

Title: Exhaustive identification of conserved upstream open reading frames with potential translational regulatory functions from animal genomes

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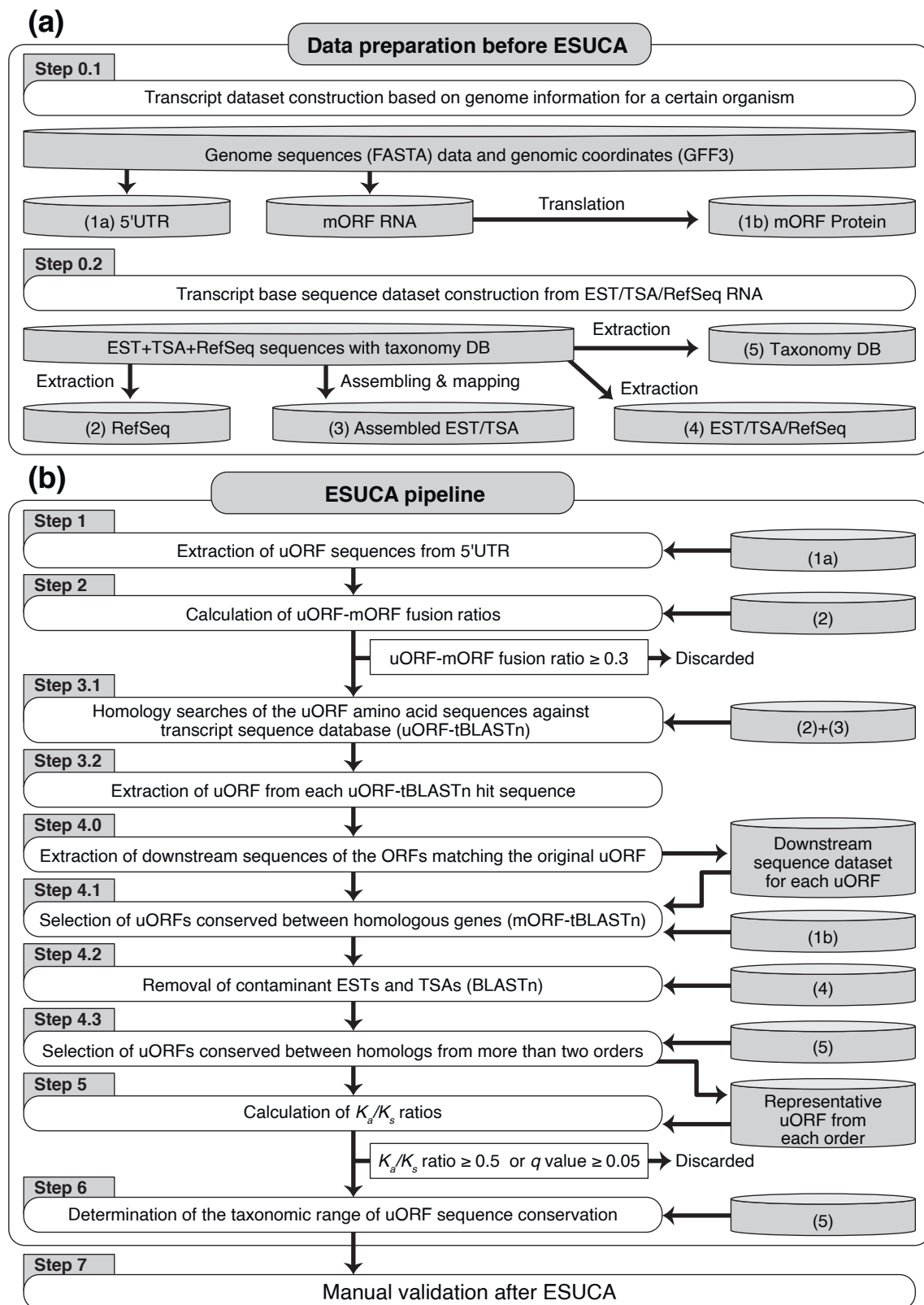
Correspondence may also be addressed to Motoyuki Itoh. Email: mito@chiba-u.jp

#Joint first authors.

Supplementary Figures: S1 to S6

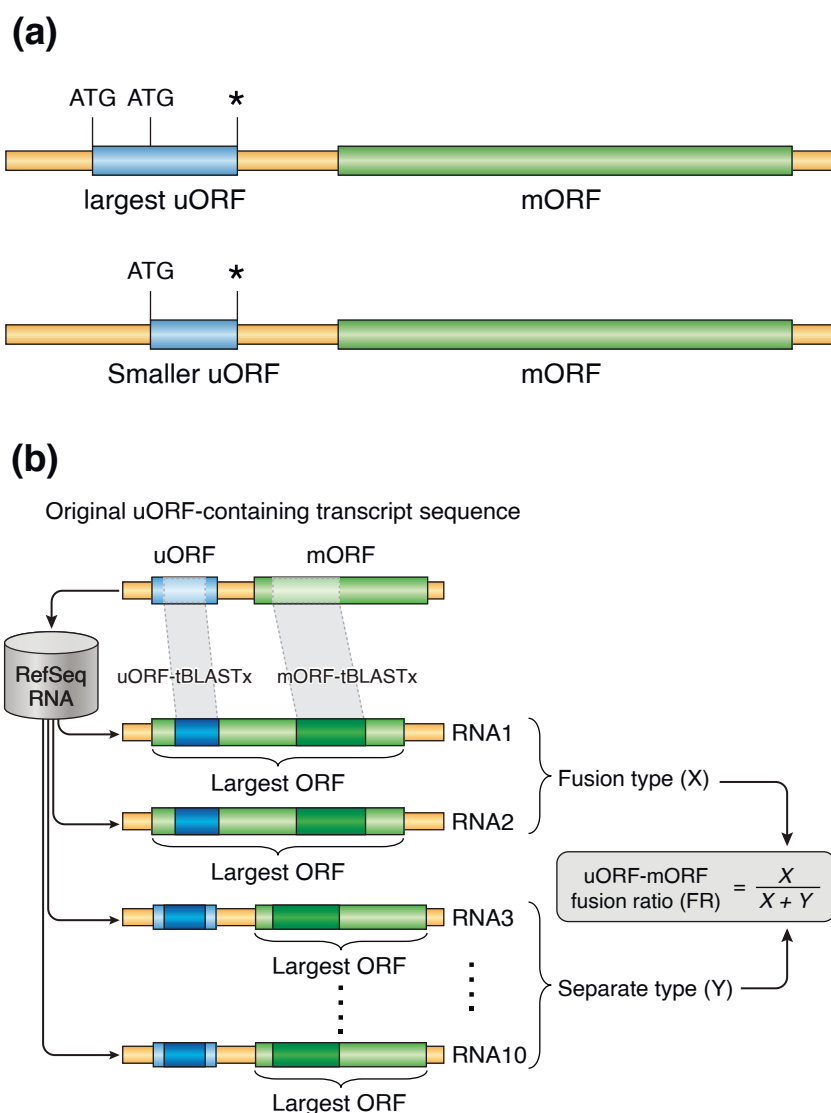
Supplementary Tables: S1 to S5

Supplementary Figure S1



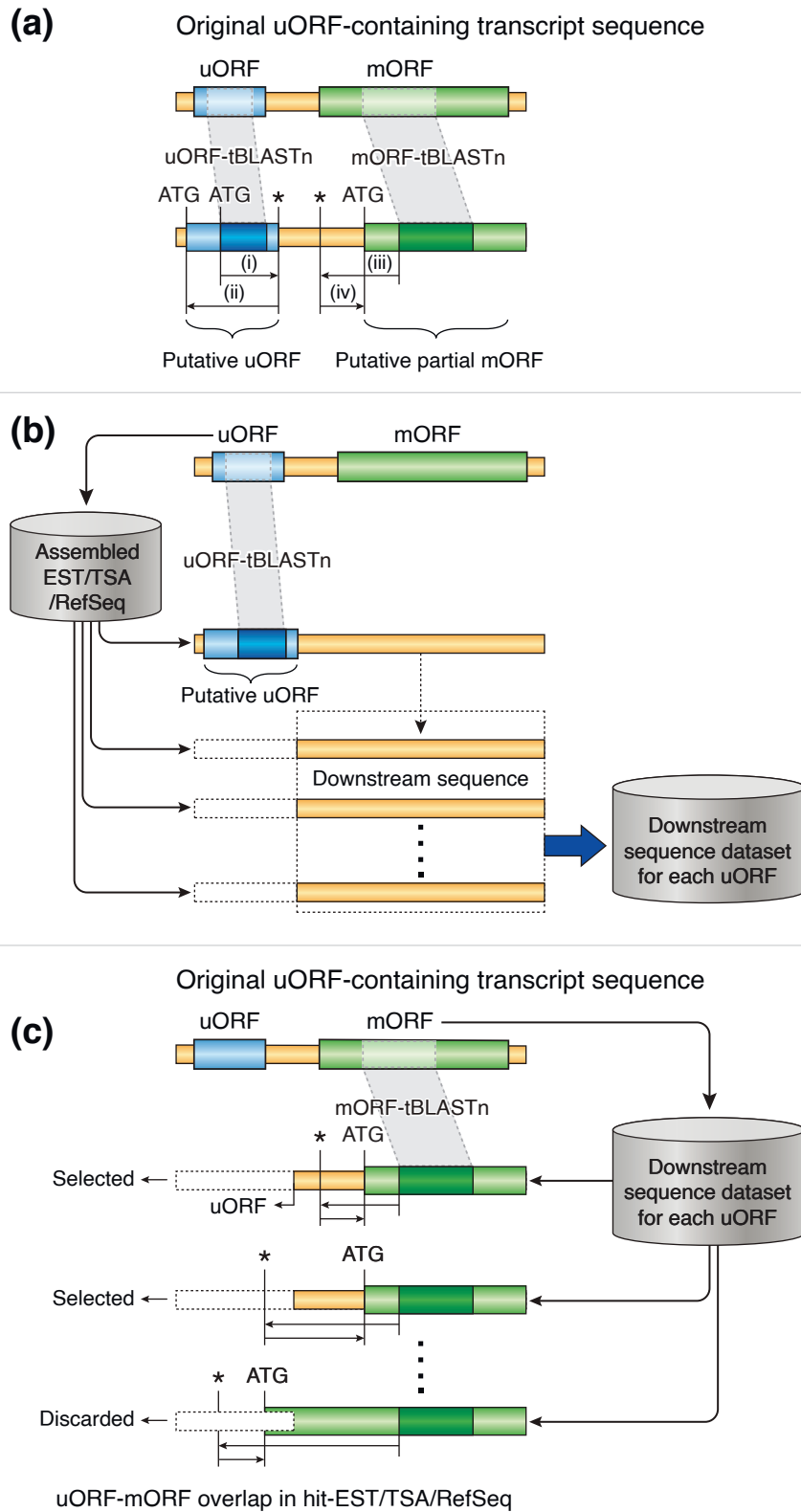
Supplementary Figure S1. Identification of animal CPuORFs using ESUCA. (a) Data preparation. (b) Outline of the ESUCA pipeline. Numbers with parenthesis indicate datasets labeled with the same numbers in (a).

Supplementary Figure S2



Supplementary Figure S2. Extraction of the largest uORF sequences and calculations of uORF-mORF fusion ratio. **(a)** Extraction of the largest uORF sequences from the 5'-UTR. Extraction of the largest uORF sequences from the 5'-UTR. After data preparation for ESUCA (Supplementary Fig. S1b), we conducted the extraction of uORF sequences by searching the 5'-UTR sequences for an ATG codon and its nearest downstream in-frame stop codon at step 1 of ESUCA (Supplementary Fig. S1b). Sequences starting with an ATG codon and ending with the nearest in-frame stop codon were extracted as uORF sequences. When multiple uORFs shared the same stop codon in a transcript, only the longest uORF sequence was used for further analyses. **(b)** Outline for uORF-mORF fusion ratio calculations. For each original uORF-containing transcript sequence, RefSeq RNAs containing both sequences similar to the uORF and the mORF of each uORF-containing transcript were selected using uORF-tBLASTx and mORF-tBLASTx from the RefSeq RNA database (database (2) in Supplementary Fig. S1a). For example, the selected RNA sequences are RNA1, 2, 3...10, as illustrated. Based on whether the uORF-tBLASTx-hit region was included in the largest RefSeq RNA ORF, the selected RefSeq RNAs were classified into two types, namely fusion (X) (RNA1 and 2) and separate types (Y) (RNA3-10). For each original uORF-containing transcript, the uORF-mORF fusion ratio was calculated as $X/(X + Y)$.

Supplementary Figure S3

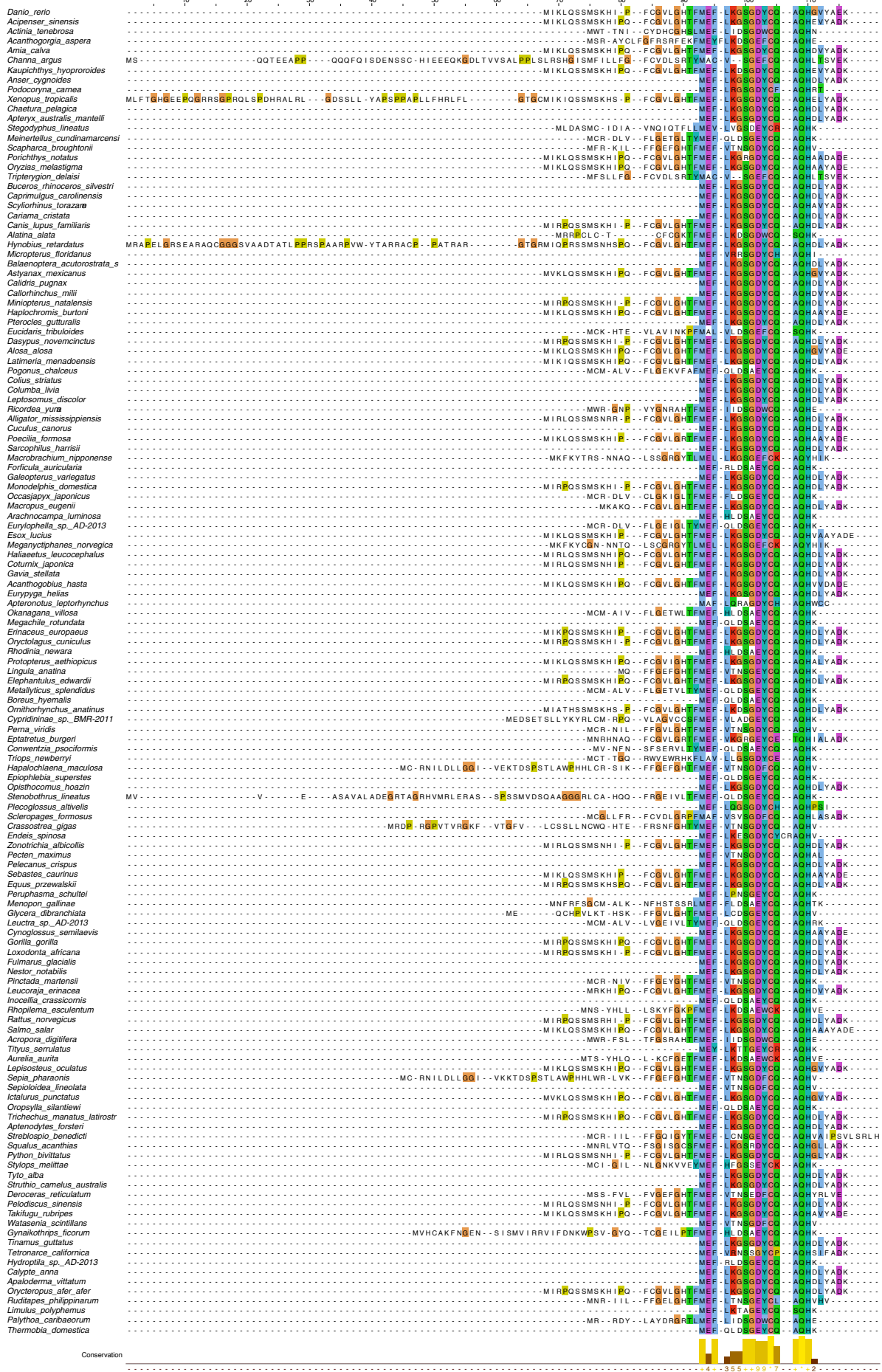


Supplementary Figure S3. Outline of homology searches for uORFs with amino acid sequences conserved between homologous genes. **(a)** For each original uORF-containing transcript, sequences containing both similar regions to the uORF and the mORF of uORF-containing transcripts were selected using uORF-tBLASTn (step 3.1 of ESUCA) and mORF-tBLASTn (step 4.1 of ESUCA). A transcript sequence database consisting of RefSeq RNAs (database (2) in Supplementary Fig. S1a) served as data source, while an assembled EST/TSA (database (3) in Supplementary Fig. S1a) was generated at step 0.2 of data preparation for ESUCA. Asterisks represent stop codons. At step 3.2 of ESUCA, the largest tBLASTn-hit region-overlapping uORF was extracted. **(b)** Detailed illustration of step 4.0 of ESUCA. Putative uORF extraction and downstream sequence dataset construction were conducted systematically for each uORF-tBLASTn hit sequence. **(c)** Detailed illustration of step 4.1 of ESUCA. After mORF-tBLASTn, the 5'-most in-frame ATG codon located downstream of the selected stop codon was identified as the initiation codon of the putative partial or intact mORF. uORF-mORF overlaps were discarded as fusion types, according to the positional relationship between them, when found in the hit-assembled EST/TSA+RefSeq sequences.

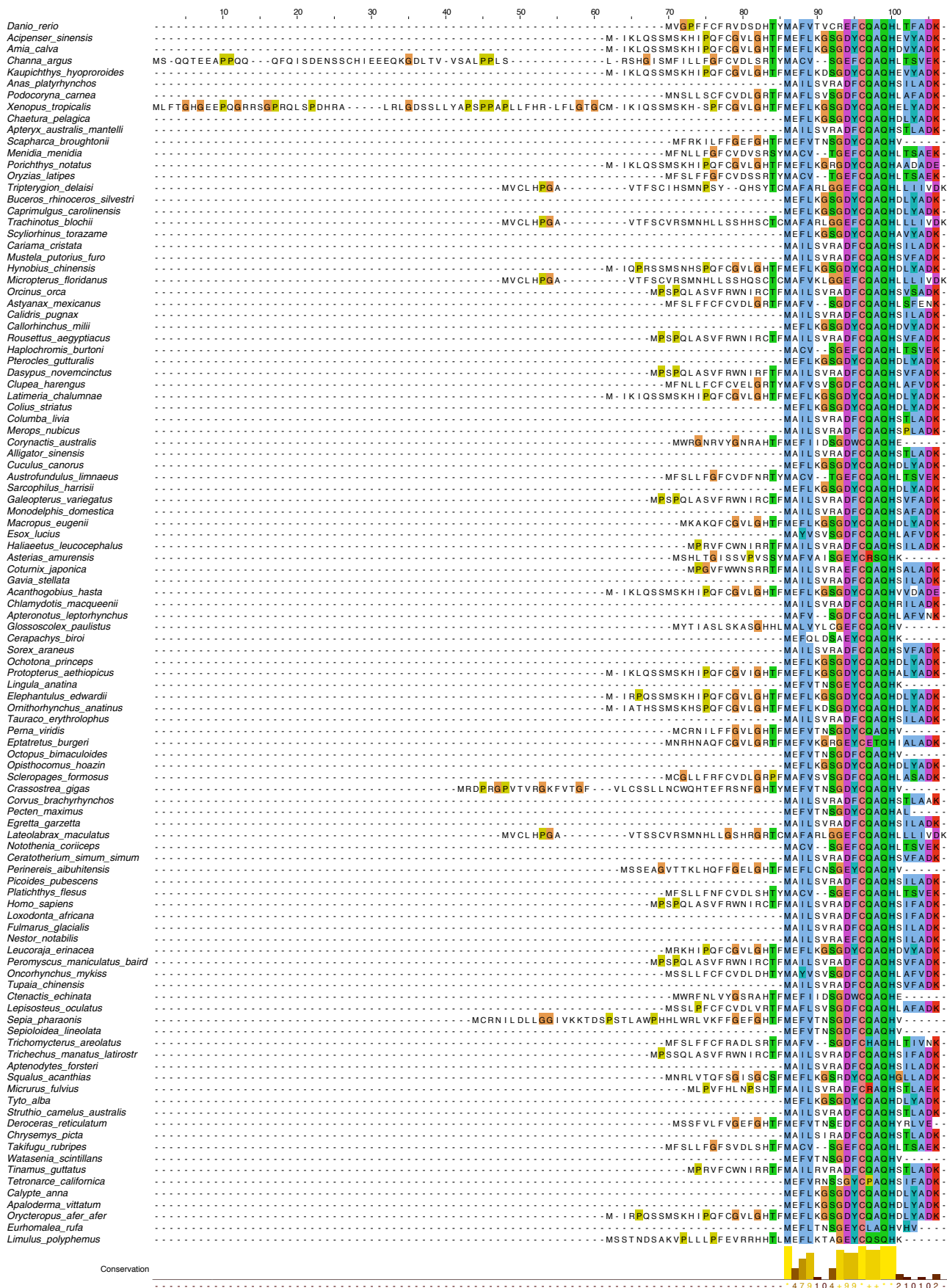
Supplementary Figure S4

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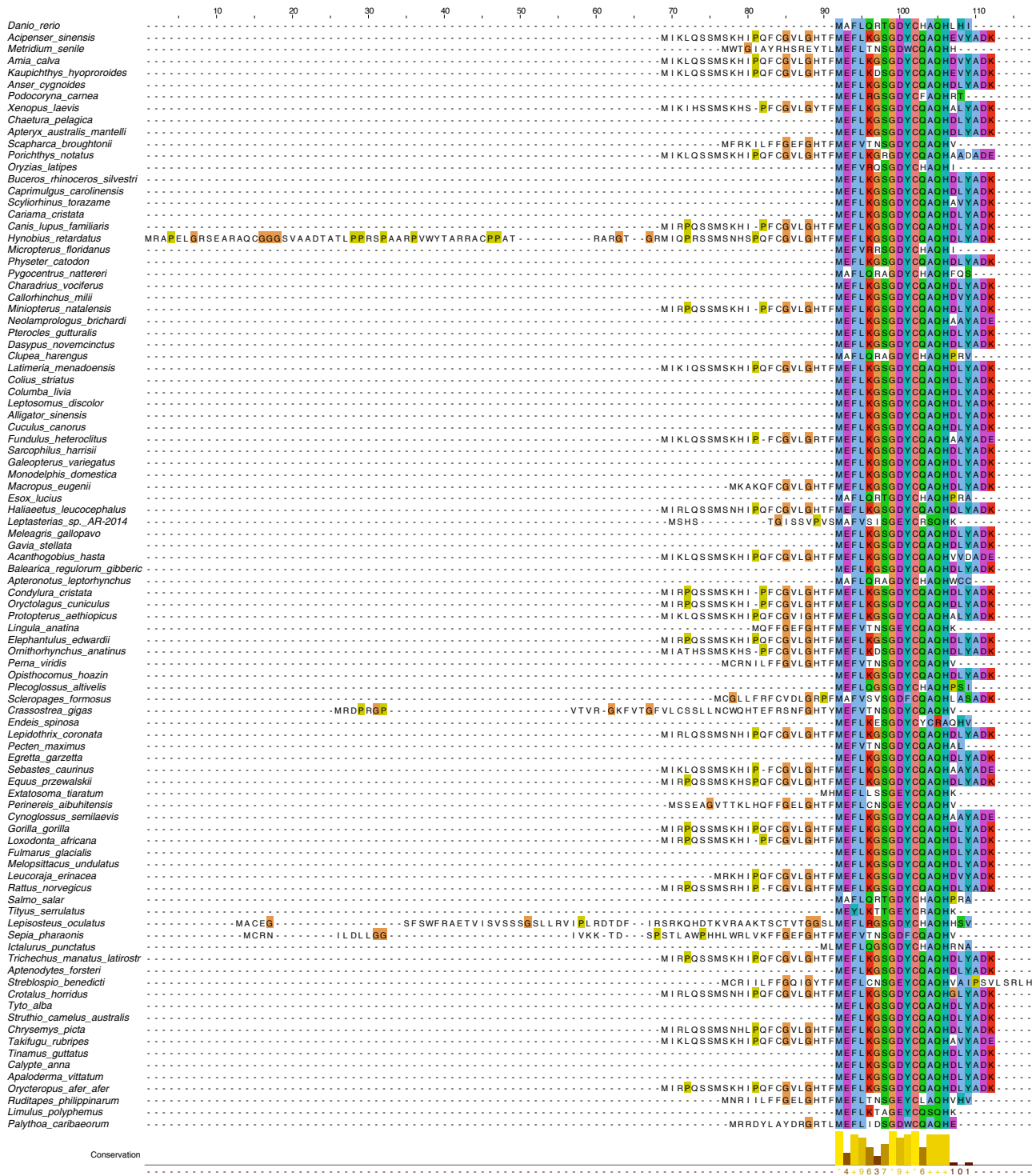


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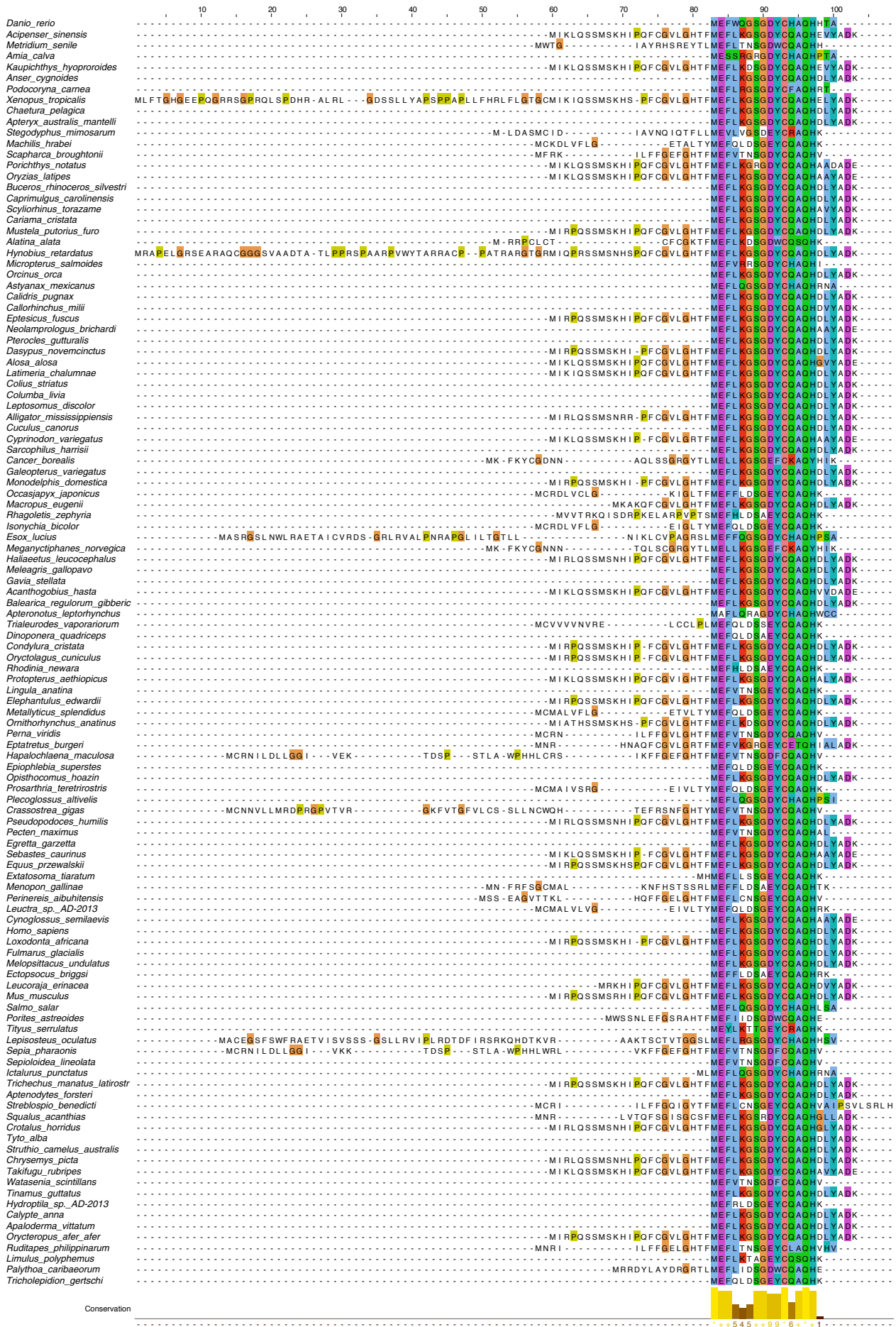
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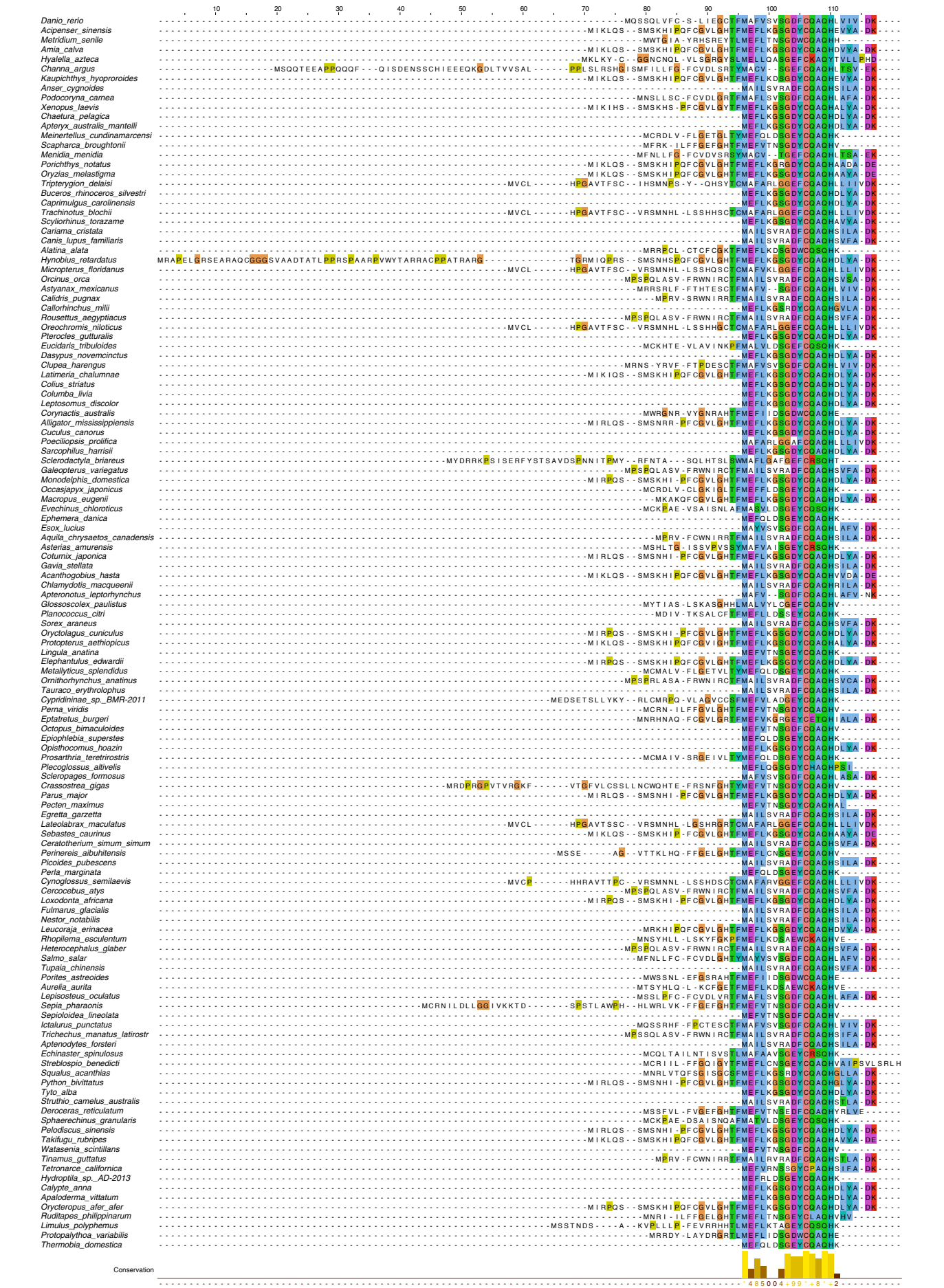
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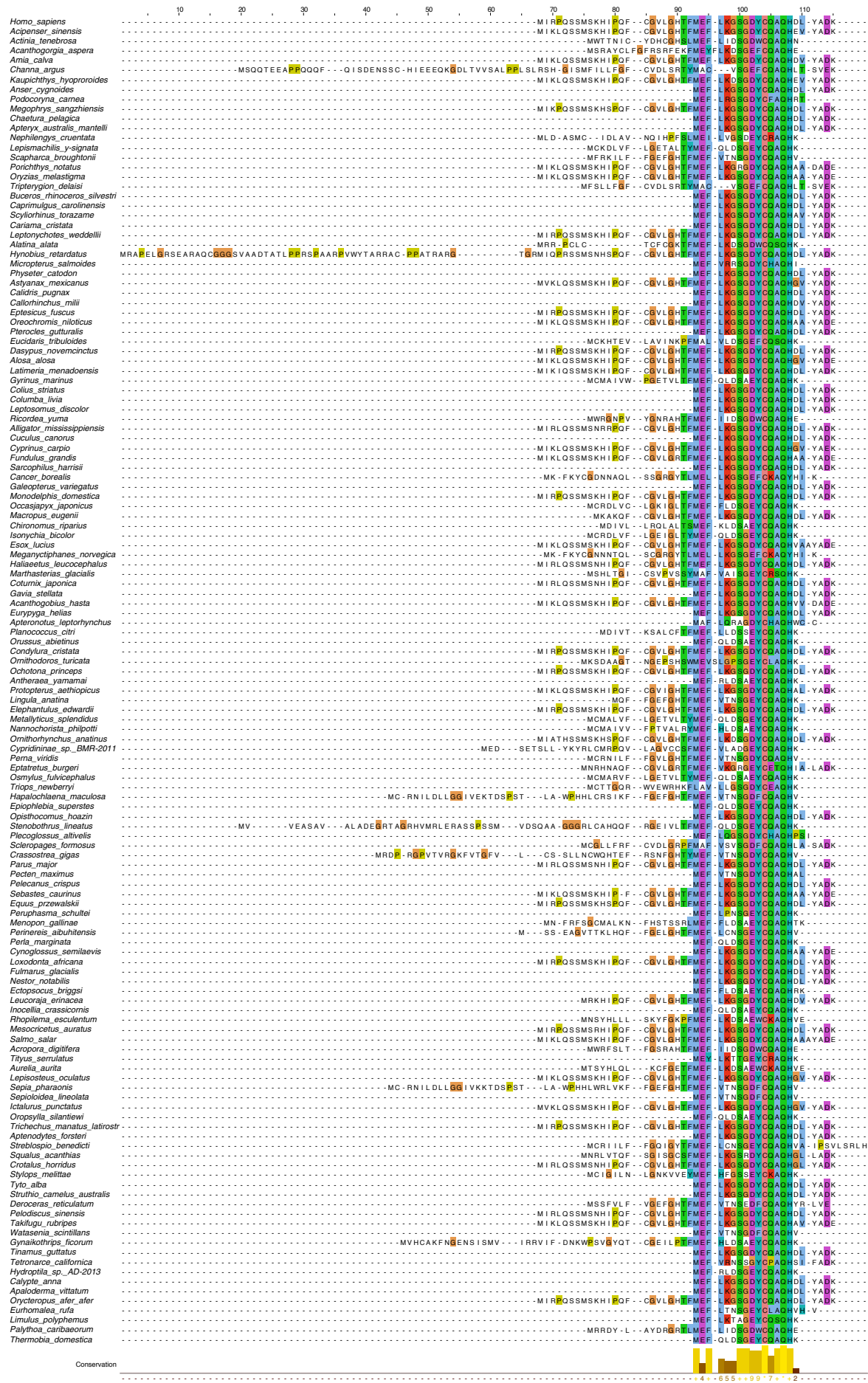
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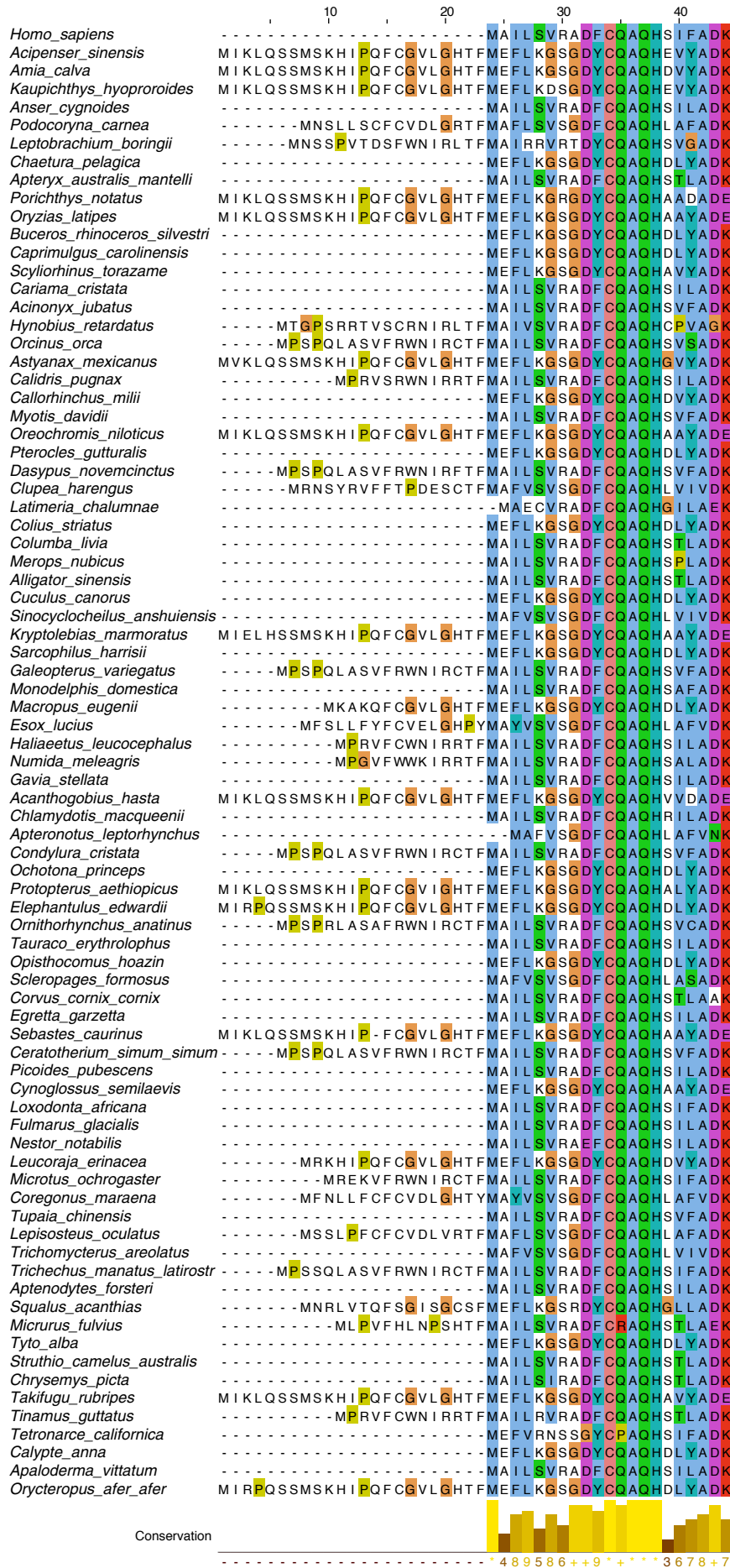
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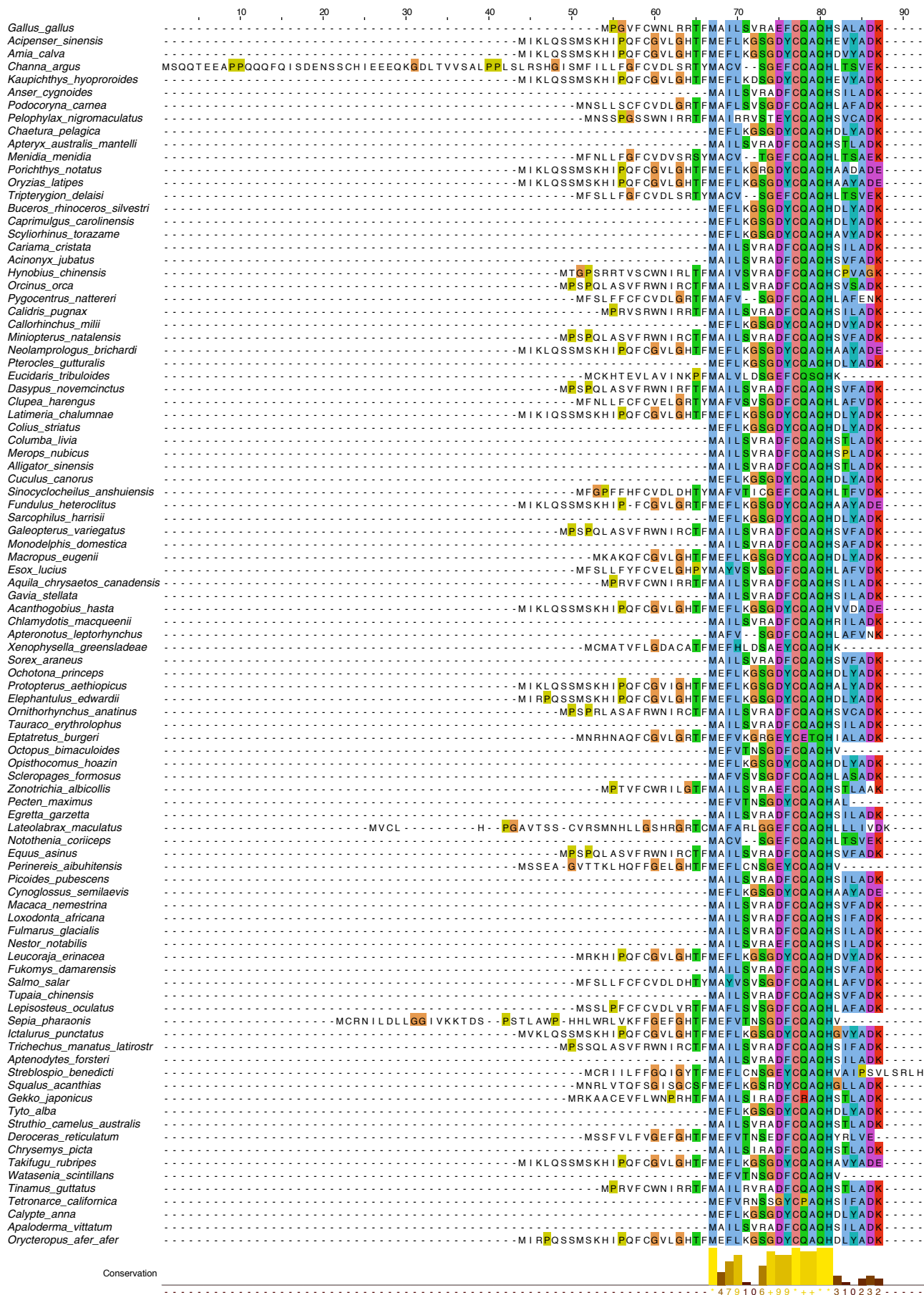


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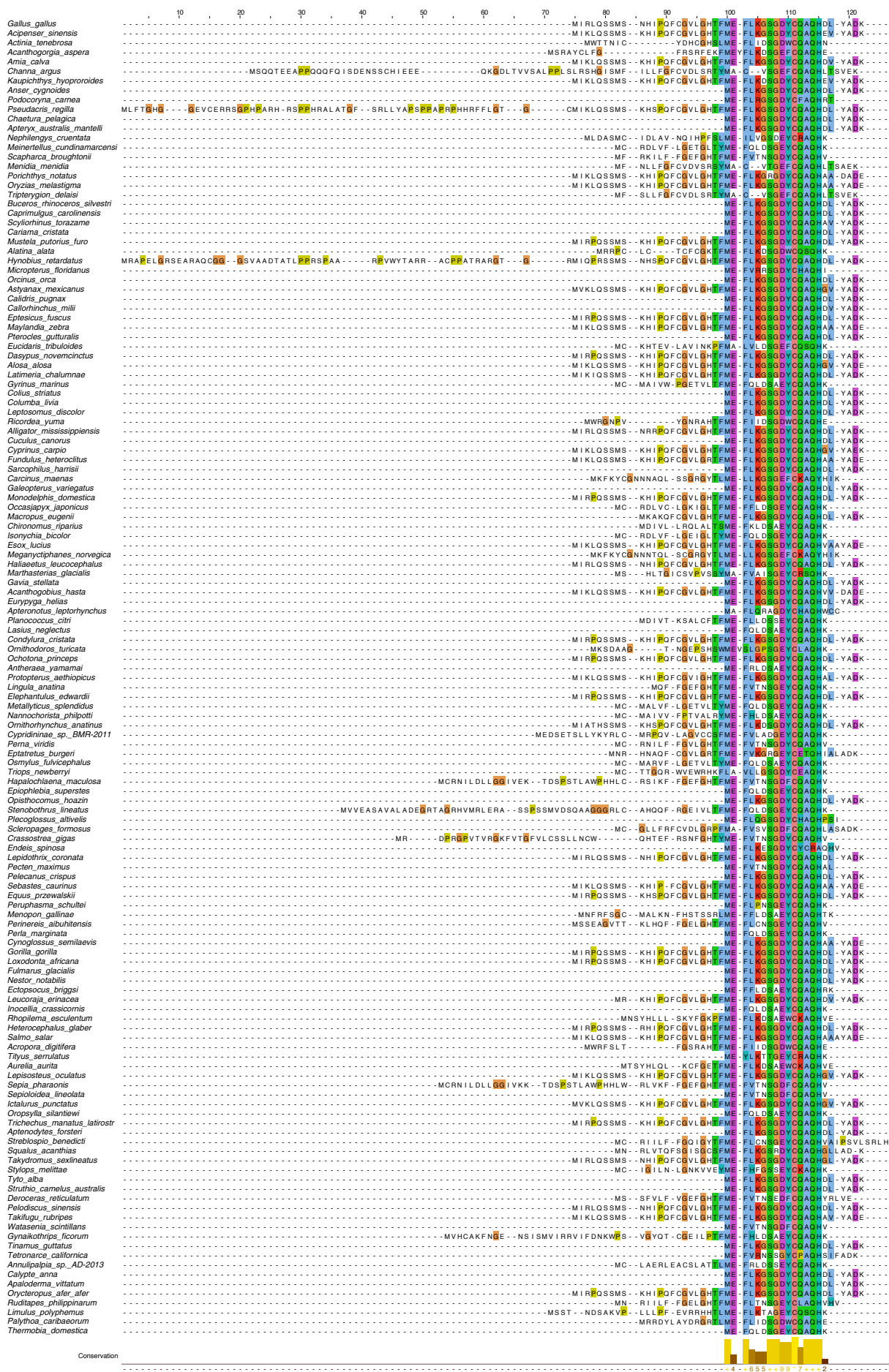
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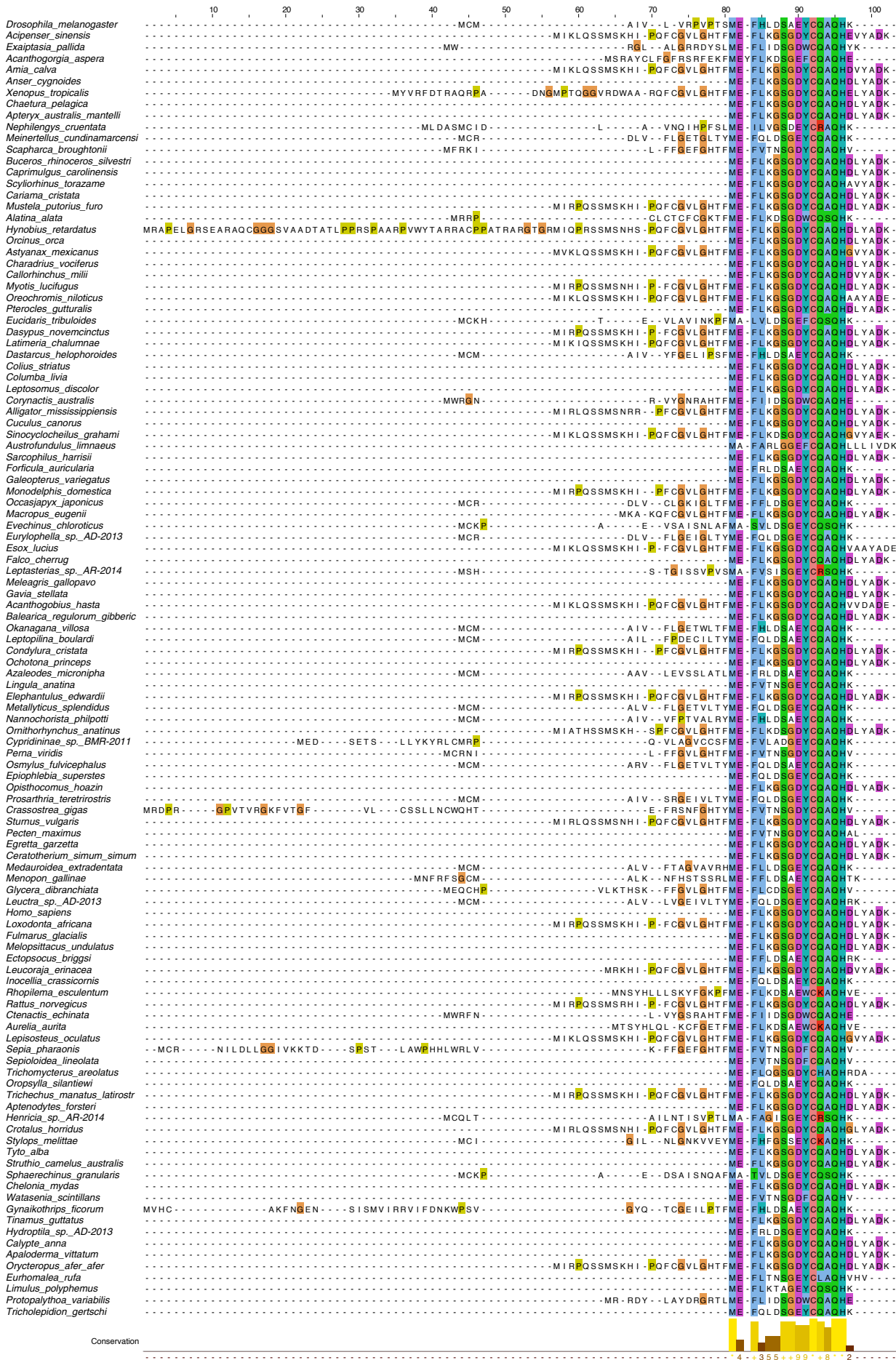


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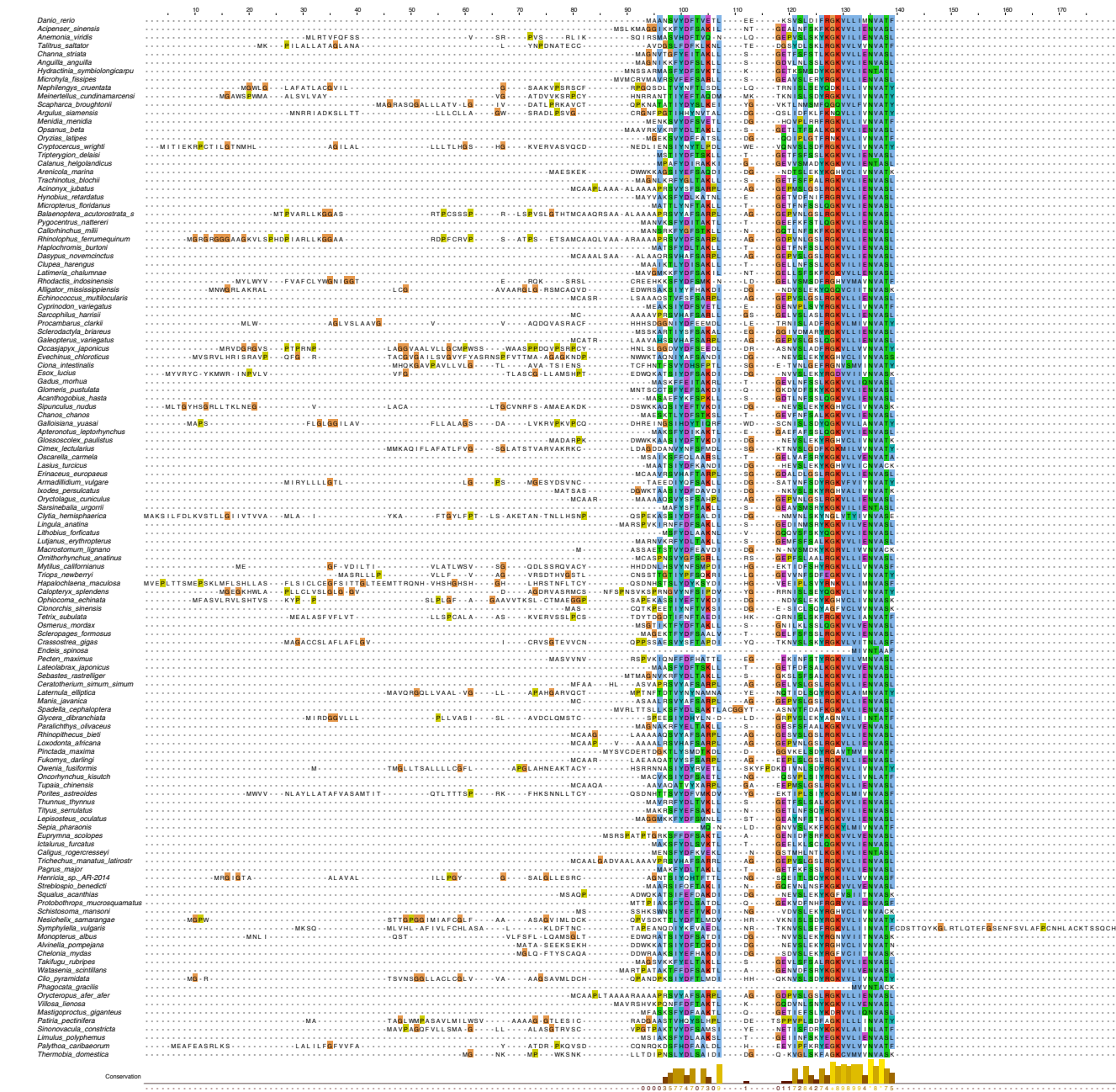
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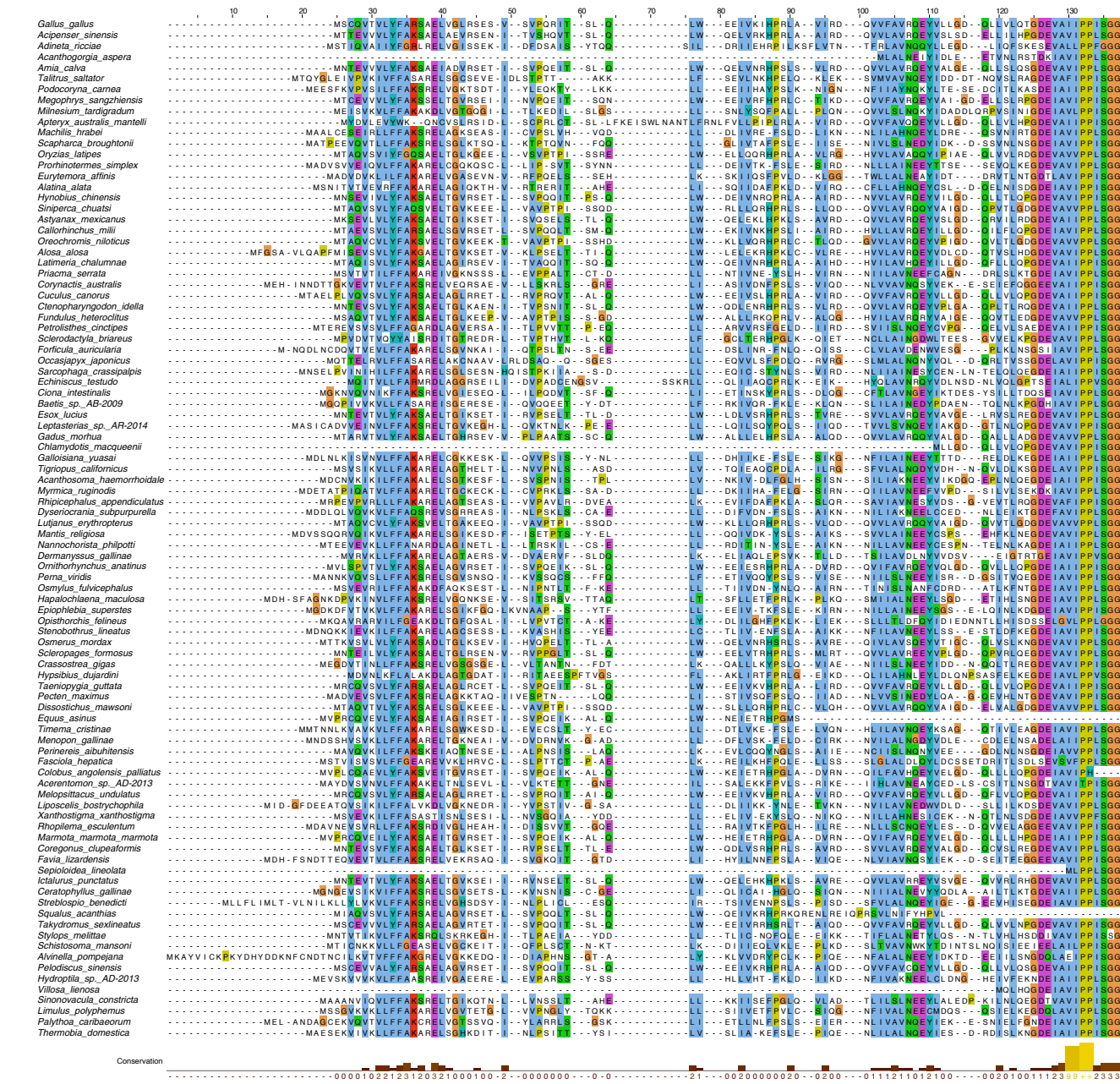
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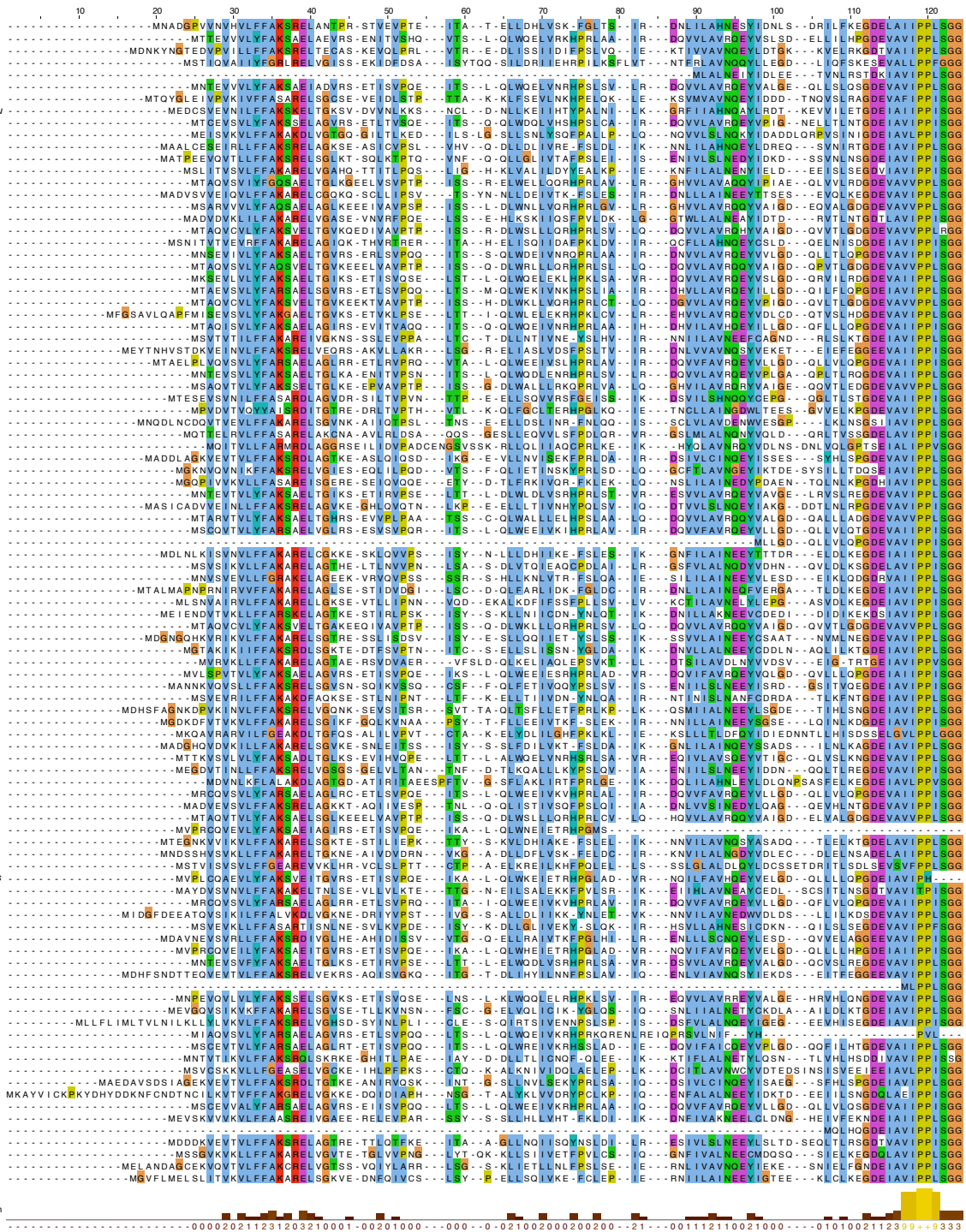
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HG0003

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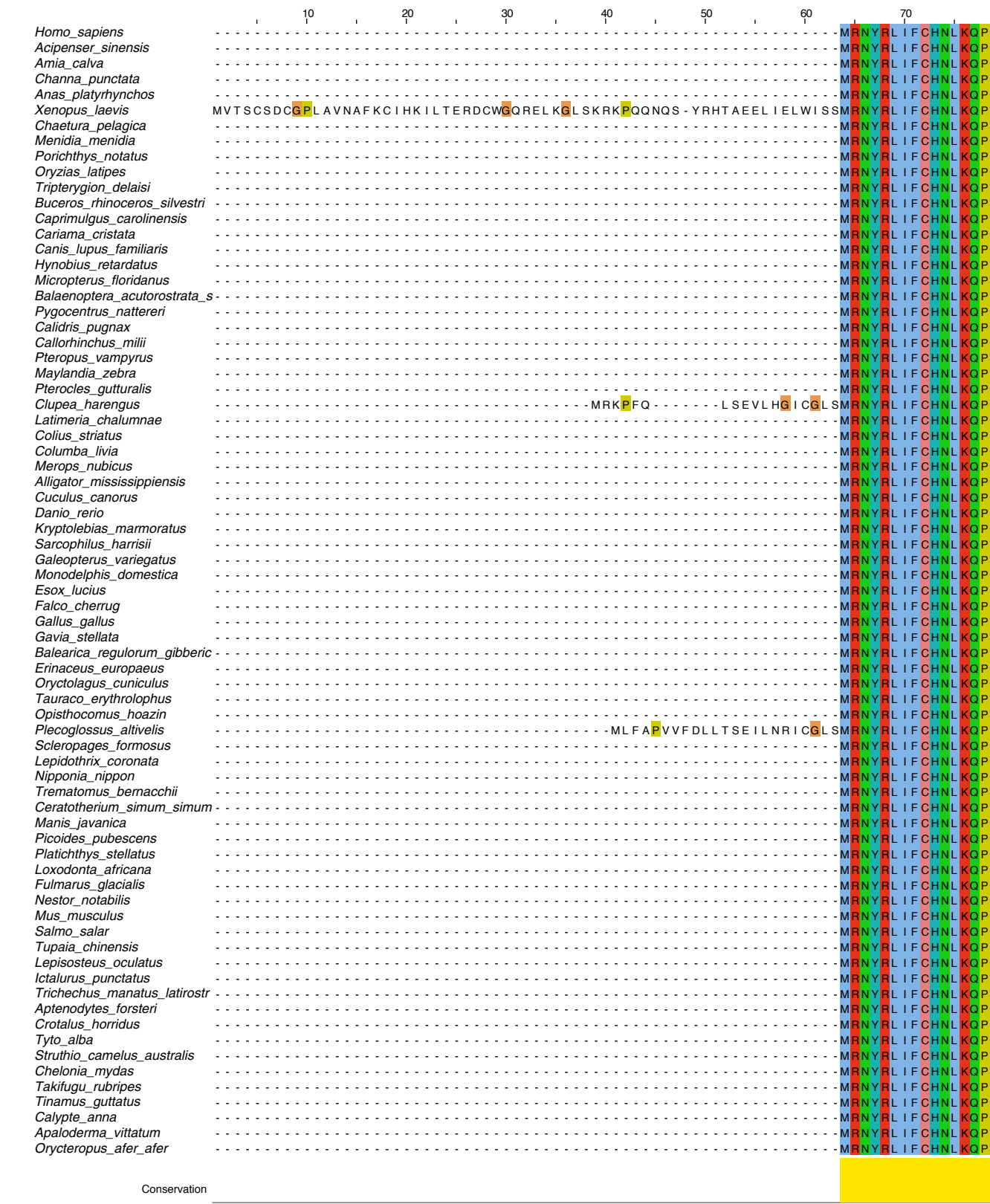


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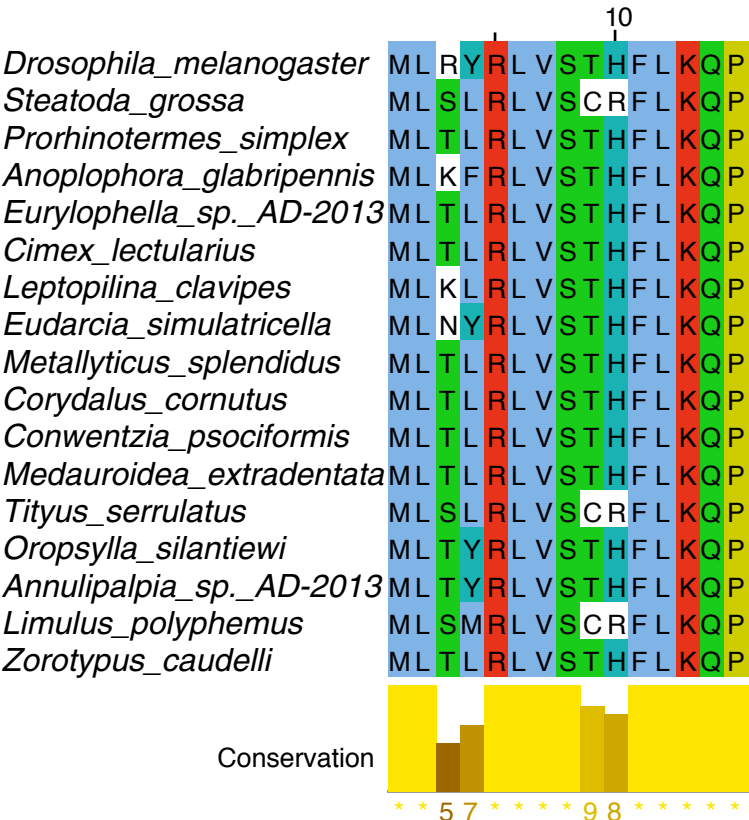
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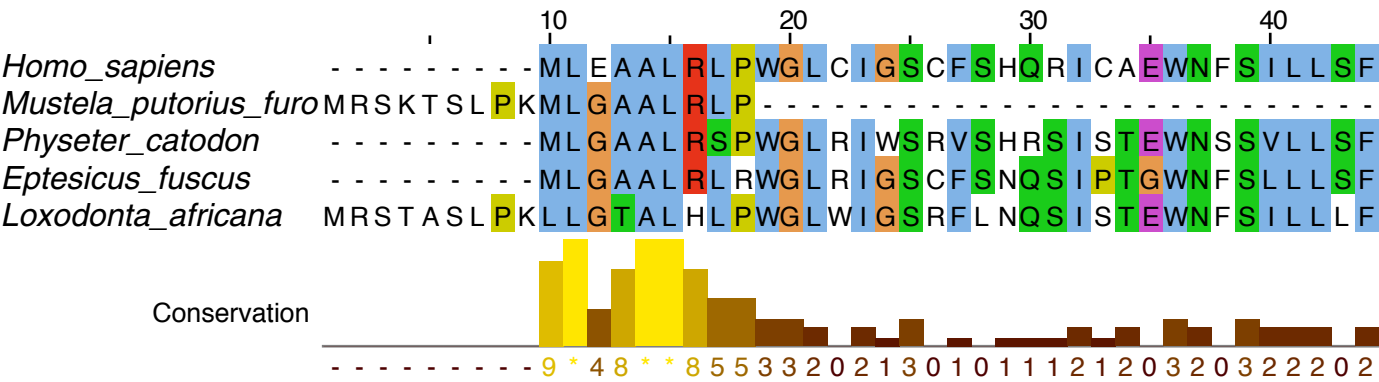
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Amia_calva	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Channa_punctata	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Anas_platyrhynchos	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Xenopus_laevis	MVTSCSDCGPLAVNAFKCIHKILTERDCWGGORELKGLSKRKPPQQNQS-YRHTAEELIELWISS							MRNYRLIFCHNLKQP
Chaetura_pelagica	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Menidia_menidia	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Porichthys_notatus	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Tripterygion_delaisi	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Buceros_rhinoceros_silvestri	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Caprimulgus_carolinensis	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
Cariama_cristata	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Balaenoptera_acutorostrata_s	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Falco_cherrug	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Opisthocomus_hoazin	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Scleropages_formosus	-	-	-	-	-	-	-	MRNYRLIFCHNLKQP
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Conservation								



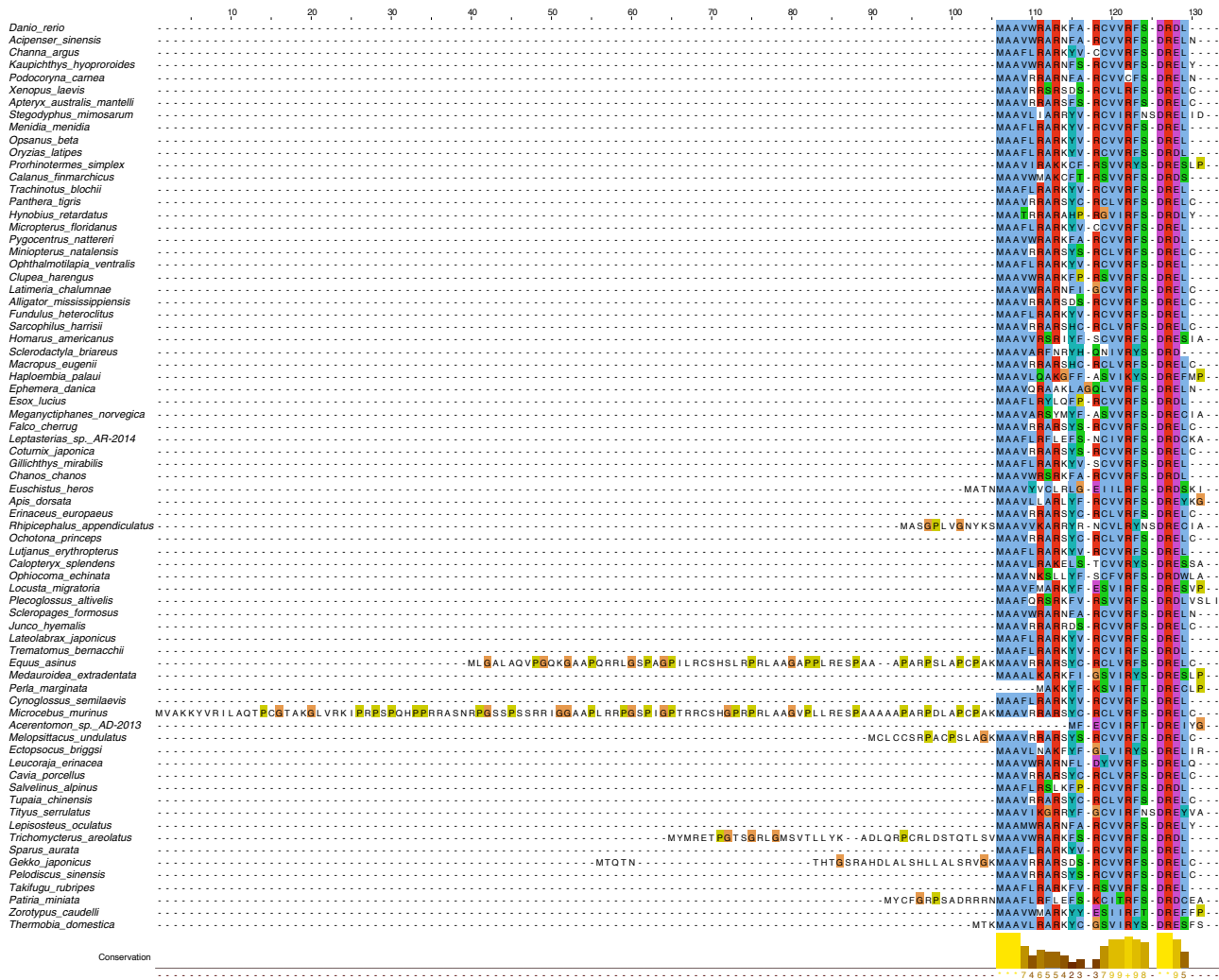
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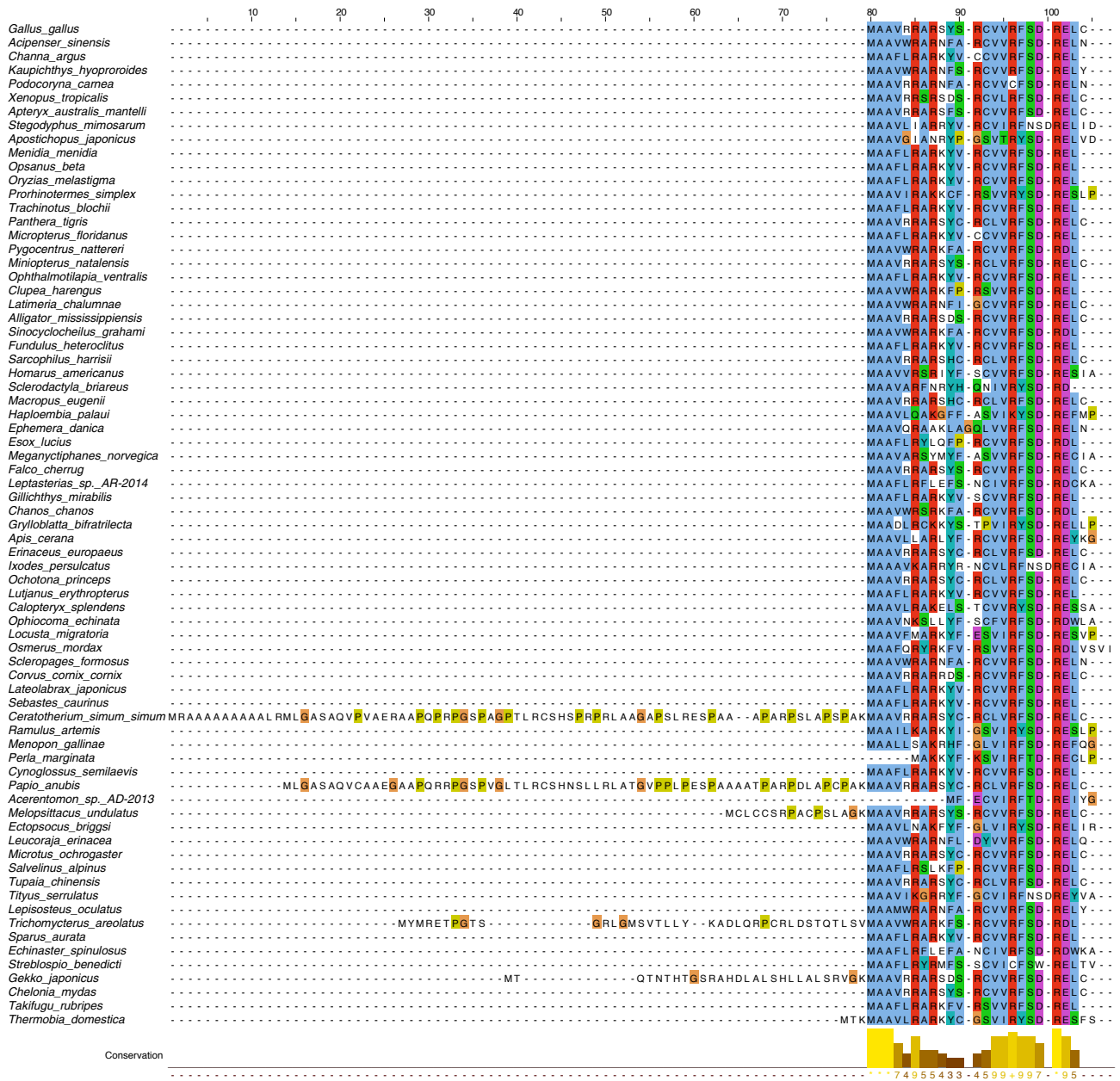
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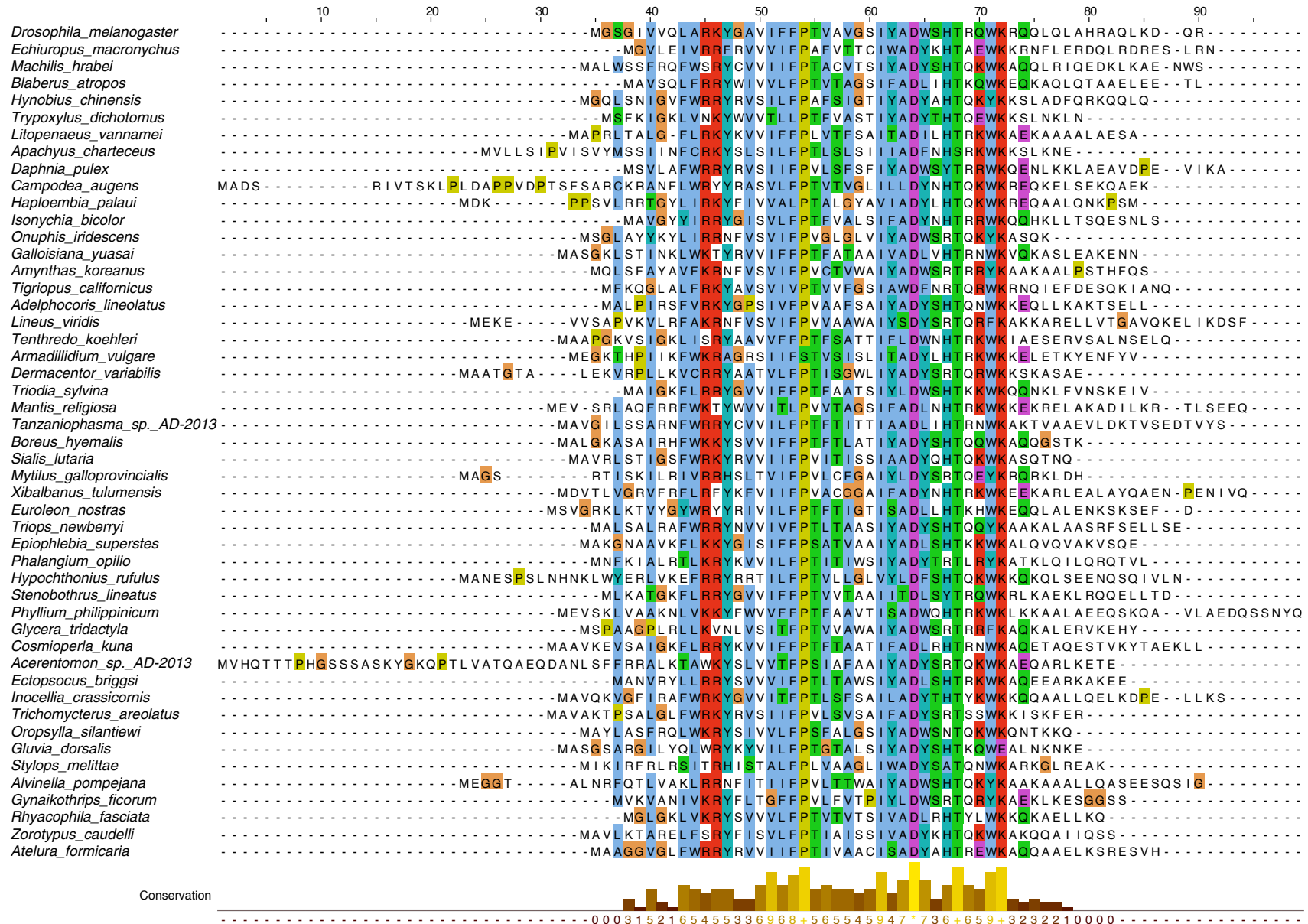


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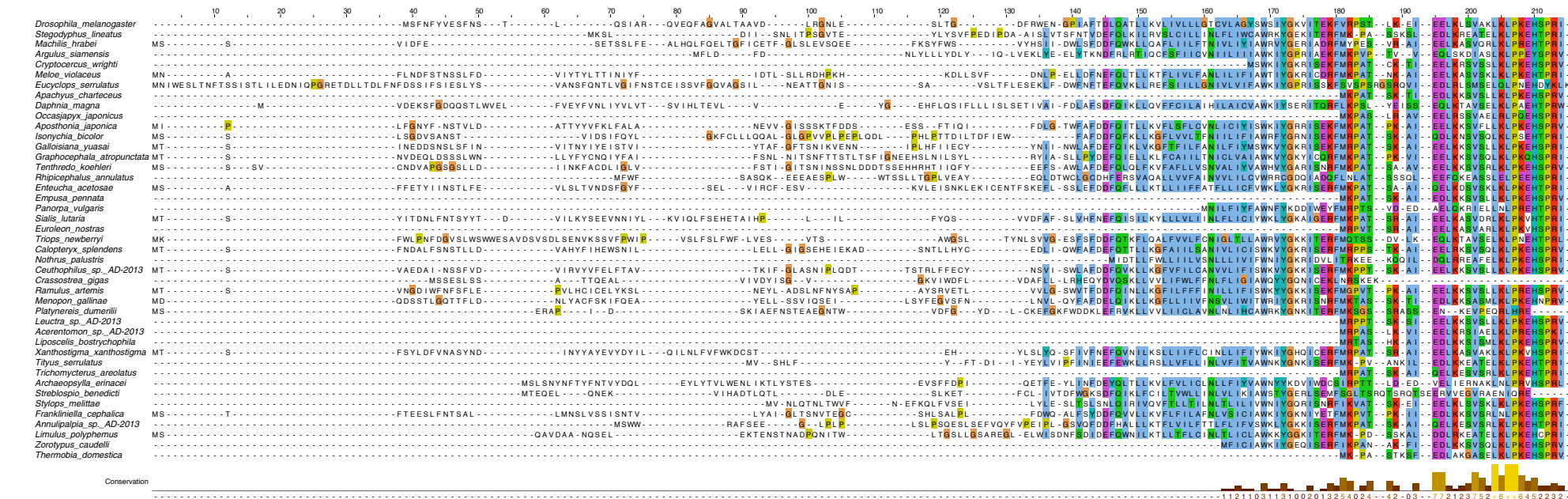


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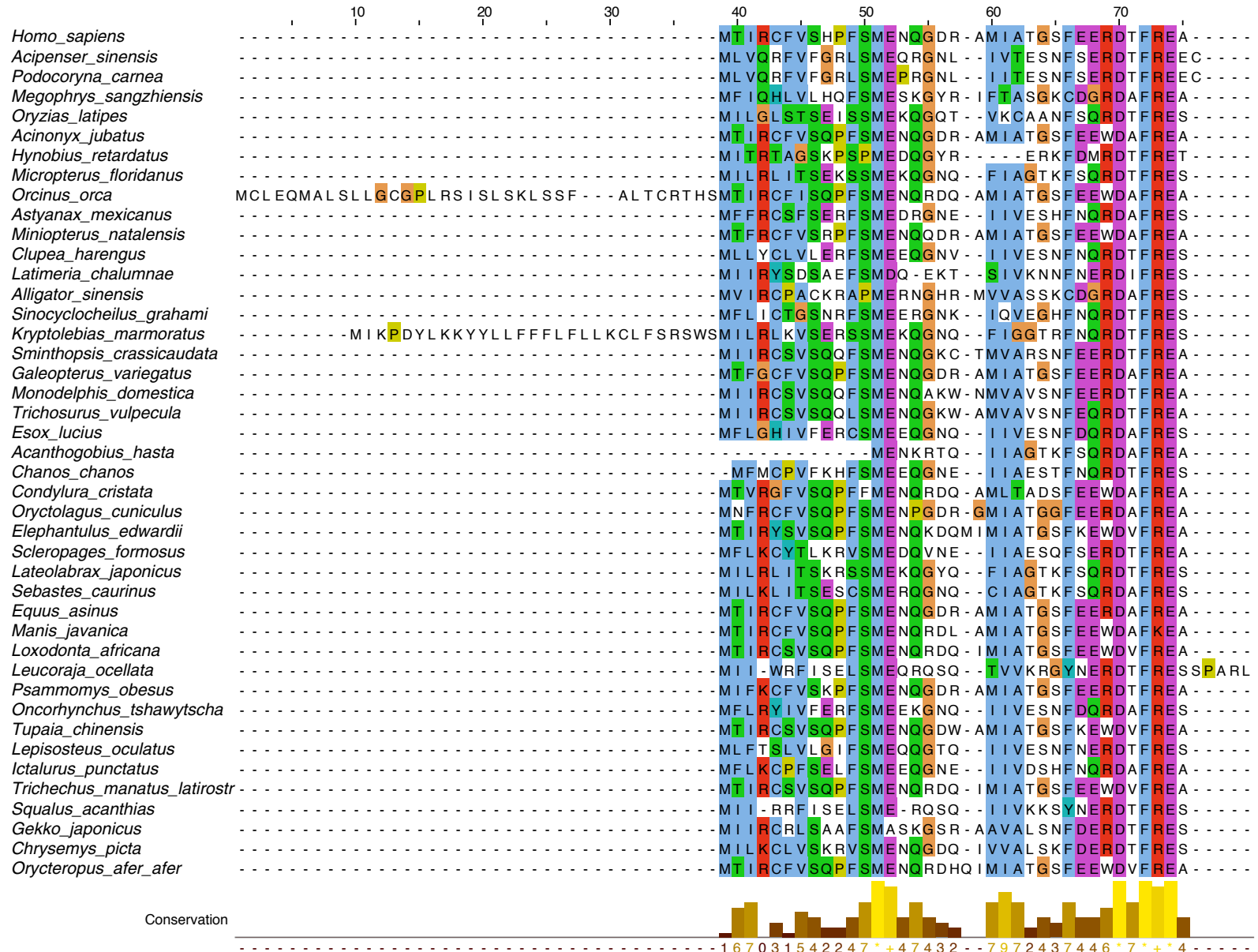
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HG0008

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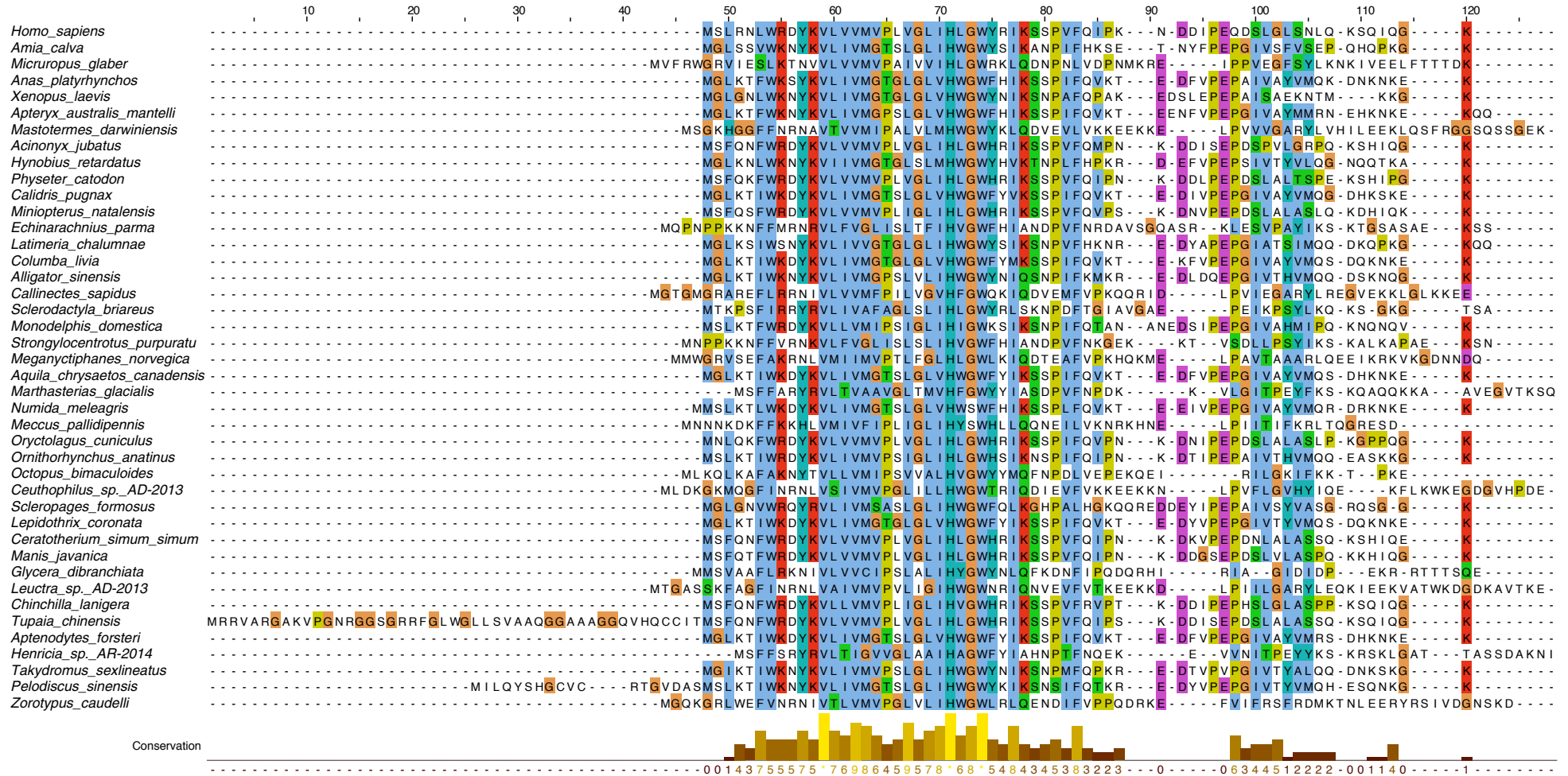
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<i>Latrodectus_geometricus</i>	- - - - -	-	MT	VSQRQVLSLYKELLKYSKNLKYTDKSYLLNRLKNEFLNRLQNASFINQIQRGKNFLSKRLL					
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<i>Calopteryx_splendens</i>	- - - - -	-	MCQ	PSPSQVLS	LYRSLRYSNQLKYTDKKFYIKRIRKESNRLIP-KERGQYERGLVLLHNKRV				
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<i>Prosarthria_teretirostris</i>	- - - - -	-	MNA	PTAHEVLR	LYRKLLQYGGKQLKLT	DKKYFFDRIRKEFKTNKTLTNQEDVT	FQFKRGLALL	ENKRVV	
<i>Ramulus_artemis</i>	- - - - -	-	MNT	PARVQVLR	LYRDLLRYGQNLQLTDKDYFCKRVREEFRRNRVLENKNDLLFHFNKGESLLKTKRVV				
<i>Menopon_gallinae</i>	- - - - -	-	MCV	PTTREVL	TLYKRLLRYGRQLKYTDQDYYSKRIKQEFQSNKDVKGN-EAIFHYE	KGQLQLLLKRVV			
<i>Perla_marginata</i>	- - - - -	-	MSG	PTAKQVI	QLYRDLLRYSKHLKFTDKNFFT	KVRKREFKTKRL	SNEEDIQFHYKGLILLKNKSVI		
<i>Polydesmus_angustus</i>	- - - -	-	MSASV	VGKSGQIL	HLRYQLLRYGRTLTYTDKNYYYGRIRBAEFEKHREAE	L-KTQLFQYKKGKALL	ENGRIL		
<i>Acerentomon_sp._AD-2013</i>	- -	-	MCWQMG	GIPTNGQIL	KLYRSLRYSSTLQYTDKDFFKRVQQEFHRNGA	ITAPNEIKFQY	EKGISFLSRKRLV		
<i>Liposcelis_bostrychophila</i>	- - - - -	-	MSA	PSRTQVLR	LYKDLRYGGEELTYTNKTYFKNRVKN	EFLSAKSAKDNKEIDNLYQKGVALLMR	RRVV		
<i>Xanthostigma_xanthostigma</i>	- - - - -	-	MEV	PSSTQVLR	LYRQLIRYGGKQLQYTDKNYYYKRVIAEFKRN	NLEDPKEIKFQFEKGGKSL	KKRSVI		
<i>Trichomycterus_areolatus</i>	- - - - -	-	MSRS	EILKLYKQL	RYGQQLRLTDKSYYQERINQEFKQHKNLASNKDIT	FNFEKGSLL	EKGLVM		
<i>Ctenocephalides_felis</i>	- - - - -	-	MNT	PSAAQVLR	LYKNLLRYGQNLQYTDKDYFCNRIKREFRNNK	TCSTEDLIFNFVCI	- - - - -		
<i>Stylops_melittae</i>	- - - - -	-	-	MRLKVLN	LYKSLMRYGKSLRLTDNEYFLERIRSEFRRNKDL	YSNQEIDYHFKKGETLLKKLLV			
<i>Symphylella_vulgaris</i>	- - - - -	-	MN	PIRVQIL	SLYKTLRLRYADNLKYS	DTNYLKQVRVVEFSQHRS	LAKKIDIEFYFKRGKSFLERKRLV		
<i>Frankliniella_cephalica</i>	- - - - -	-	MSTL	INSN	QVLQLYRSLIRYGGQSLKLT	DQKYLLKRVBKEFRAN	DLQDPEKIEFMYKKGVSLLDRKRLI		
<i>Philopotamus_ludificatus</i>	- - - - -	-	MS	KREIL	KLYKQLLRYGQQLRLTDKTYFQQRIVNEFKNNKDL	SKSDDITFNFKGGQLL	KNKRLV		
<i>Zorotypus_caudelli</i>	- - - - -	-	MN	PGKPGIL	LYKSLIRYGNLKYTDKKYFIERIQEFKNRK	ELNEEDIKFAFGKGVSVL	NNKRLI		
<i>Atelura_formicaria</i>	- - - - -	-	MVA	PSSKQVLR	LYRLMRYGRQLKYTGKDYYSKRVREEFKRNKSL	ENDEKKIFHFEKGGALL	SQKRII		

Conservation

- - - - - 0 0 0 2 3 2 7 5 5 * + 9 3 + 8 7 + 8 5 3 + 3 7 8 8 7 4 9 7 1 3 9 9 4 3 + * 3 3 3 7 3 5 0 0 0 5 4 2 6 3 6 5 9 + 3 3 7 + 4 4 4 3 9 9

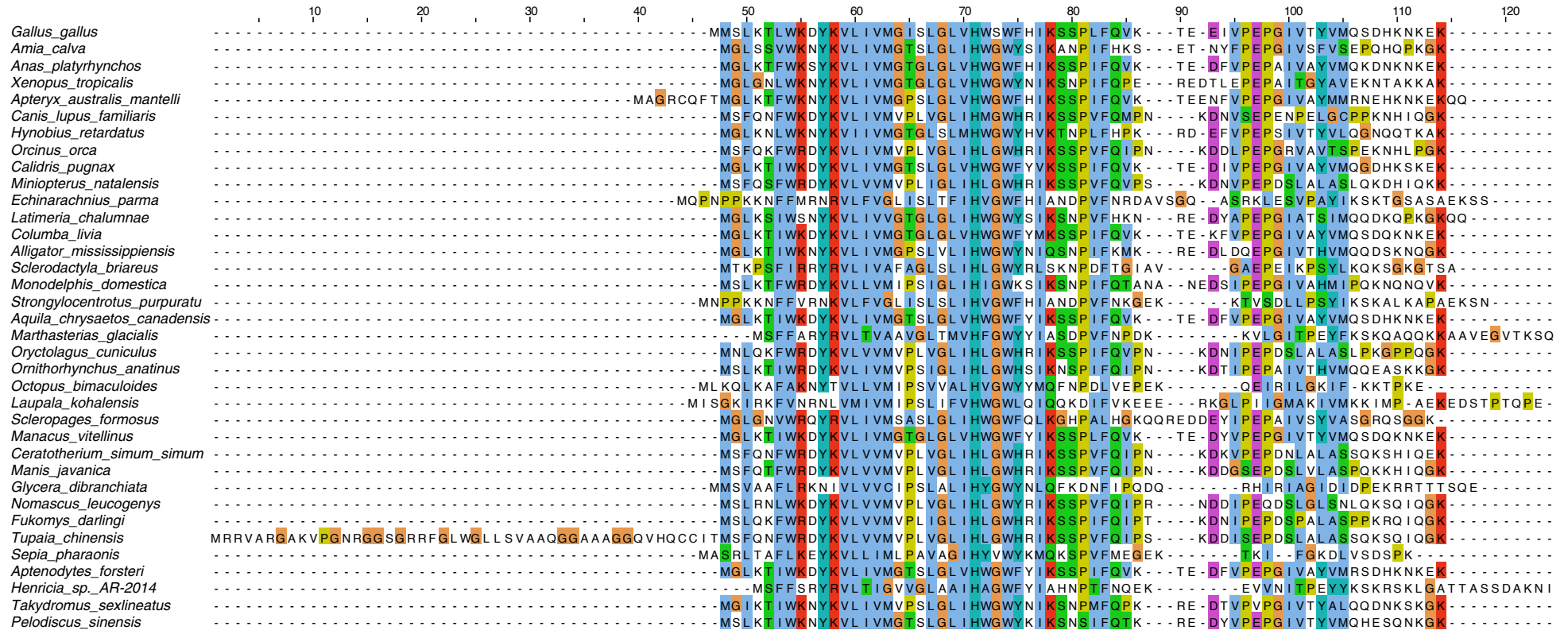
HG0010.1

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HG0010.1

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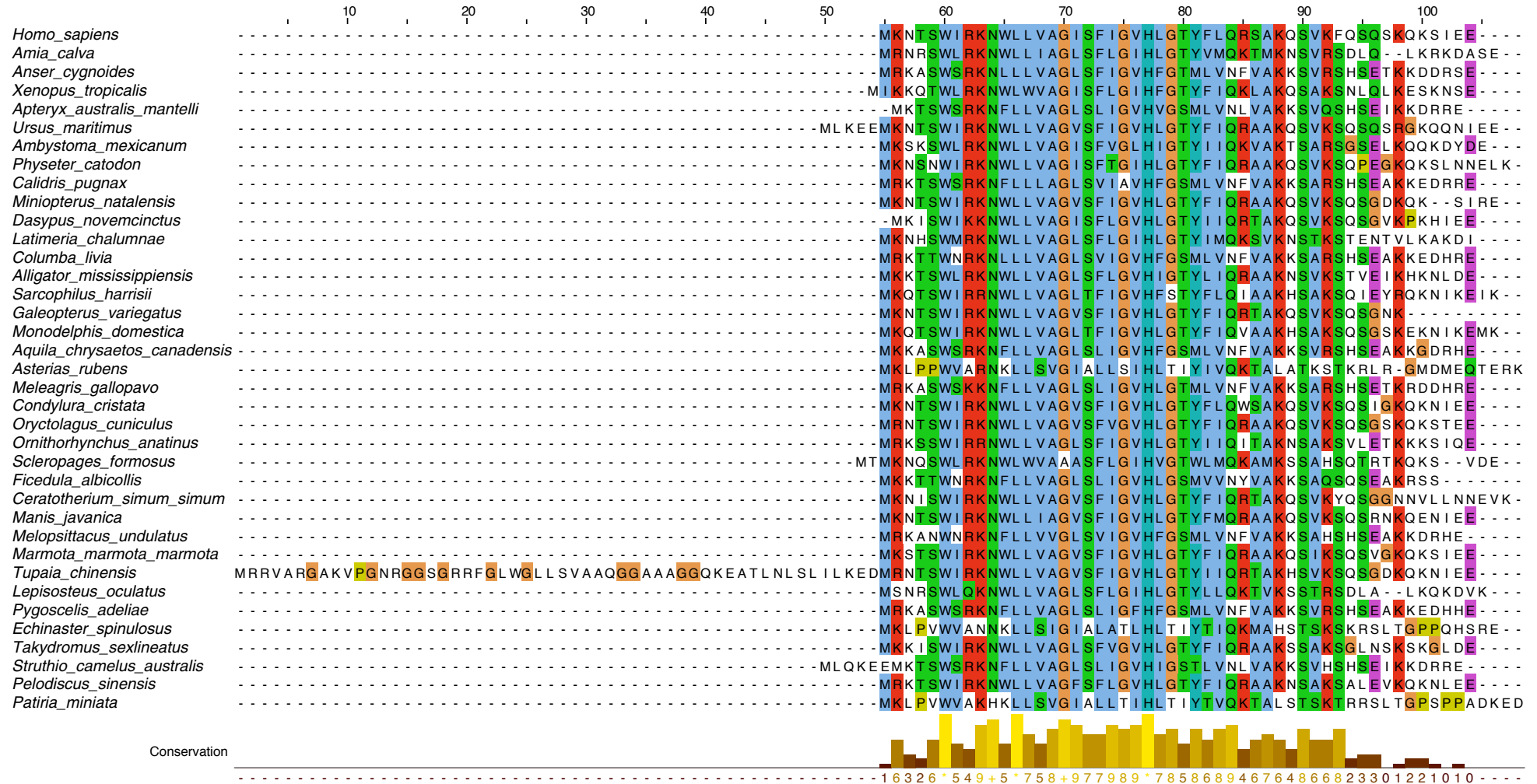


Conservation



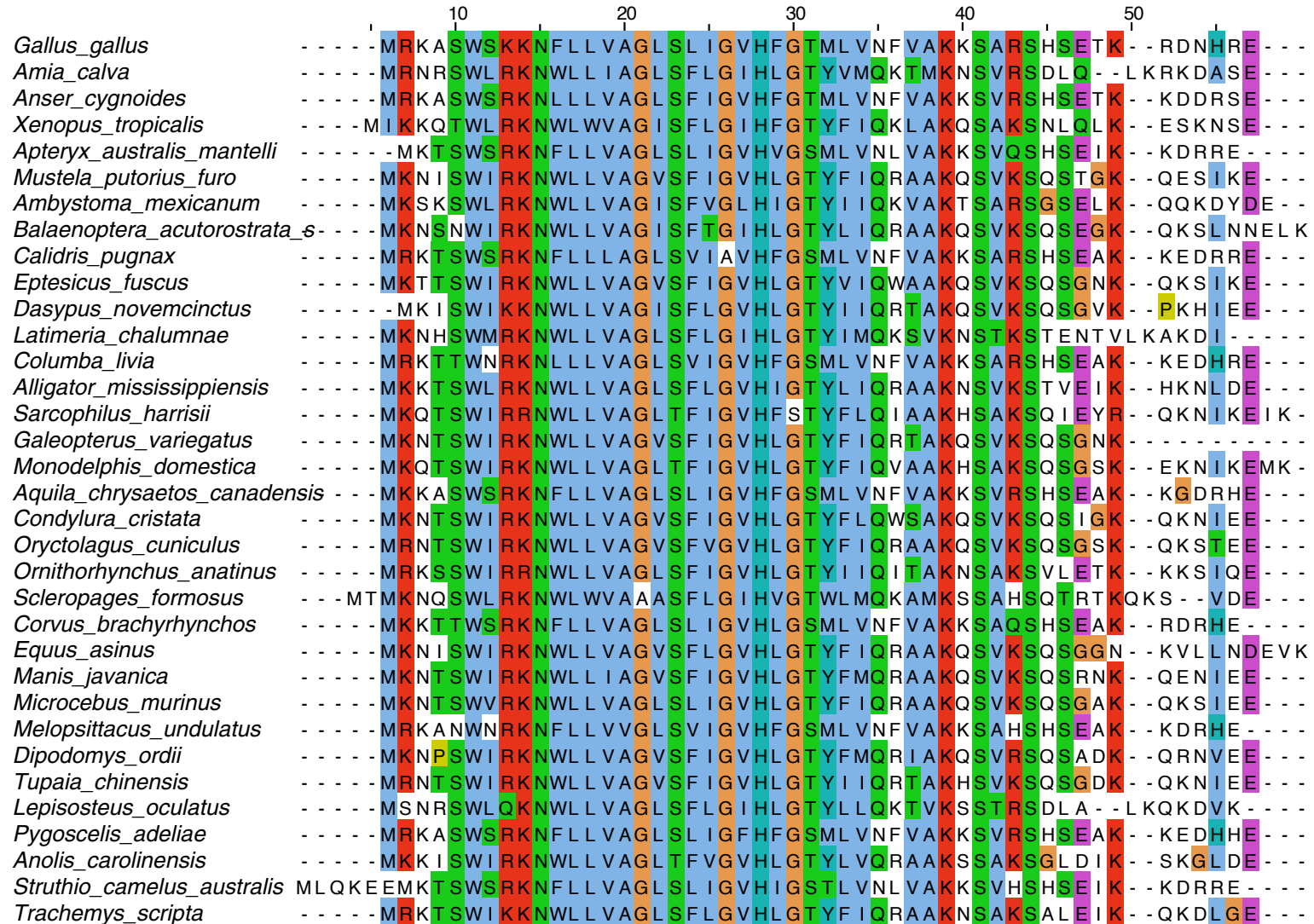
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HG0010.2

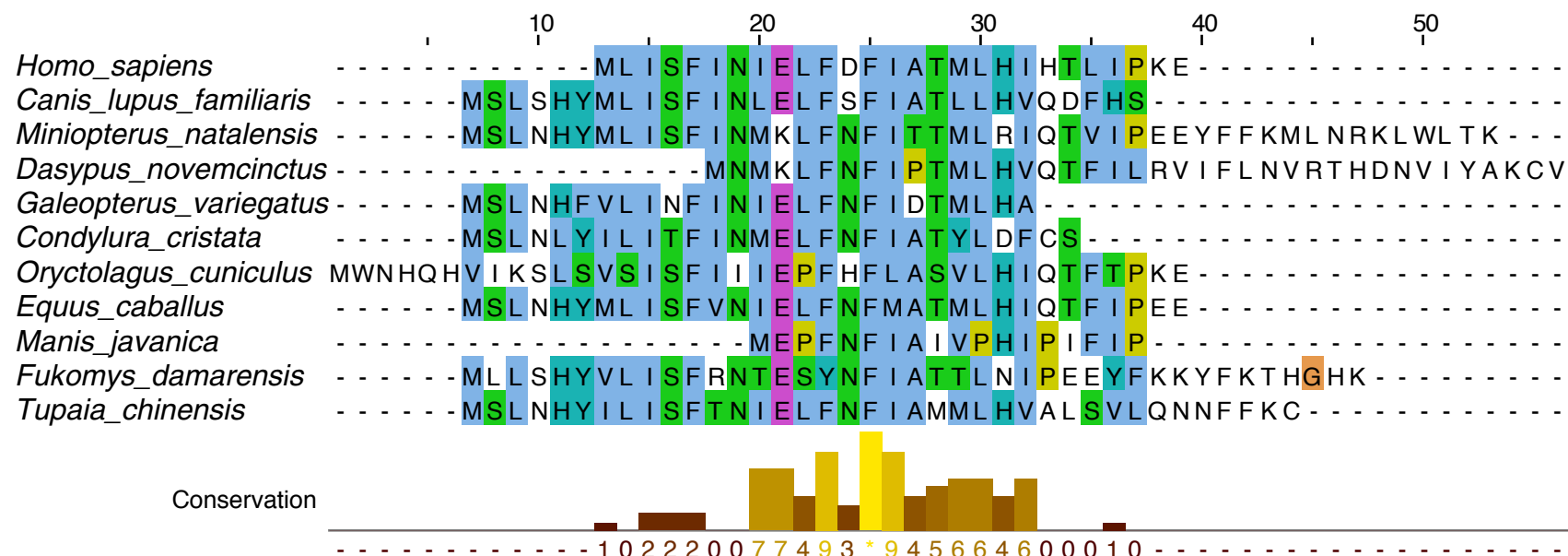
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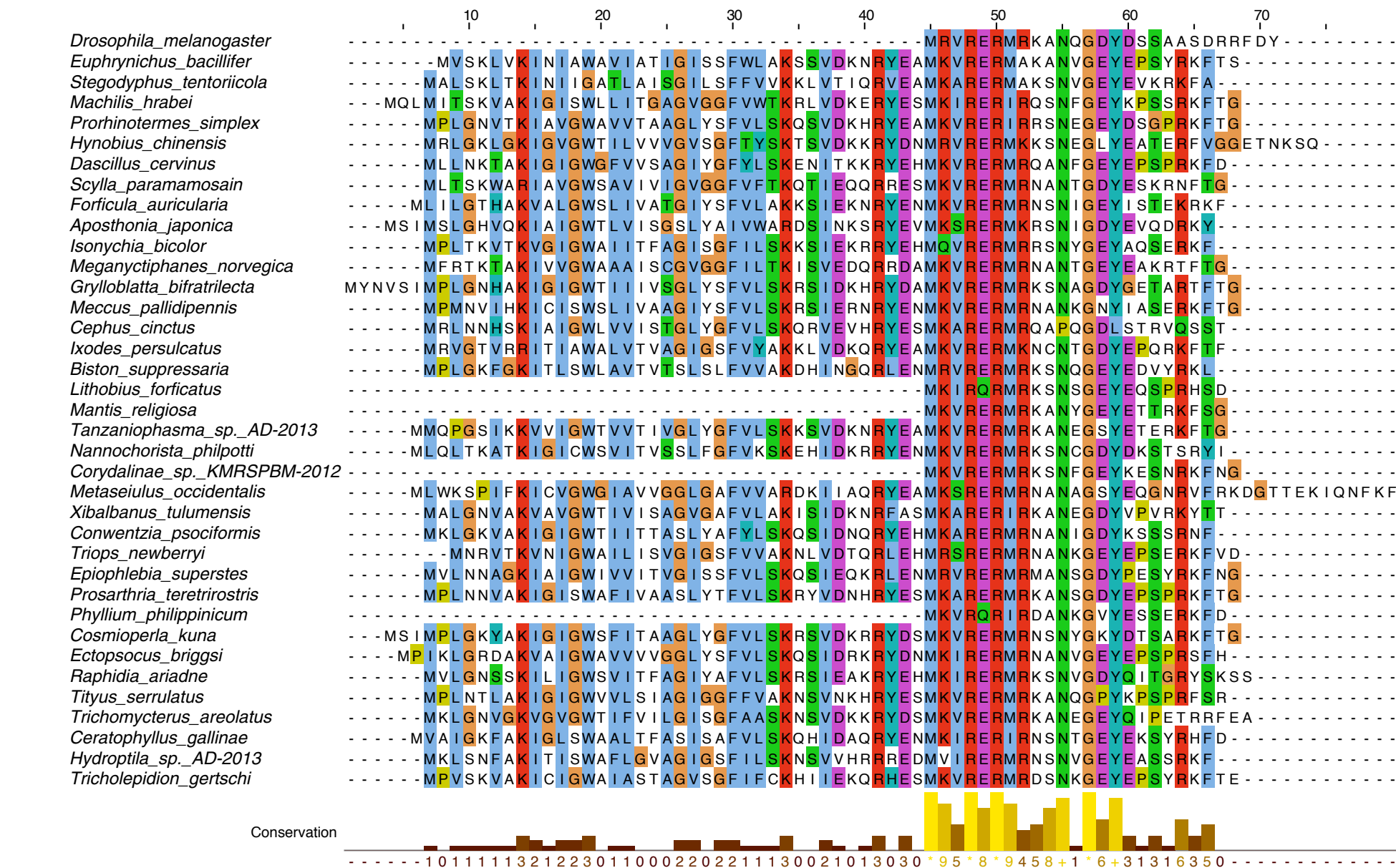
Conservation

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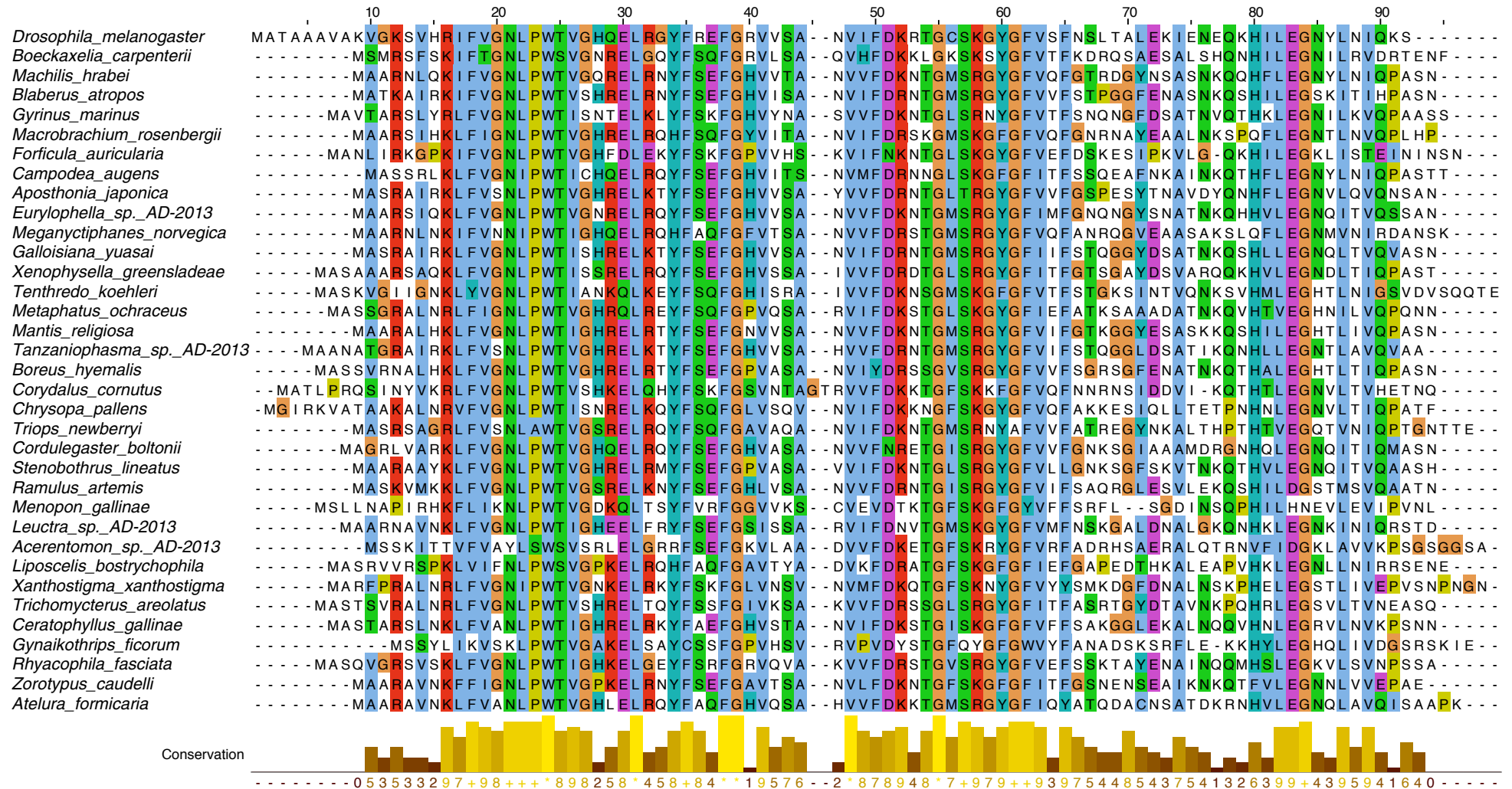


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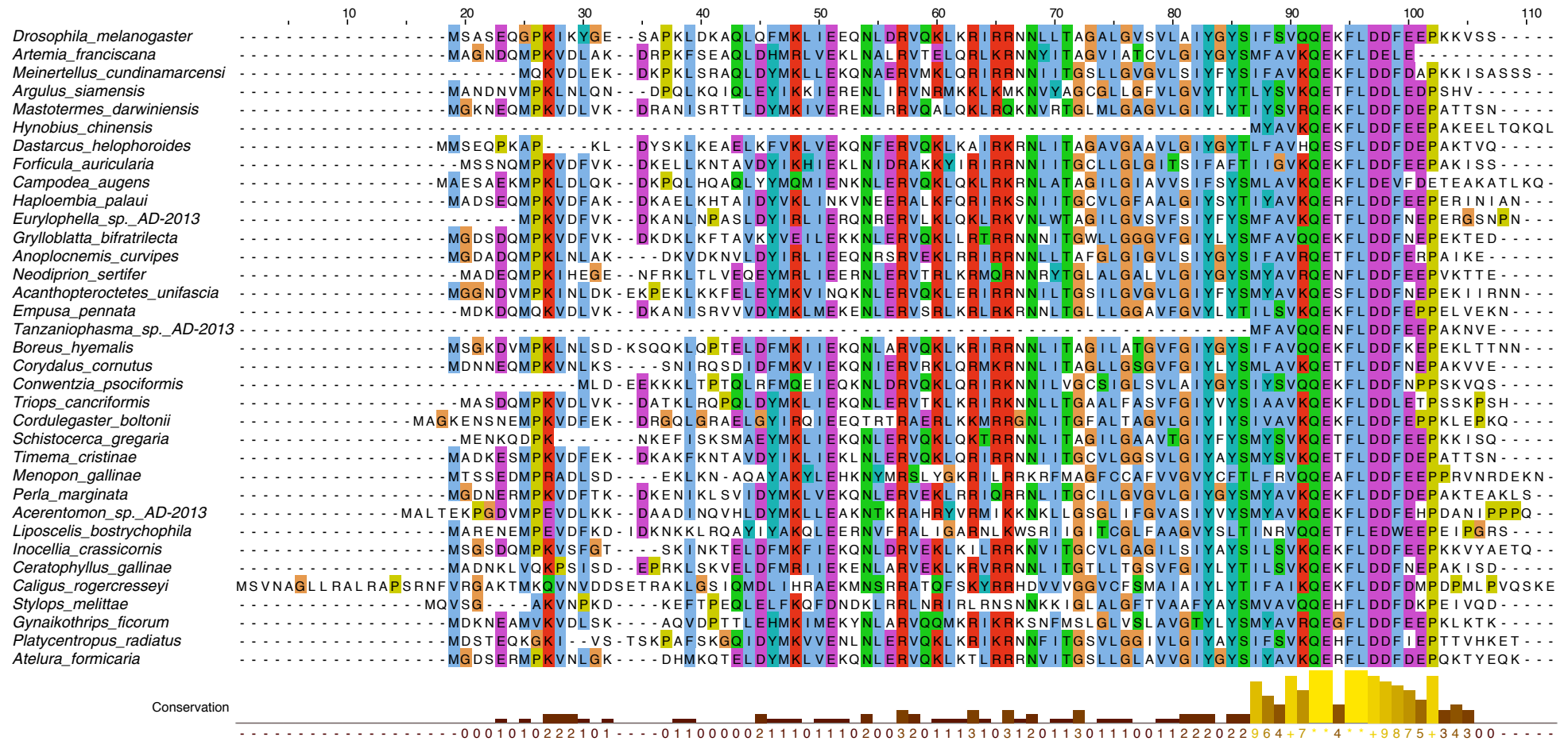


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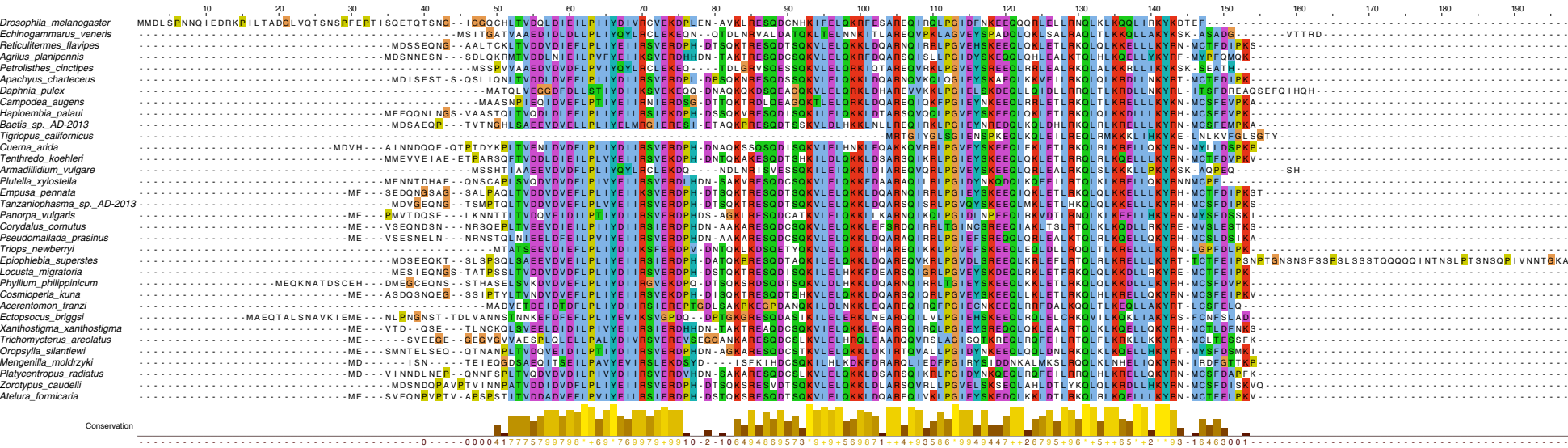


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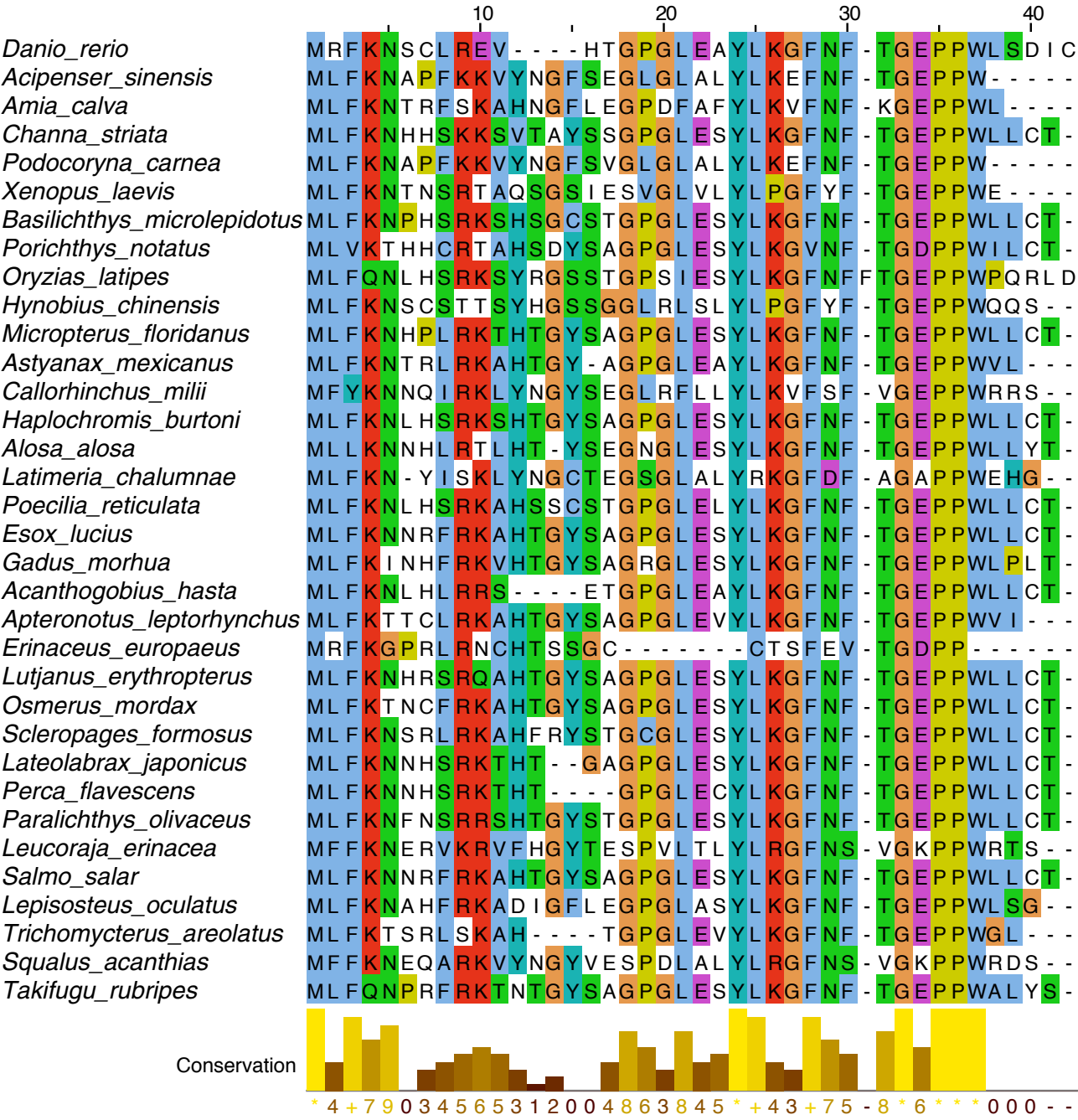
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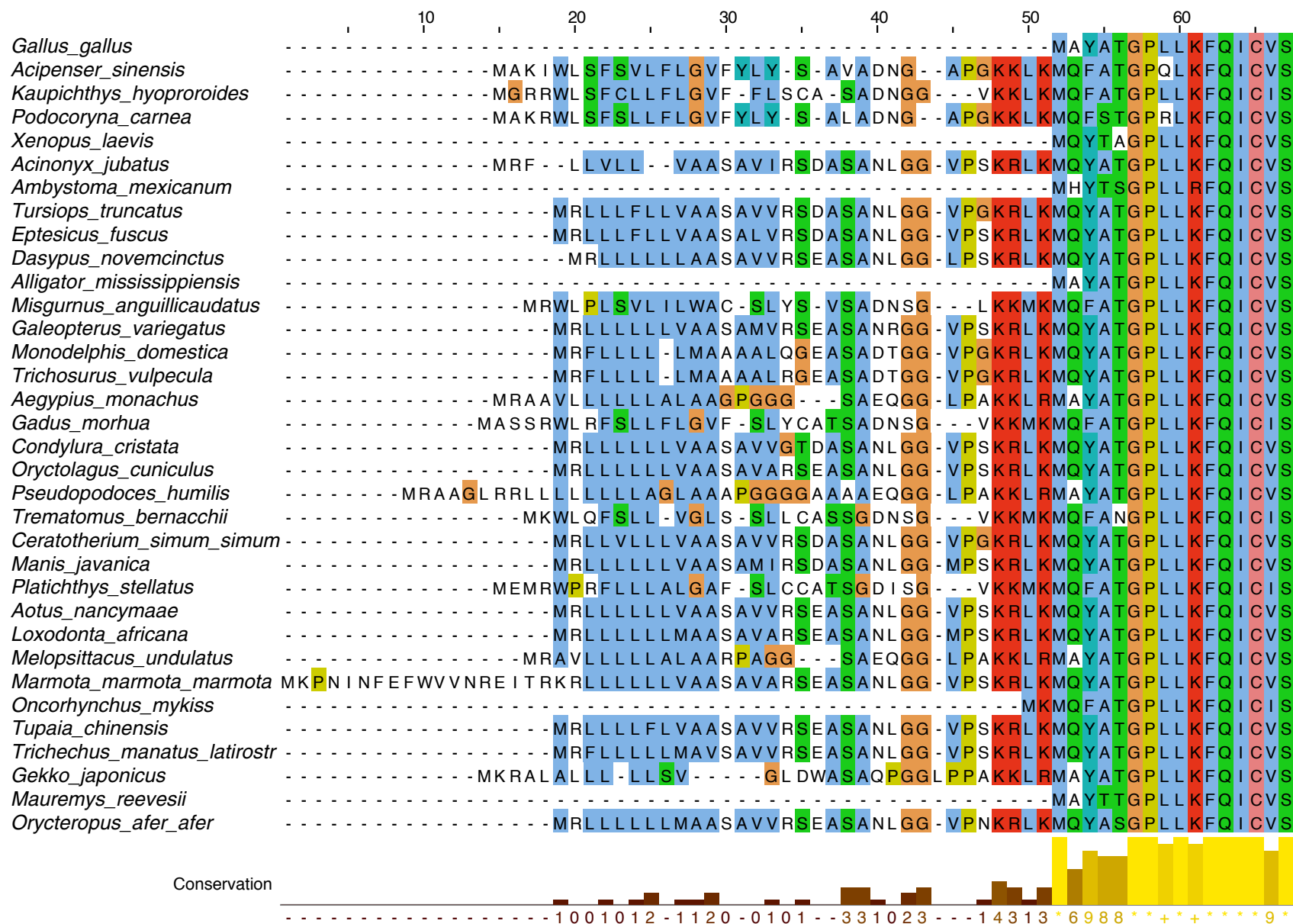


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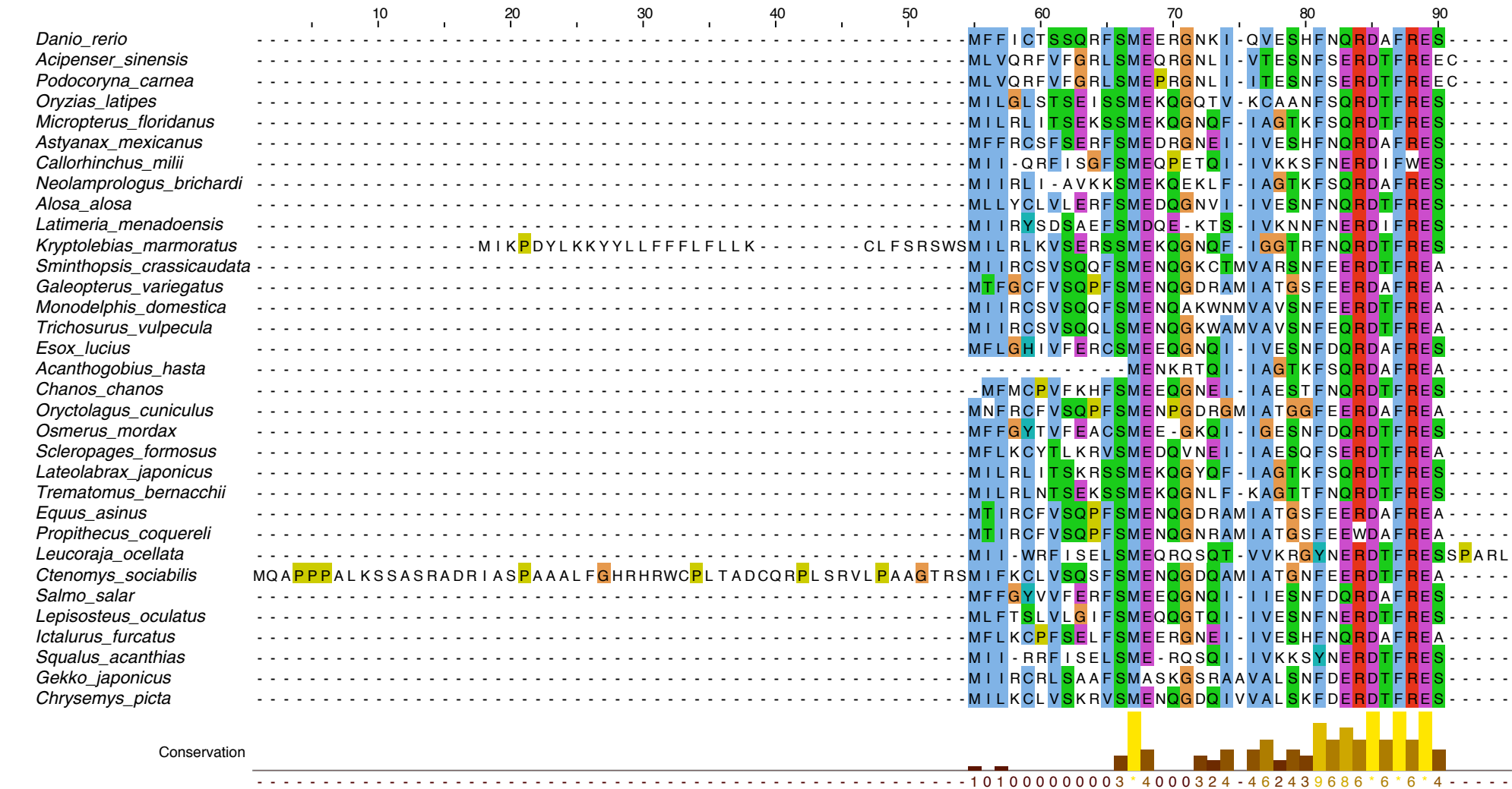


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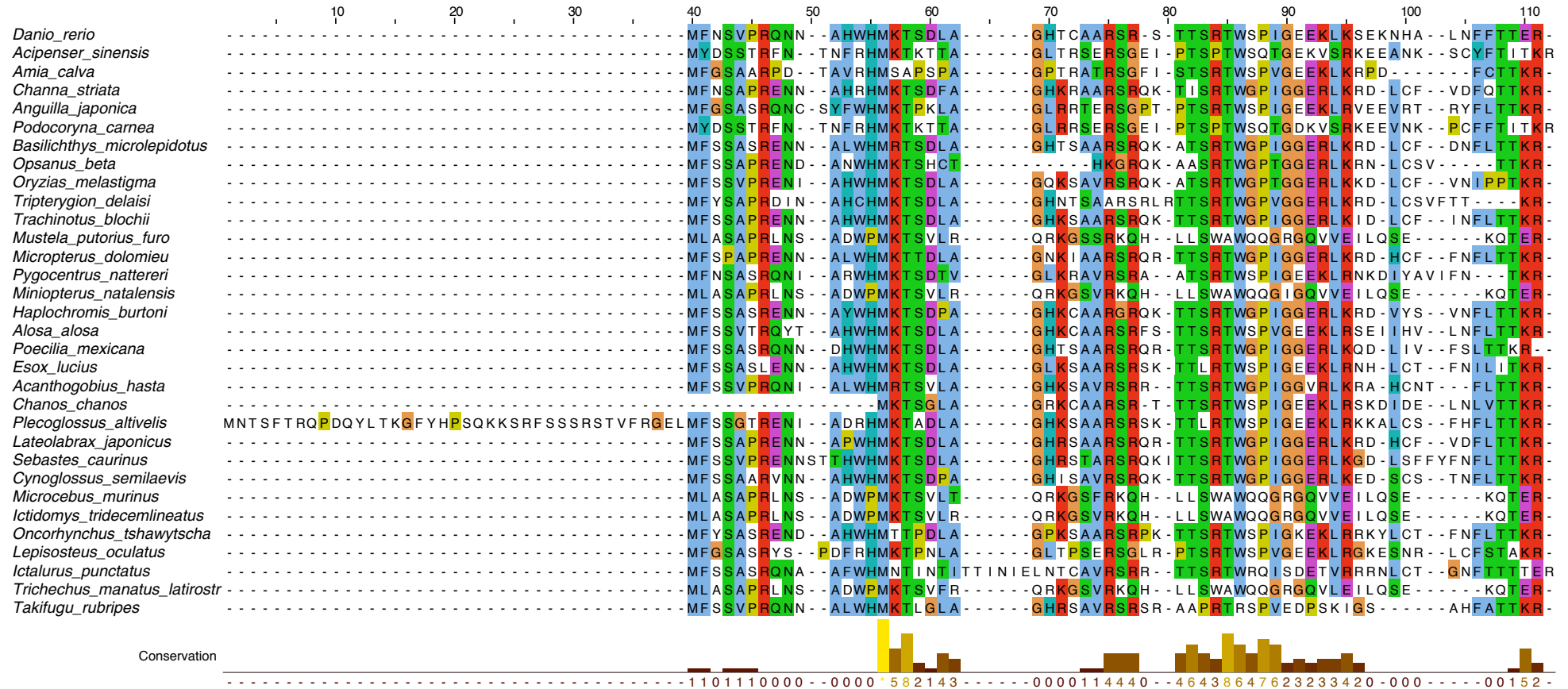
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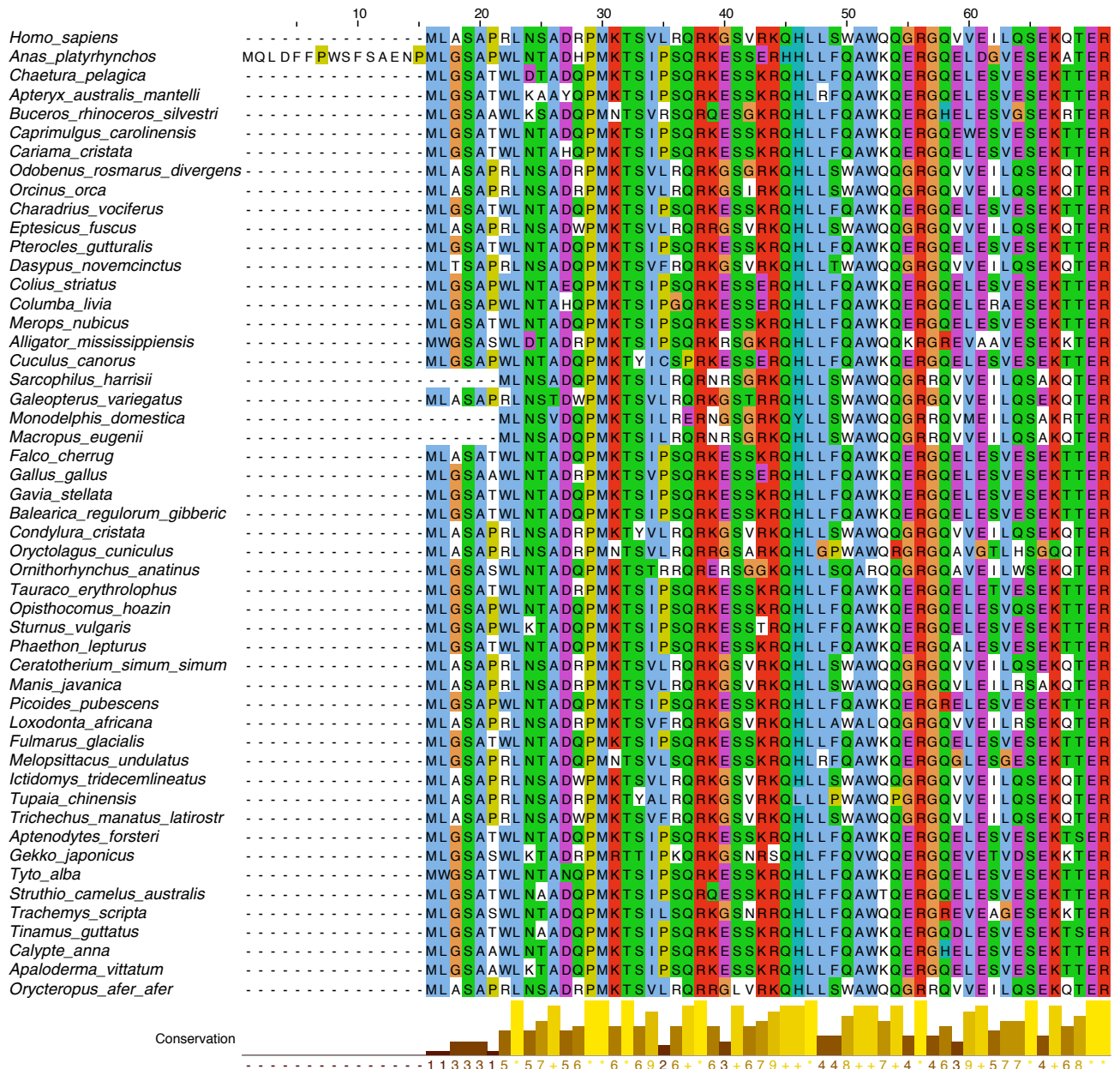
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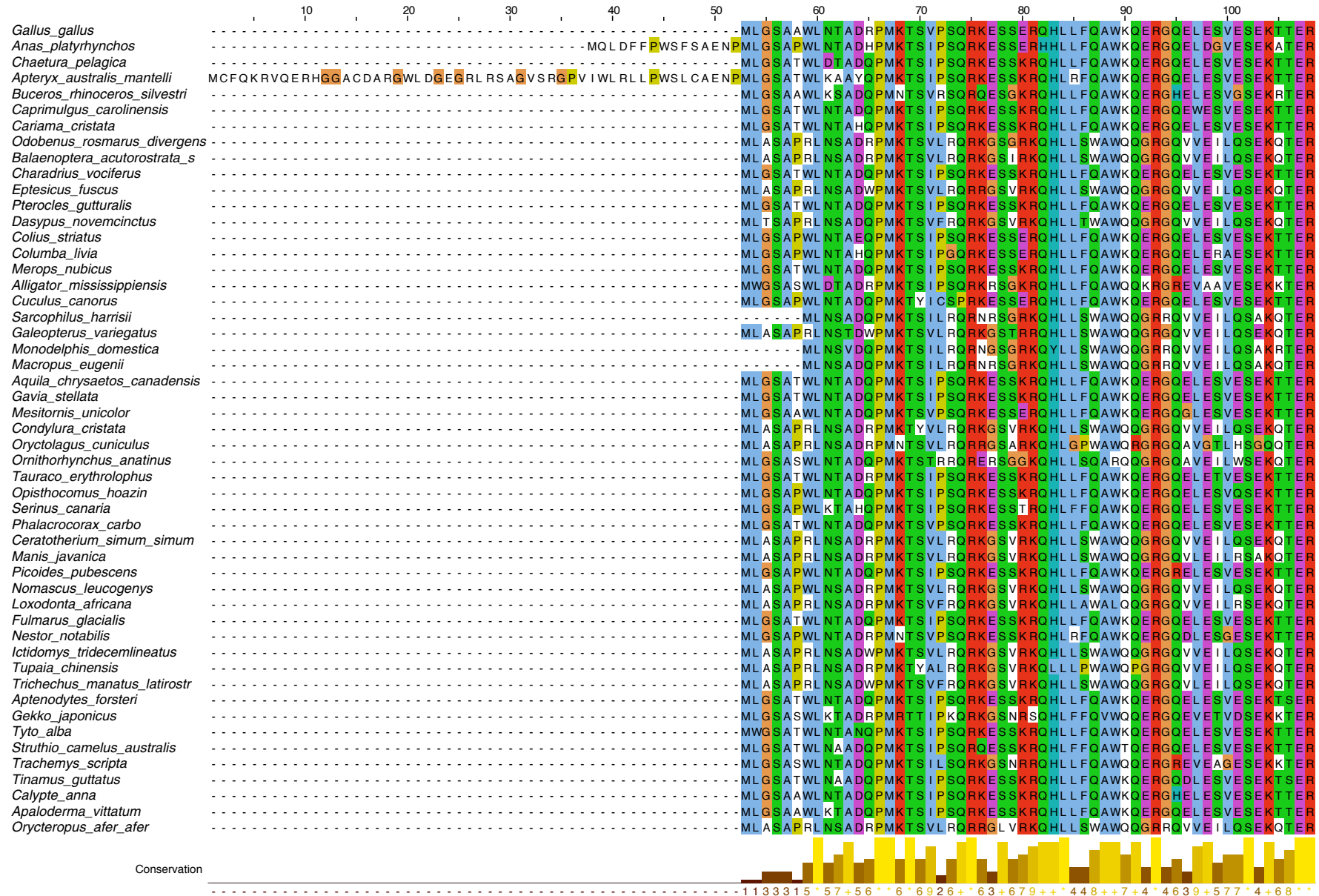
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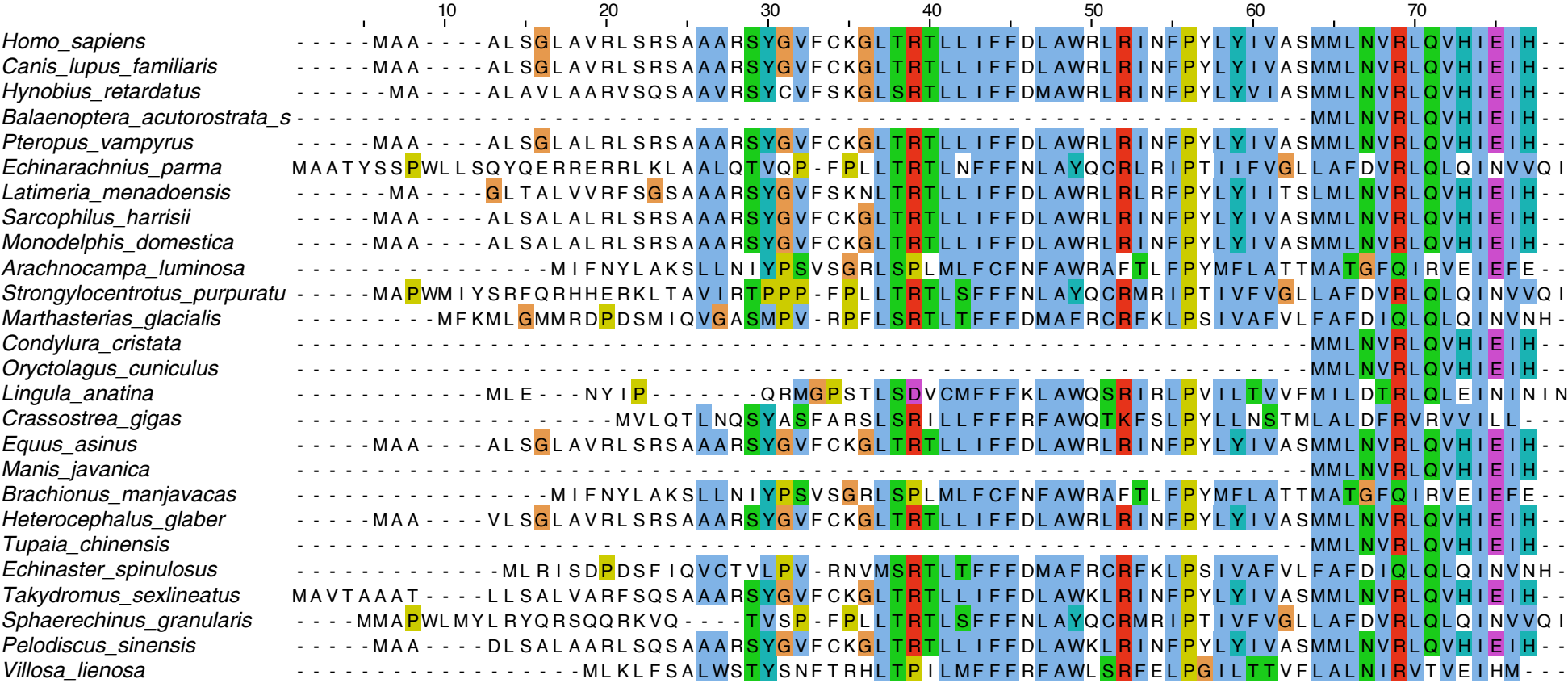
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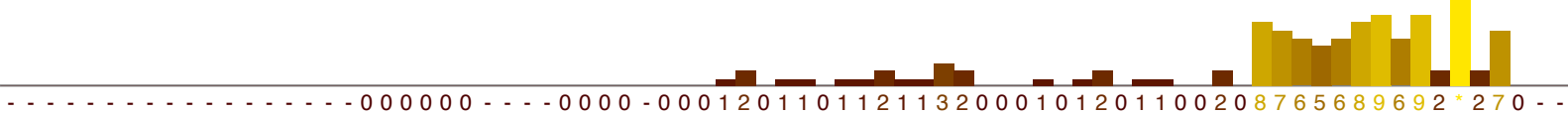


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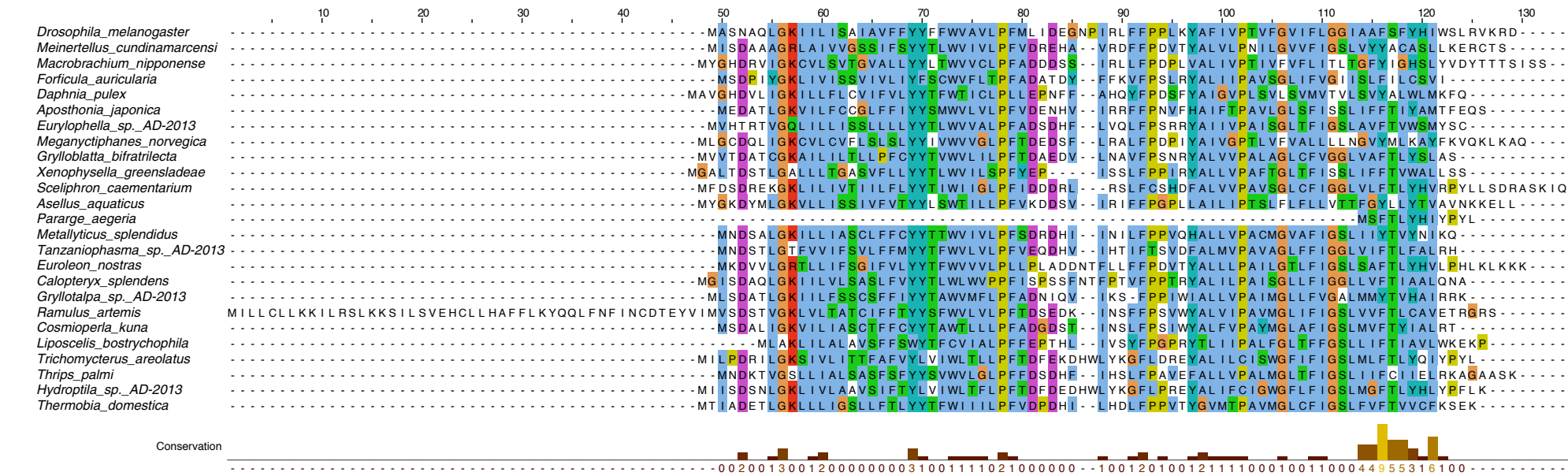


Conservation



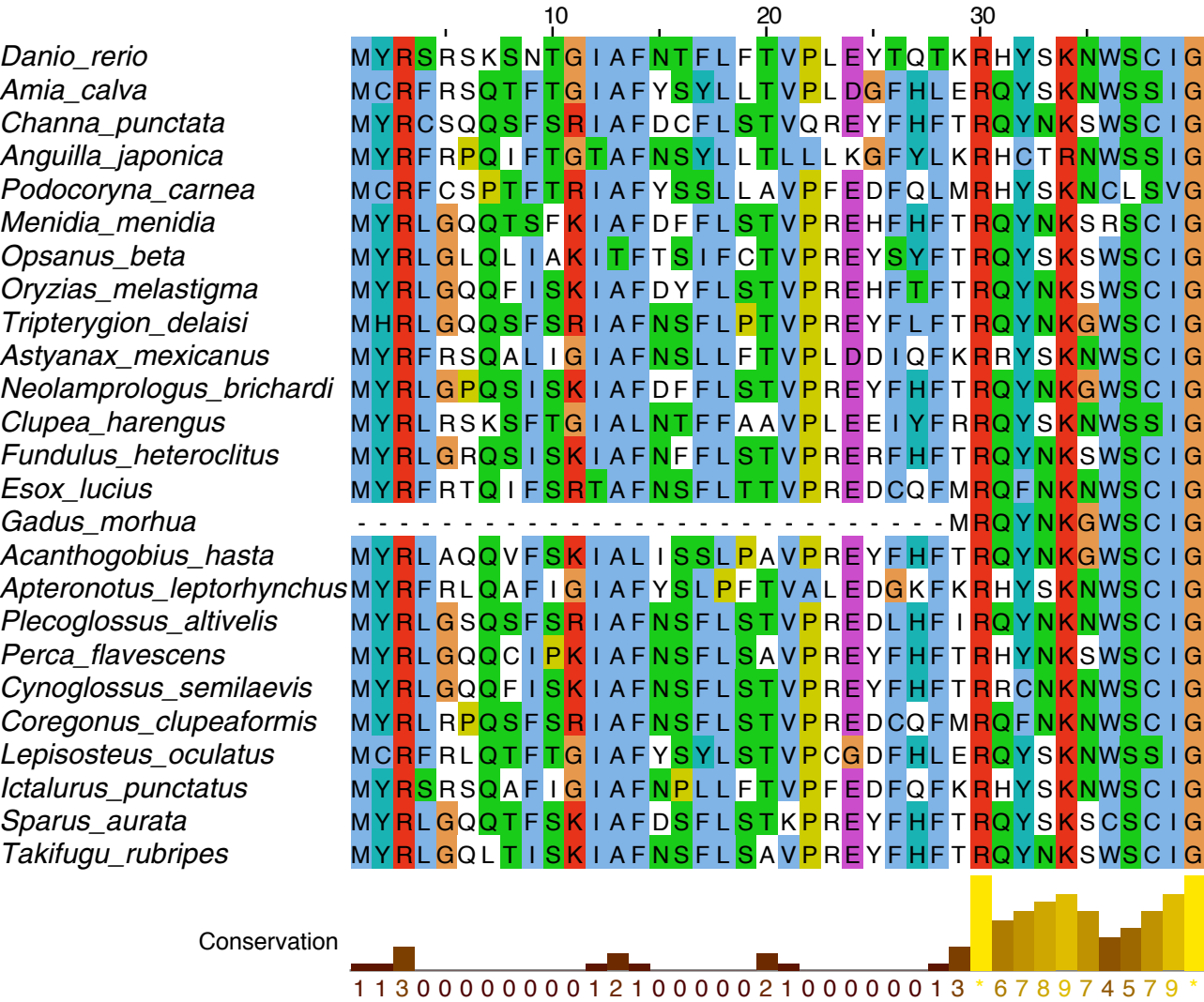
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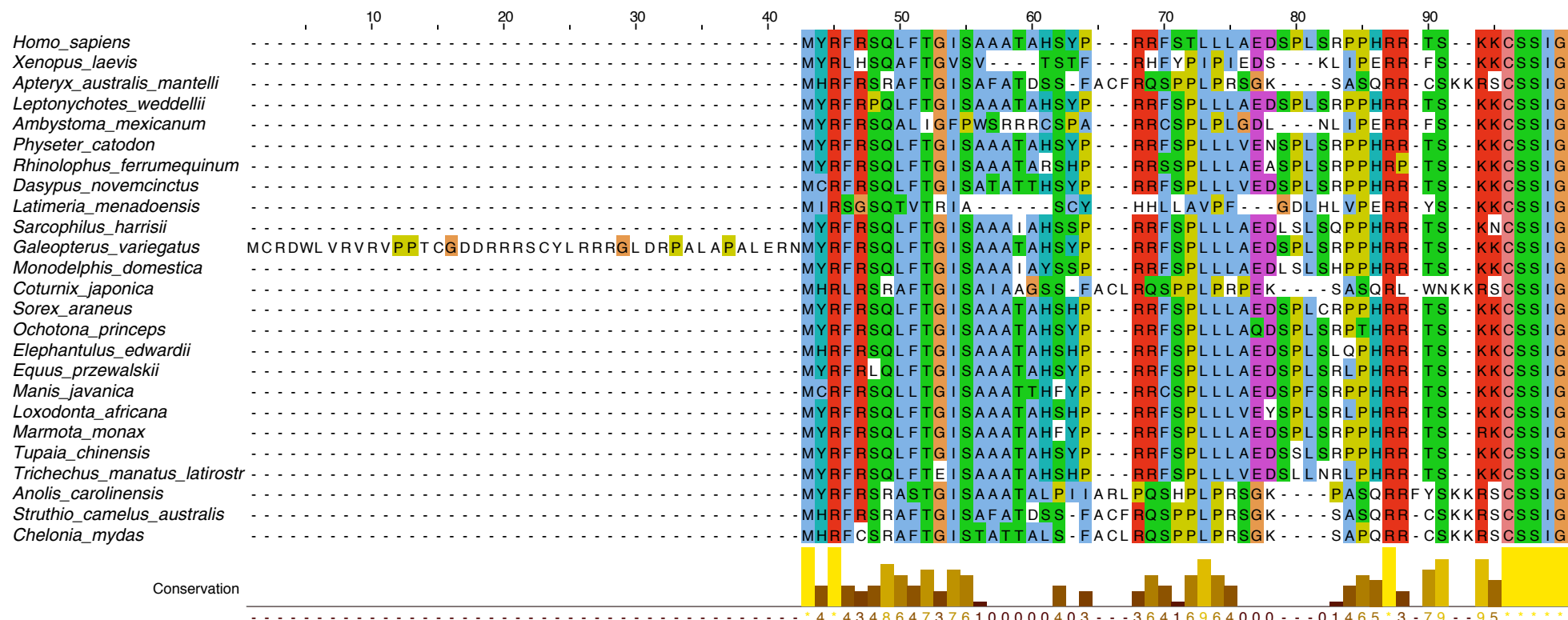


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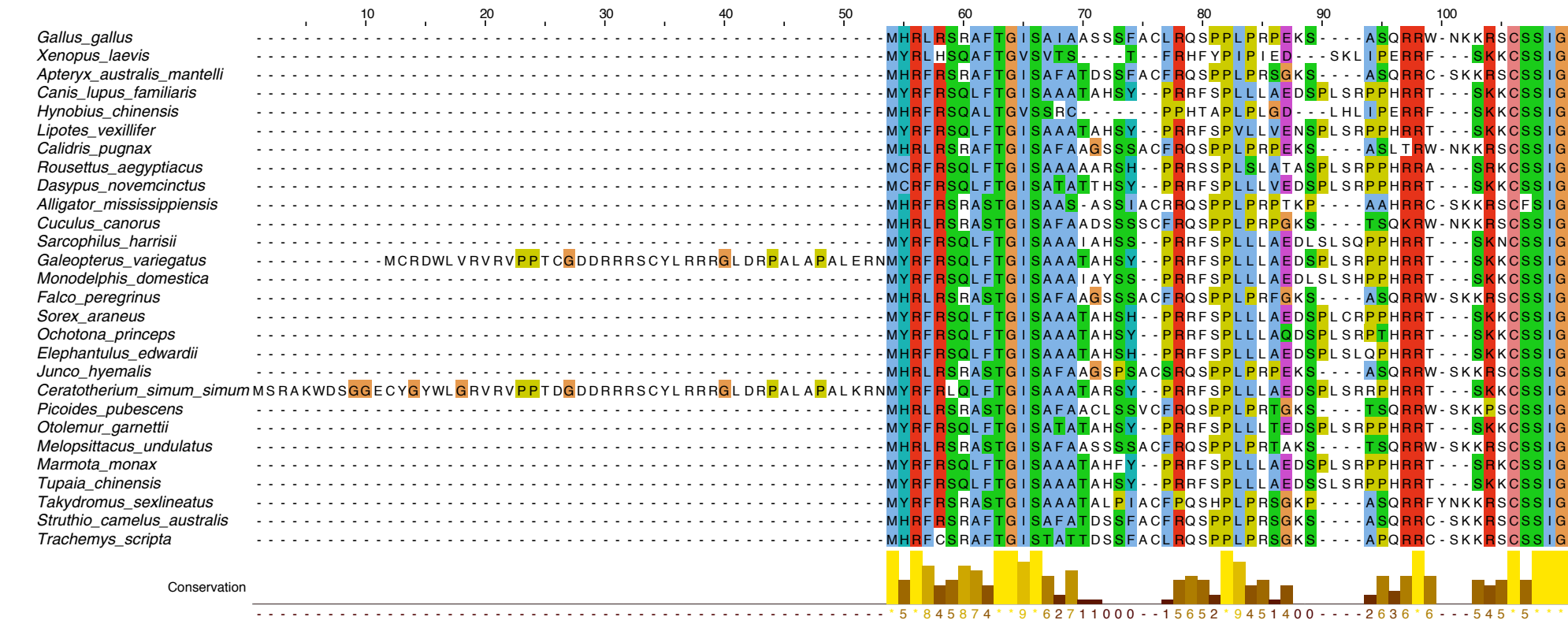


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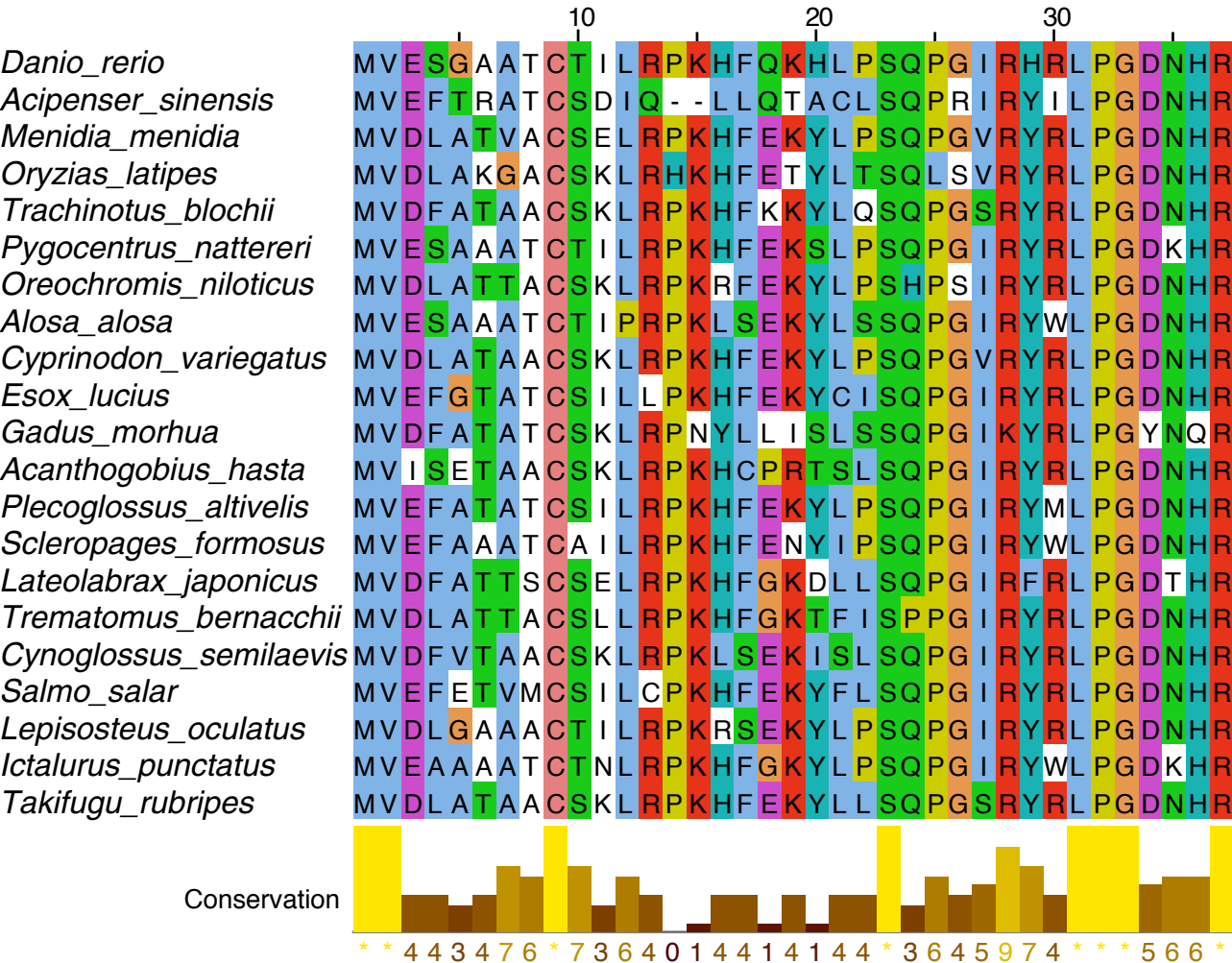
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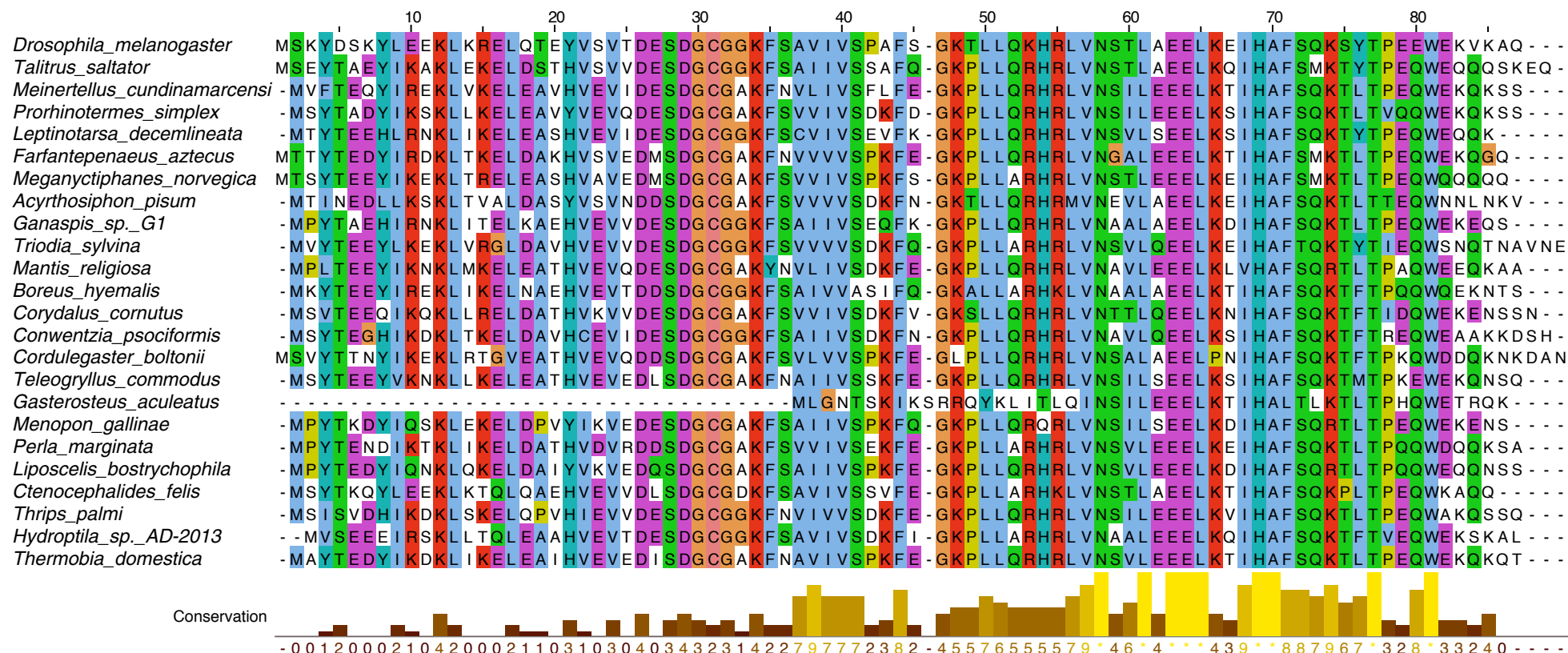


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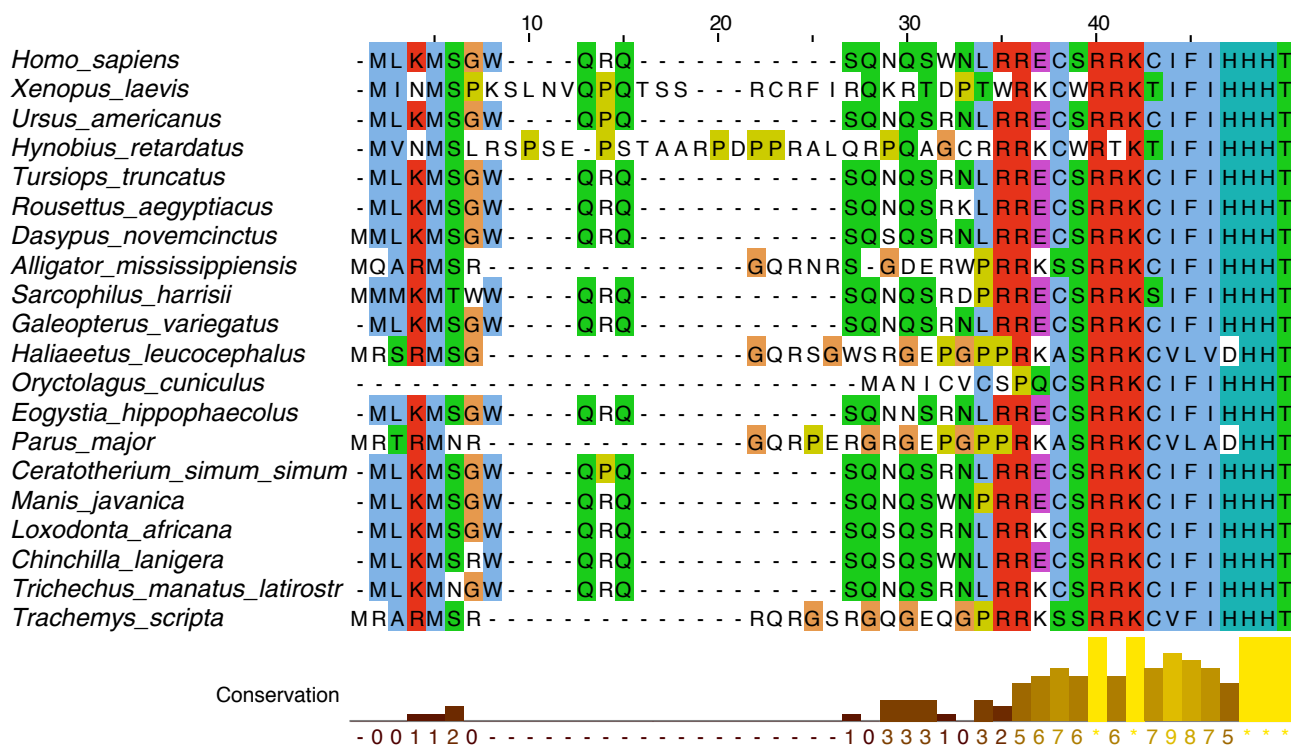


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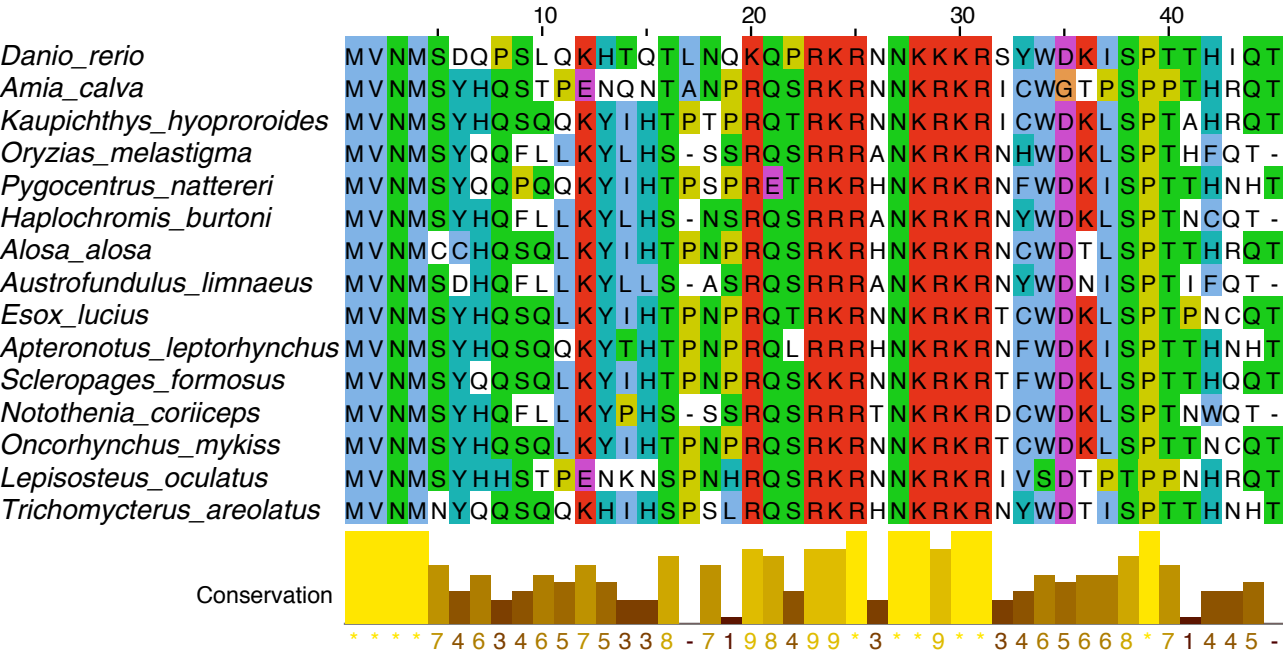
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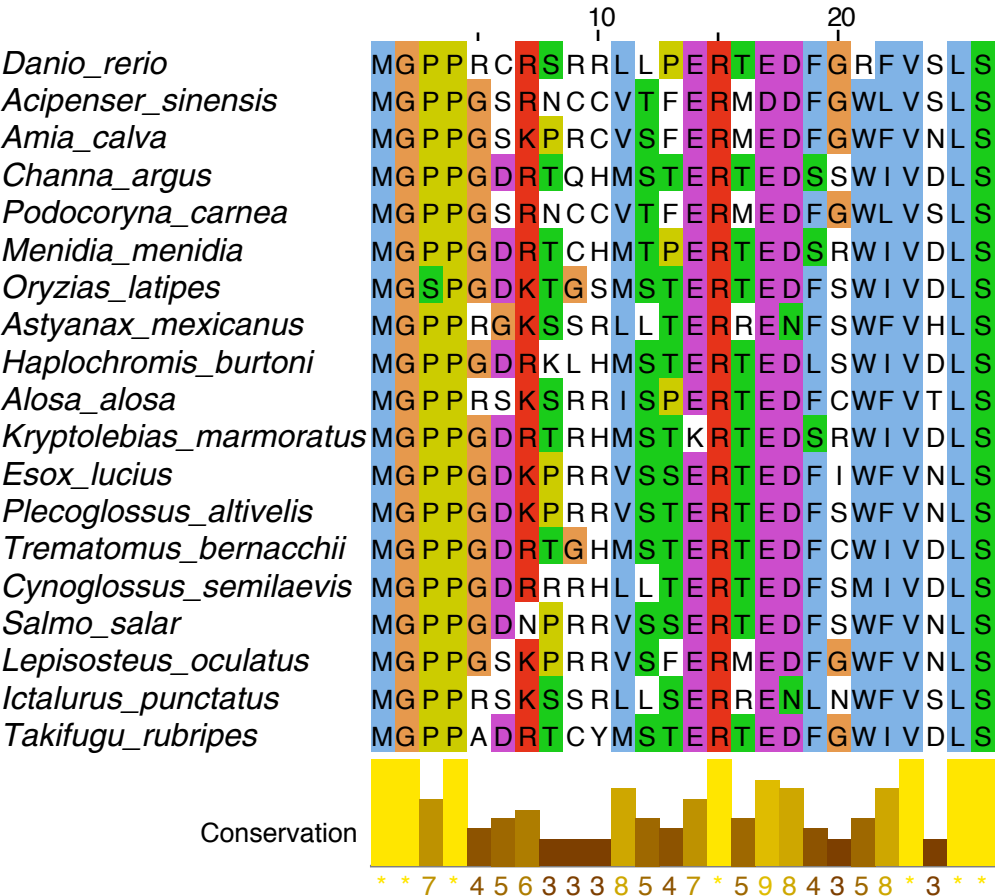
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HG0023.2

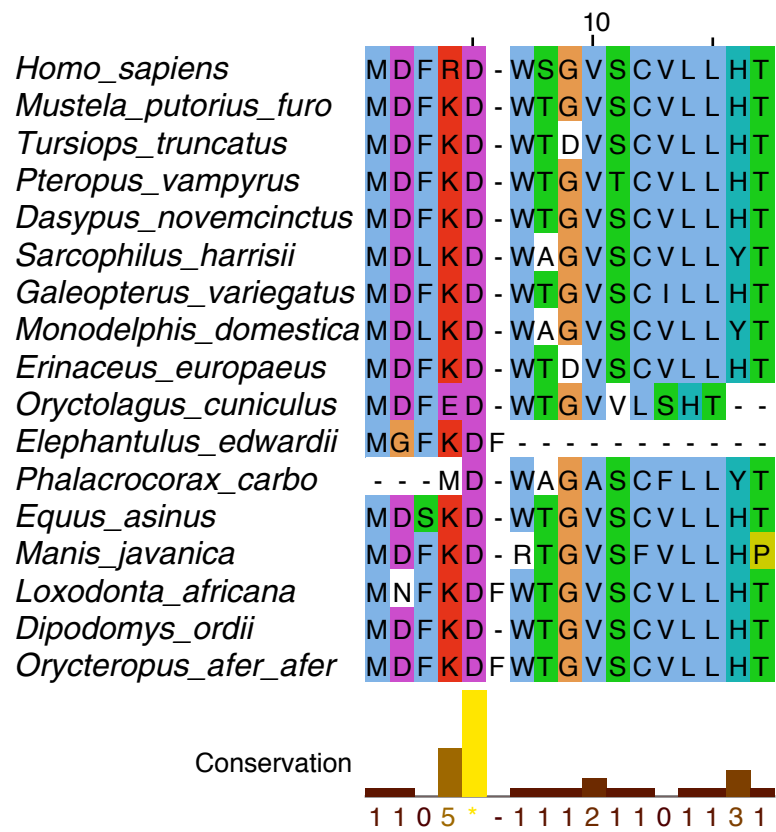
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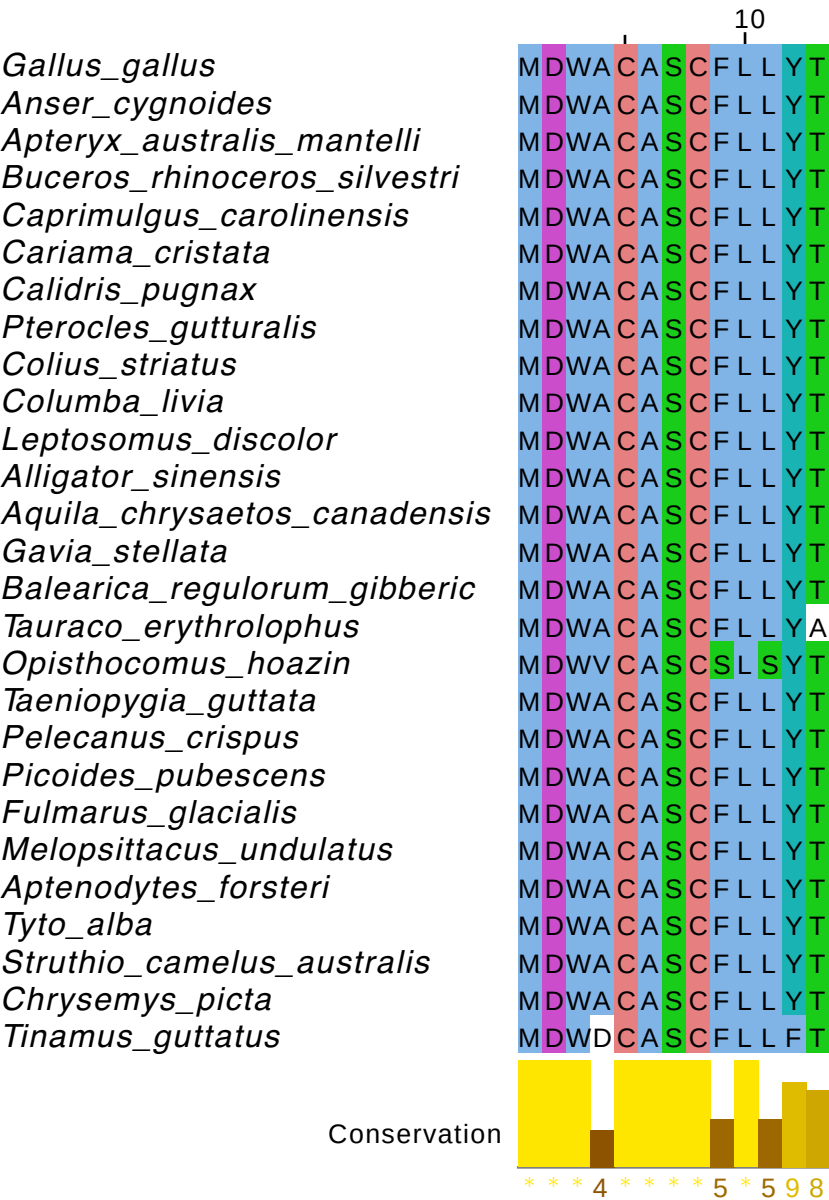
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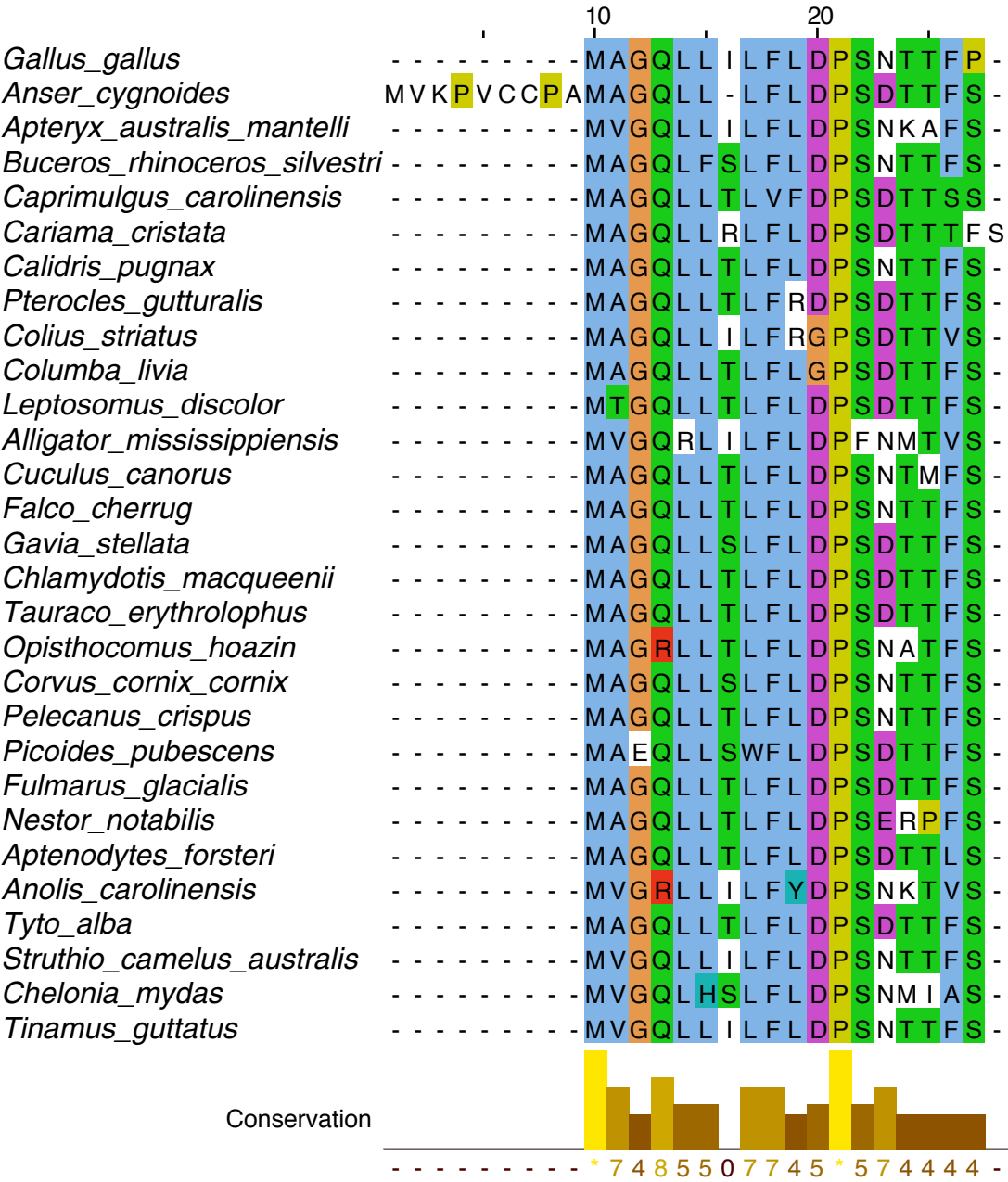
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HG0024.3

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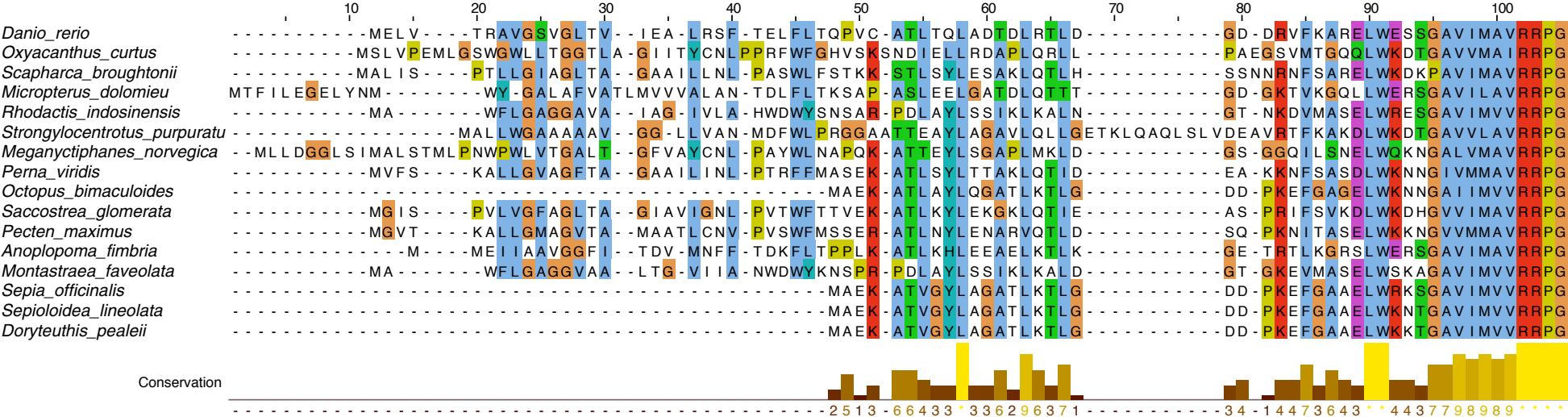


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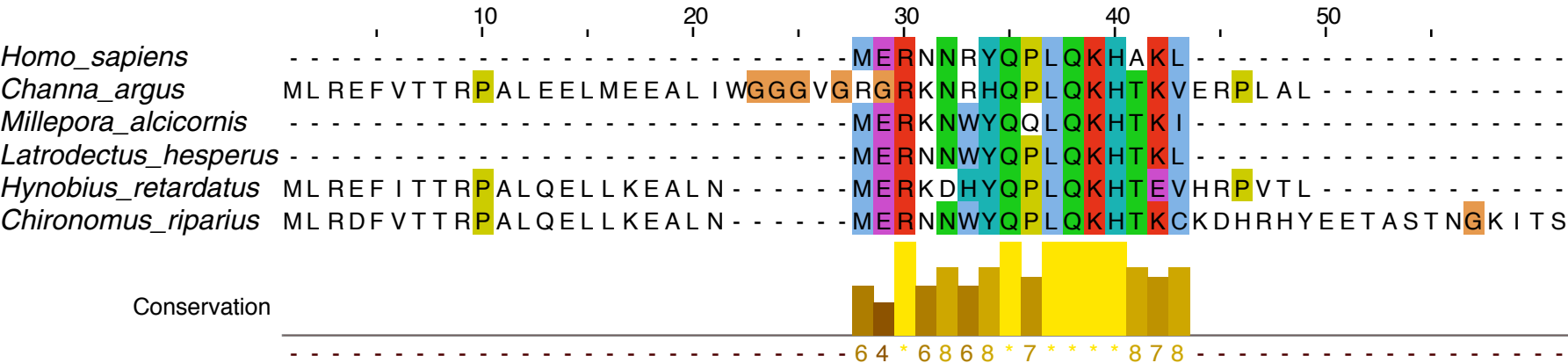
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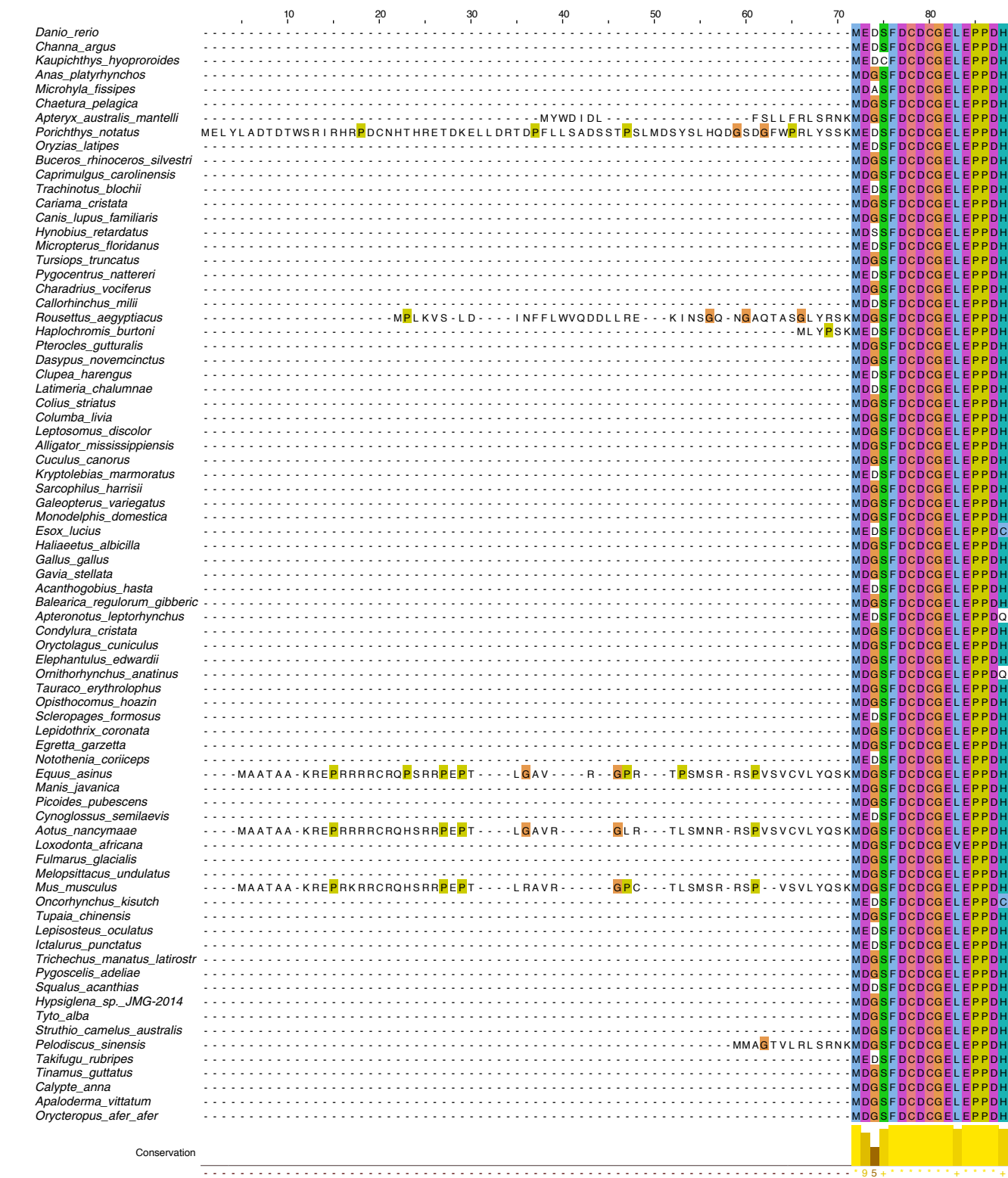
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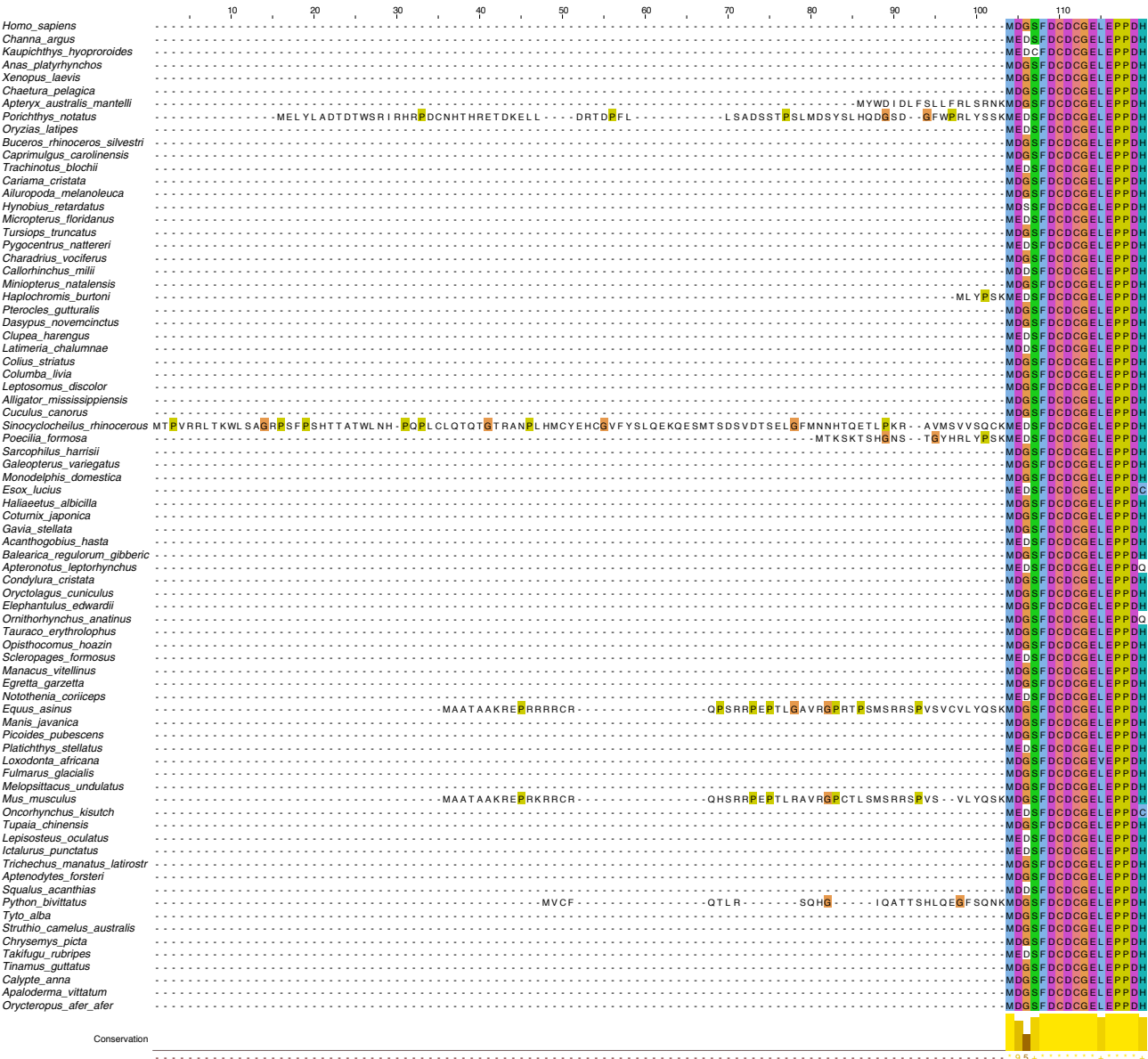
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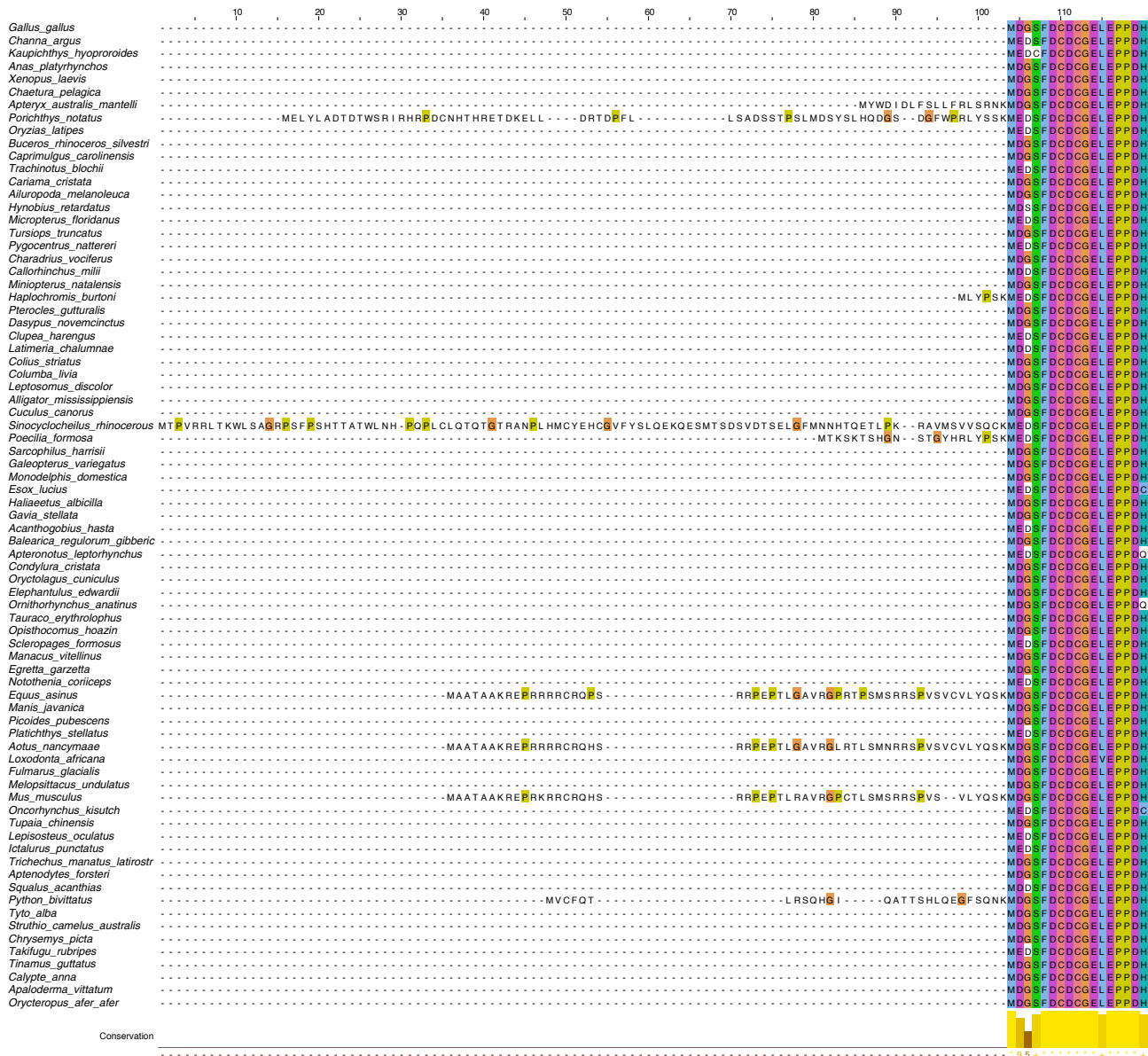
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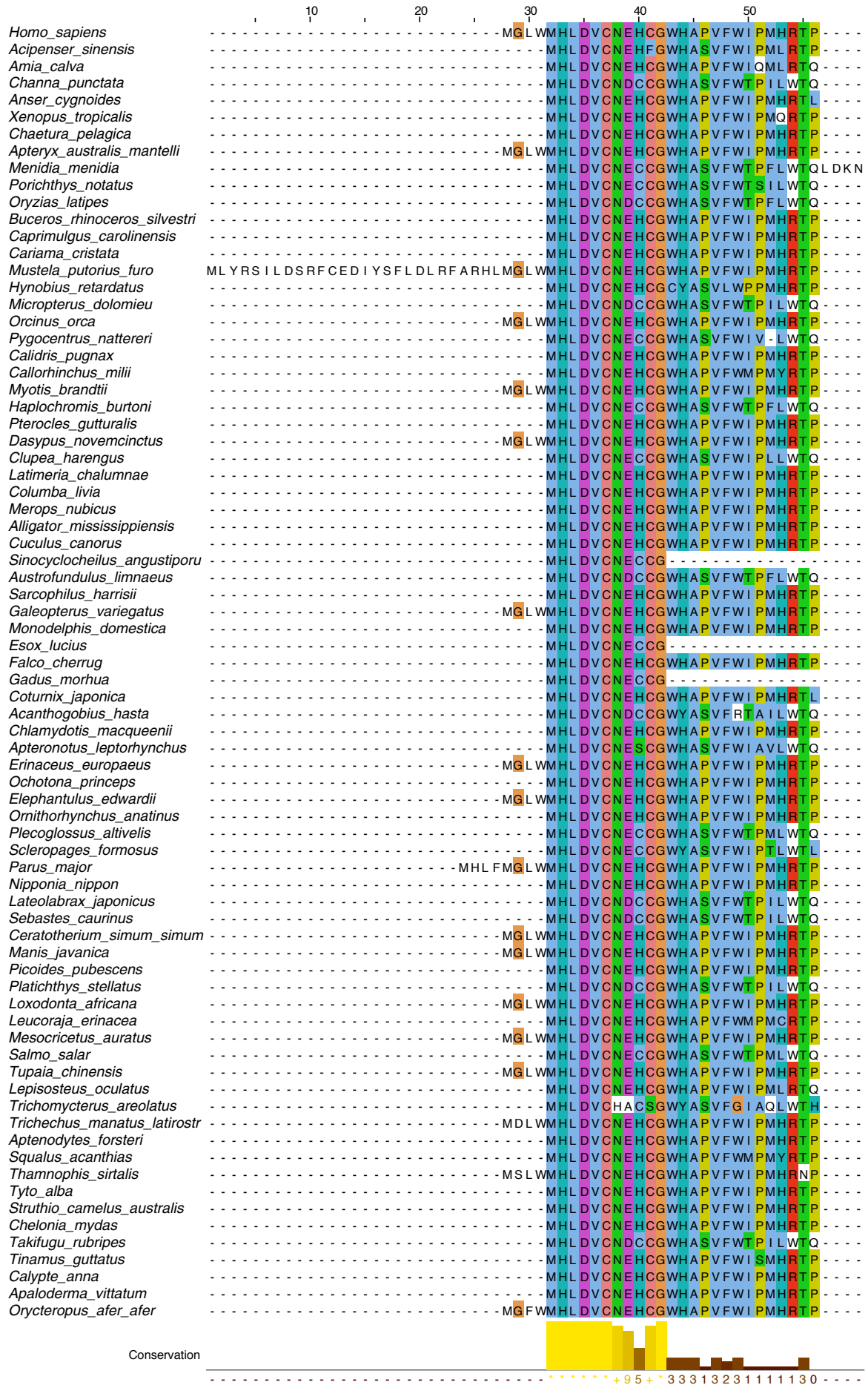
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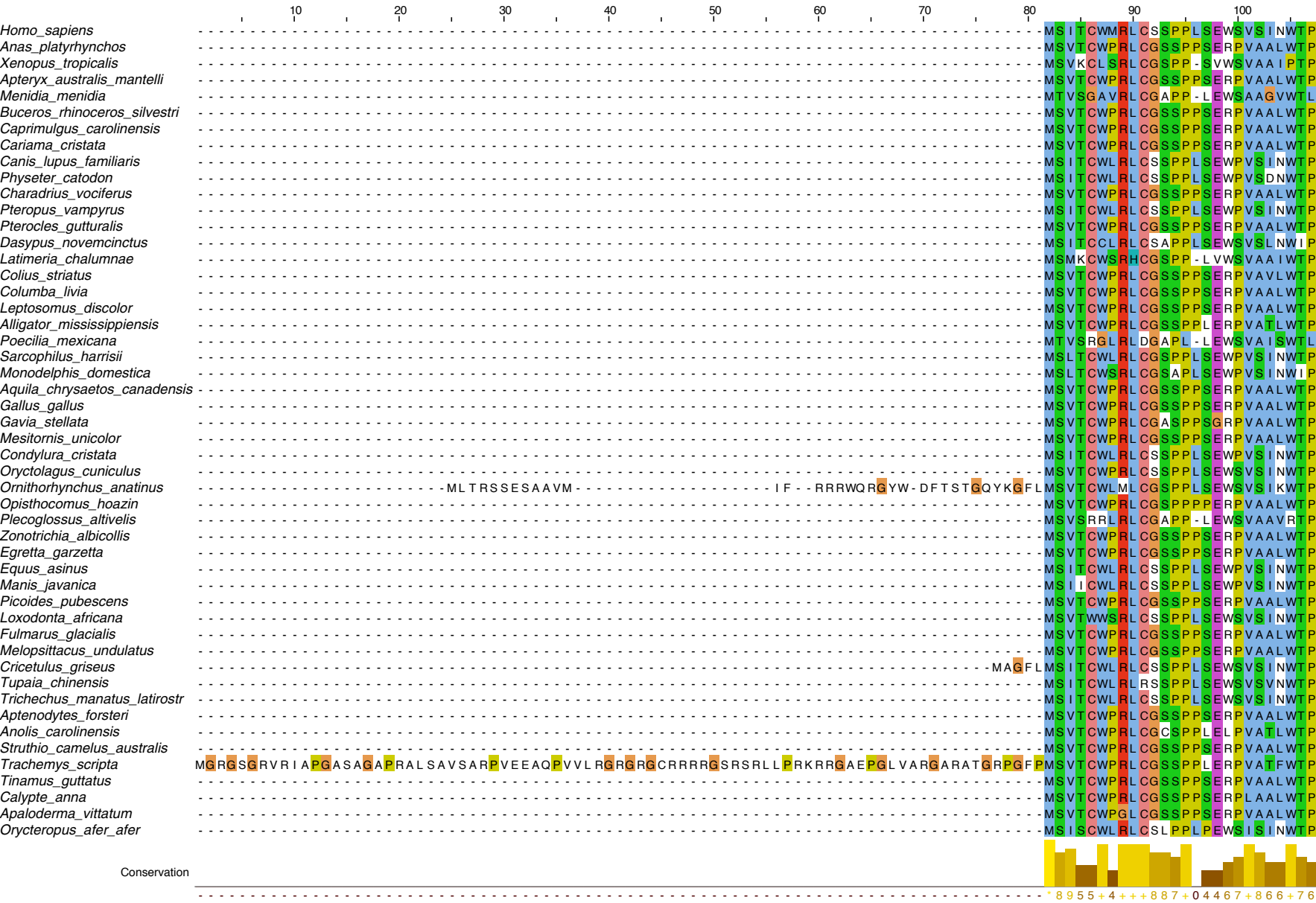
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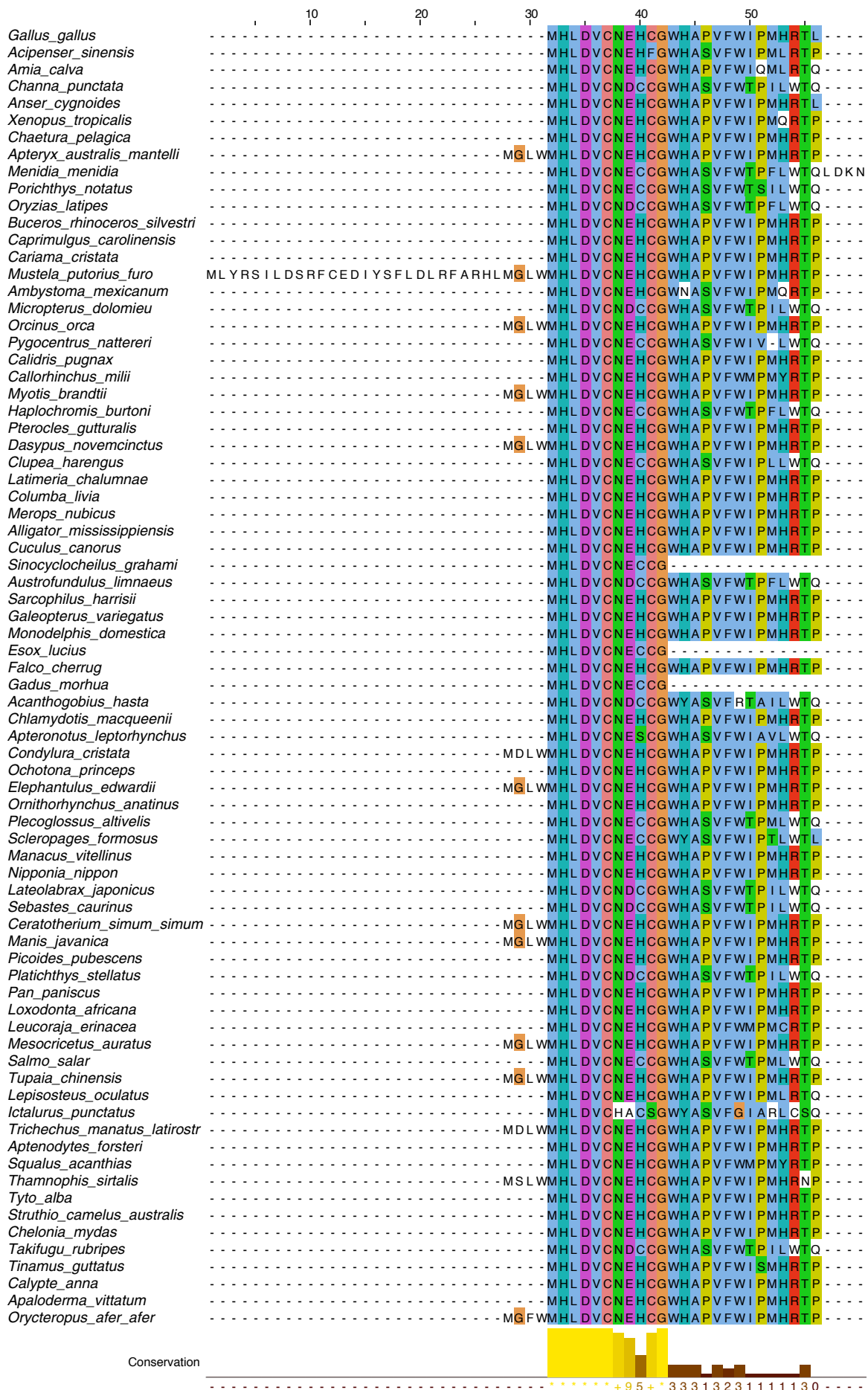


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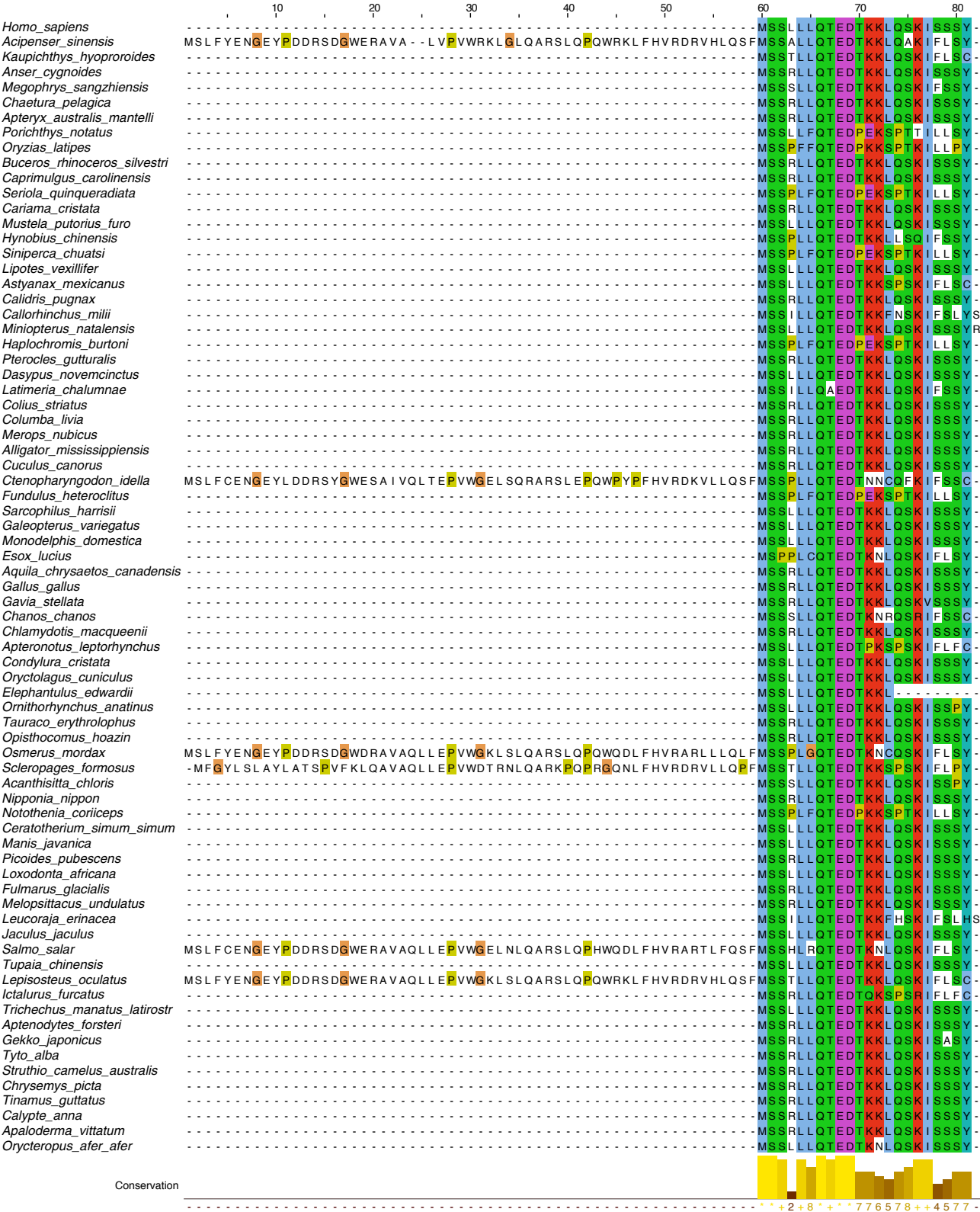


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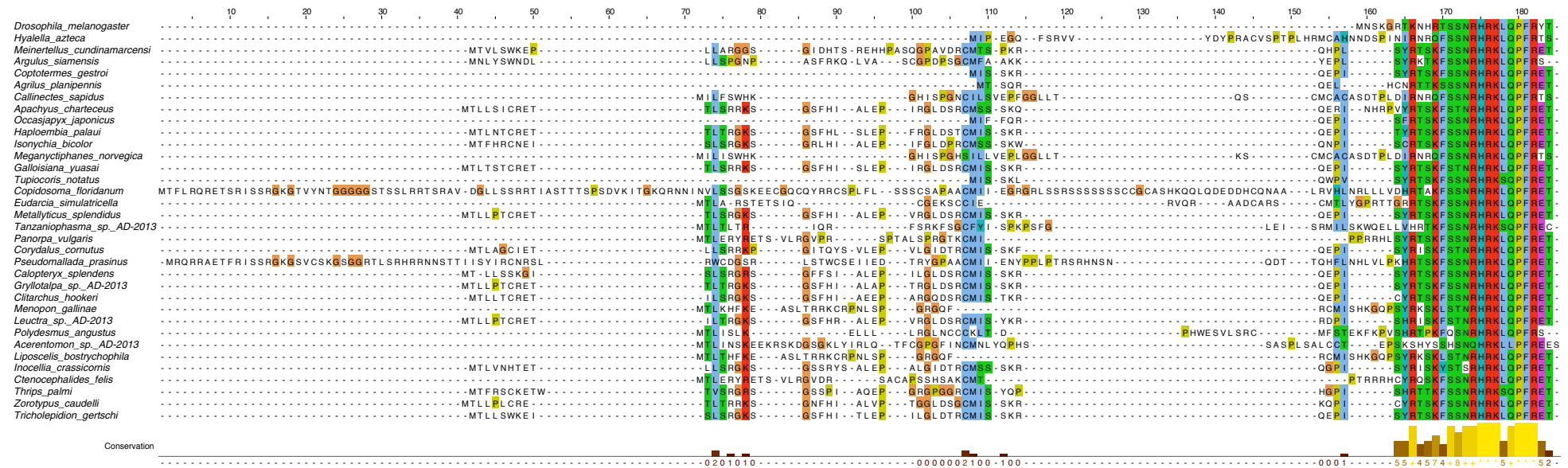


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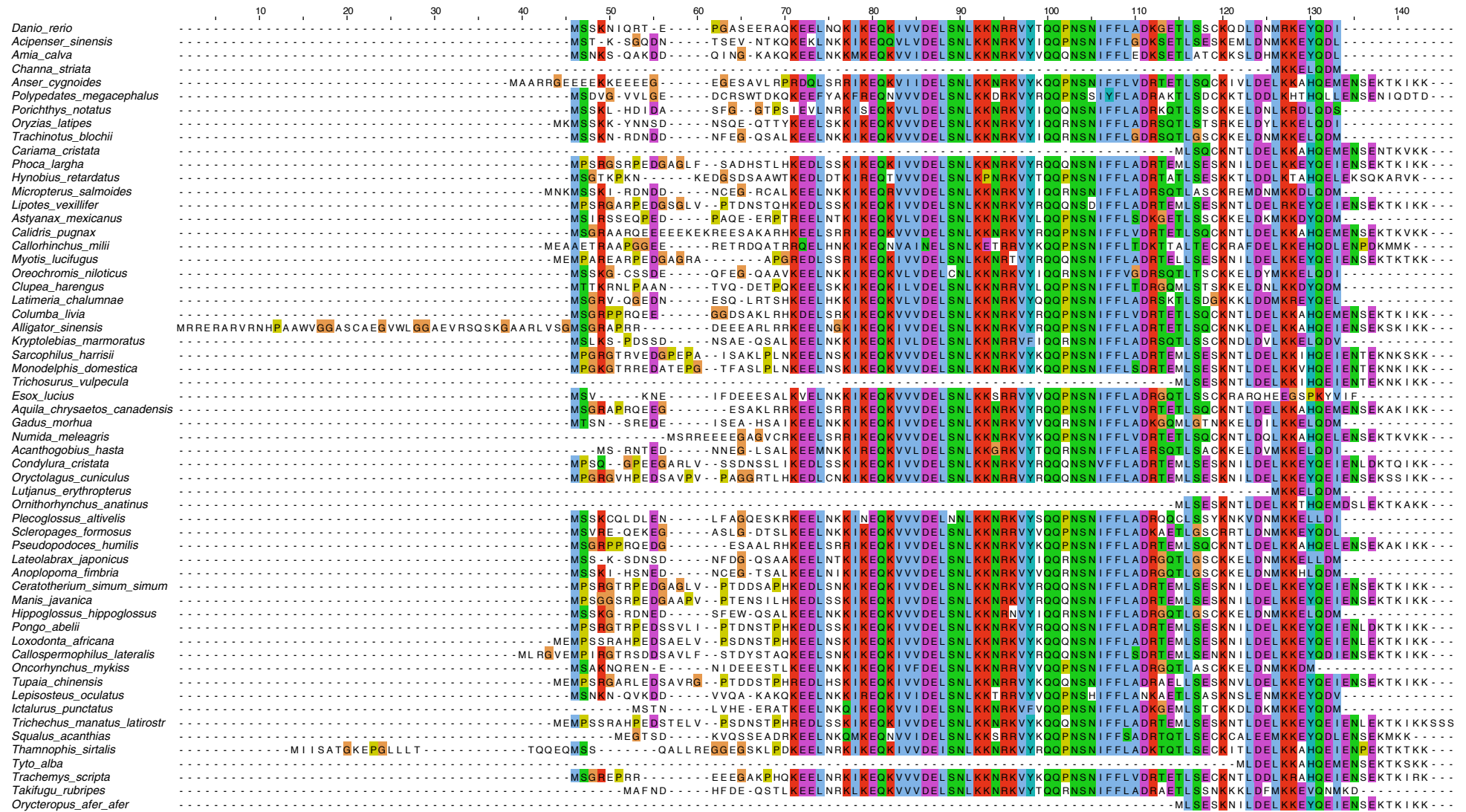
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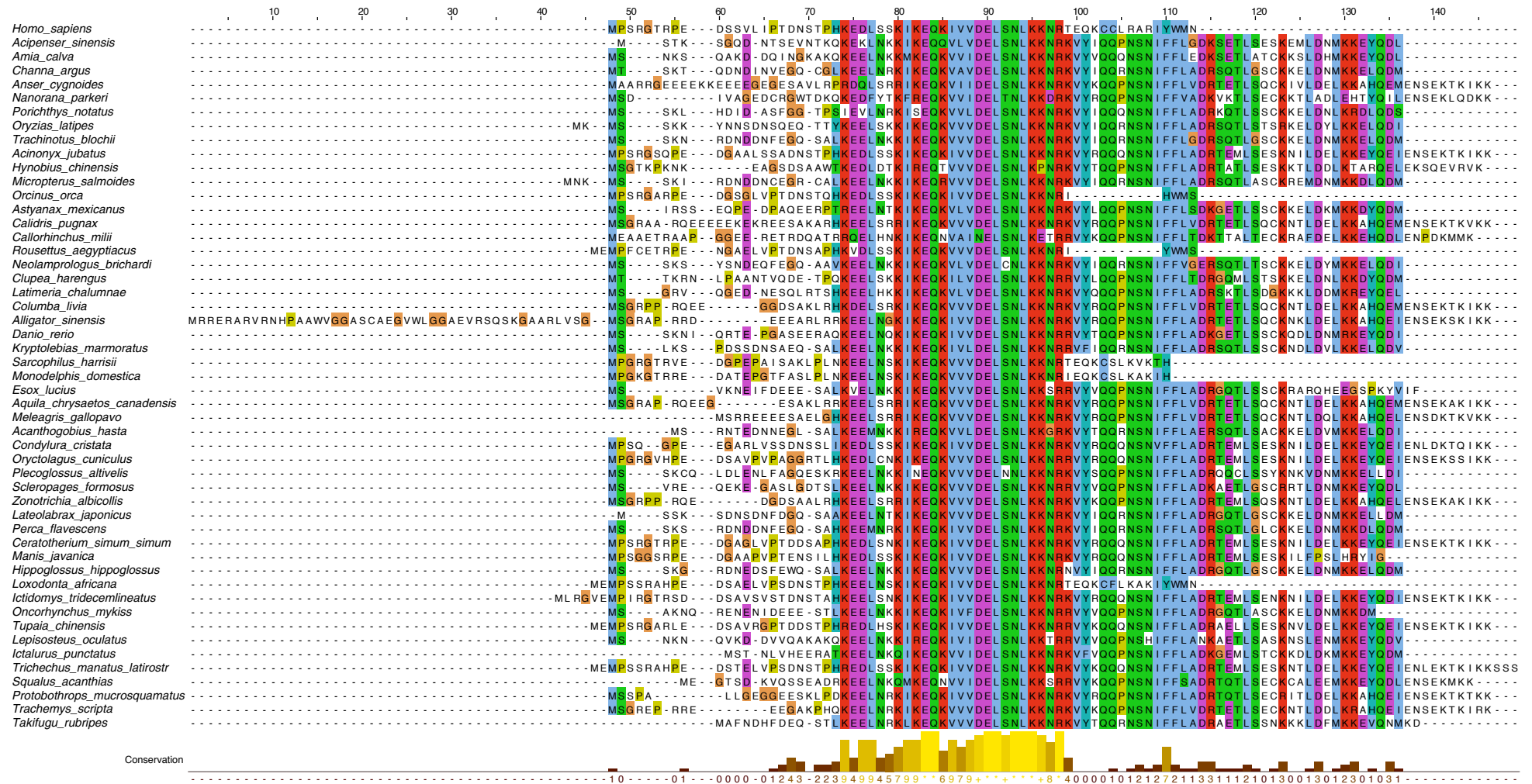
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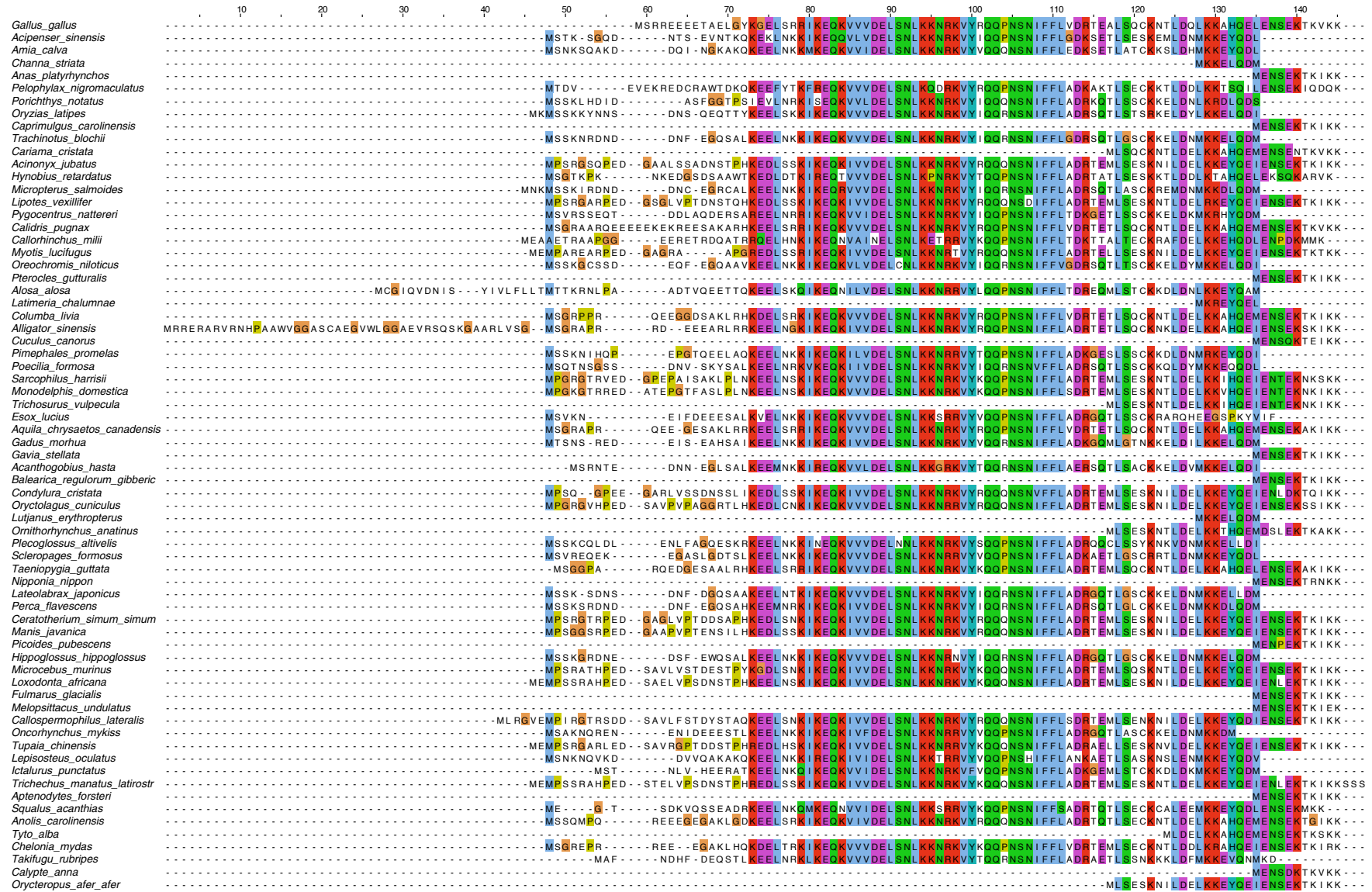
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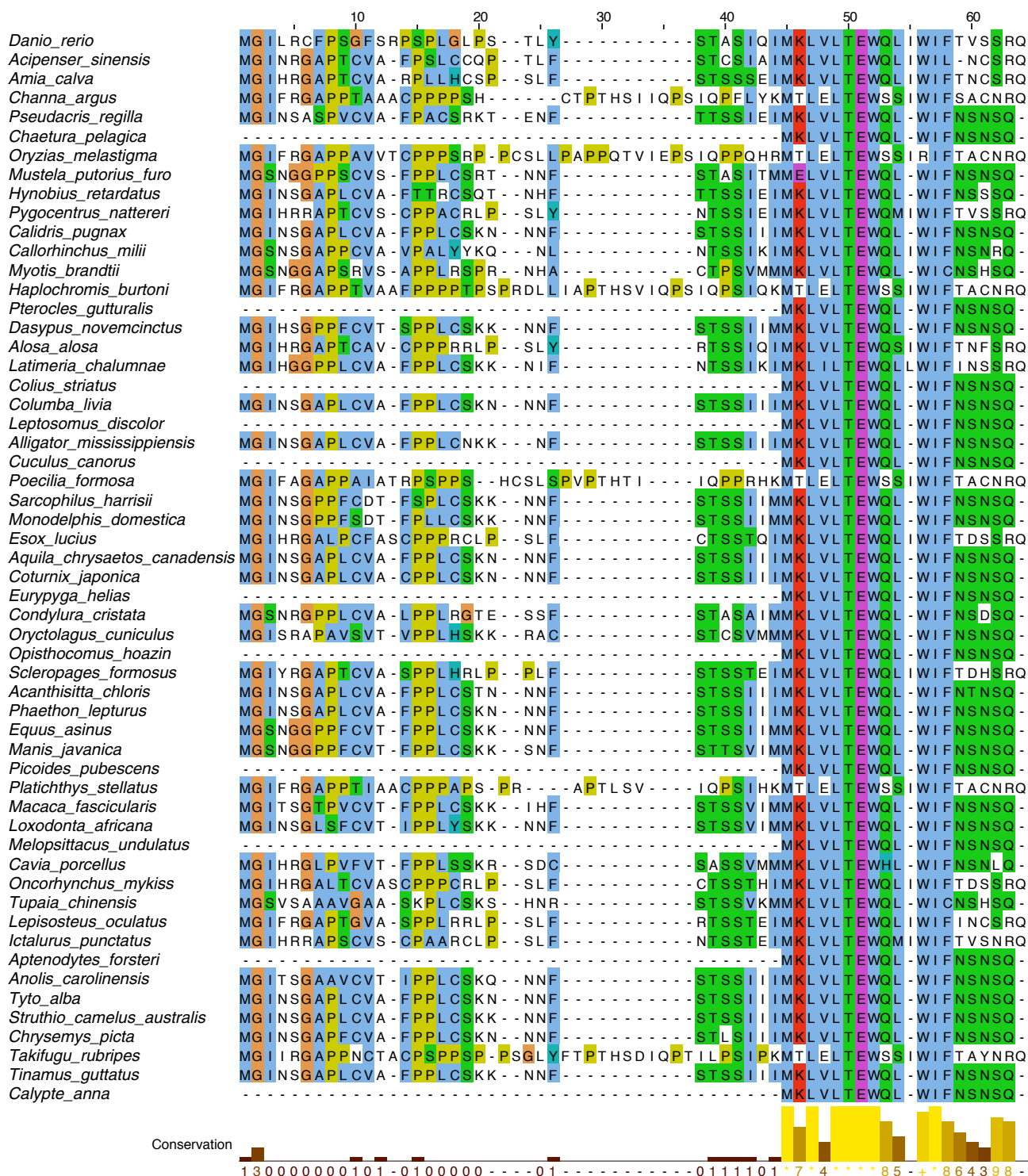


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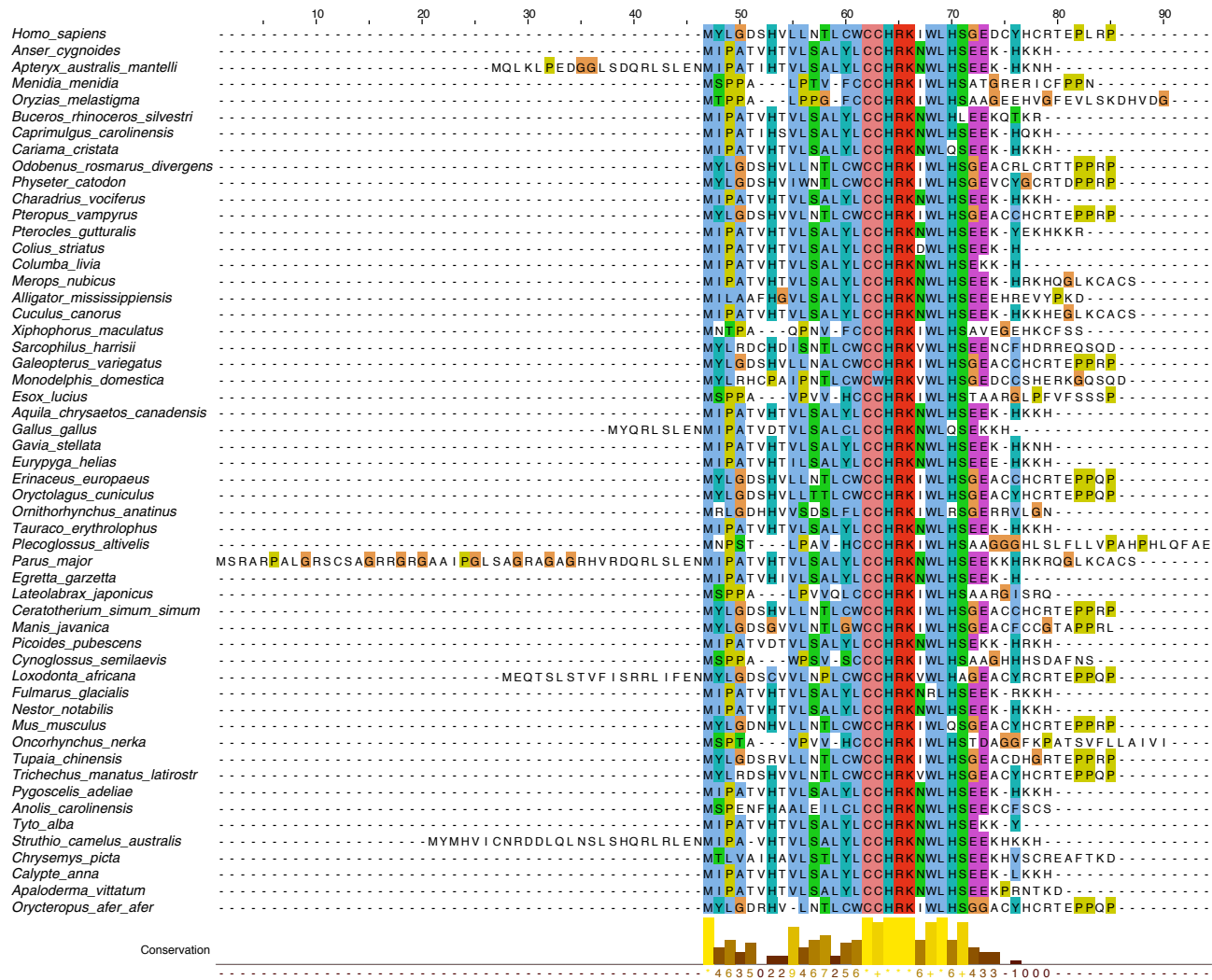


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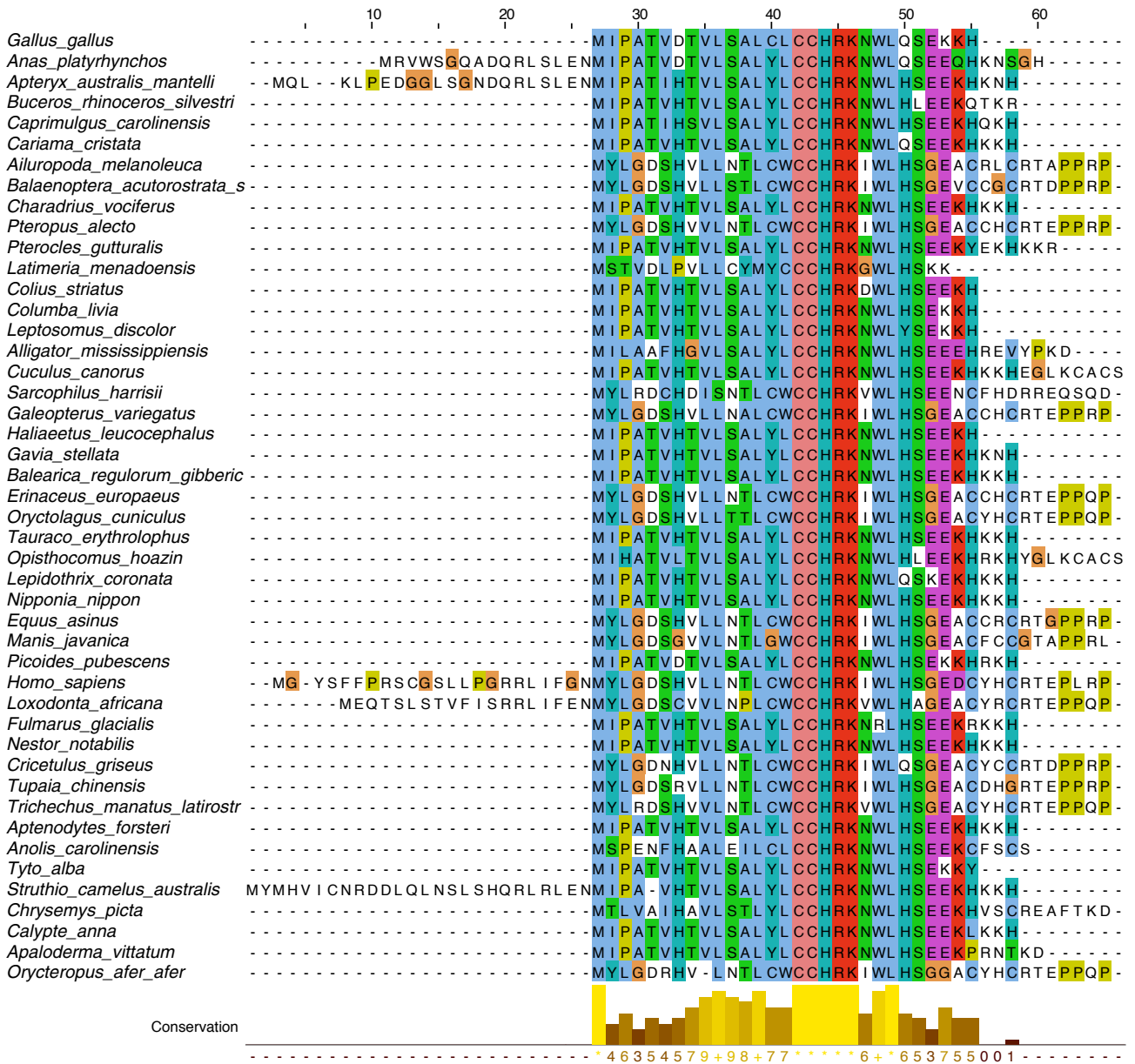
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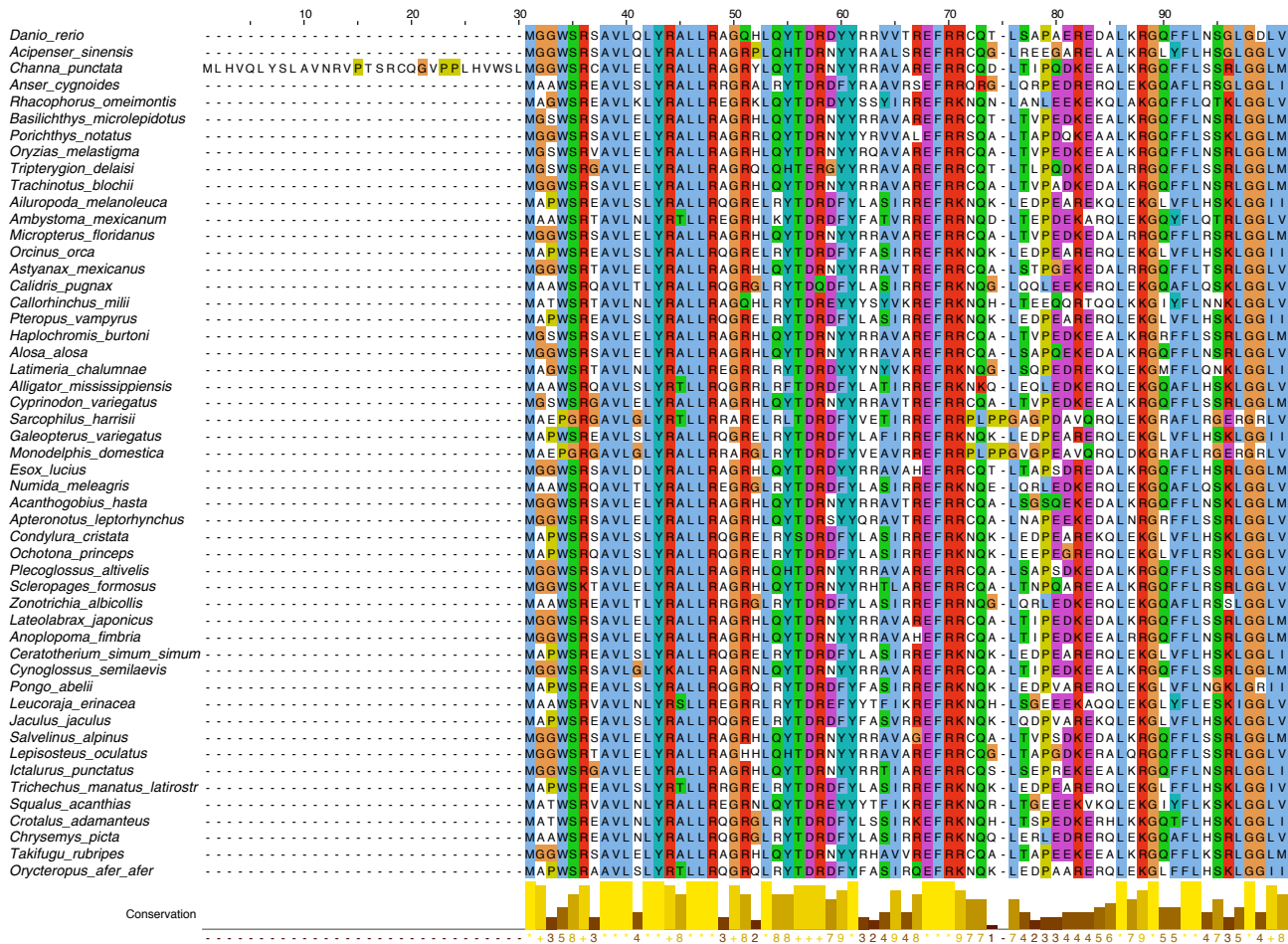
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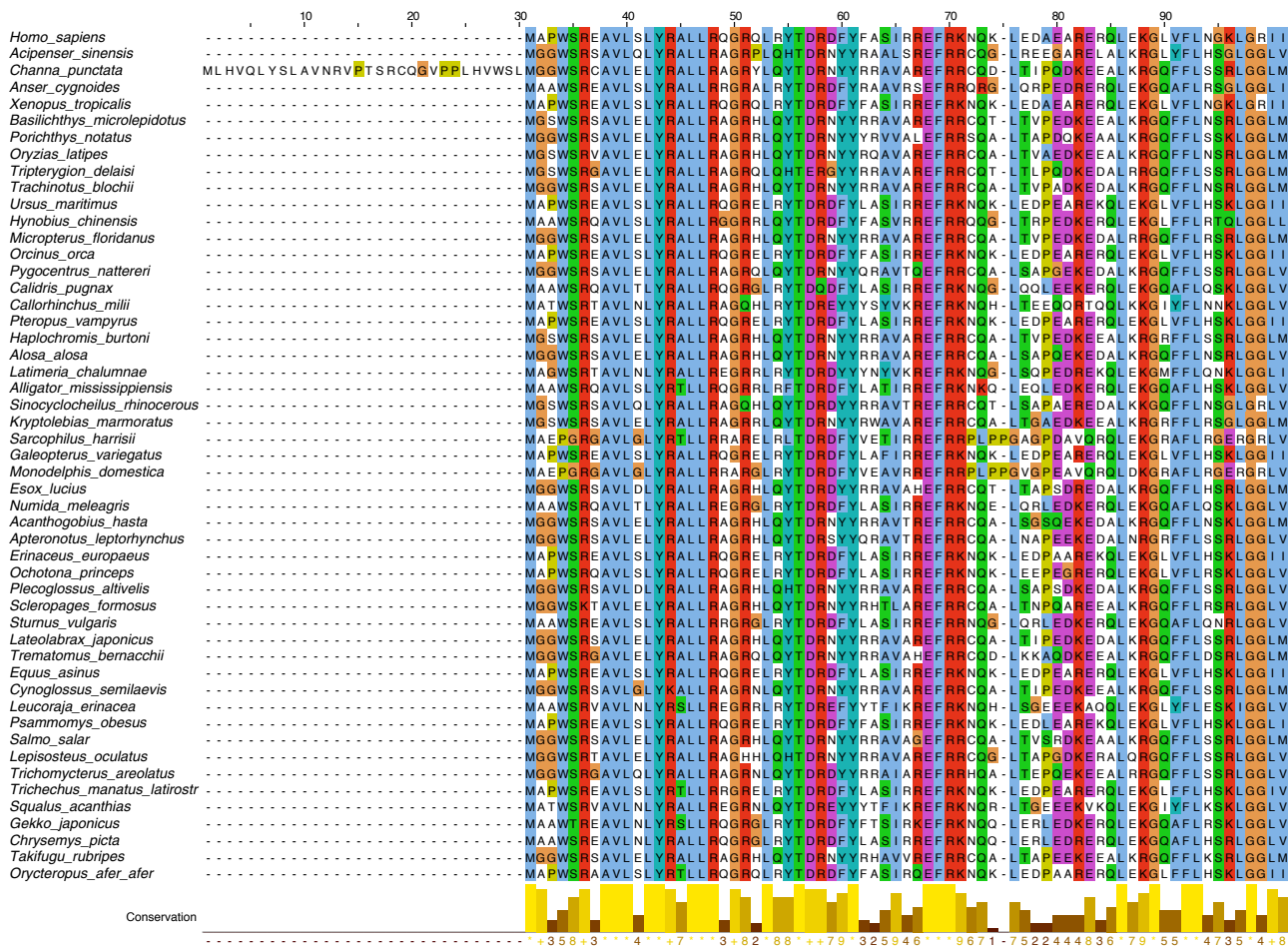


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ENSG00000100335 (MIEF1)



ENSG00000197147 (LRRC8B)



HG0035

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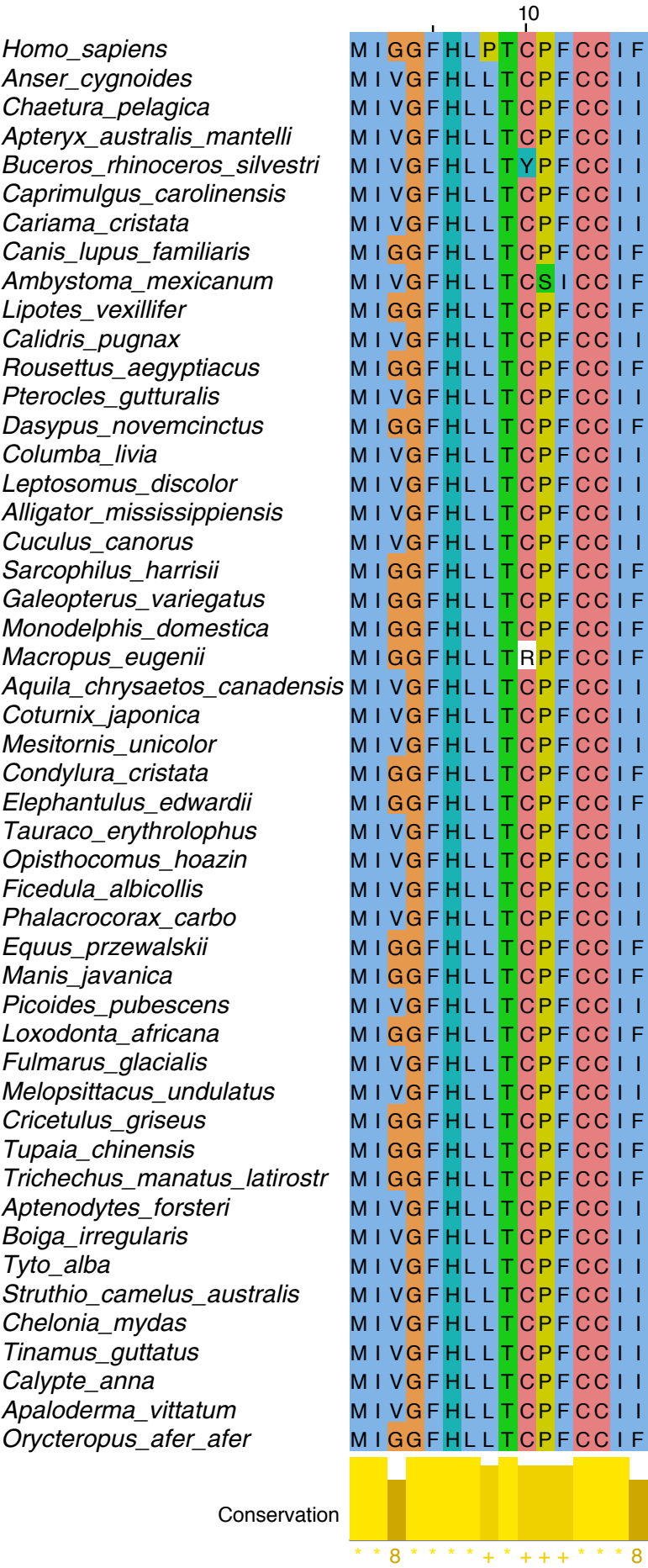
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<i>Leptobranchium_boringii</i>	-----	-----	MKSNAEMSRIKH	KRCRPPD
<i>Chaetura_pelagica</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Buceros_rhinoceros_silvestri</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Caprimulgus_carolinensis</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Cariama_cristata</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Felis_catus</i>	-----	MLAAHKCR	MKTNT	EMVCLRNFKRCRPPD
<i>Ambystoma_mexicanum</i>	-----	-----	-----	MQCTRKFKRCRPPD
<i>Physeter_catodon</i>	-----	-----	MKTIT	EMVCLRNFKRCRPPD
<i>Charadrius_vociferus</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
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<i>Pterocles_gutturalis</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Dasypus_novemcinctus</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
<i>Colius_striatus</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Columba_livia</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Merops_nubicus</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Alligator_mississippiensis</i>	-----	-----	MKANAKMACPRNF	KRCRPPD
<i>Cuculus_canorus</i>	-----	-----	MKANVKMACPRNF	KRCRPPD
<i>Sarcophilus_harrisii</i>	-----	-----	MKTKA	EMVCLRNFKRCRPPD
<i>Galeopterus_variegatus</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
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<i>Balearica_regulorum_gibberic</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Condylura_cristata</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
<i>Oryctolagus_cuniculus</i>	-----	-----	MKKNT	EMVCLRNFKRCRPPD
<i>Elephantulus_edwardii</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
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<i>Egretta_garzetta</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Ceratotherium_simum_simum</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
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<i>Picoides_pubescens</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Homo_sapiens</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
<i>Loxodonta_africana</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
<i>Melopsittacus_undulatus</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Nannospalax_galili</i>	-----	-----	MKTNS	EMVCLRNFKRCRPPD
<i>Tupaia_chinensis</i>	-----	-----	MKTNT	DMVCLRNFKRCRPPD
<i>Trichechus_manatus_latirostr</i>	-----	-----	MKTNT	EMVCLRNFKRCRPPD
<i>Aptenodytes_forsteri</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Anolis_carolinensis</i>	-----	-----	MKT	LVRMACPRNFKRCRPPD
<i>Tyto_alba</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Struthio_camelus_australis</i>	-----	-----	MKTNAKMACPRNF	KRCRPPD
<i>Chelonia_mydas</i>	MRVLFWKRE	PTELESHLKCLSR	MKI	NAKMACPRNFKRCRPPD
<i>Tinamus_guttatus</i>	-----	-----	MKTNAKMACPRNF	KRCRPPD
<i>Calypte_anna</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
<i>Apaloderma_vittatum</i>	-----	-----	MKTNVKMACPRNF	KRCRPPD
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Conservation

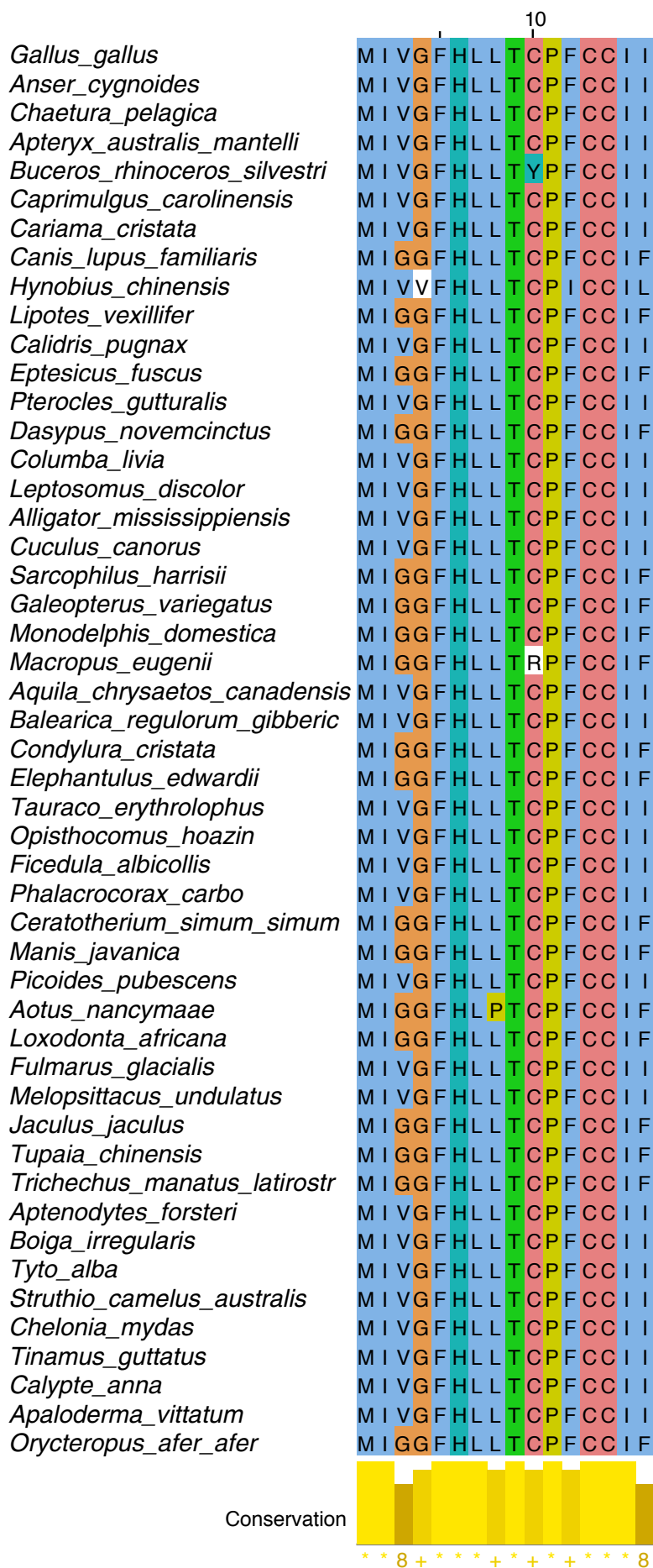


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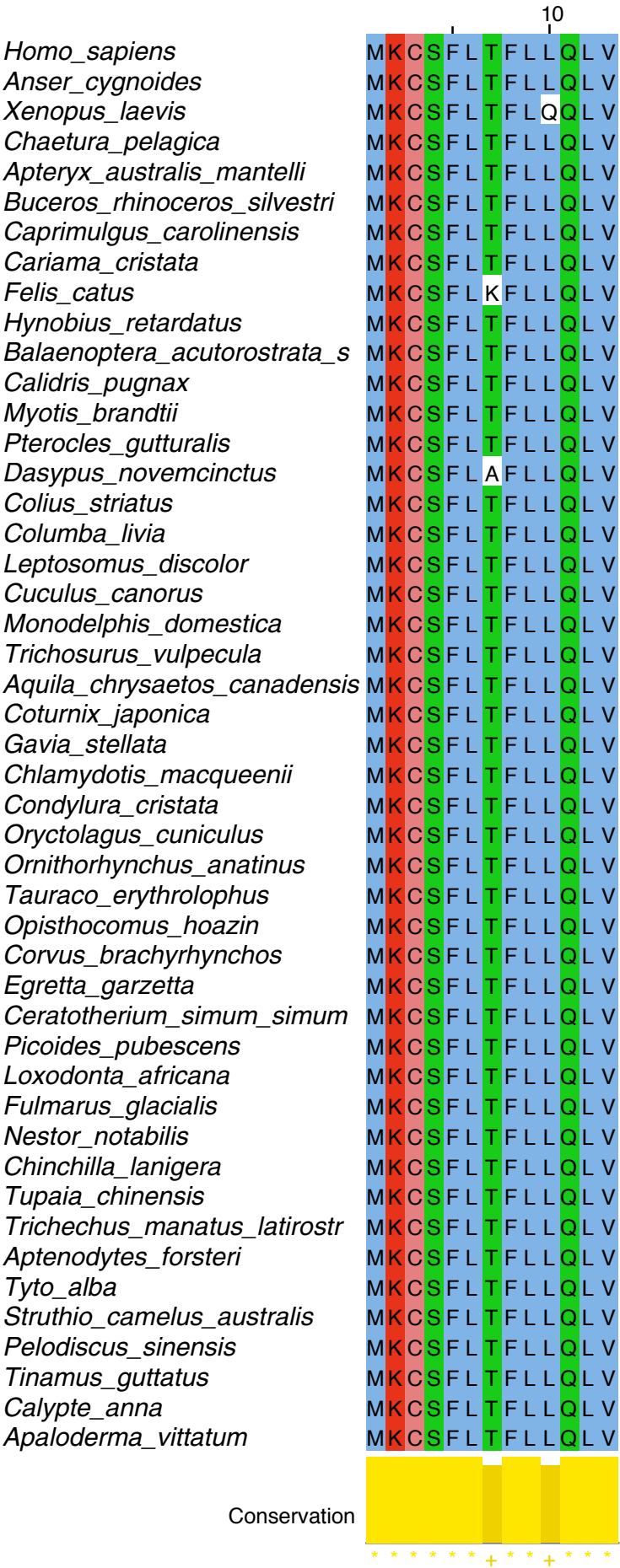


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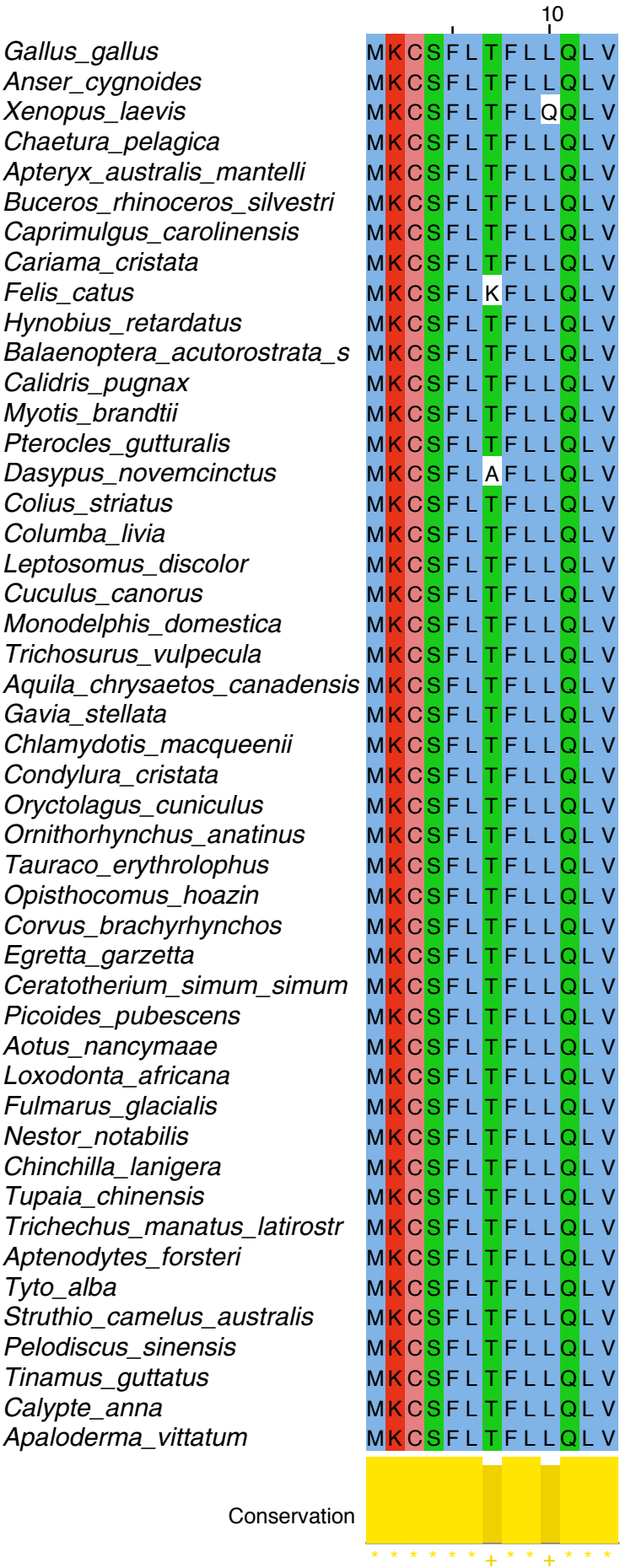
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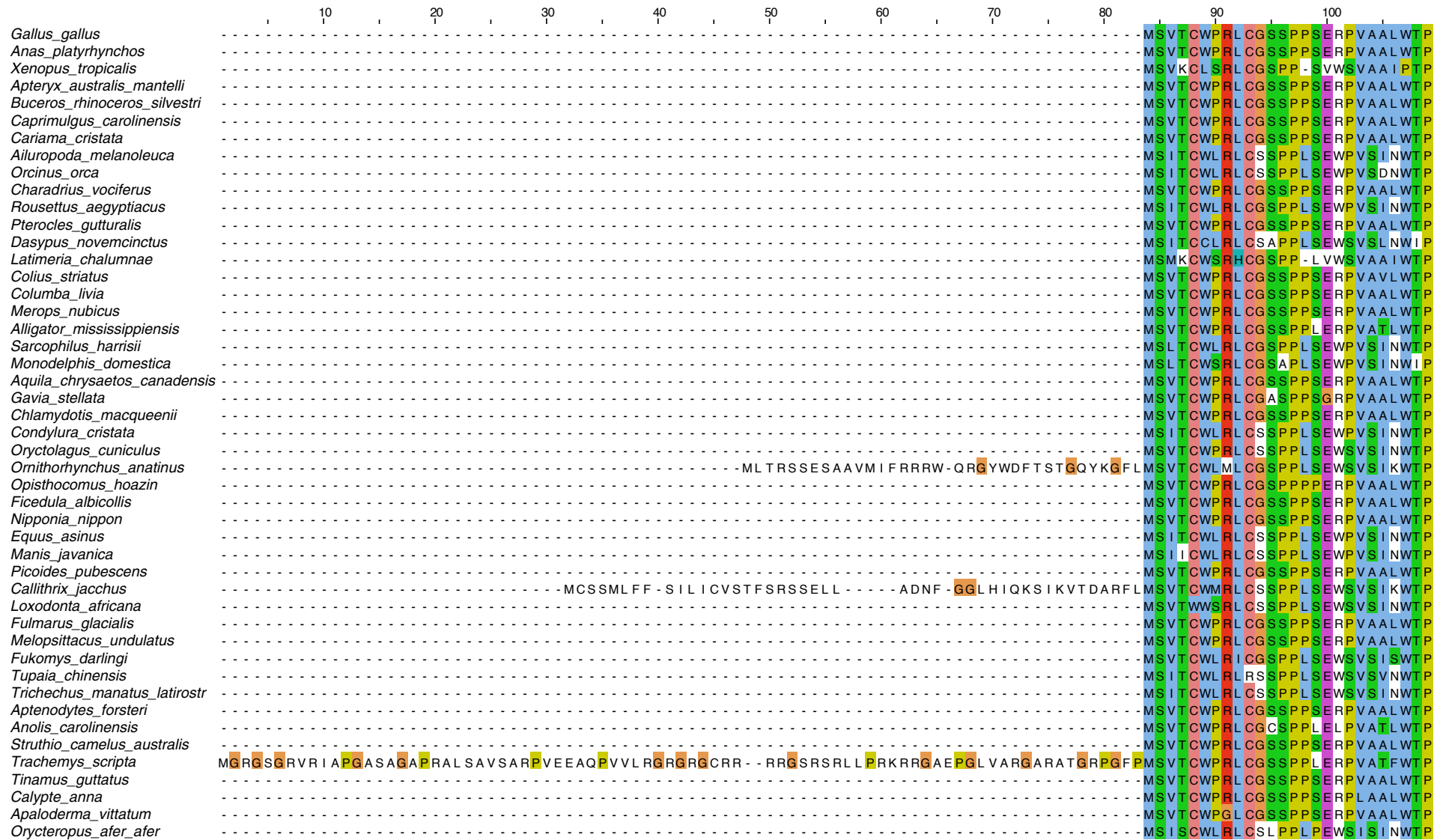
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HG0038

ENSGALG00000006571



Conservation

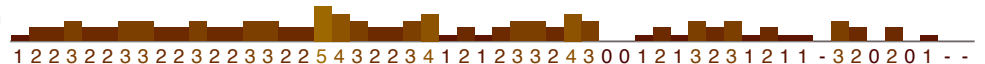
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HG0039.1

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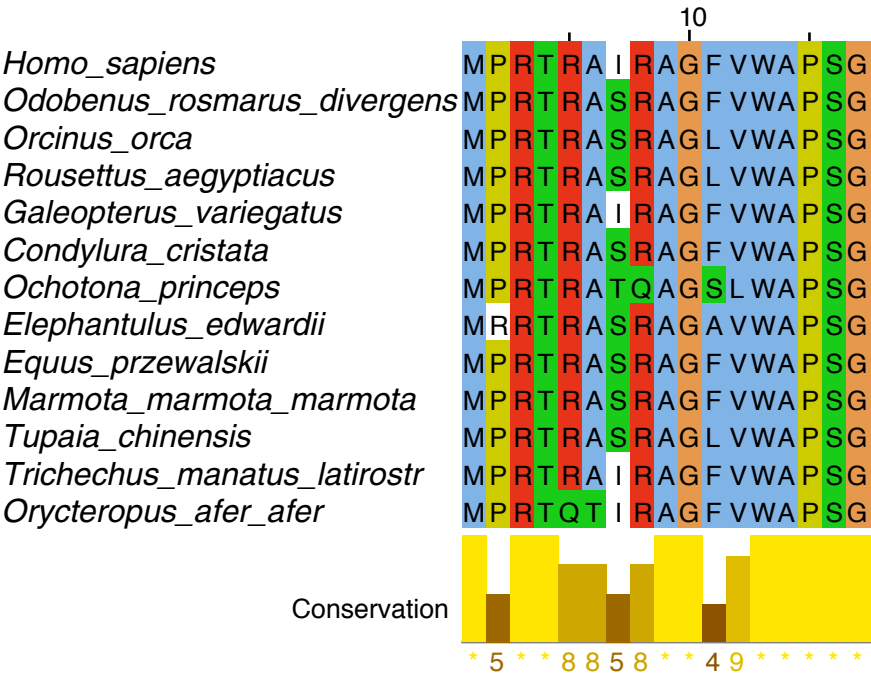
	10	20	30	40	50
<i>Homo_sapiens</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Acipenser_sinensis</i>	- -				
<i>Amia_calva</i>	M I I W I N Y R L L A V L S V I I H D S S L G K R P R S S V P K R G Q S L M E L G P L L H - A I S L H T - -				
<i>Anser_cygnoides</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Xenopus_tropicalis</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G A E F D G V G C T F S I A I C C A P K G				
<i>Chaetura_pelagica</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L S C - A I F L H T - -				
<i>Apteryx_australis_mantelli</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L L T - -				
<i>Buceros_rhinoceros_silvestri</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Ursus_maritimus</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Orcinus_orca</i>	M I I W I N Y R L L A G L S V I I H D S R L G K R P T A Y V P K R G Q S L M E L G G L F Y - A I C L H T - -				
<i>Calidris_pugnax</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Callorhinchus_milii</i>	M I I W I N Y R G F -				
<i>Eptesicus_fuscus</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Dasypus_novemcinctus</i>	M I I W I N Y R L L A G V S V I I H D S G P A G S P R A C V P K K G Q S L M E L G G L V L D A I C L R T - -				
<i>Latimeria_chalumnae</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P R A Y V P K K R G R V S W S W Y F Y M P F S T T P R G				
<i>Colius_striatus</i>	- -				
<i>Columba_livia</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Cuculus_canorus</i>	- -				
<i>Galeopterus_variegatus</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L Y T - -				
<i>Falco_cherrug</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Coturnix_japonica</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Gavia_stellata</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Mesitornis_unicolor</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Apteranotus_leptorhynchus</i>	M I T W I V S K L L A T L S V I I R D S G L G K G A R N M S N Q R -				
<i>Condylura_cristata</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Oryctolagus_cuniculus</i>	M I I W I N Y R L L A G L S V I I H D S G L G K E P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Elephantulus_edwardii</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K R G Q S L M E L G G L F - A V C L R T - -				
<i>Opisthocomus_hoazin</i>	- -				
<i>Geospiza_fortis</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Nipponia_nippon</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Ceratotherium_simum_simum</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Manis_javanica</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Picoides_pubescens</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Loxodonta_africana</i>	M T I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L R T - -				
<i>Melopsittacus_undulatus</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L Y T - -				
<i>Callospermophilus_lateralis</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L H T - -				
<i>Salmo_salar</i>	- -				
<i>Tupaia_chinensis</i>	M I I W I N Y R L L A G L S V I I H D S G L G K S P T A Y V P K K G Q S L M E L G G L F Y - A I C L L T - -				
<i>Lepisosteus_oculatus</i>	M I I W I N Y R L L V V L S V I I H D S S L G K R P R S Y V P K K G Q S L M E L V P L L H - A I S L H T - -				
<i>Trichechus_manatus_latirostr</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L R T - -				
<i>Pygoscelis_adeliae</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Squalus_acanthias</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Q R A K K R G E E K I - - - - - - - - - - - - - - - - - - -				
<i>Struthio_camelus_australis</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Trachemys_scripta</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R R T A Y V P K K G Q S L M E L G V L L Y - A I F L H T - -				
<i>Tinamus_guttatus</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Calypte_anna</i>	M I I W I N Y R L L A V L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G V L L C - A I F L H T - -				
<i>Orycteropus_afer_afer</i>	M I I W I N Y R L L A G L S V I I H D S G L G K R P T A Y V P K K G Q S L M E L G G L F Y - A I C L R T - -				

Conservation



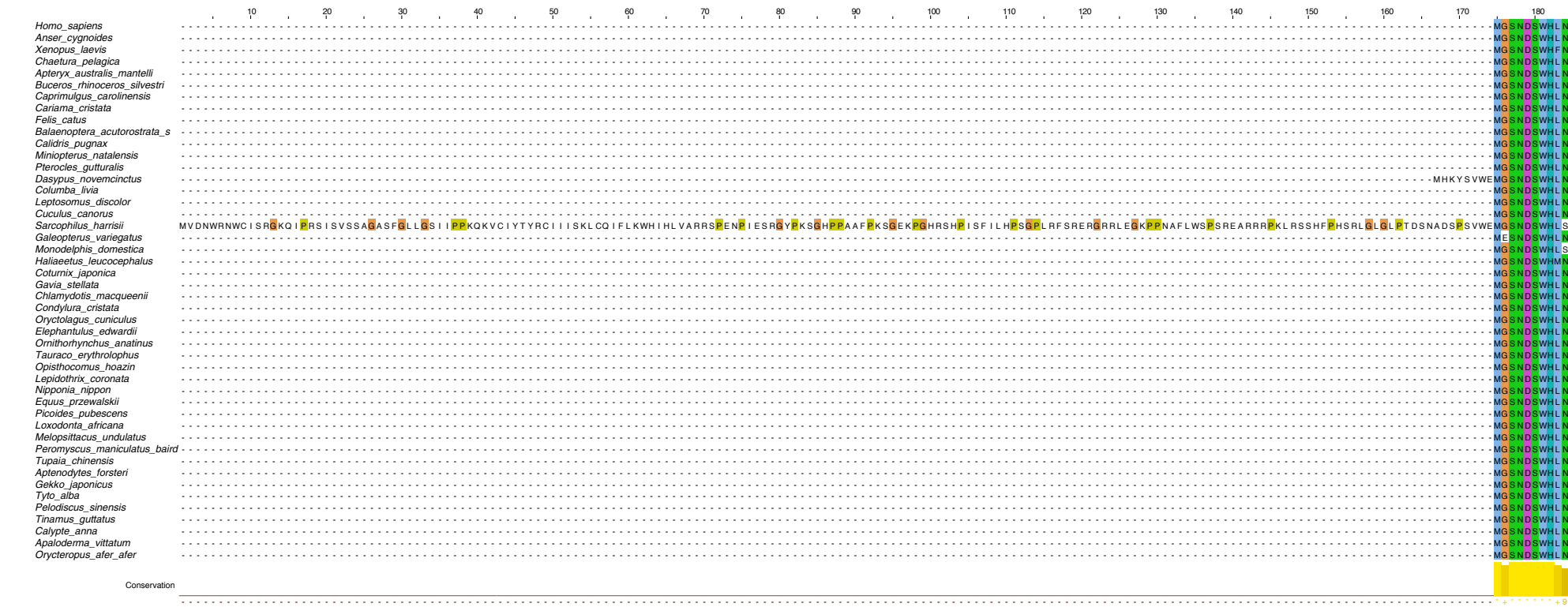
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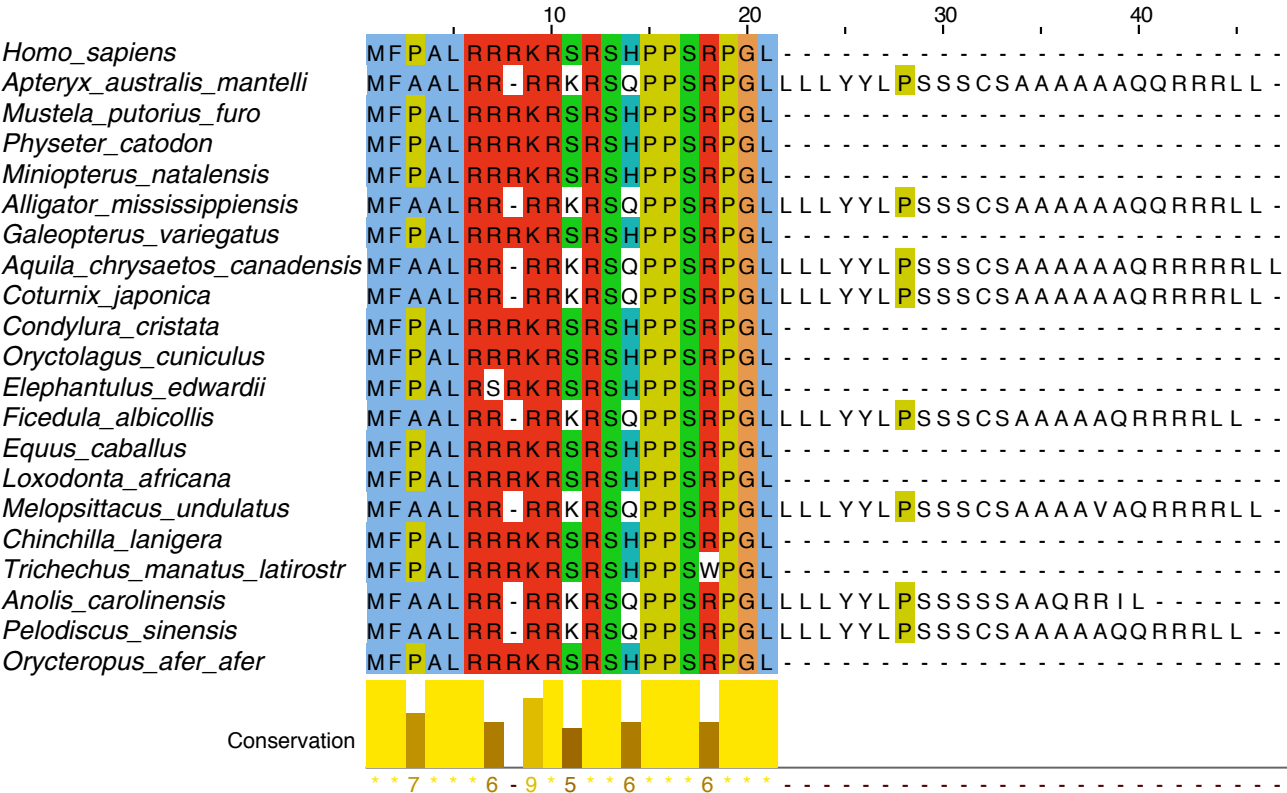
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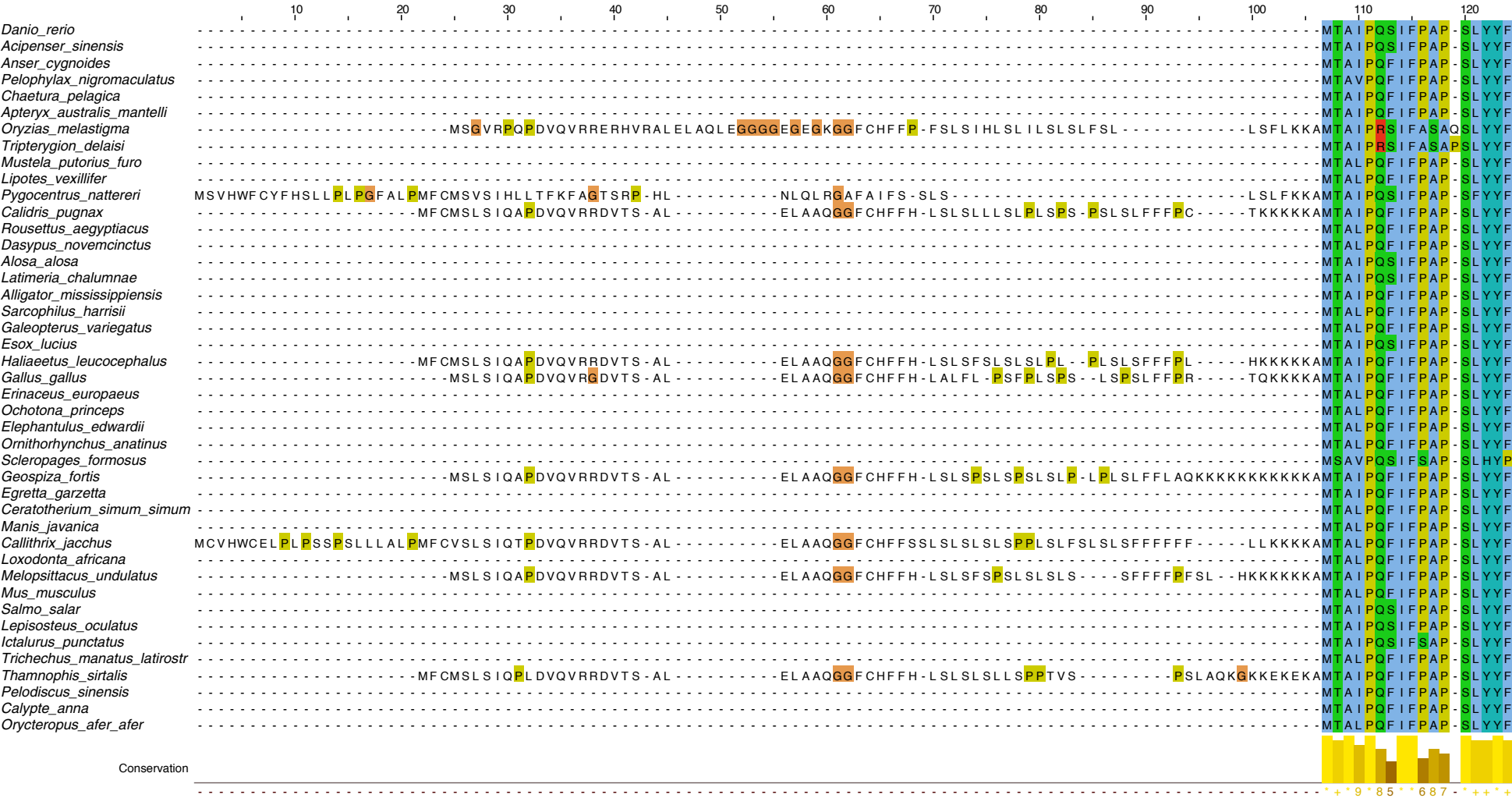
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HG0041

ENSDARG00000061352 (bcl11aa)



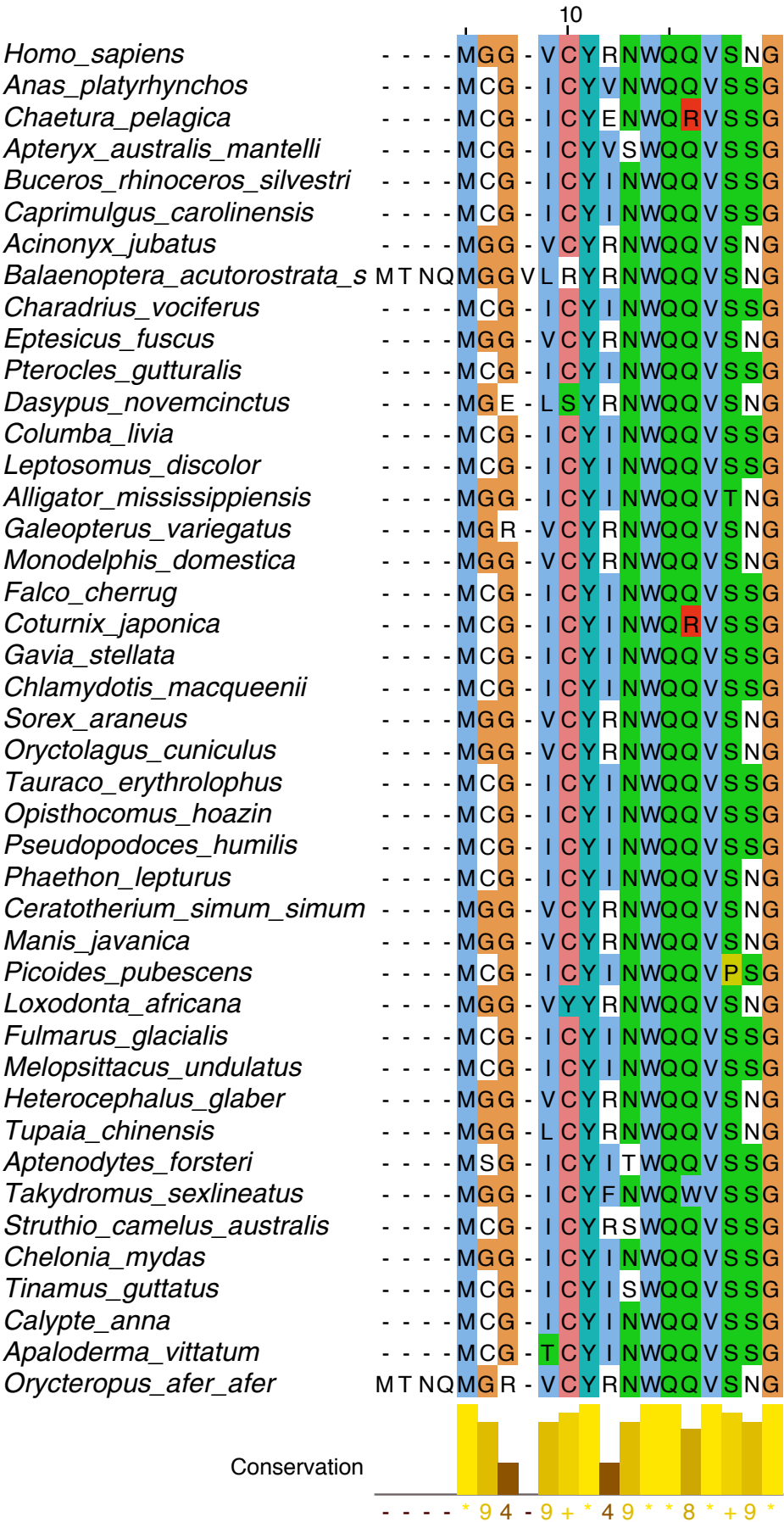
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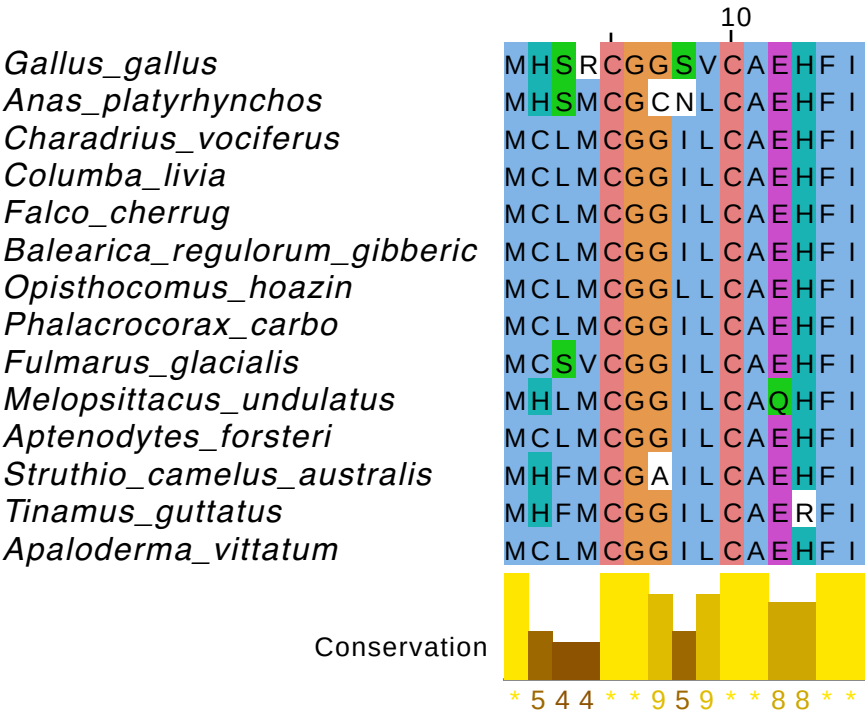


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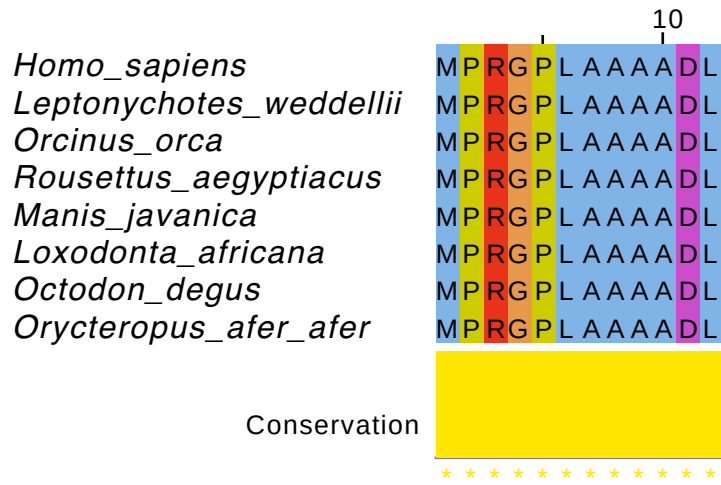






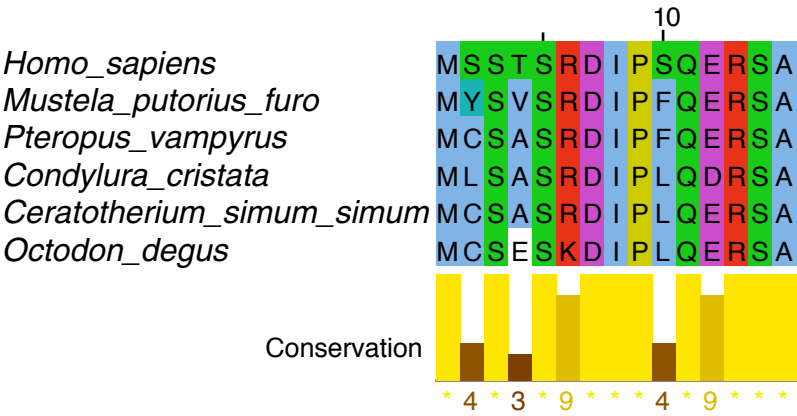
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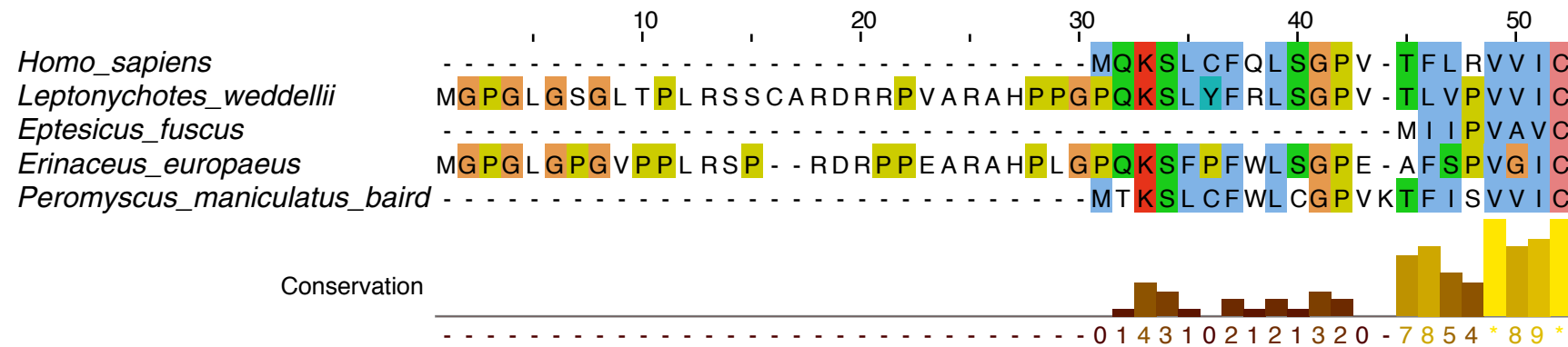
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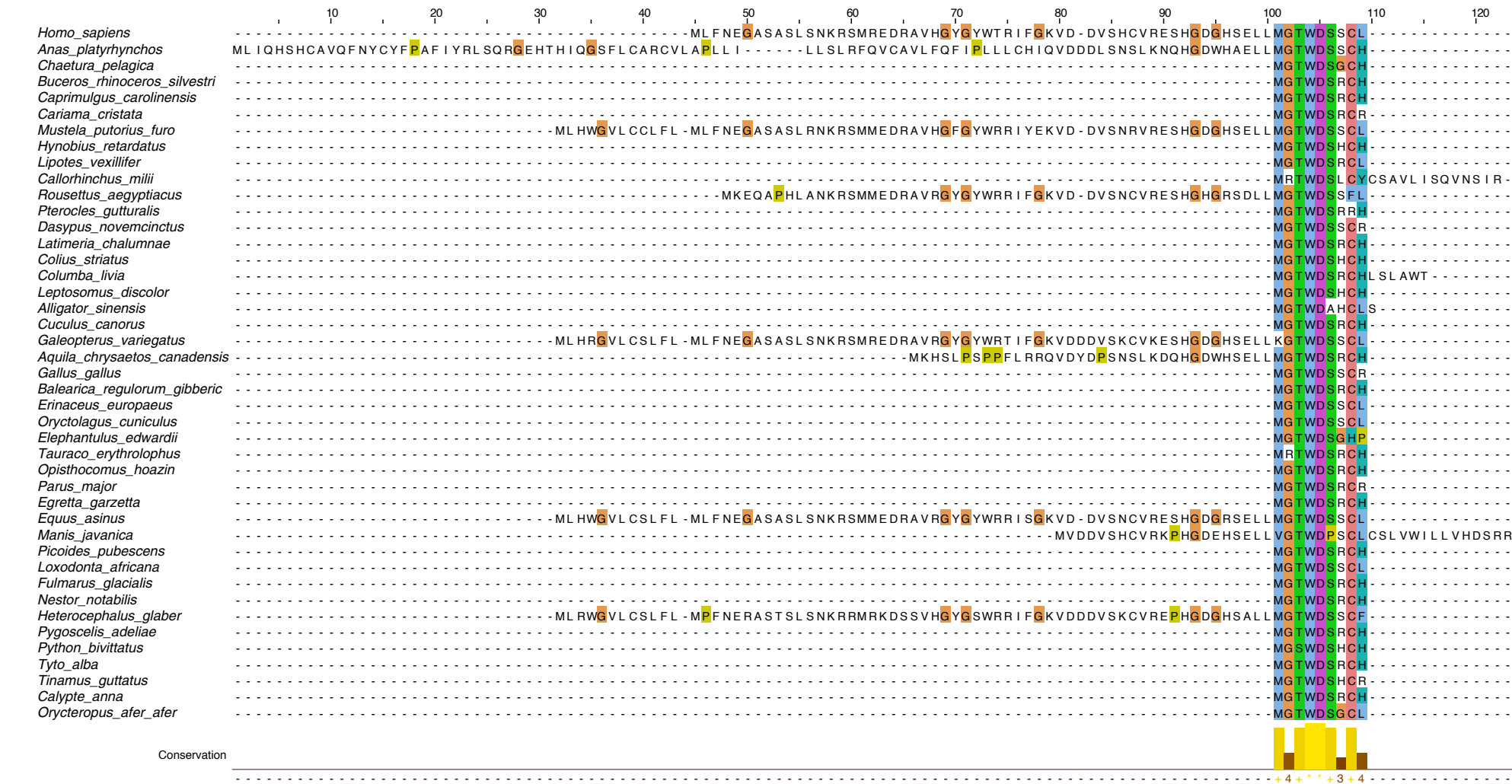
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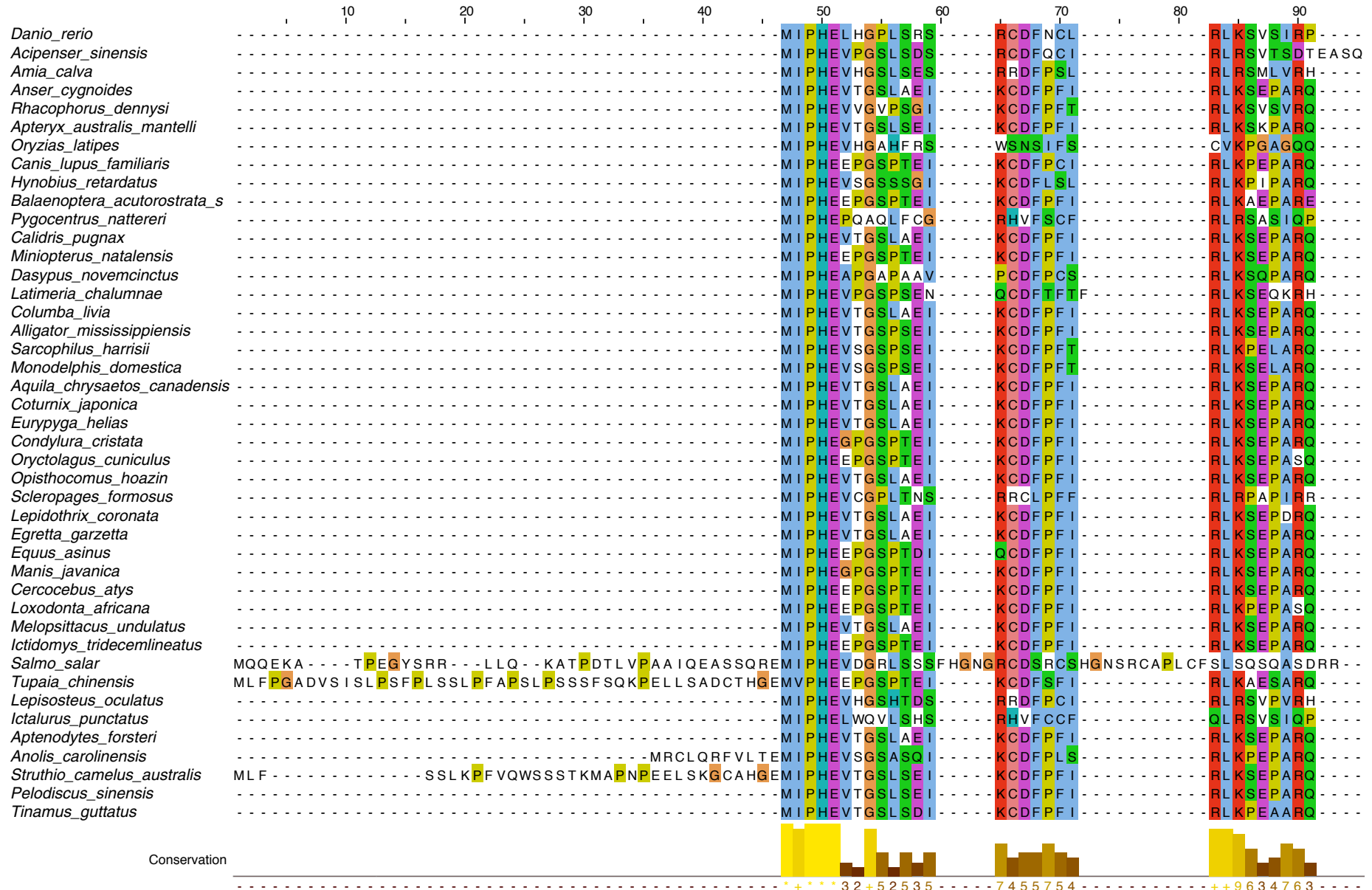
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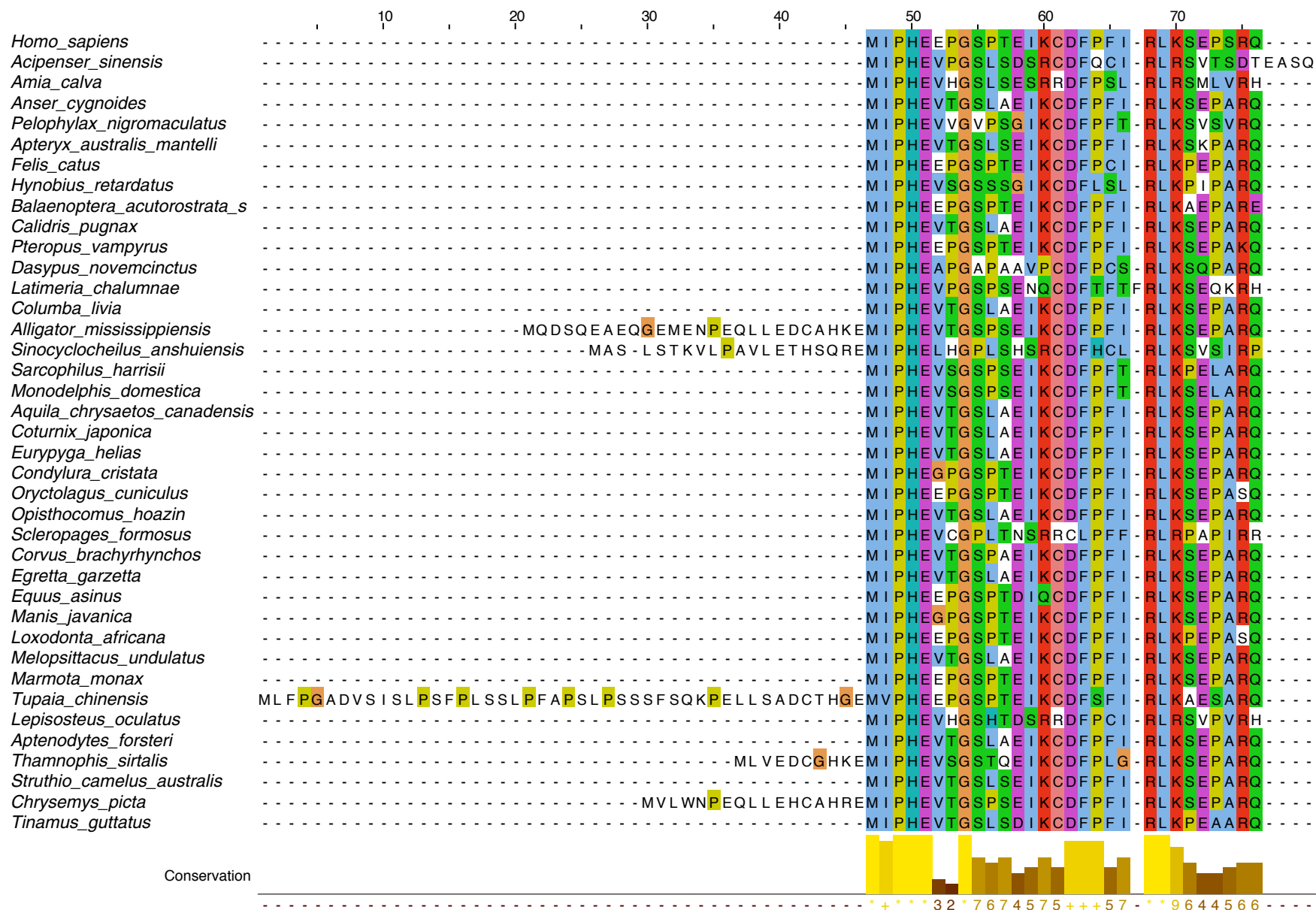


HG0044

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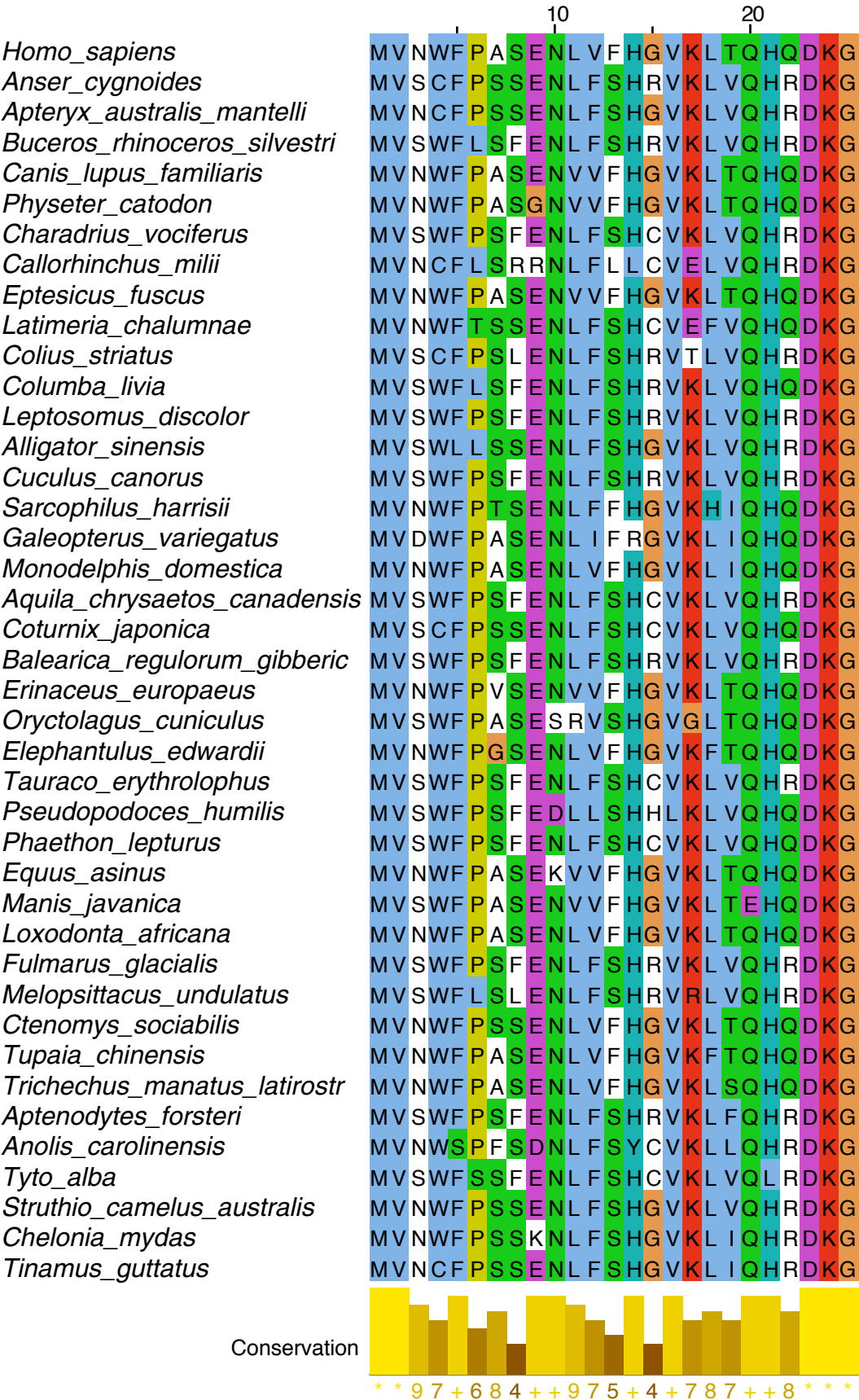


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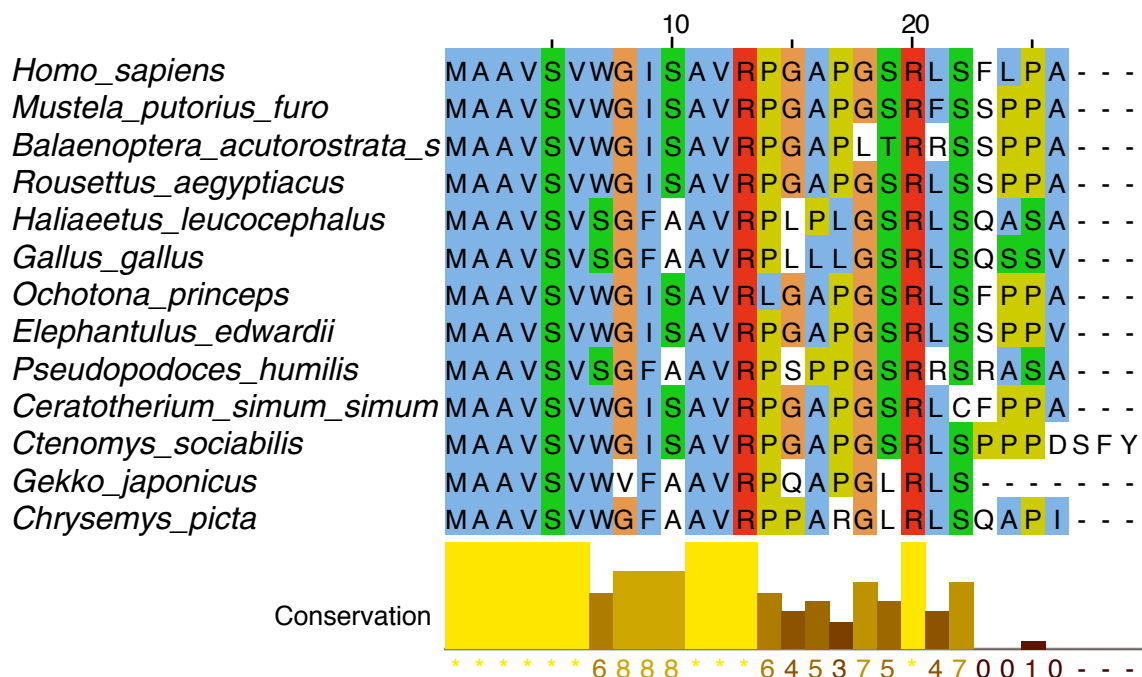
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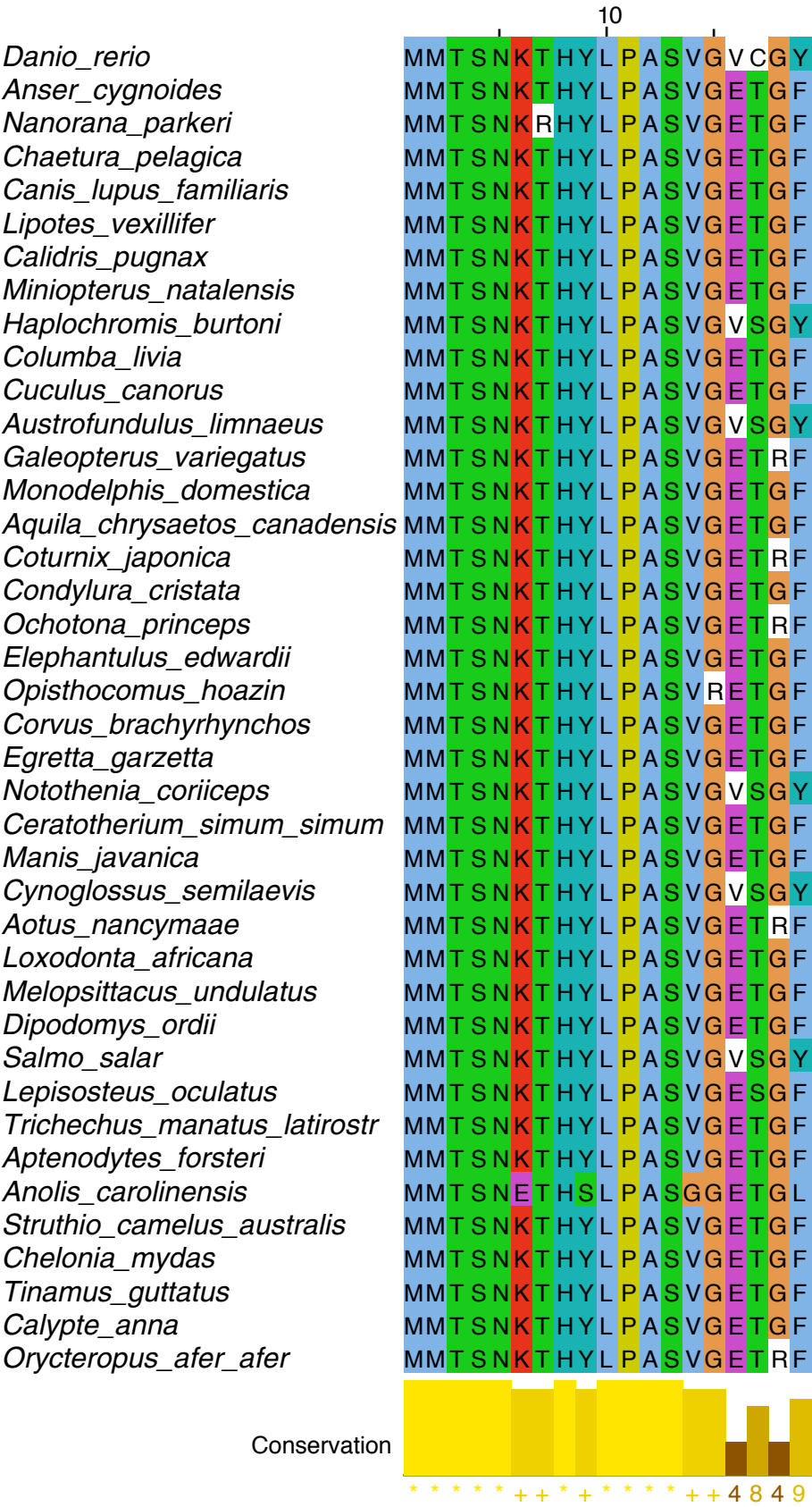
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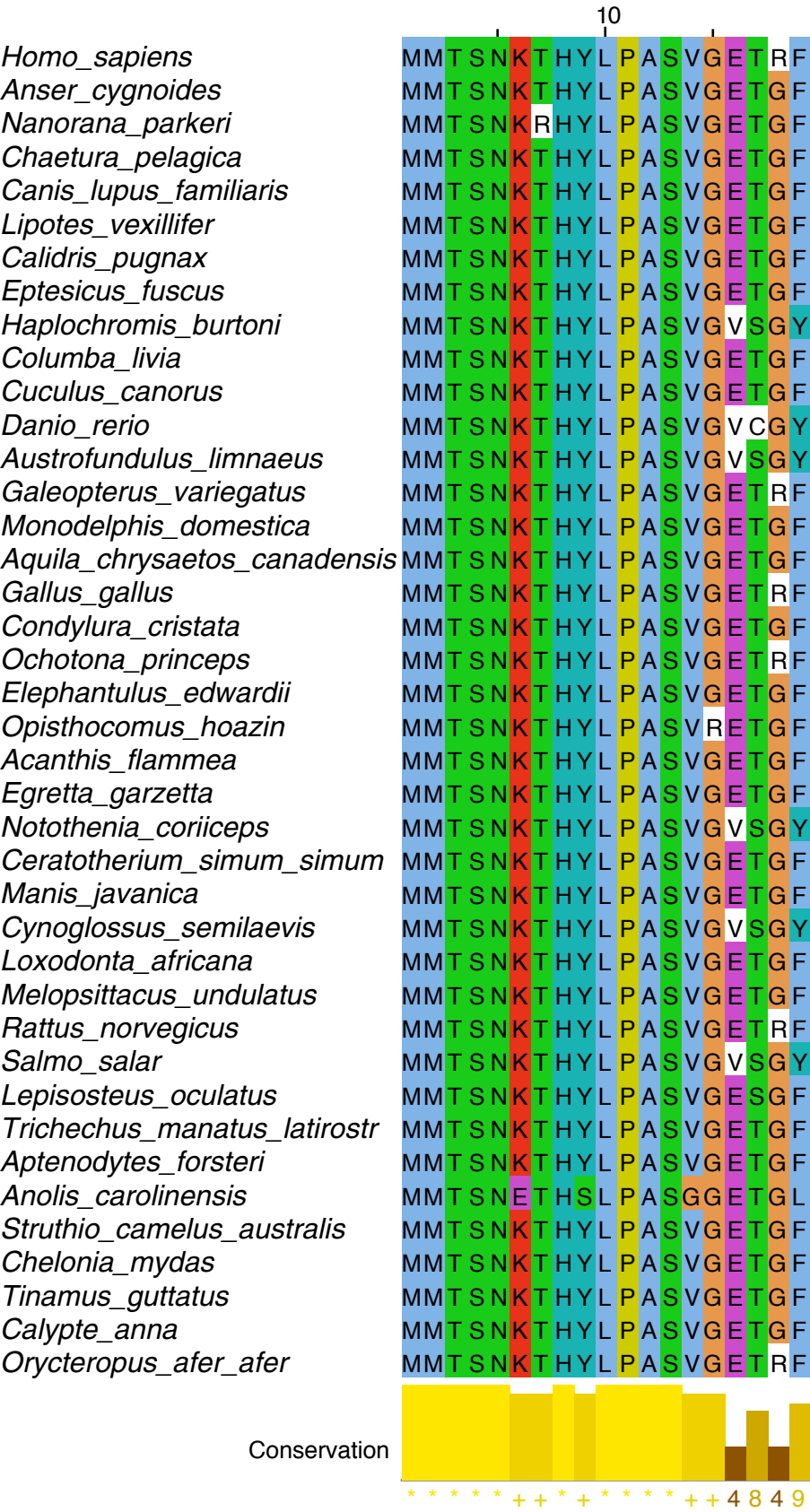
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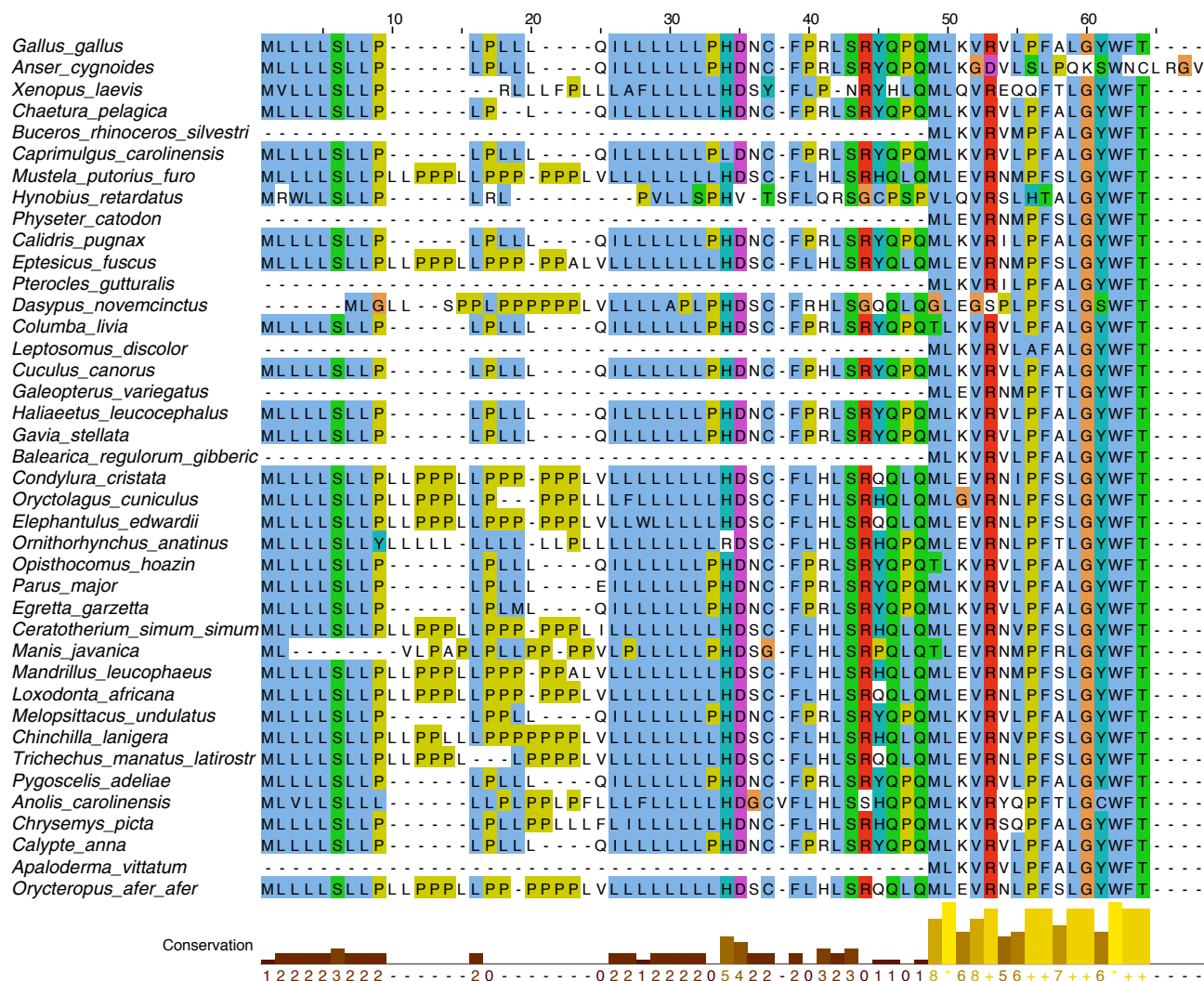


HG0046

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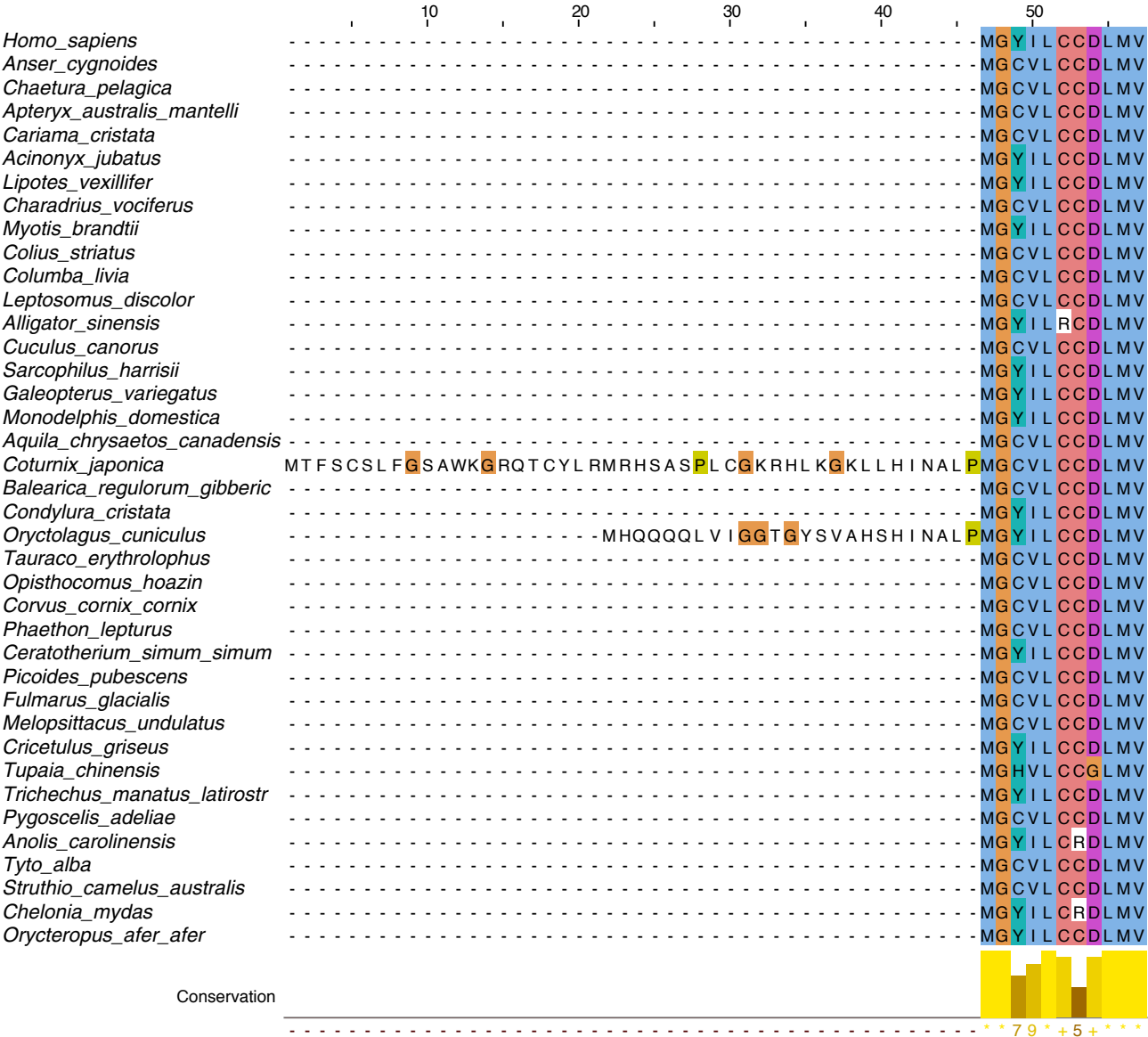


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HG0048

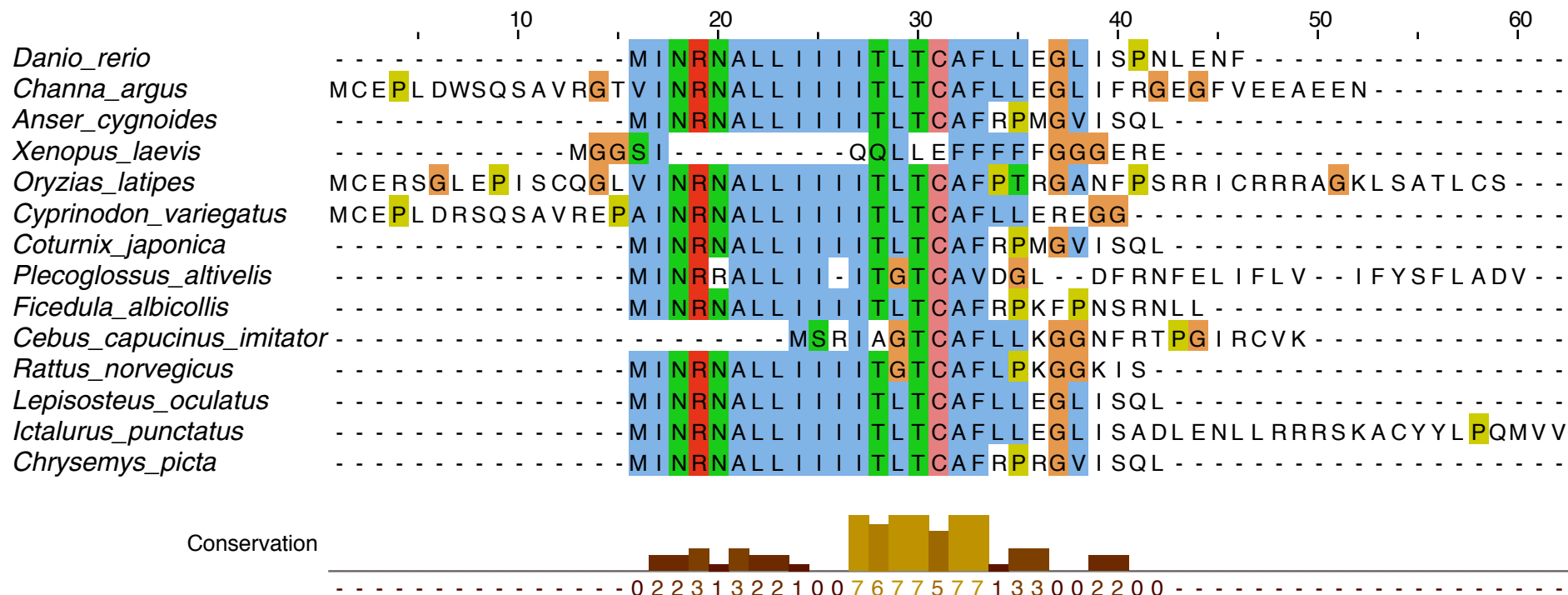
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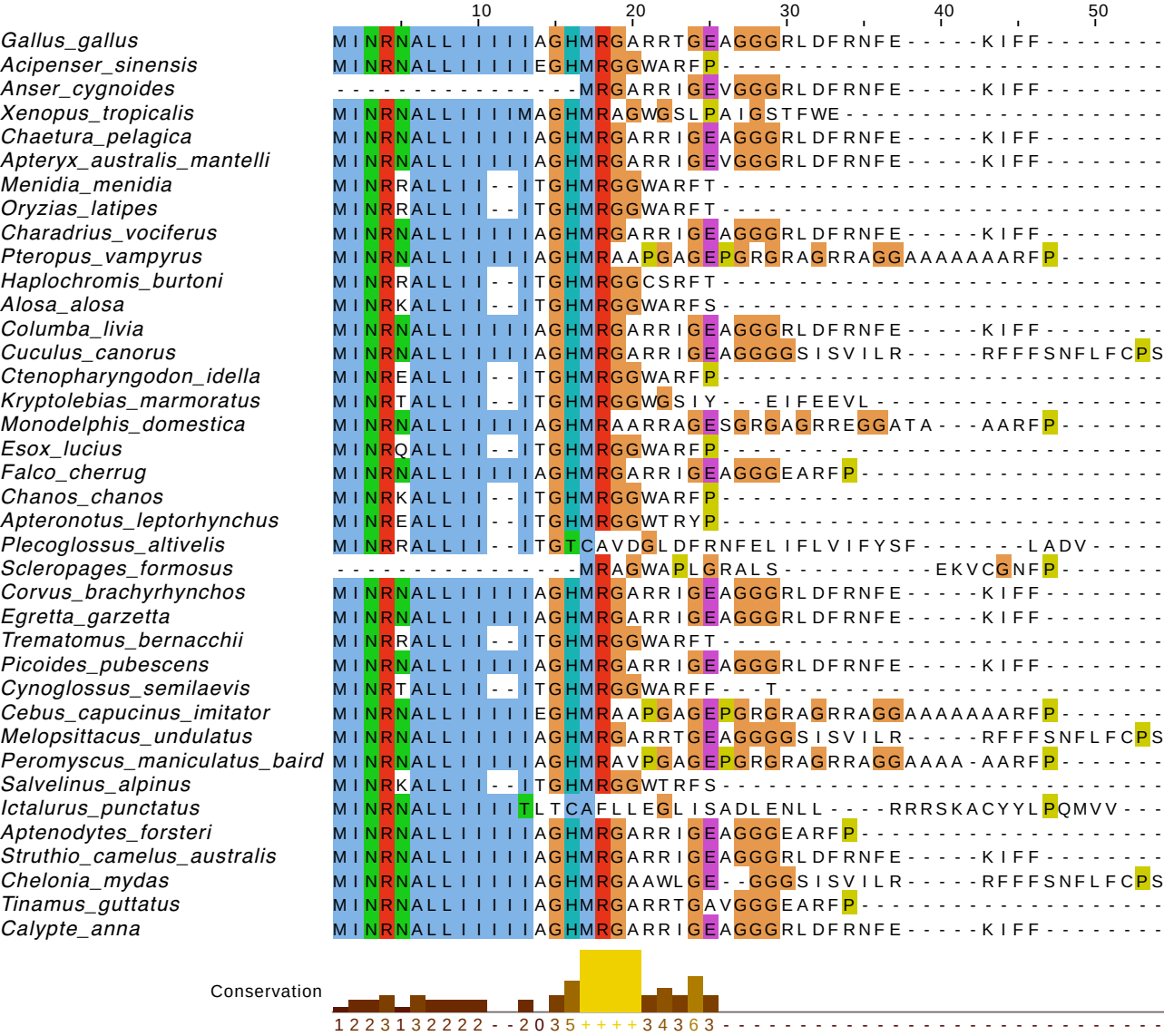


ENSDARG00000044485 (sall4)



HG0049

ENSGALG00000039238



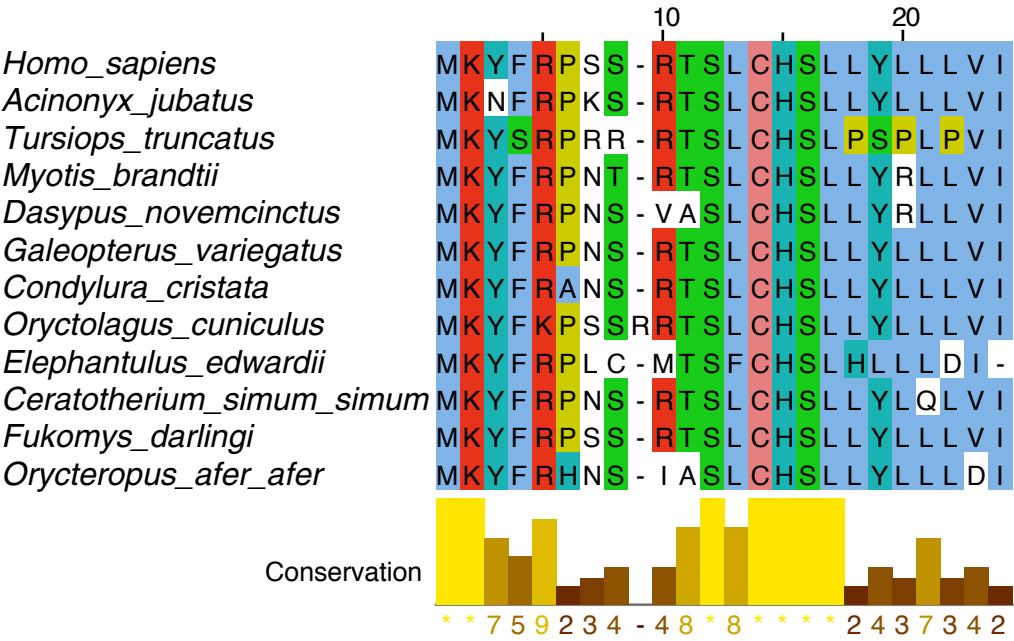
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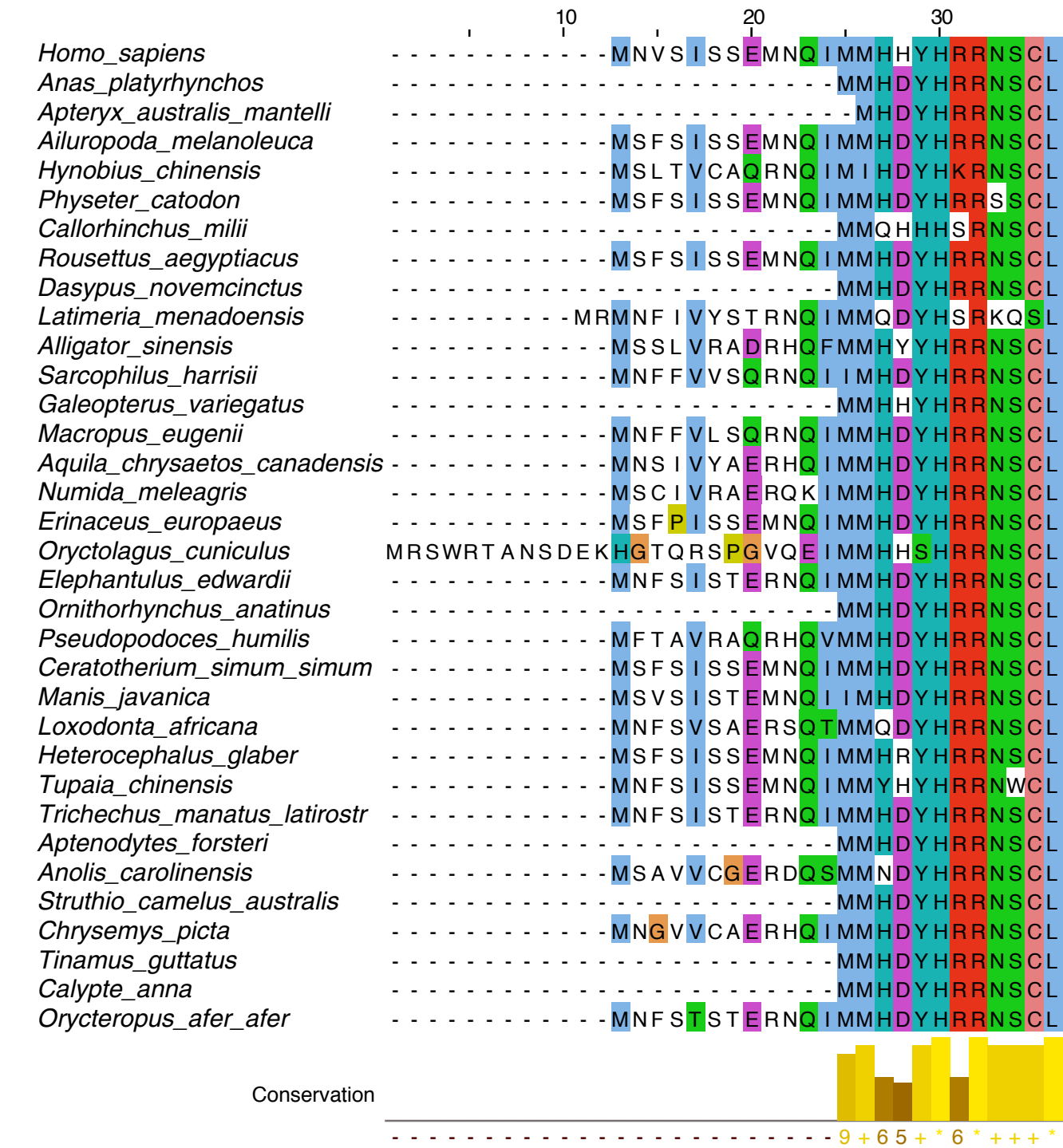
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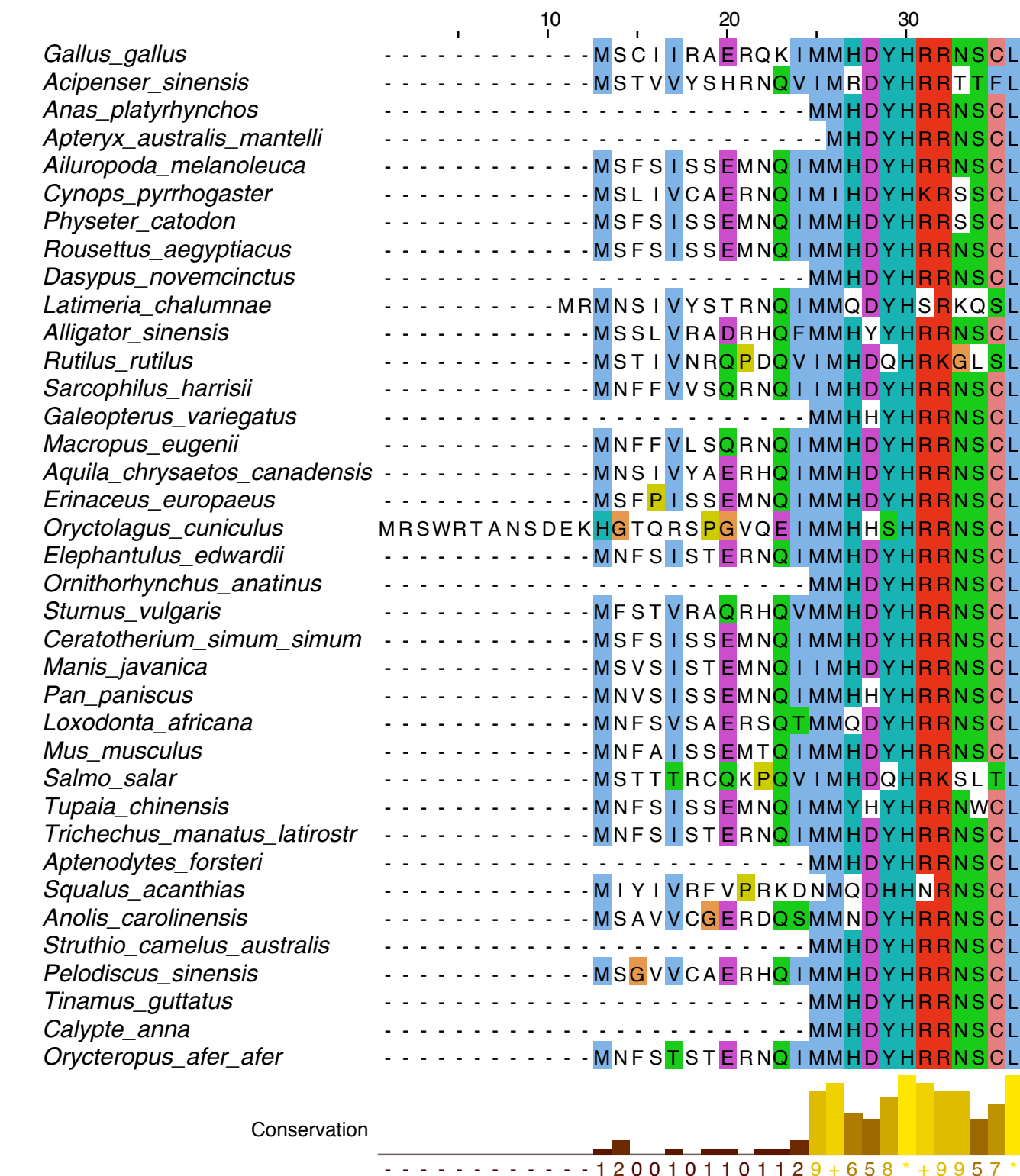


HG0051

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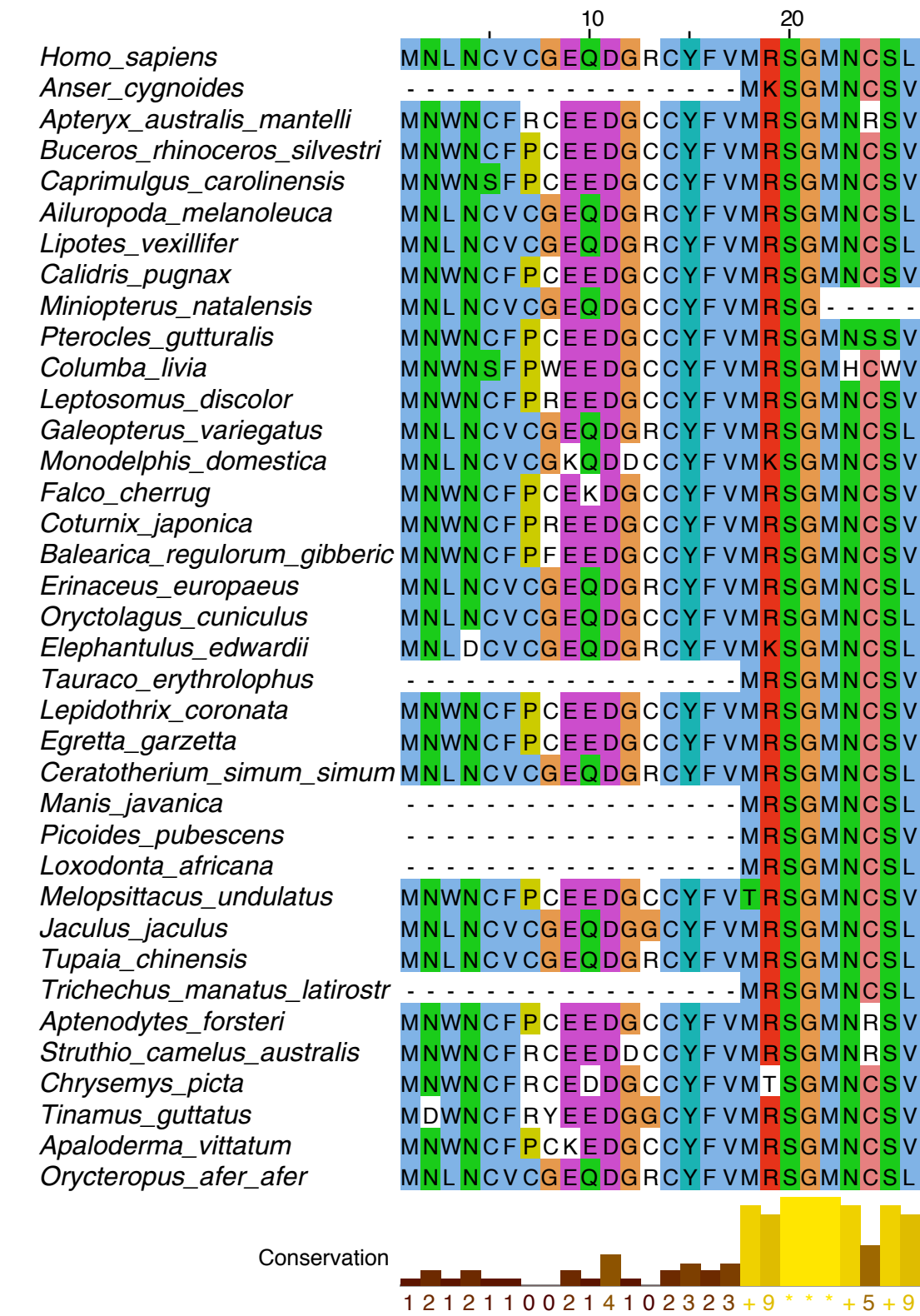


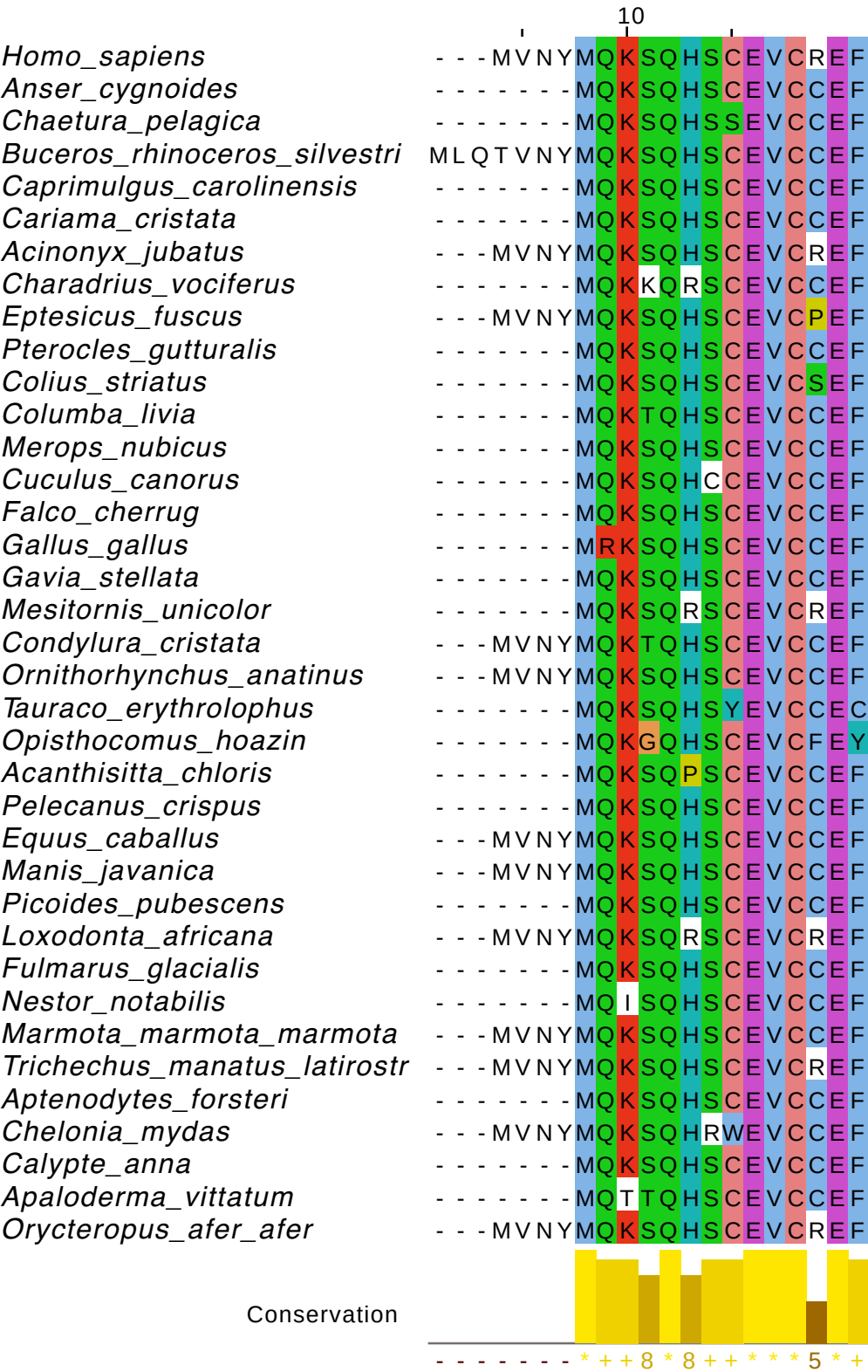
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HG0052

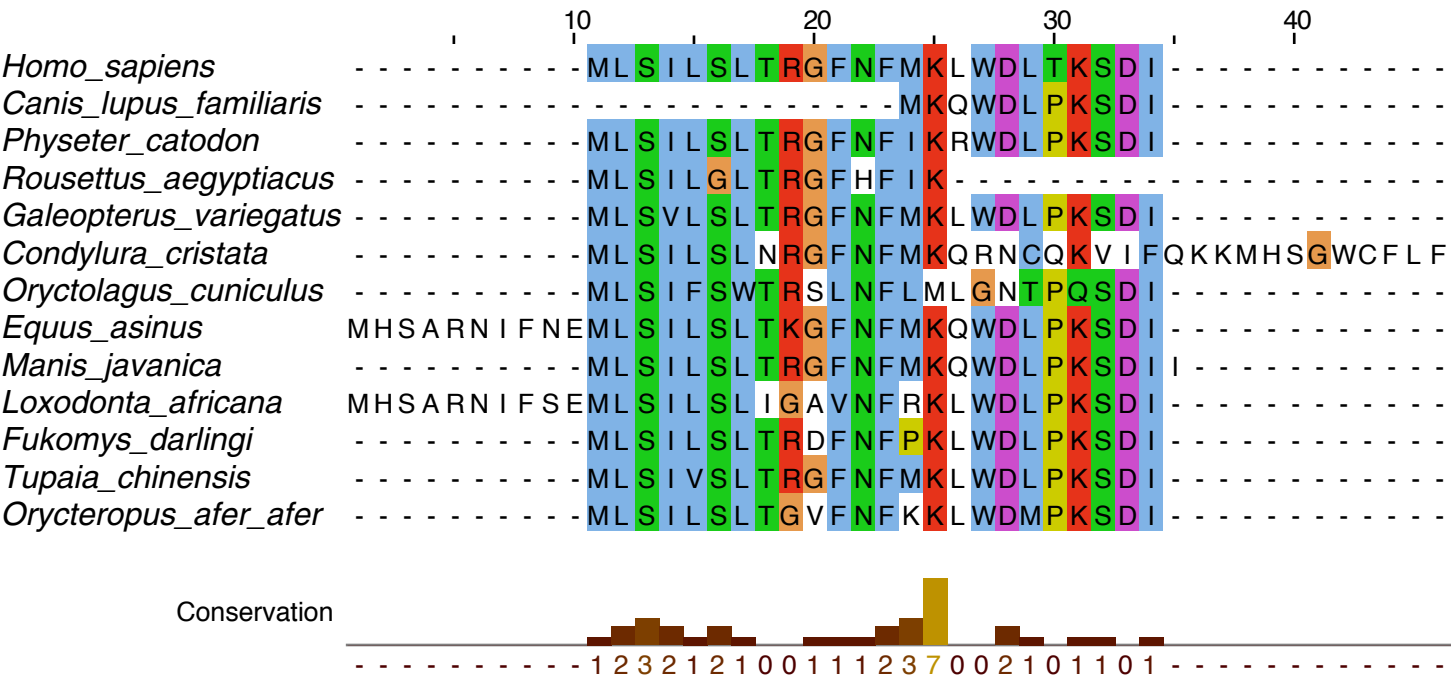
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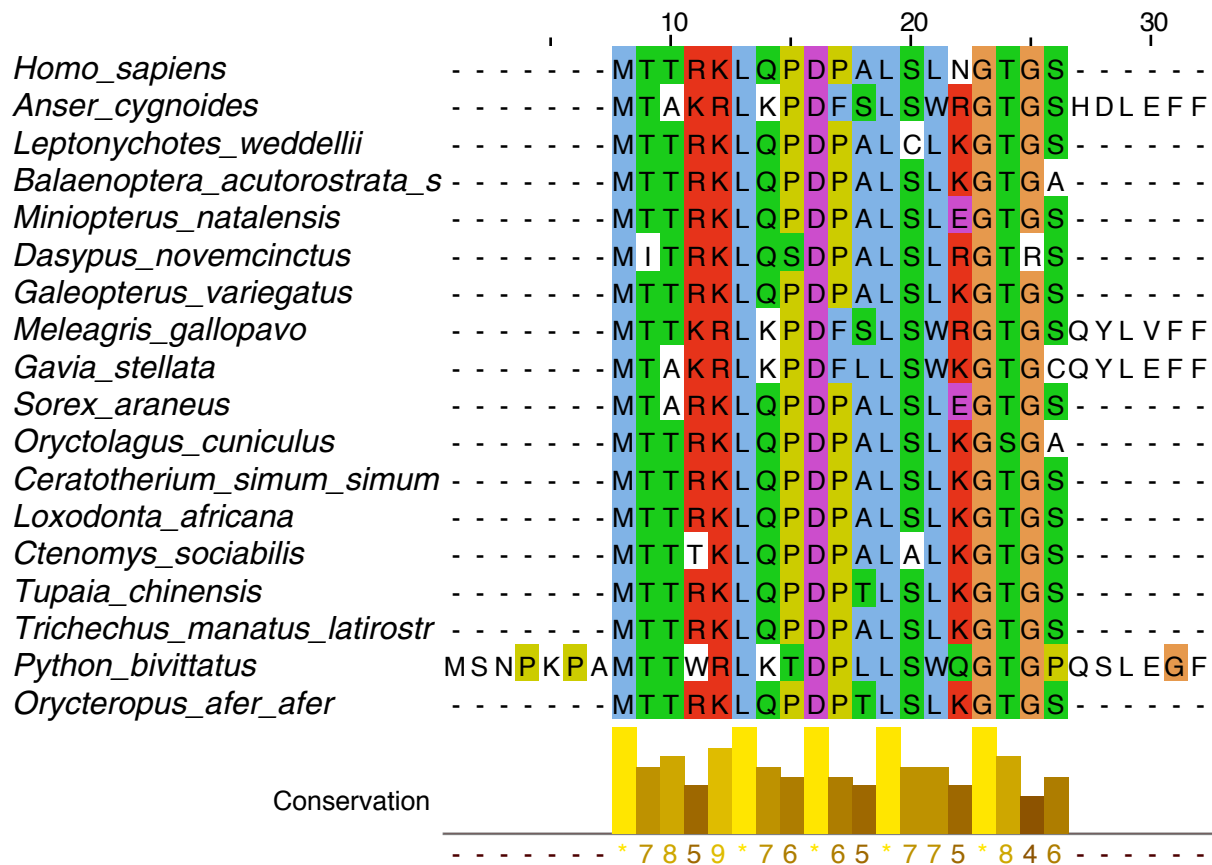
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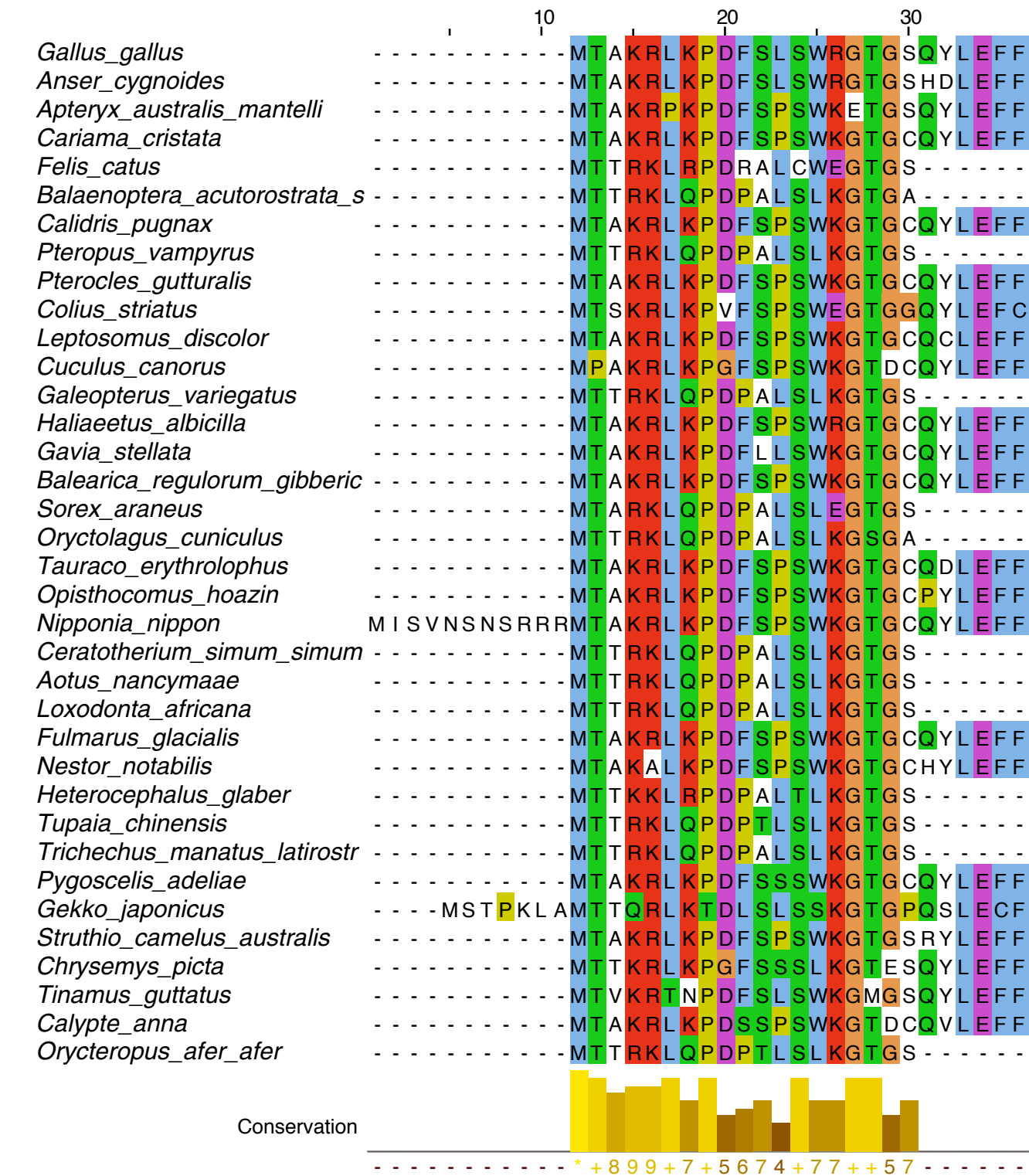
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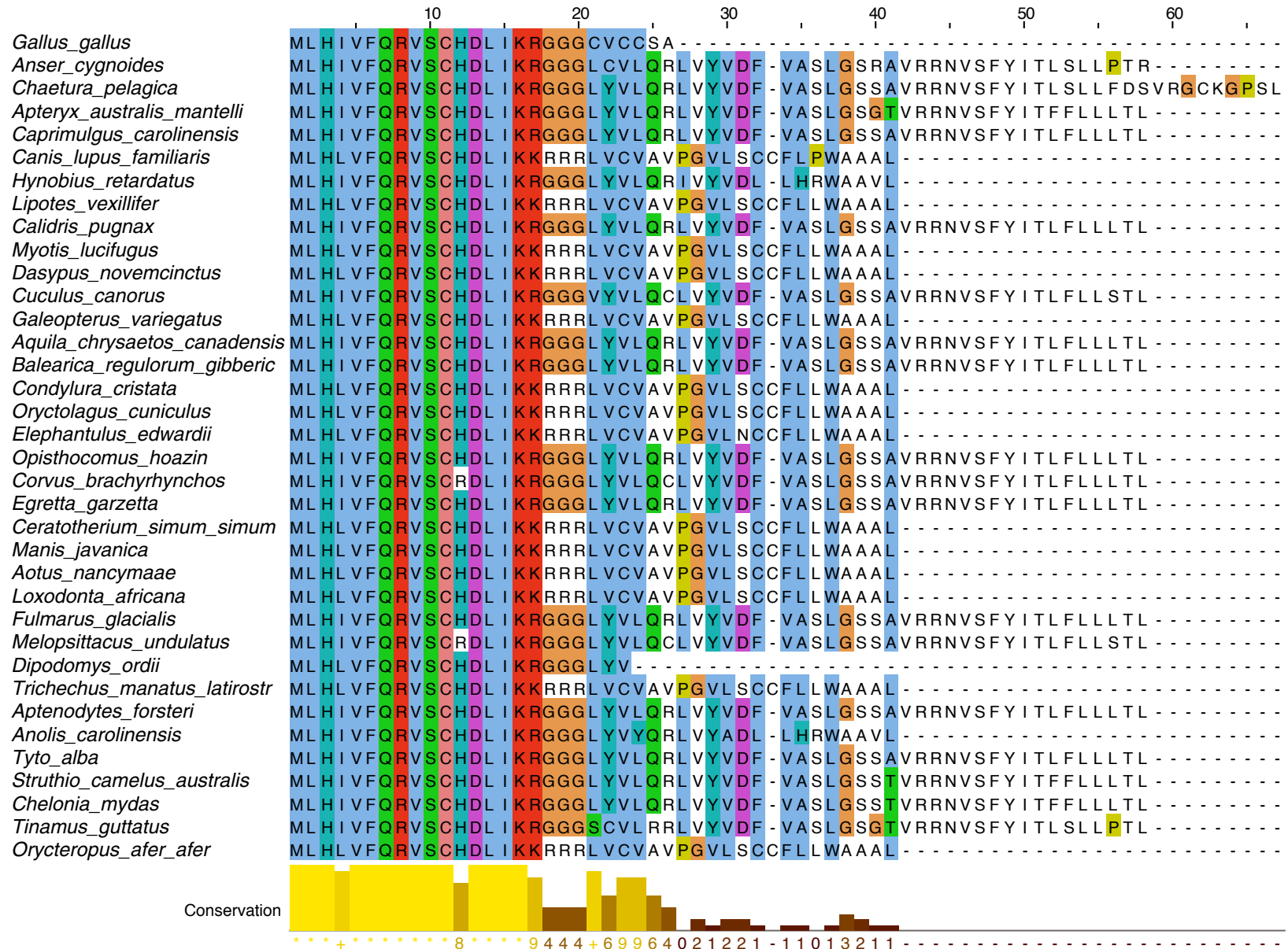
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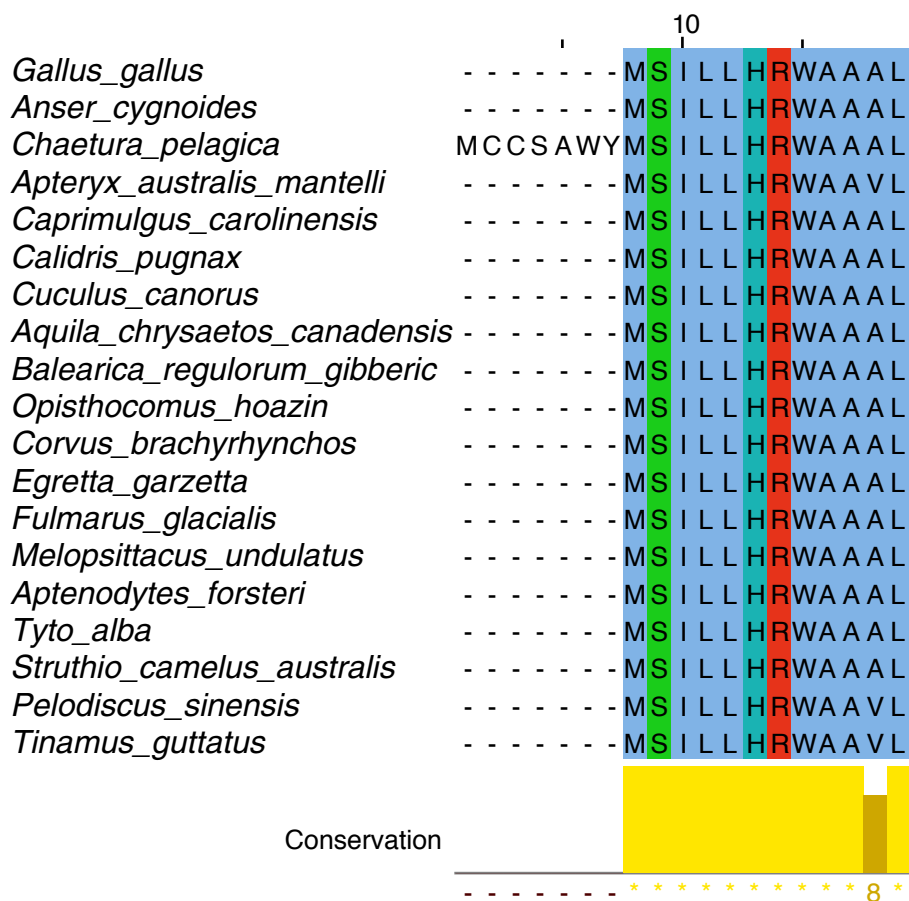
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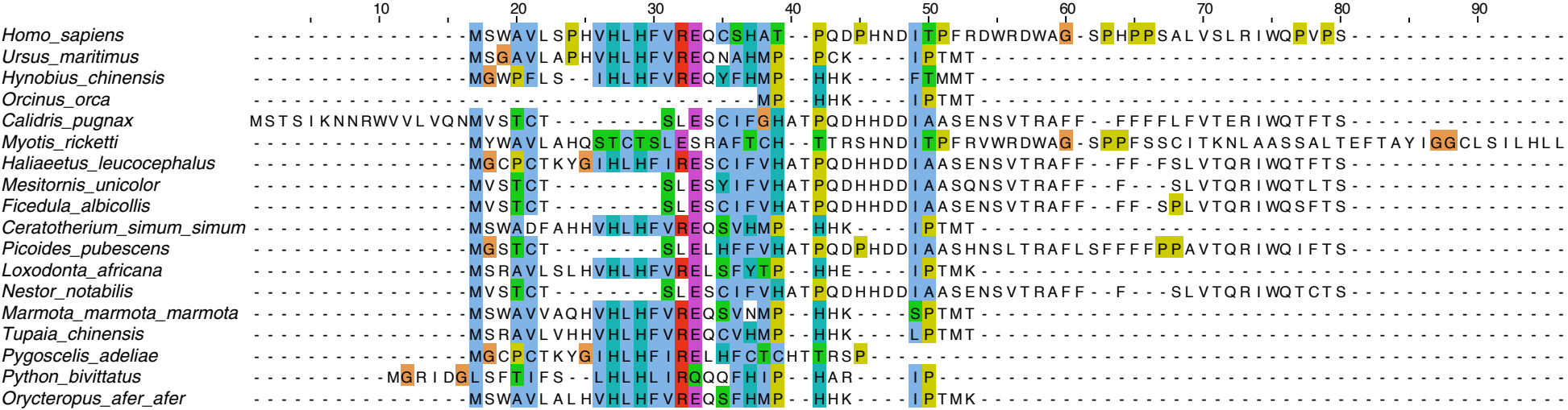
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HG0056

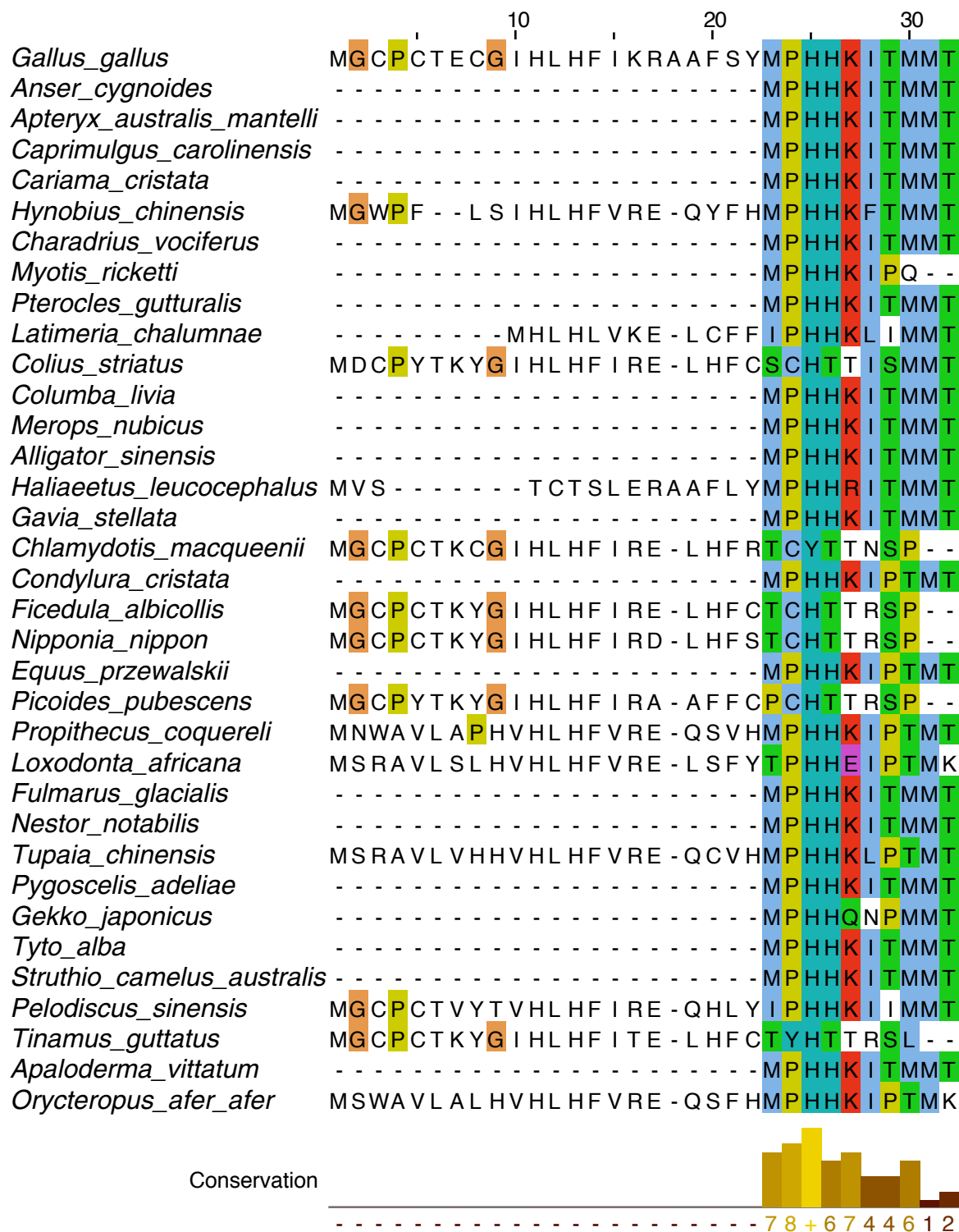
ENSG00000139329 (LUM)



Conservation



ENSGALG00000011271 (LUM)

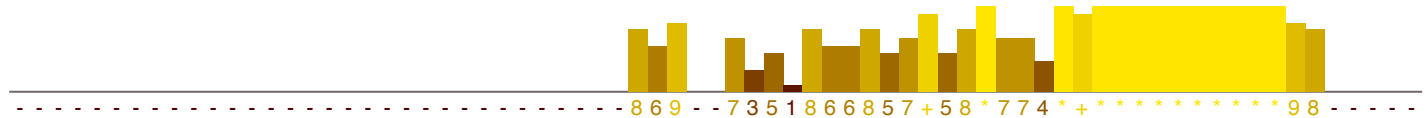


HG0057

ENSG00000280987 (MATR3)

	10	20	30	40	50	60	70
<i>Homo sapiens</i>	---	---	MLGAQWRRNQ	PSRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFEAKLT
<i>Anas platyrhynchos</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Apteryx australis mantelli</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Buceros rhinoceros silvestri</i>	---	MMHK--	LNCICLKGL	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV
<i>Caprimulgus carolinensis</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Cariama cristata</i>	---	---	MTK---	PACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Odobenus rosmarus divergens</i>	---	---	MLGAQWRRNQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFE----
<i>Calidris pugnax</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TVFEVKFA
<i>Miniopterus natalensis</i>	---	---	MLGAQWRRNQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFEAKLT
<i>Pterocles gutturalis</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Colius striatus</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TVFEVKFA
<i>Columba livia</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Merops nubicus</i>	---	---	MTK---	PACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Cuculus canorus</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TILK----
<i>Monodelphis domestica</i>	---	---	MLGTQW	---	---	---	---
<i>Gallus gallus</i>	MLAVQGRPP	RCRFALLFFT	PLPEHXIA	PRGPGARS	---	HRRXRAEL	SGVSQL EEDL
<i>Gavia stellata</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Chlamydotis macqueenii</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Condylura cristata</i>	---	---	MLGAQWRRNQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFE----
<i>Oryctolagus cuniculus</i>	---	---	MLGAQWRRNQ	SPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFE----
<i>Tauraco erythrolophus</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TVLK----
<i>Opisthocomus hoazin</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TVF----
<i>Acanthisitta chloris</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TVFEVKFA
<i>Egretta garzetta</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Ceratotherium simum simum</i>	---	---	MLGAQWRRKQ	PLRAAESCLL	FL SLKKIL	QSLLILFLGV	TIFE----
<i>Picoides pubescens</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Loxodonta africana</i>	---	---	MLGAQGRRSQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFE----
<i>Fulmarus glacialis</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	RSLLILFLGV	TIFEVKFA
<i>Melopsittacus undulatus</i>	---	---	MTK---	PACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Jaculus jaculus</i>	---	MRA-S	SRSAAAML	GAQWRRRQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV
<i>Trichechus manatus latirostr</i>	---	---	MLGAQWRRSQ	PPRAAESCLL	VL SLKKIL	QSLLILFLGV	TIFE----
<i>Aptenodytes forsteri</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Tyto alba</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Struthio camelus australis</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA
<i>Tinamus guttatus</i>	---	---	MTK---	TACFSTEL	SGVSQL EEDL	QSLLILFLGV	TIFEVKFA

Conservation



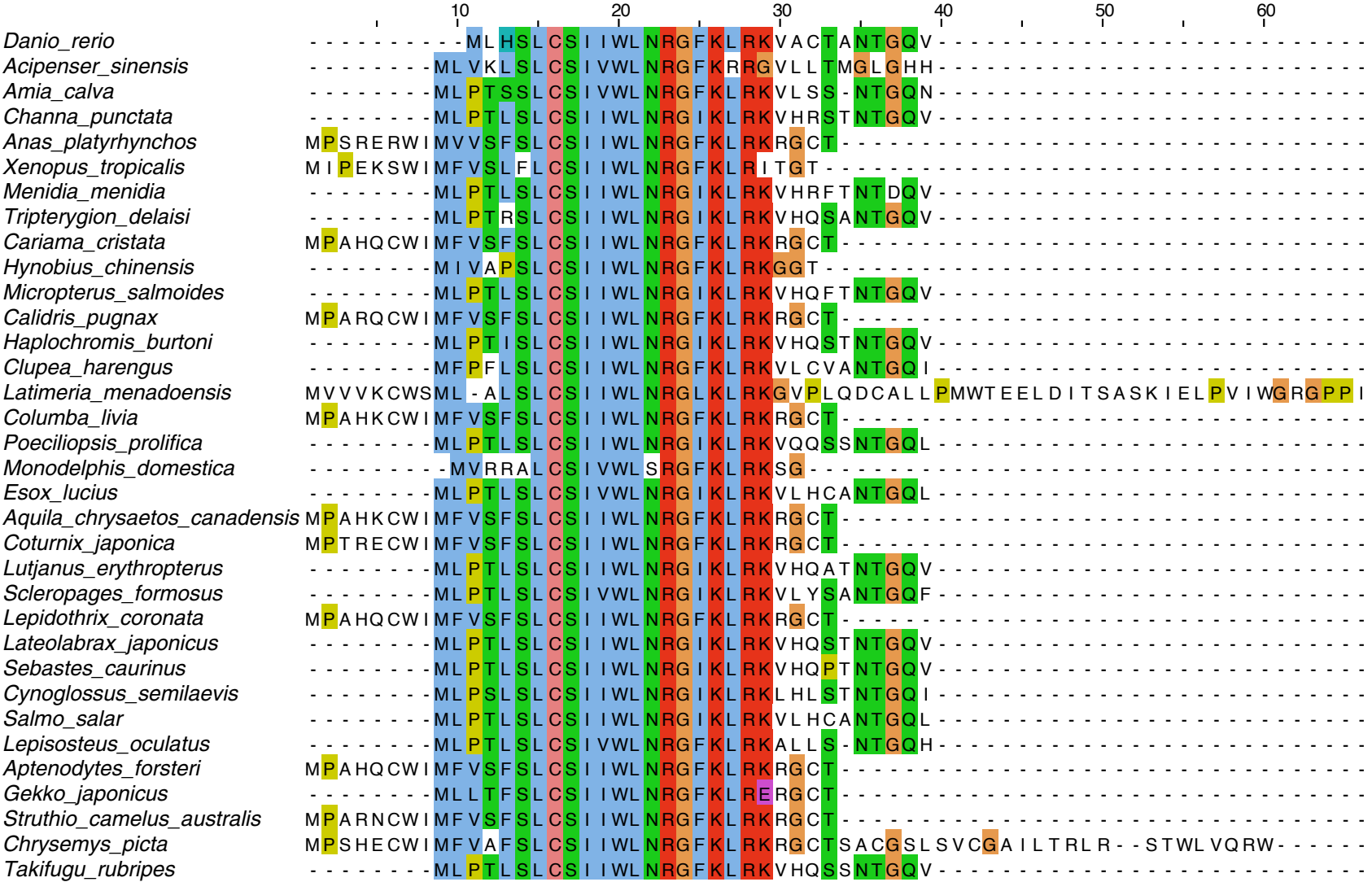
HG0058

ENSG00000180332 (KCTD4)



HG0059.1

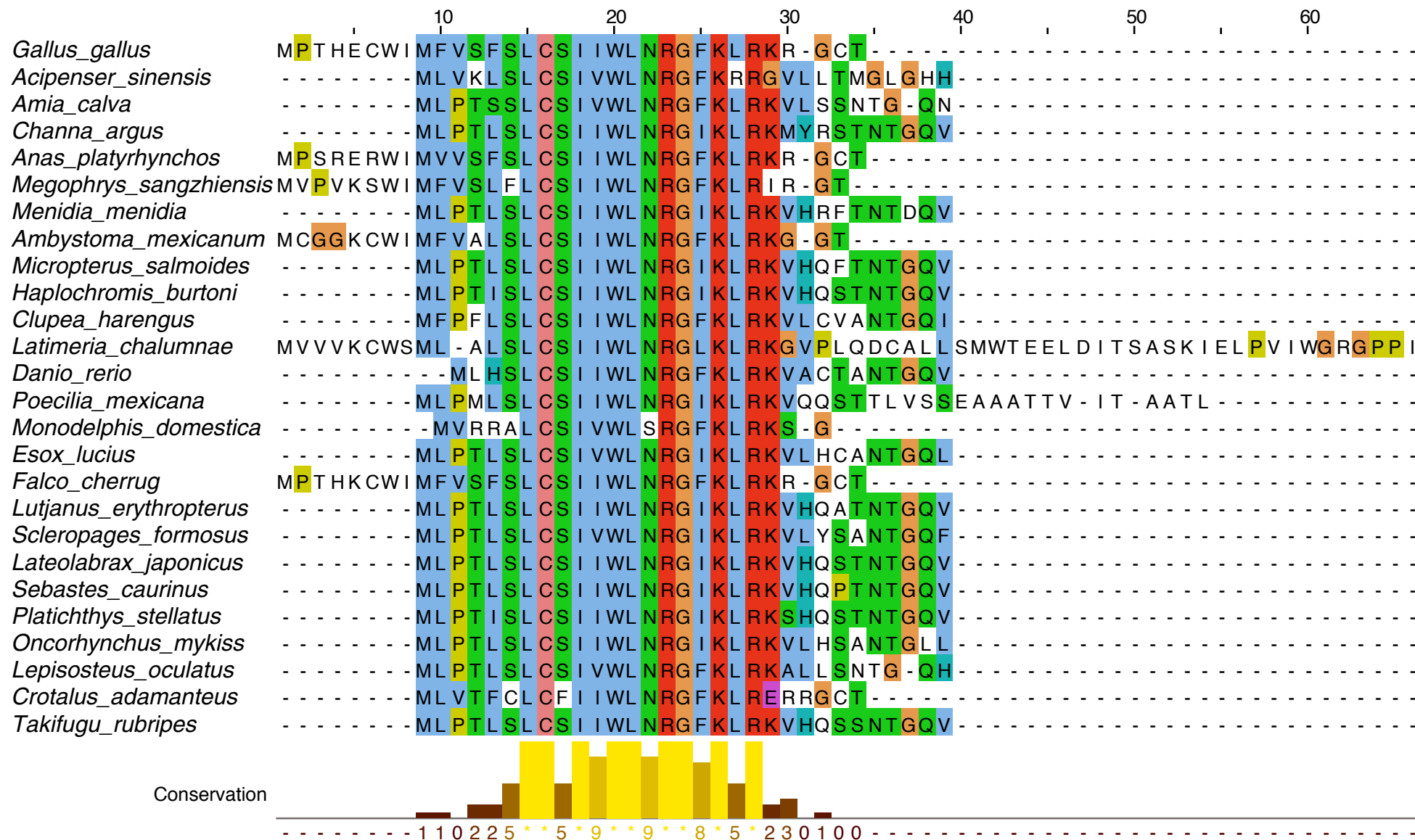
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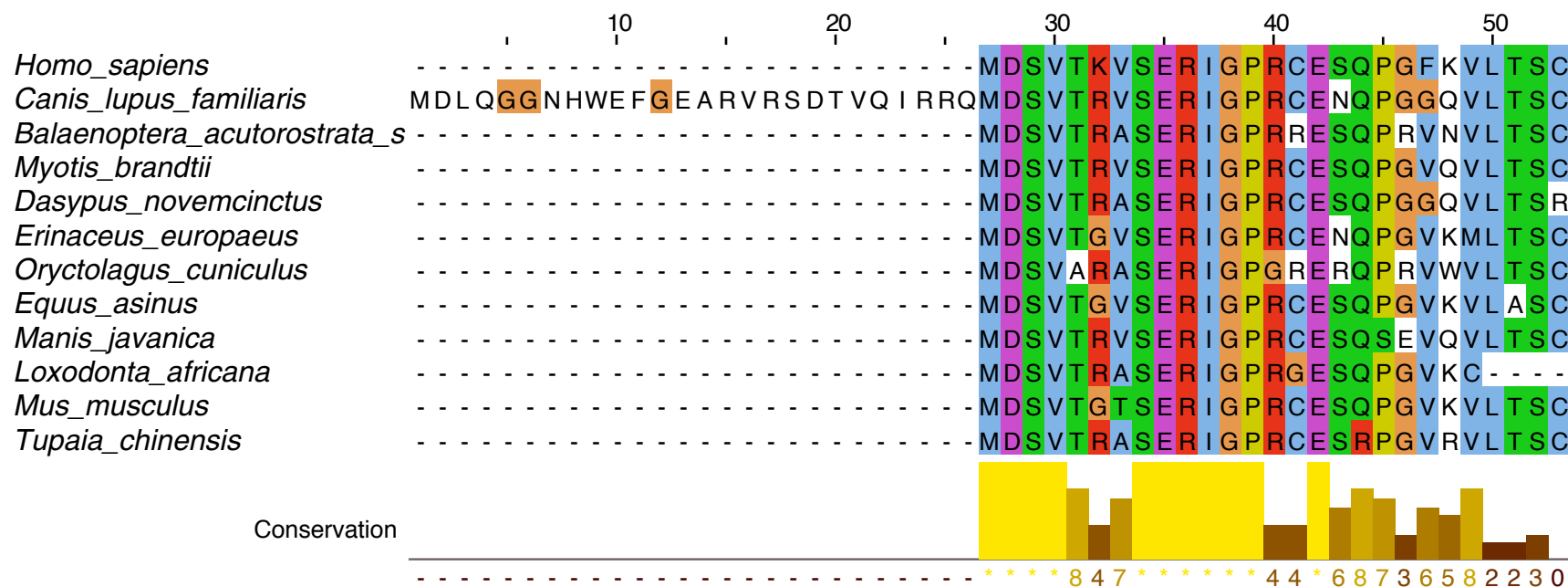
Conservation

1 8 7 7 4 + * * * * 9 * * + * * 8 * * + 3 3 3 0

ENSGALG00000003428

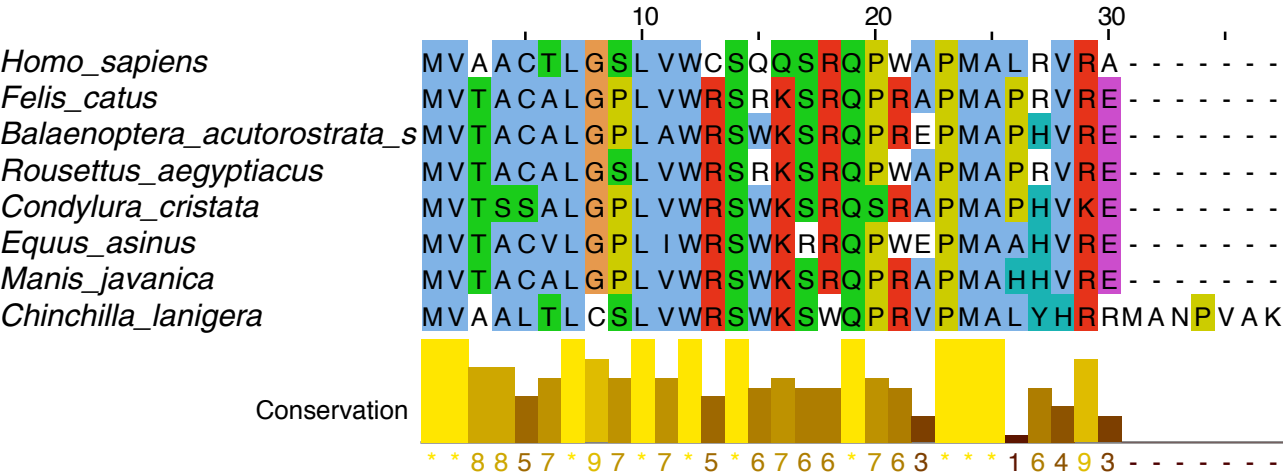


ENSG00000145675 (PIK3R1)



HG0059.3

ENSG00000105647 (PIK3R2)



HG0059.4

ENSG00000145675 (PIK3R1)

Homo_sapiens

Dasypus_novemcinctus

Equus_asinus

Loxodonta_africana

Nannospalax_galili

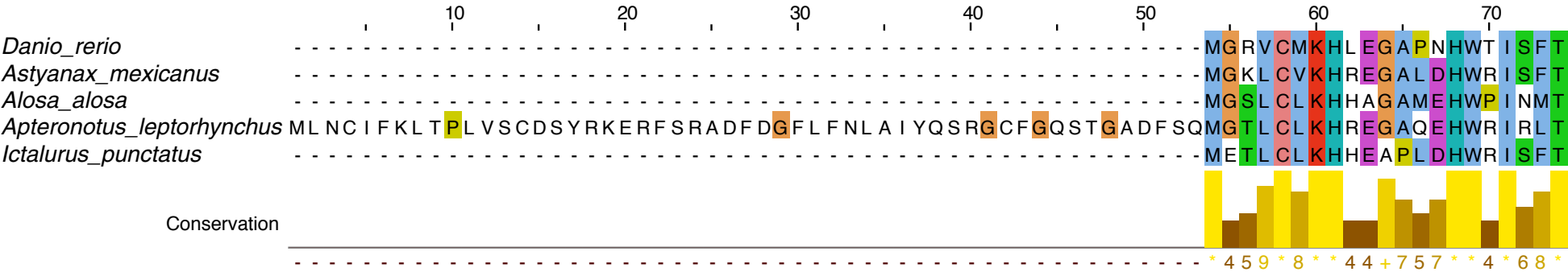
Tupaia_chinensis

Conservation

★ ★ ★ ★ ★ ★ ★ ★ ★ ★

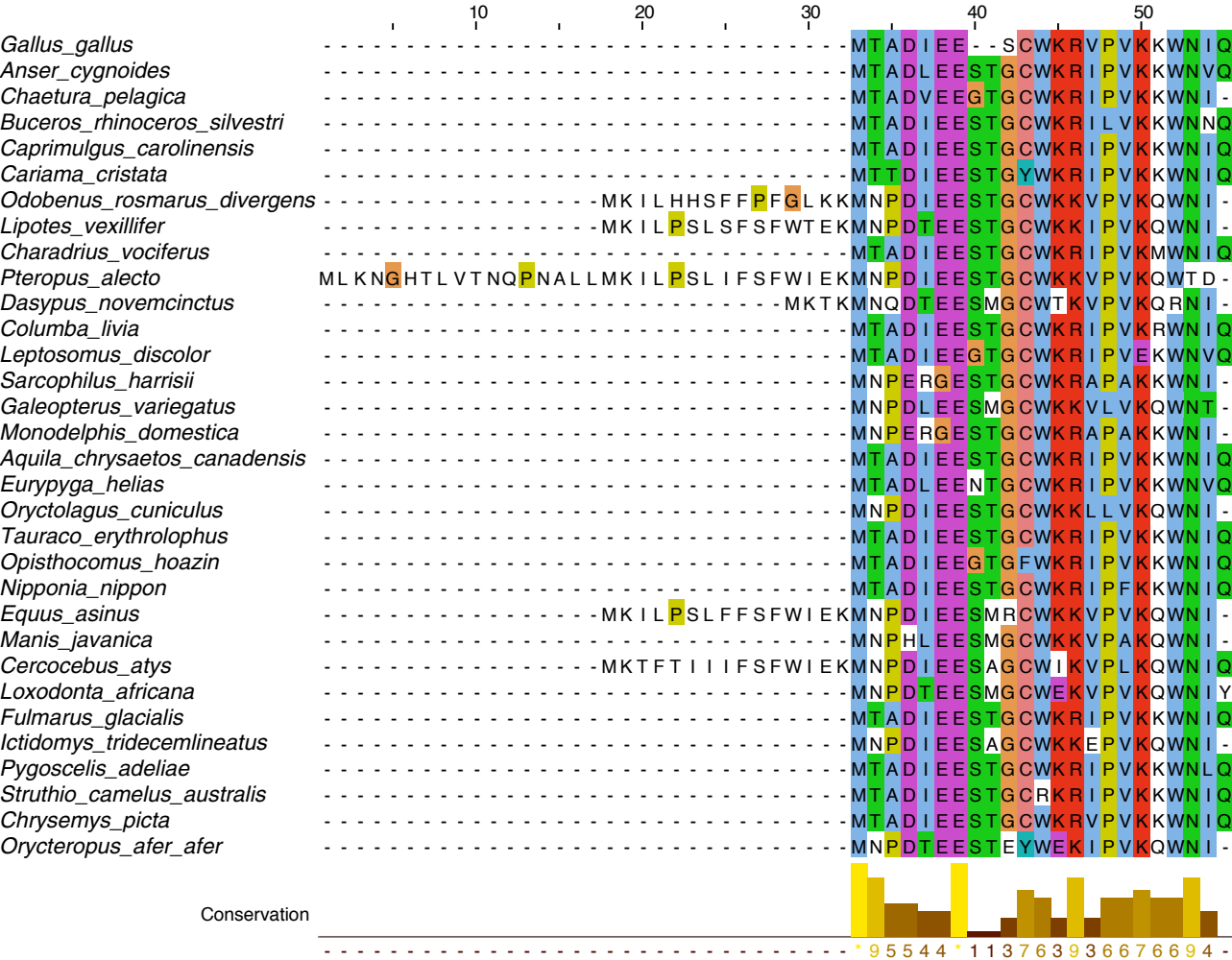
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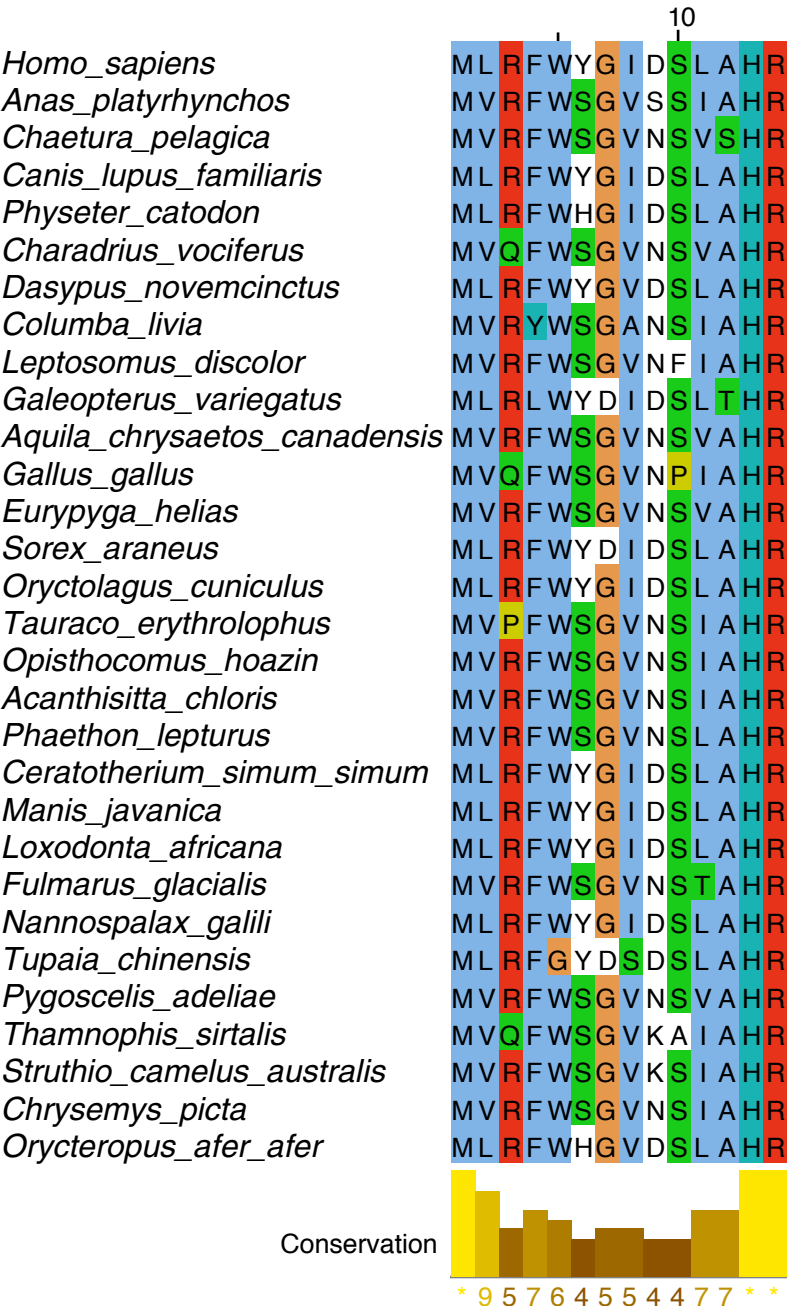
ENSG00000049192 (ADAMTS6)

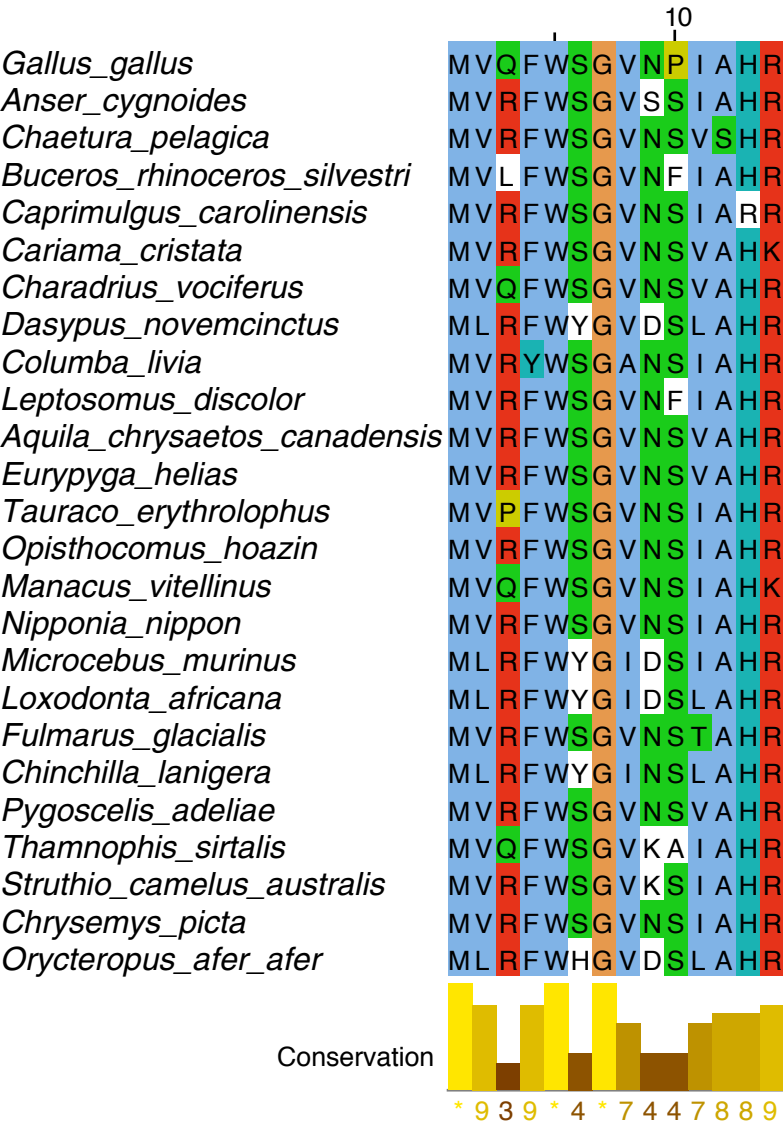


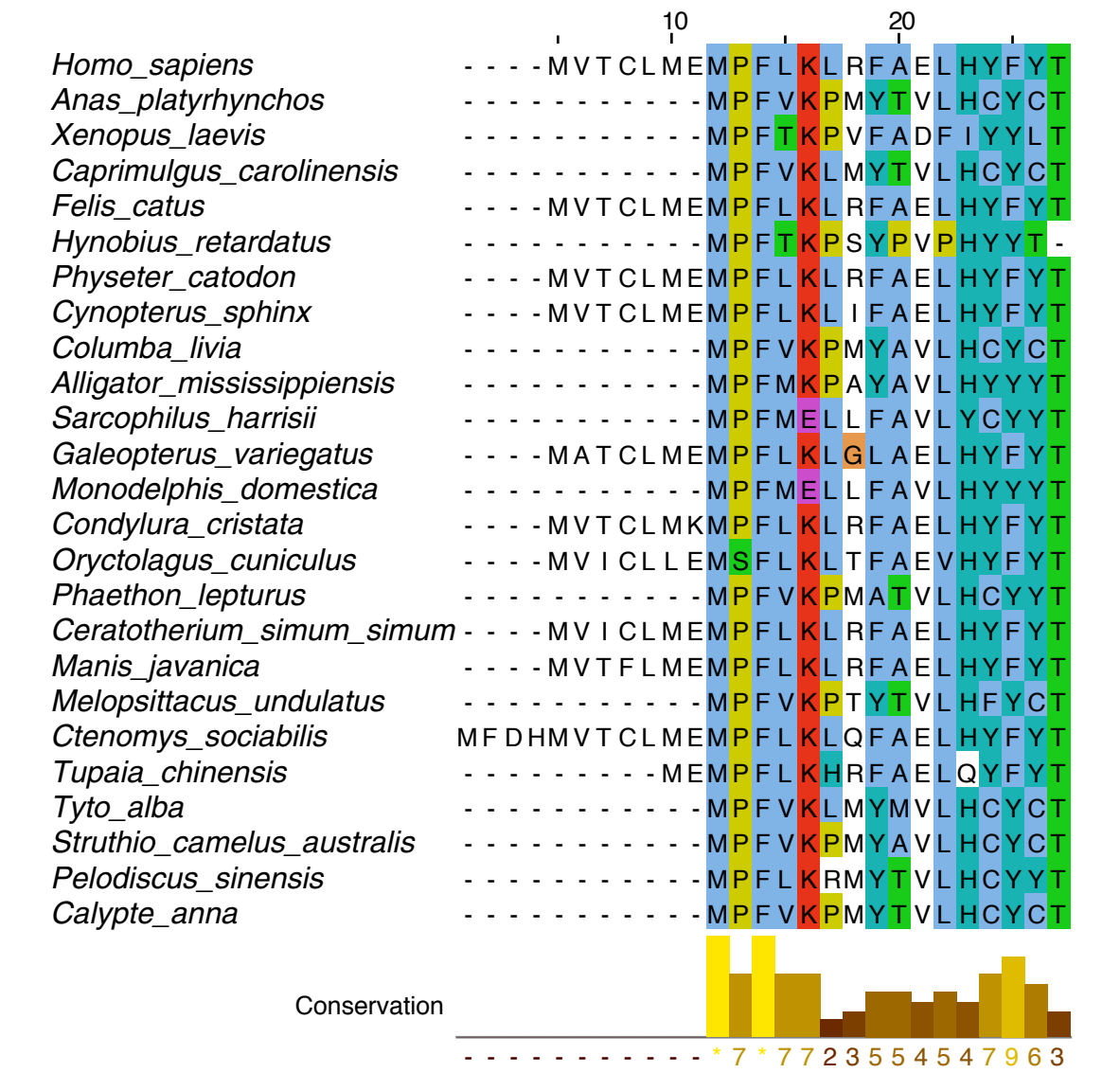


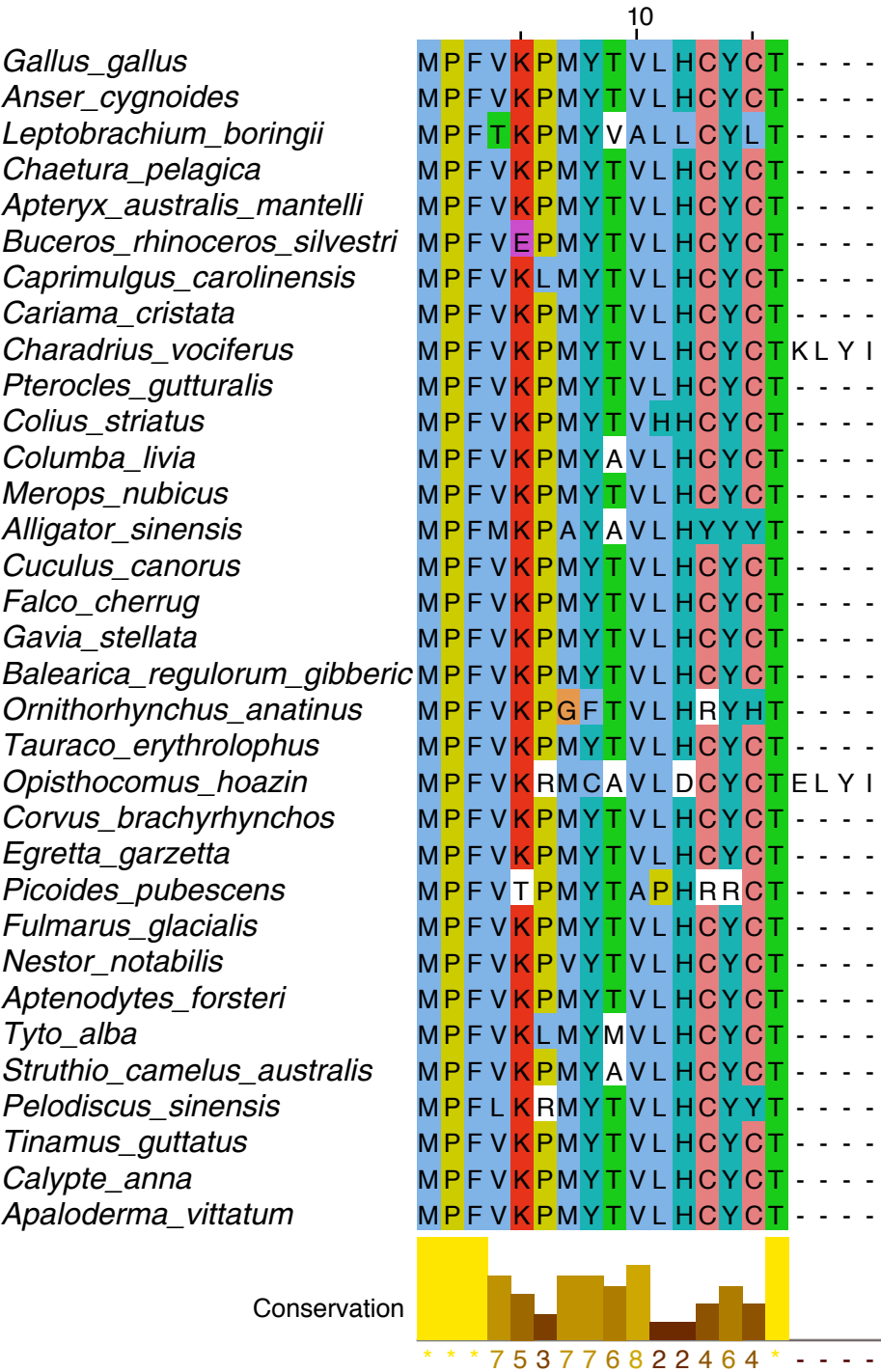
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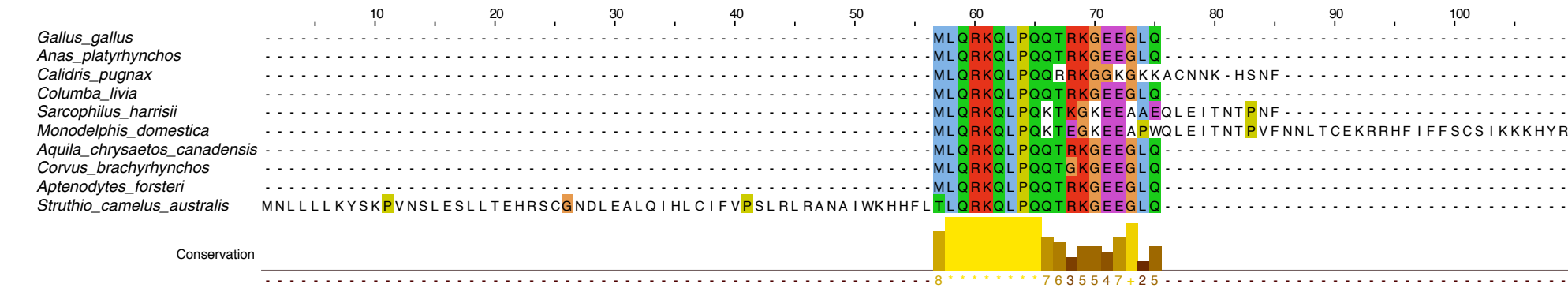






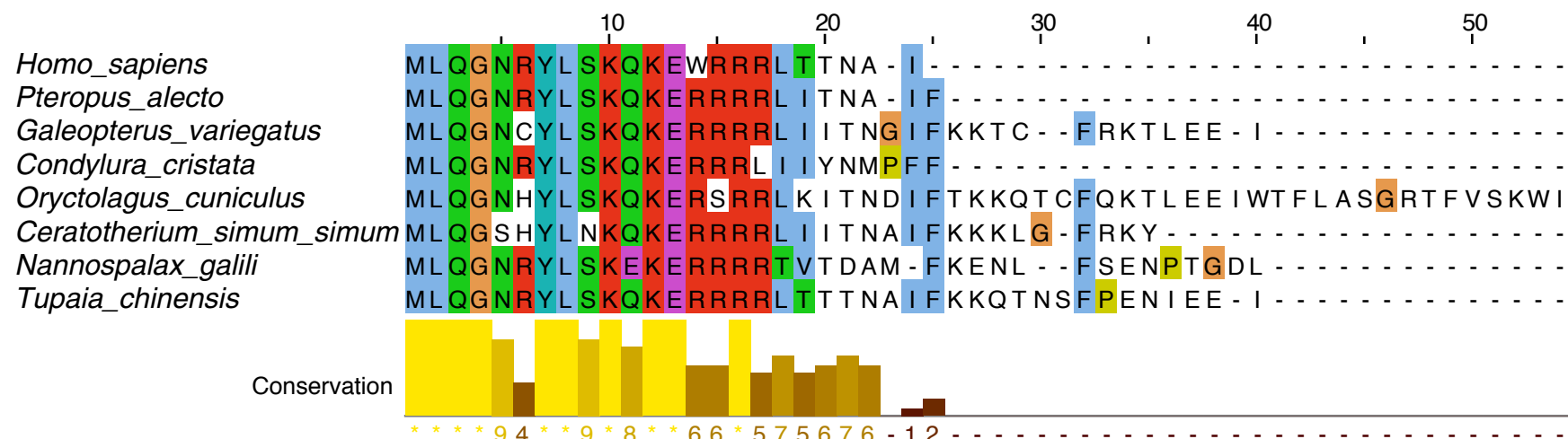


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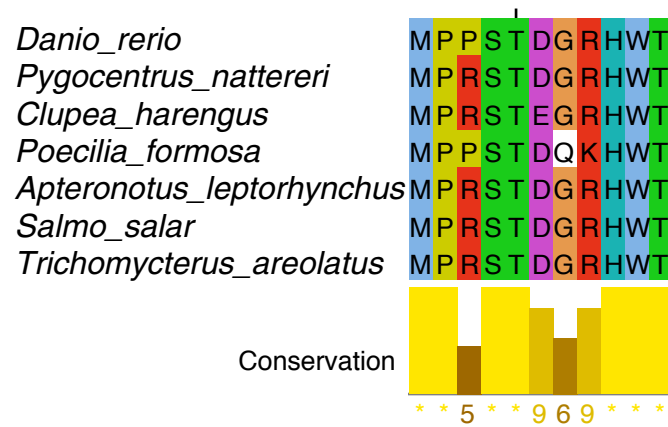
HG0061.3

ENSG00000166398



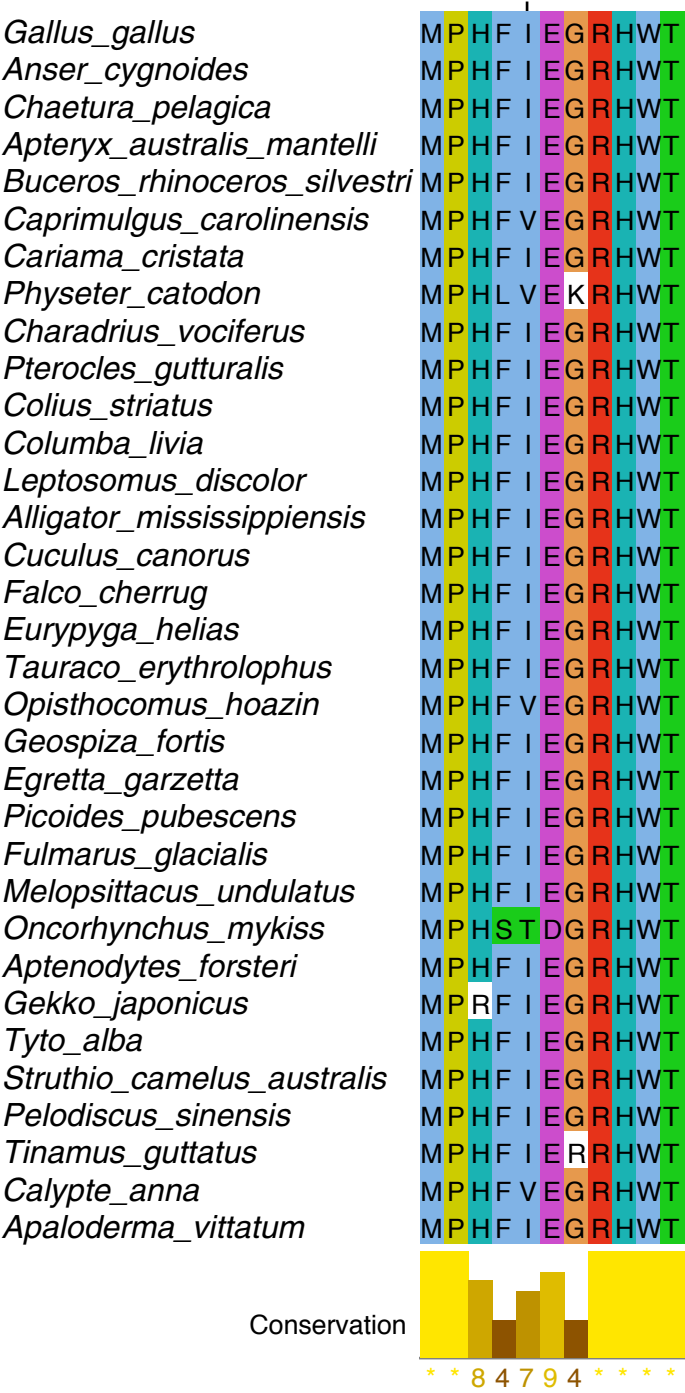
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ENSDARG00000075569 (gpbp1l1)



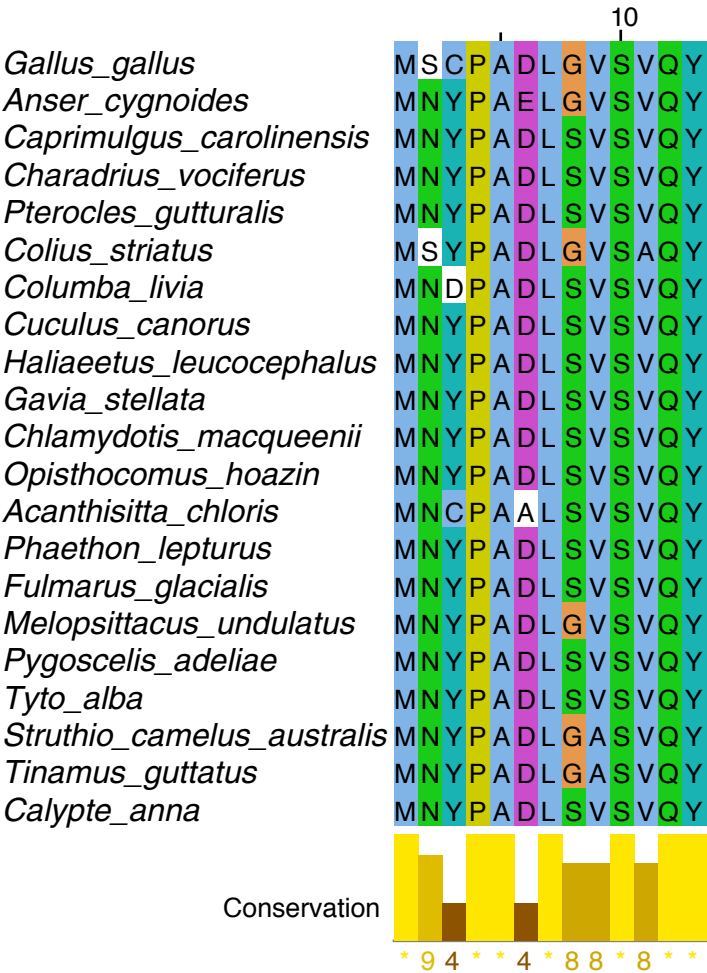
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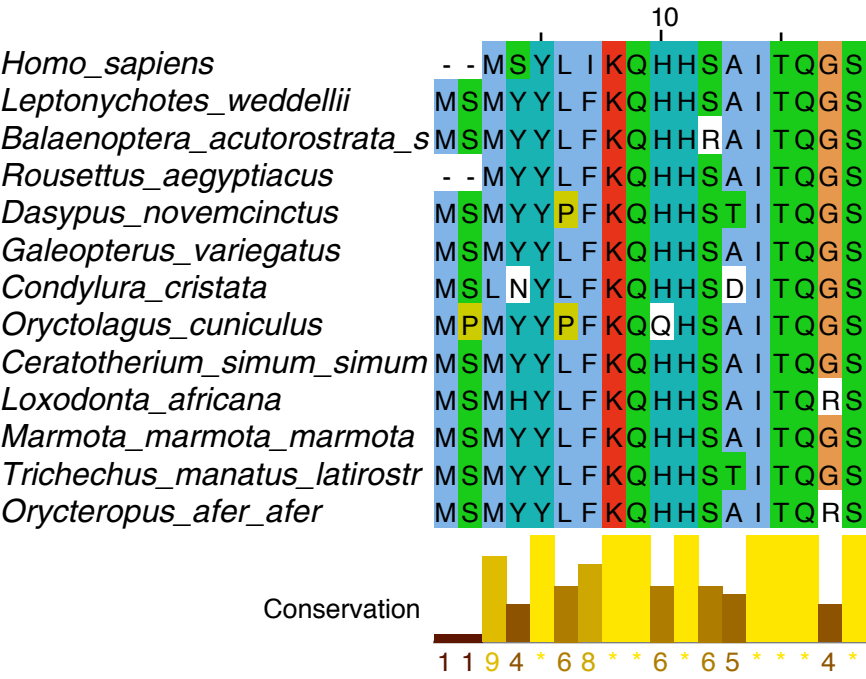
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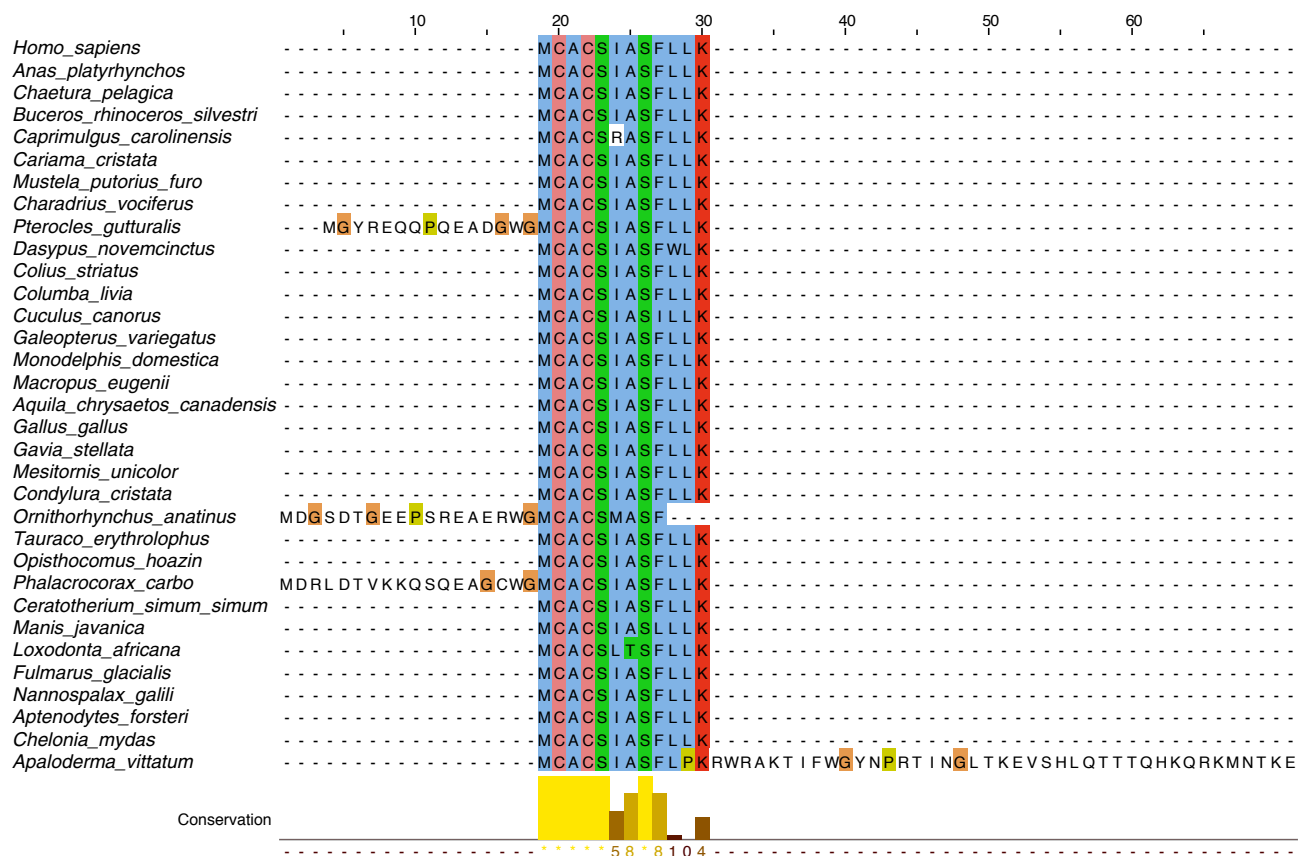


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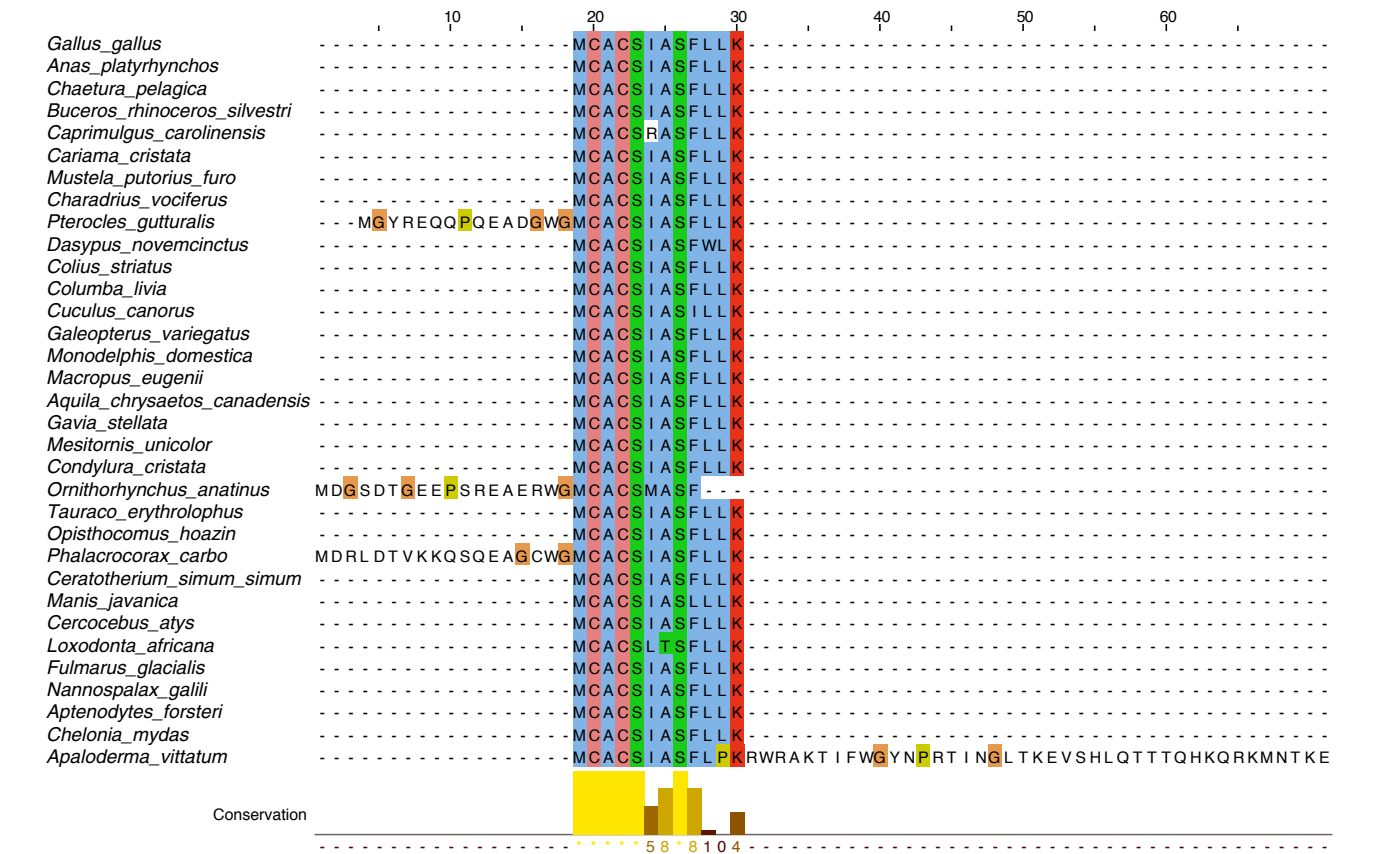


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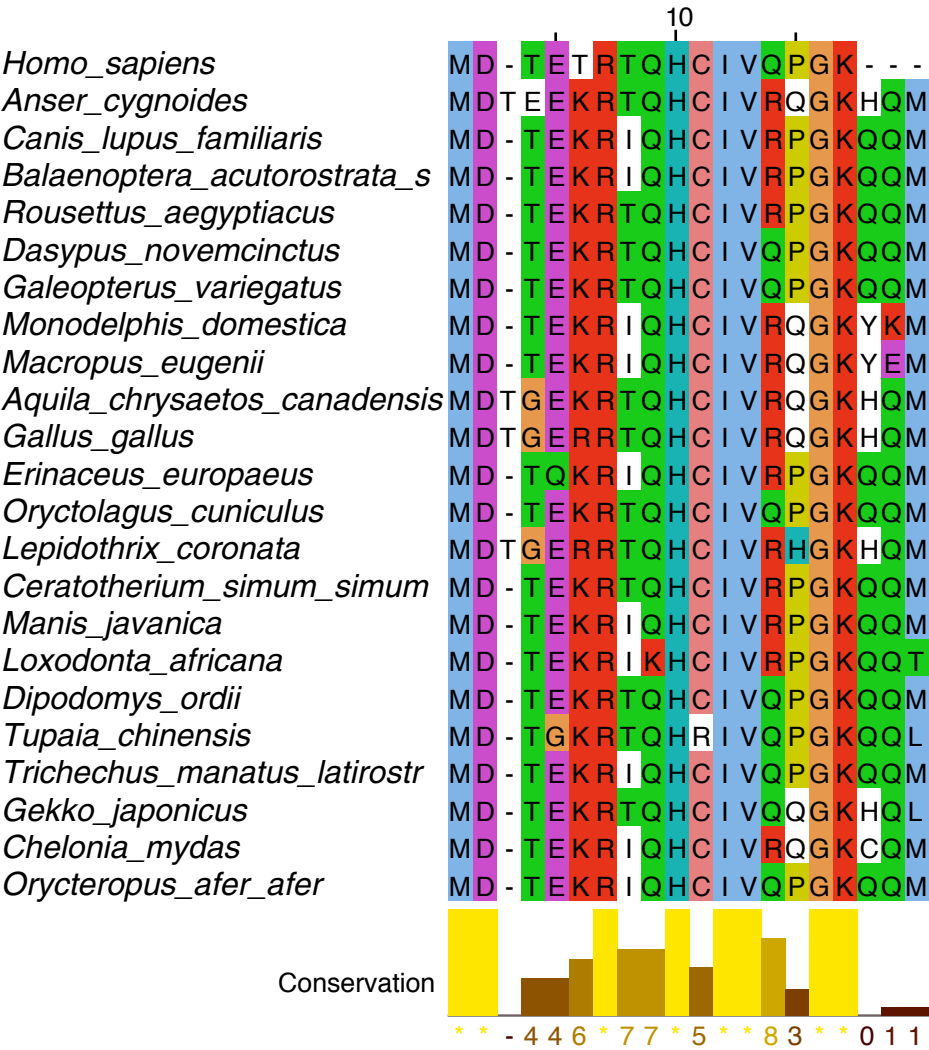
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ENSGALG00000002477



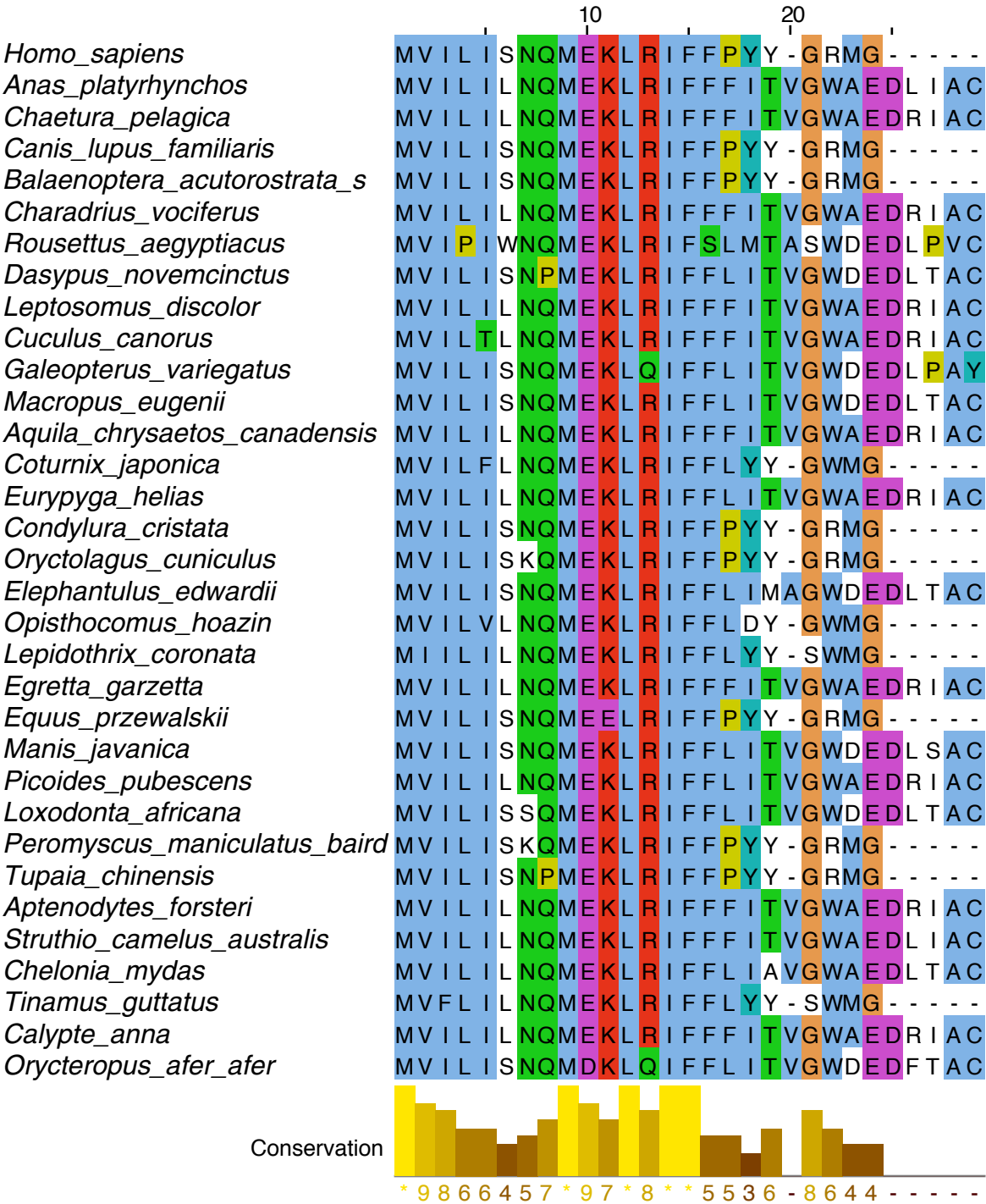
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ENSG00000162630 (B3GALT2)



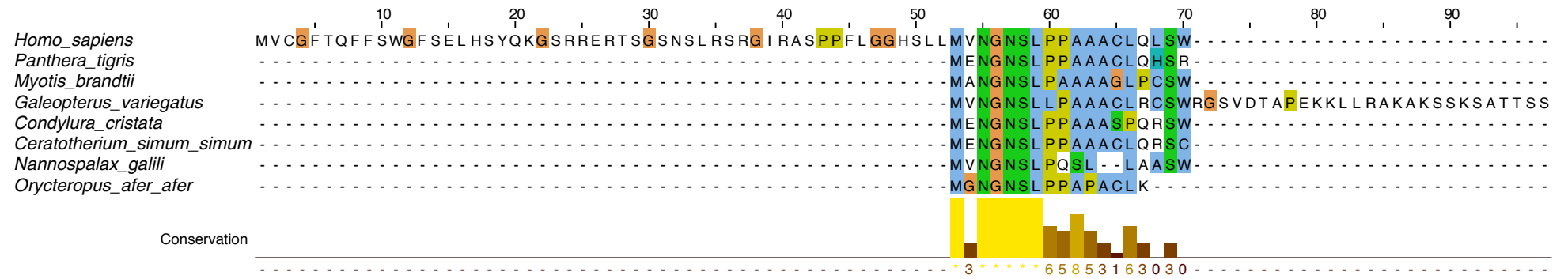
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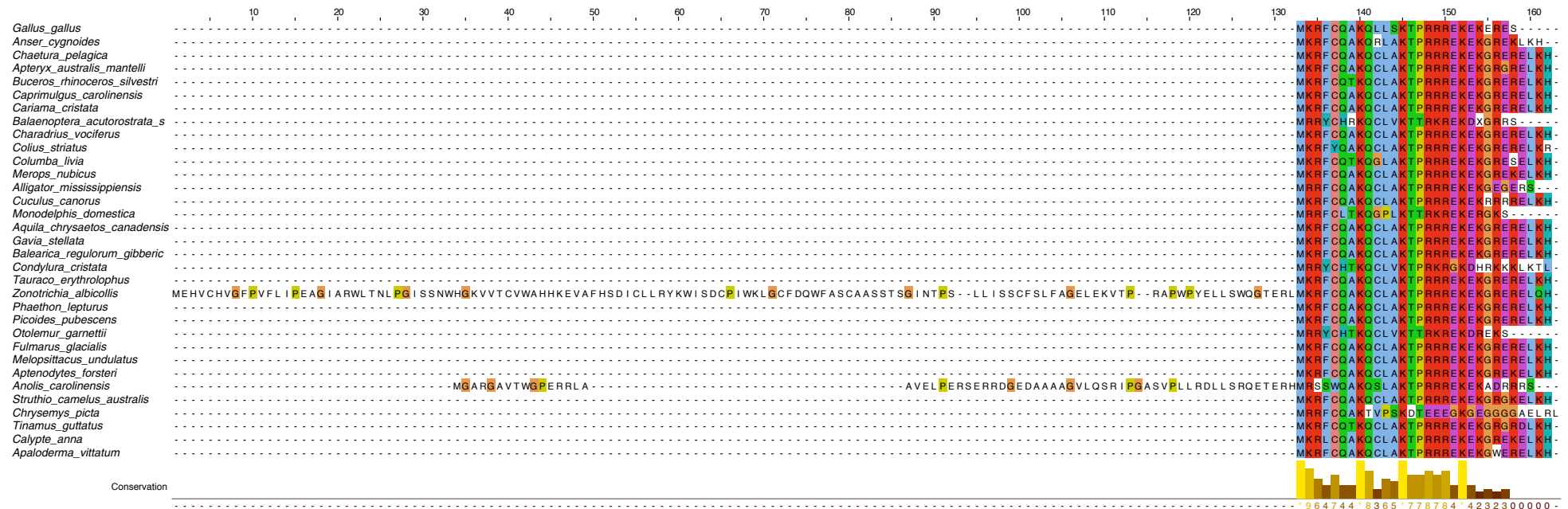


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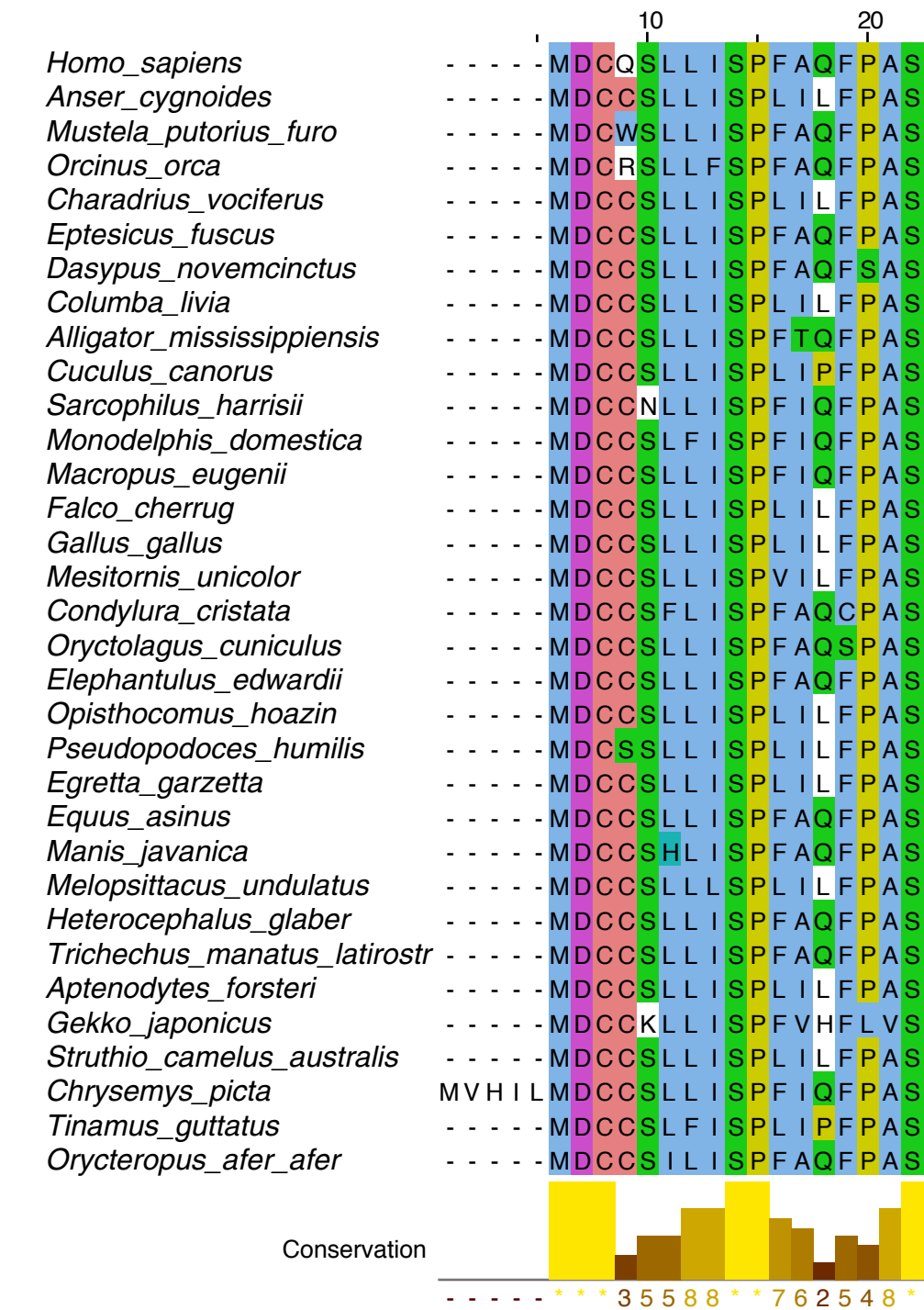


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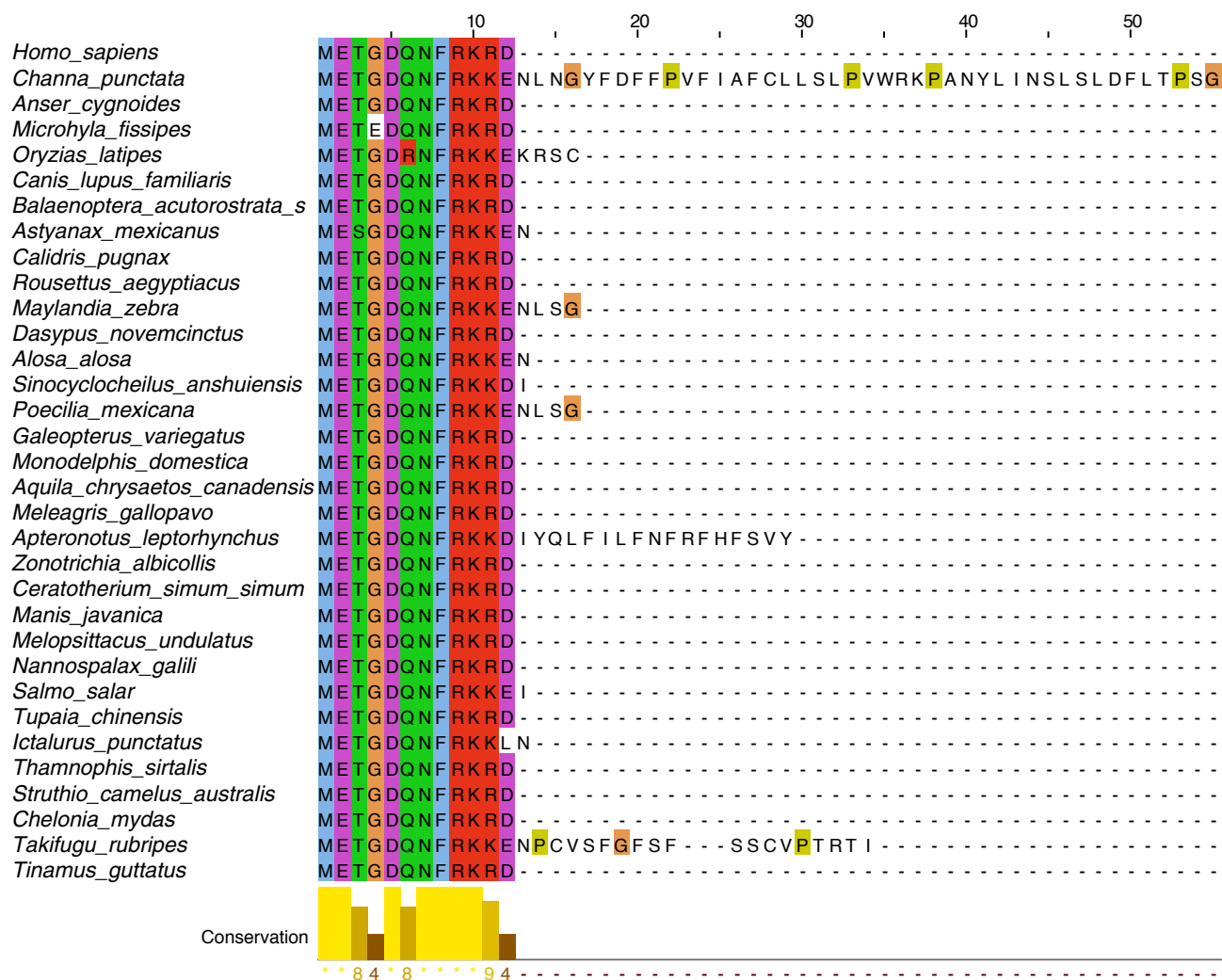


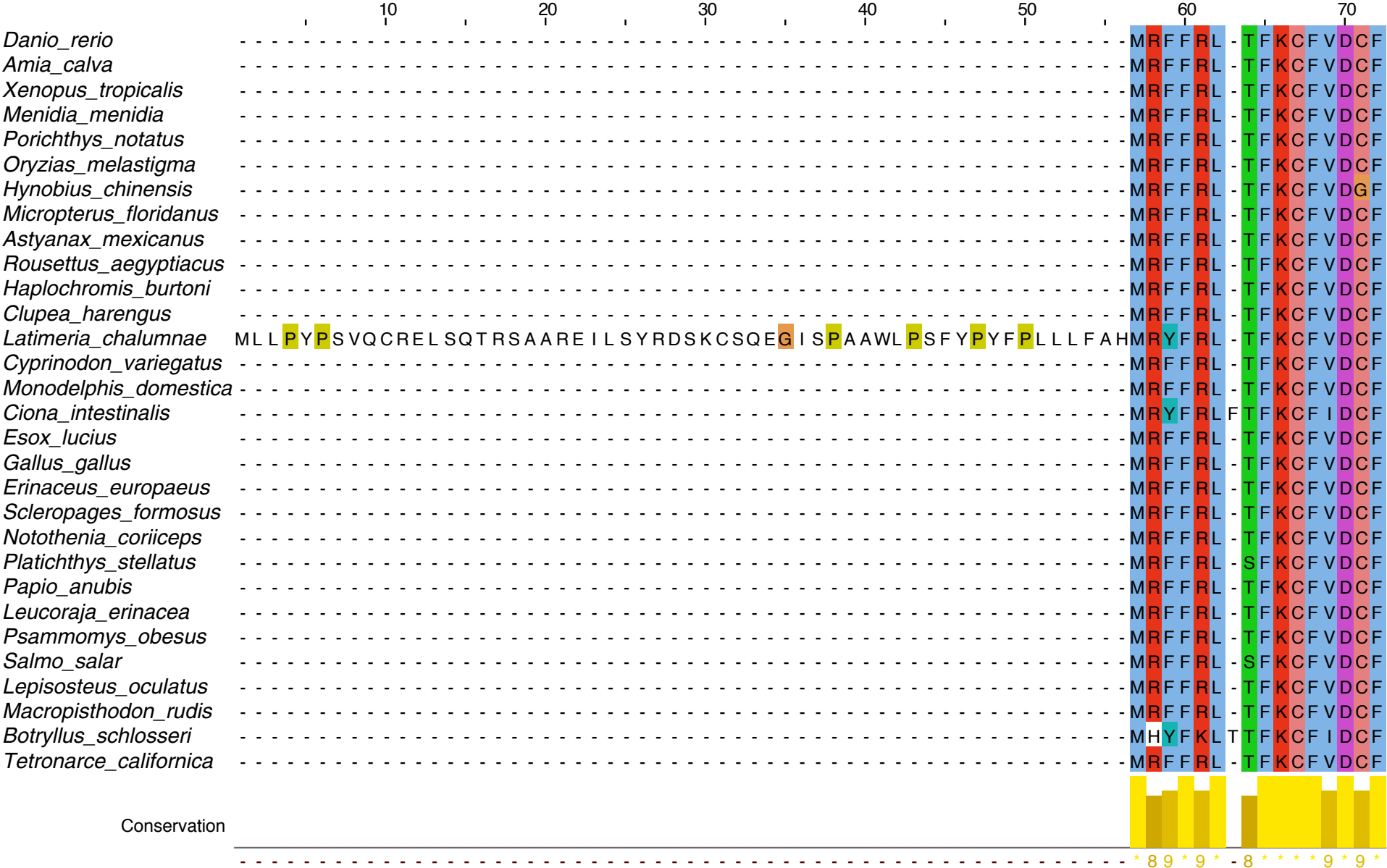
HG0066

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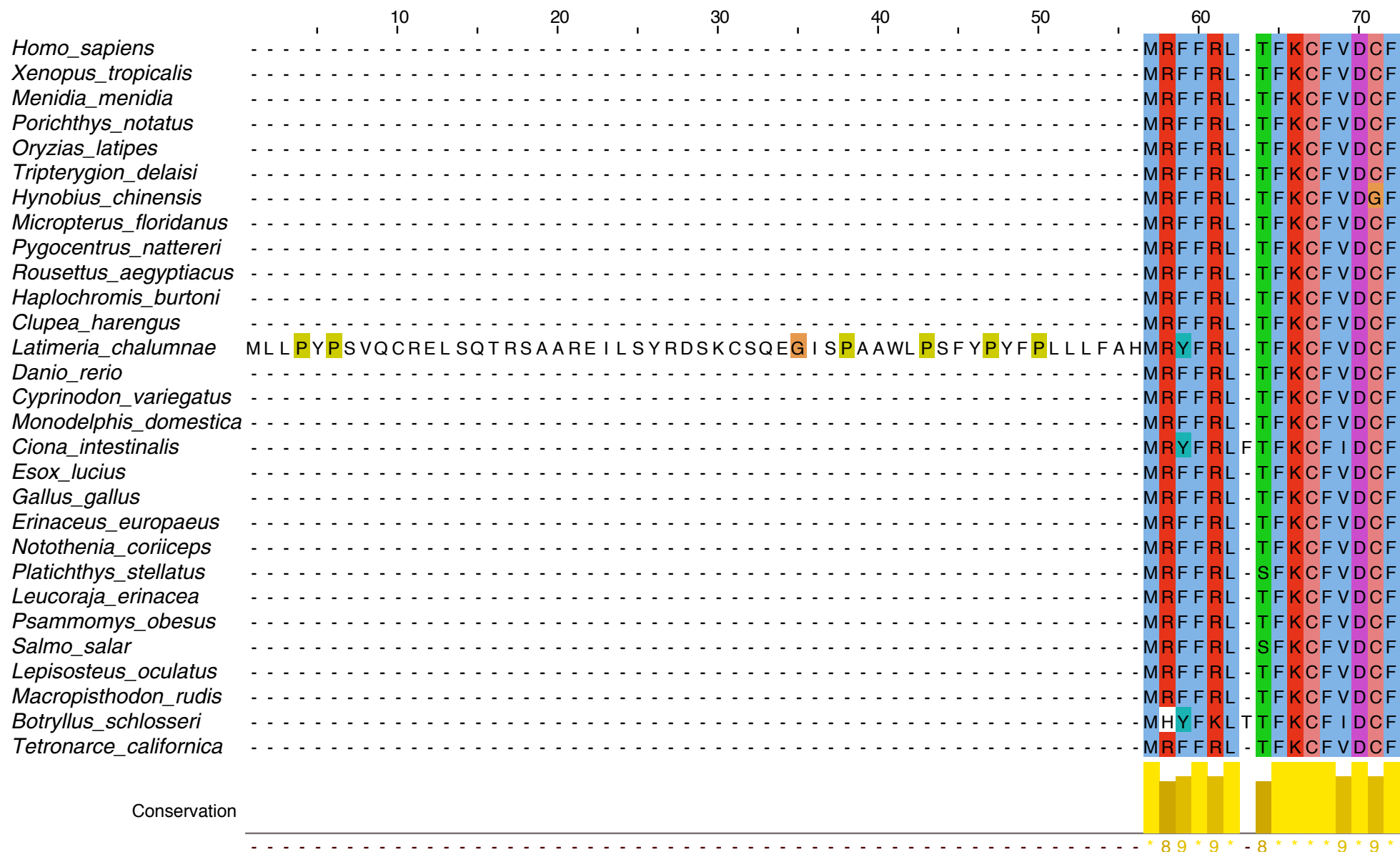


ENSG00000166862 (CACNG2)

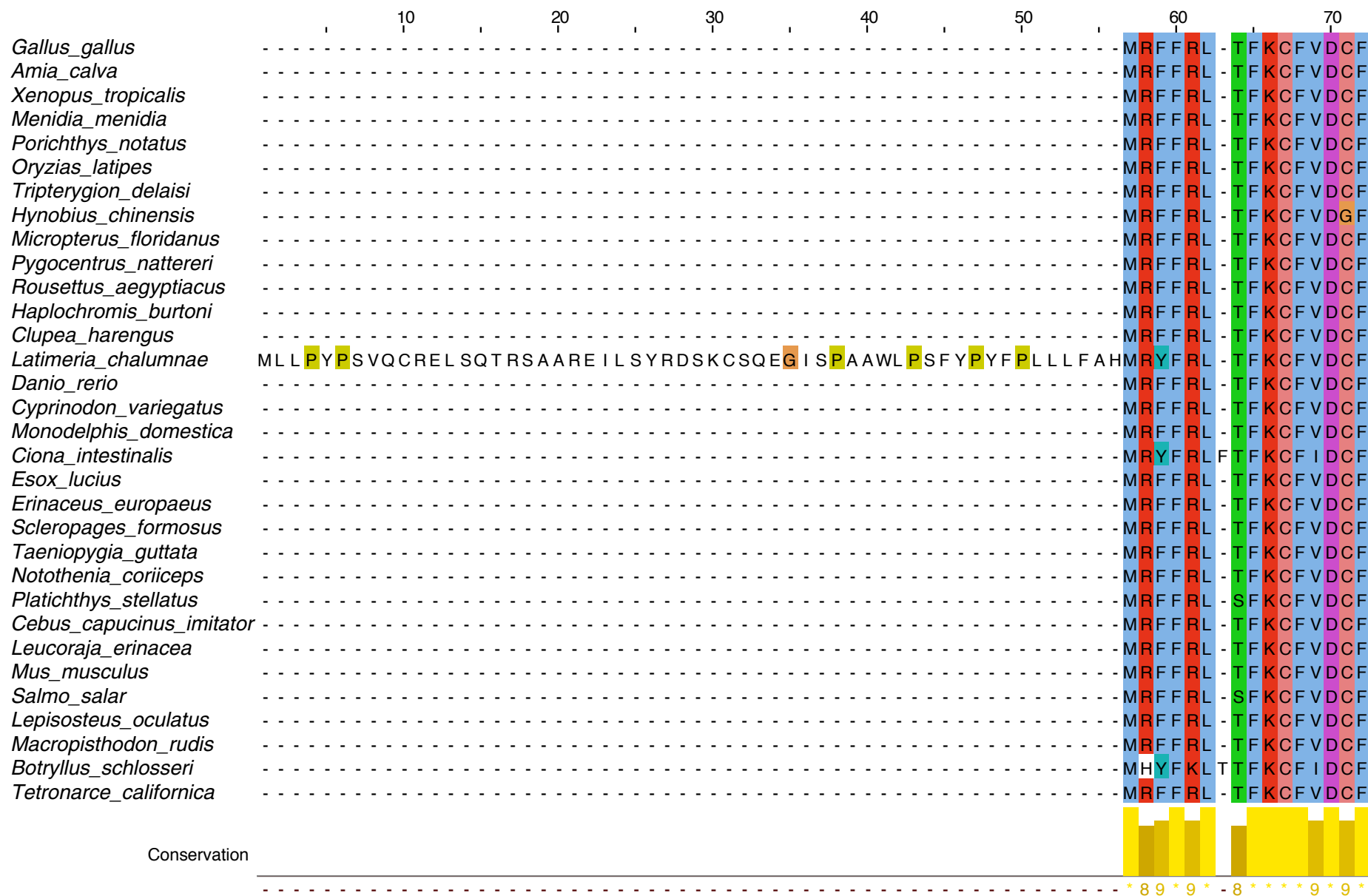




ENSG00000130821 (SLC6A8)

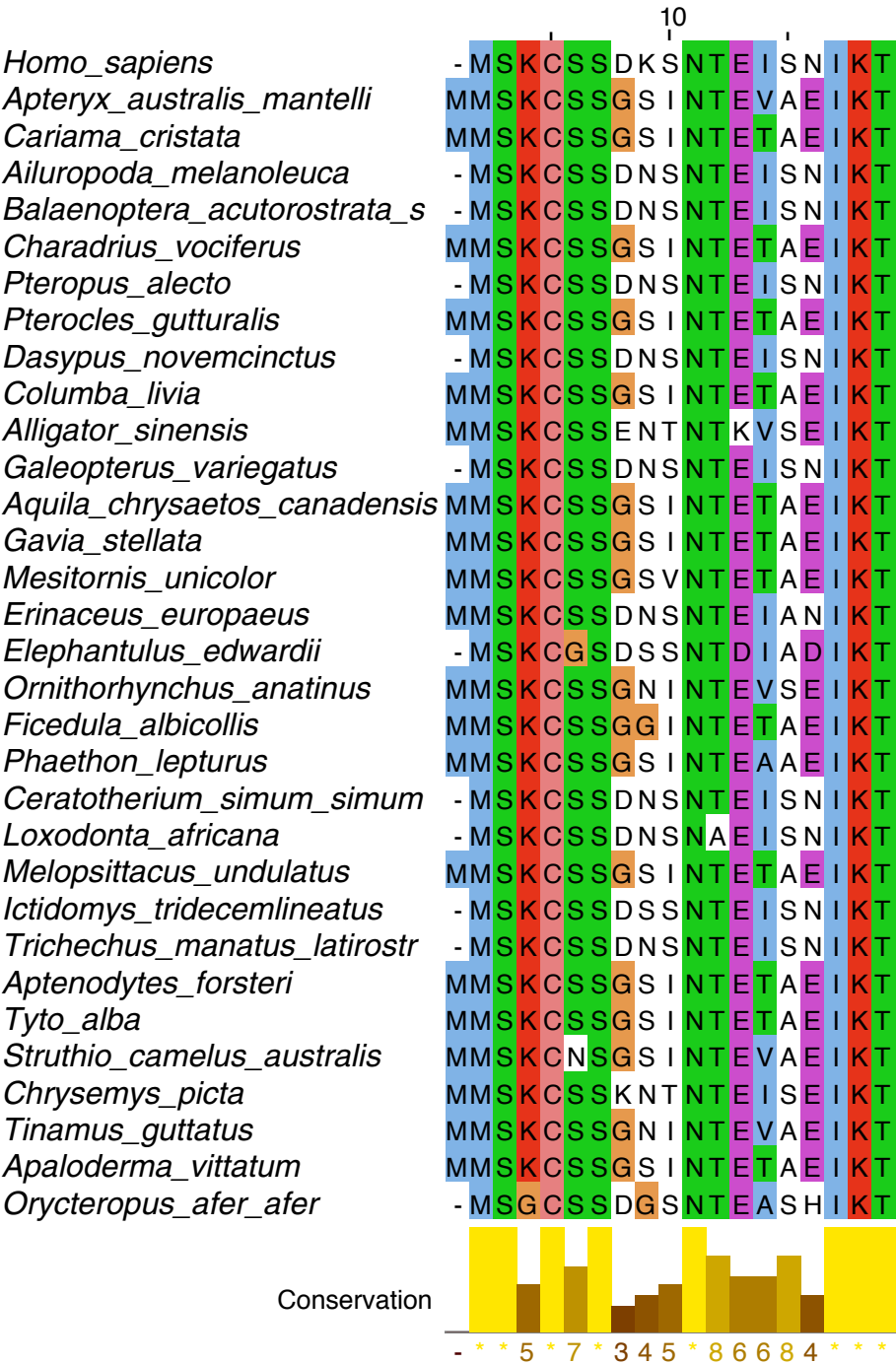


ENSGALG00000041419



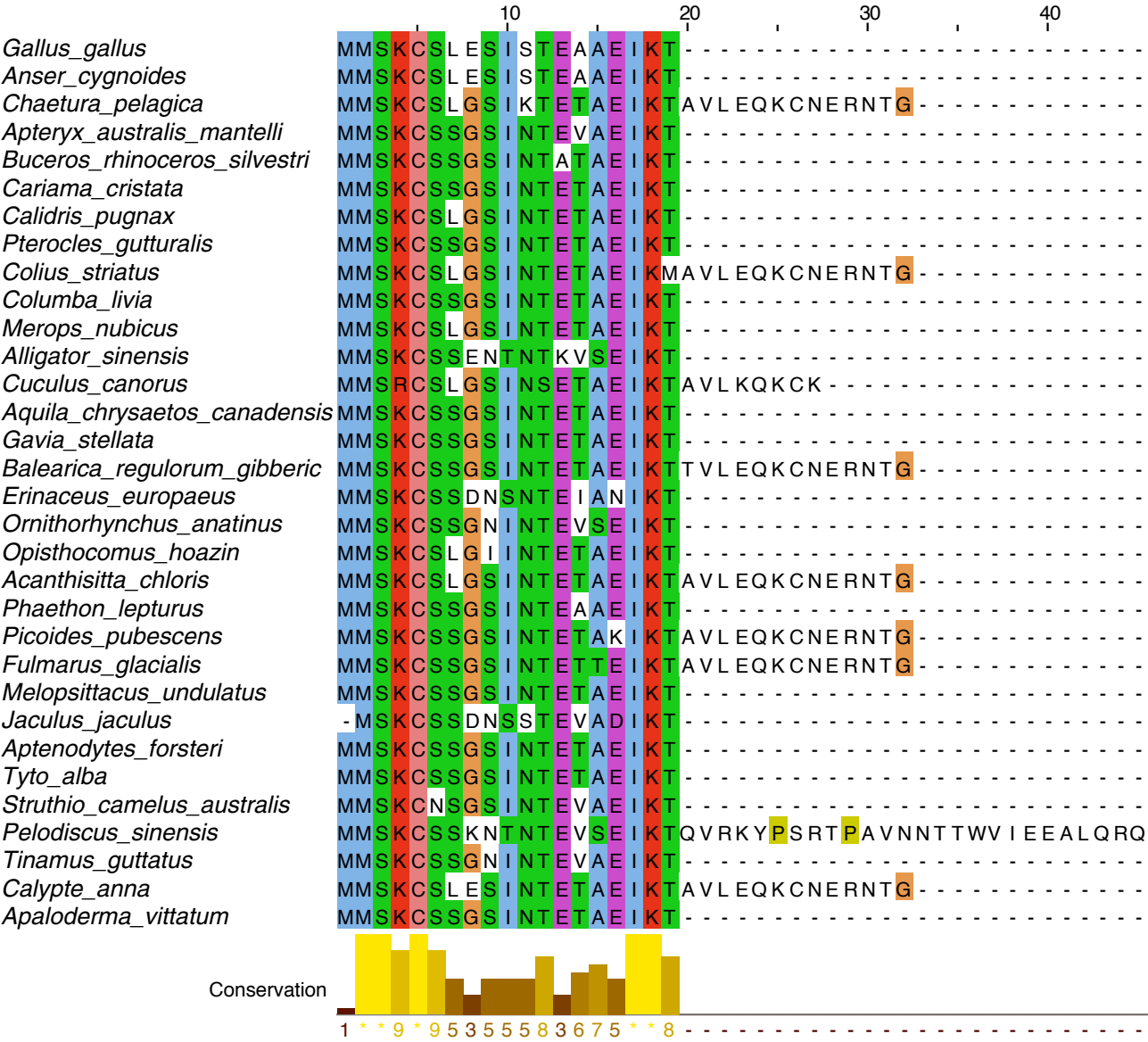
HG0069

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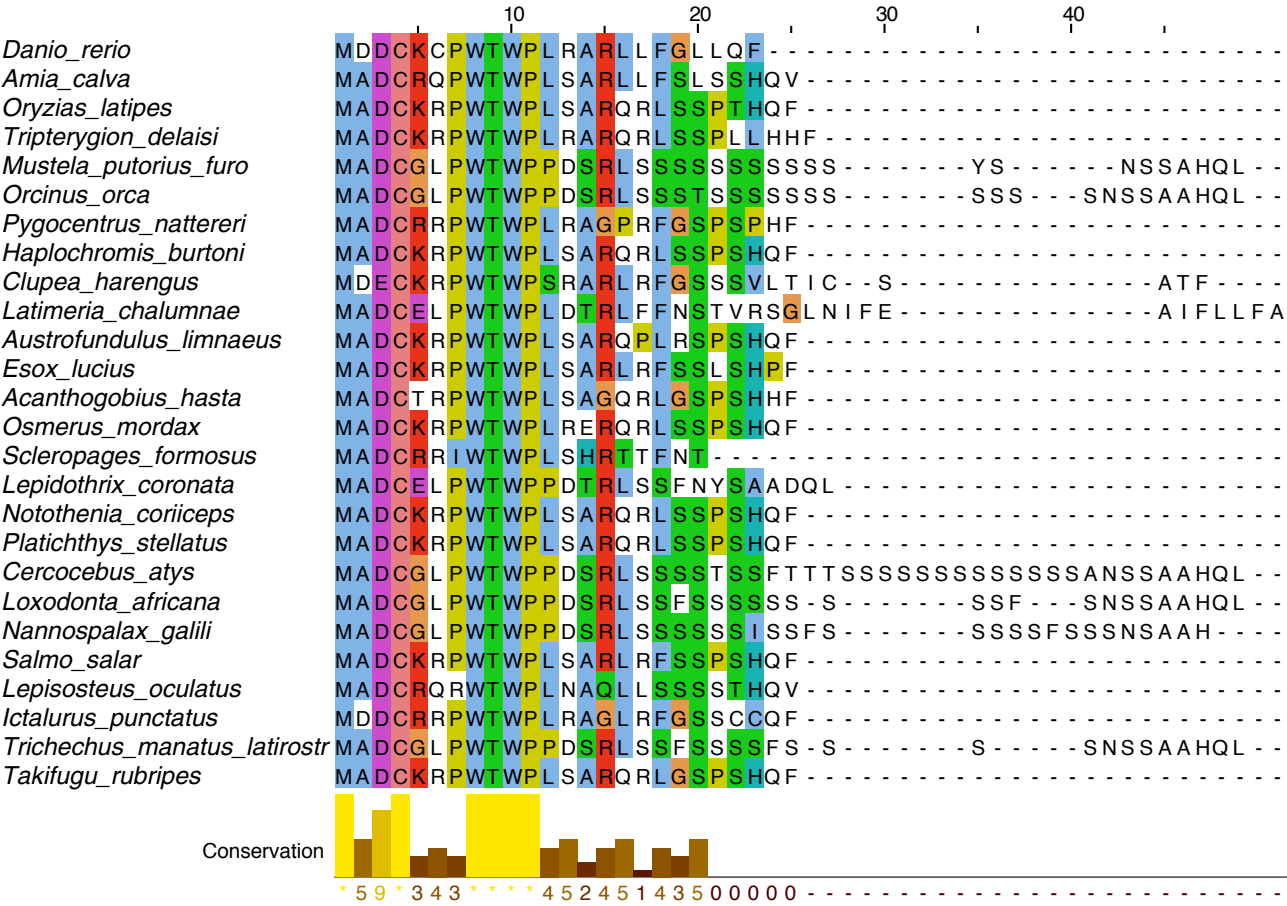
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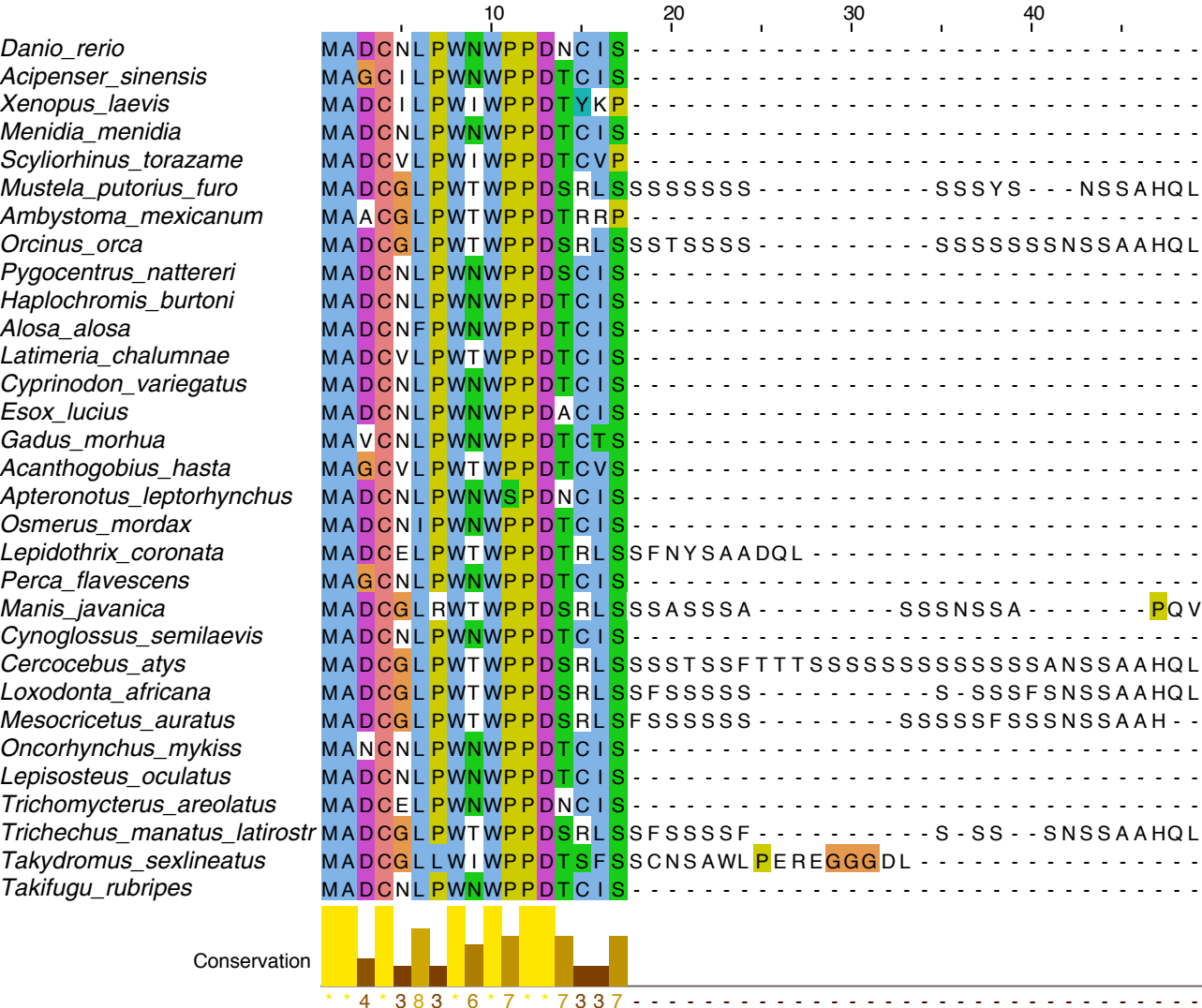
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ENSDARG00000040926 (nr2f2)



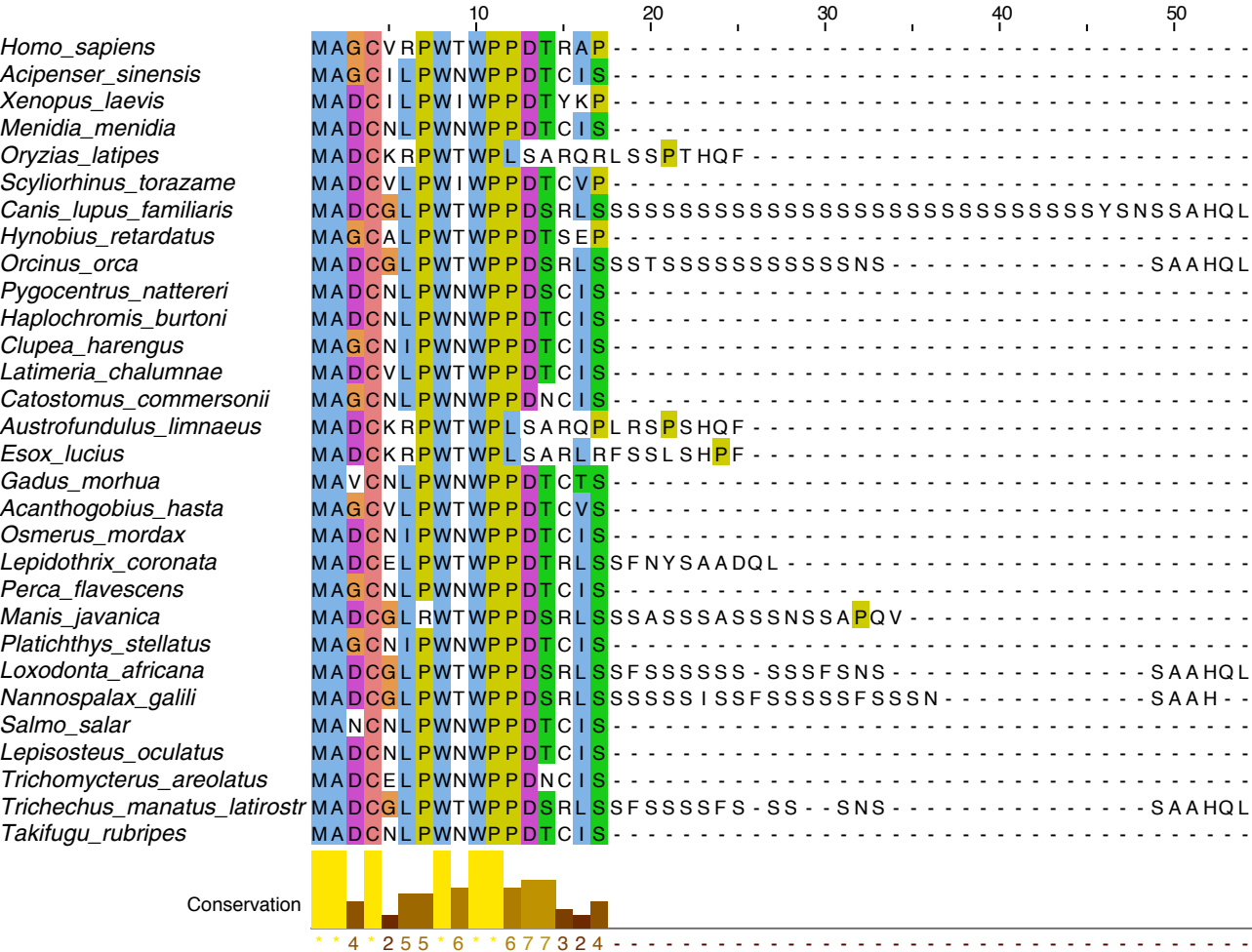
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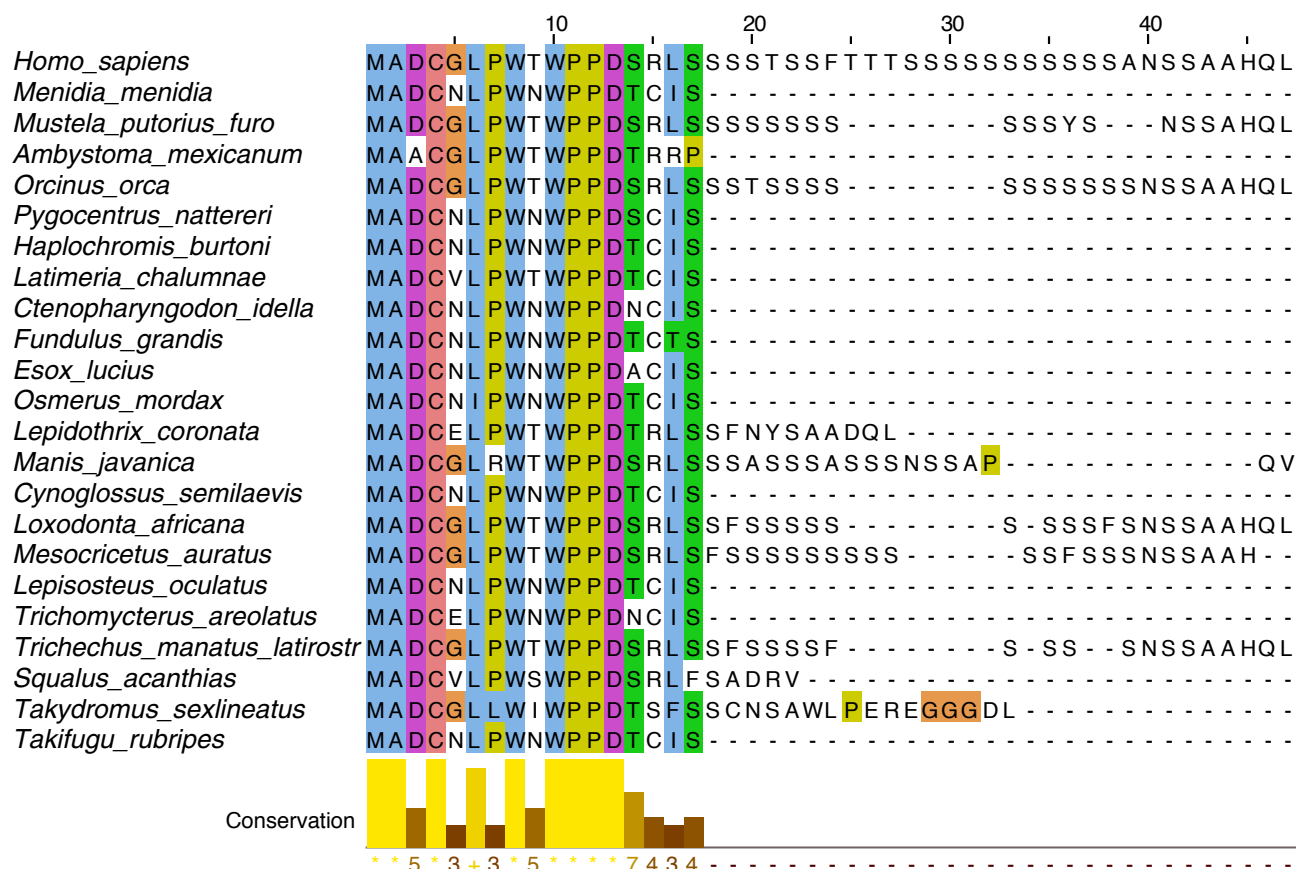


HG0070

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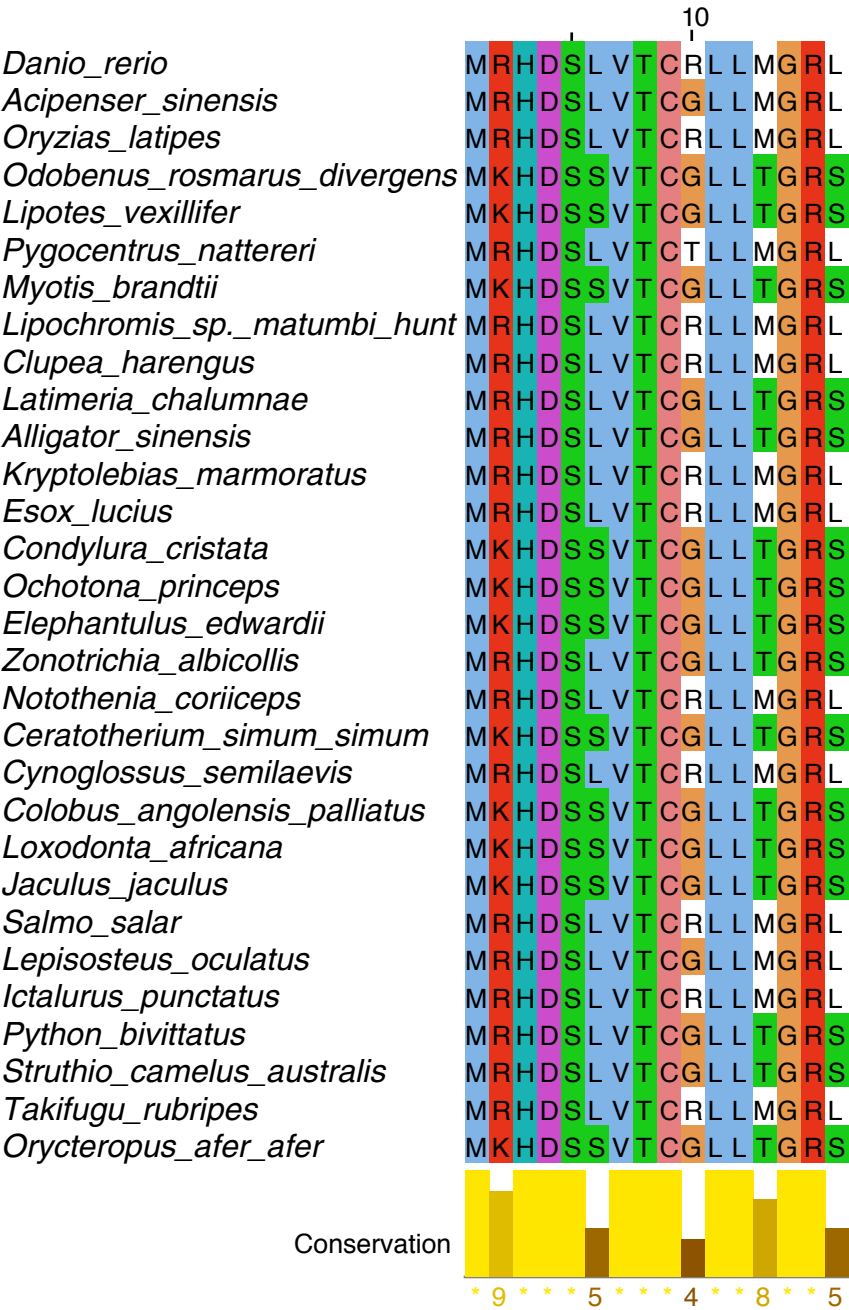


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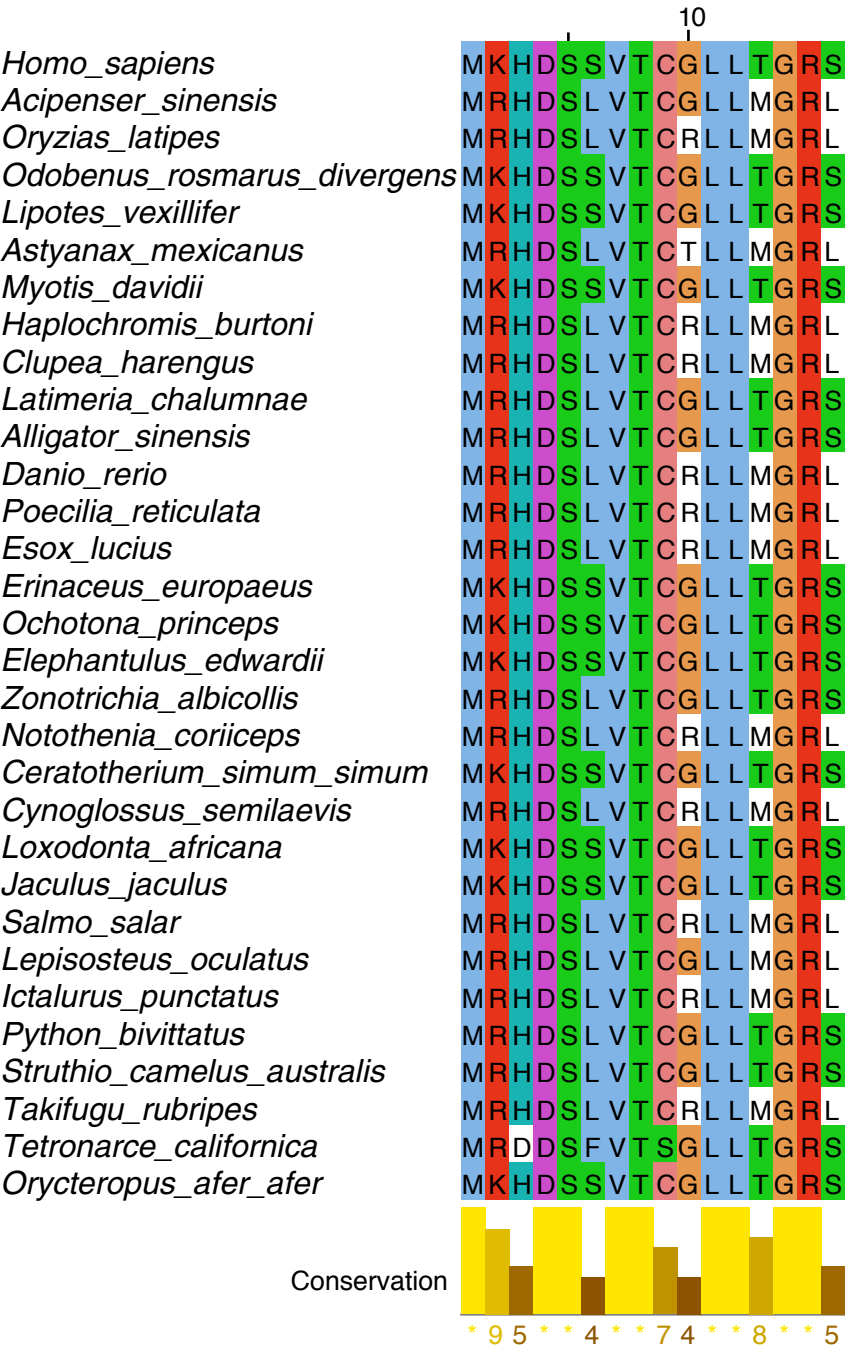
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ENSDARG00000098240 (meis2a)



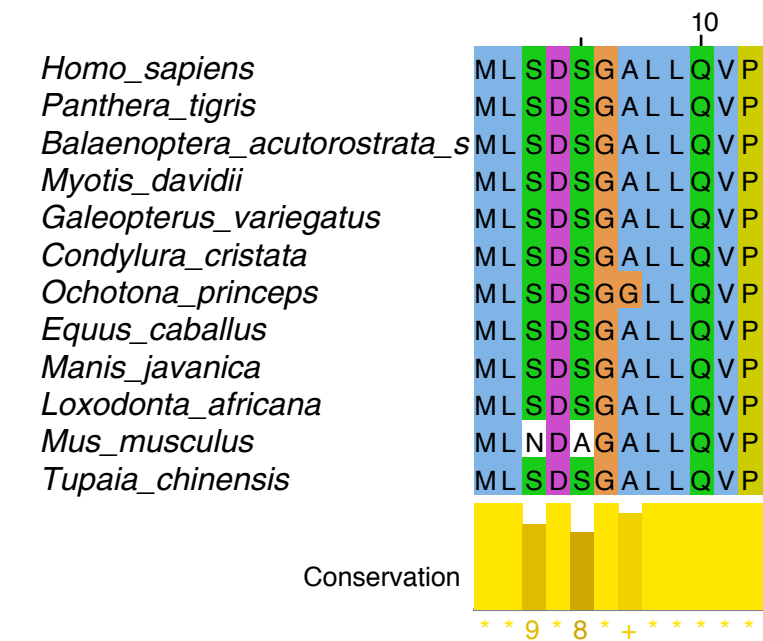
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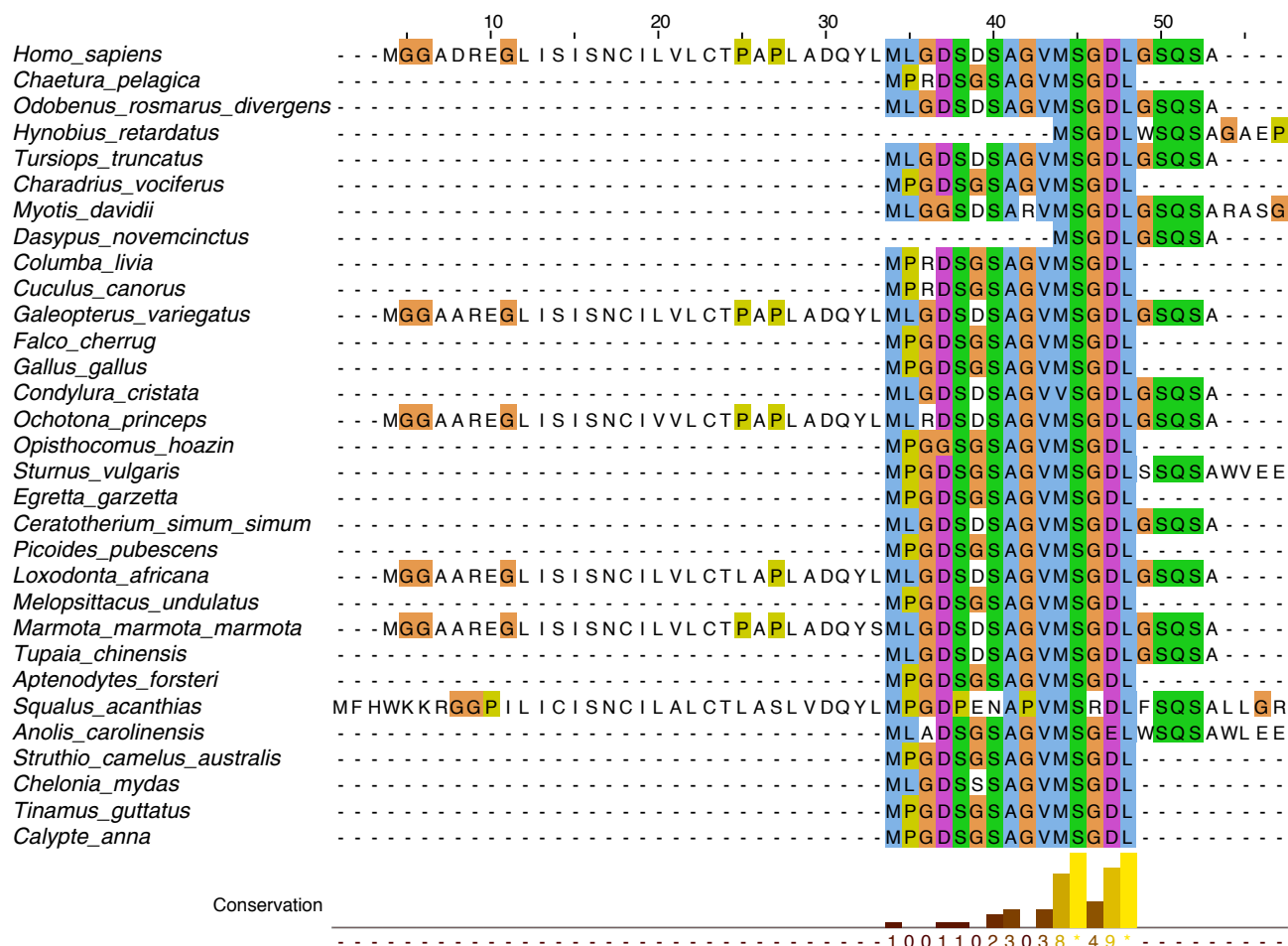


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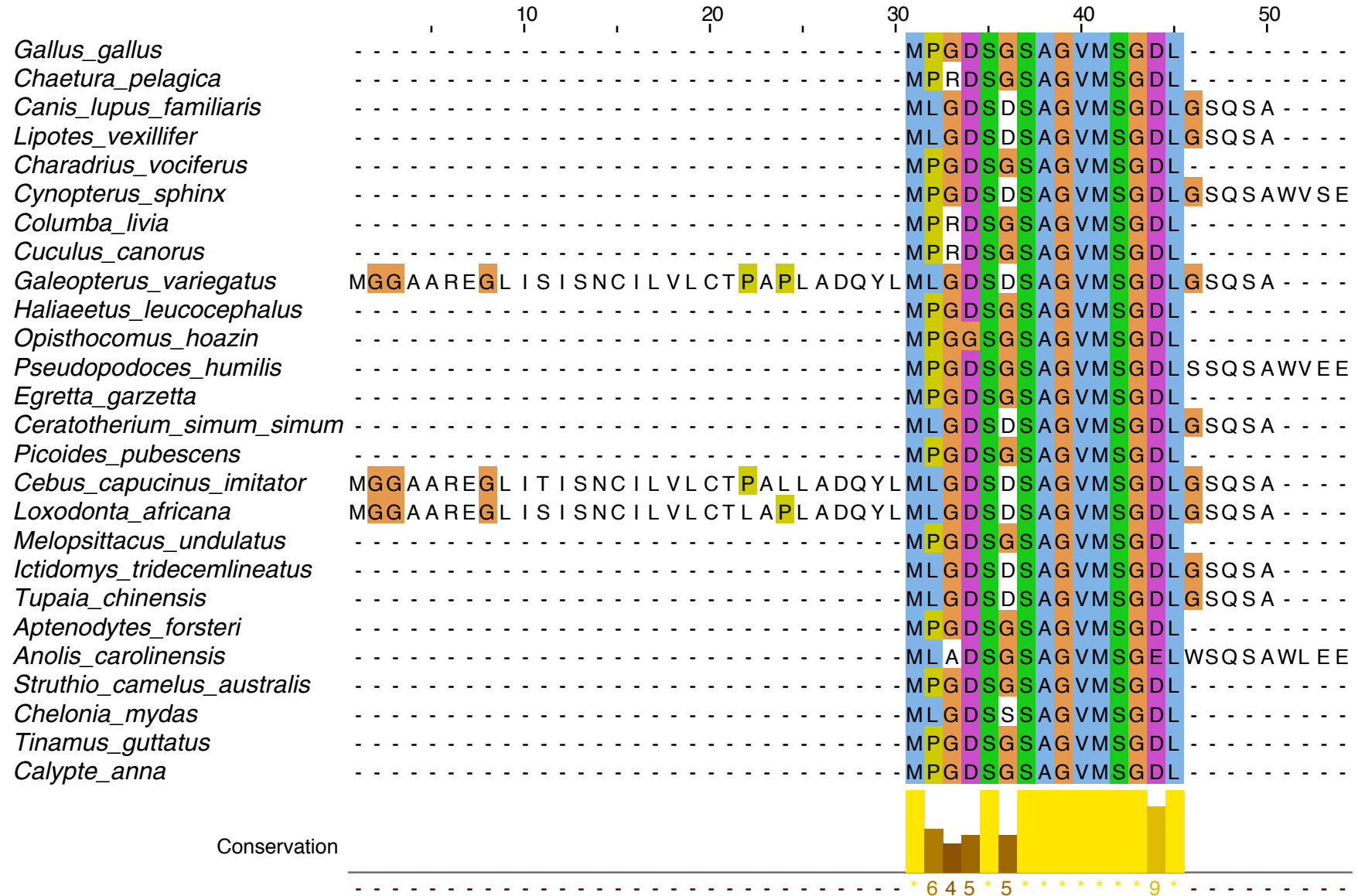


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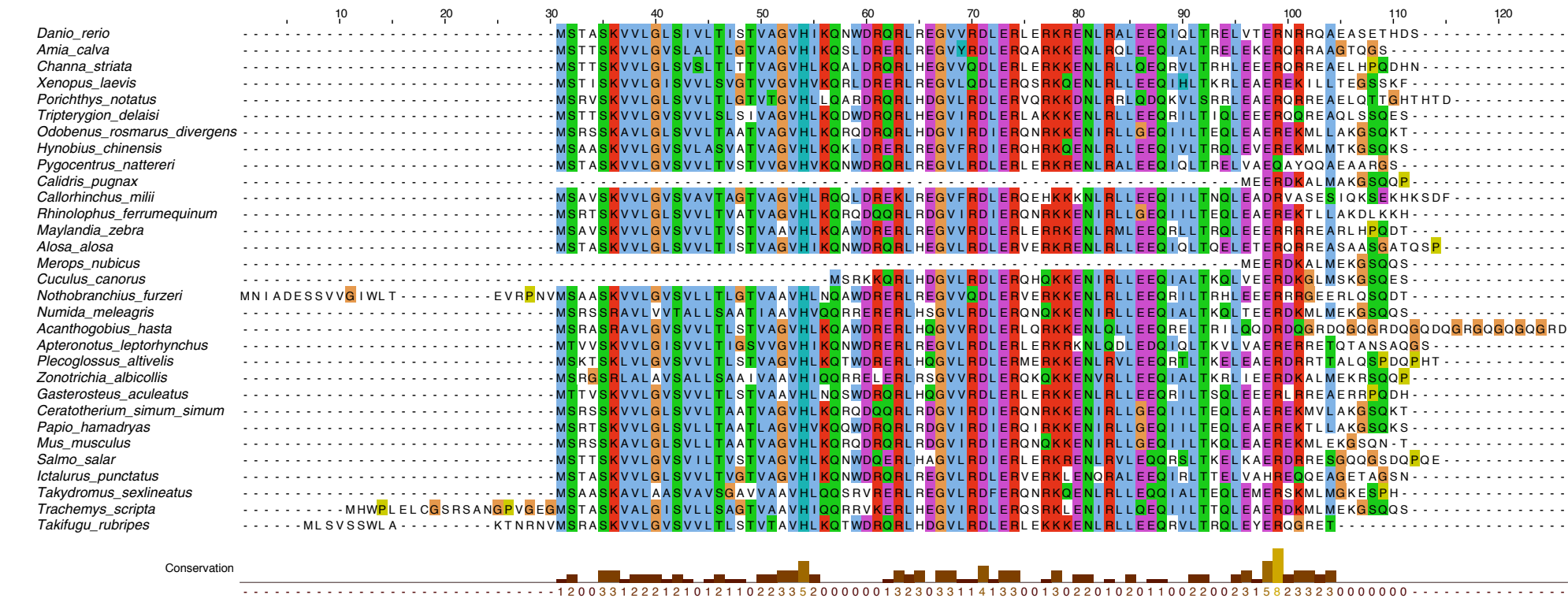
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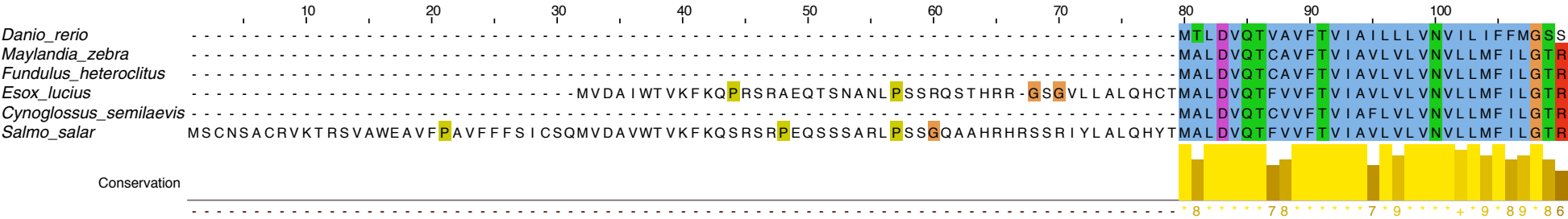
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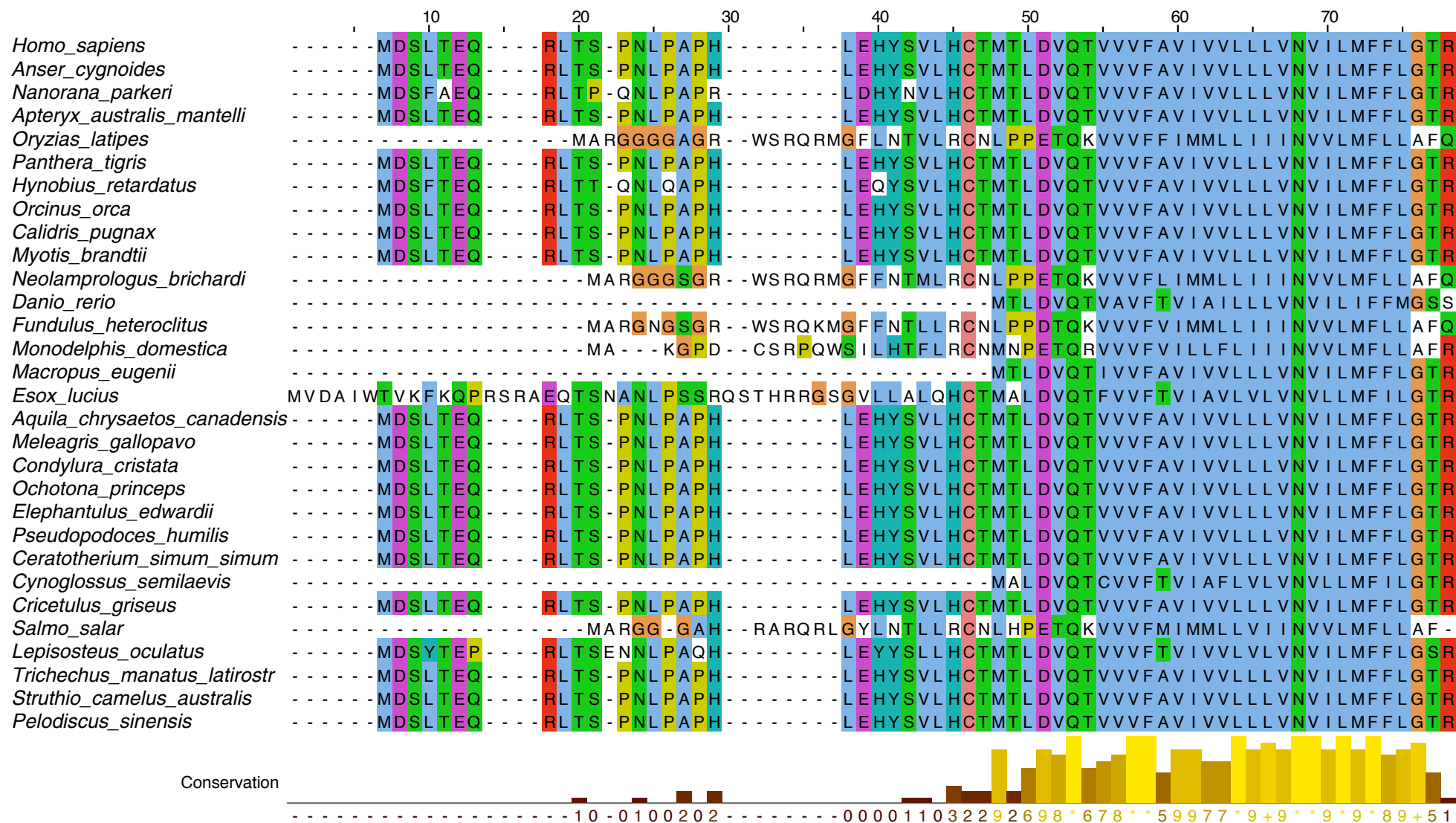


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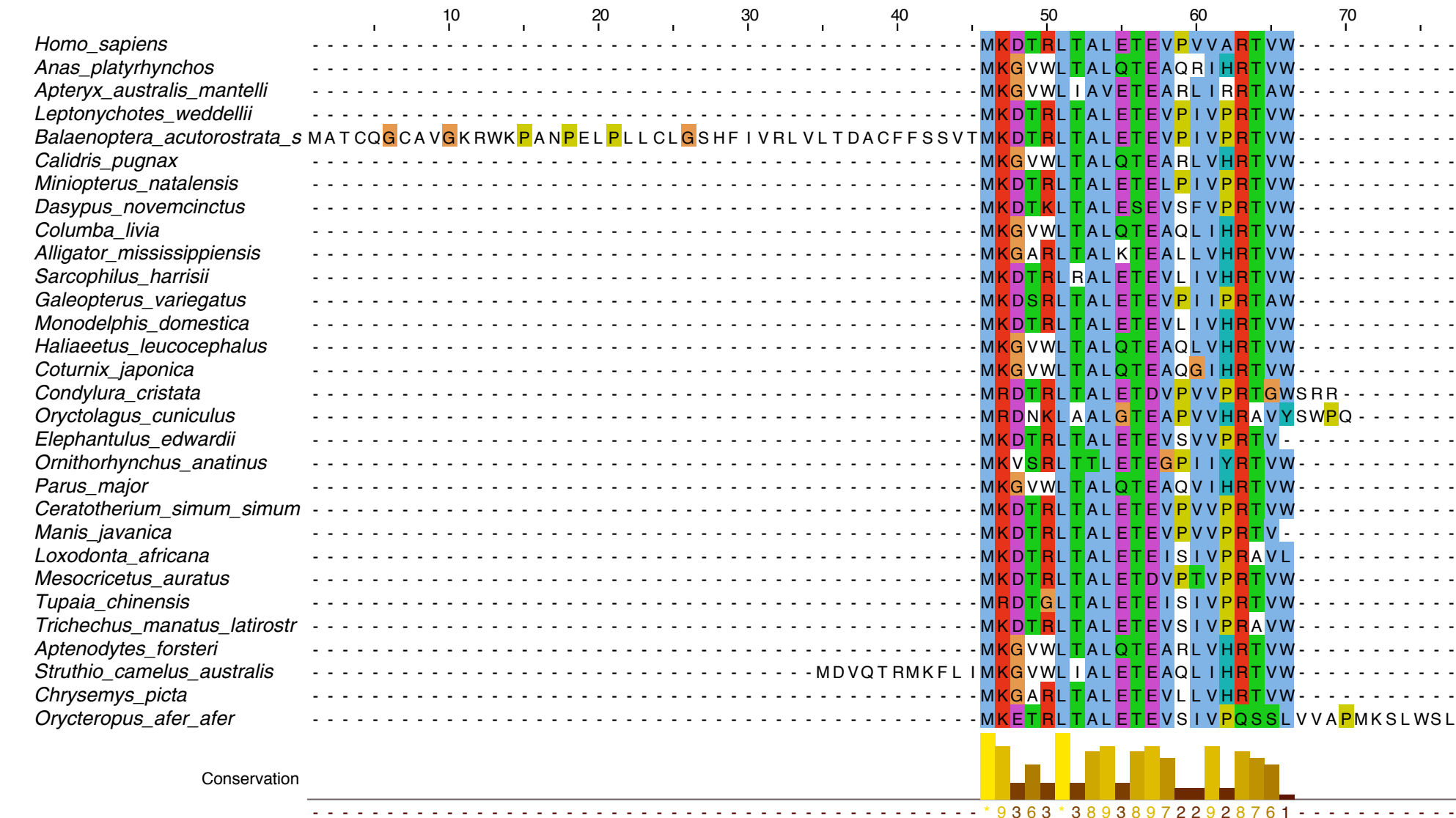


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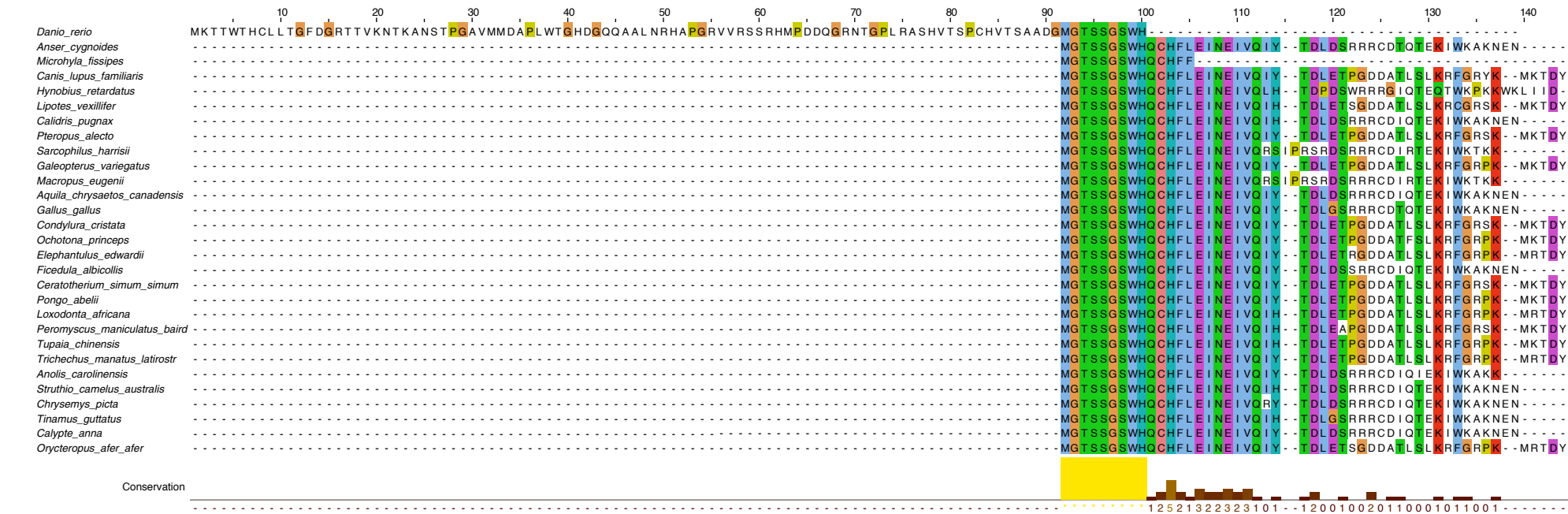
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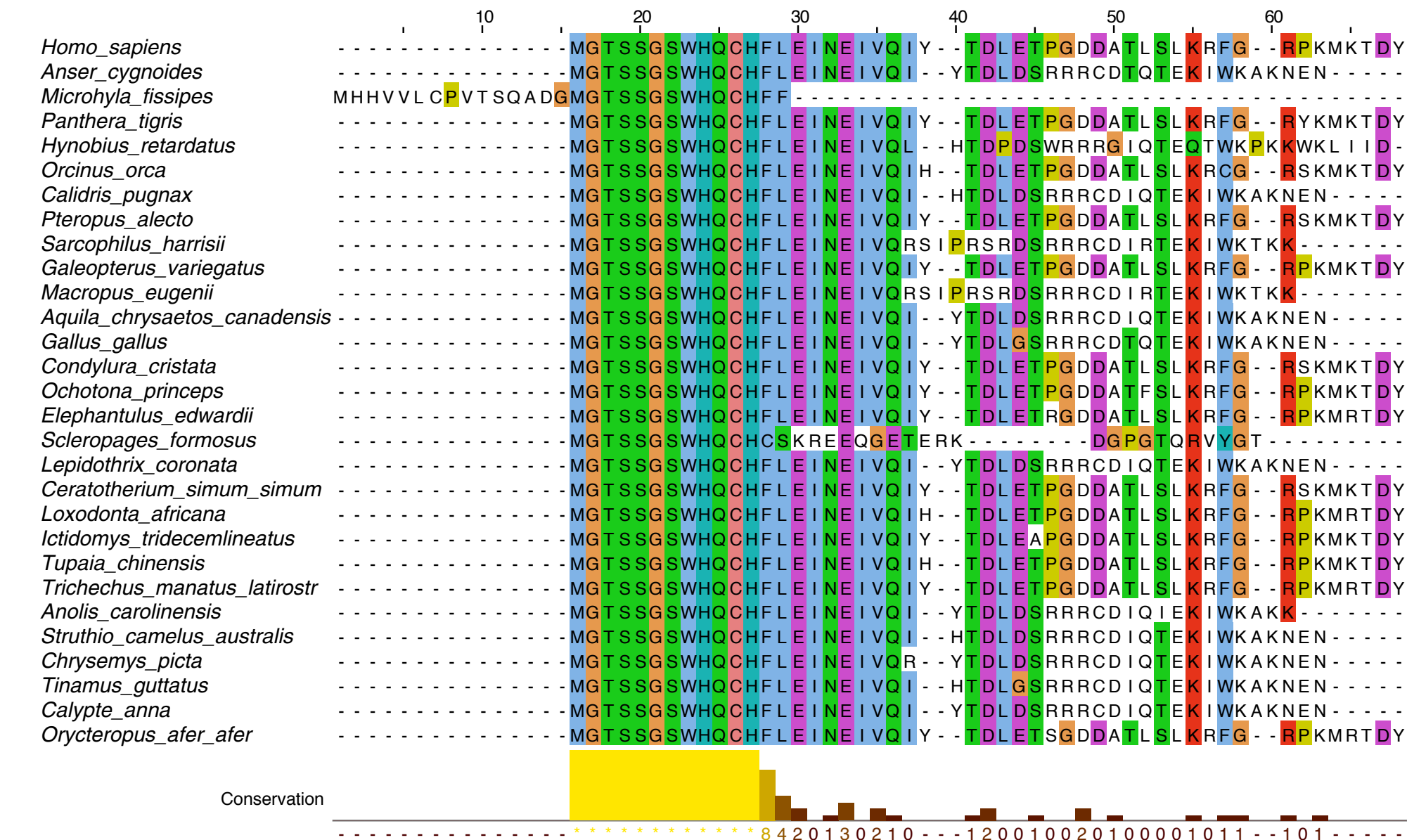


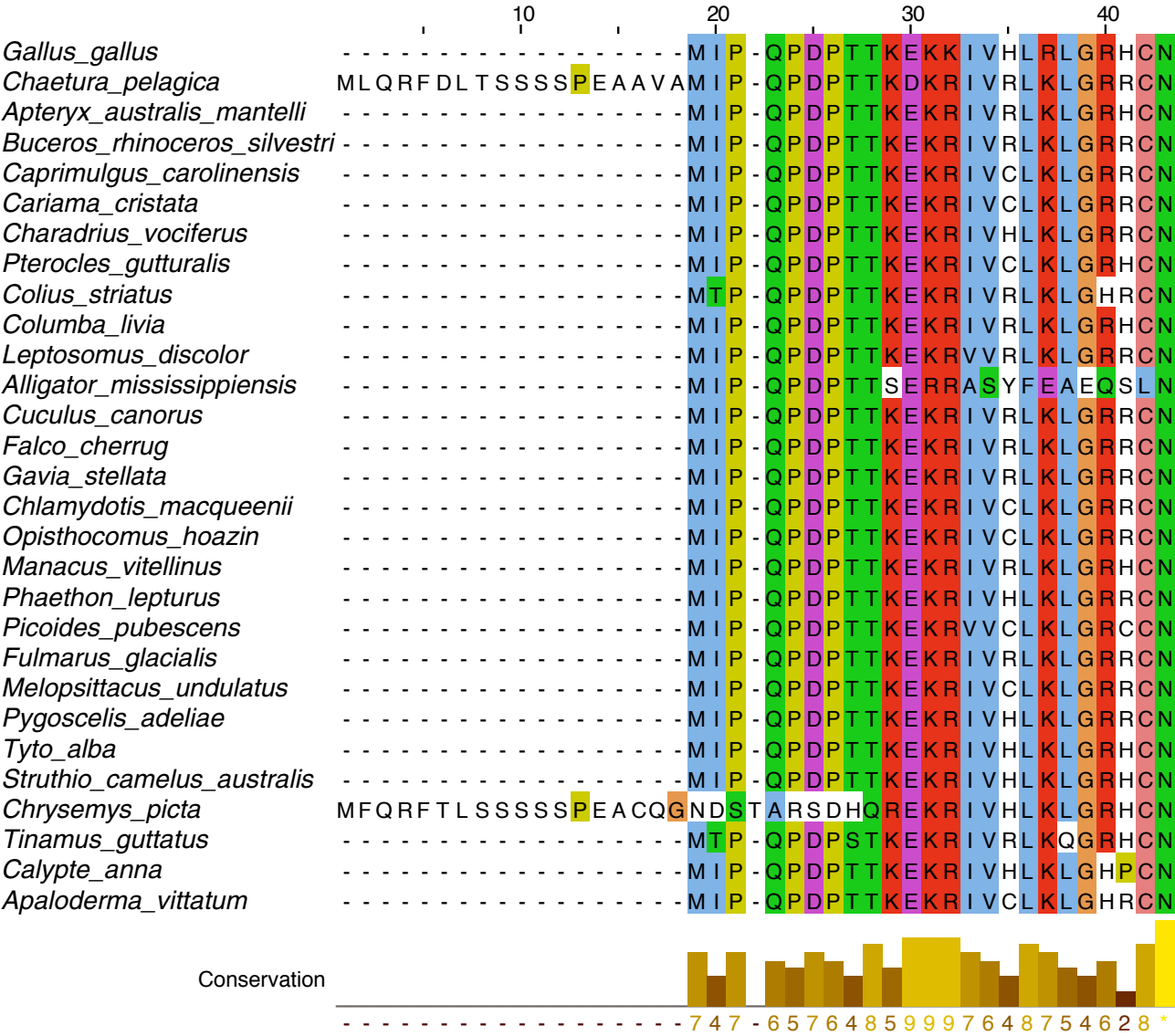
HG0076

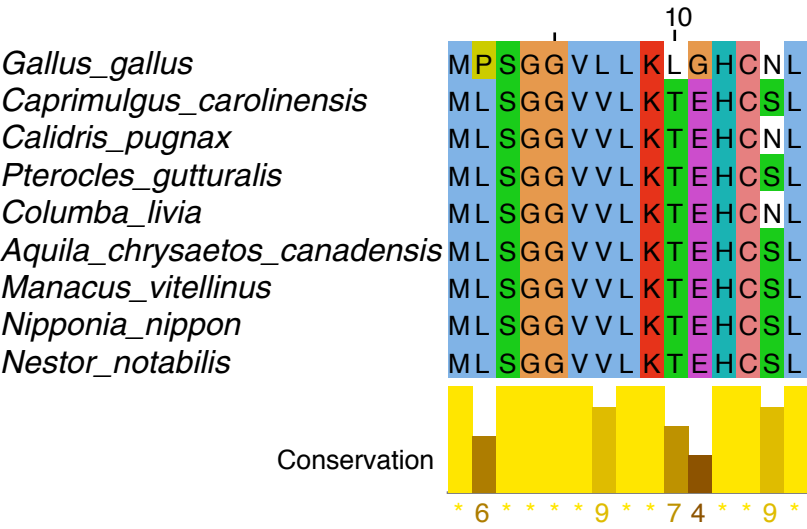
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ENSG00000164600 (NEUROD6)





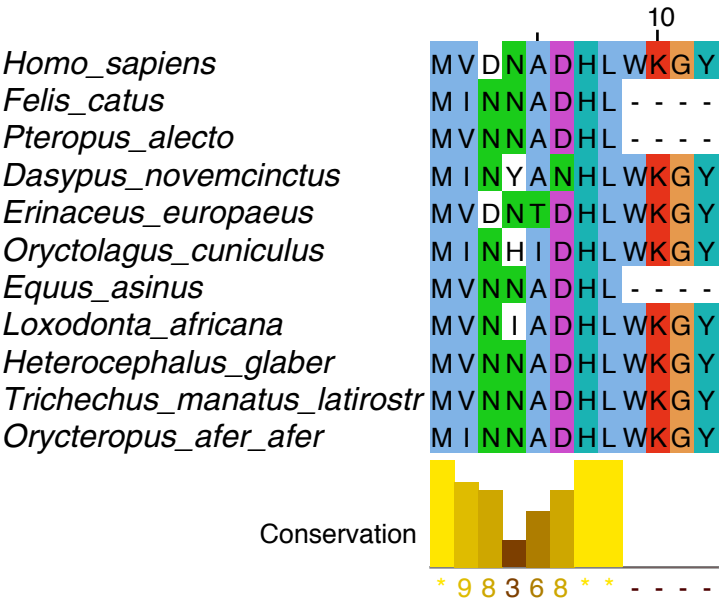


ENSGALG00000016633 (HMBOX1)

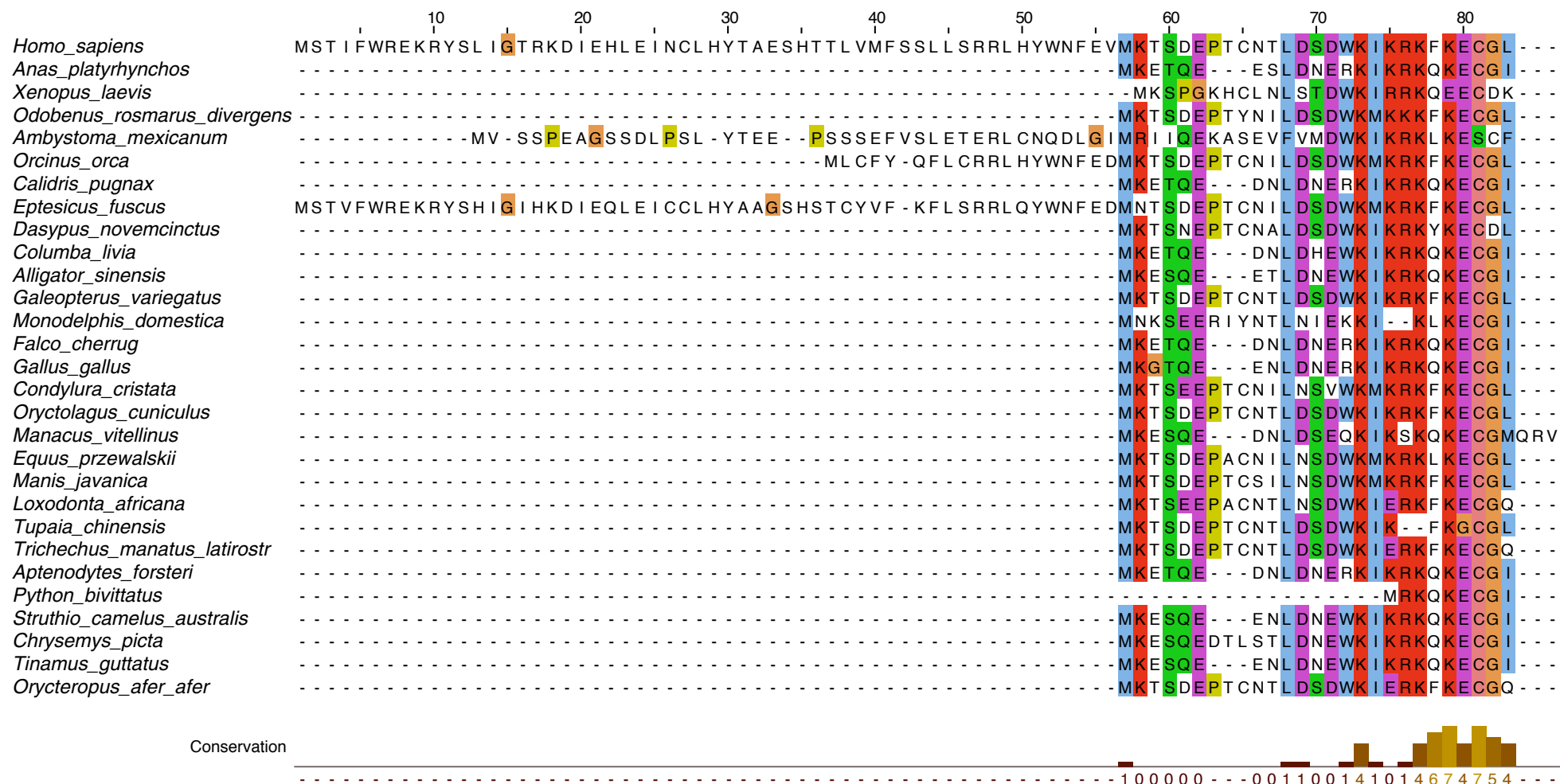


HG0078.2

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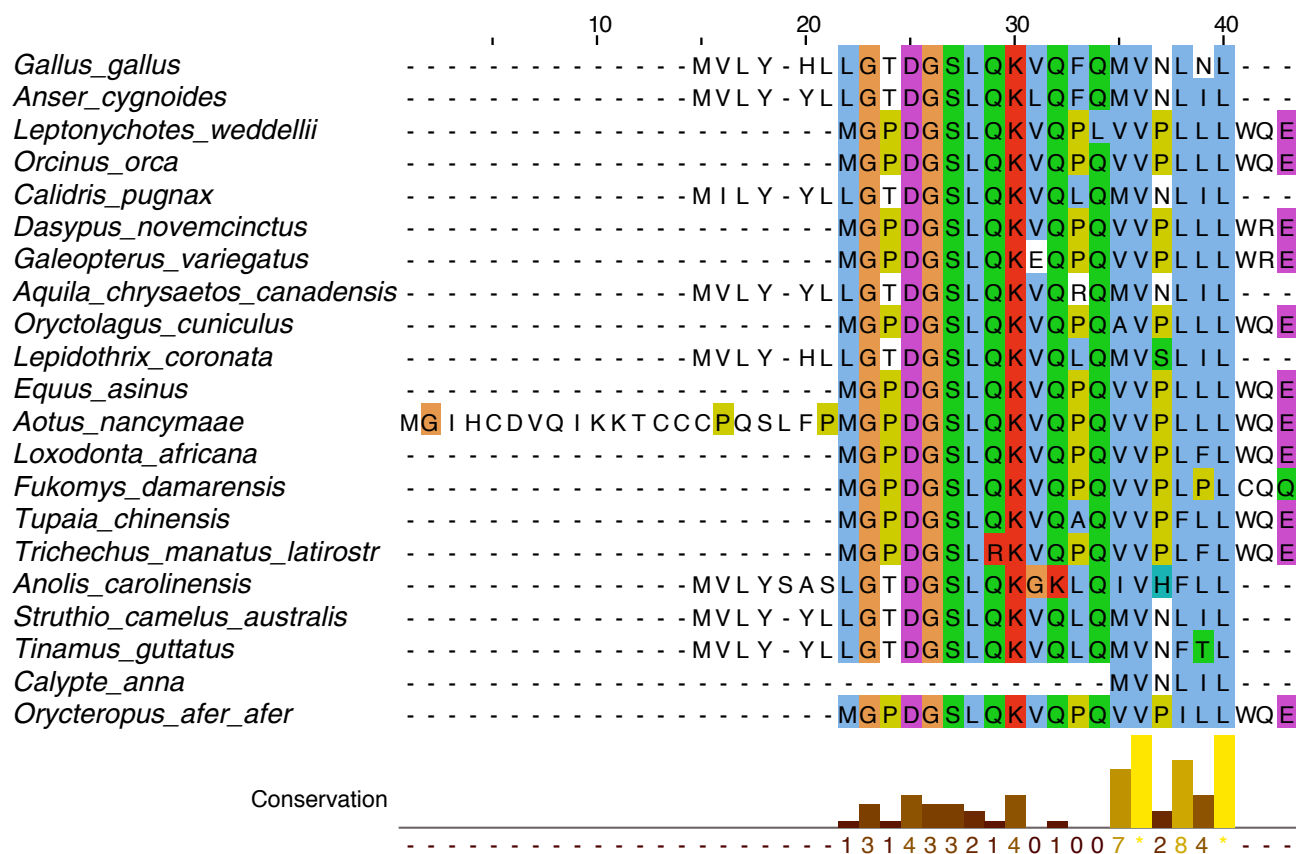
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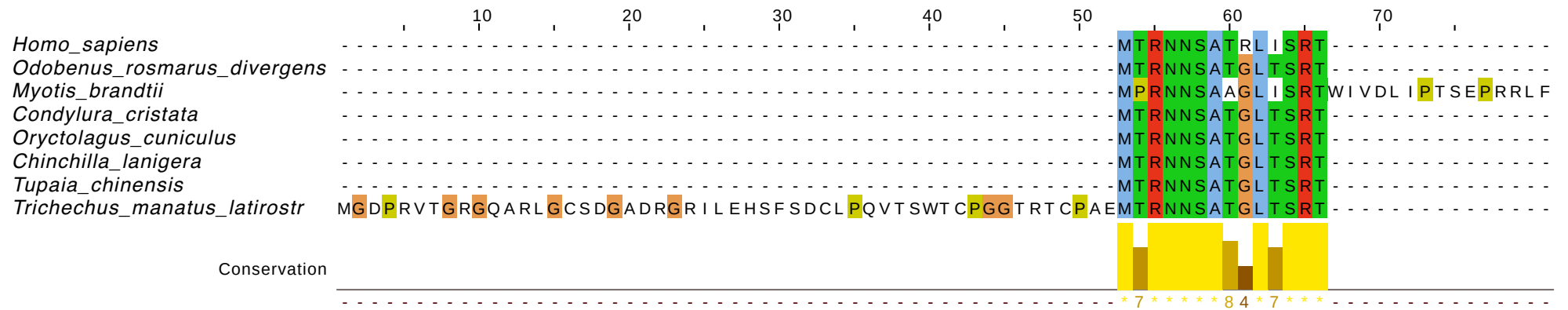
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ENSGALG00000039403

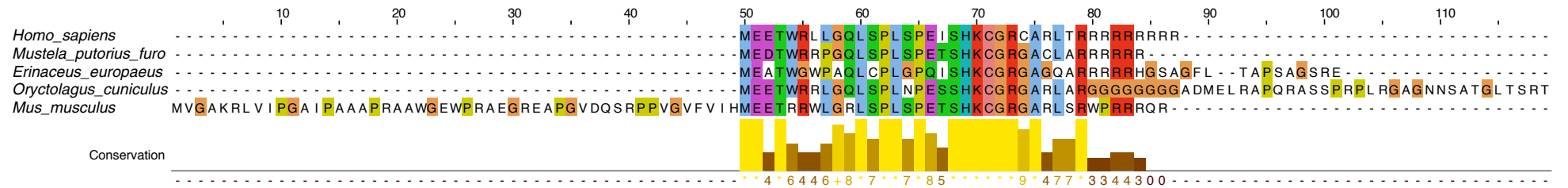


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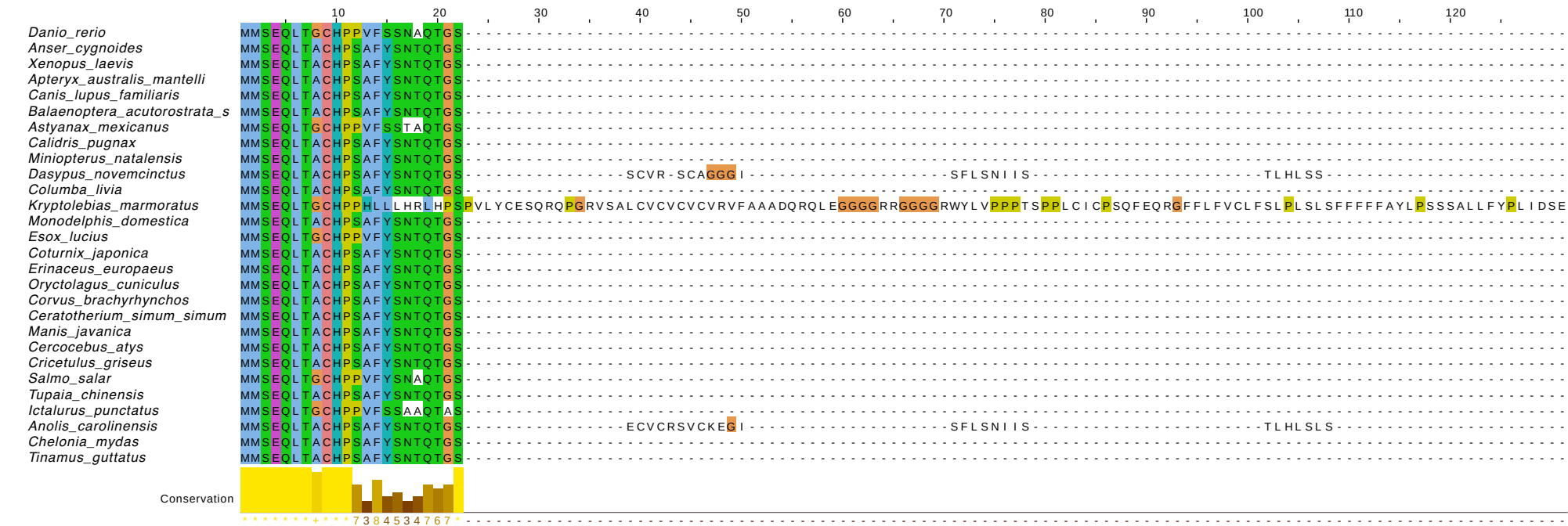
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ENSG00000179603 (GRM8)



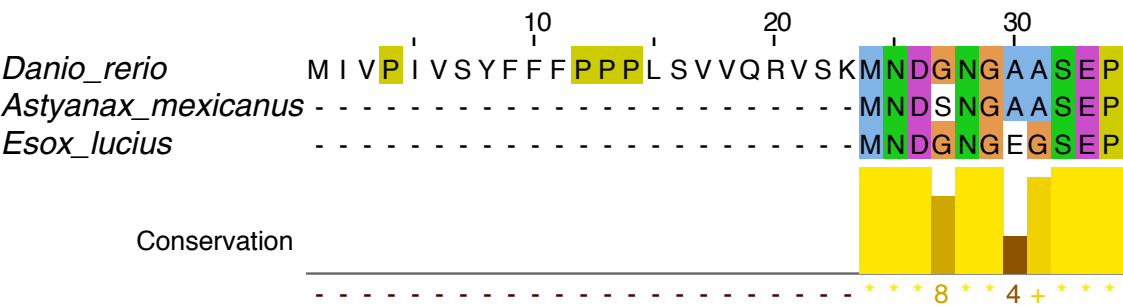
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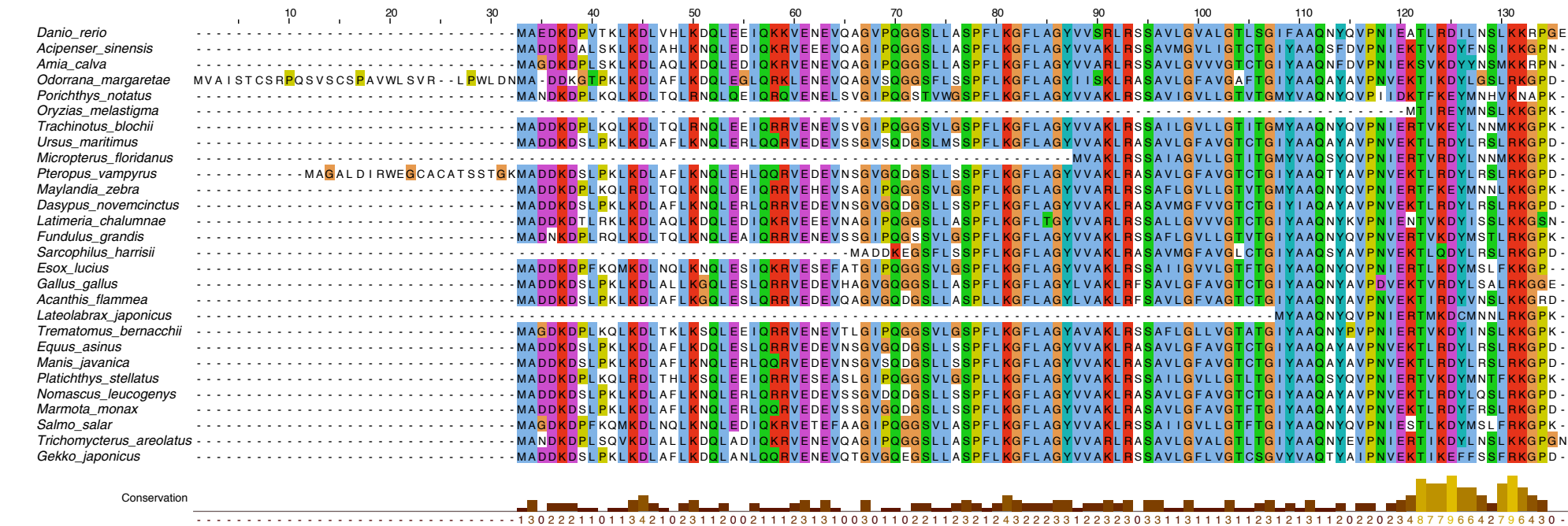
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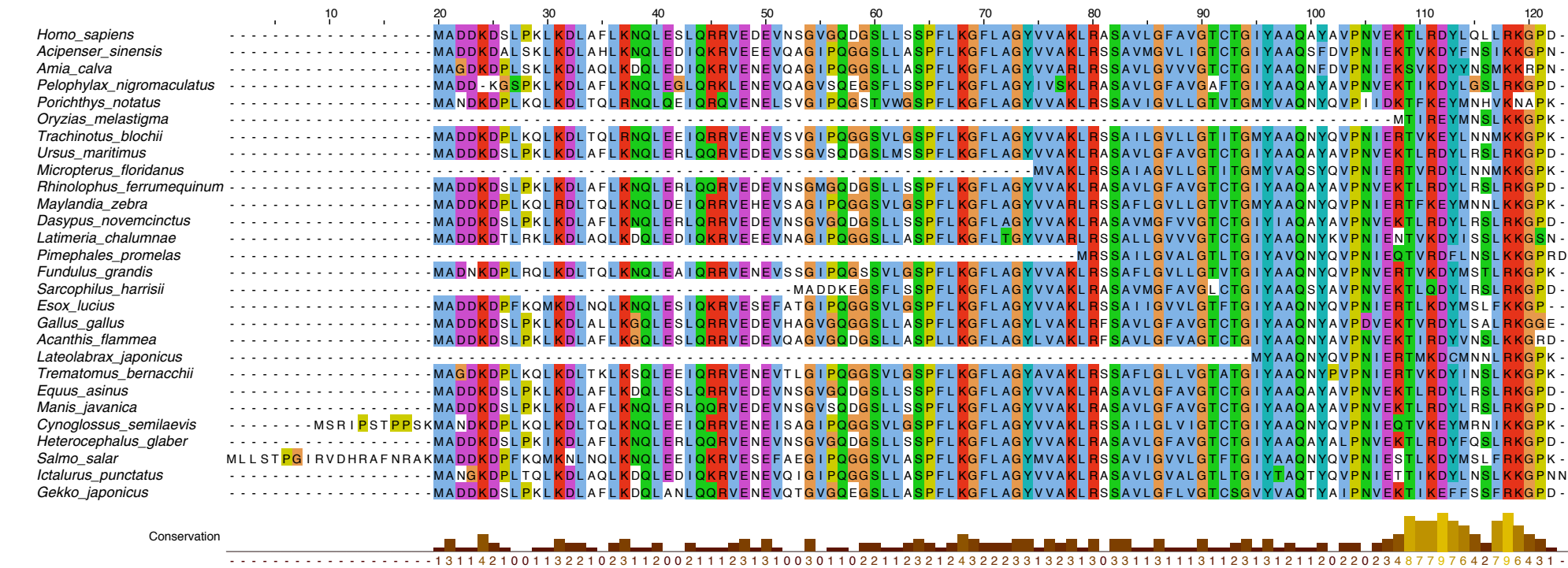
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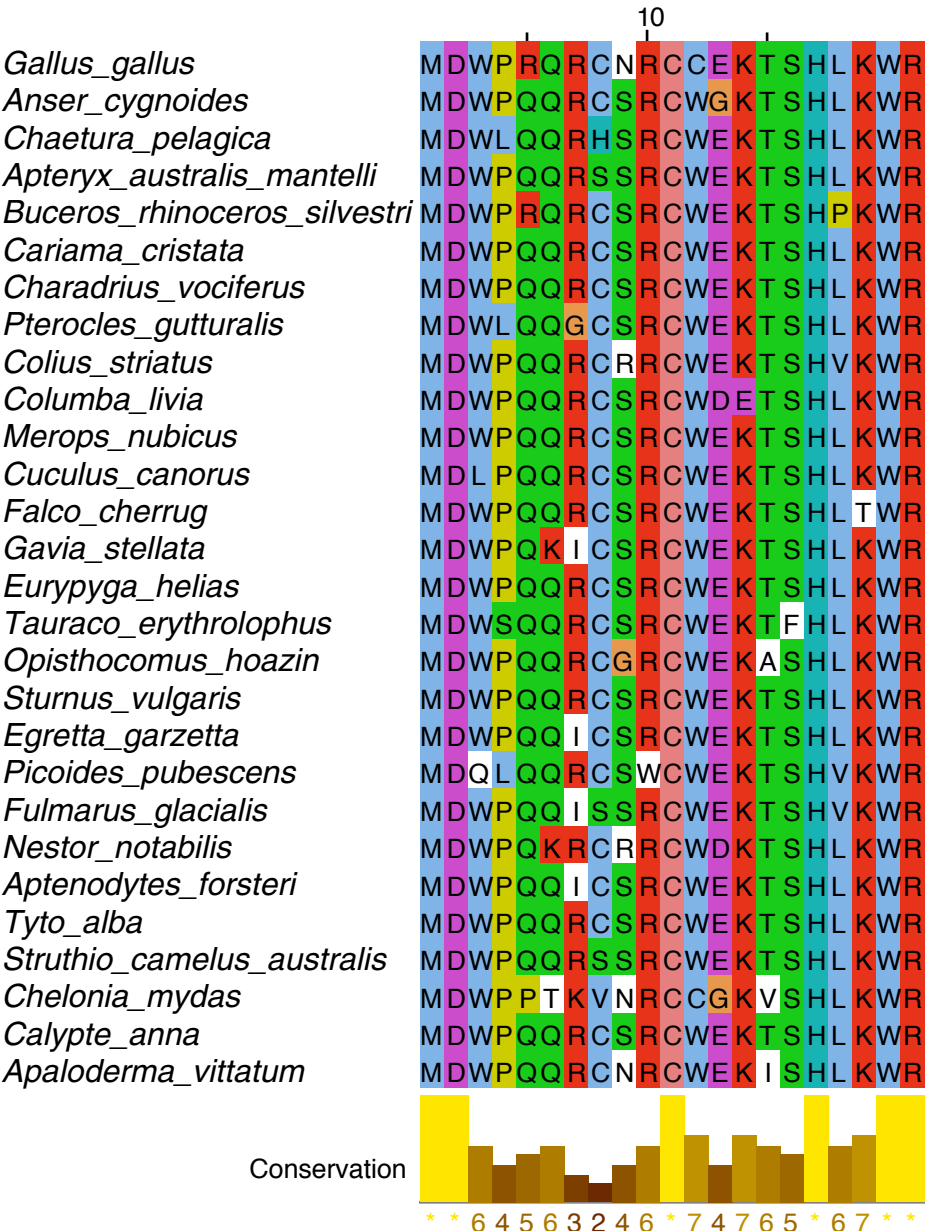
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HG0082

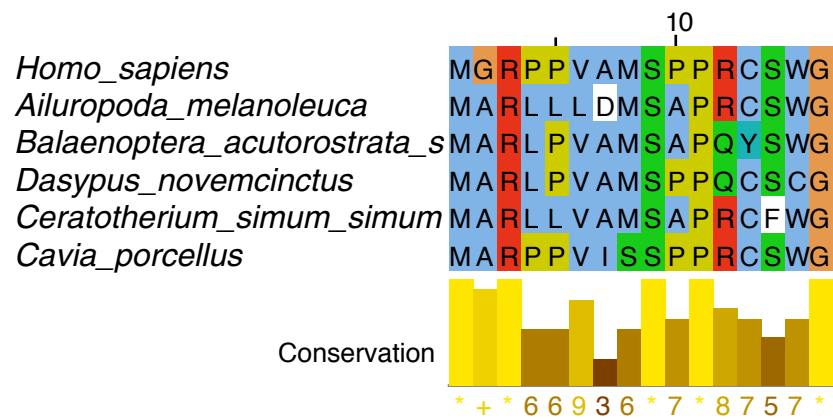
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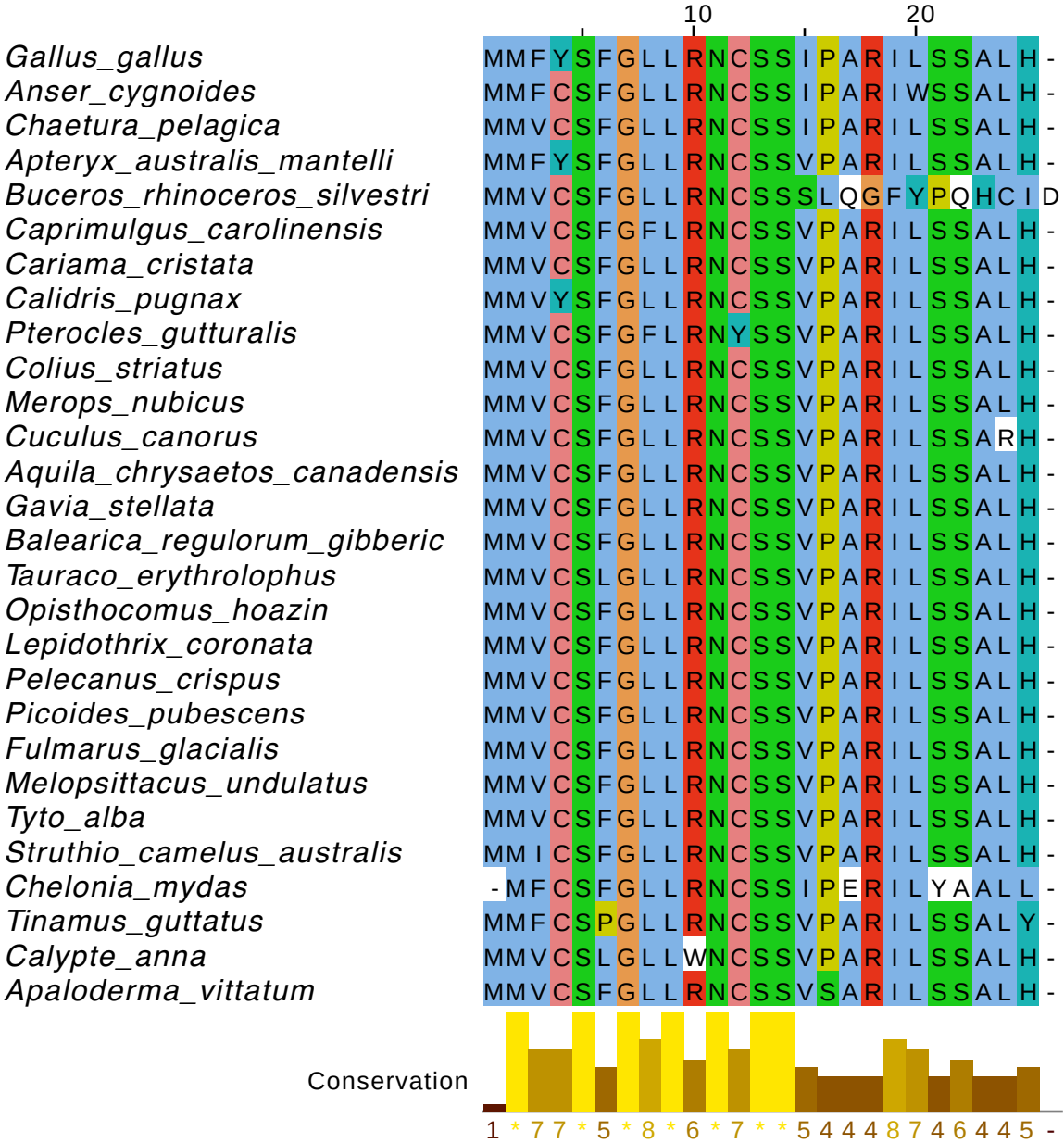




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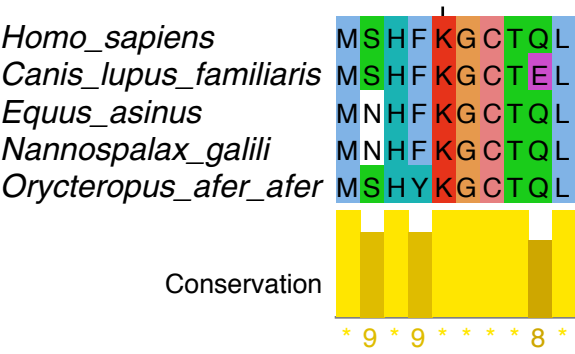
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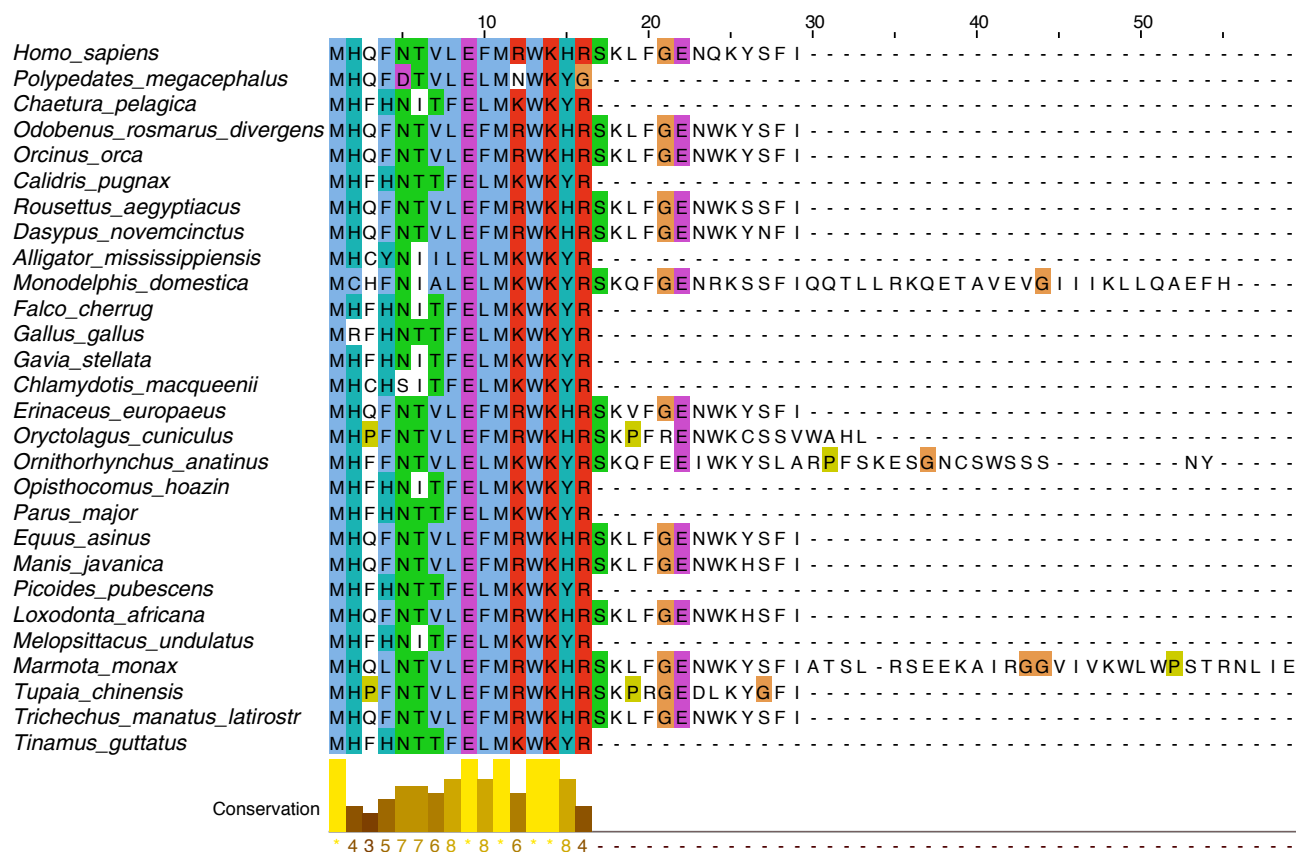


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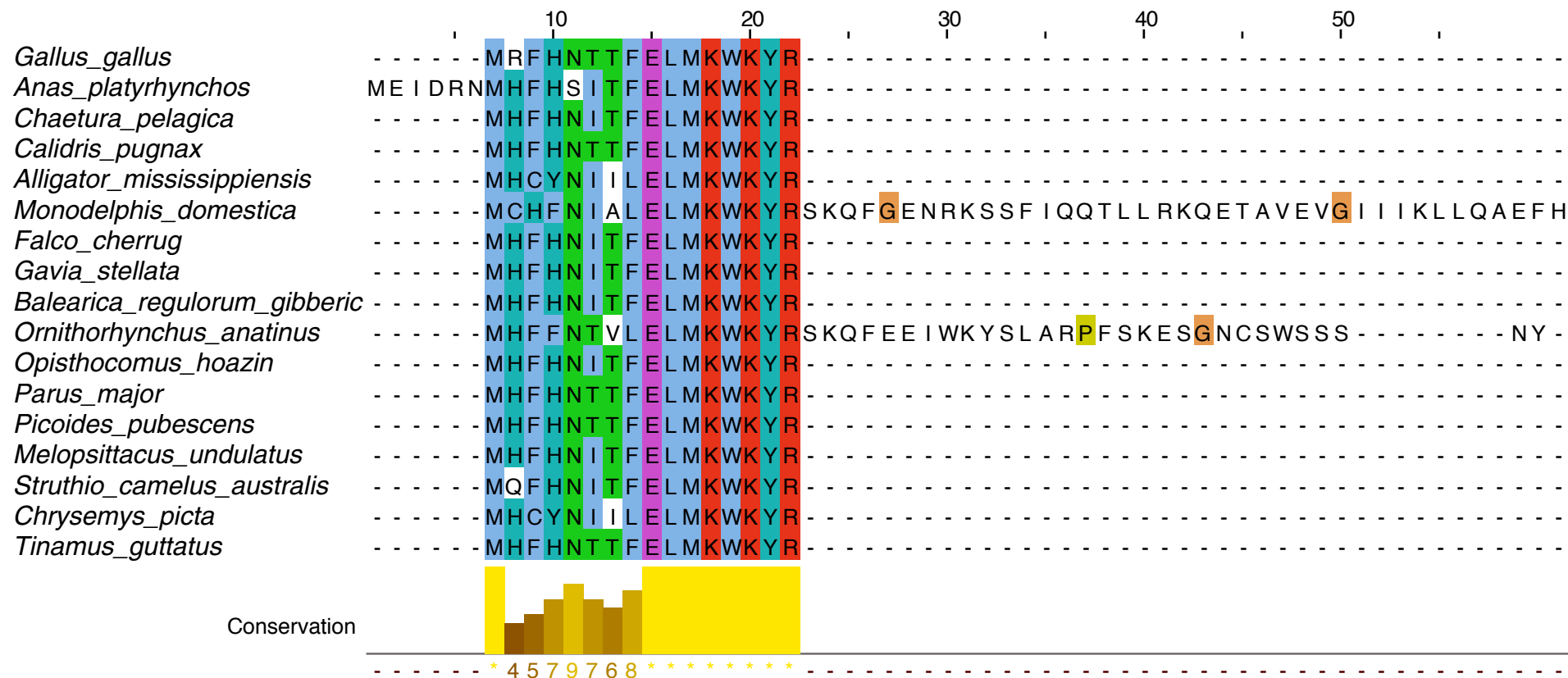
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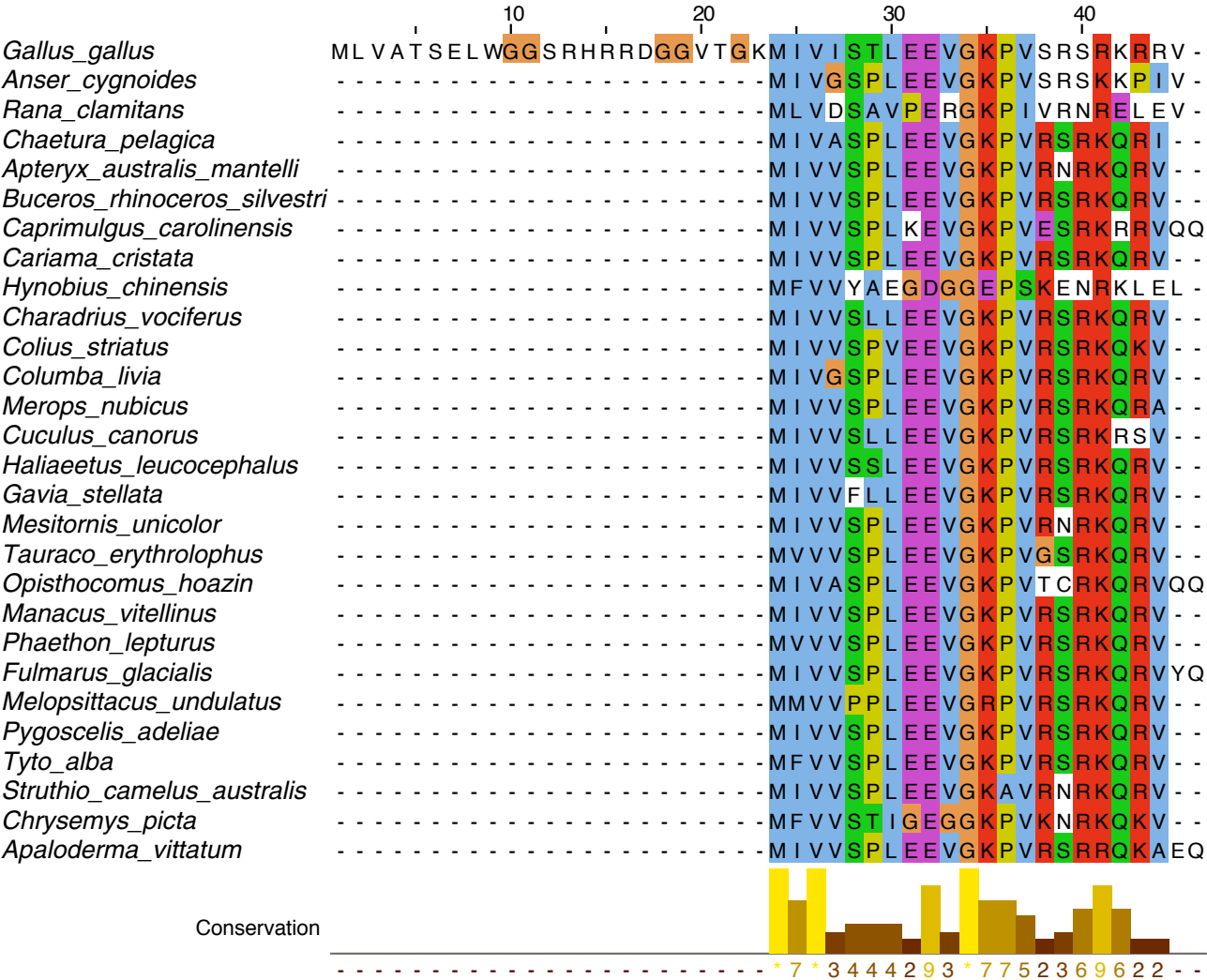


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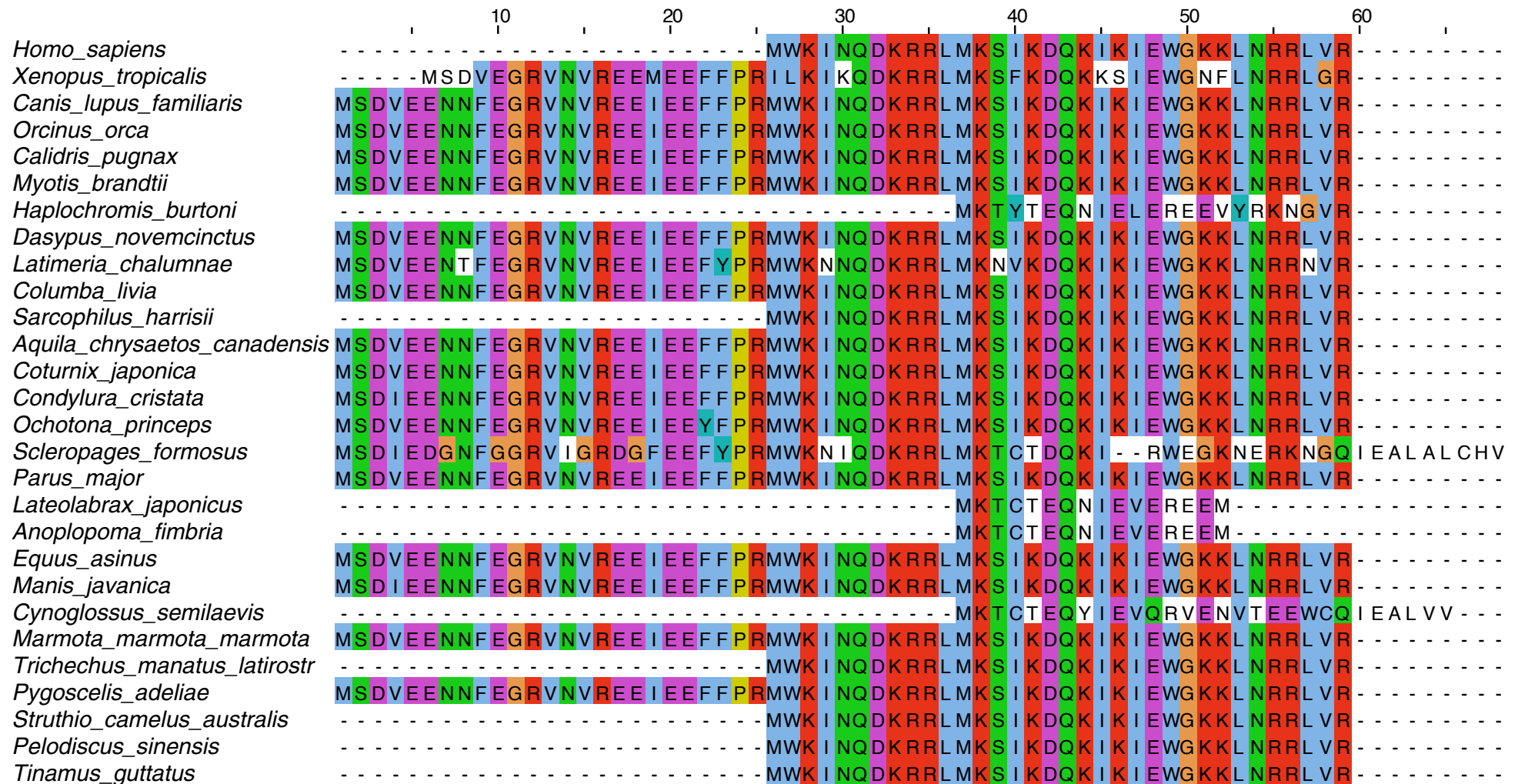
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ENSGALG00000009835 (XPOT)

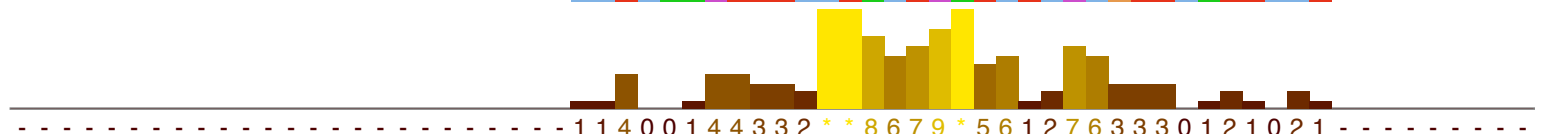


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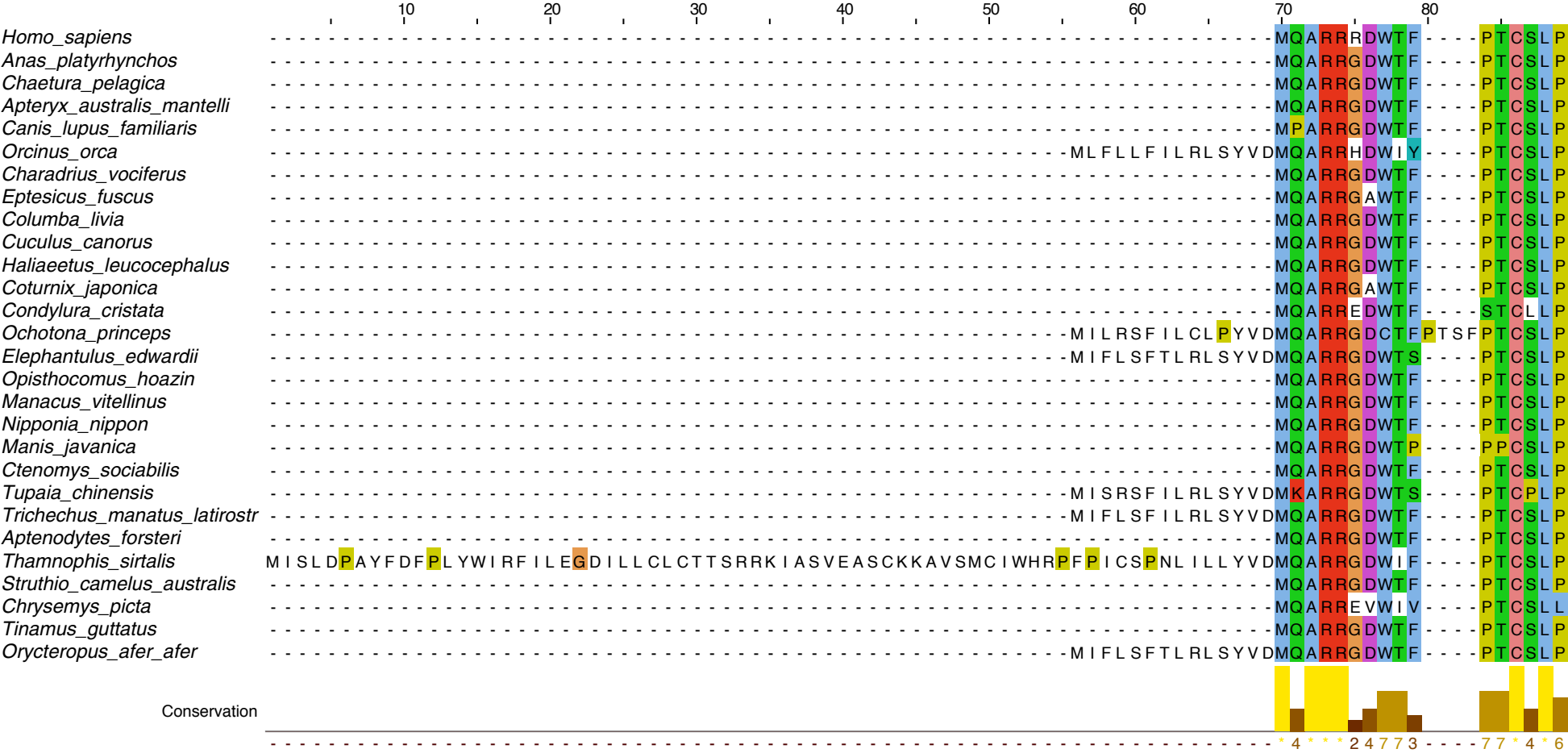


Conservation

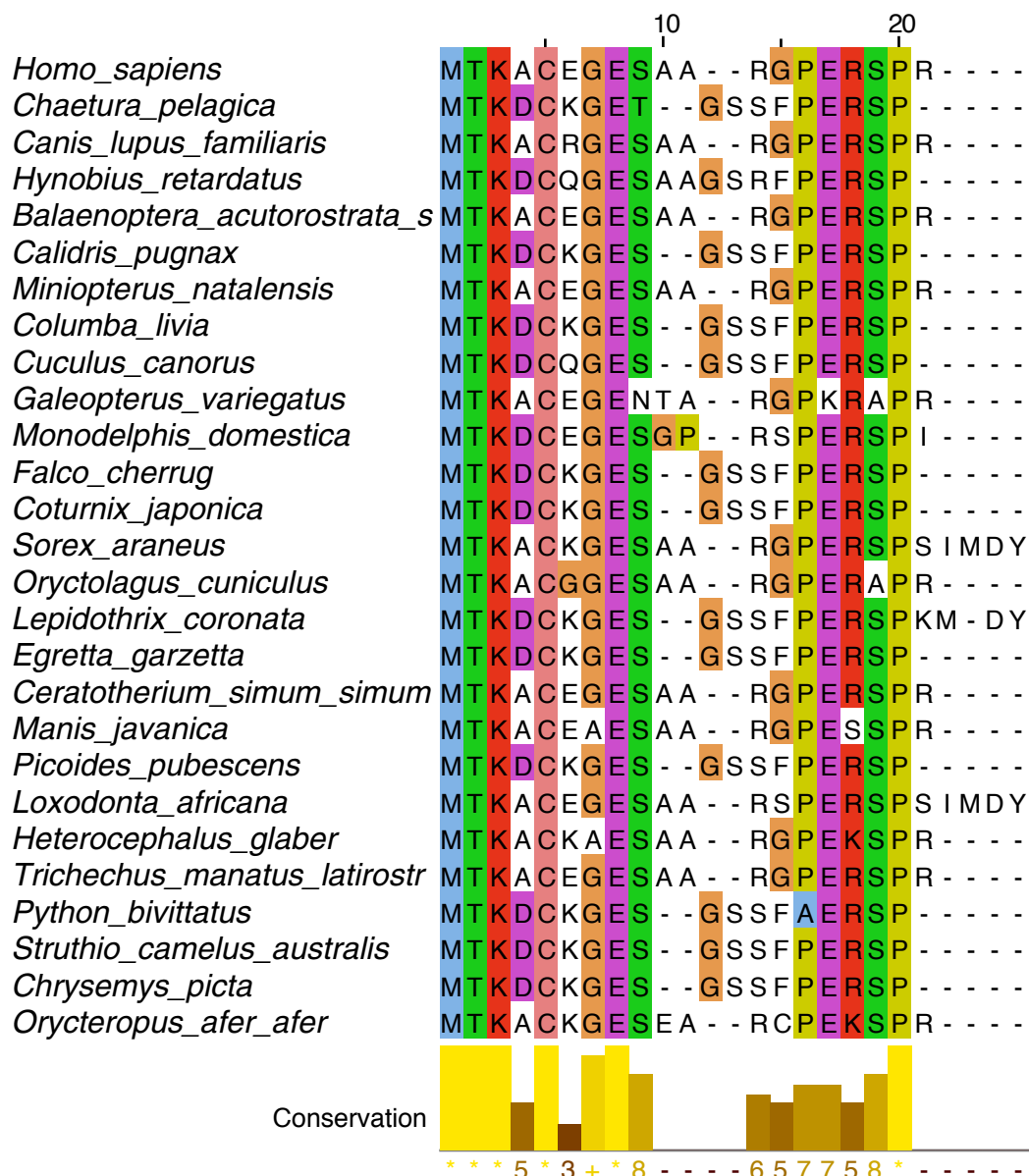


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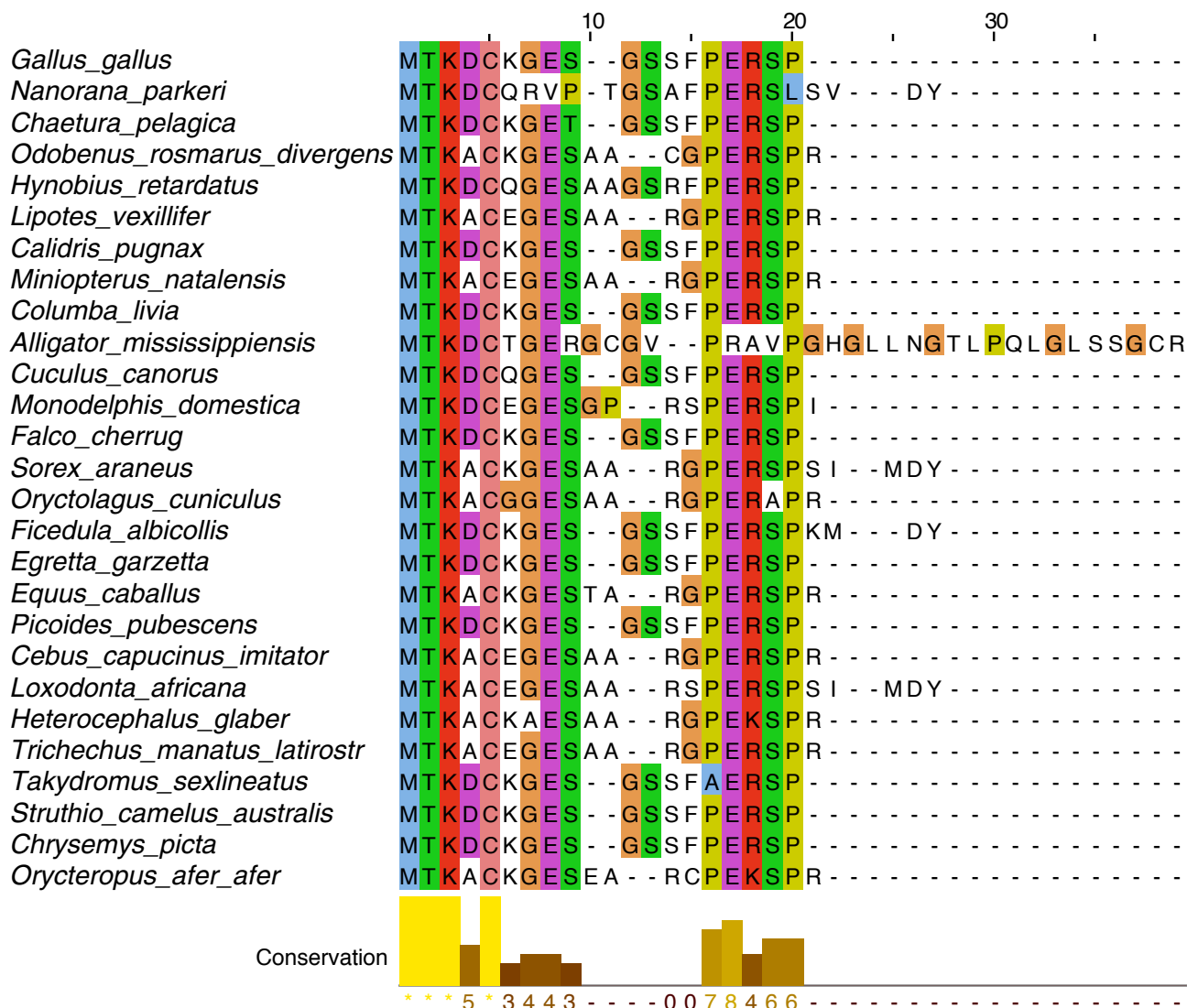
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ENSG00000092421 (SEMA6A)

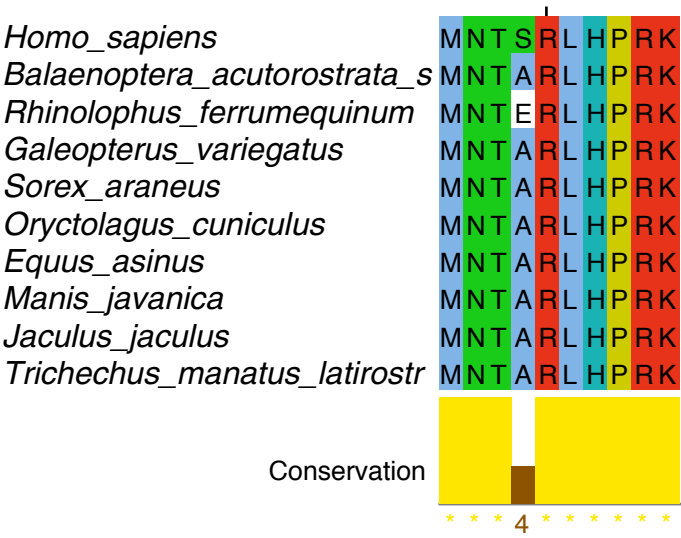


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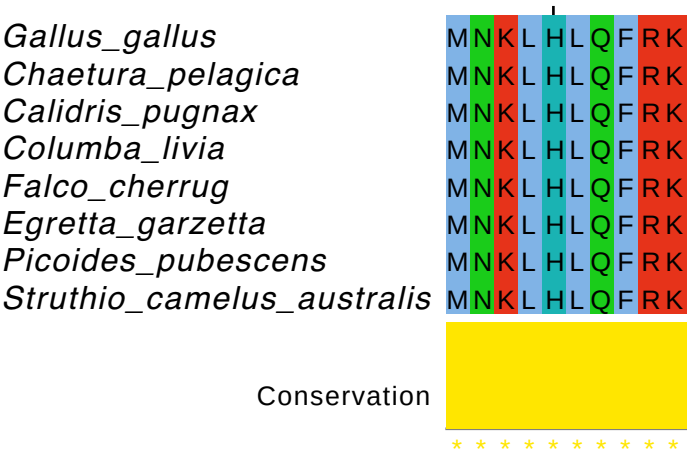
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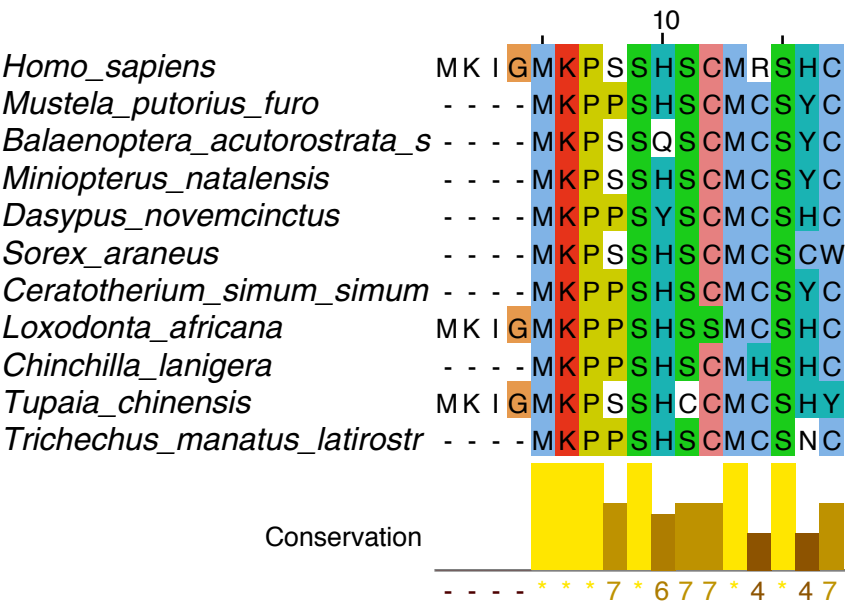
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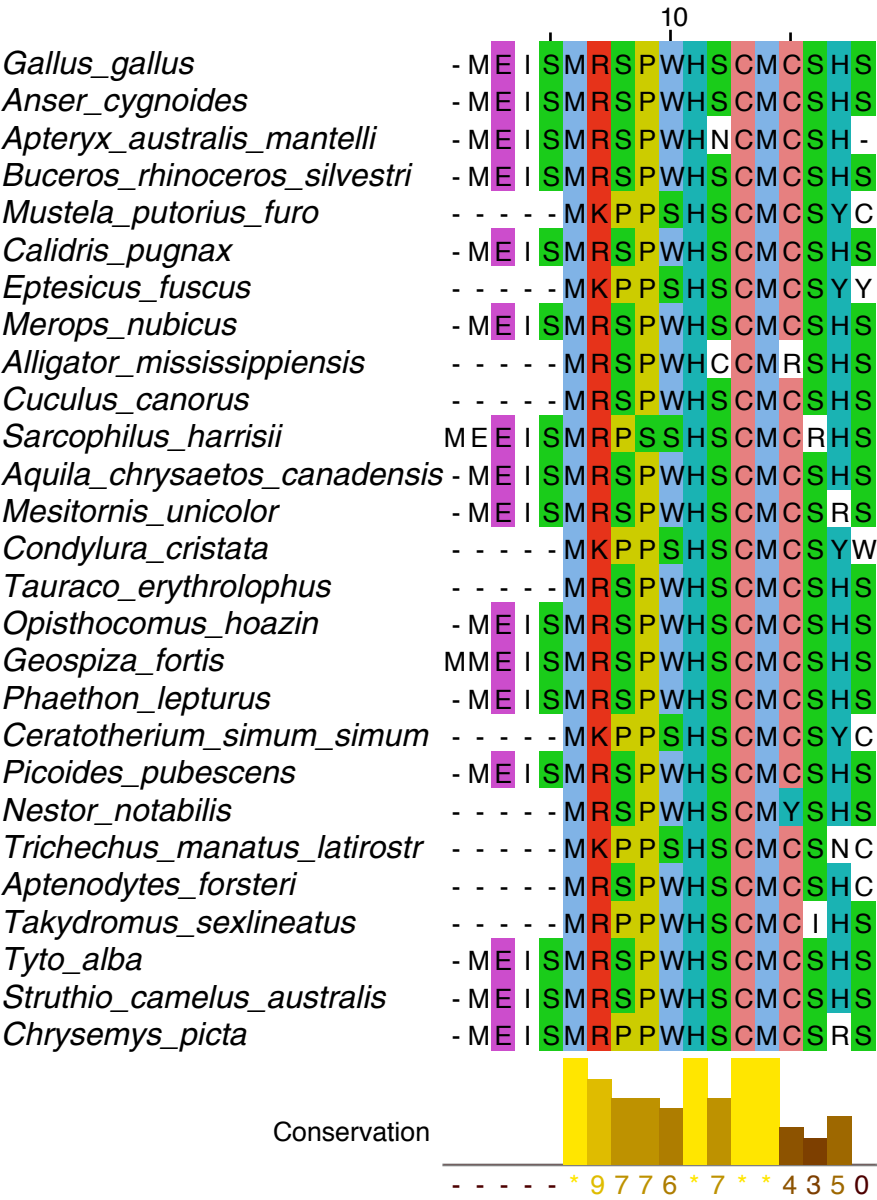
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HG0090.1

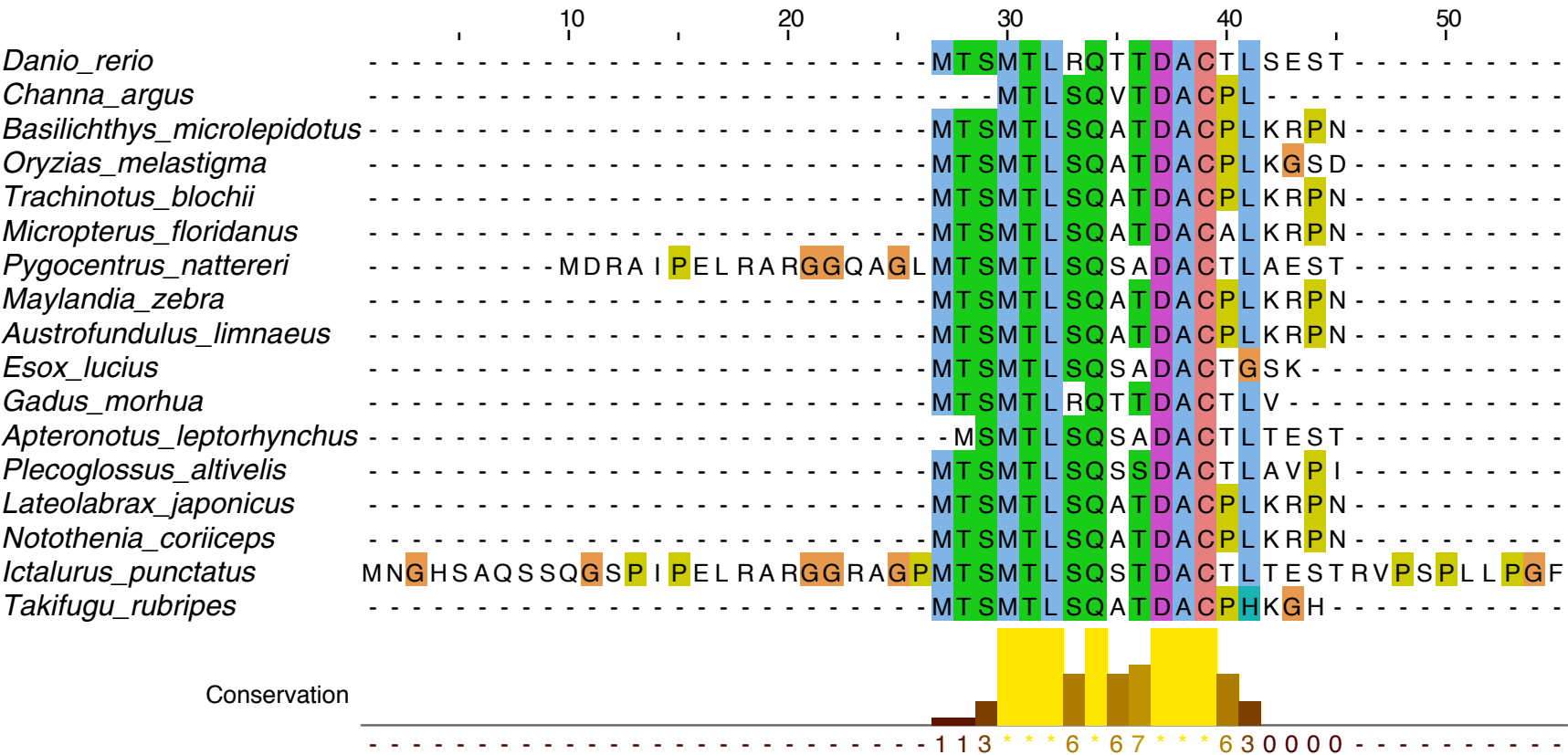
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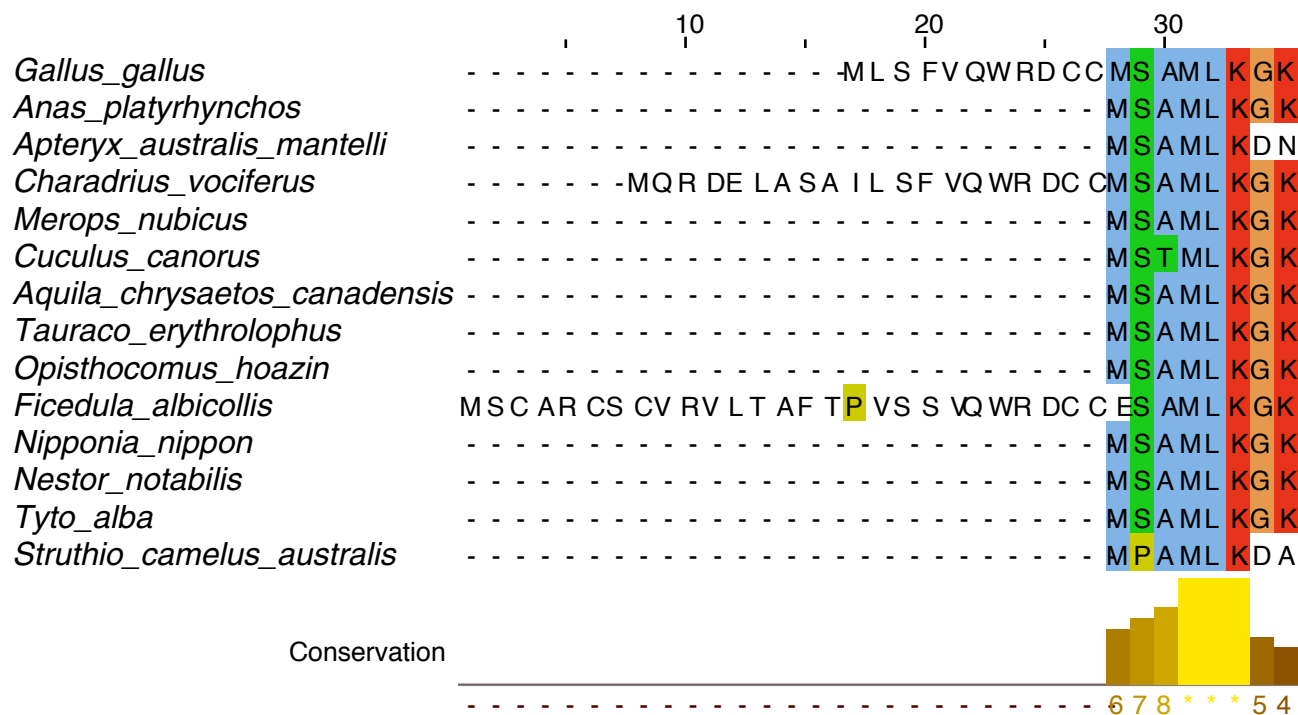


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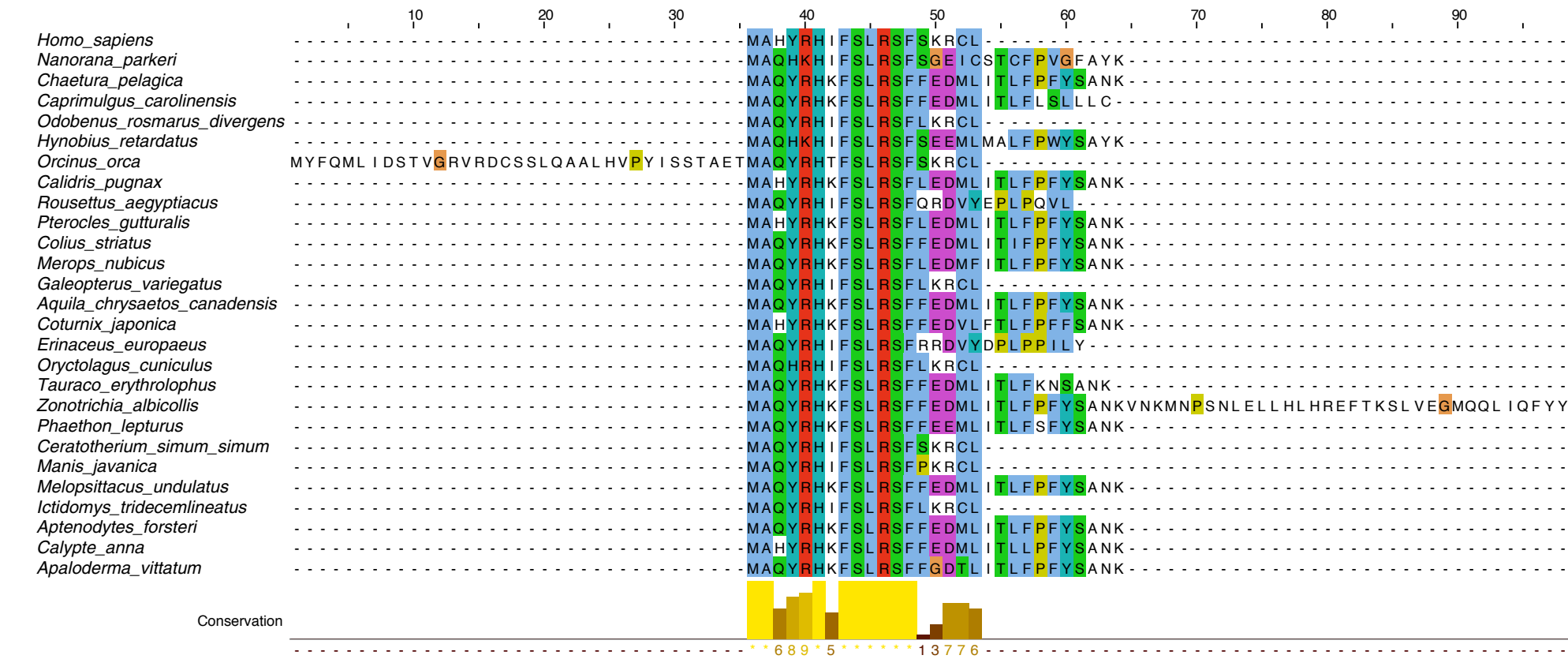


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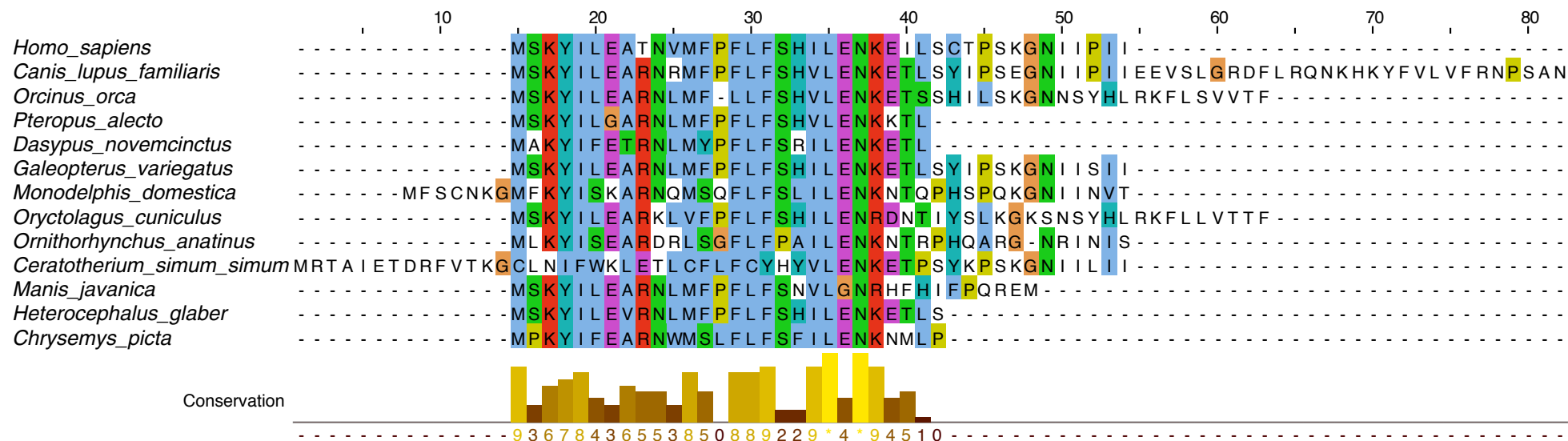
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ENSG00000172209 (GPR22)



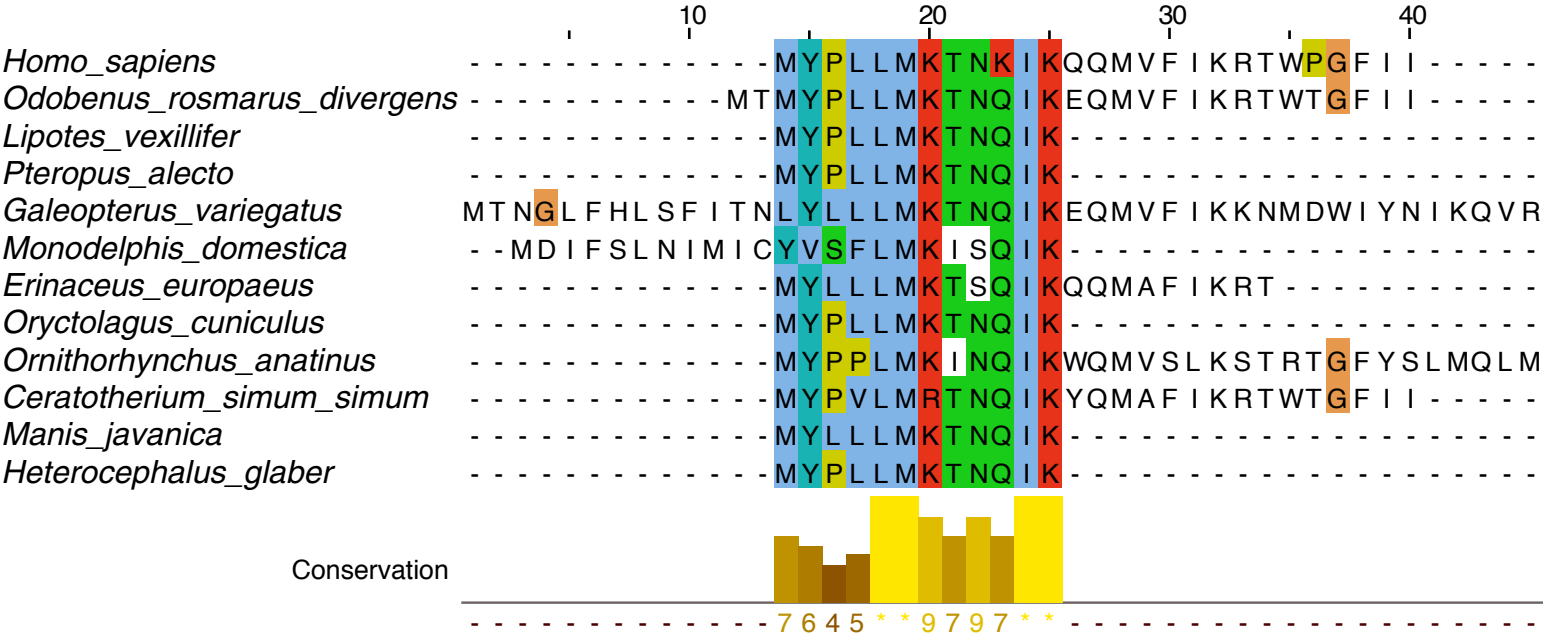
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ENSG00000172209 (GPR22)



HG0091.3

ENSG00000172209 (GPR22)



HG0092.1

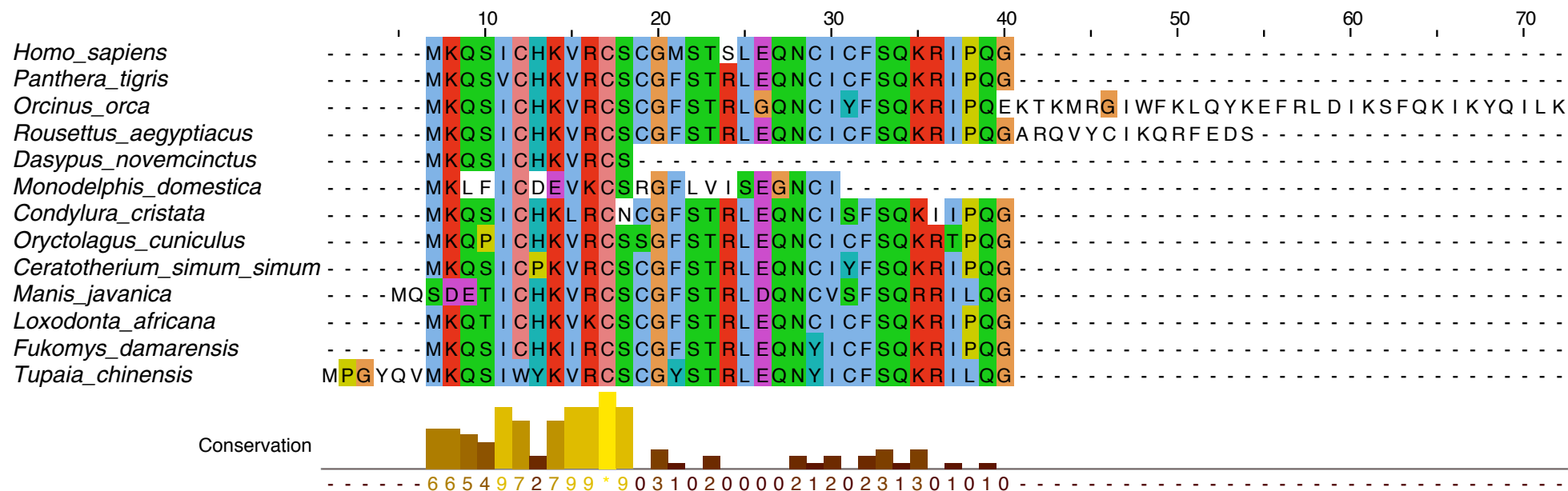
ENSGALG00000009966 (FRS2)

	10	20	30	40	50	60	
<i>Gallus_gallus</i>							MISSVTRQHDTLKYDRSPDAATEAGNINGQI
<i>Anser_cygnoides</i>		MV	IKQL	LLSCSA	AVC		LHVLGQMISVTRQHDTLKYDRTPDAATEAGNINGQI
<i>Xenopus_laevis</i>							MRHVILV
<i>Apteryx_australis_mantelli</i>		ML	HG	AKCL	MLMTL	GWK	VTFLDQMITSVTRQHDTLKYDRSPDAAAEAGNINGQI
<i>Buceros_rhinoceros_silvestri</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAES	RDHMF
<i>Charadrius_vociferus</i>	MI	-SSVTRQHDALS	MT	EALML	QQRL	GILMAKS	RDHMF
<i>Pteropus_alecto</i>	MR	G	IWF	KLQYREFRL	D	IKNFQKIKYQ	ILKR
<i>Dasypus_novemcinctus</i>							FVMSSNKKKHGILKYD
<i>Latimeria_menadoensis</i>							MKYERGP
<i>Colius_striatus</i>	MI	-SSMTRQHDTLS	MT	EALML	QQRL	GILMAKS	RDLMVF
<i>Columba_livia</i>							MISSVTRHHDTLKYDRSPDAAAE
<i>Leptosomus_discolor</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAKS	RDHMF
<i>Alligator_mississippiensis</i>							MSPFDDCSDMGACI
<i>Cuculus_canorus</i>	MI	-SSVTRQHDTSS	MT	EALML	QQRL	GILMAKS	RDHMF
<i>Sarcophilus_harrisii</i>							MQLLLFSHIRRKLHLIFSKEKFARLCKQA
<i>Aquila_chrysaetos_canadensis</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAKS	RDHMF
<i>Gavia_stellata</i>	MI	-SSVTRQHD	PL	SMTEALML	QQRL	GILMAKS	RDHMF
<i>Balearica_regulorum_gibberic</i>							MISSVTRQHDTLKYDRSPDAAAEAGNINGQI
<i>Condylura_cristata</i>							MQLWLFNQIRAKLYLFFSEDNSTRISHHTEKSHGILKYD
<i>Tauraco_erythrolophus</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAKCR	DHMF
<i>Opisthocomus_hoazin</i>							MISSVTRQHDTLKYDRSPDAAAEAGNINGQI
<i>Zonotrichia_albicollis</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAKS	RDQMF
<i>Phaethon_lepturus</i>							MISSVTRQHDTLKYDRSPDAAAEAGNINGQI
<i>Fulmarus_glacialis</i>	MI	-SSVTRQYDTLS	MT	EALML	QQRL	GILMARS	RDHMF
<i>Aptenodytes_forsteri</i>	MI	-SSVTRQHDTLS	MT	EALML	QQRL	GILMAKS	RDHMF
<i>Pelodiscus_sinensis</i>							MFVYVRRQHA
<i>Calypte_anna</i>	MI	-SSVARQHDTLS	MT	EALML	QQRL	GILMAKS	RDPMVF

Conservation

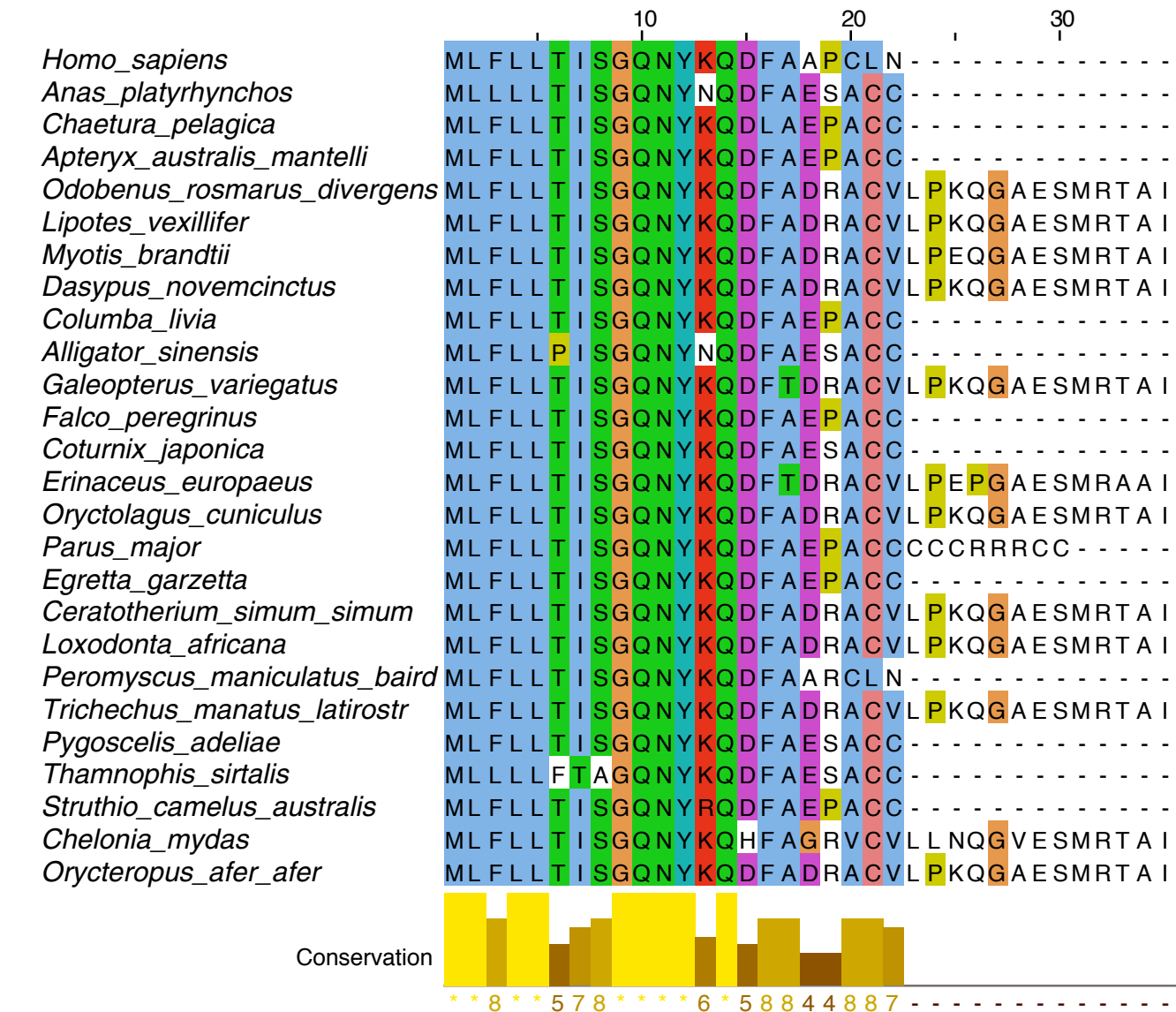


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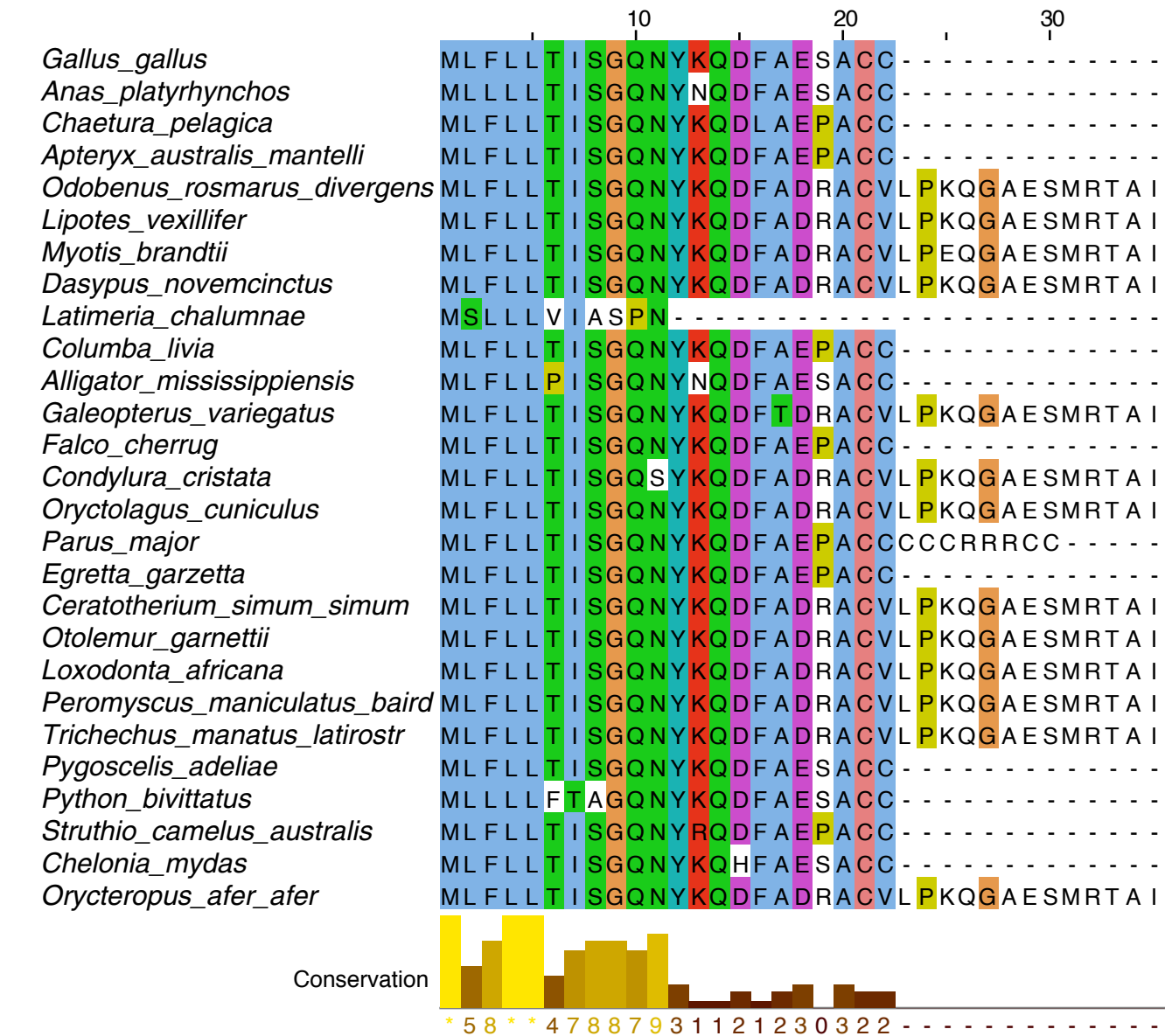
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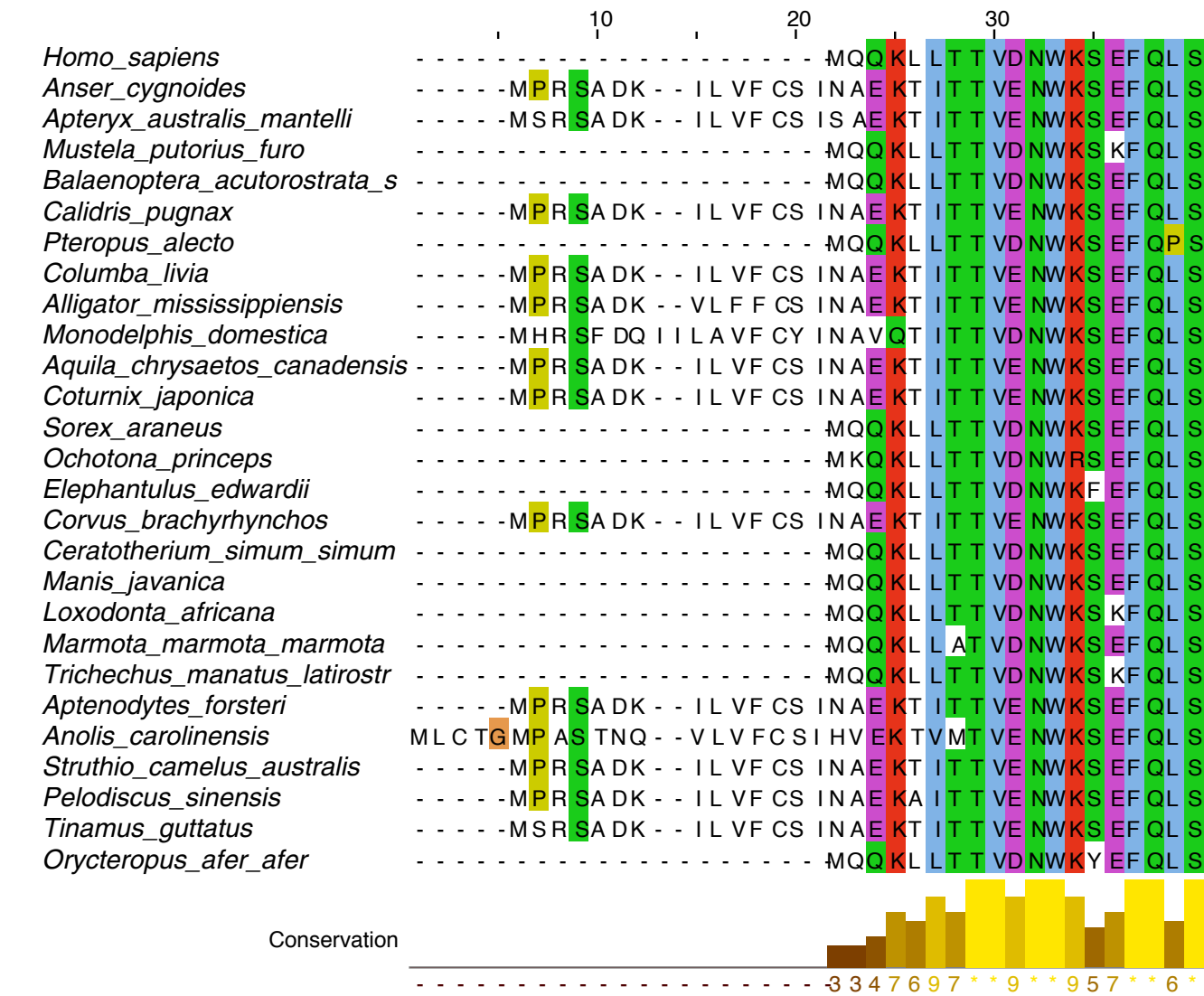
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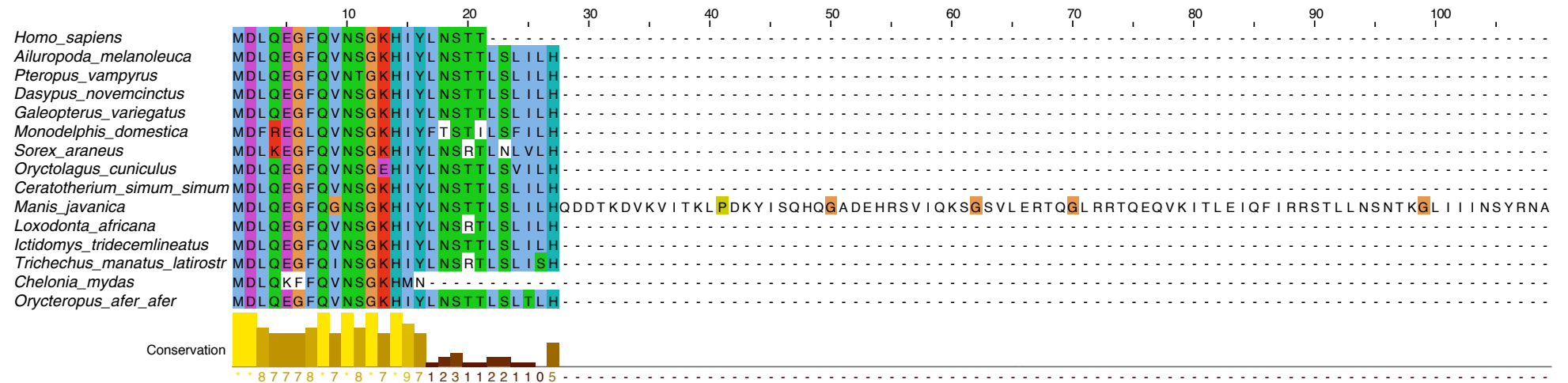


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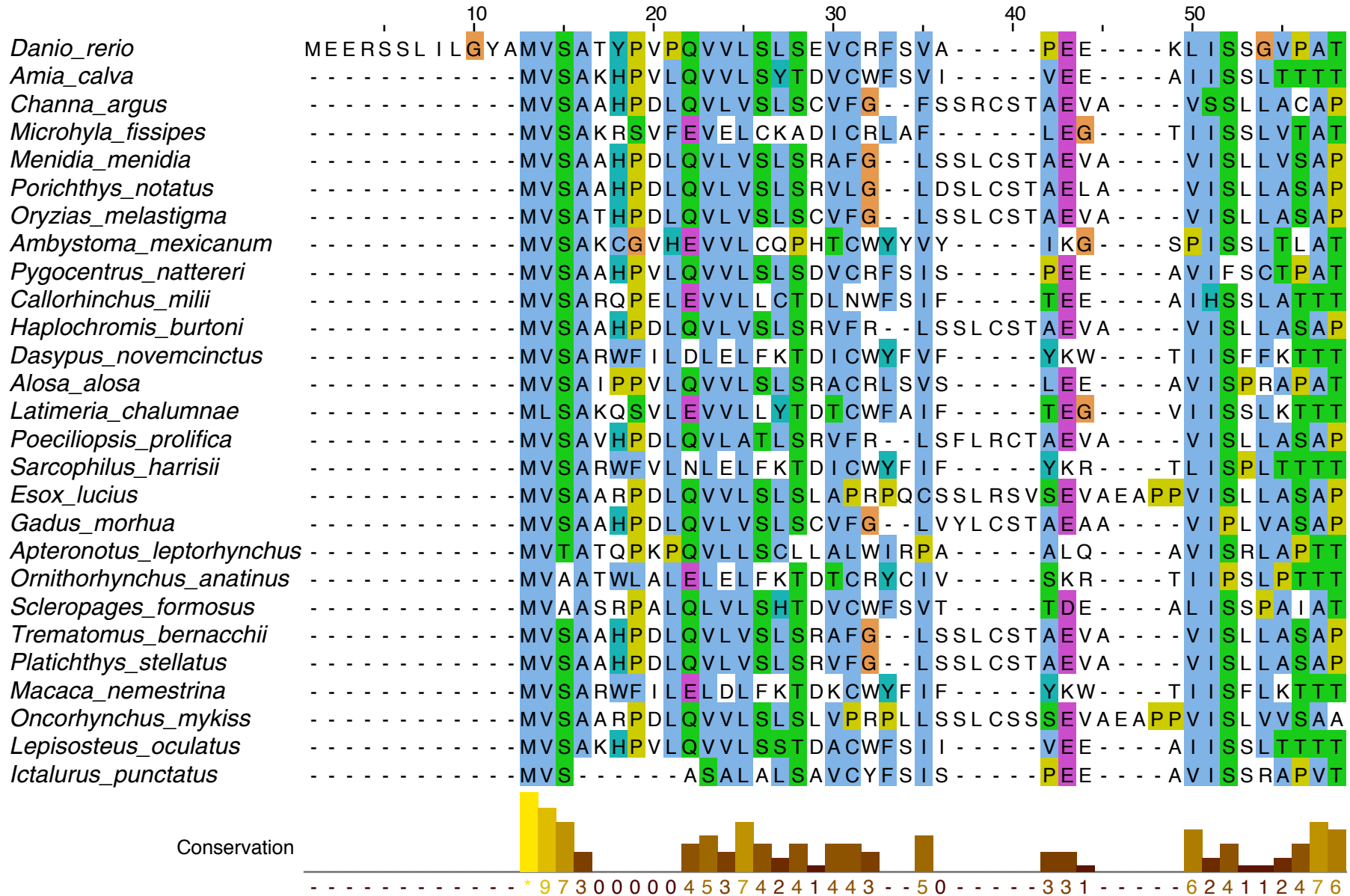


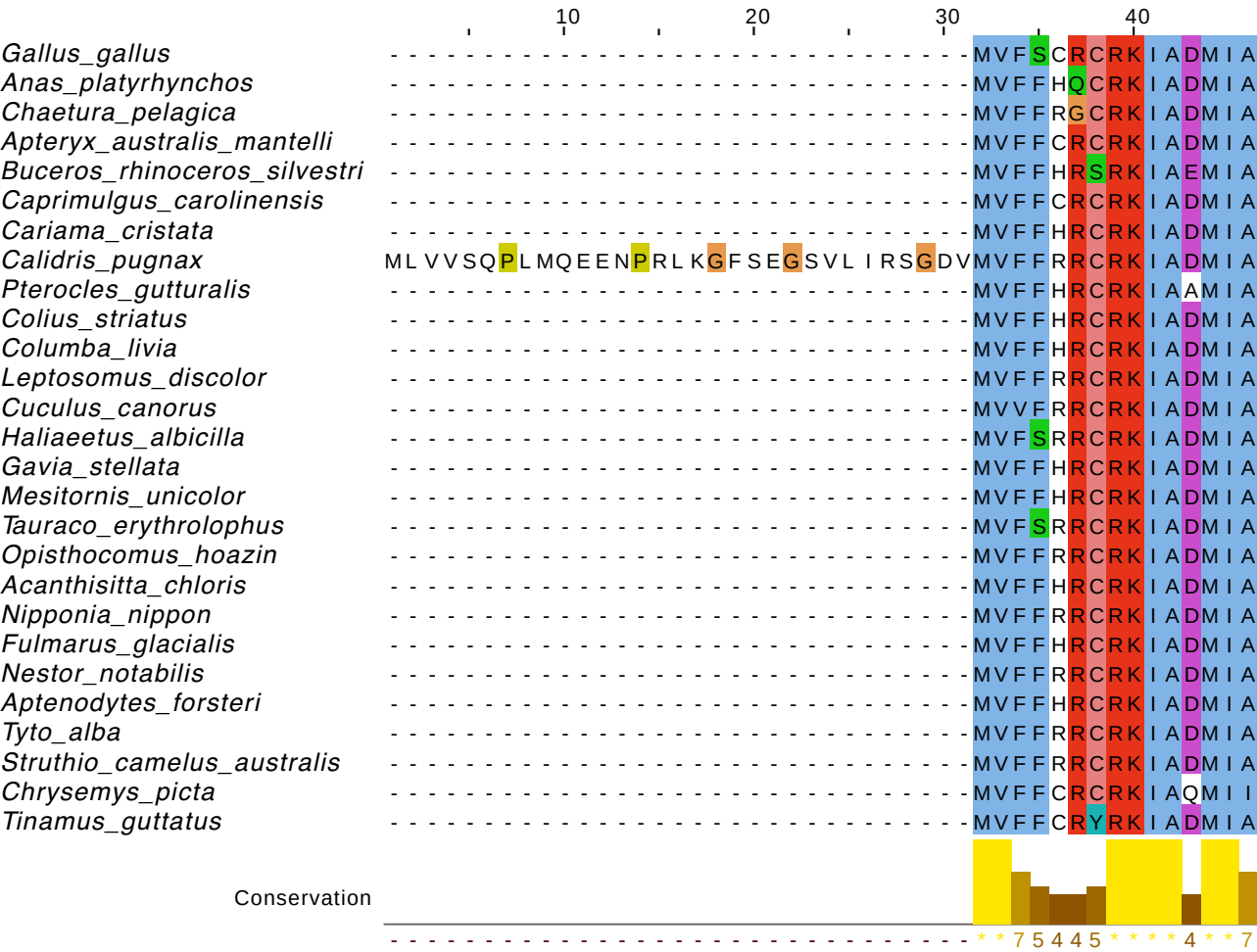
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HG0095

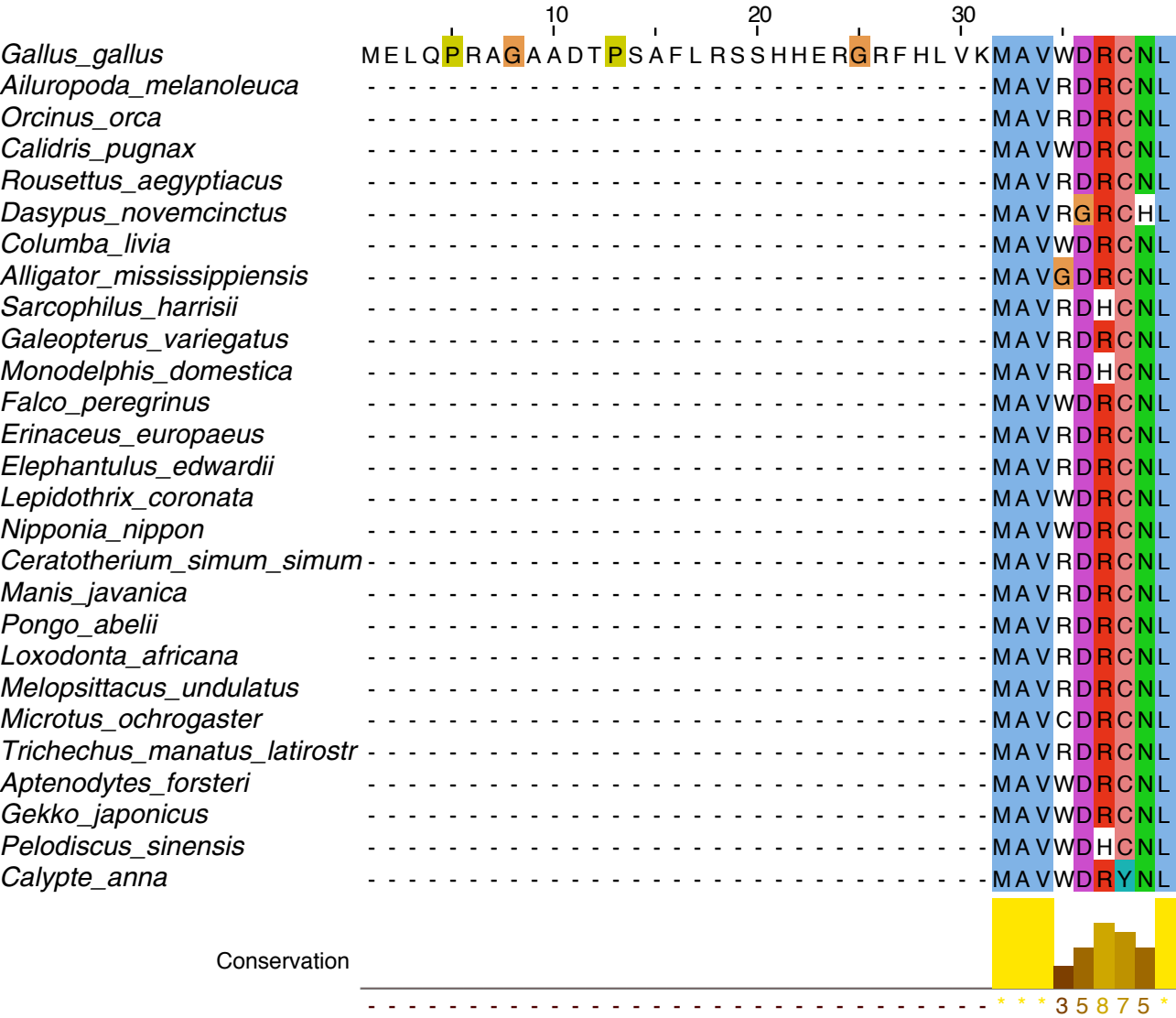
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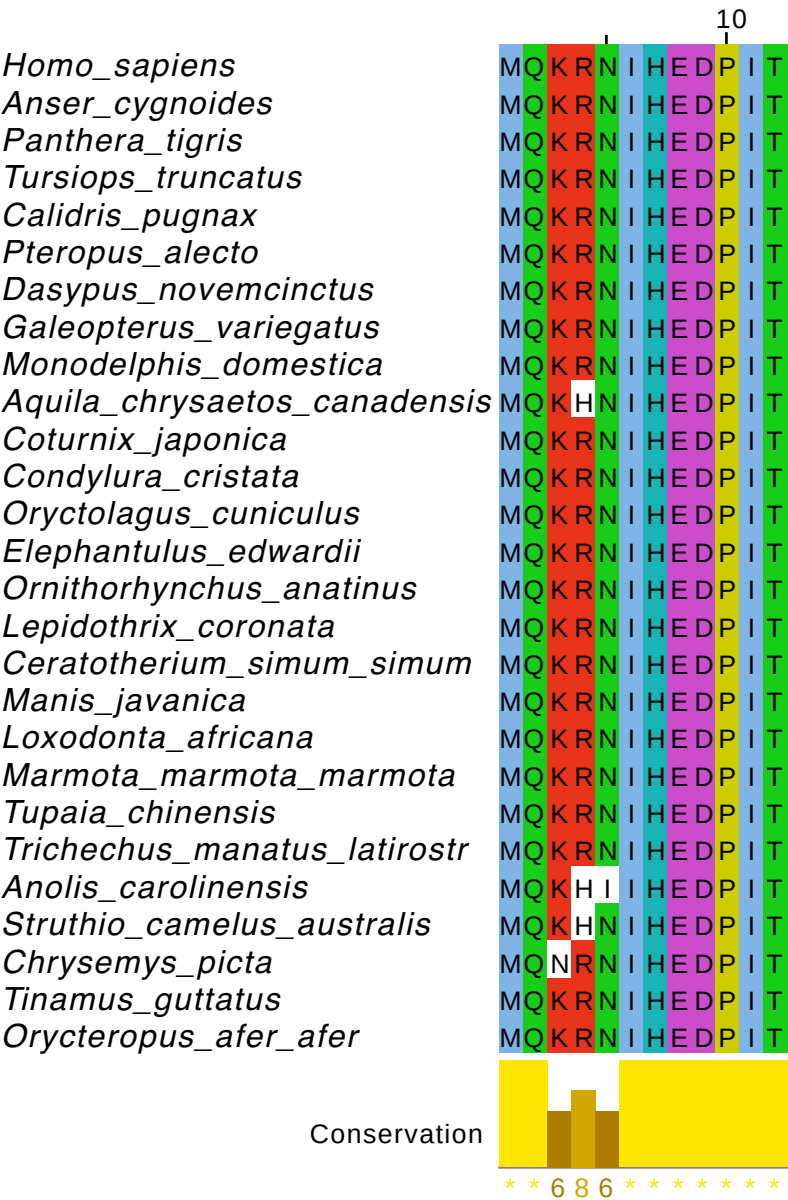
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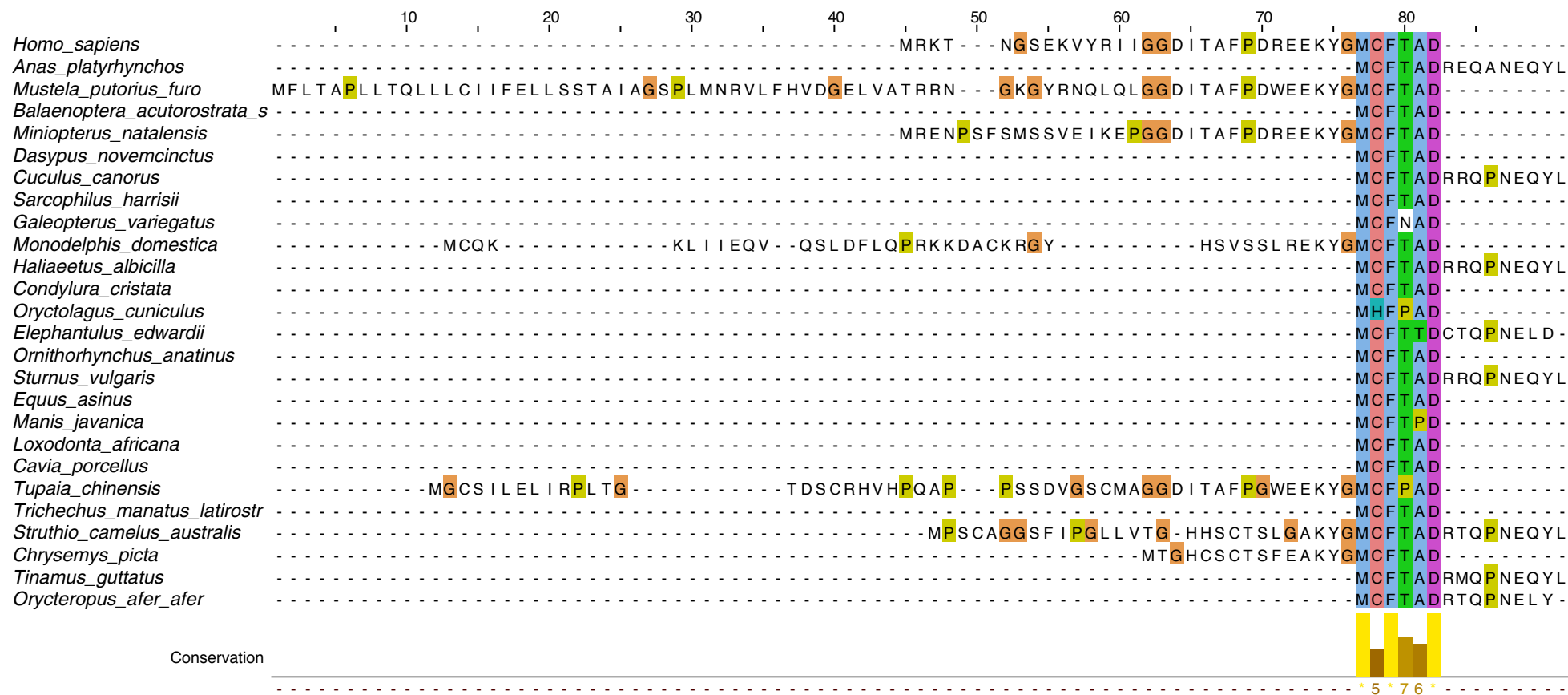


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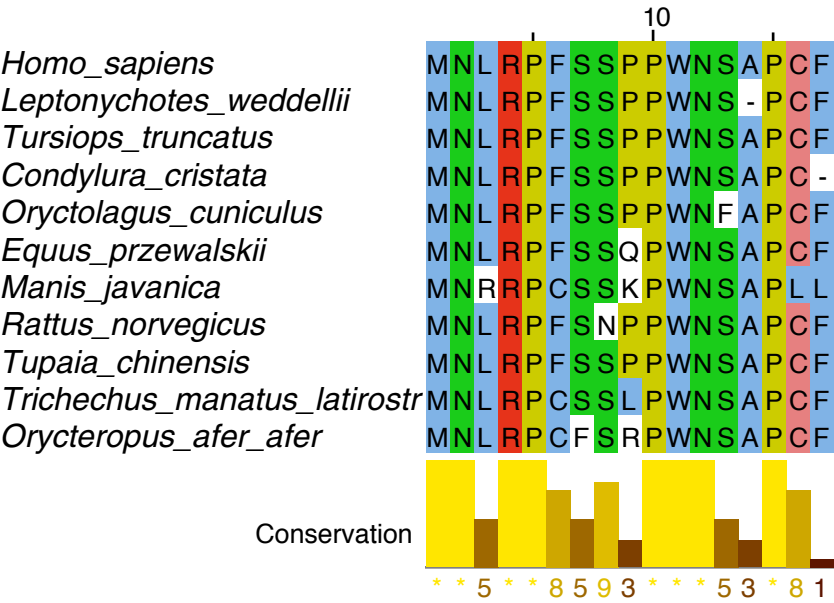


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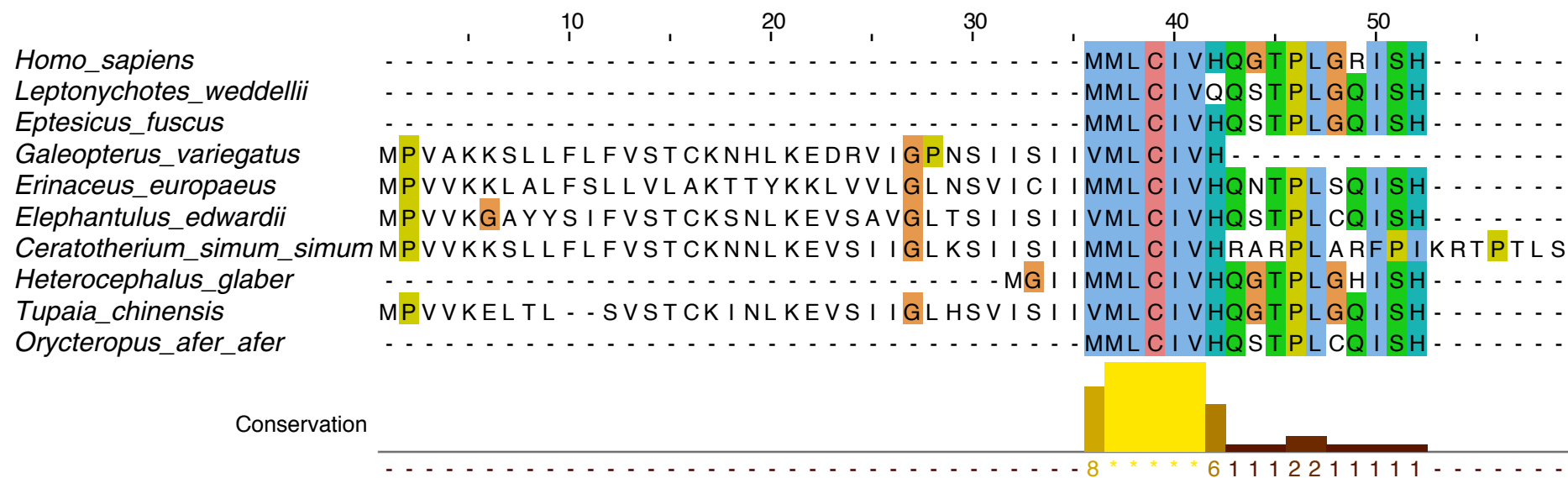
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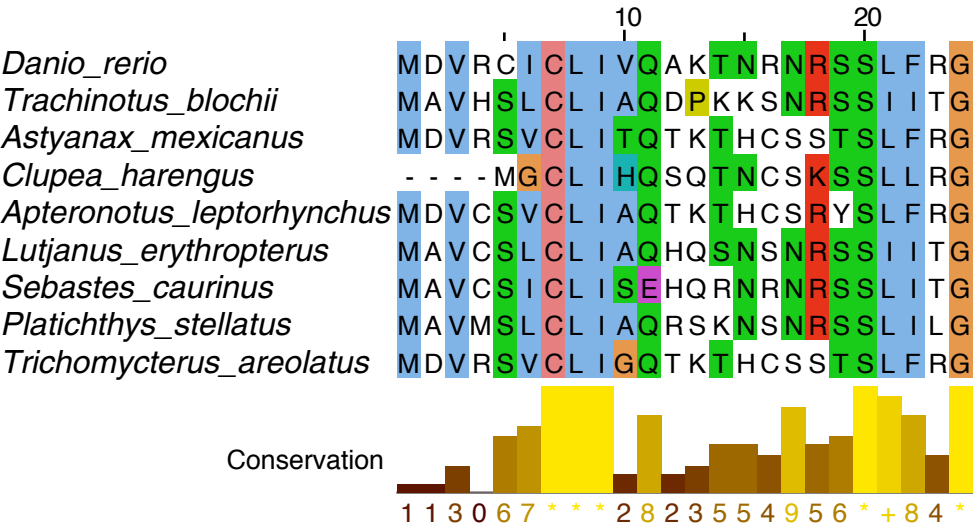
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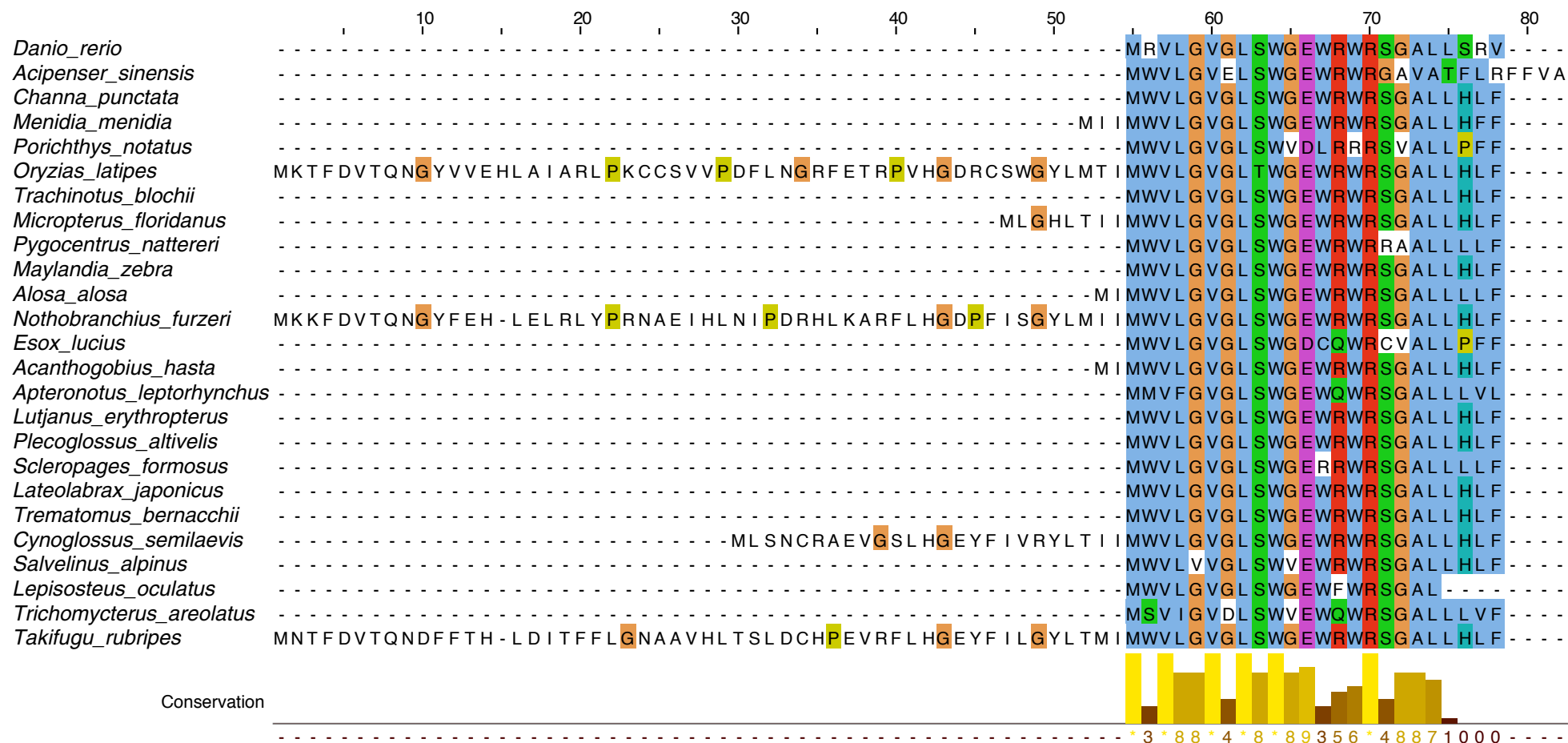


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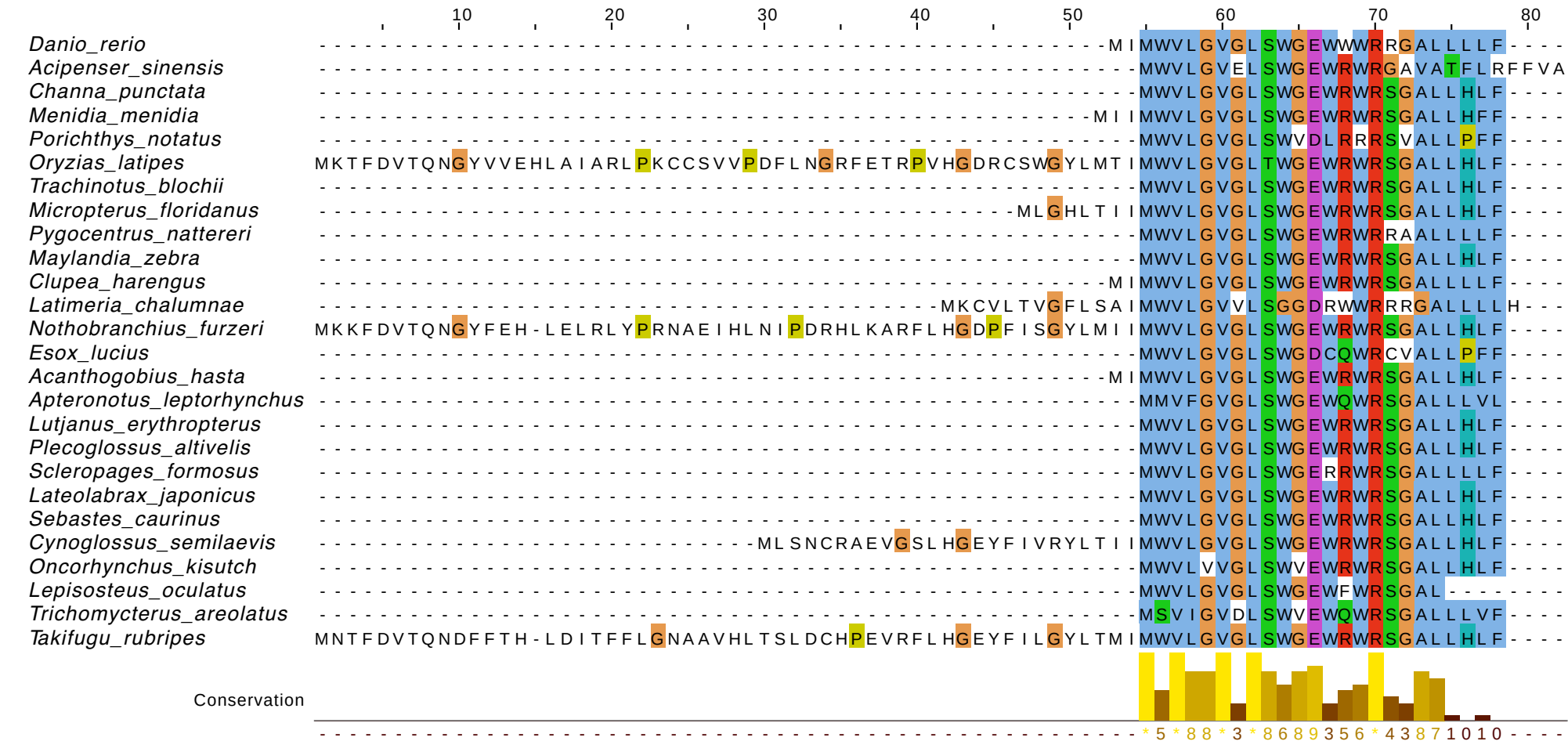


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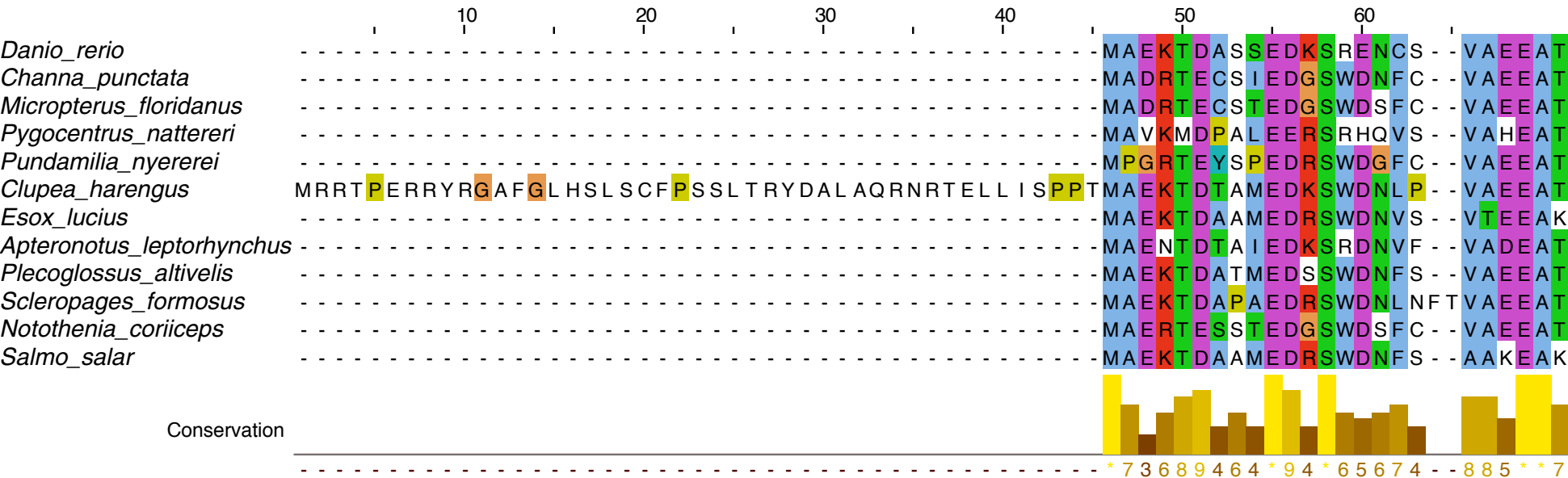
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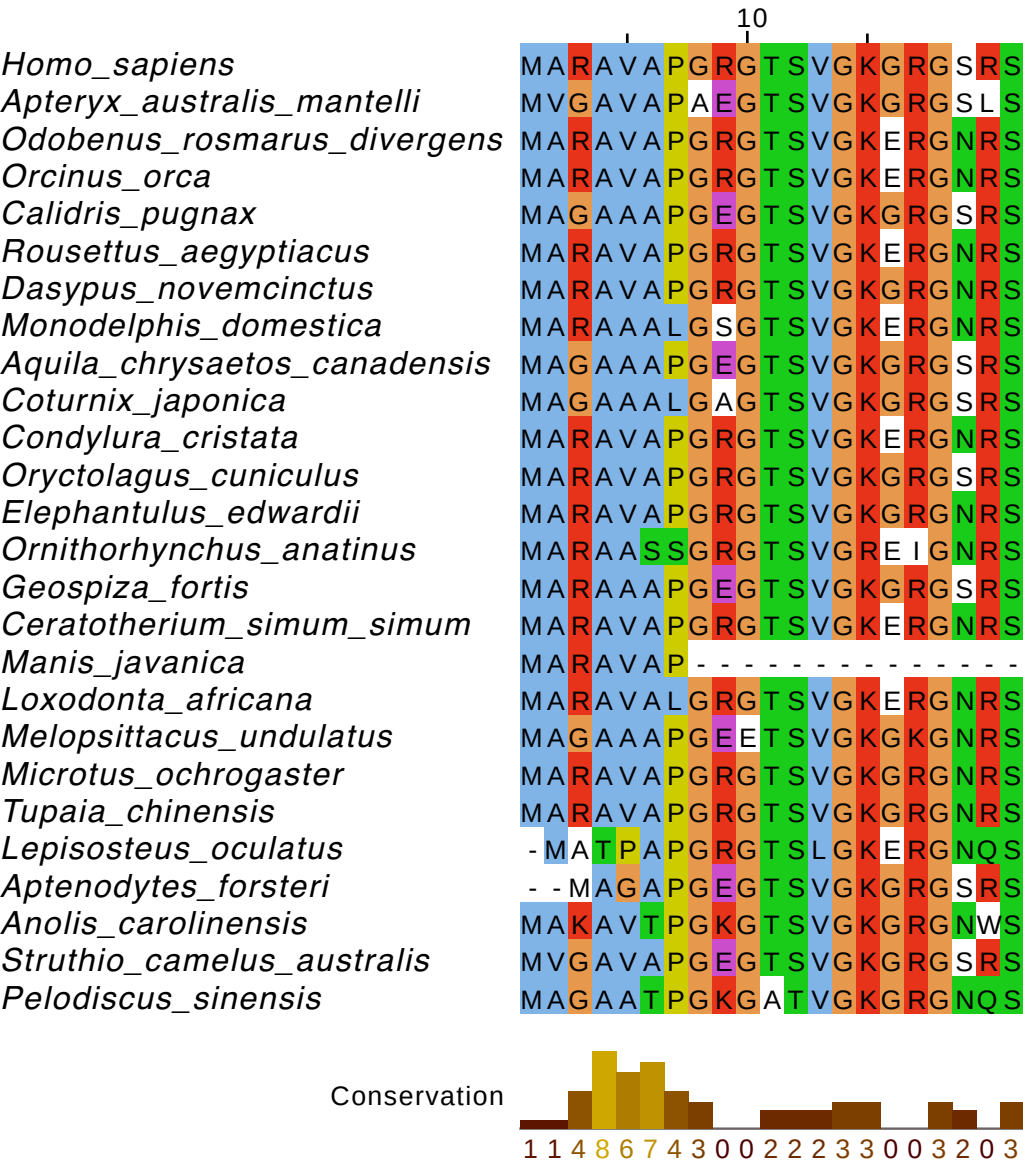
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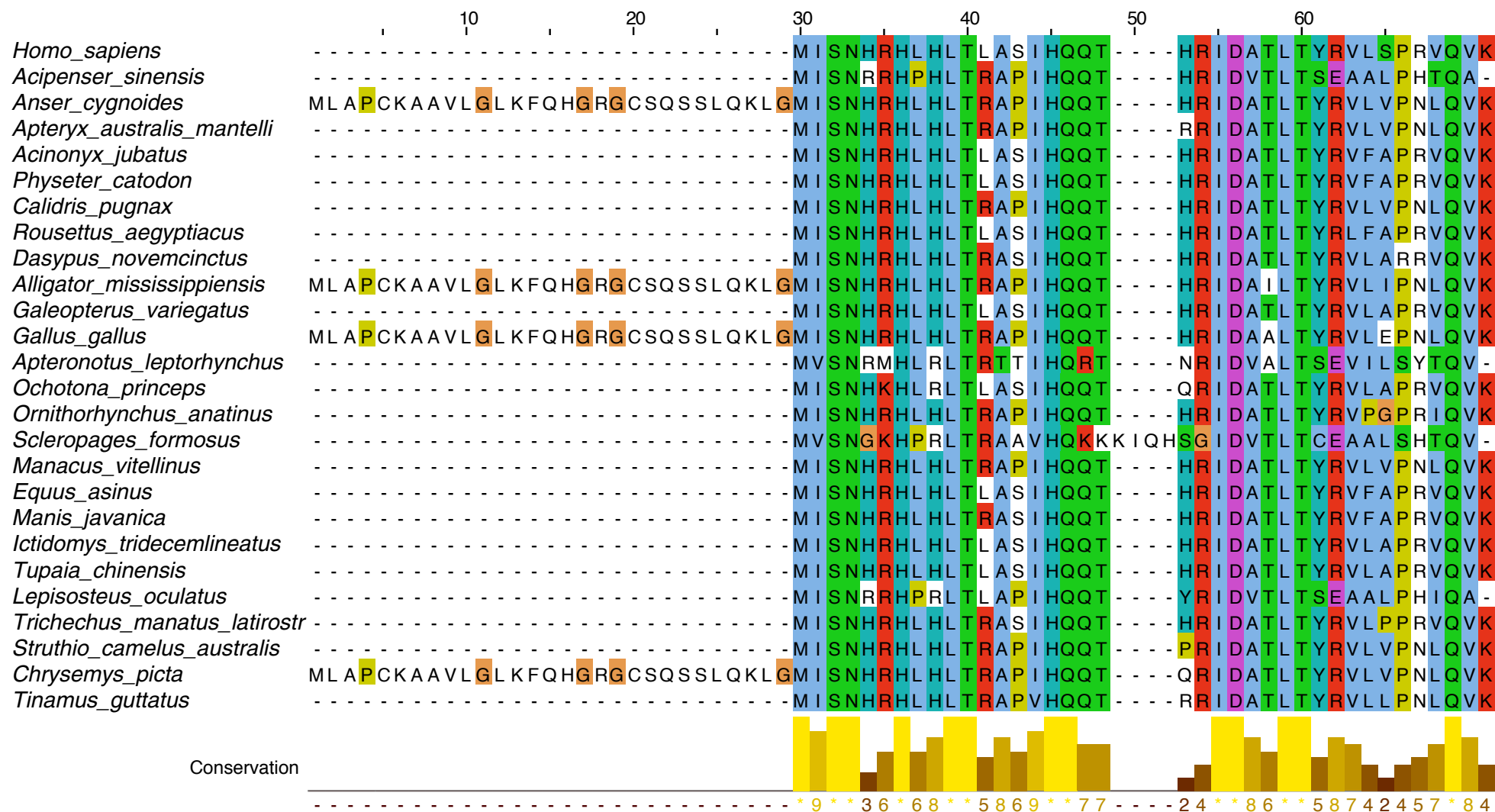


HG0101

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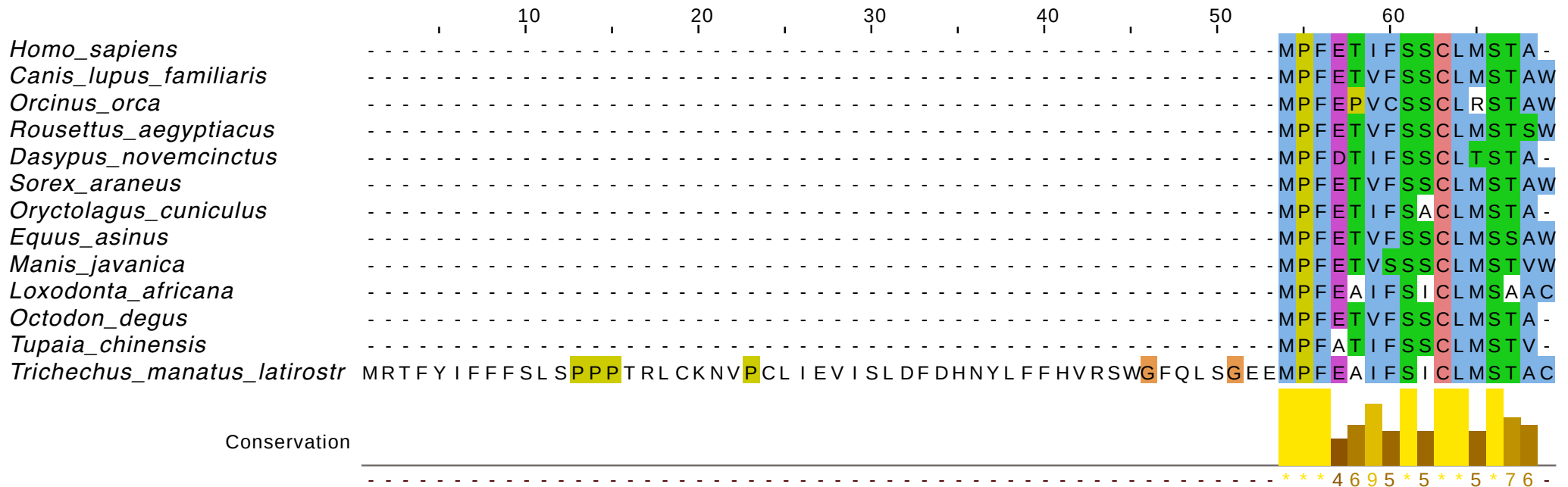


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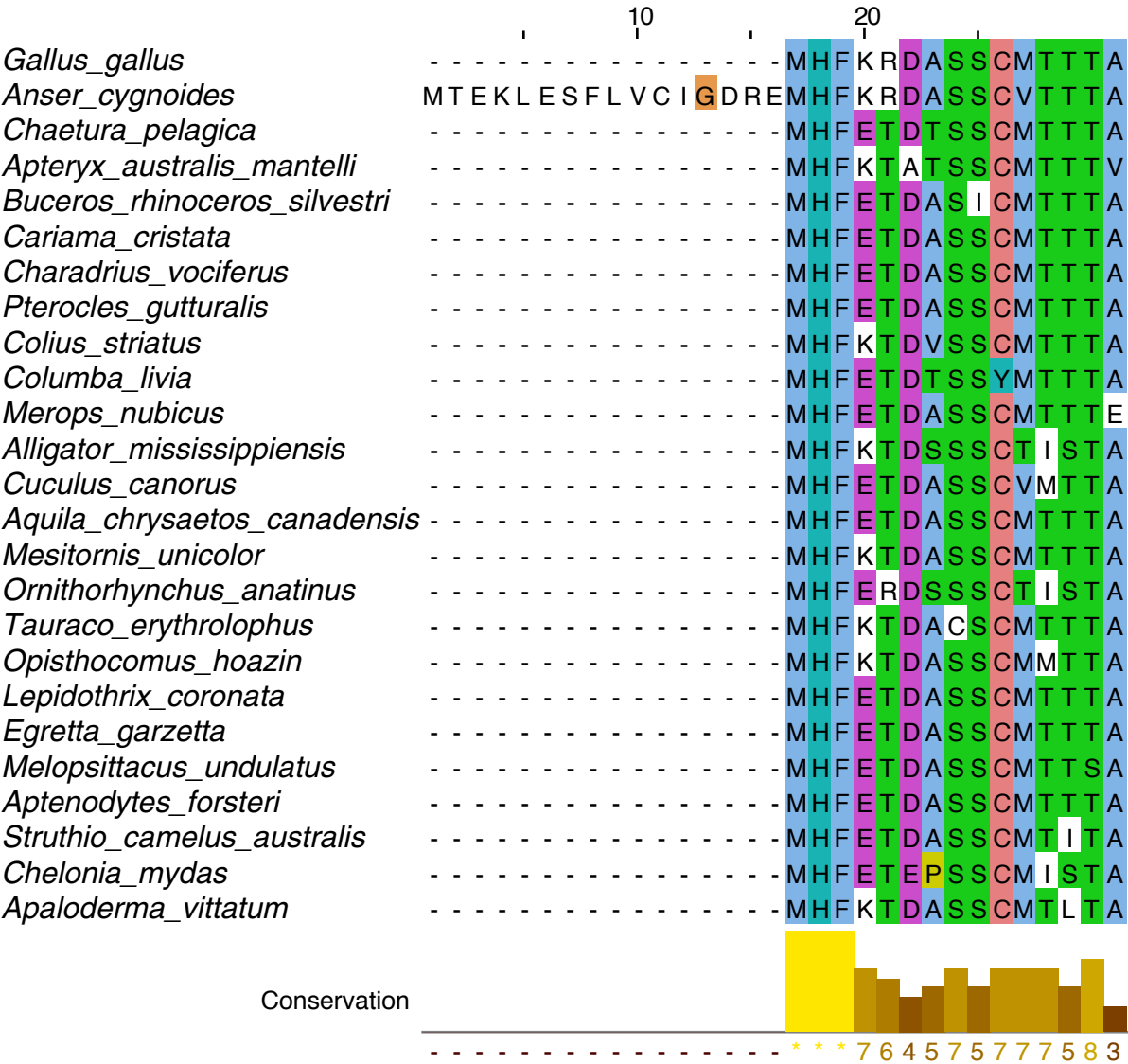
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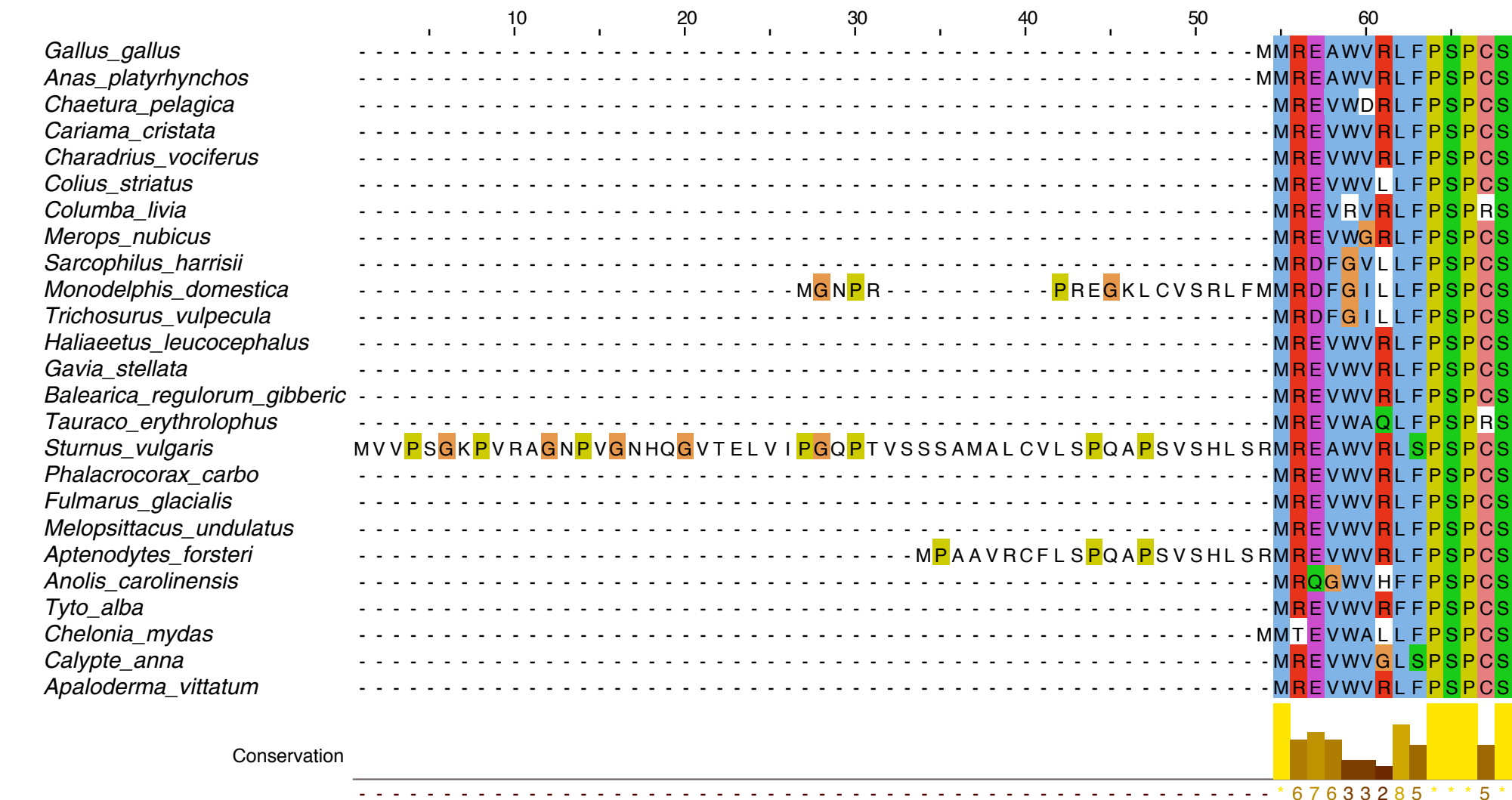


HG0103

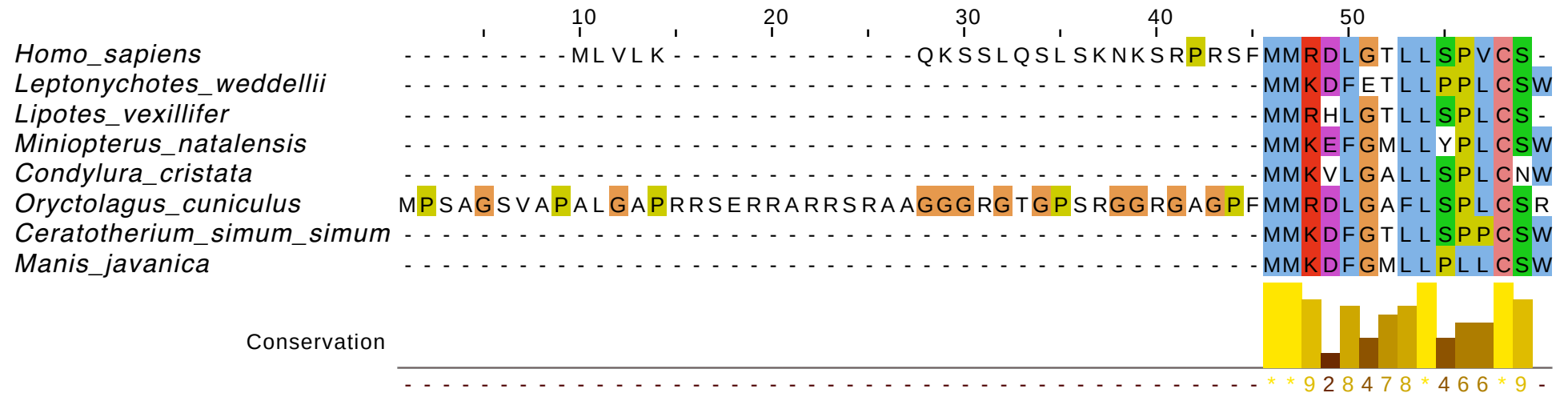
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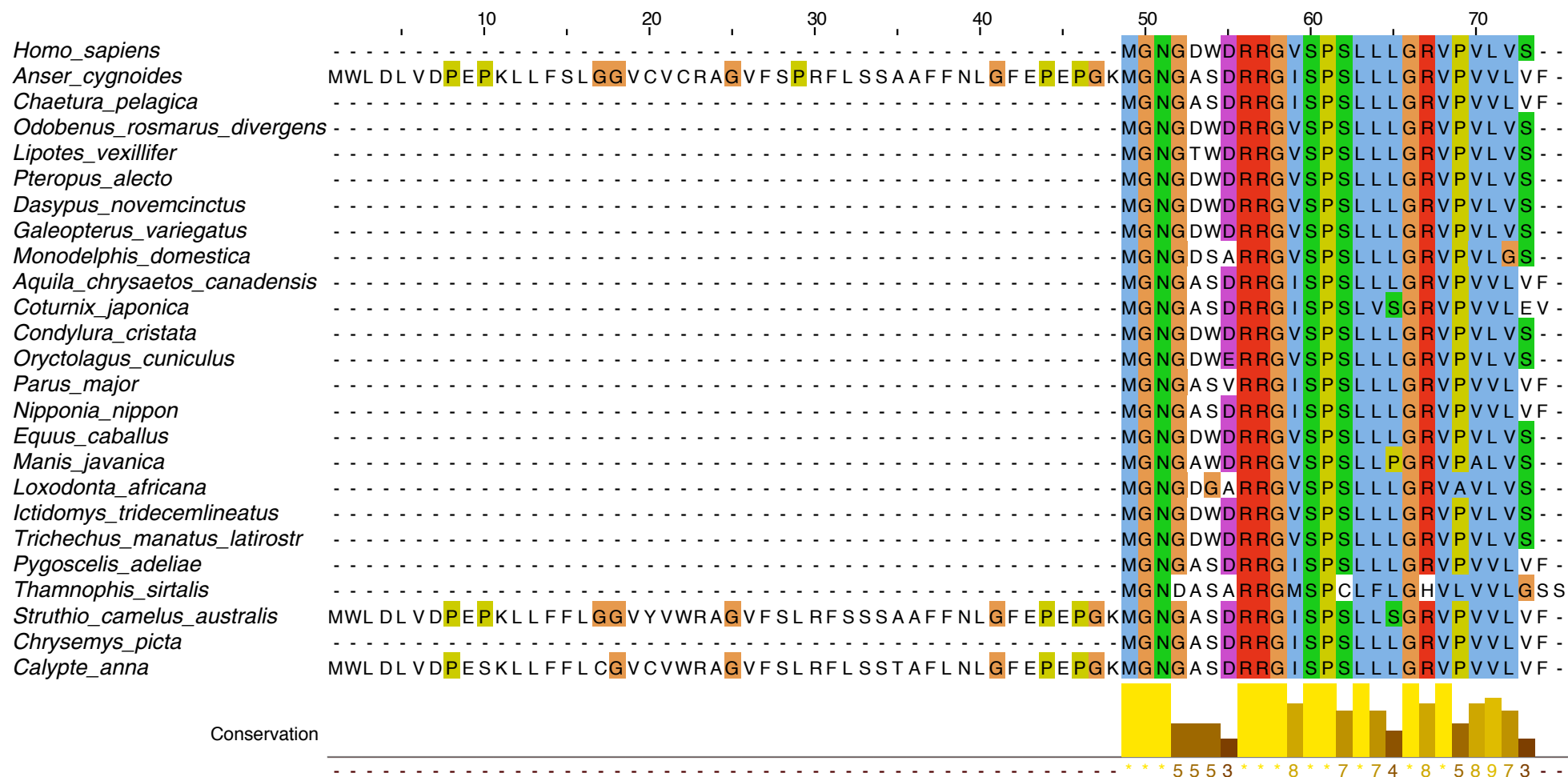
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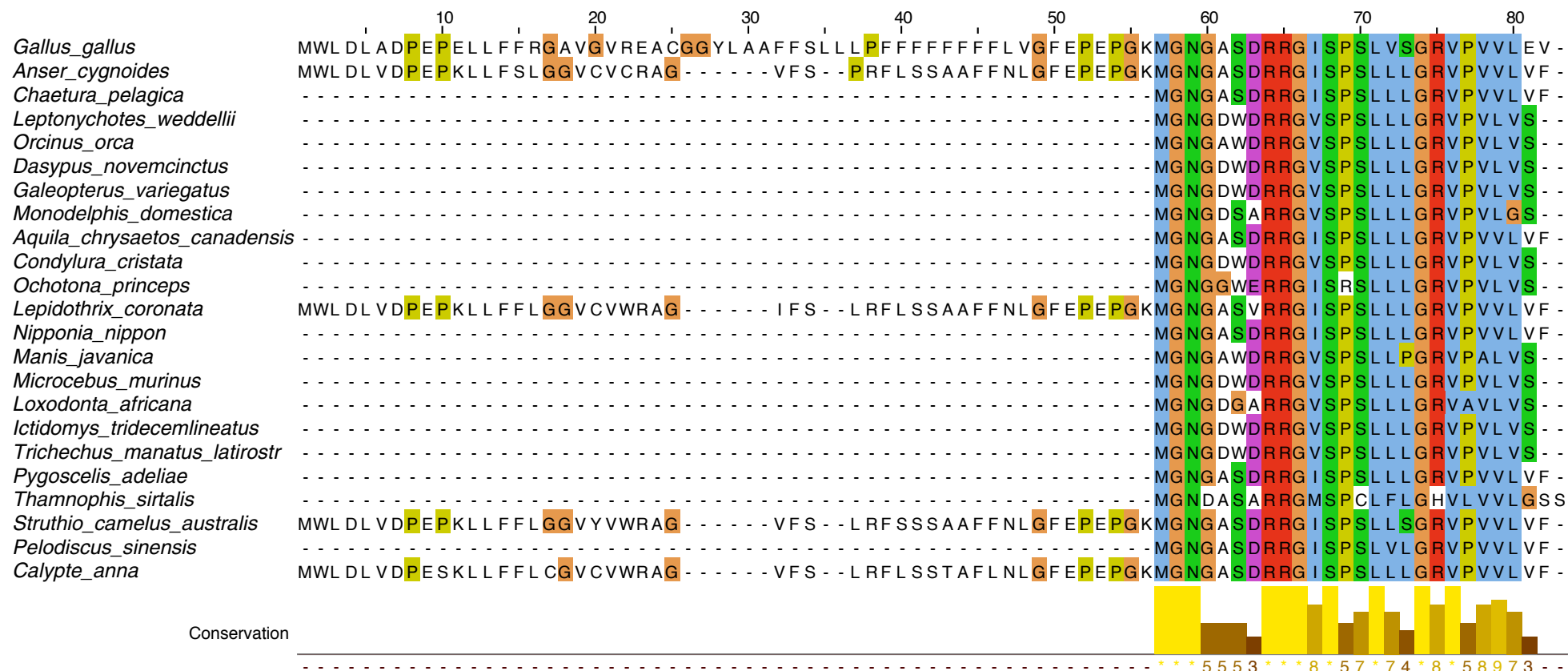
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ENSG00000135298 (ADGRB3)



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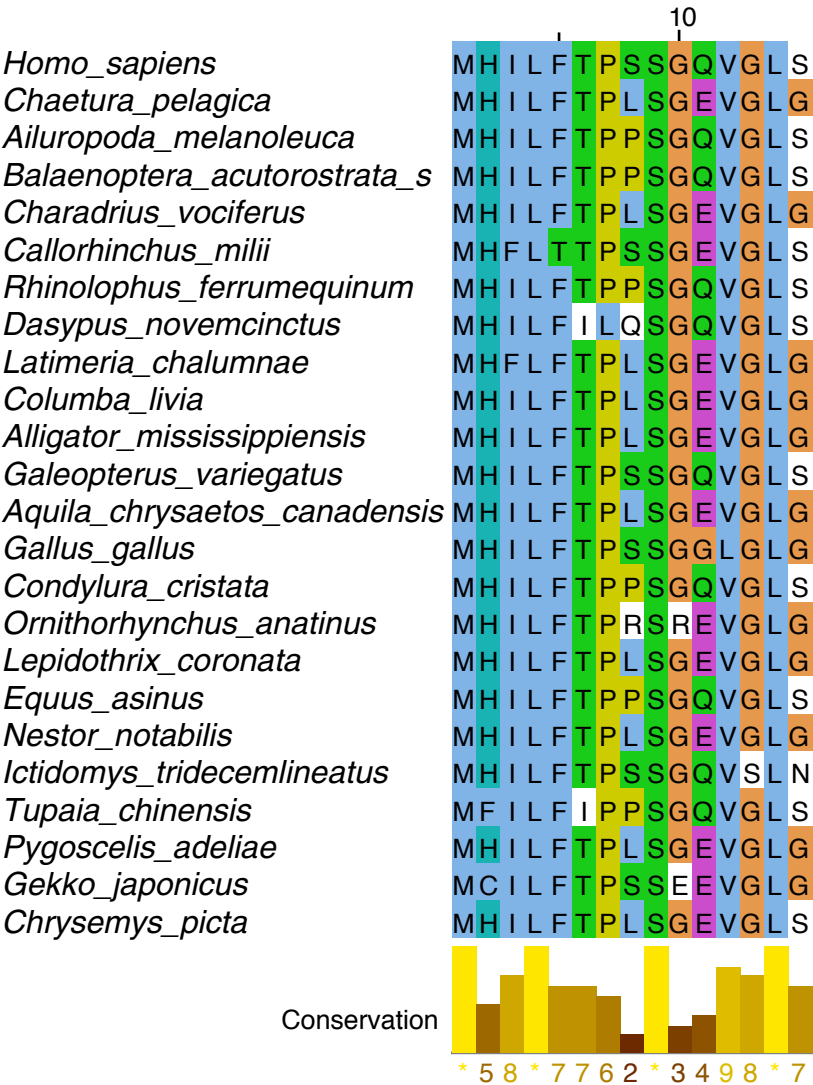


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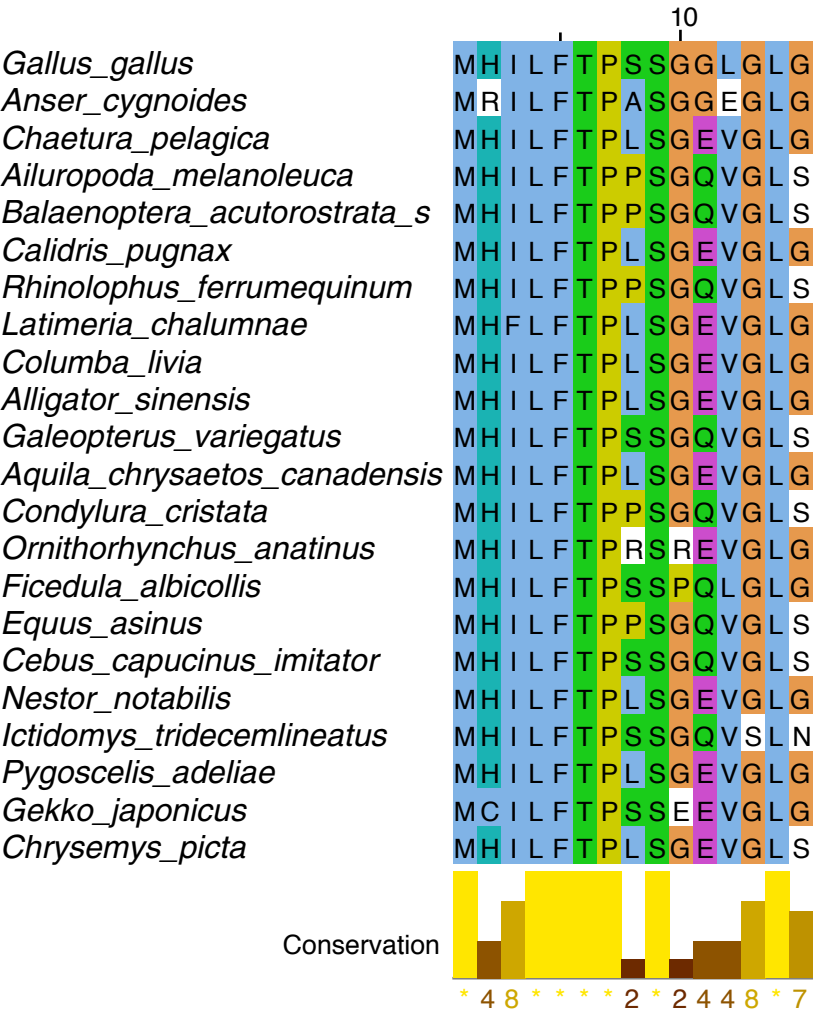
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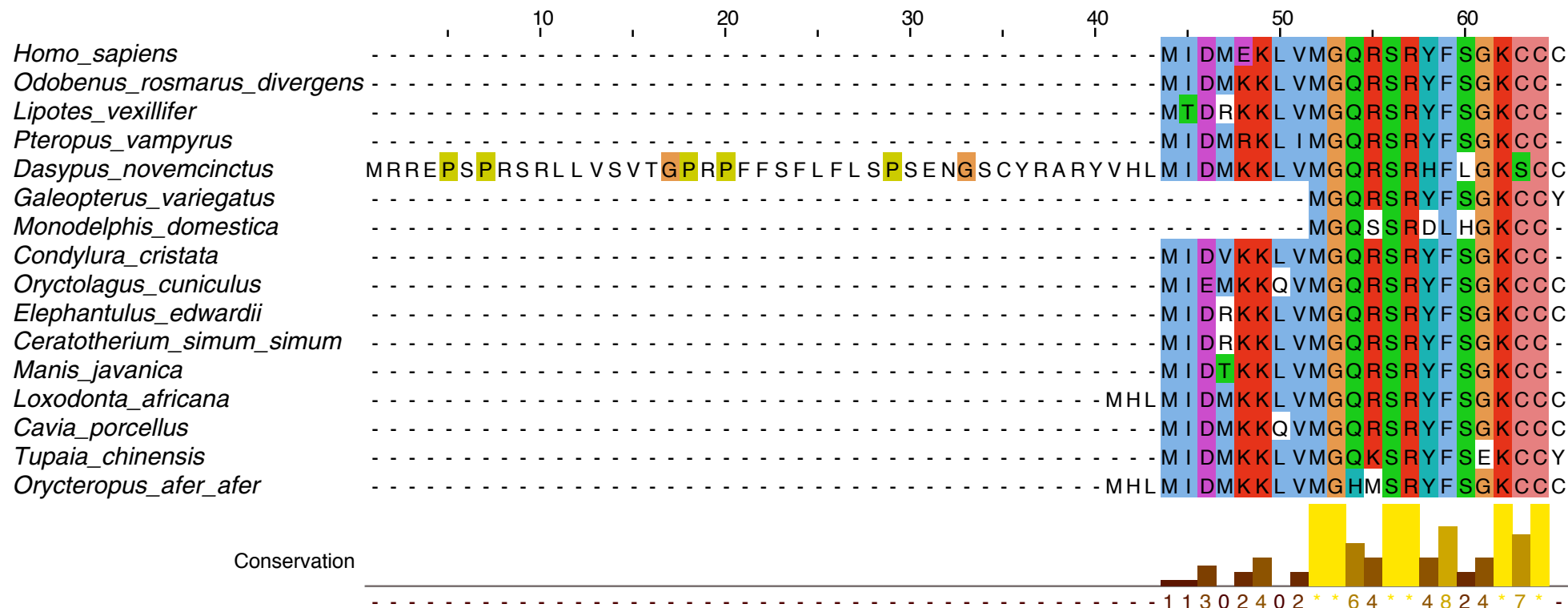


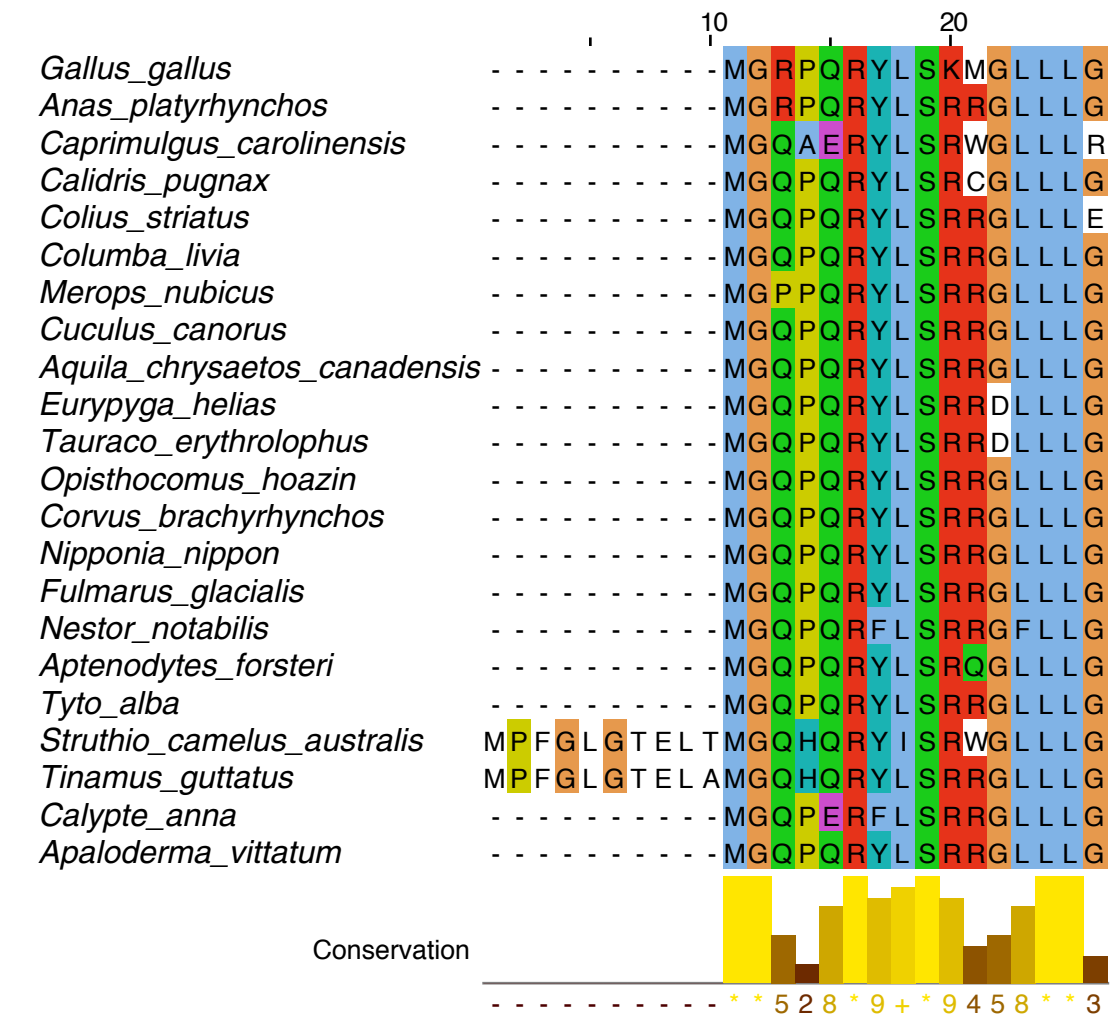
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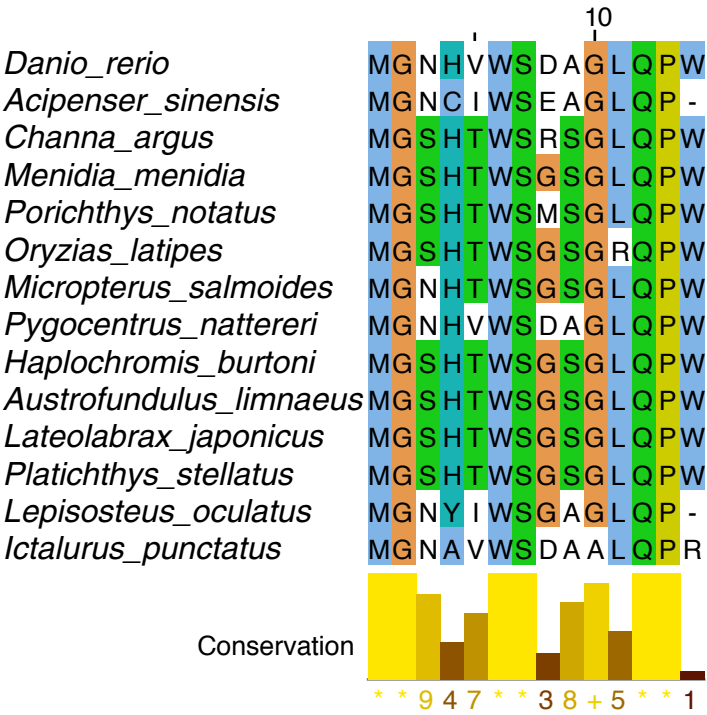
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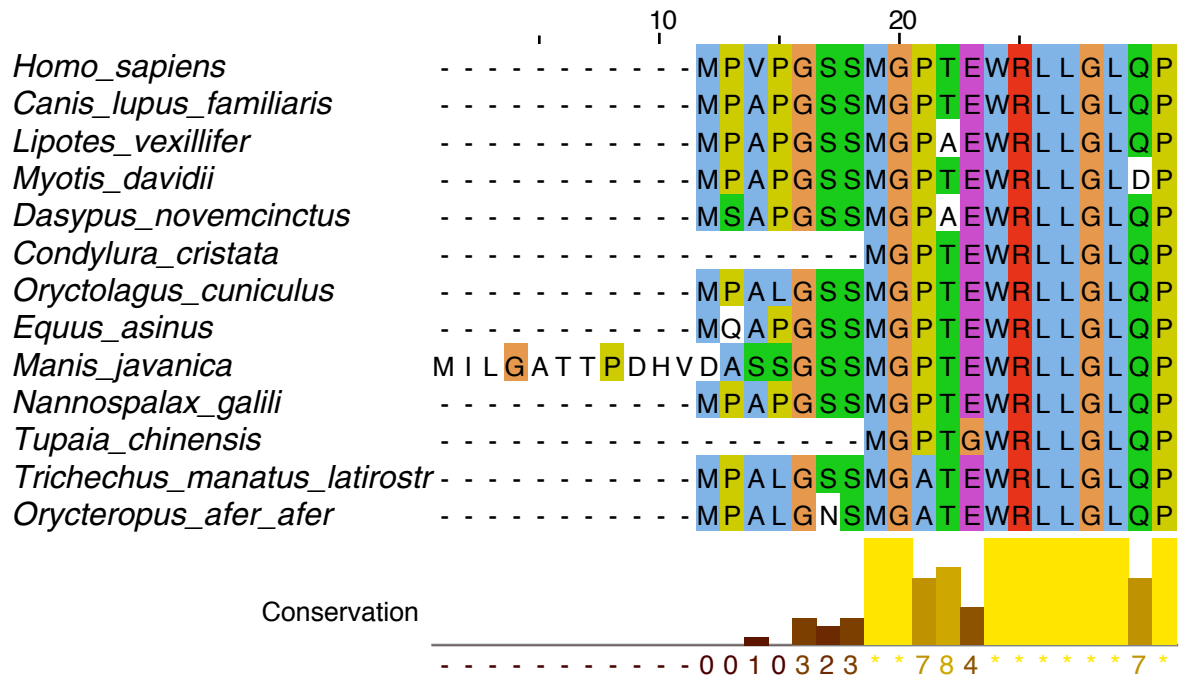


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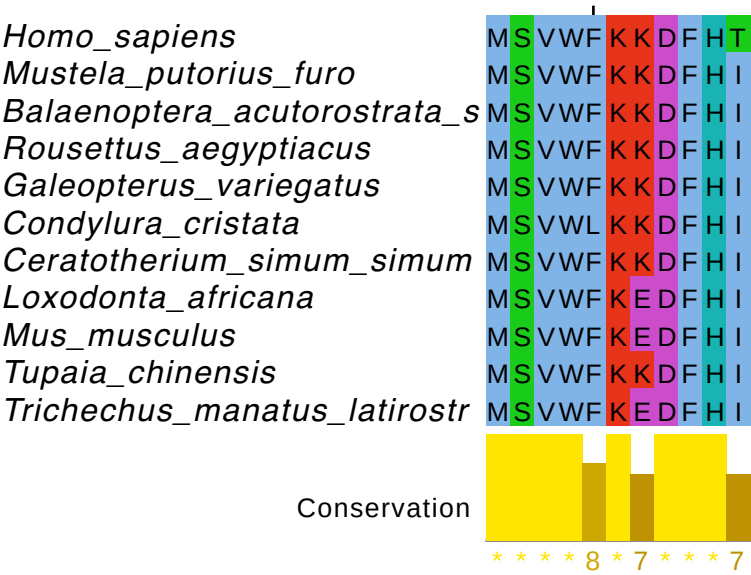


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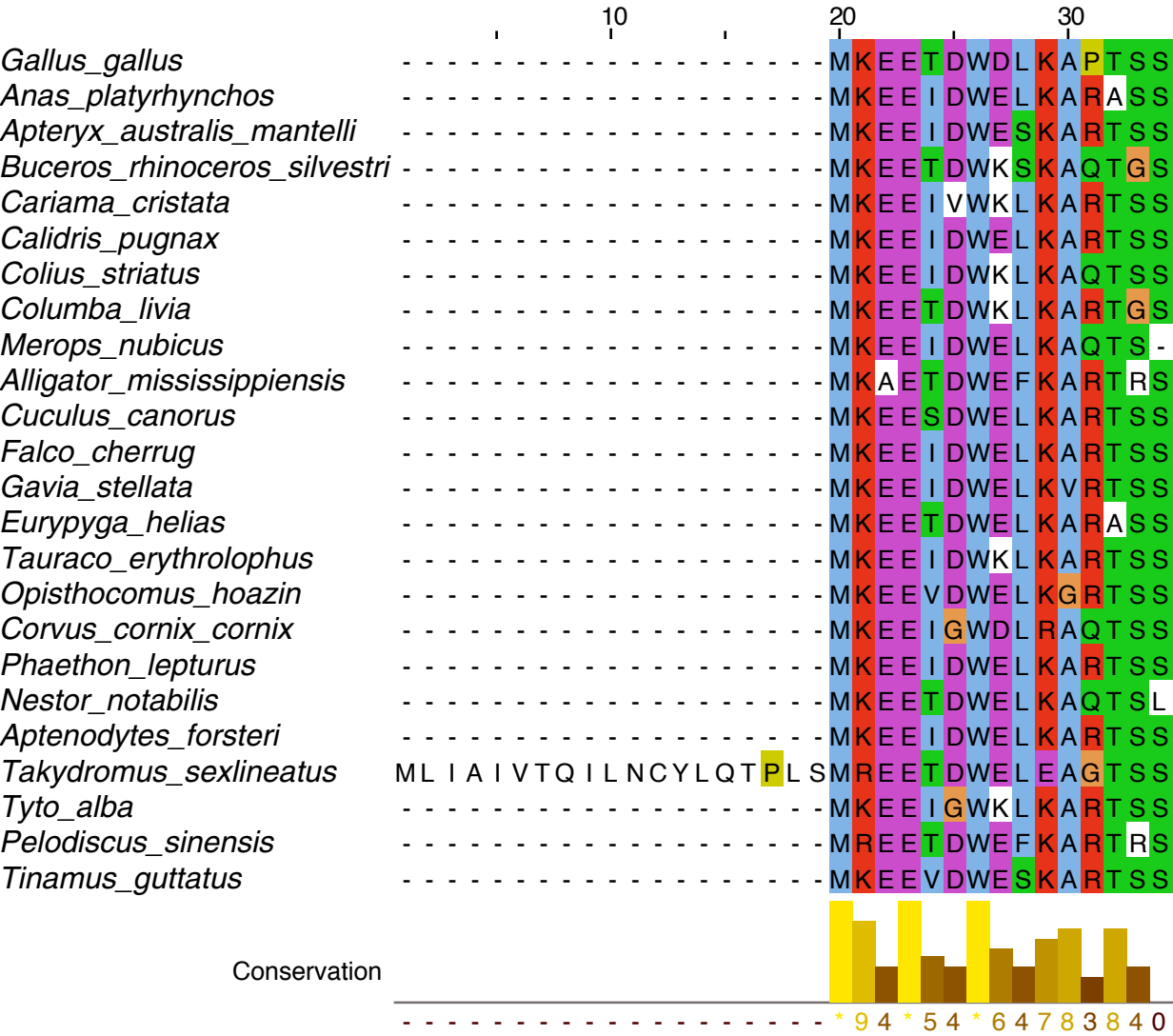
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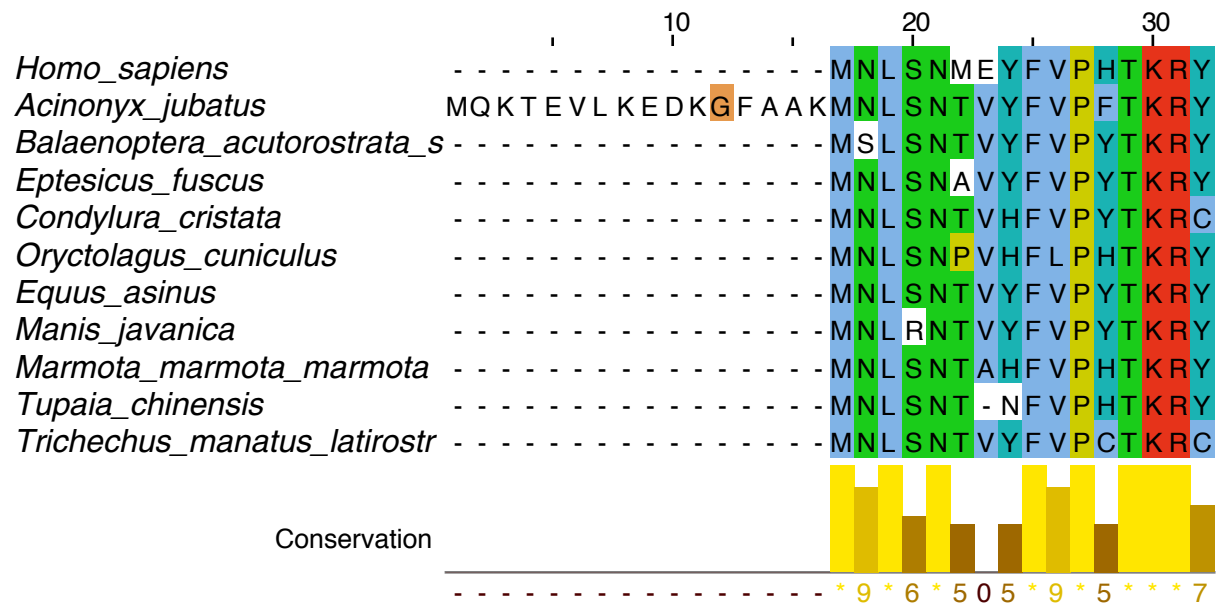
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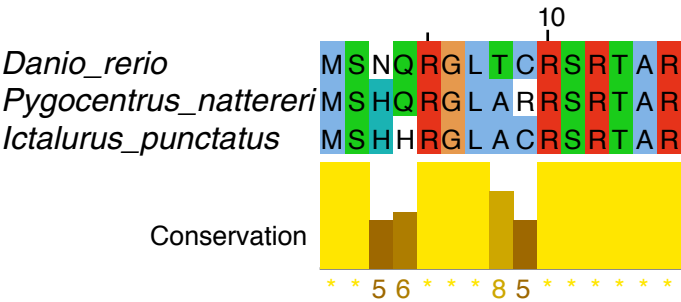
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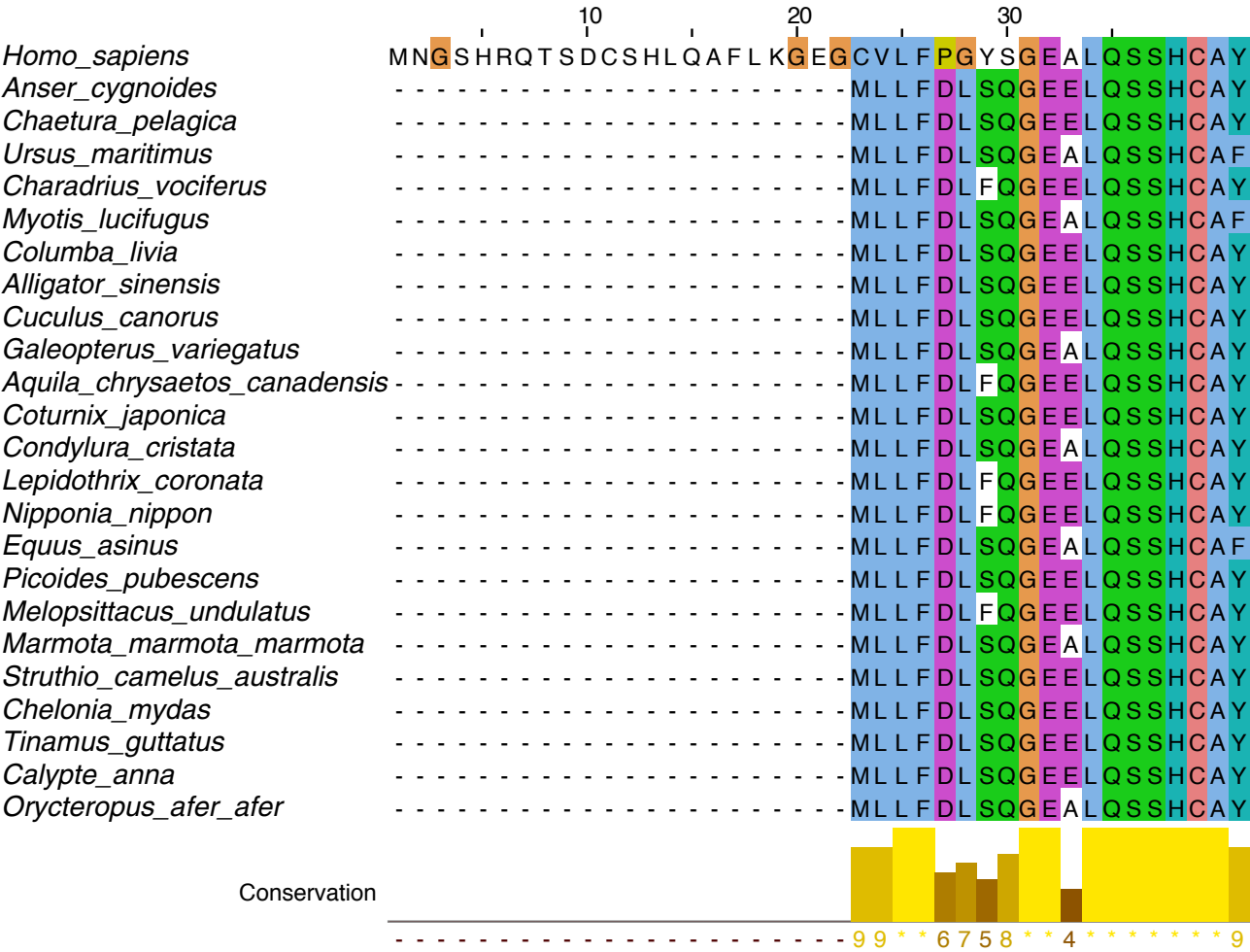
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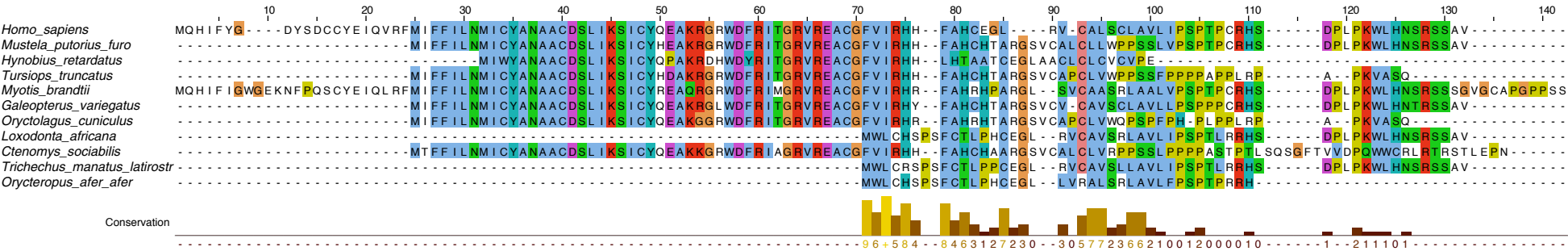
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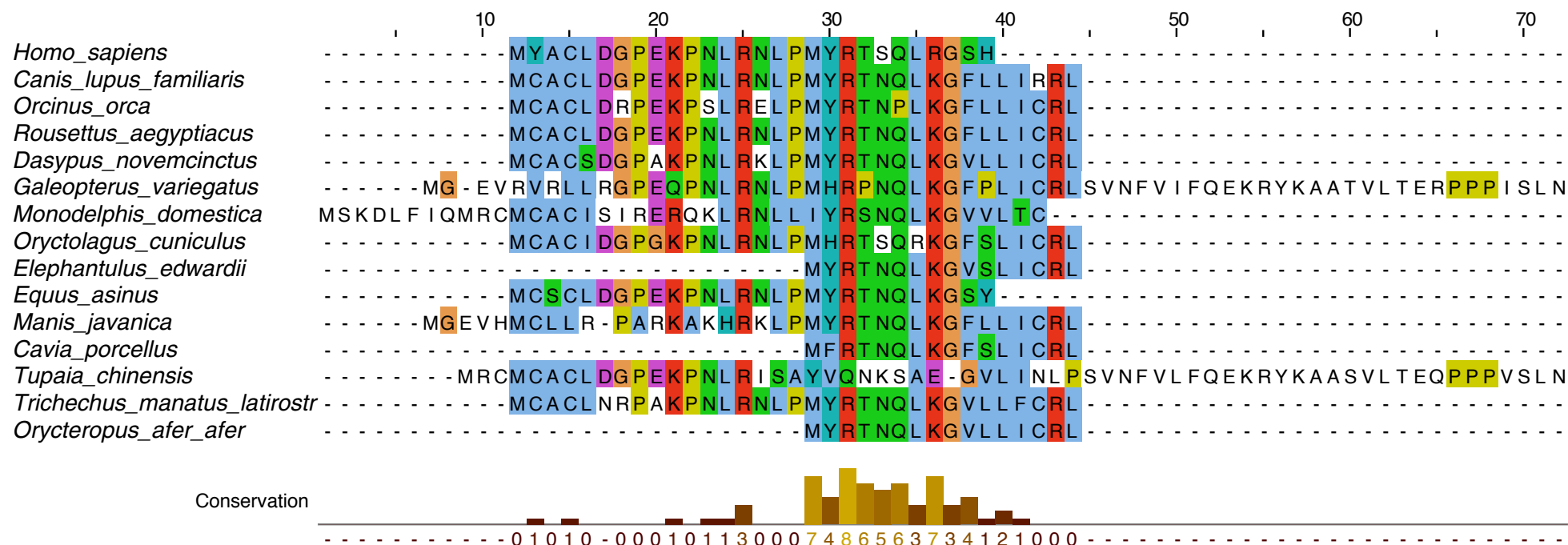


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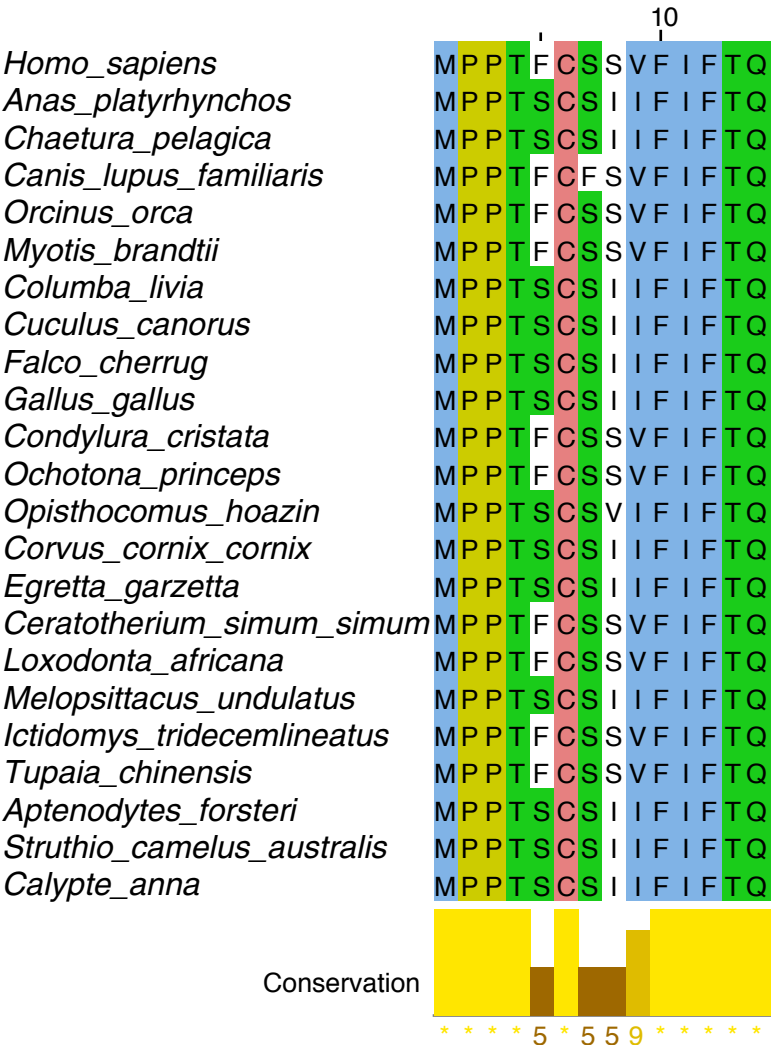


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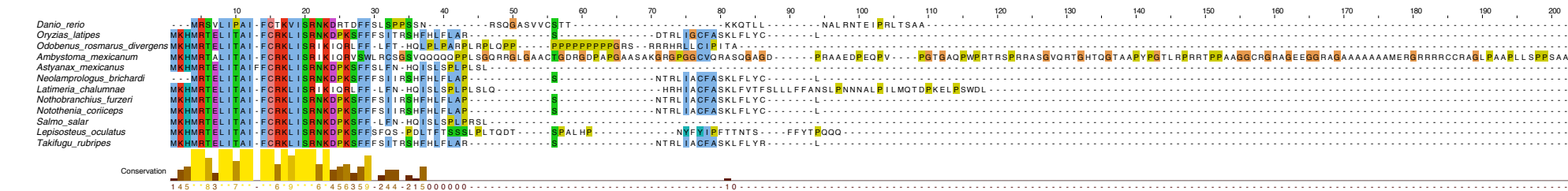
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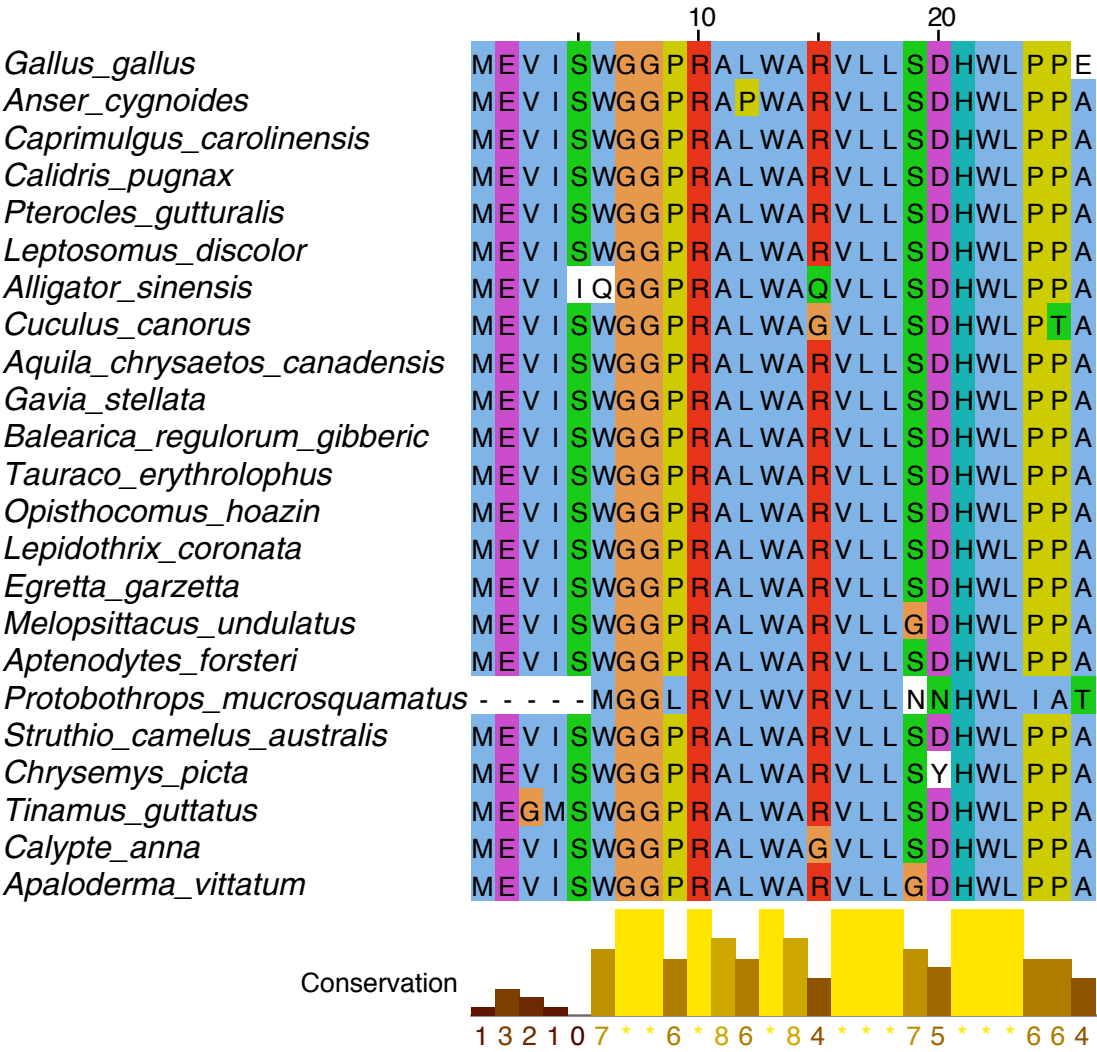
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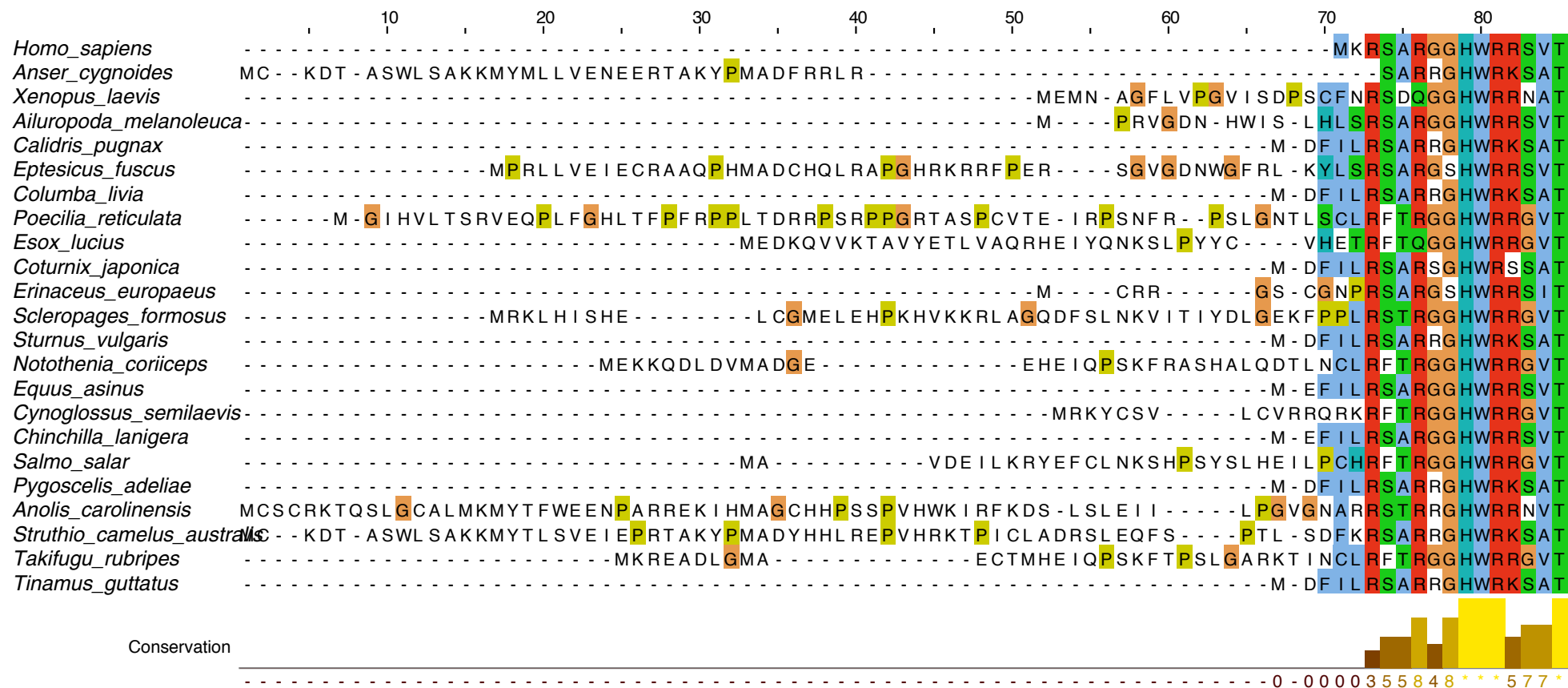


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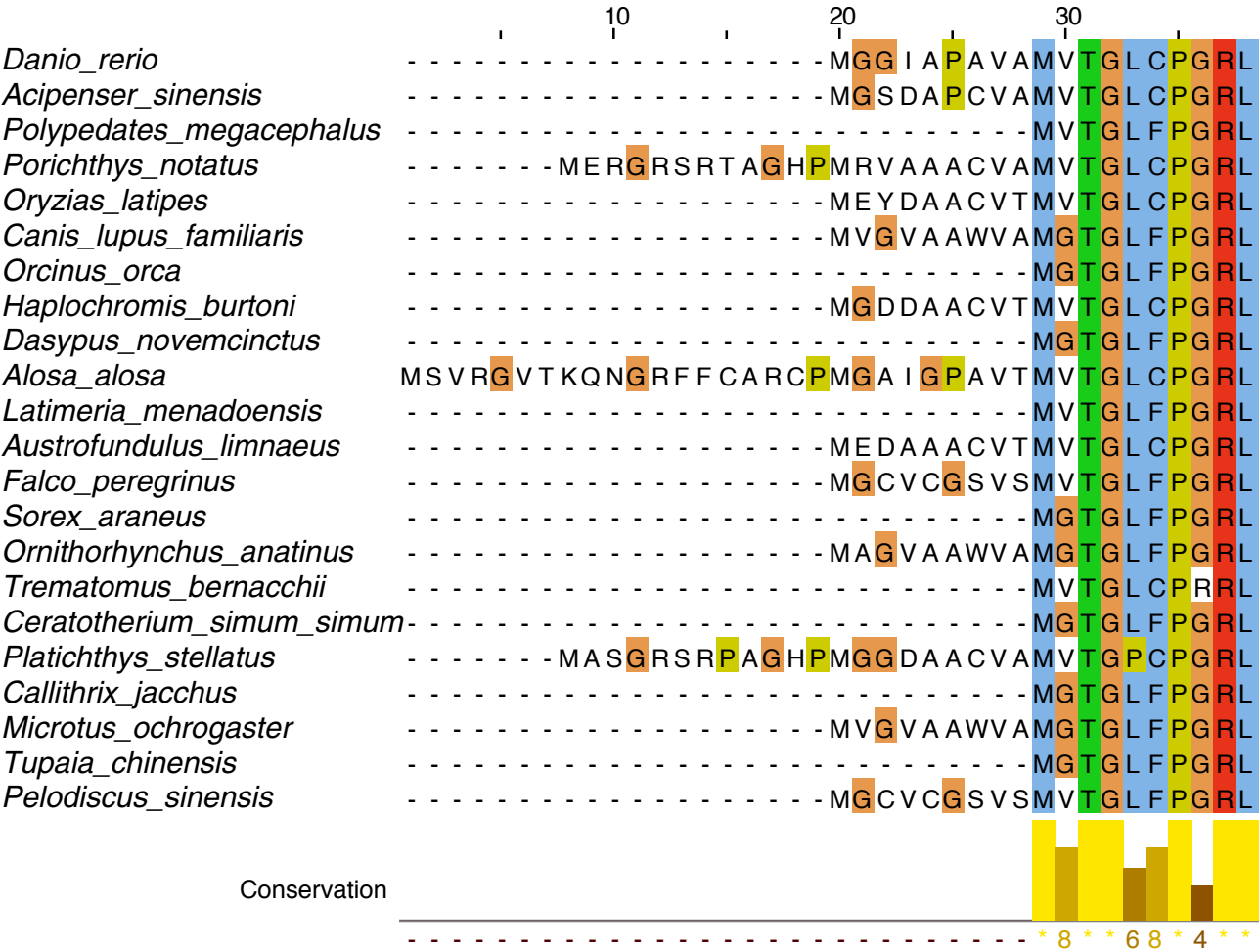


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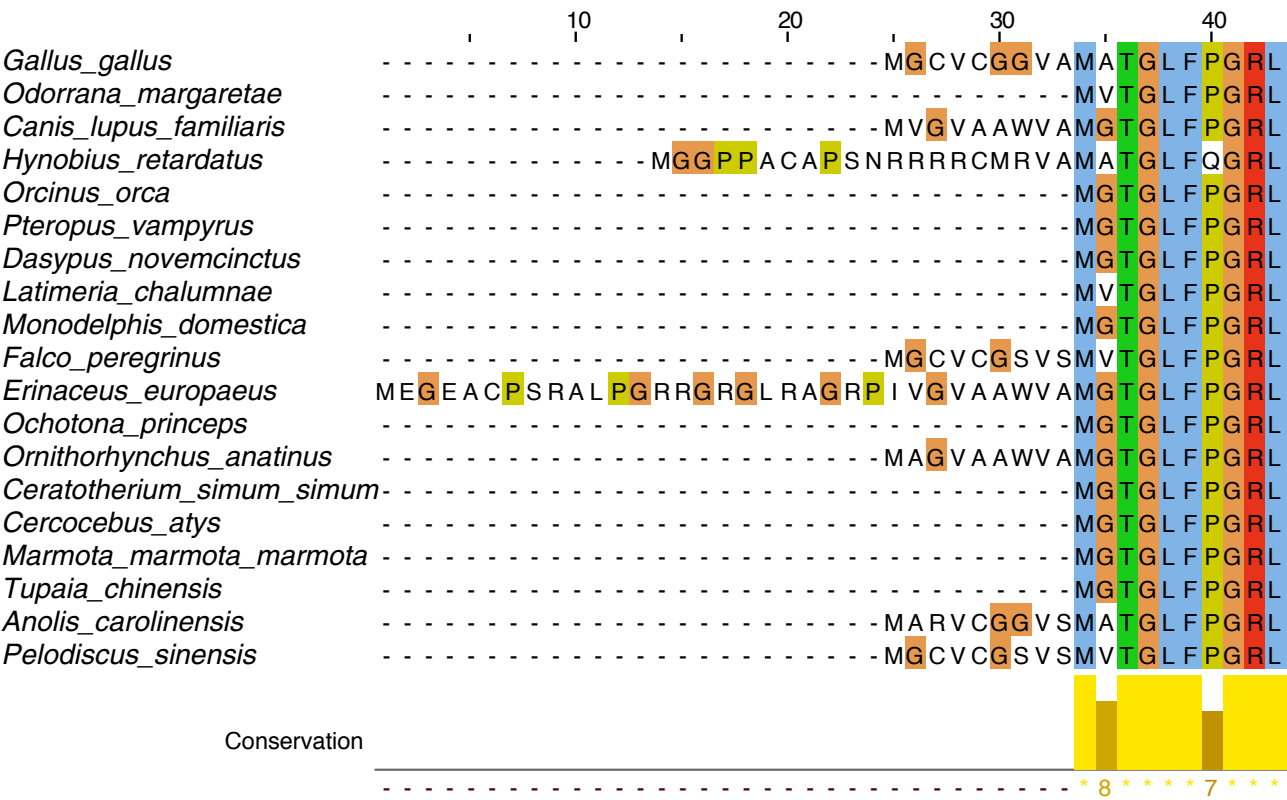
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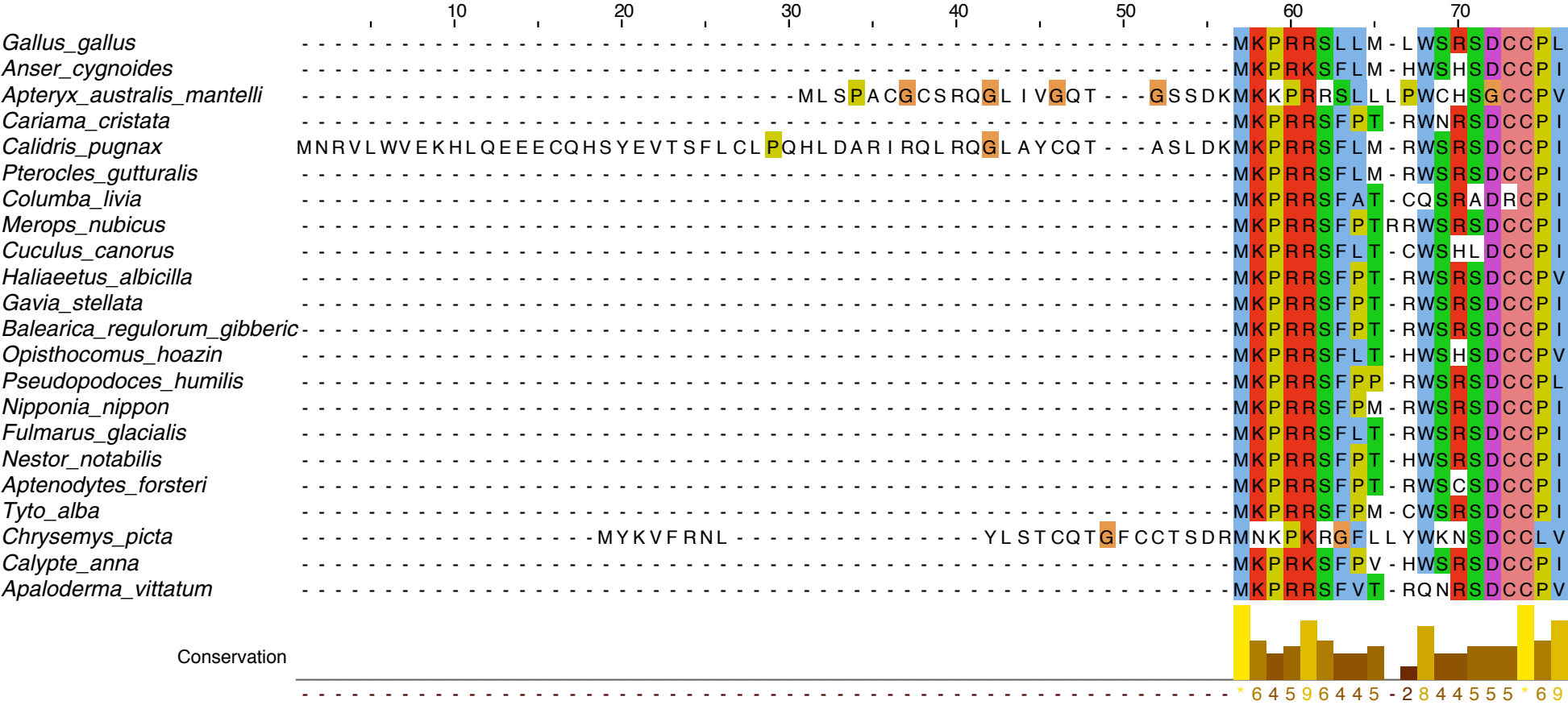
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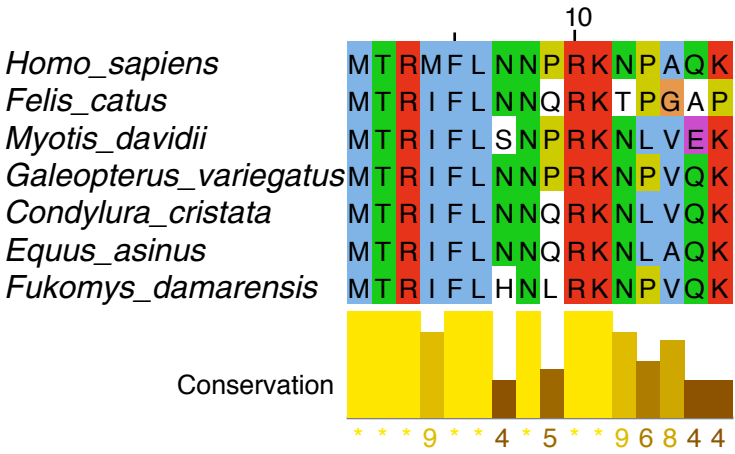
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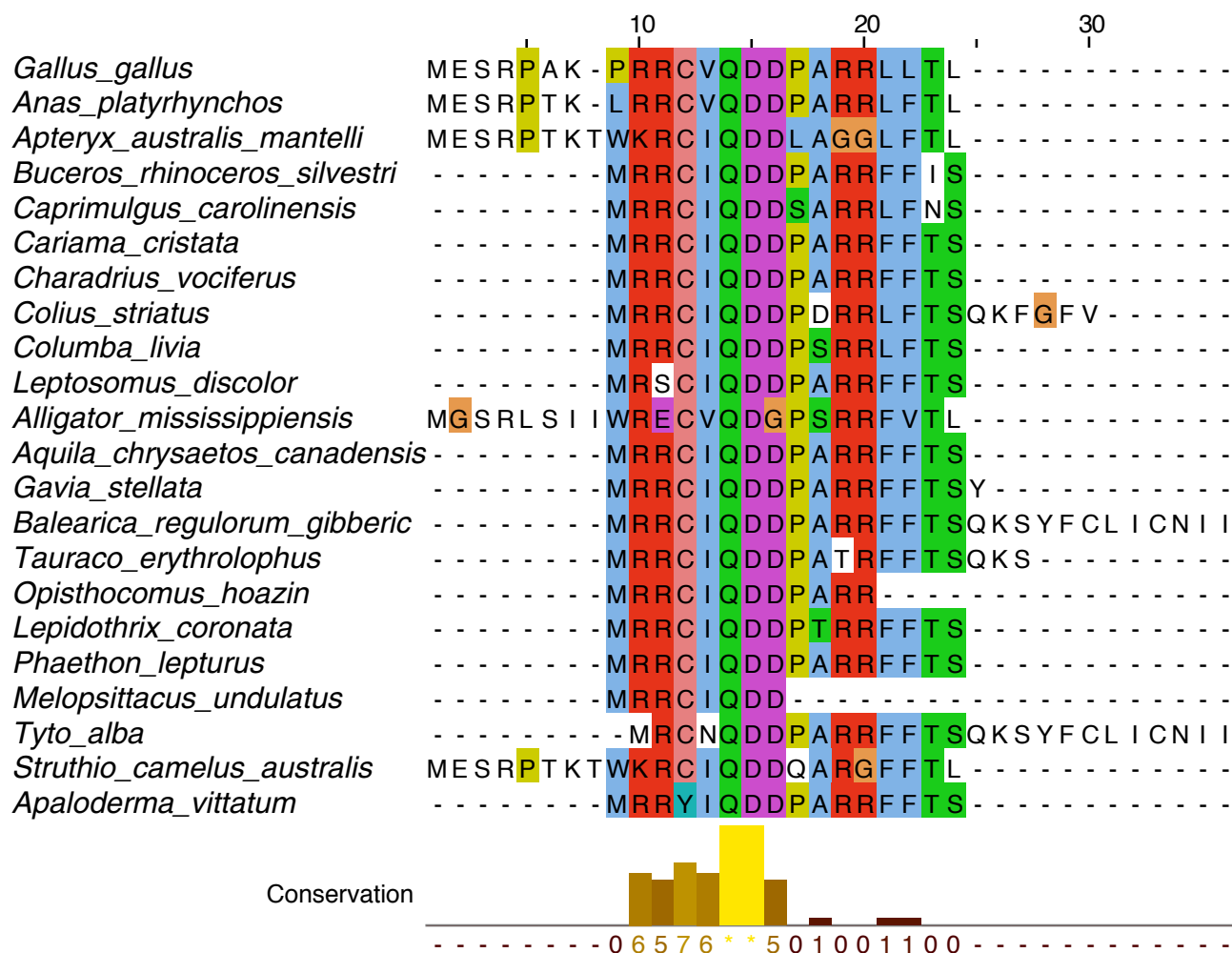


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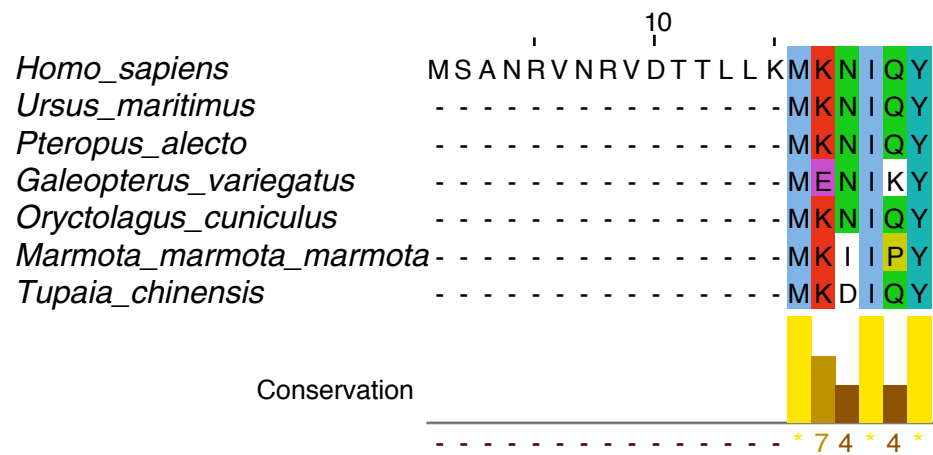


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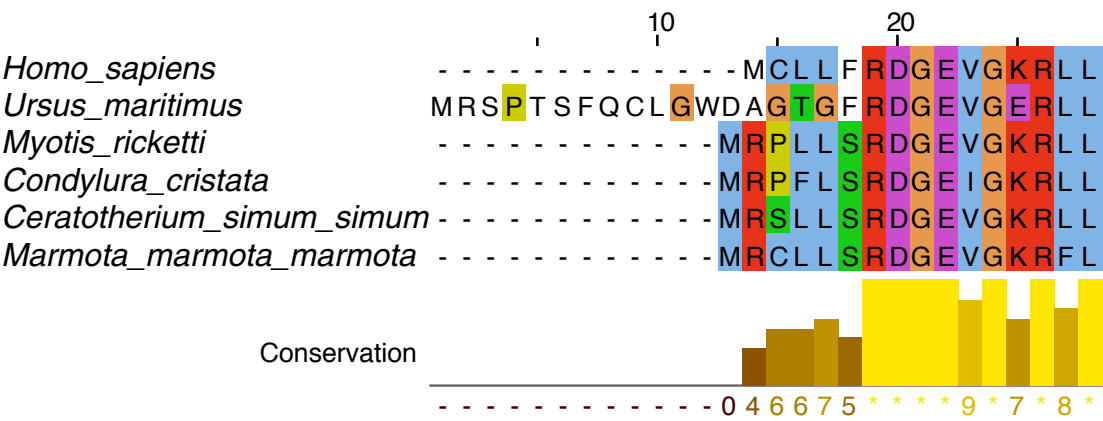
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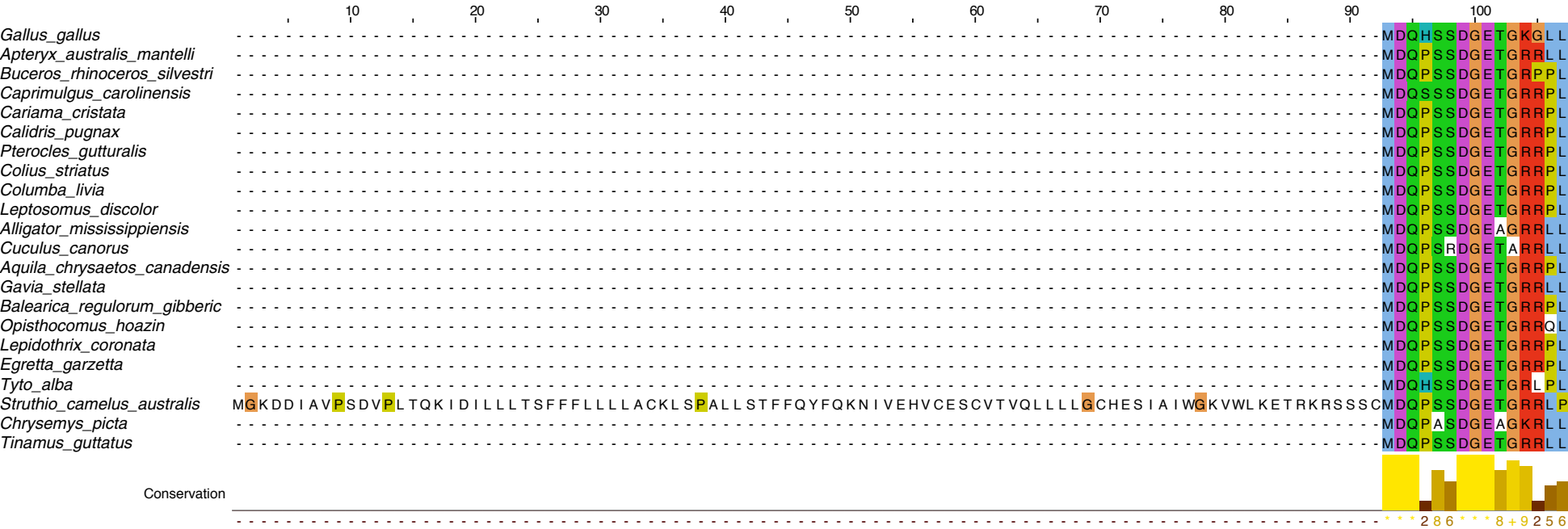


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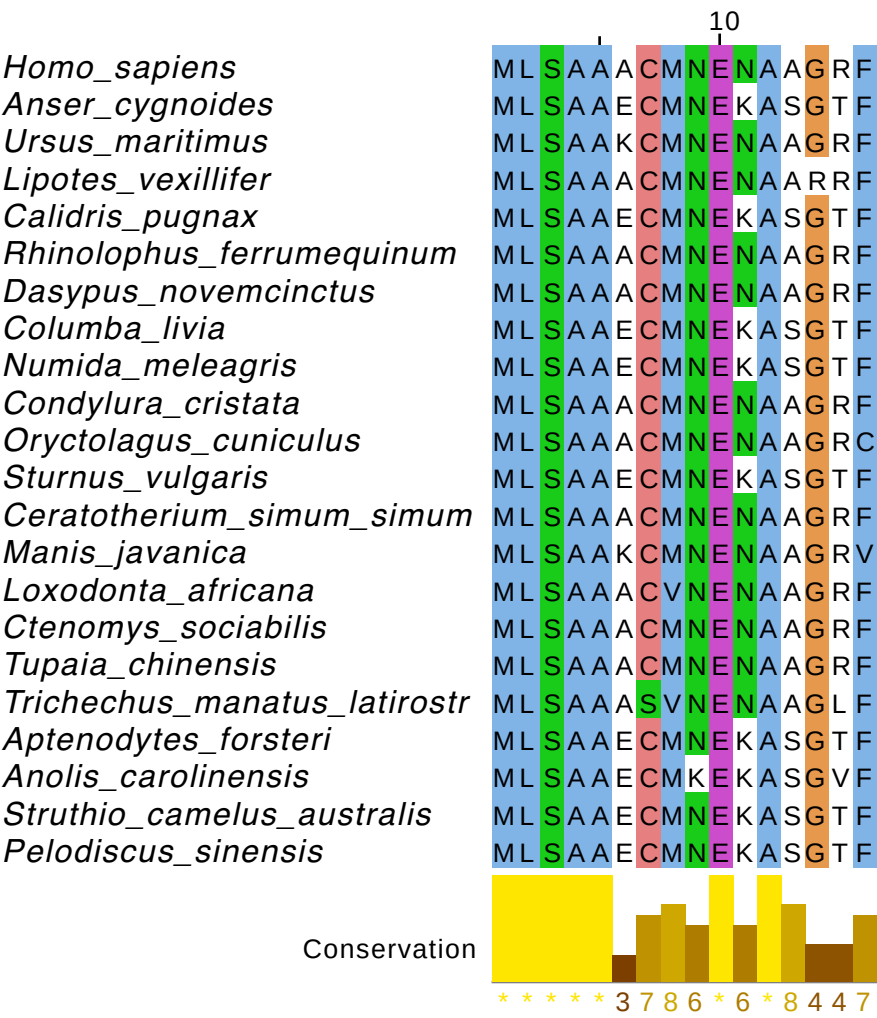


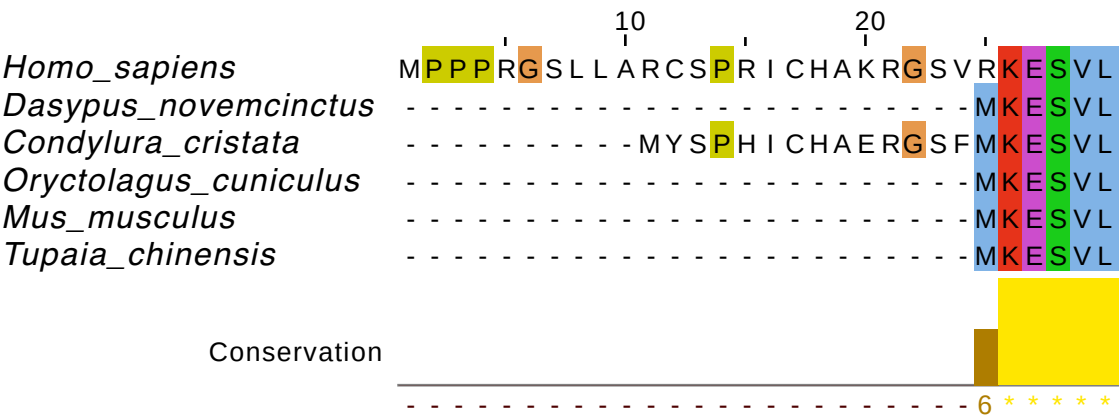
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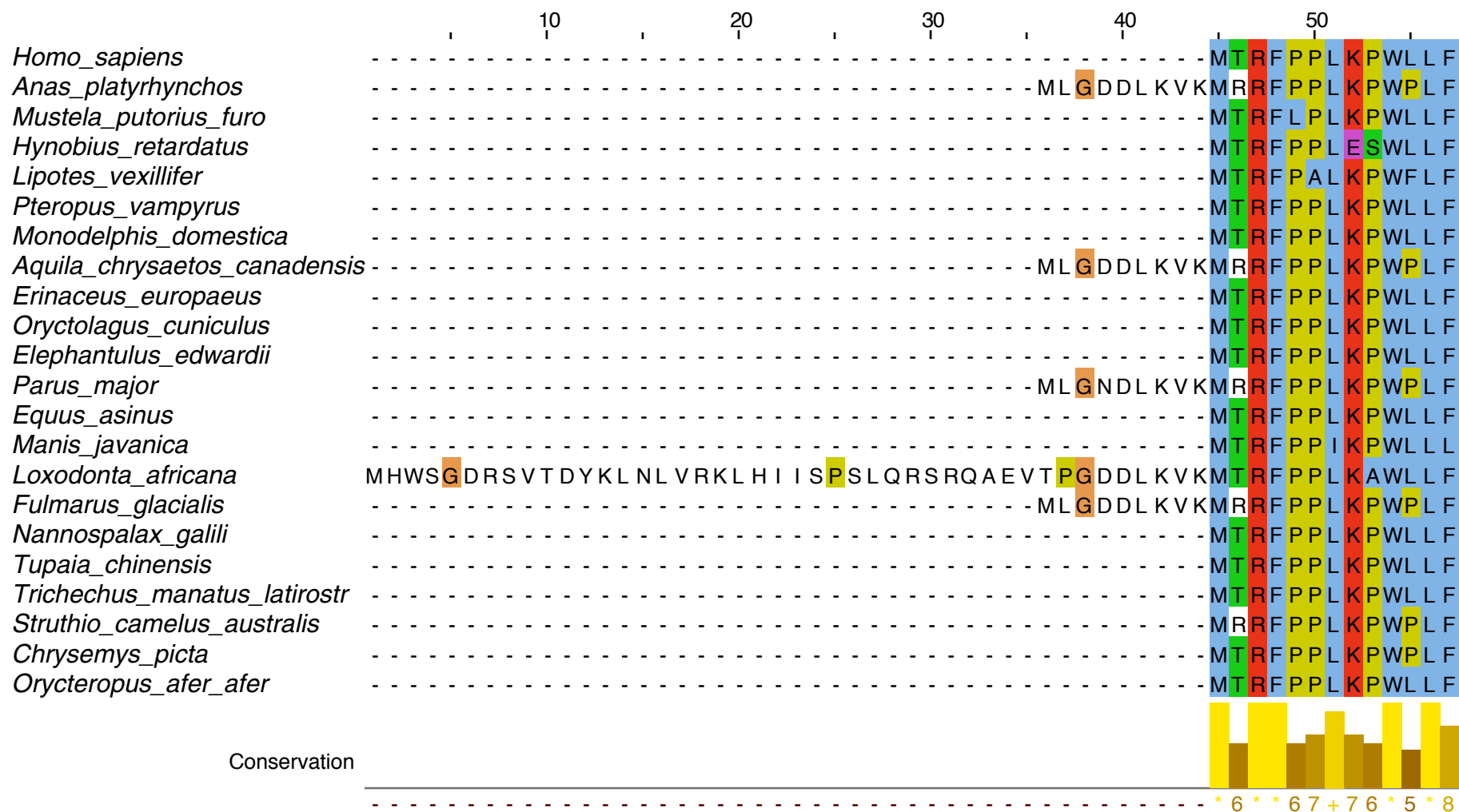
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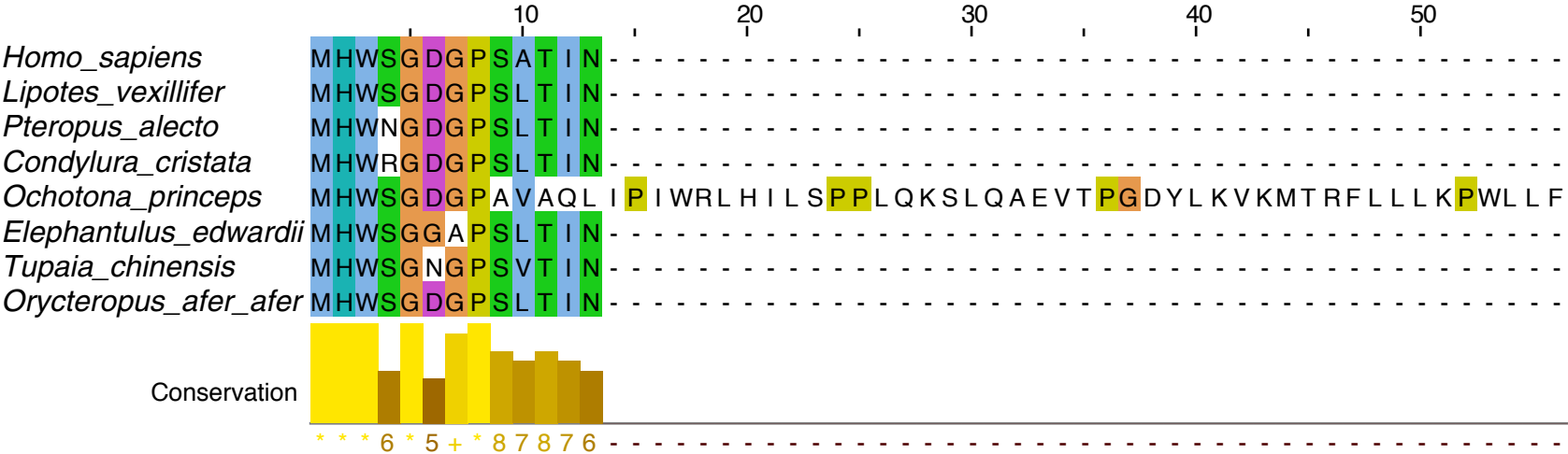


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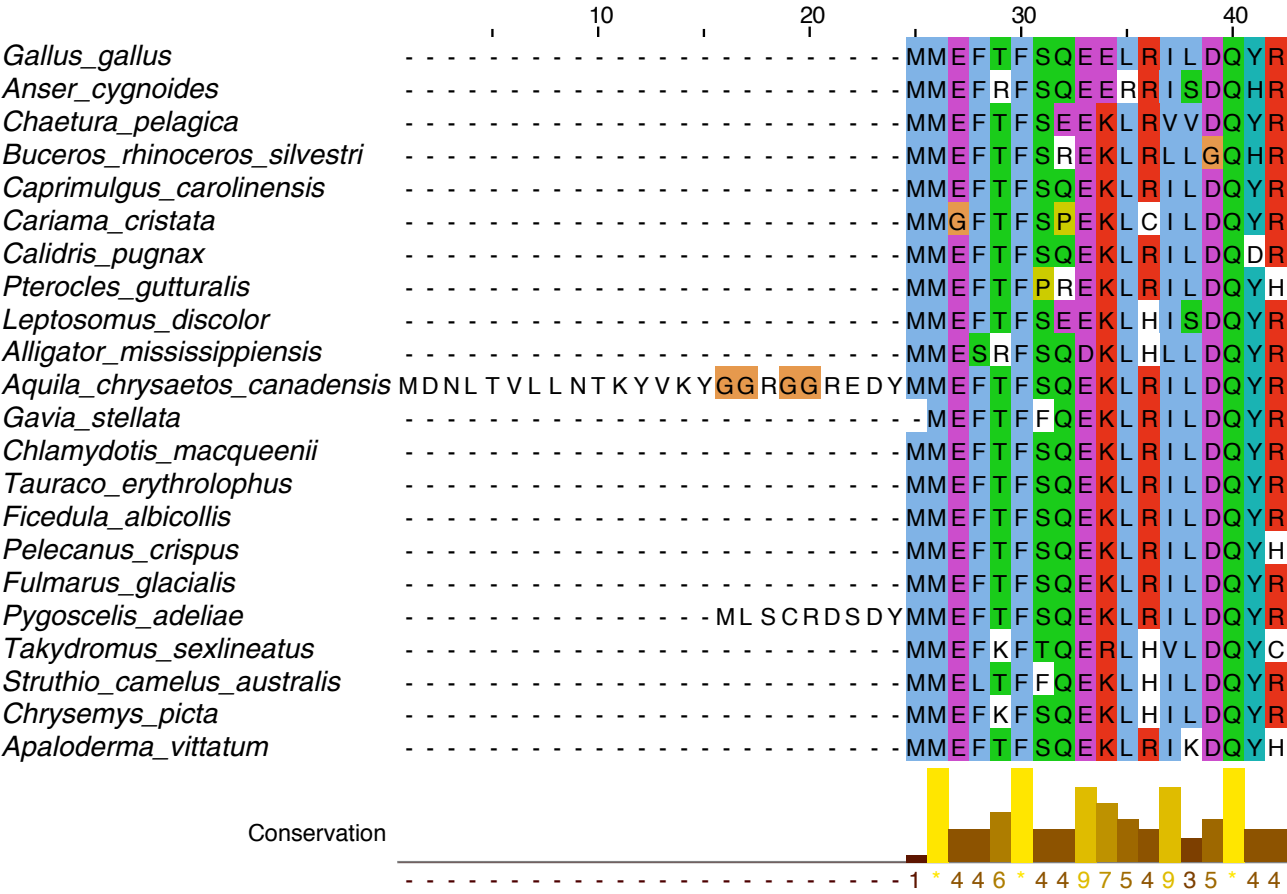
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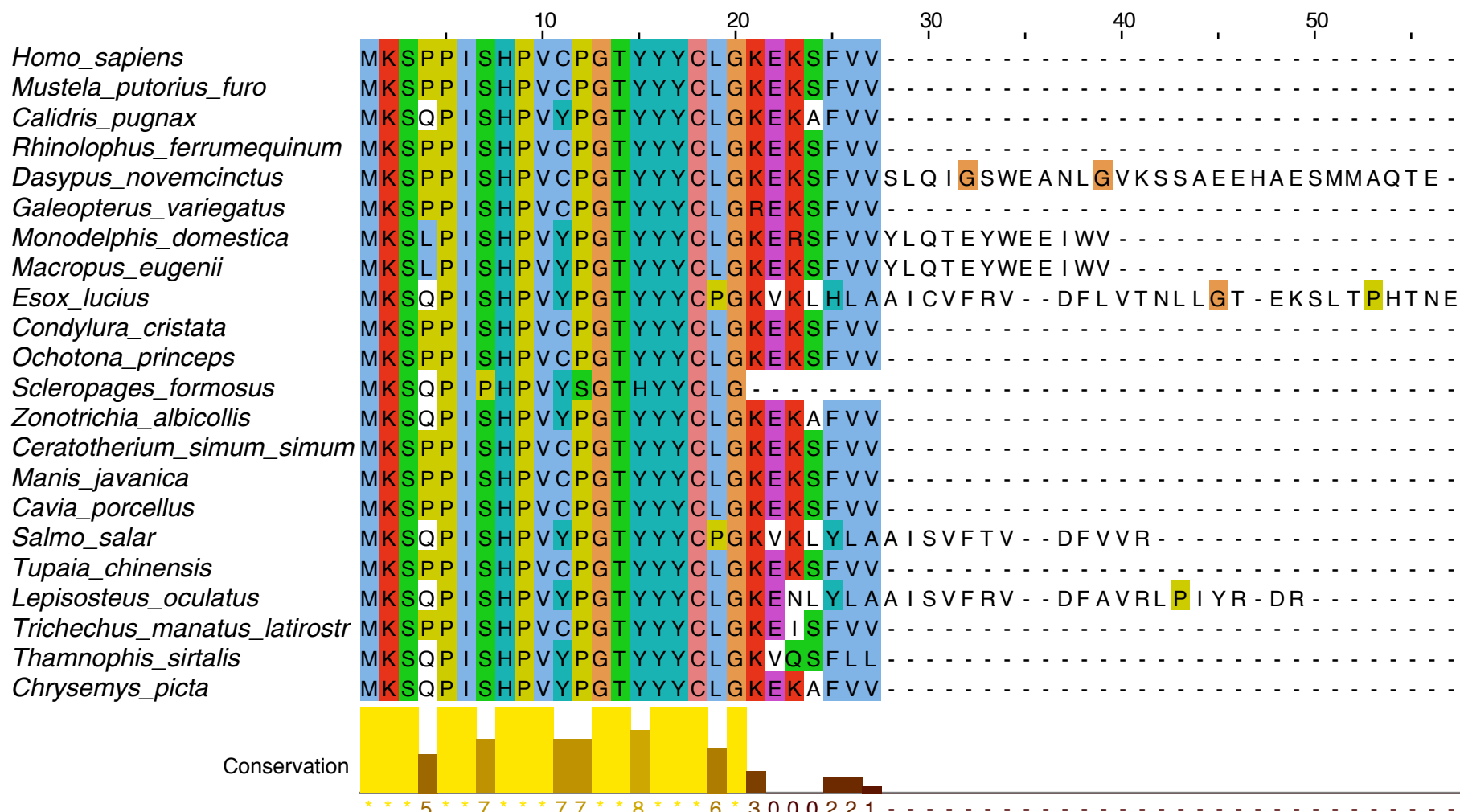


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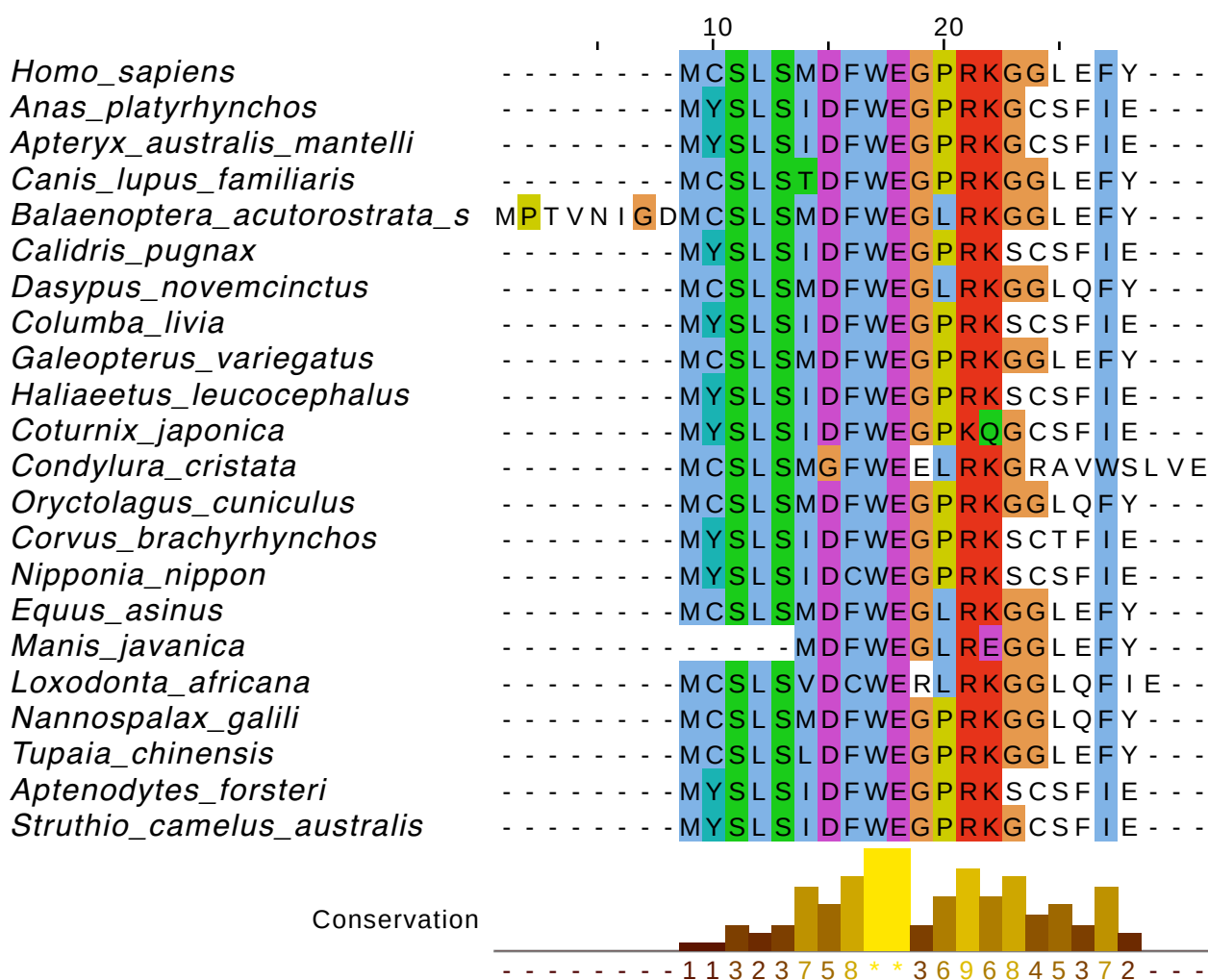
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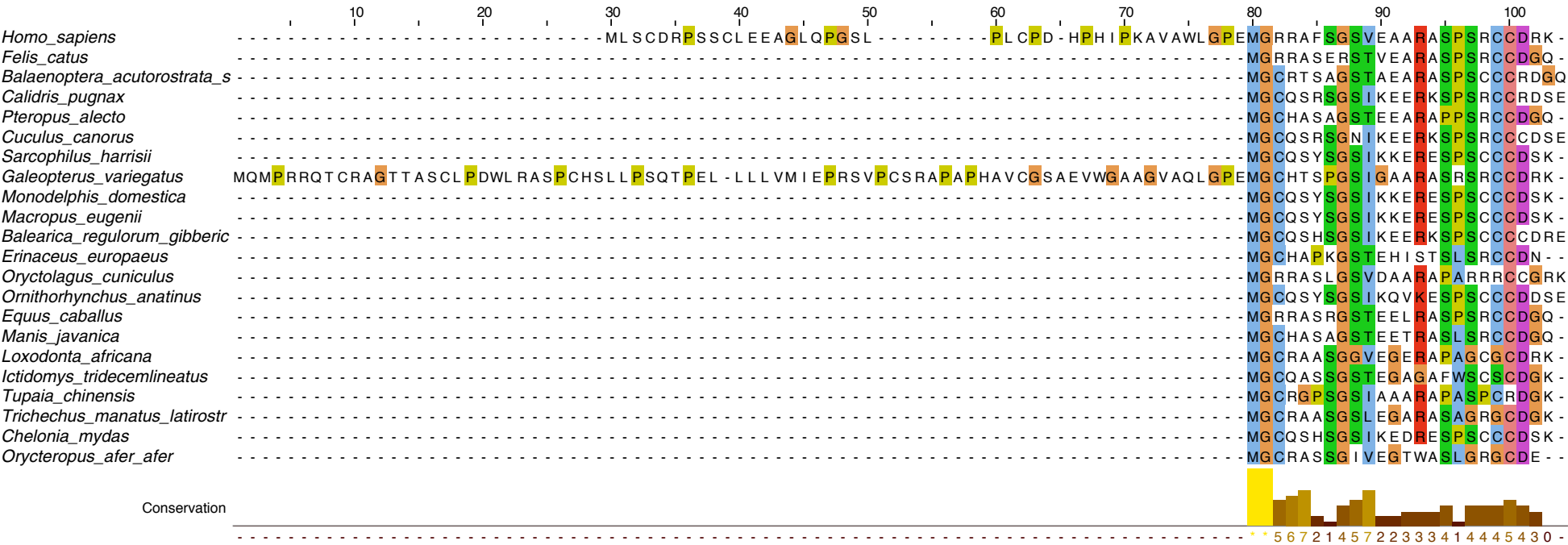
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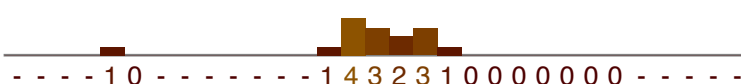
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HG0122
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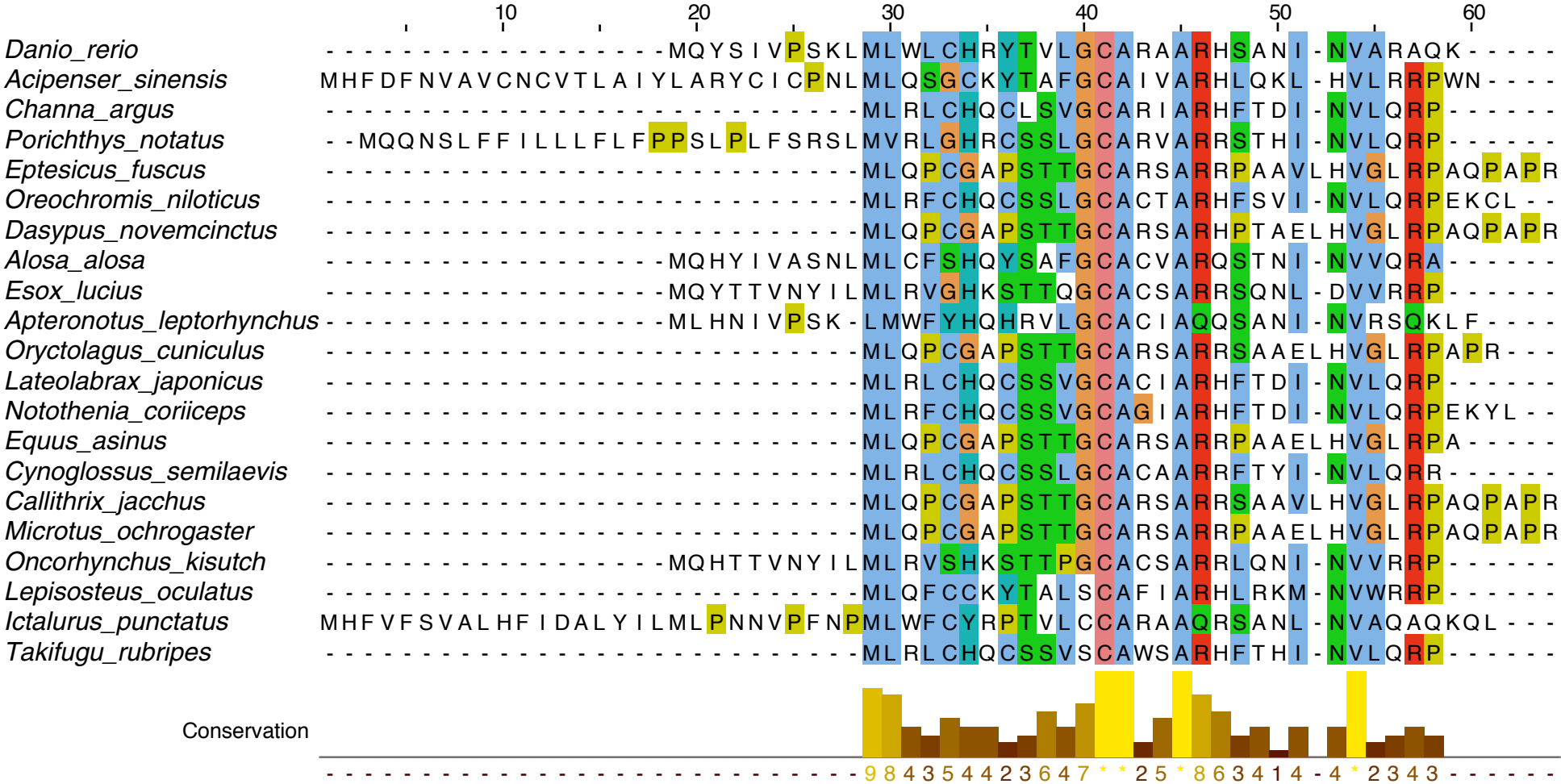


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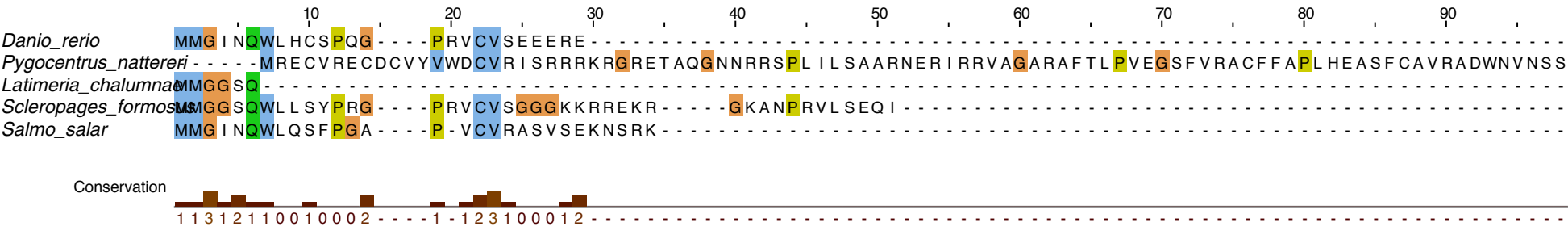
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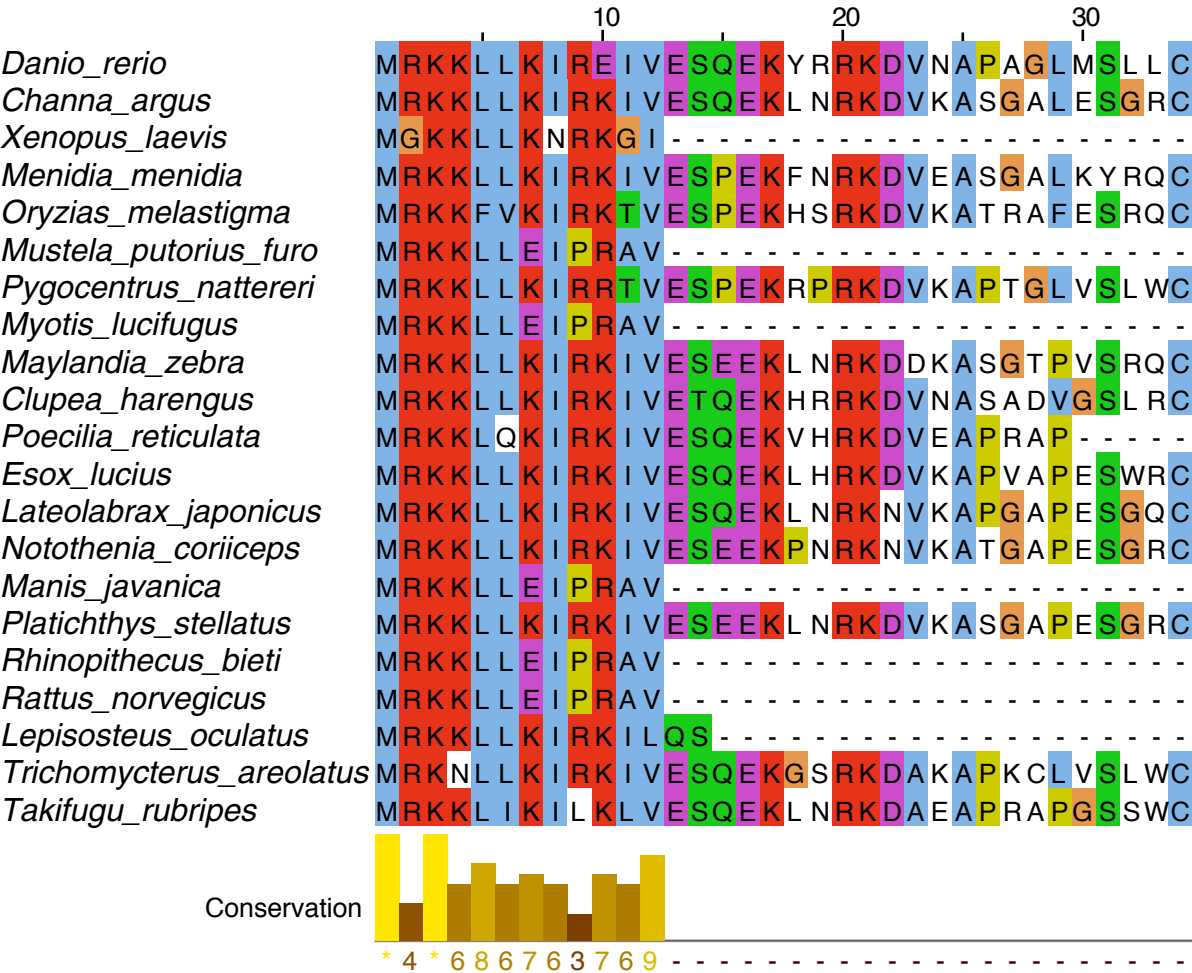
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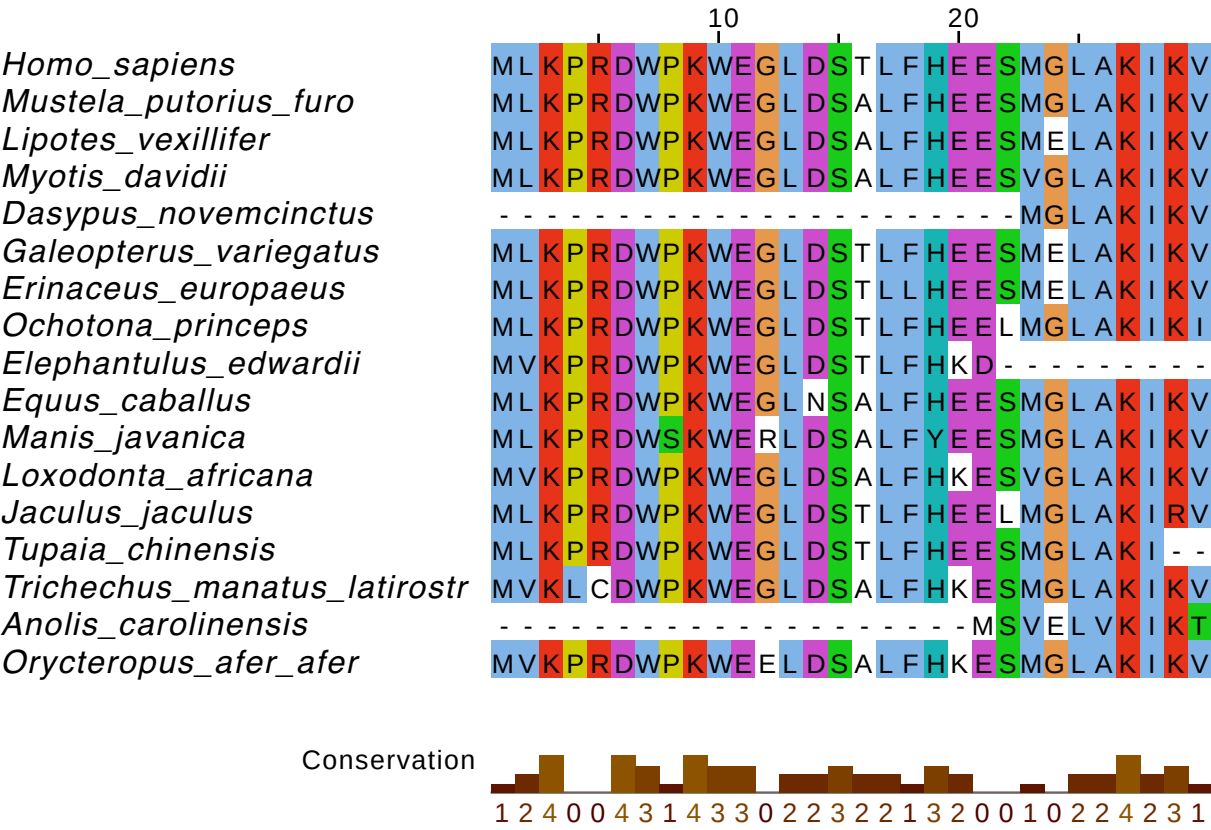
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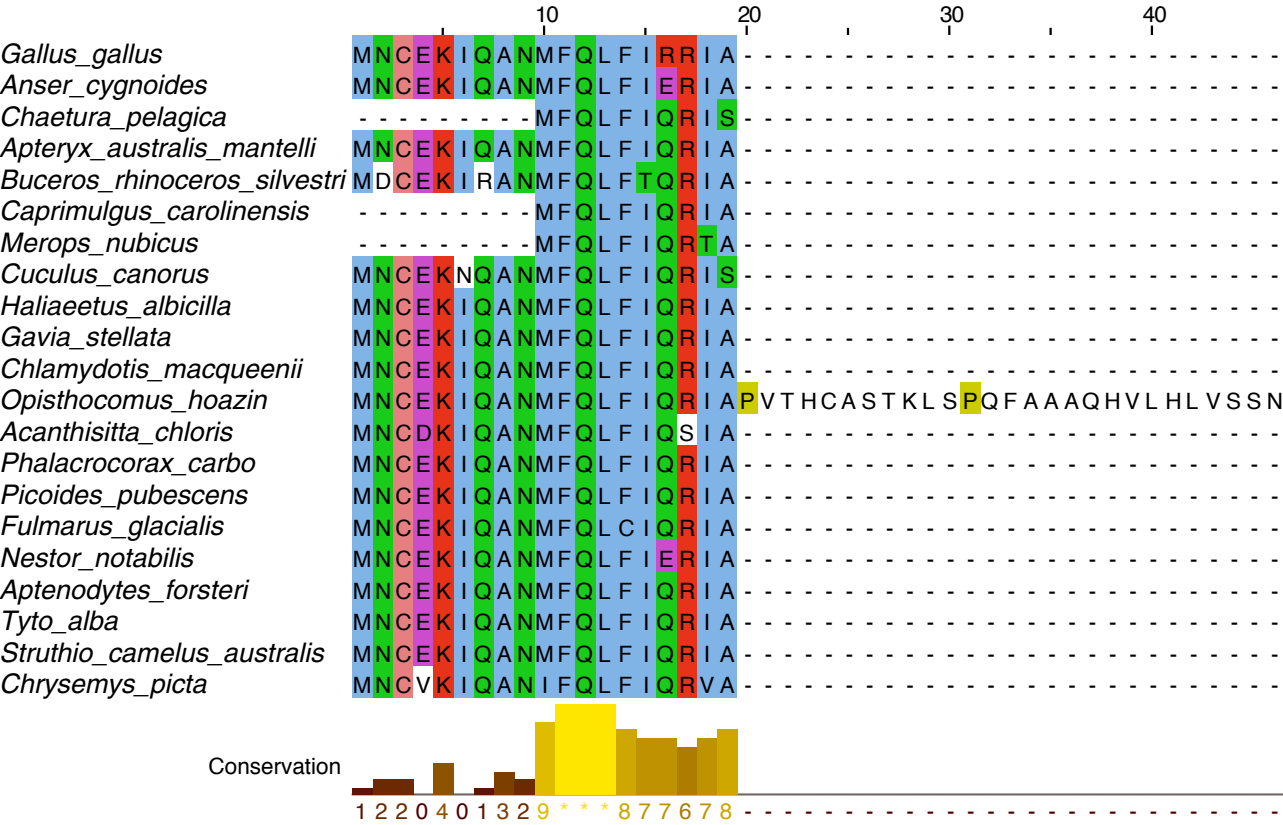
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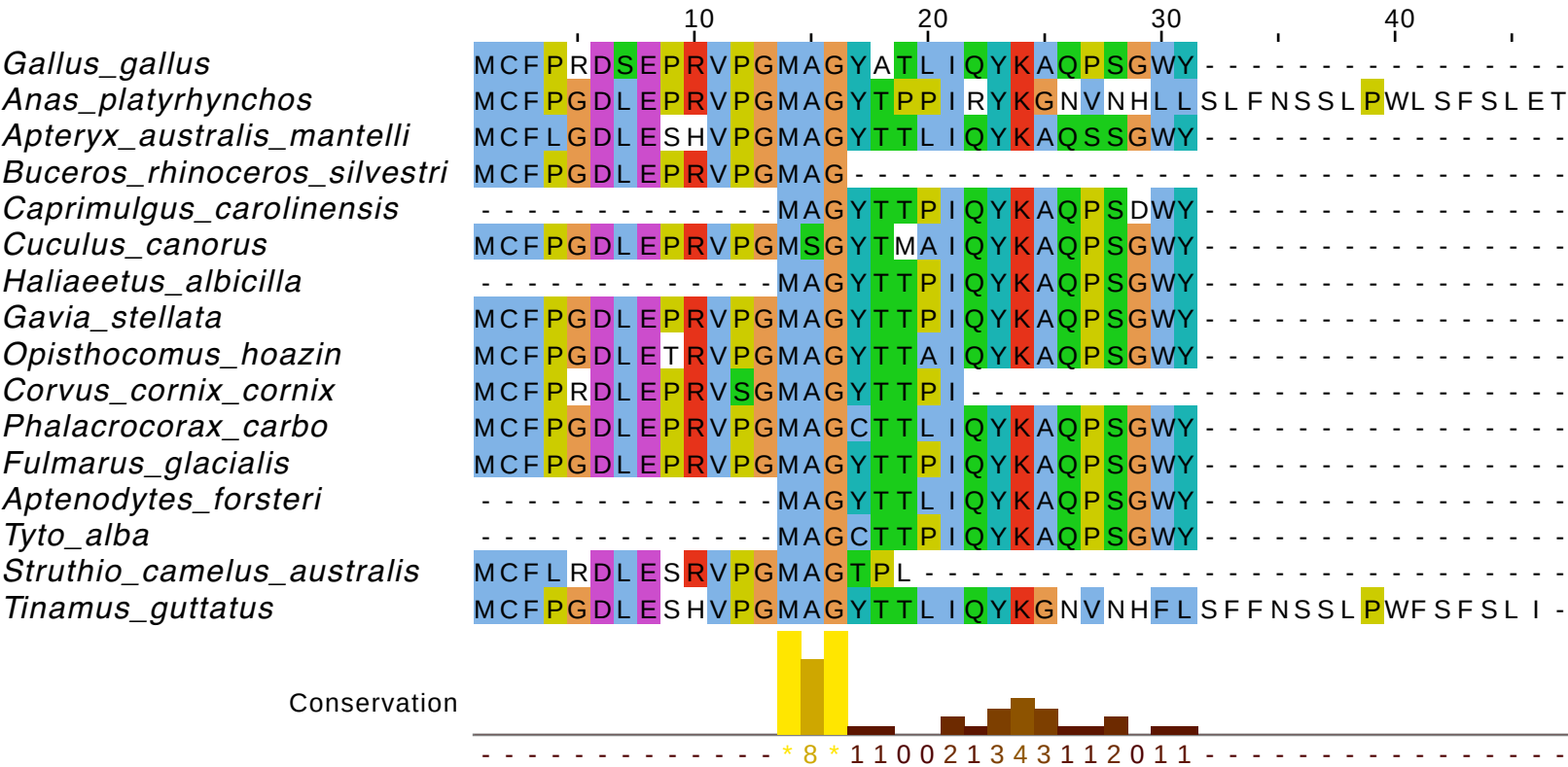
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HG0126.2

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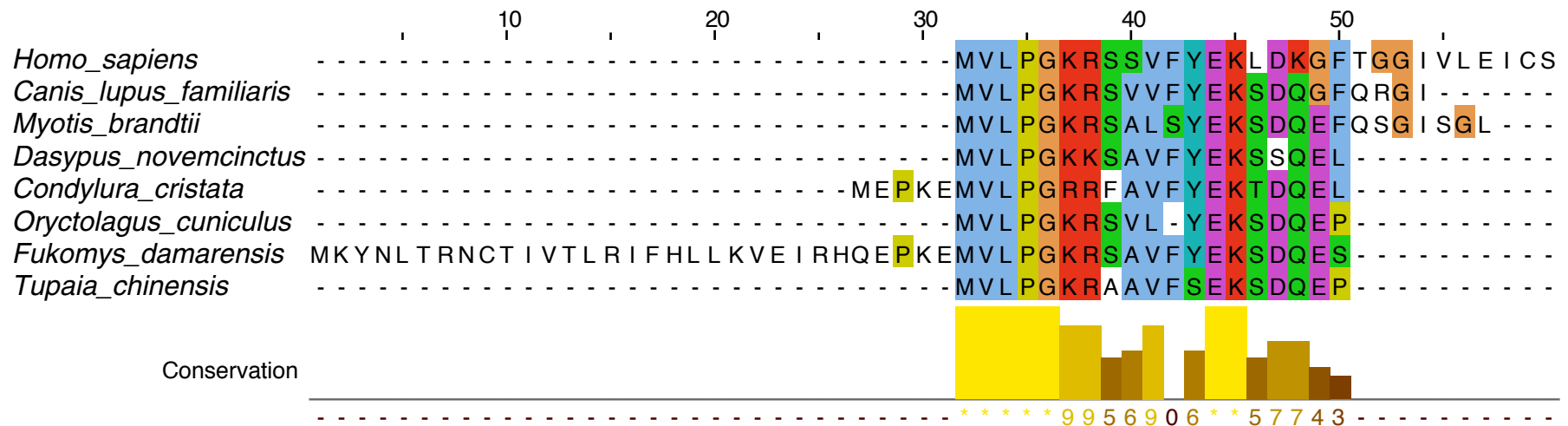


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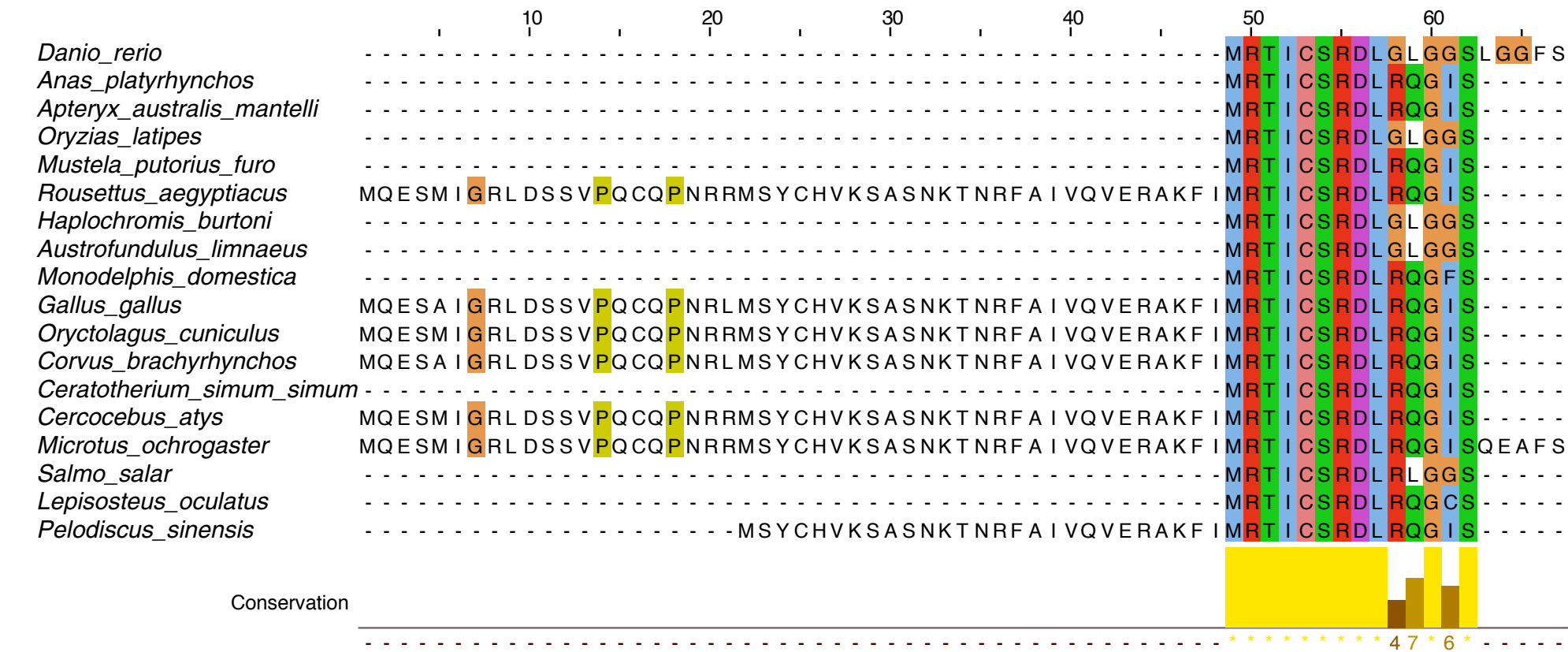
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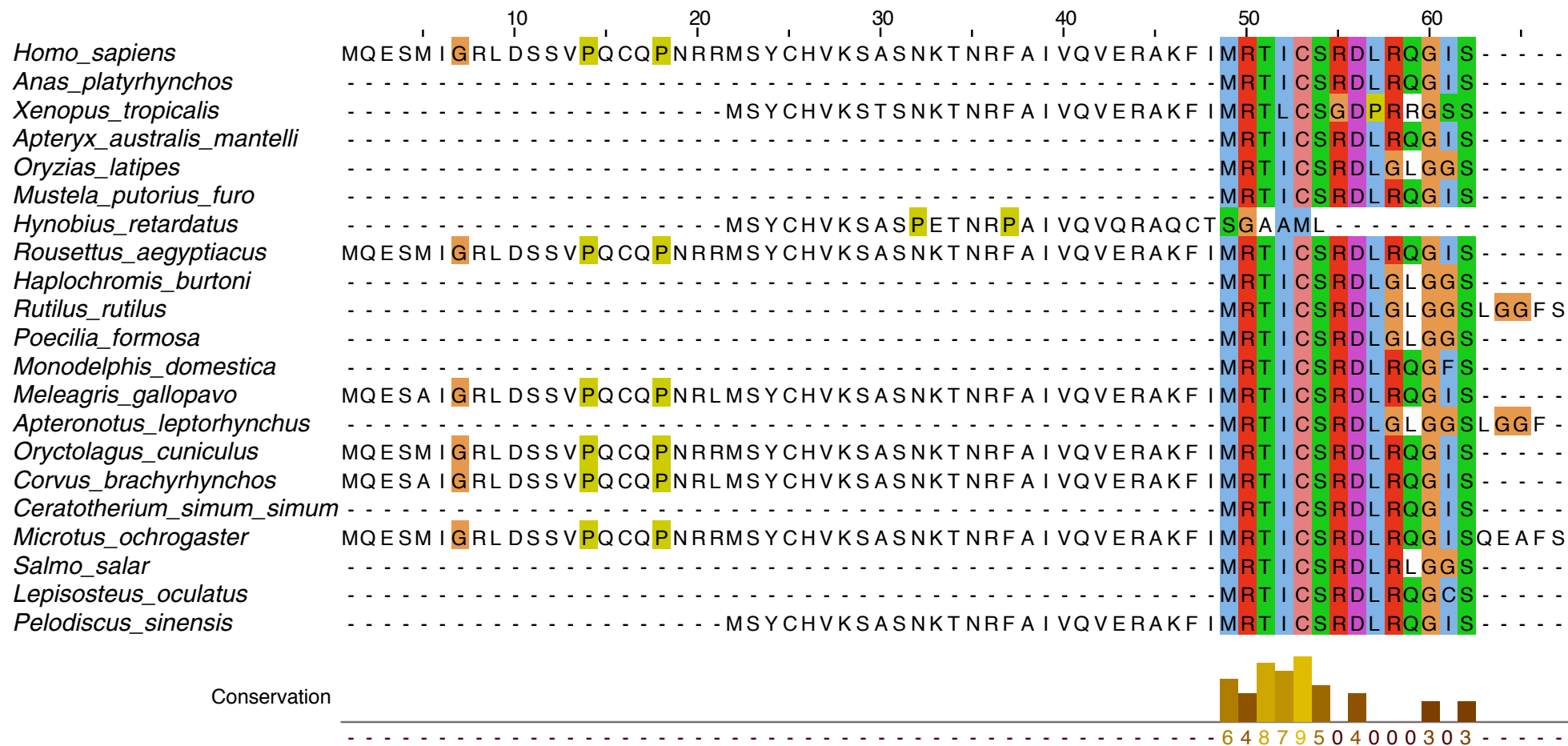


HG0128

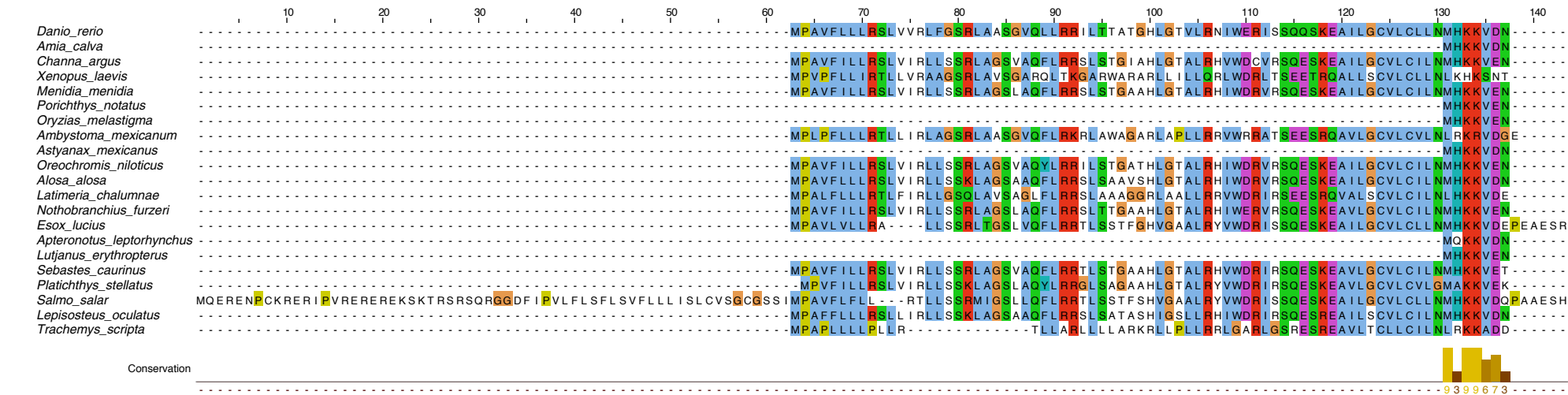
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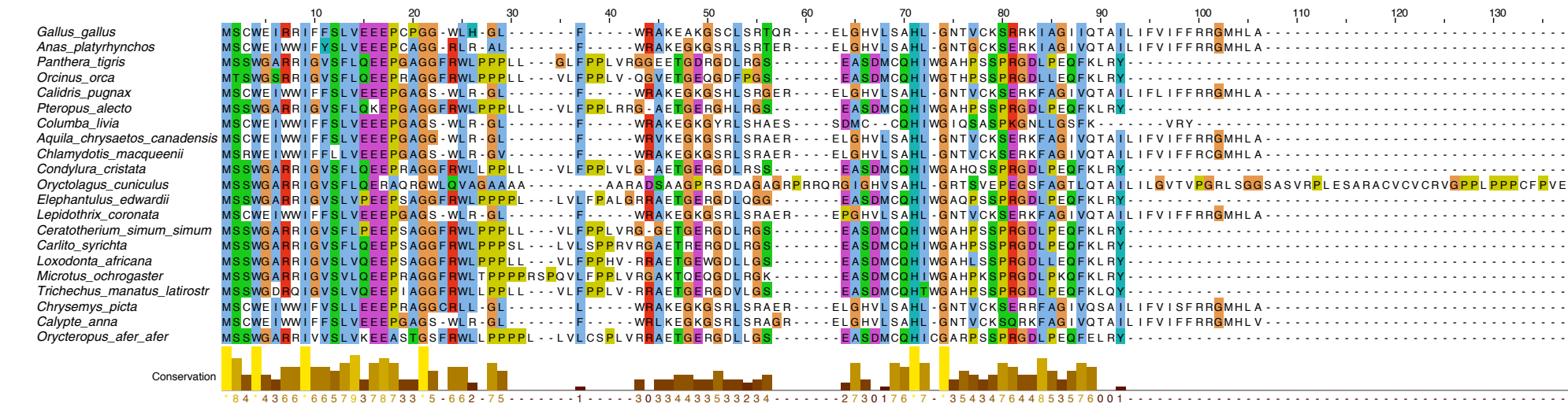
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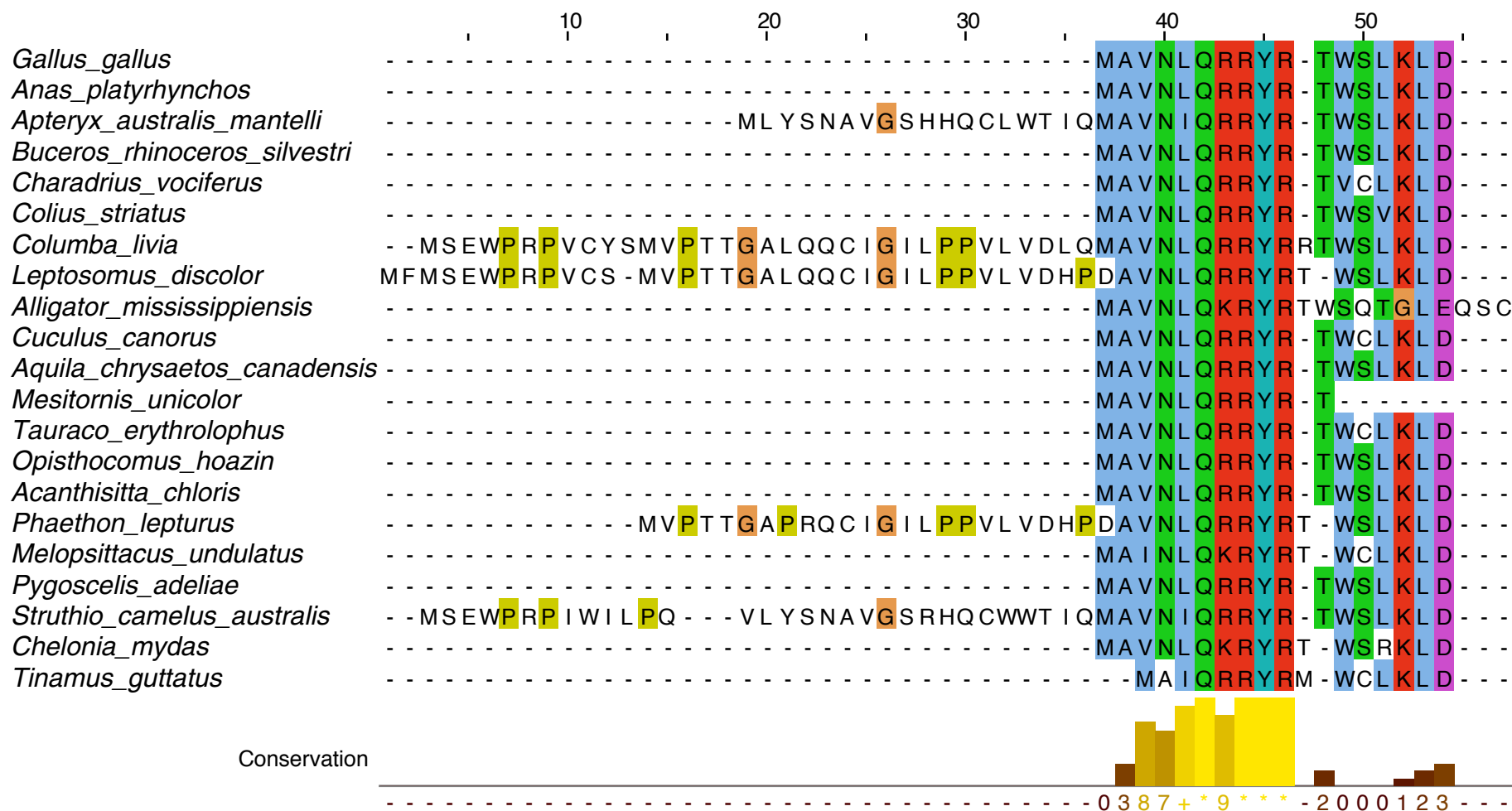
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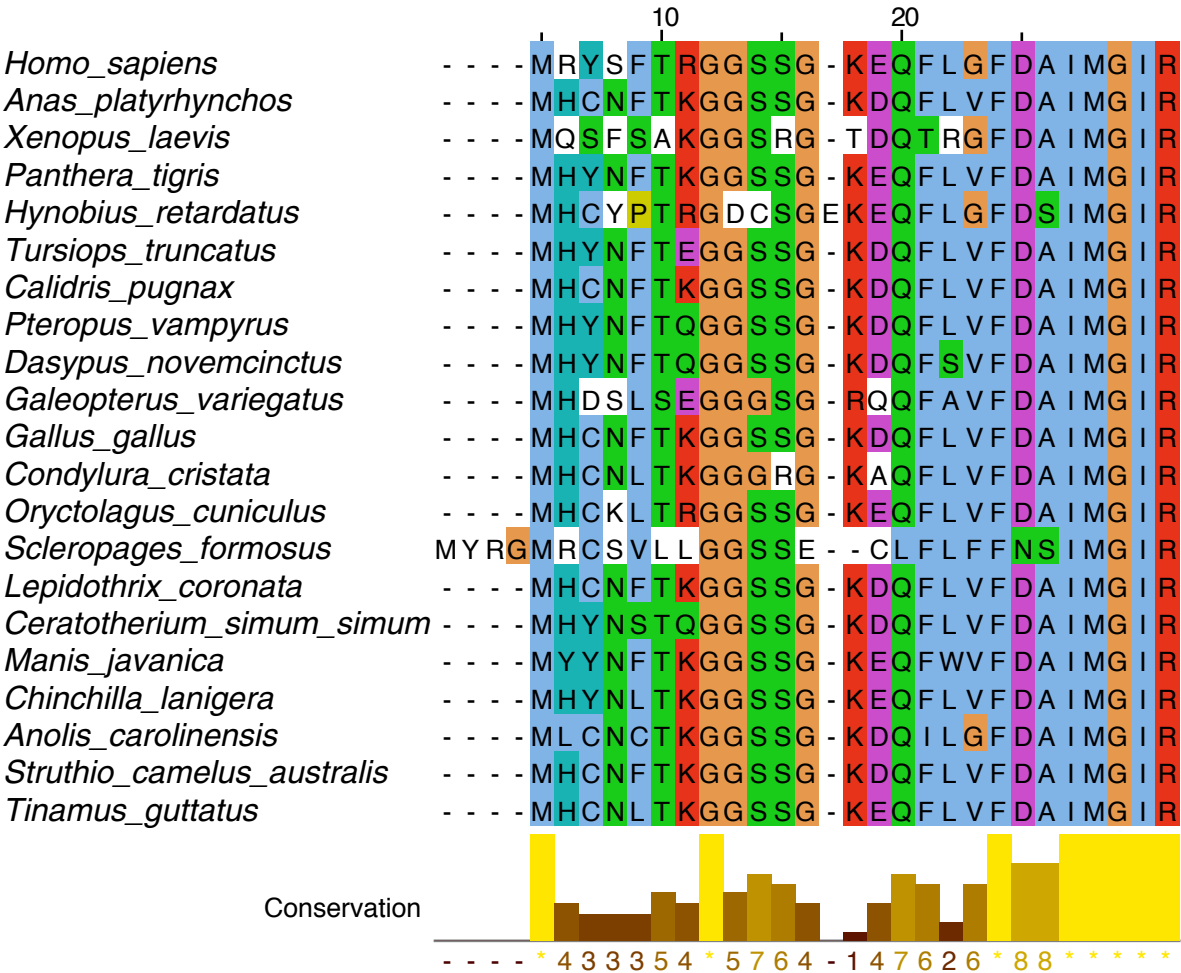


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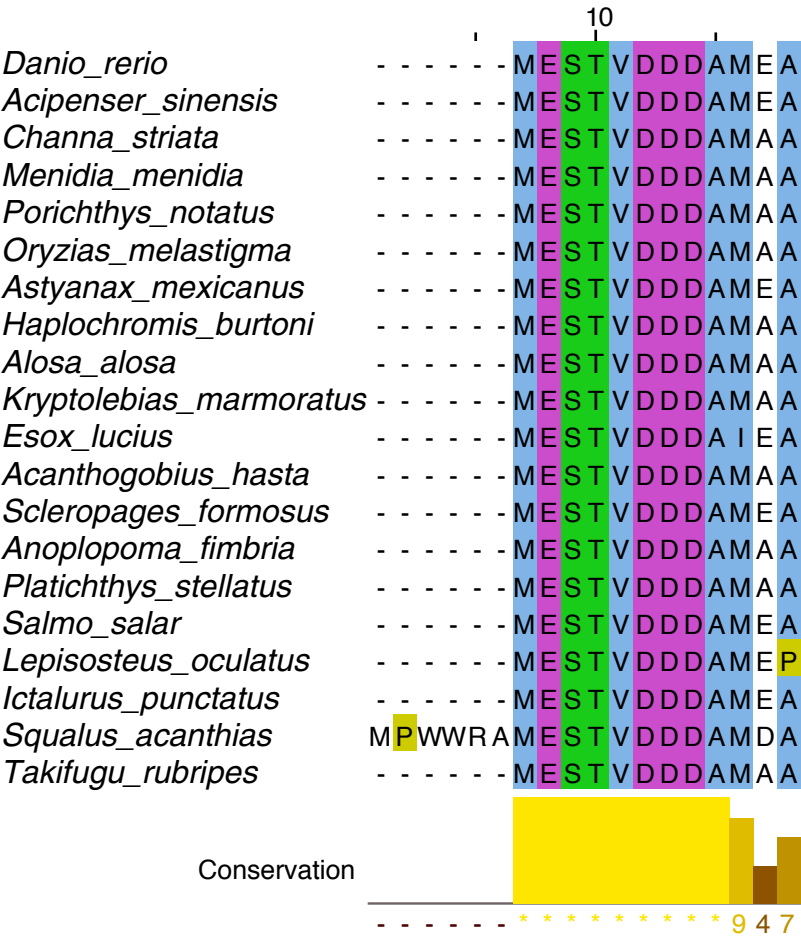
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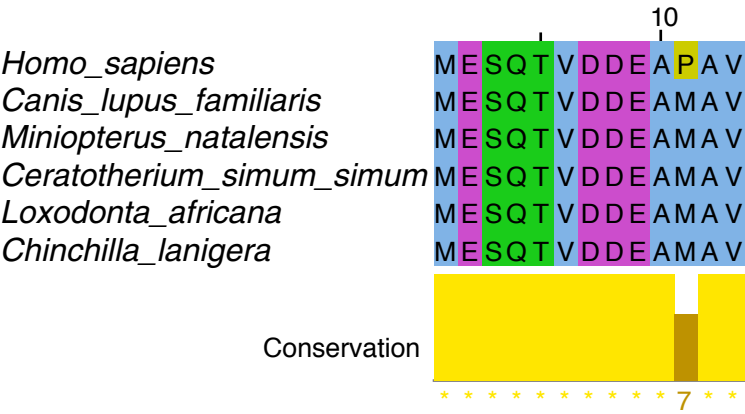
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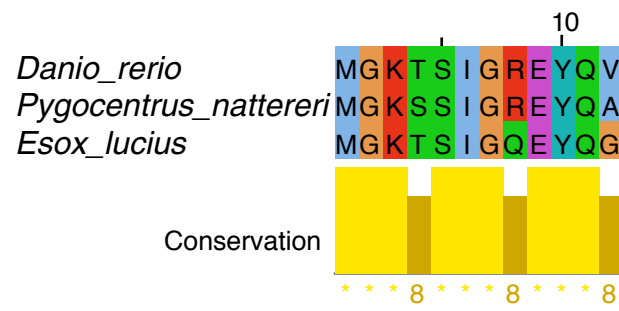
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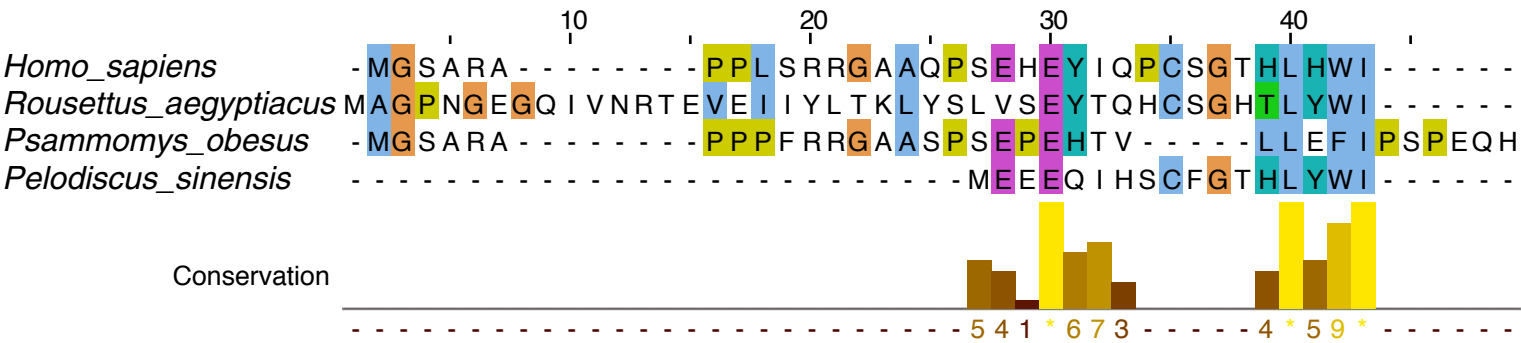
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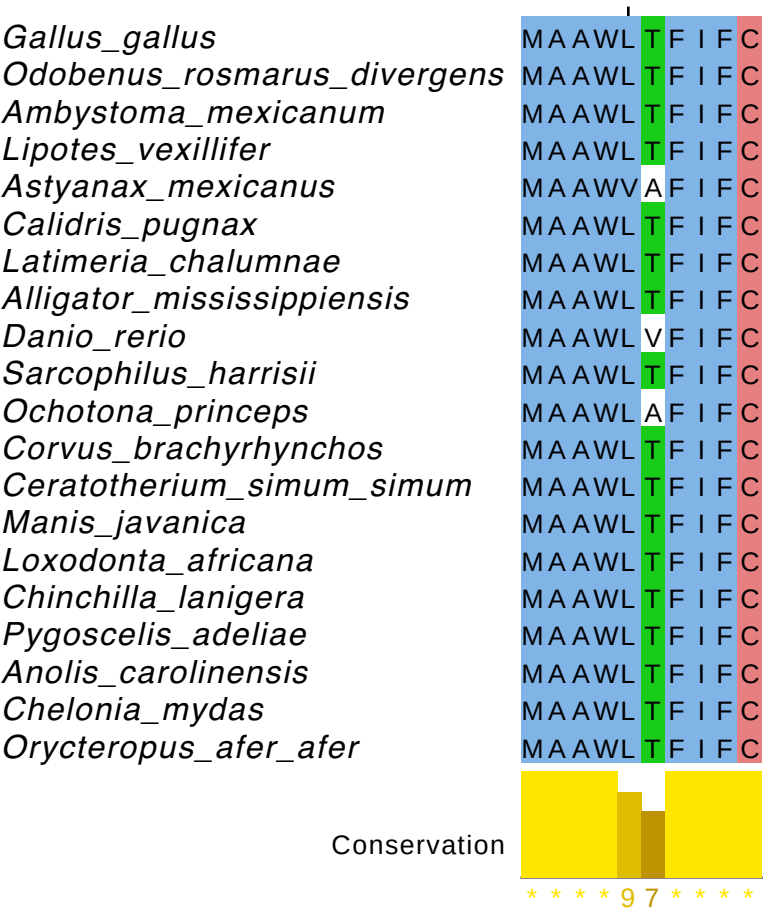
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HG0133.3

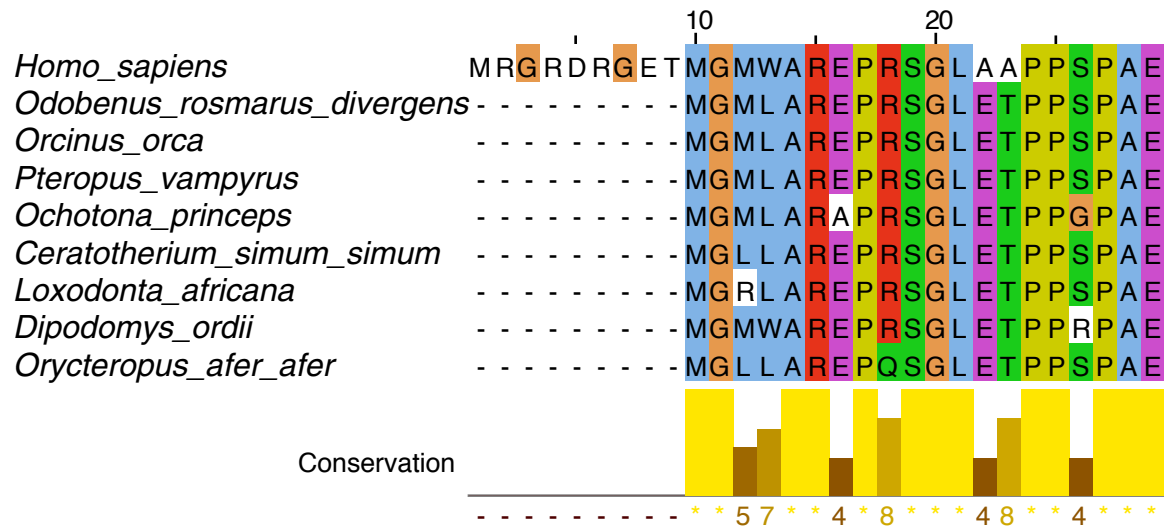
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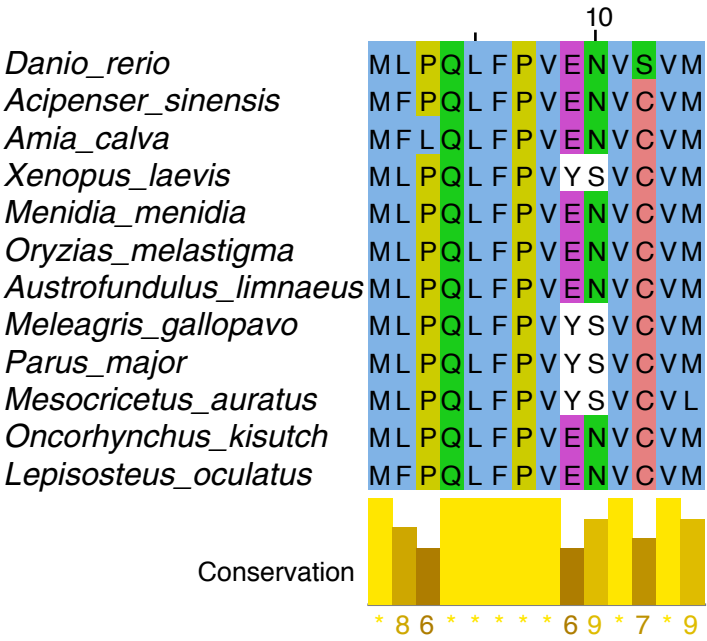
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ENSG00000168283 (BMI1)



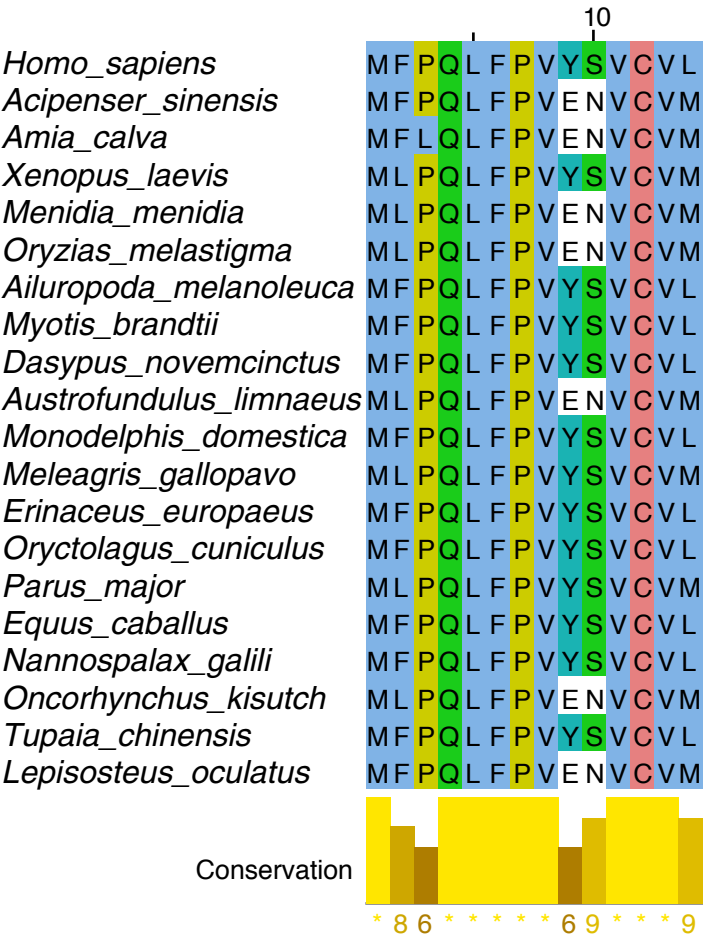
HG0135

ENSDARG00000094132 (igf1)

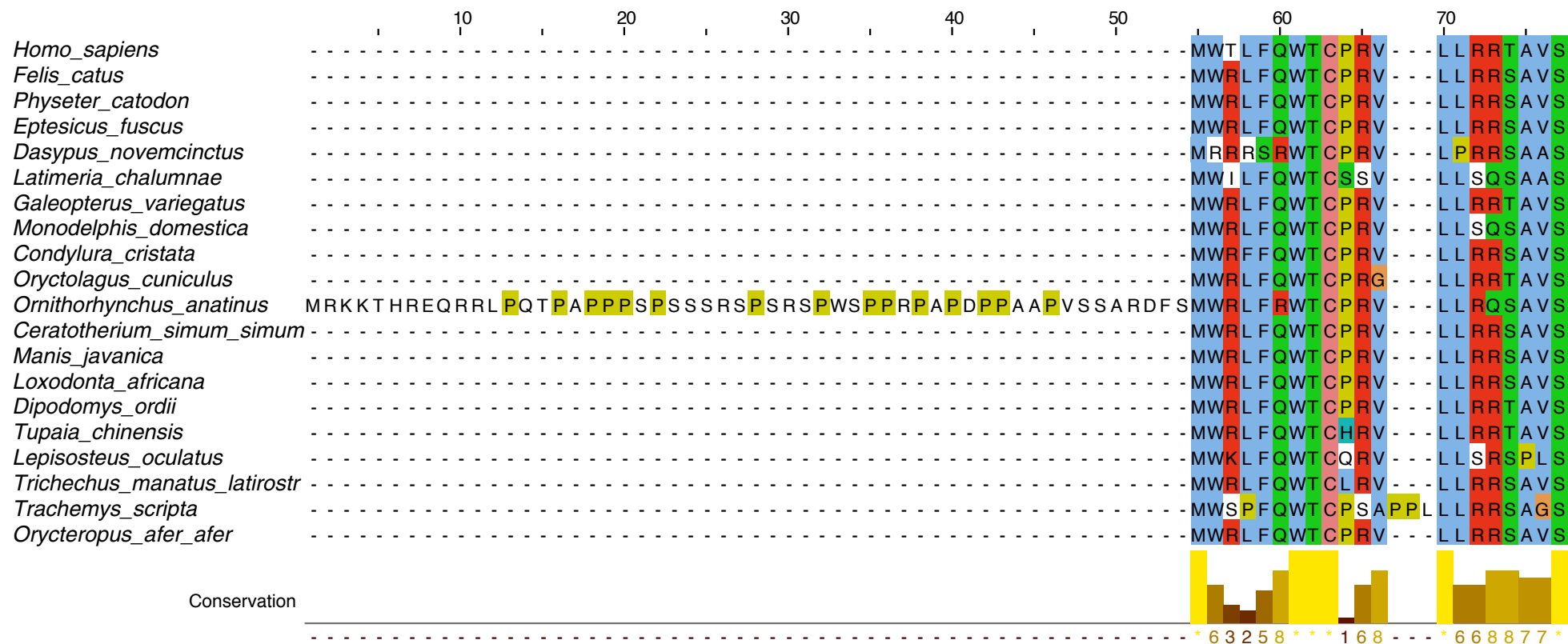


HG0135

ENSG00000017427 (IGF1)

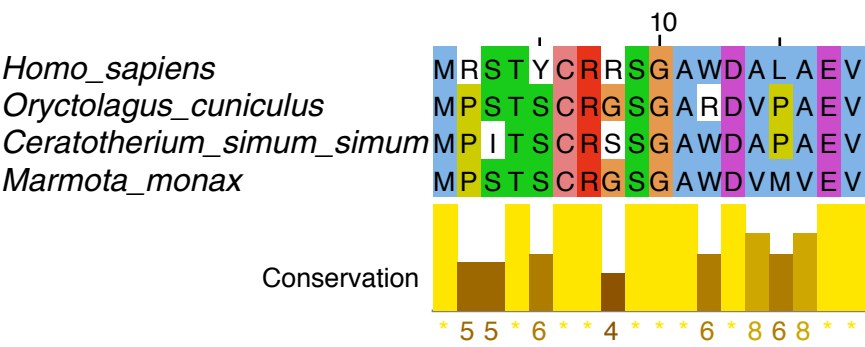


ENSG00000125845 (BMP2)



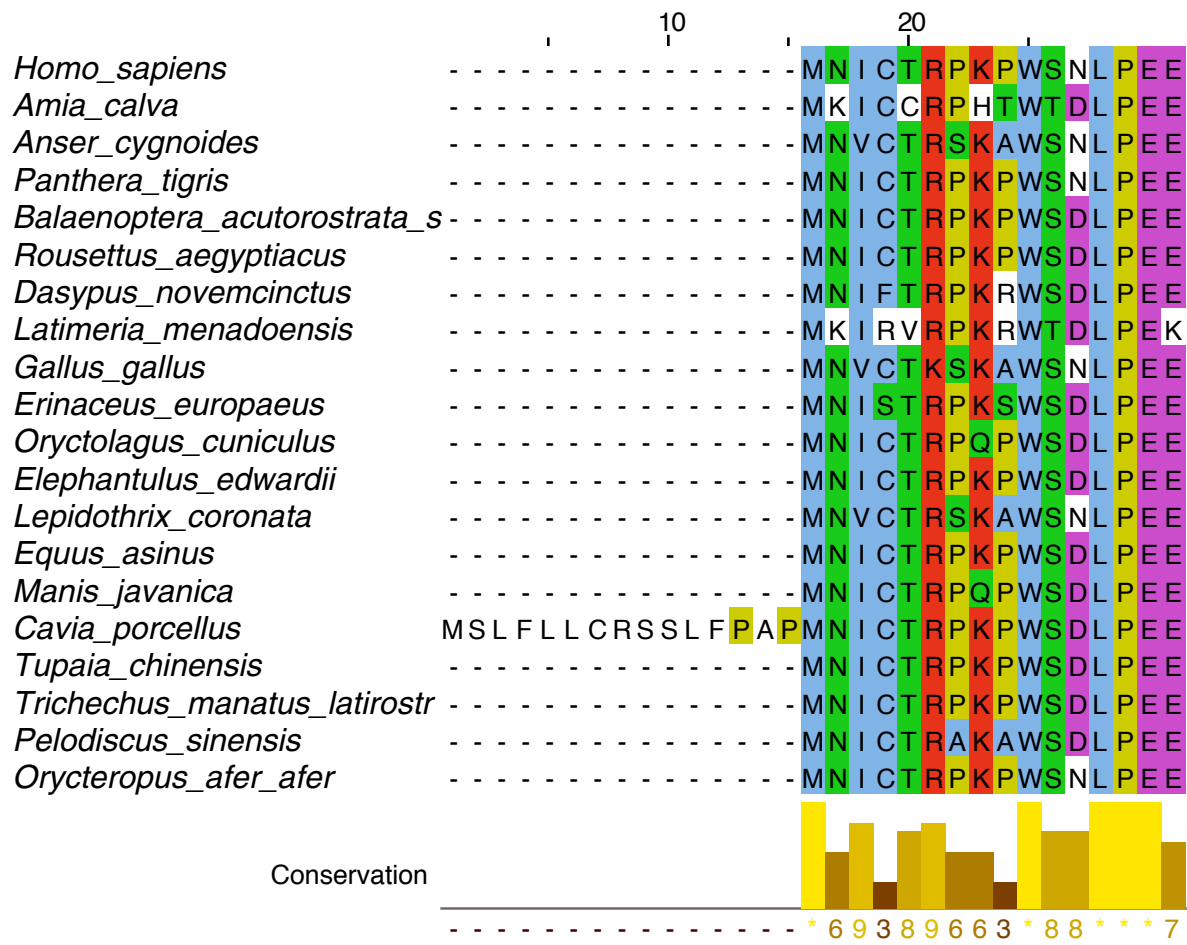
HG0136.2

ENSG00000125845 (BMP2)



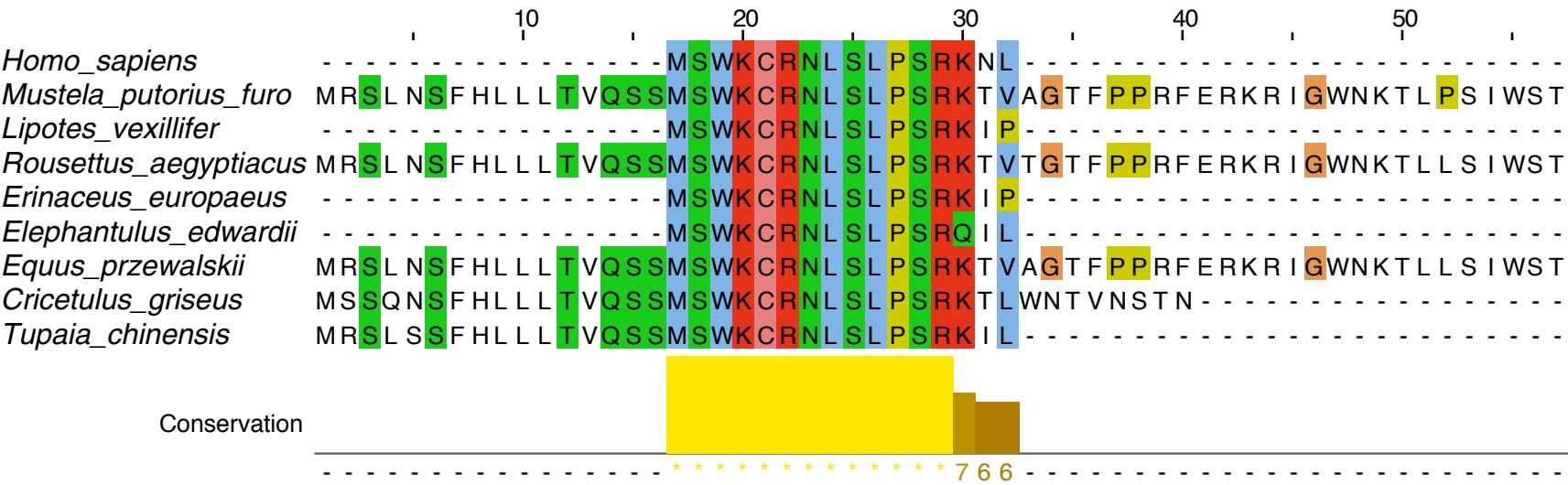
HG0137.1

ENSG00000181722 (ZBTB20)



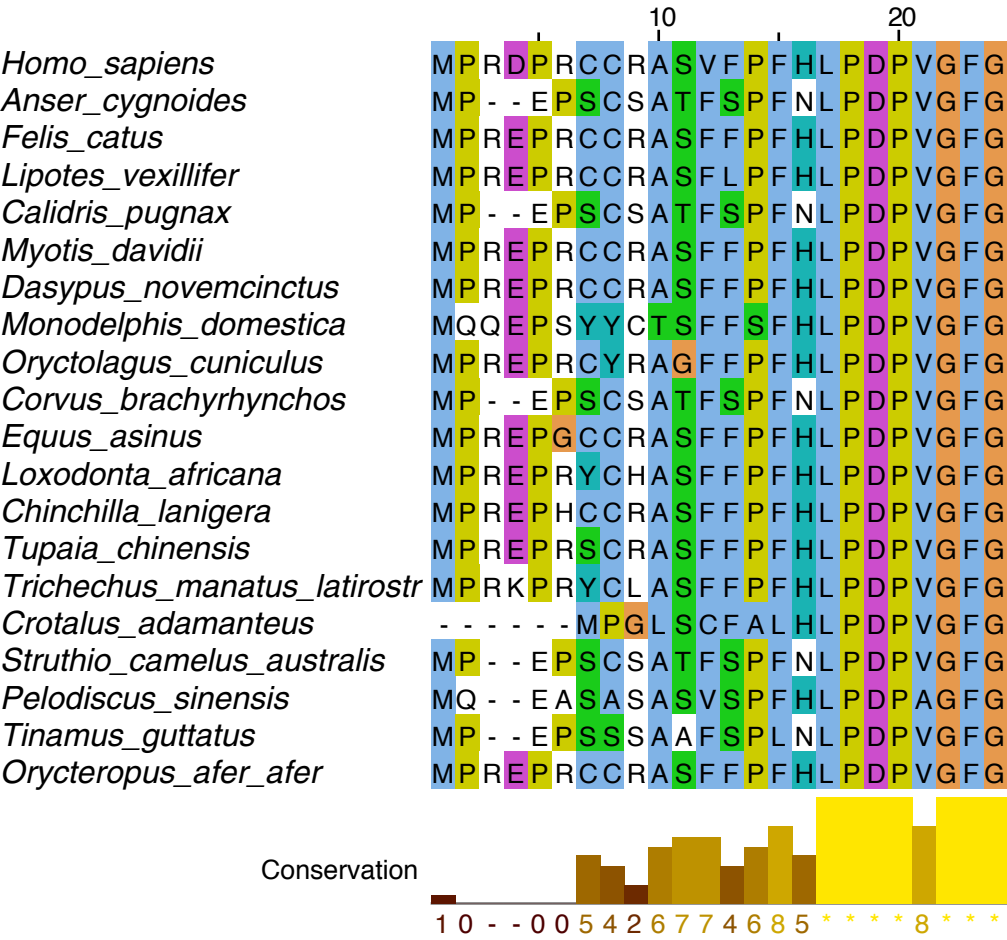
HG0137.2

ENSG00000181722 (ZBTB20)



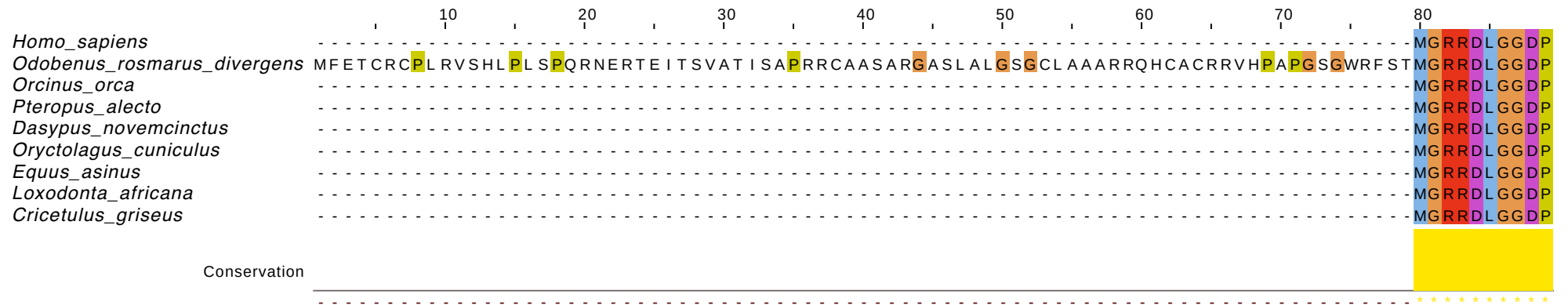
HG0138.1

ENSG00000185070 (FLRT2)

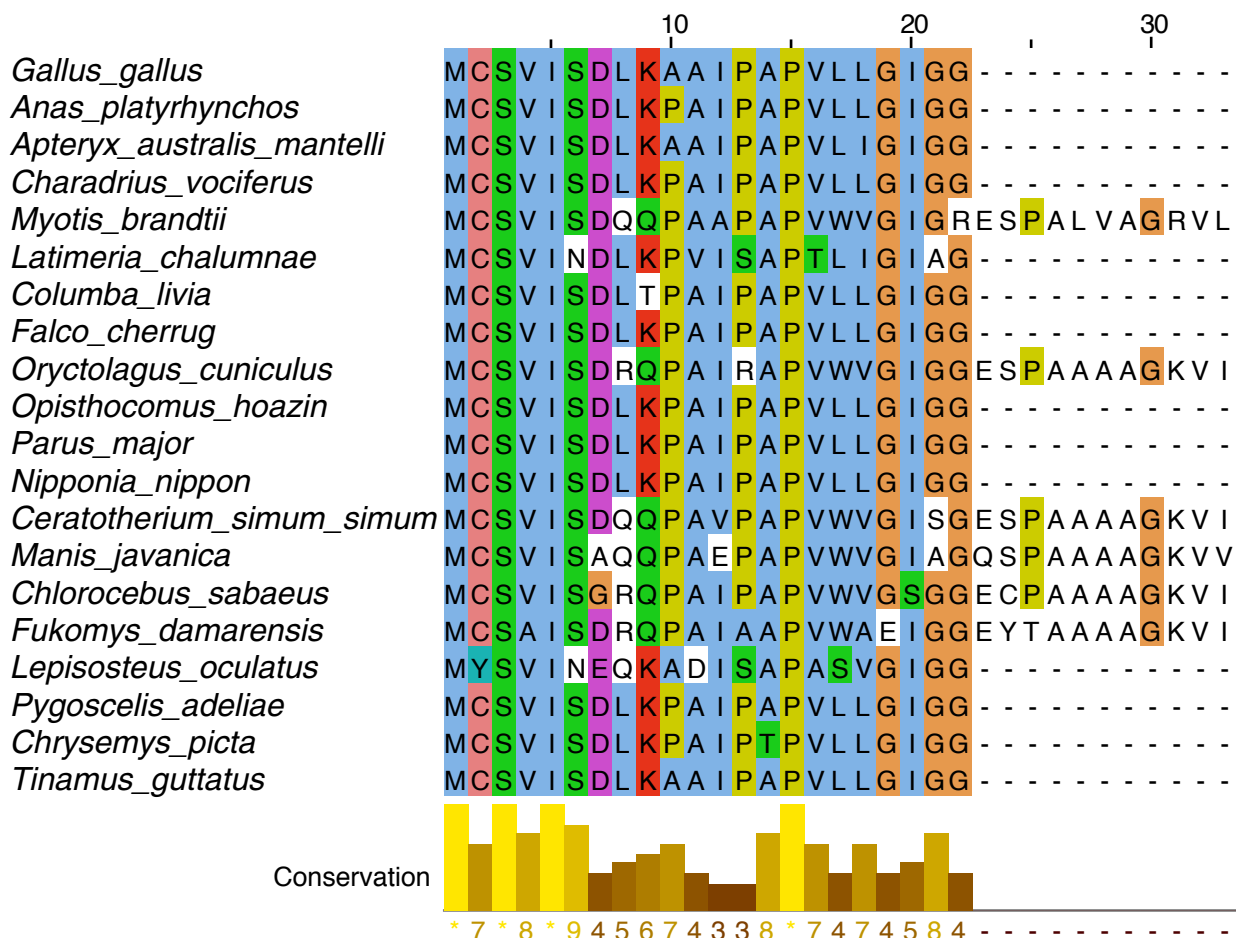


HG0138.2

ENSG00000185070 (FLRT2)

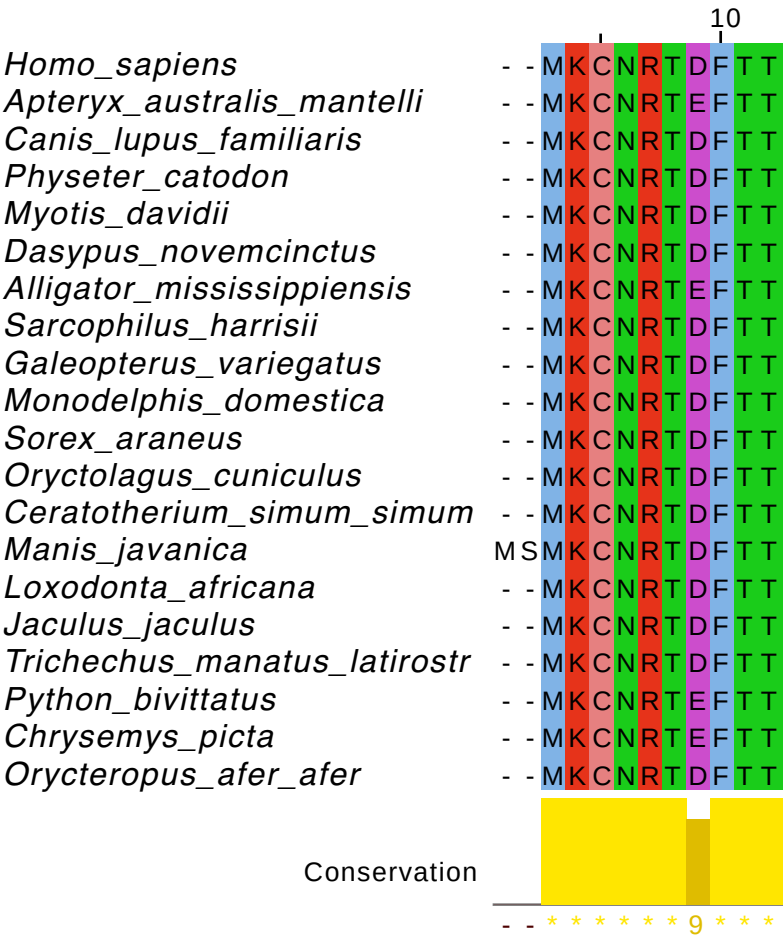


ENSGALG00000006379 (SHH)



HG0140

ENSG00000009307 (CSDE1)

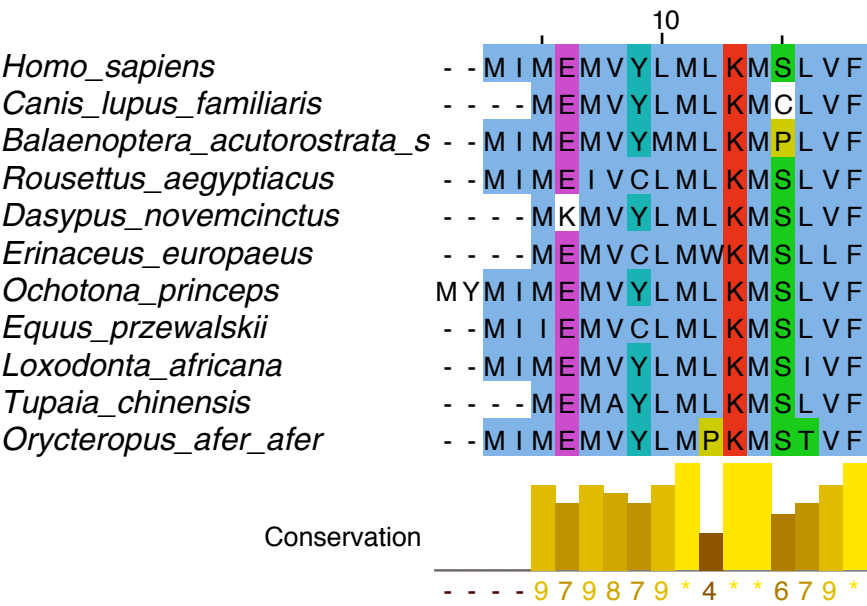


ENSGALG00000010435 (RASGRP3)



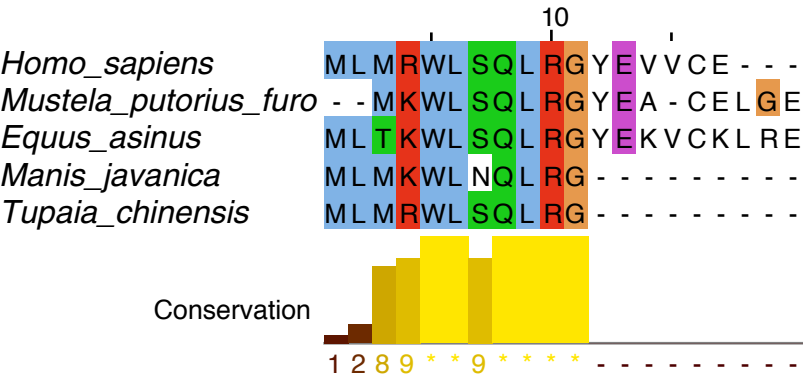
HG0141.2

ENSG00000152689 (RASGRP3)



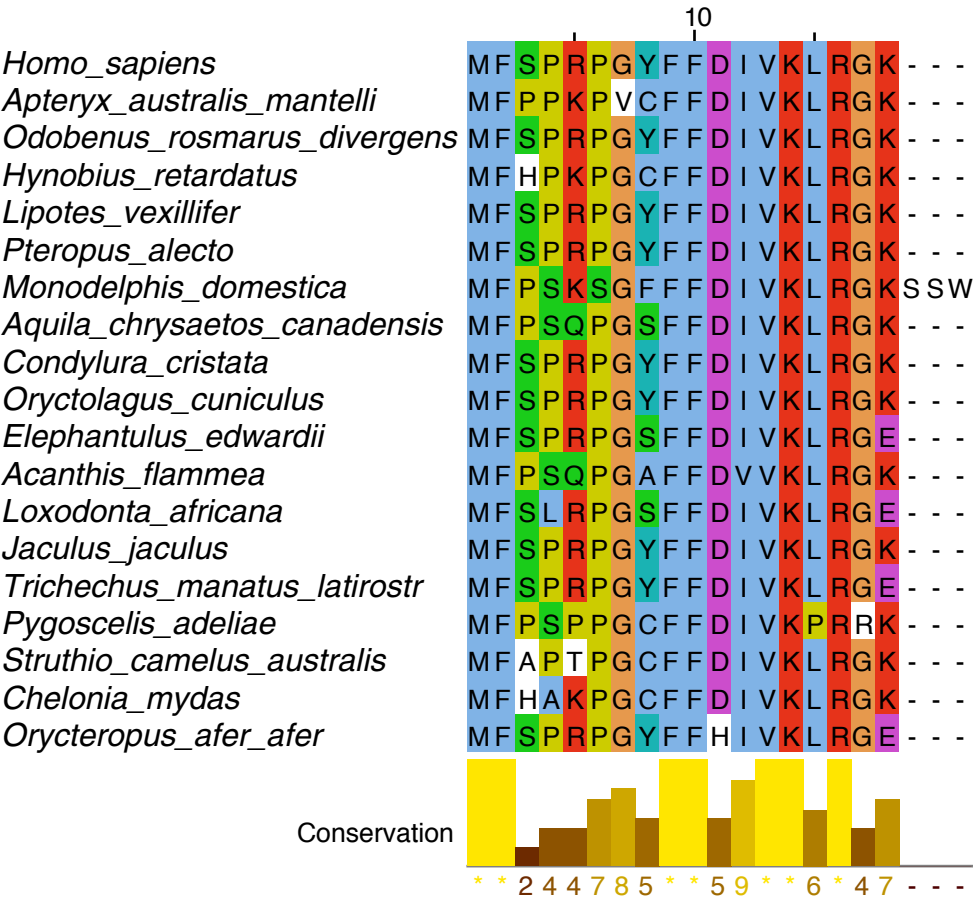
HG0141.3

ENSG00000152689 (RASGRP3)



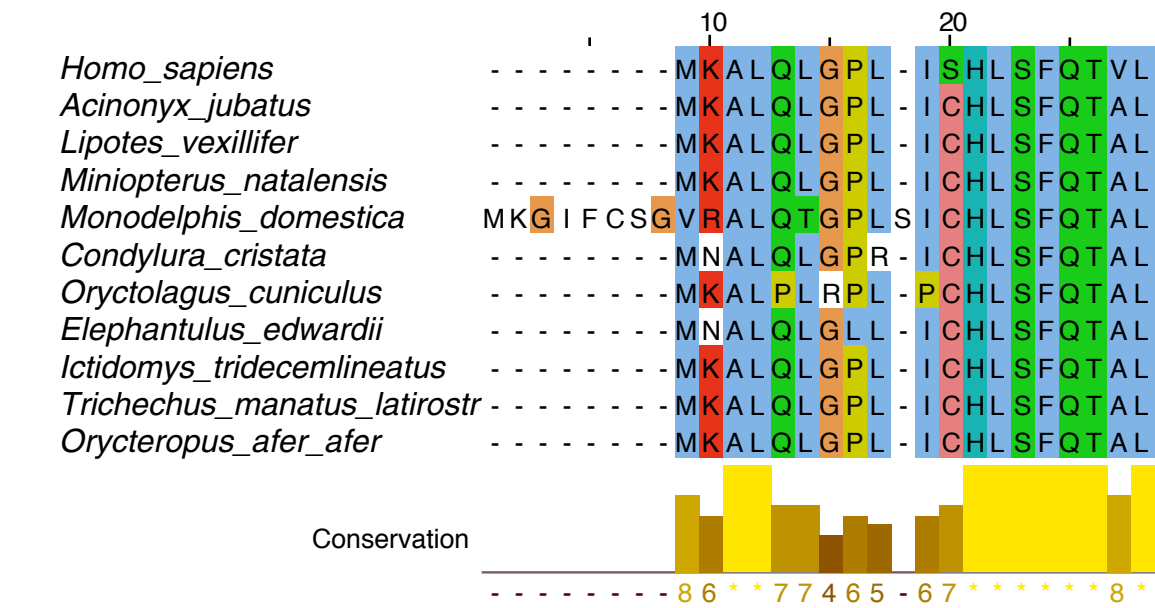
HG0142.1

ENSG00000204217 (BMPR2)



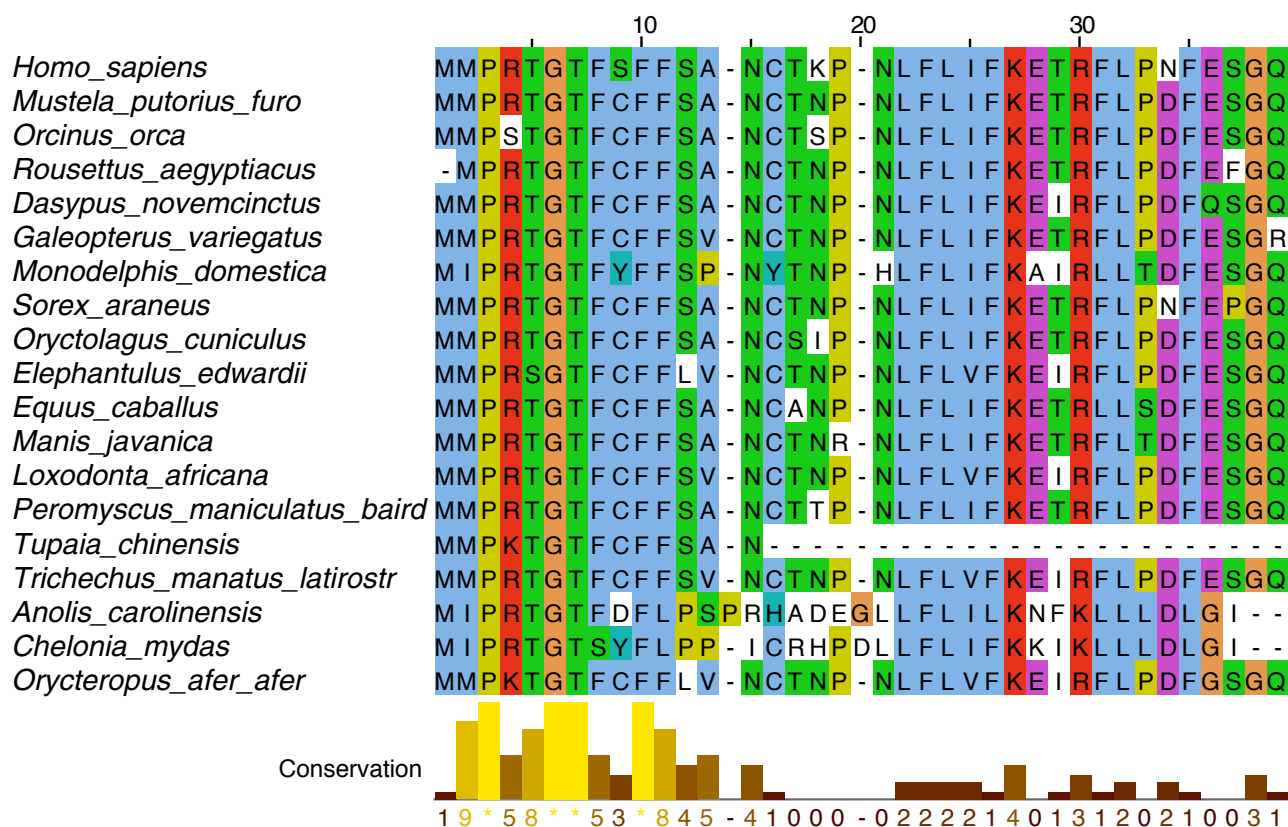
HG0142.2

ENSG00000204217 (BMPR2)



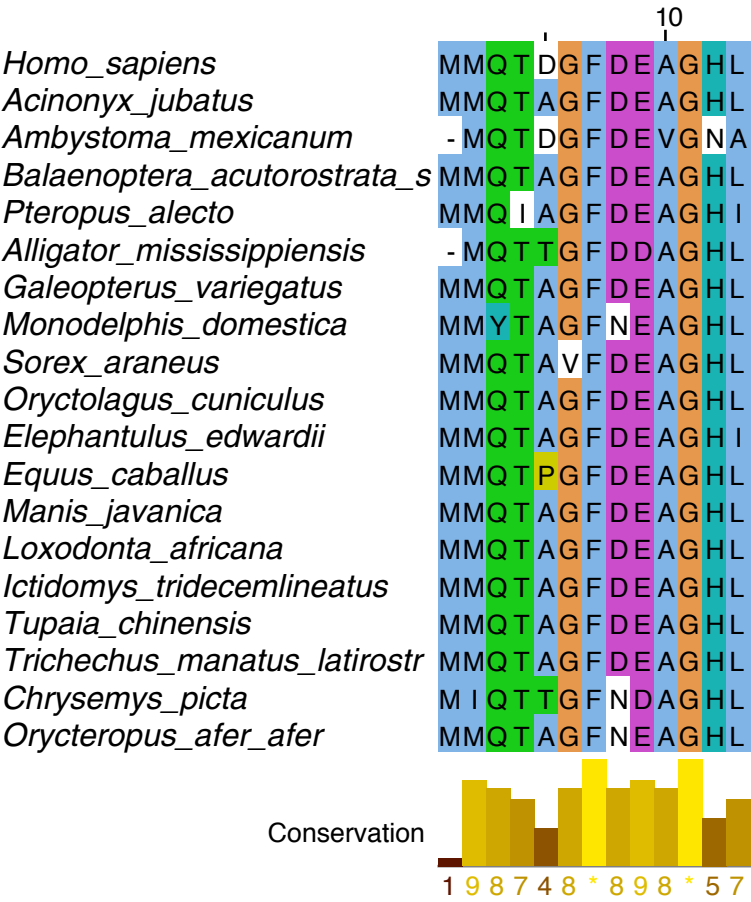
HG0143

ENSG00000101958 (GLRA2)



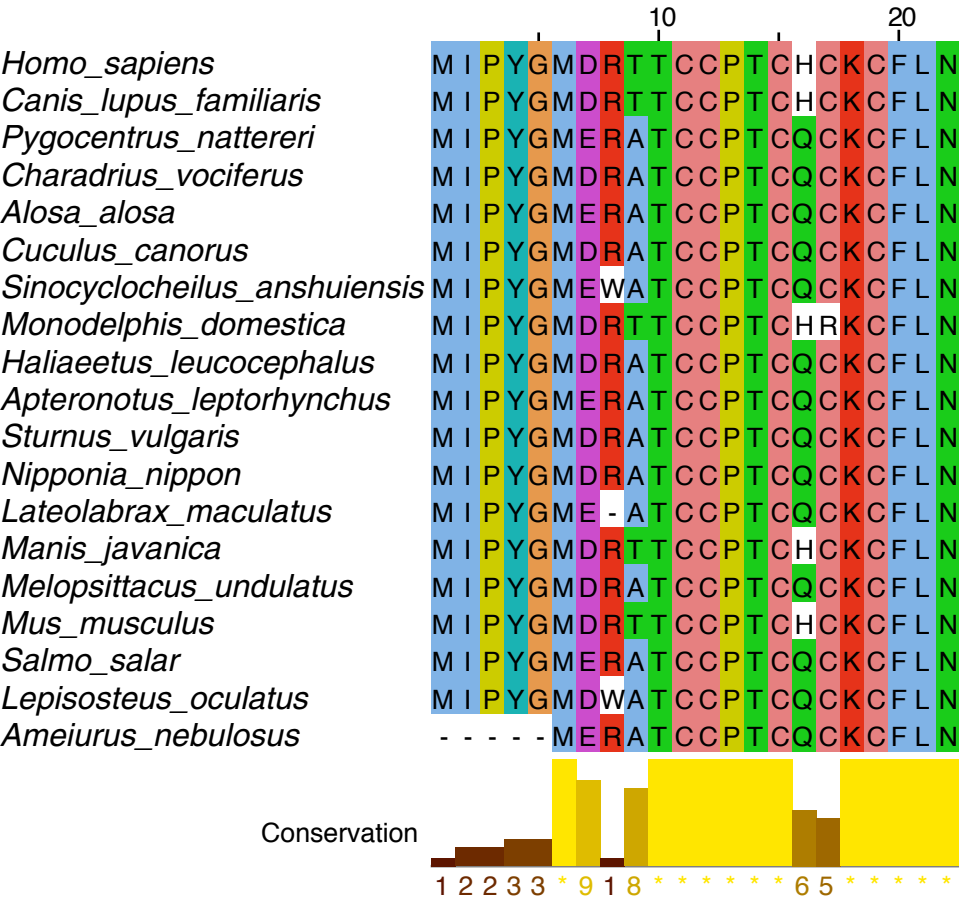
HG0144

ENSG00000117114 (ADGRL2)

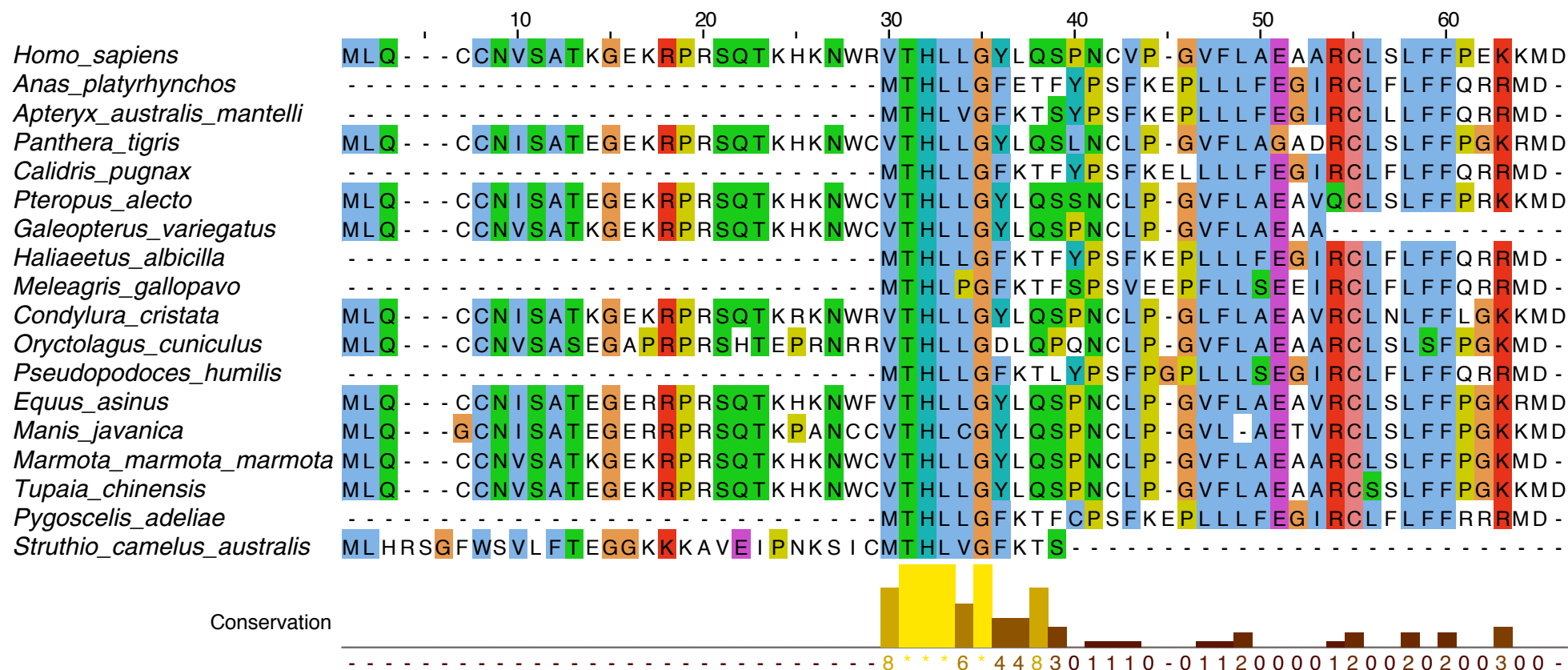


HG0145

ENSG00000162599 (NFIA)

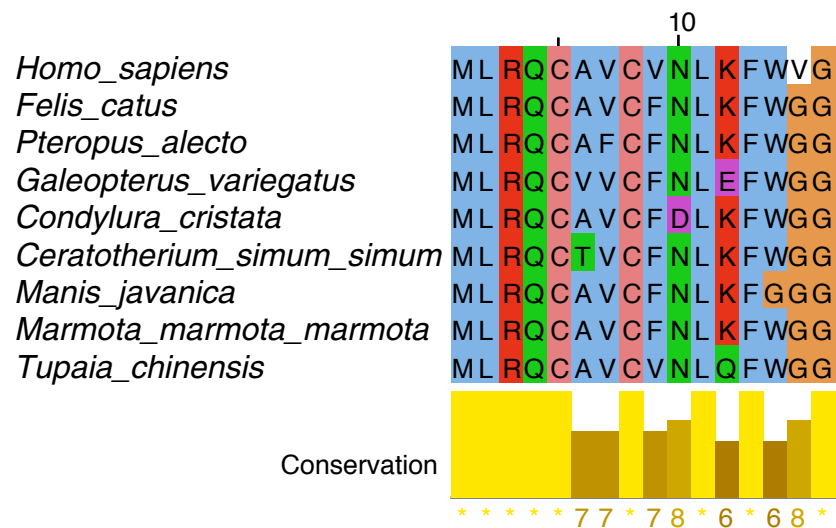


ENSG00000163681 (SLMAP)



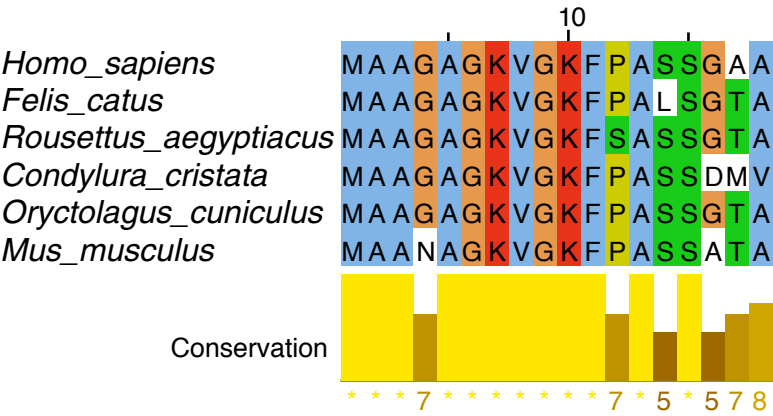
HG0146.2

ENSG00000163681 (SLMAP)



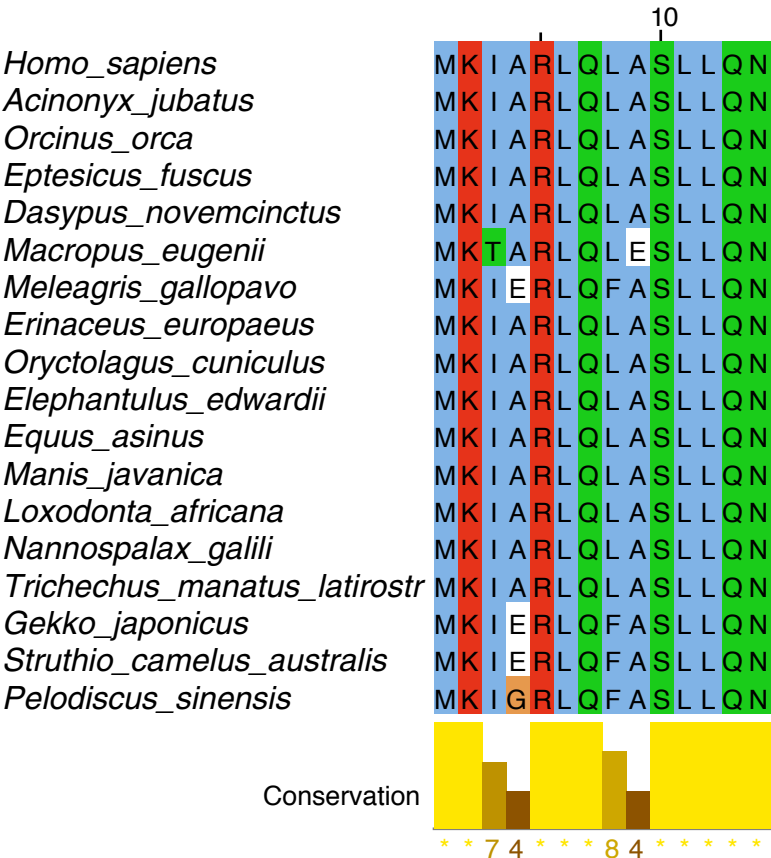
HG0146.3

ENSG00000163681 (SLMAP)



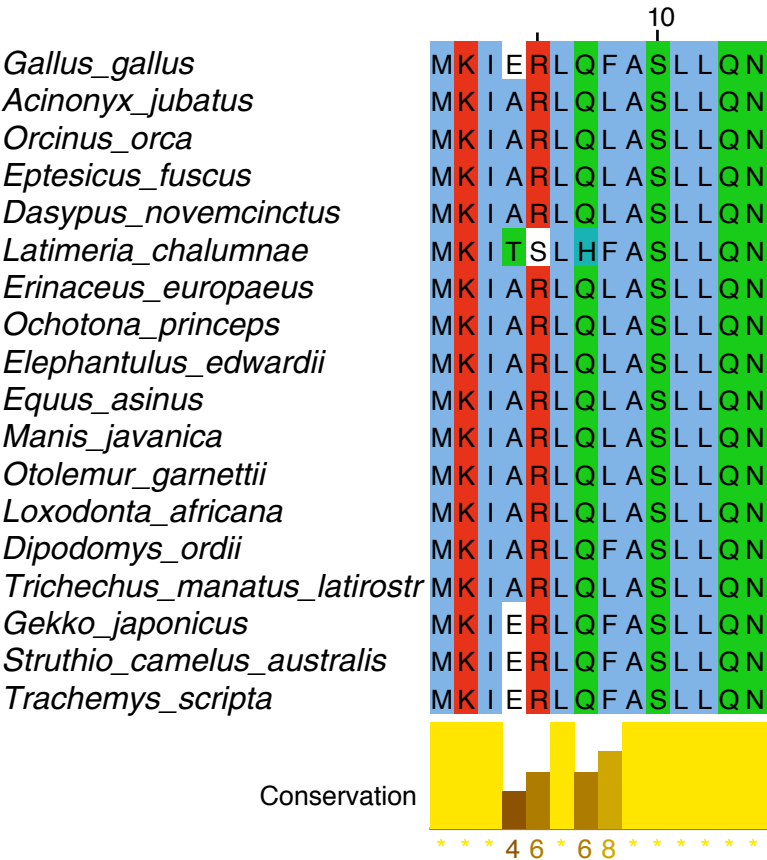
HG0147

ENSG00000108984 (MAP2K6)



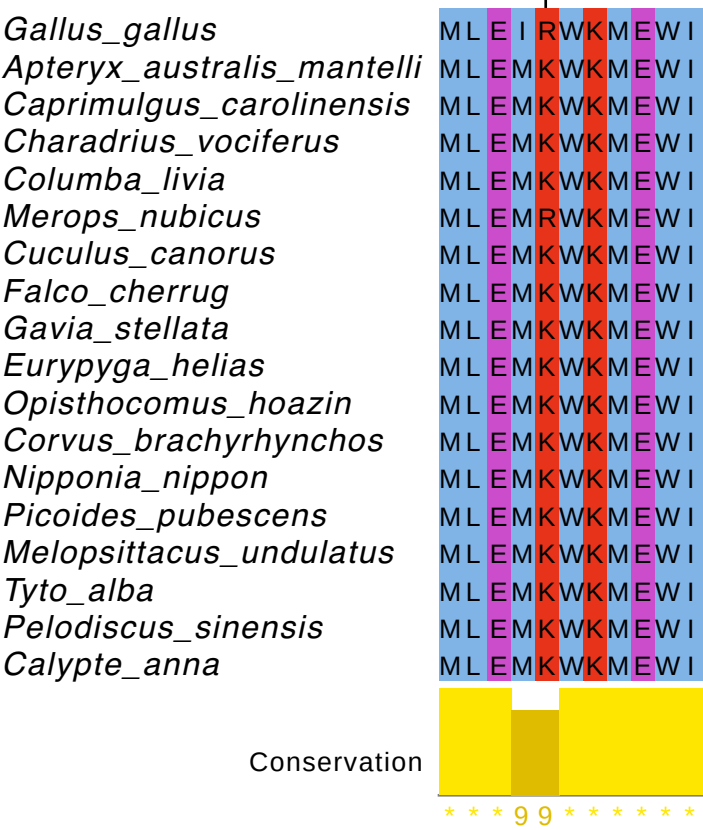
HG0147

ENSGALG00000004370 (MAP2K6)



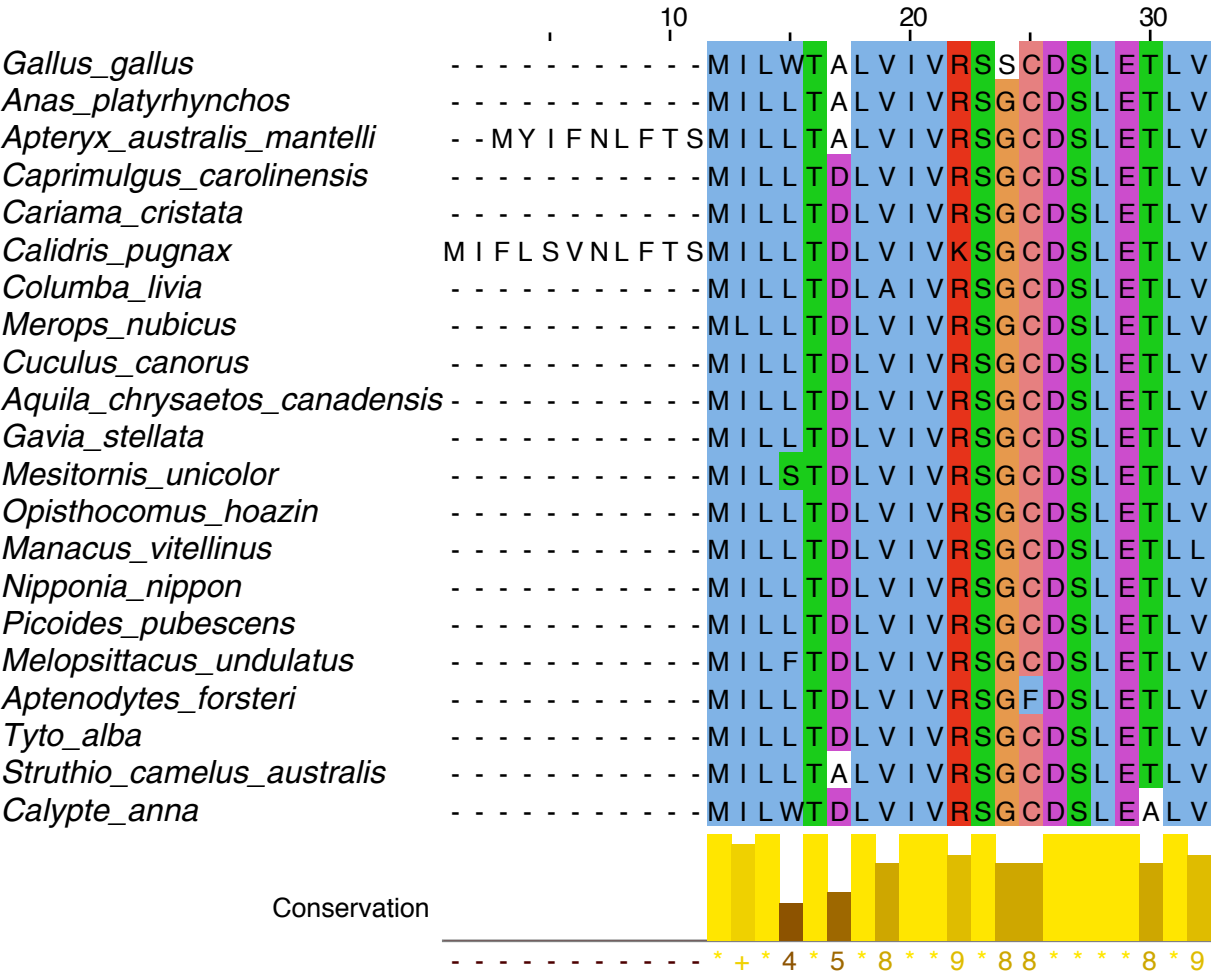
HG0148.1

ENSGALG00000011855 (RHOJ)



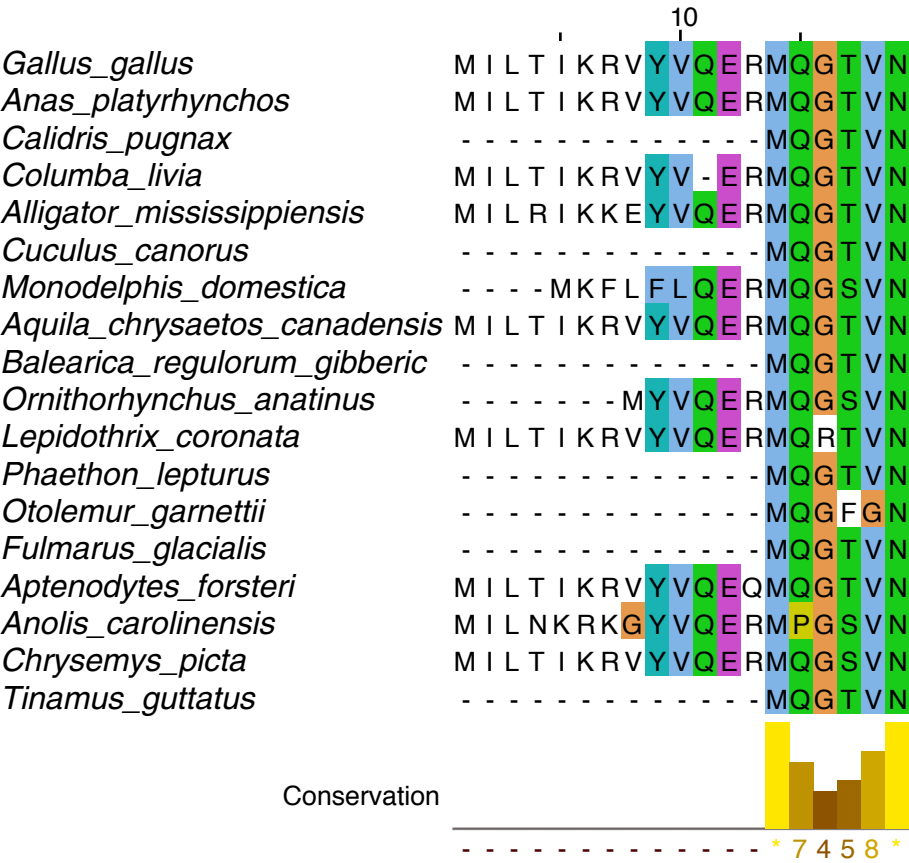
HG0148.2

ENSGALG00000011855 (RHOJ)



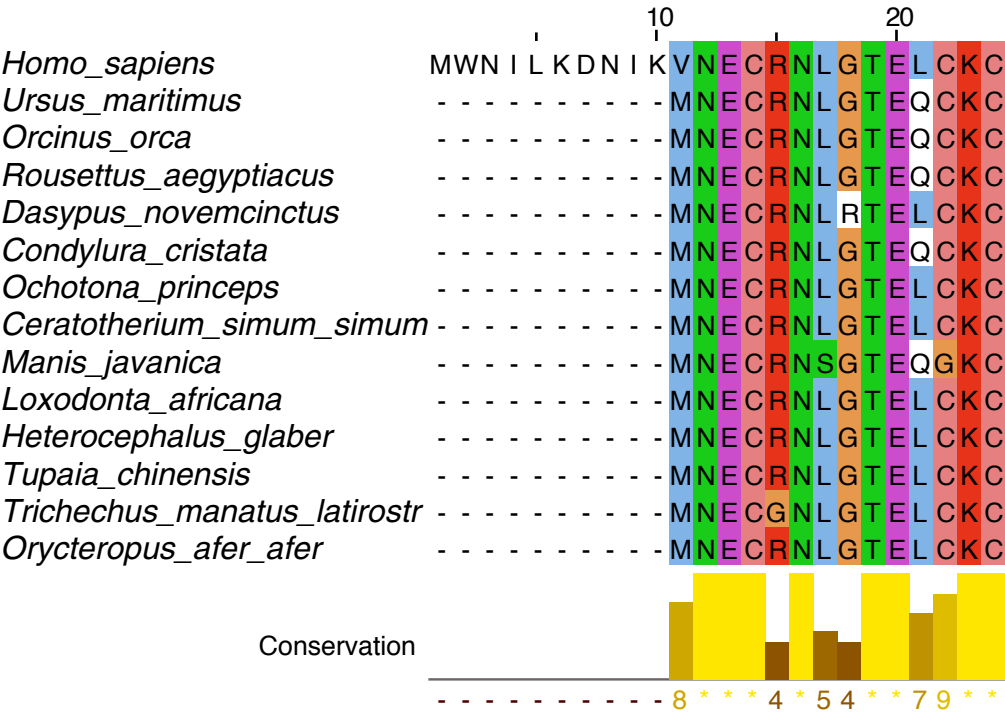
HG0149.1

ENSGALG00000014645 (MEF2C)



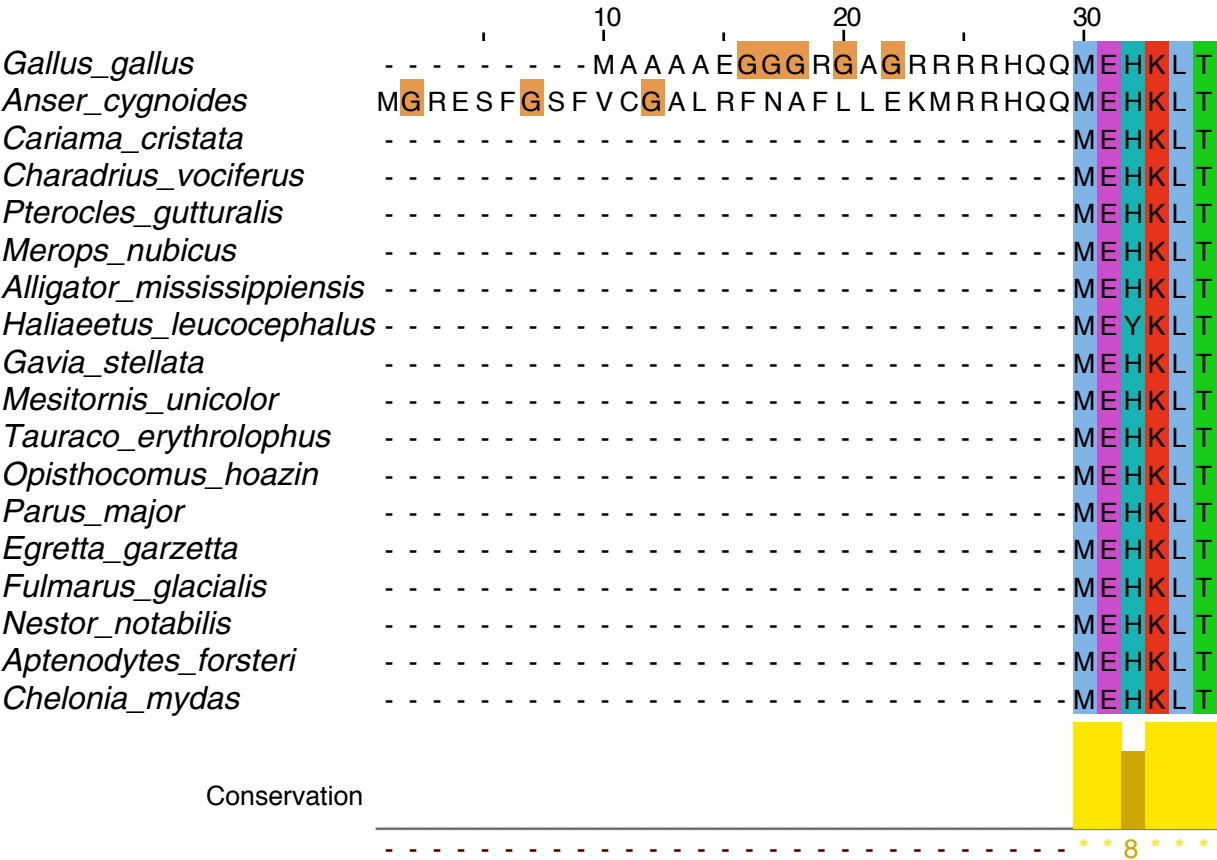
HG0149.2

ENSG00000081189 (MEF2C)



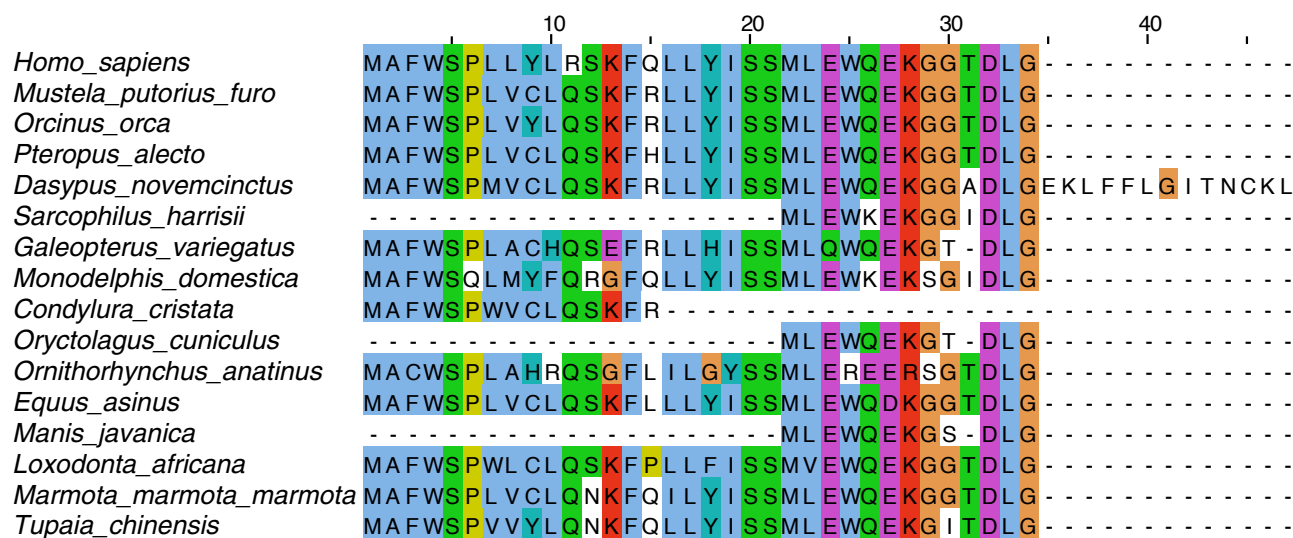
HG0150.1

ENSGALG00000032289 (IKZF5)

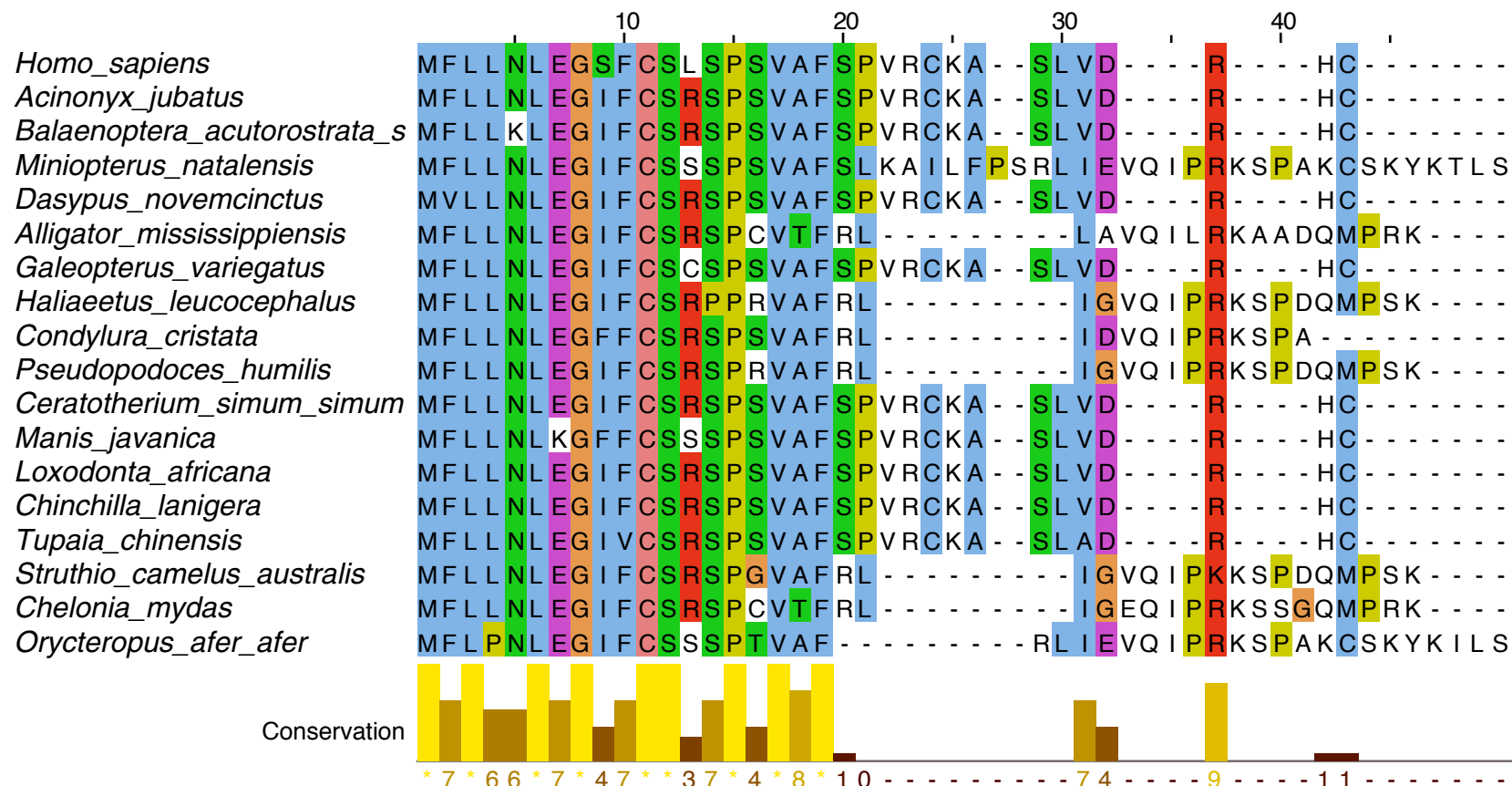


HG0150.2

ENSG00000095574 (IKZF5)

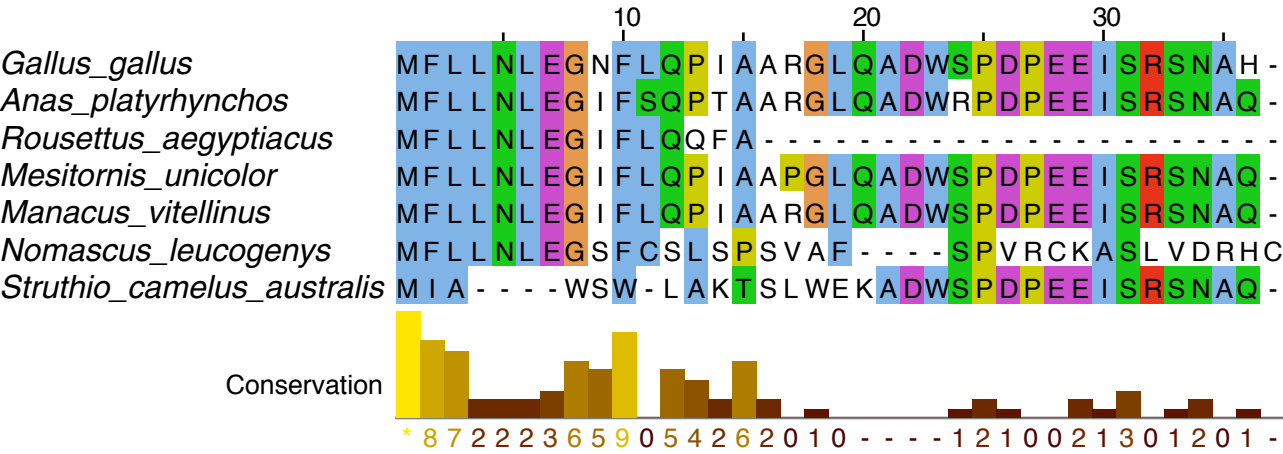


ENSG00000006468 (ETV1)



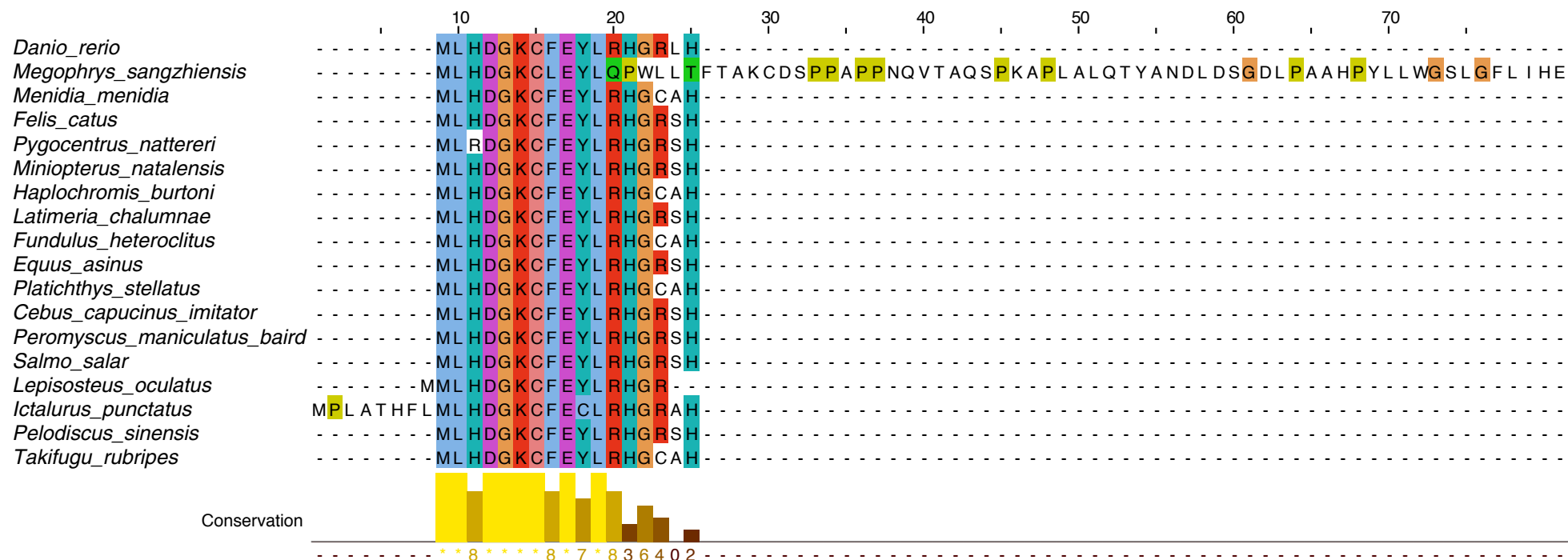
HG0151

ENSGALG00000035504 (ER81)



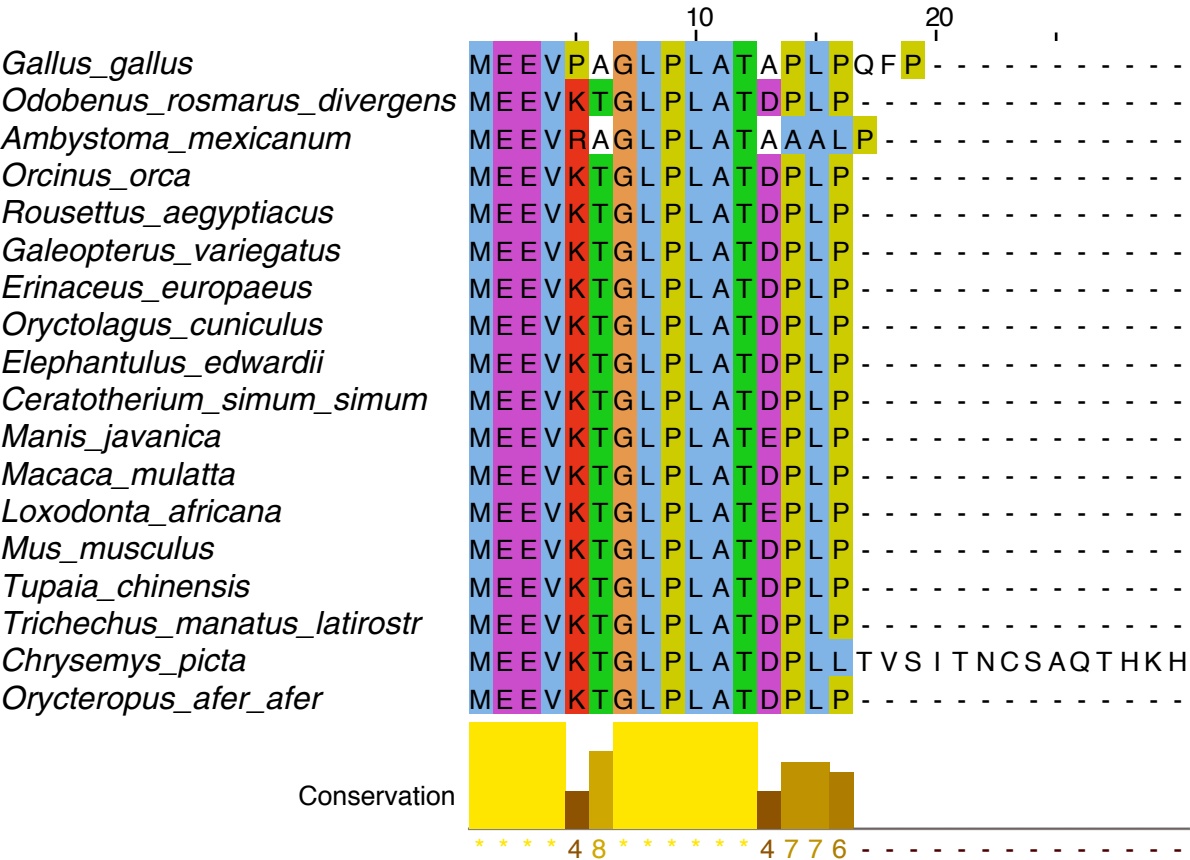
HG0152

ENSDARG00000015536 (sox6)



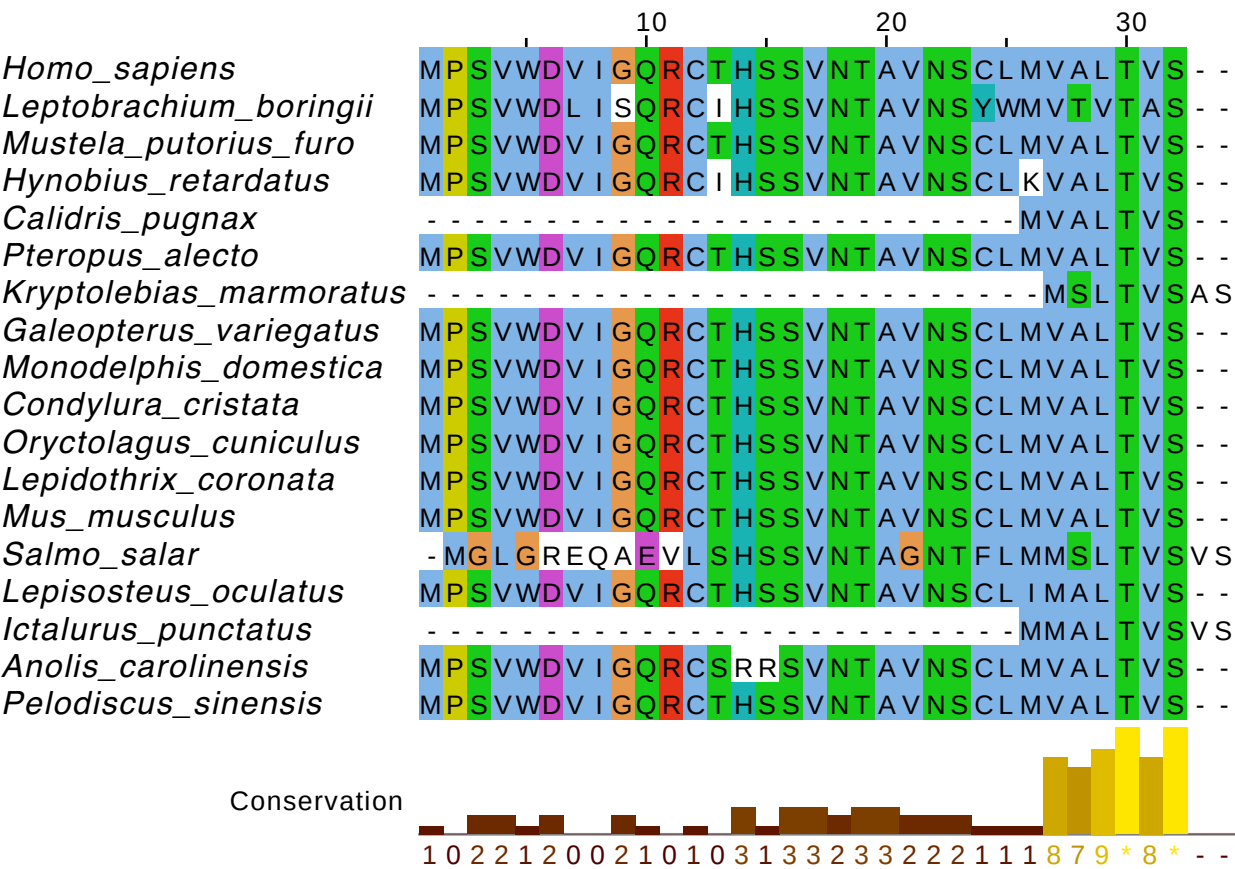
HG0153

ENSGALG00000003136 (IKZF2)



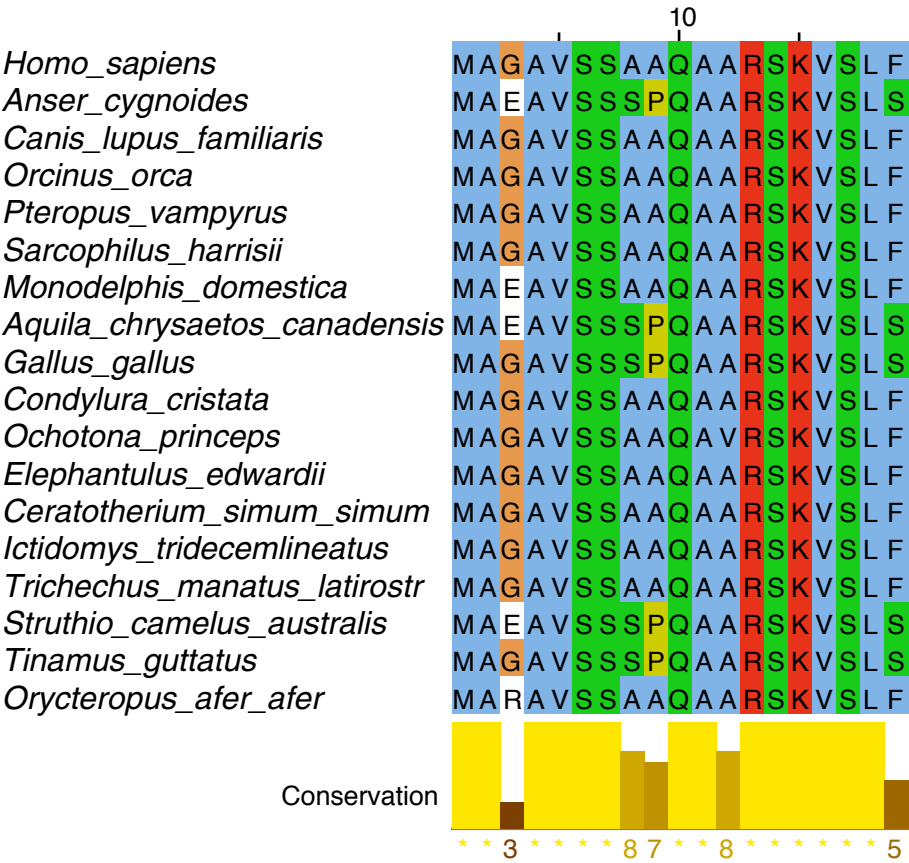
HG0154

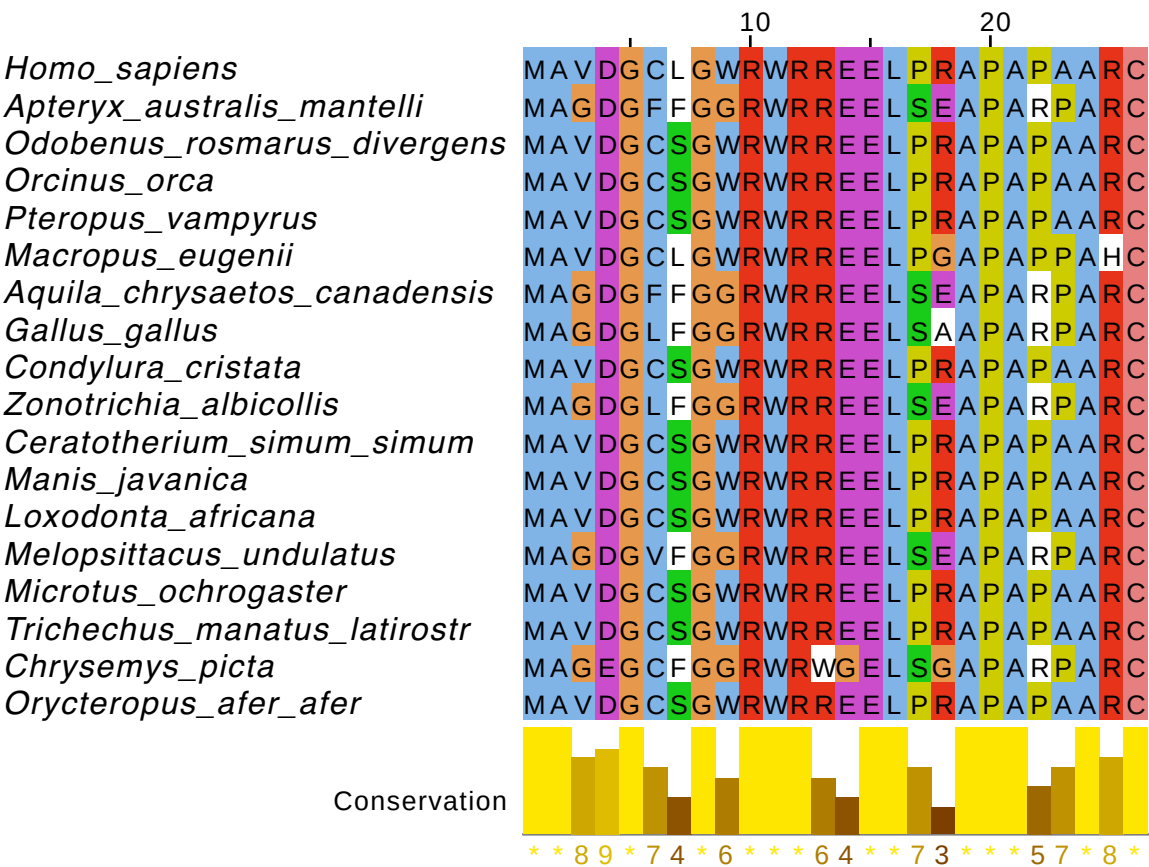
ENSG00000128573 (FOXP2)



HG0155

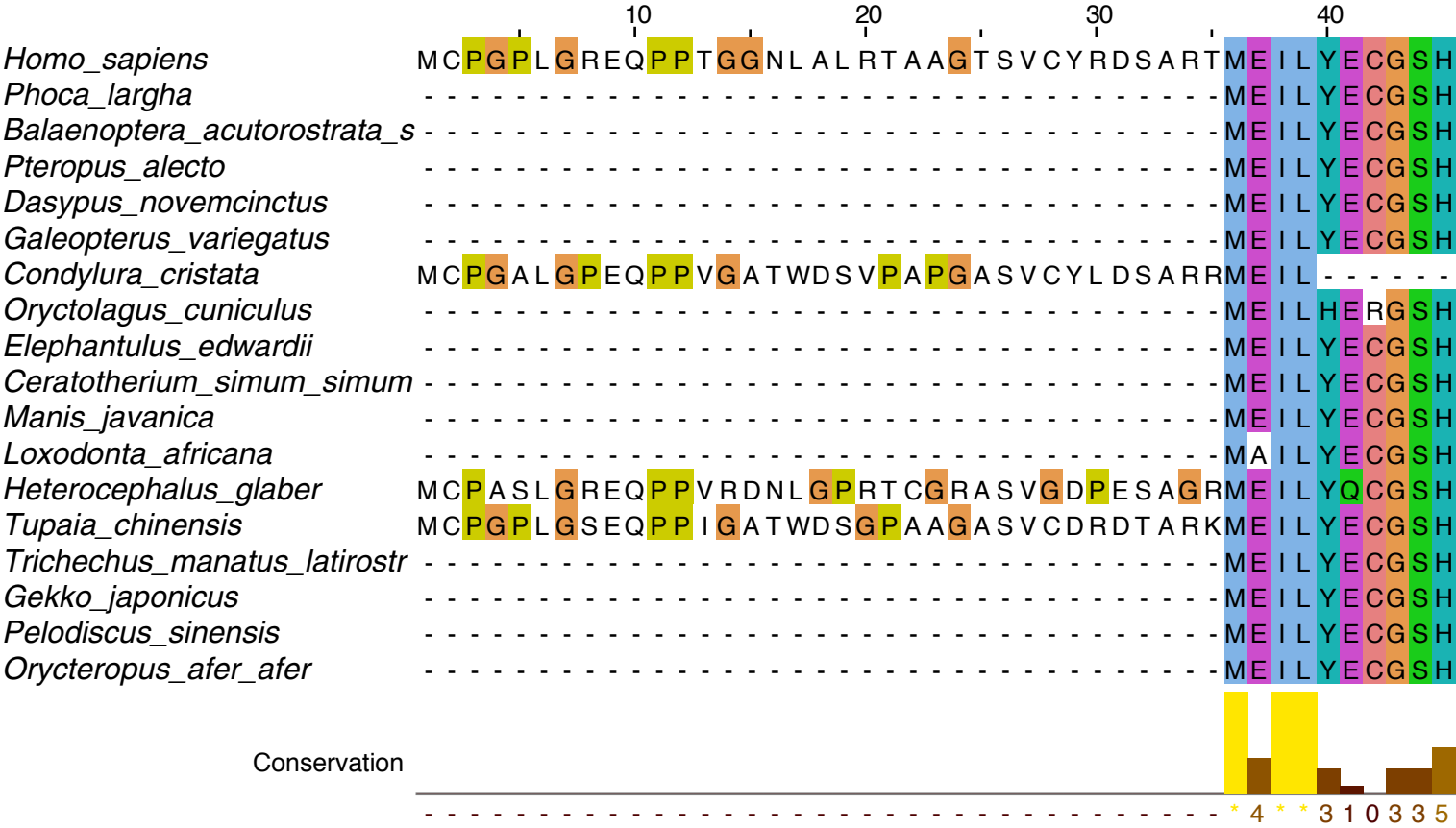
ENSG00000136535 (TBR1)





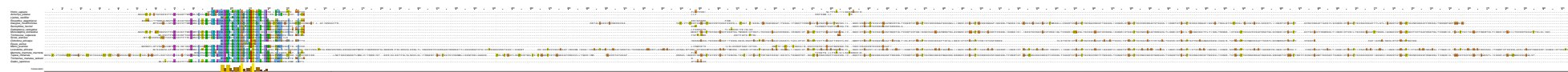
HG0157

ENSG00000173926 (3-Mar)

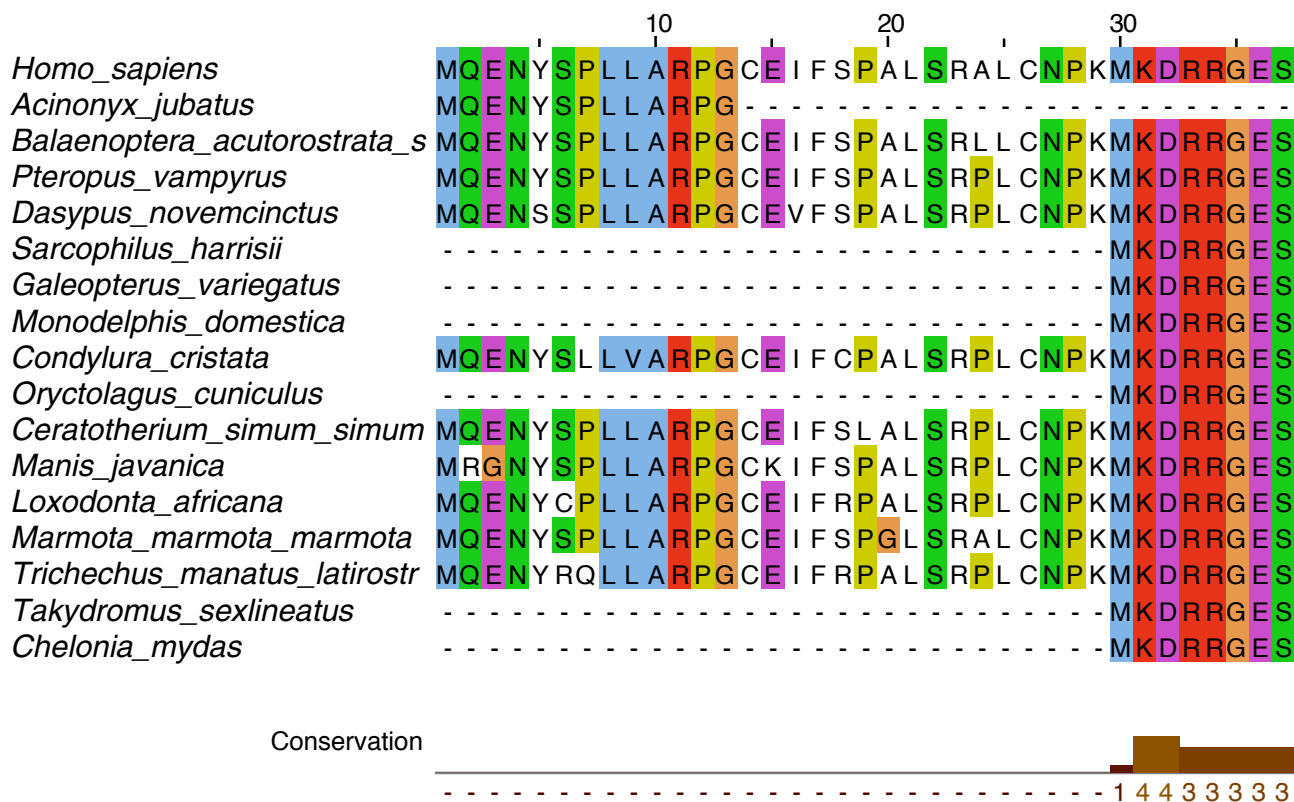


HG0158

ENSG00000198939 (ZFP2)

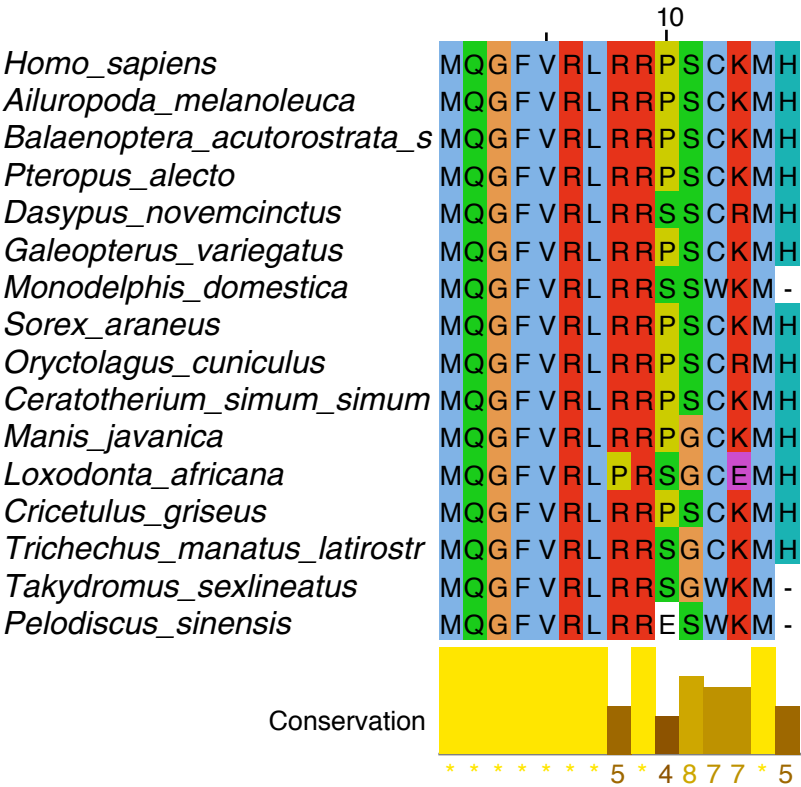


ENSG00000182197 (EXT1)



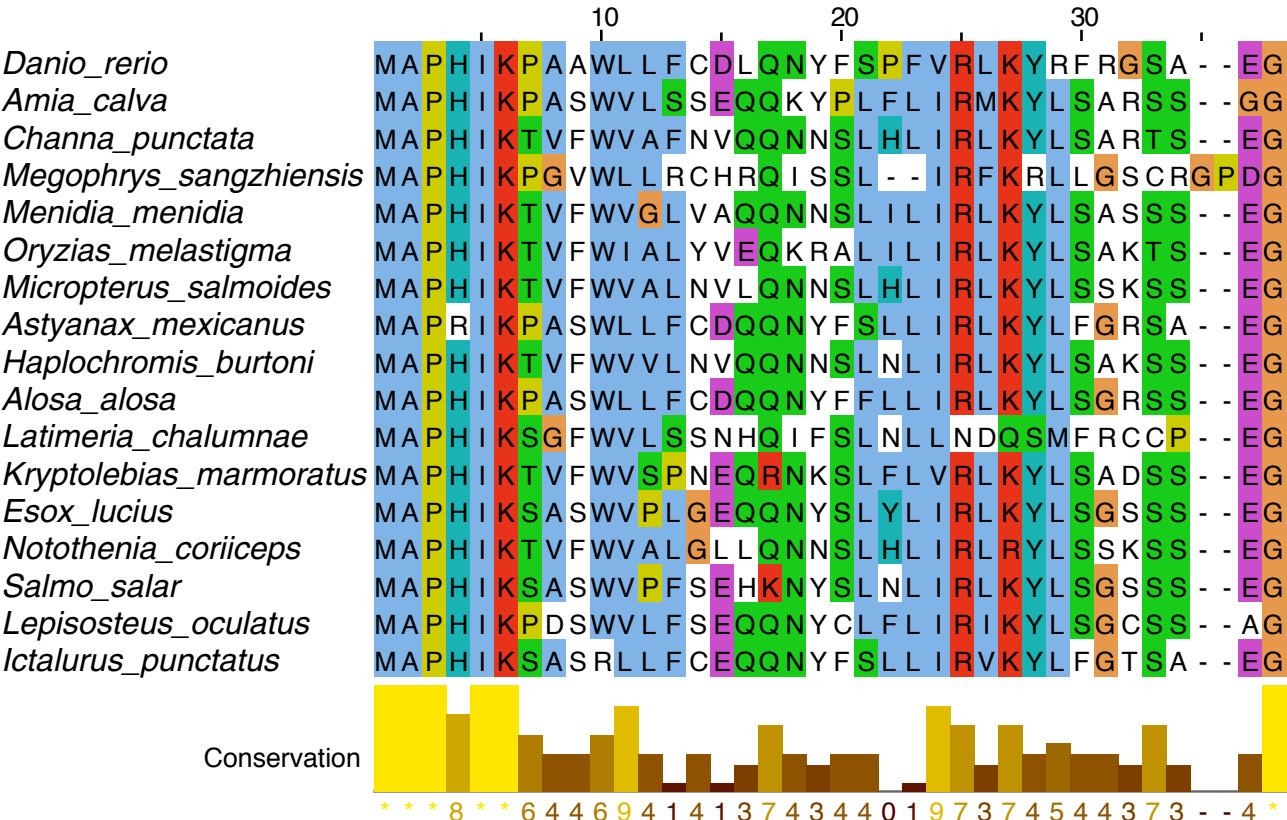
HG0159.2

ENSG00000182197 (EXT1)



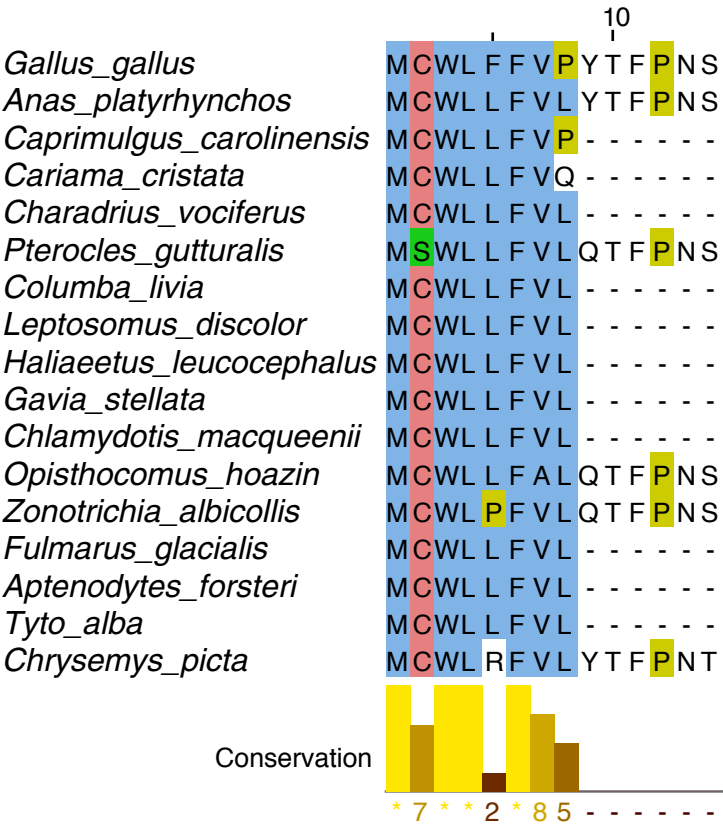
HG0160

ENSDARG00000060089 (btaf1)

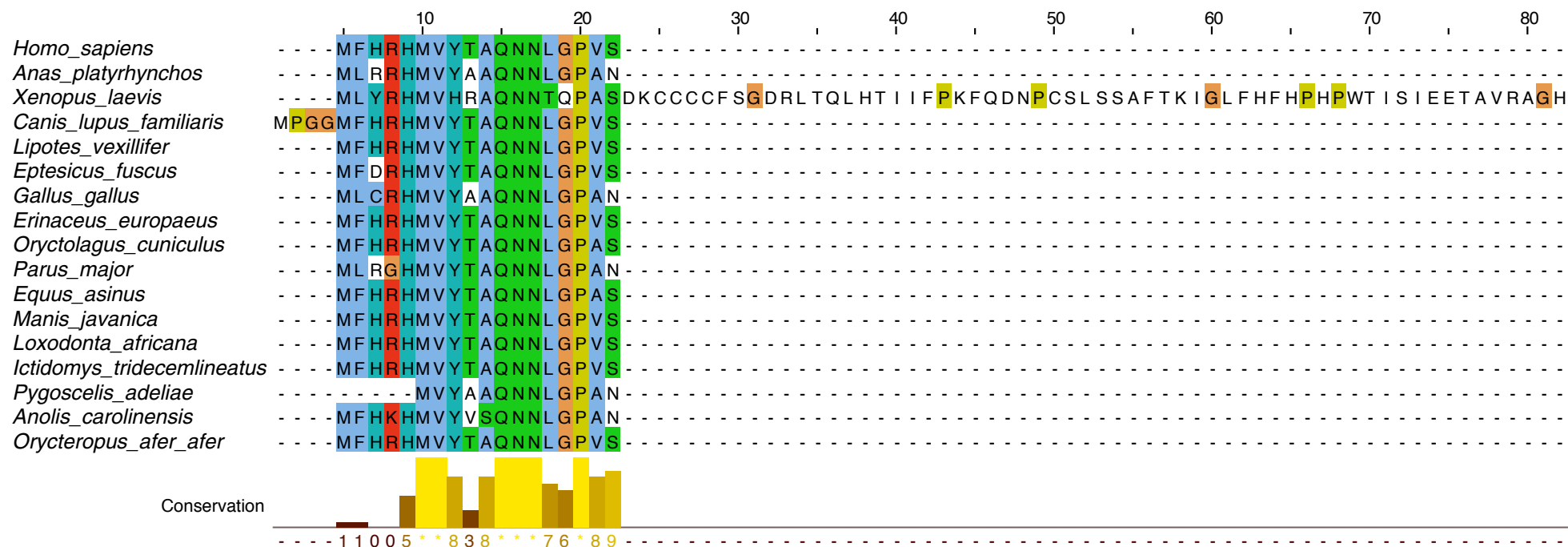


HG0161

ENSGALG00000017191

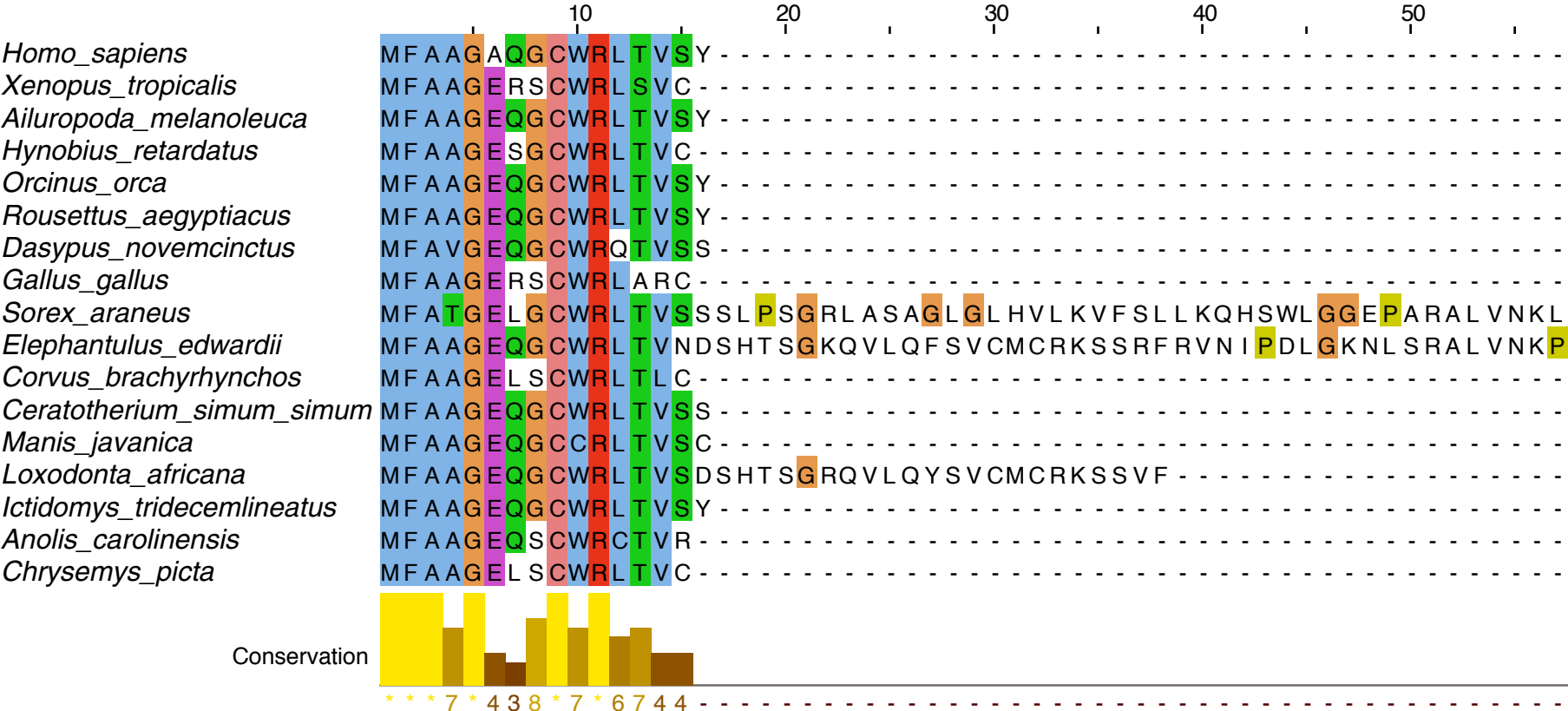


ENSG00000138347 (MYPN)



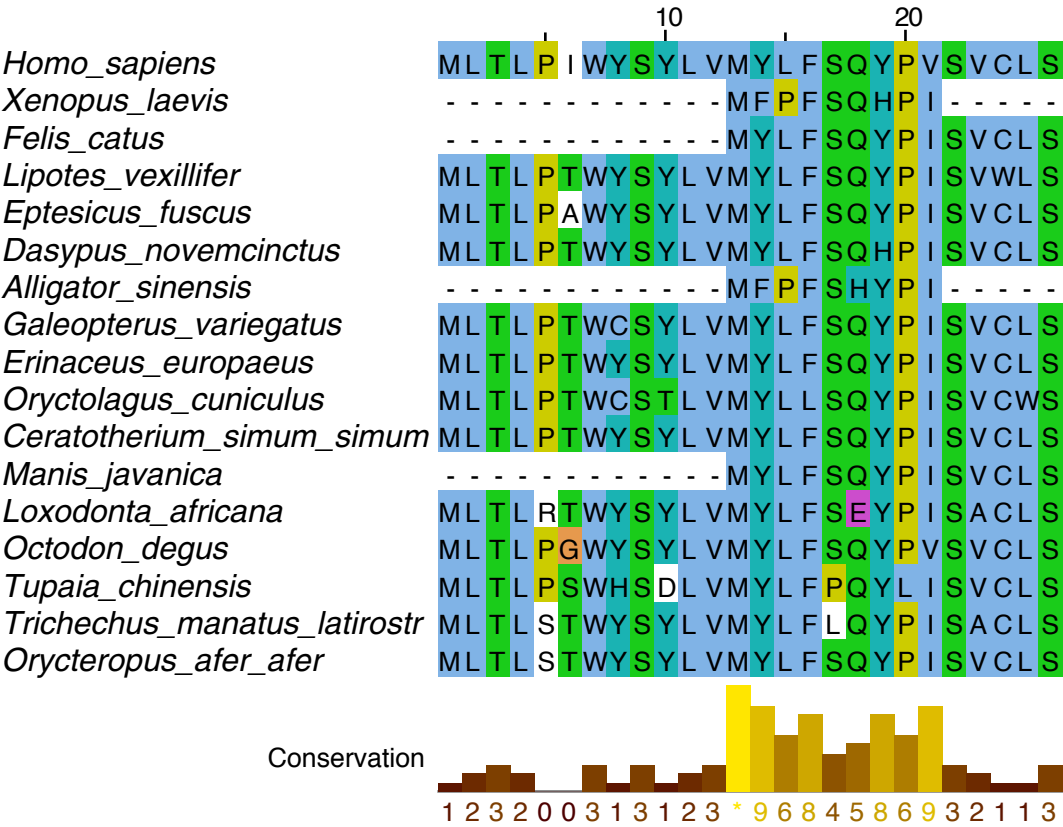
HG0163

ENSG00000146285 (SCML4)



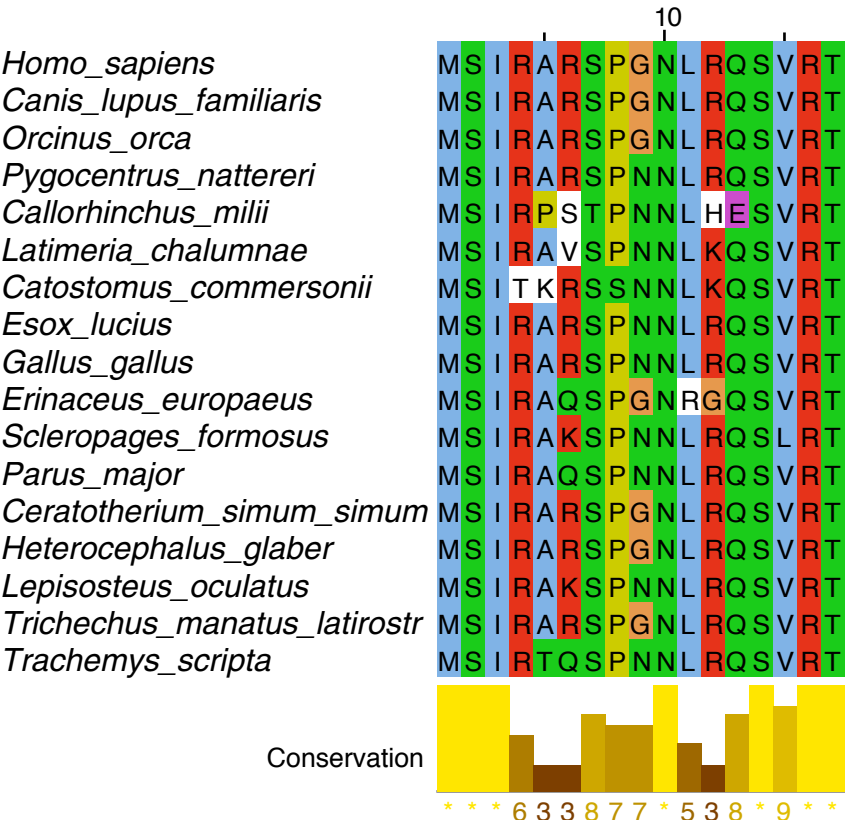
HG0164

ENSG00000151292 (CSNK1G3)



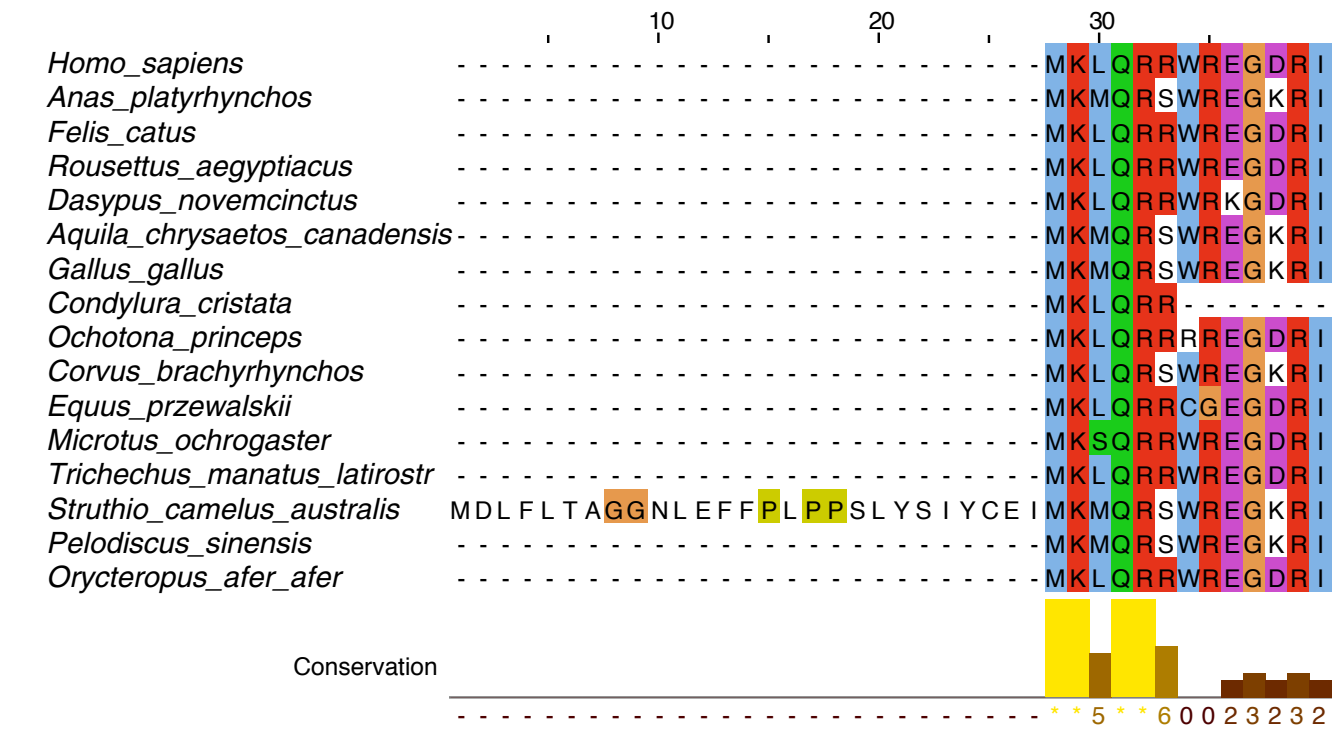
HG0165

ENSG00000177508 (IRX3)



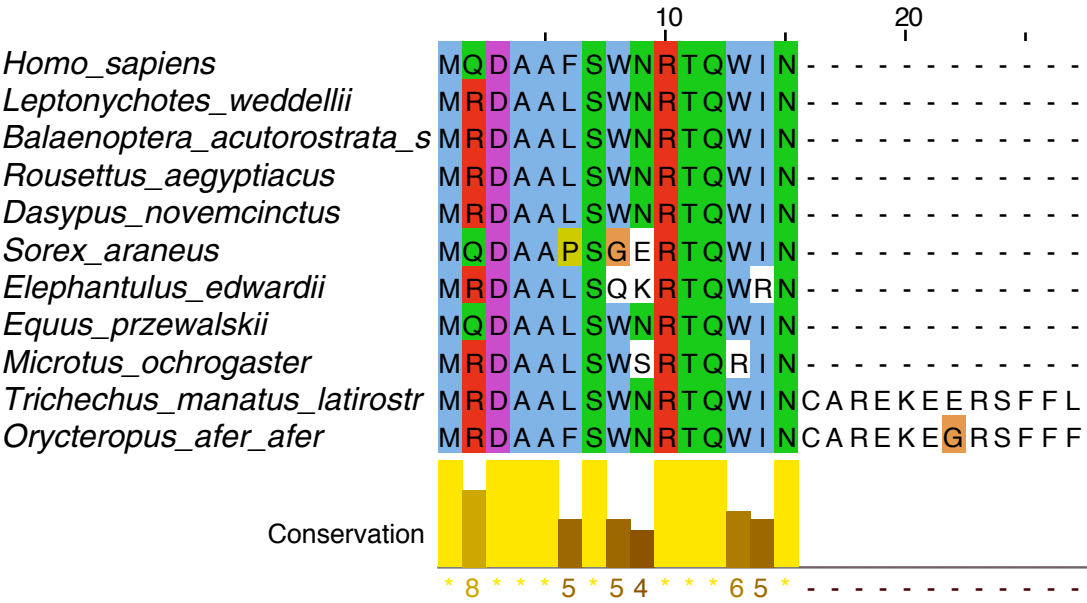
HG0166.1

ENSG00000148948 (LRRC4C)

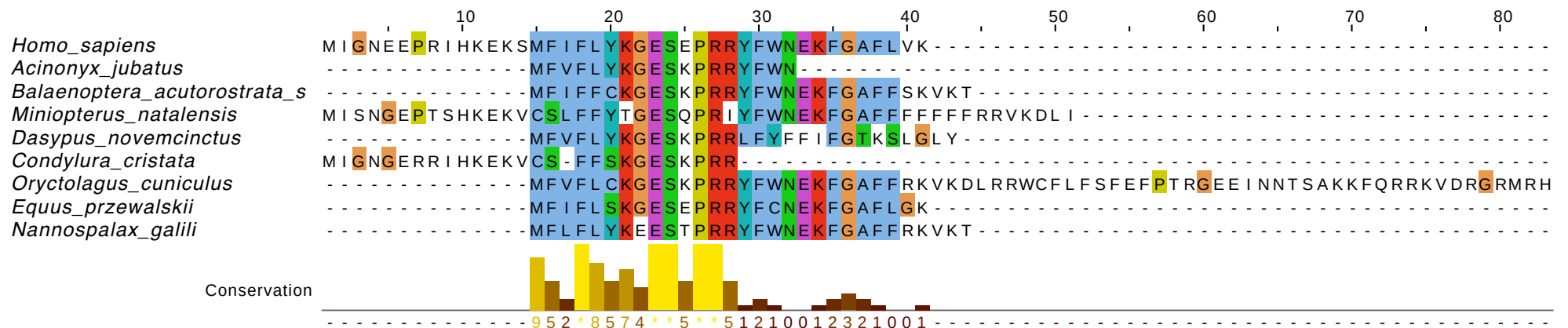


HG0166.2

ENSG00000148948 (LRRC4C)

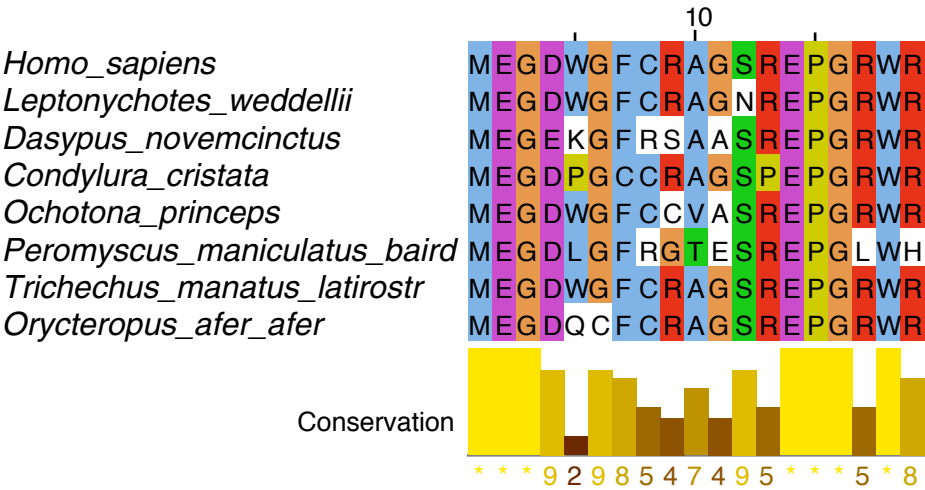


ENSG00000148948 (LRRC4C)



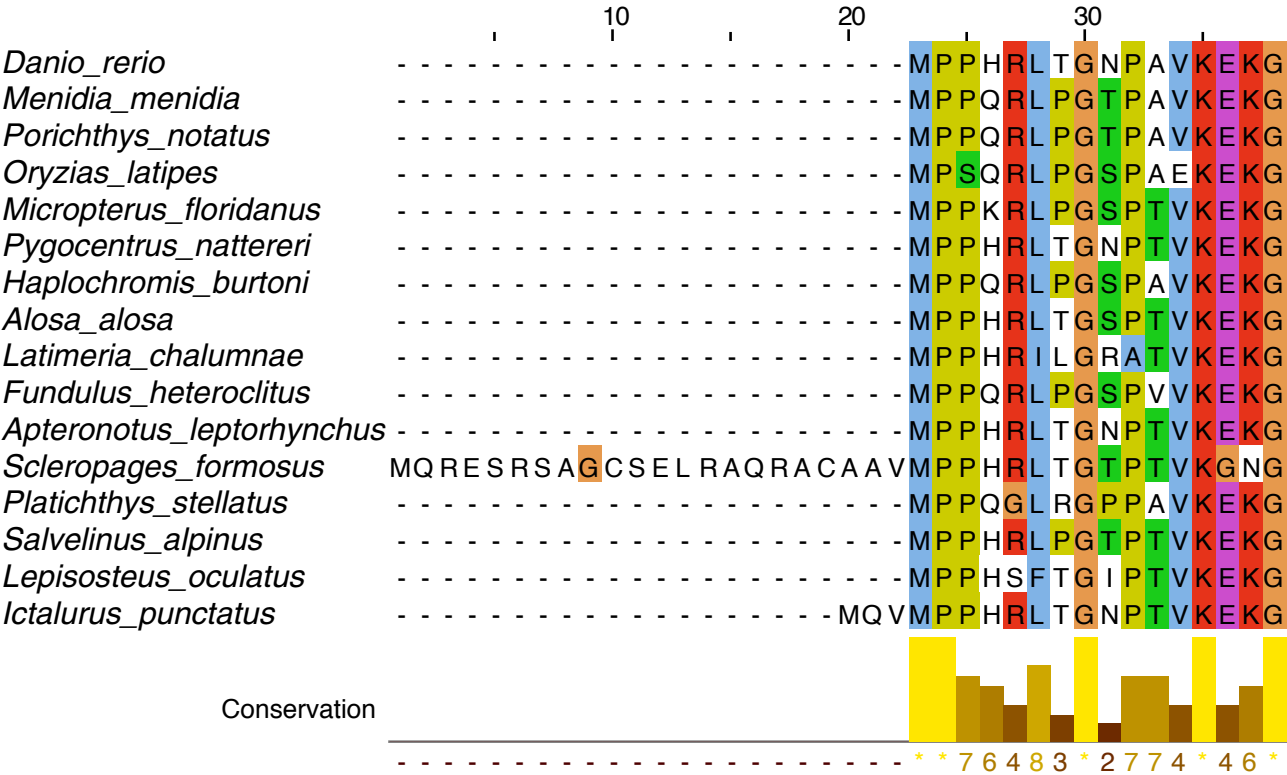
HG0166.4

ENSG00000148948 (LRRC4C)



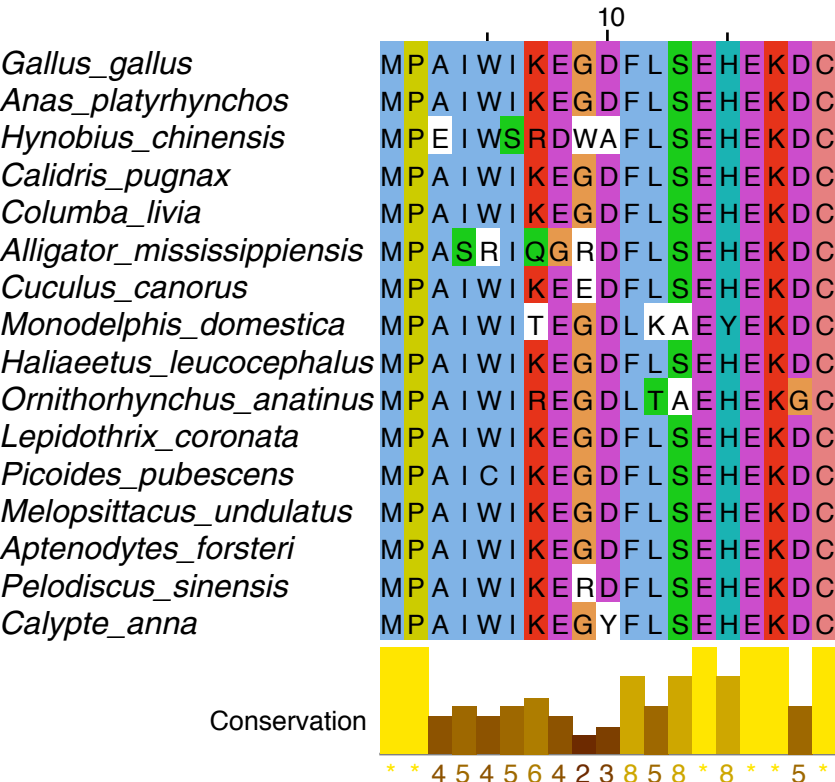
HG0167

ENSDARG00000104005 (slc4a3)



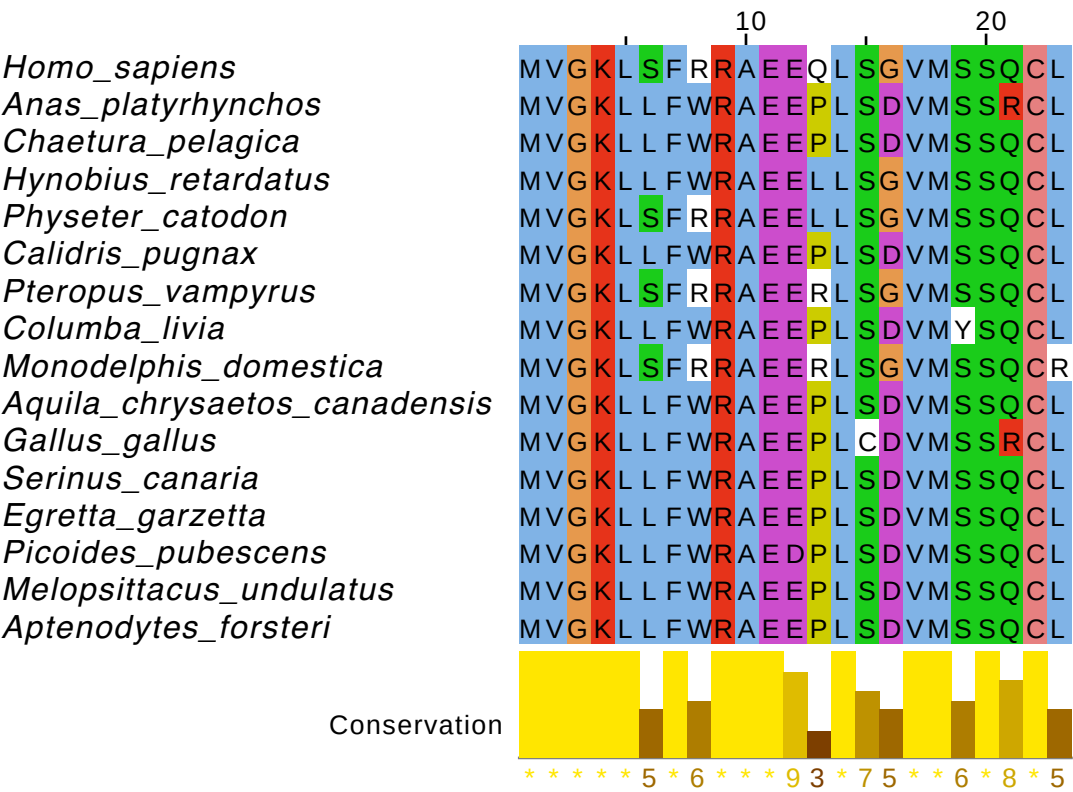
HG0168

ENSGALG00000006997 (BRINP1)

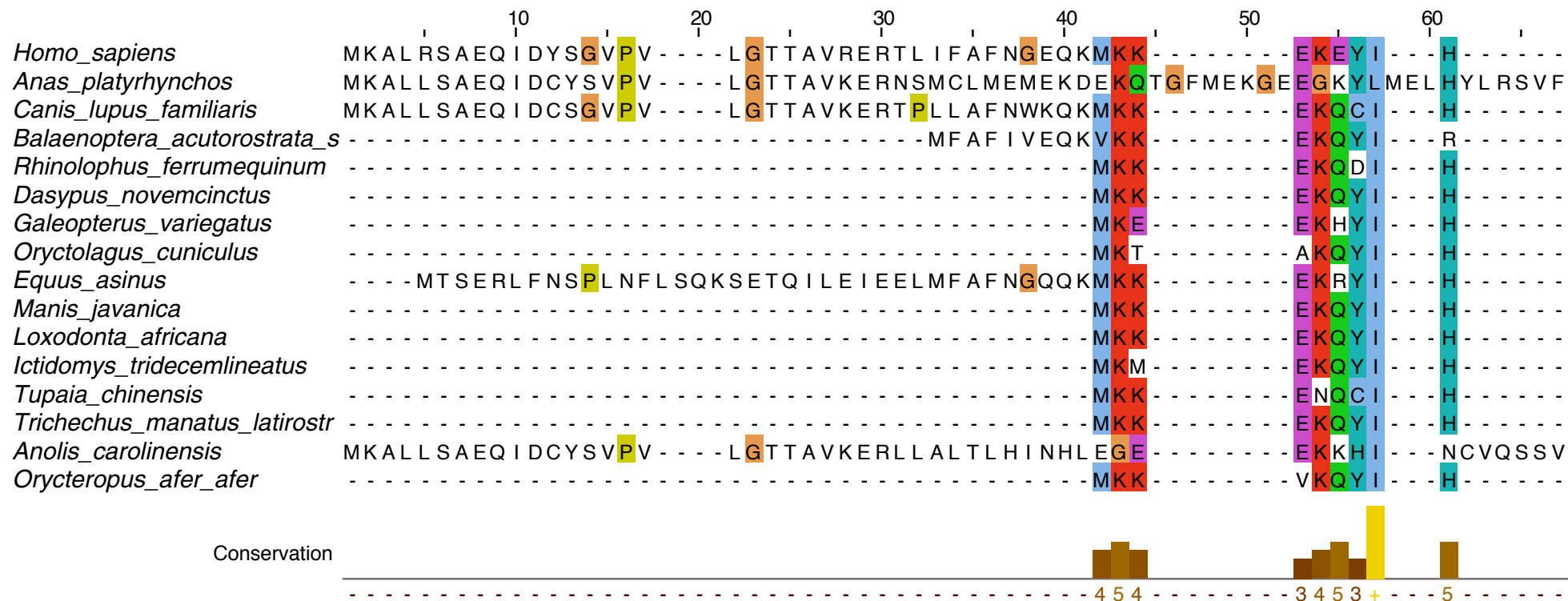


HG0169

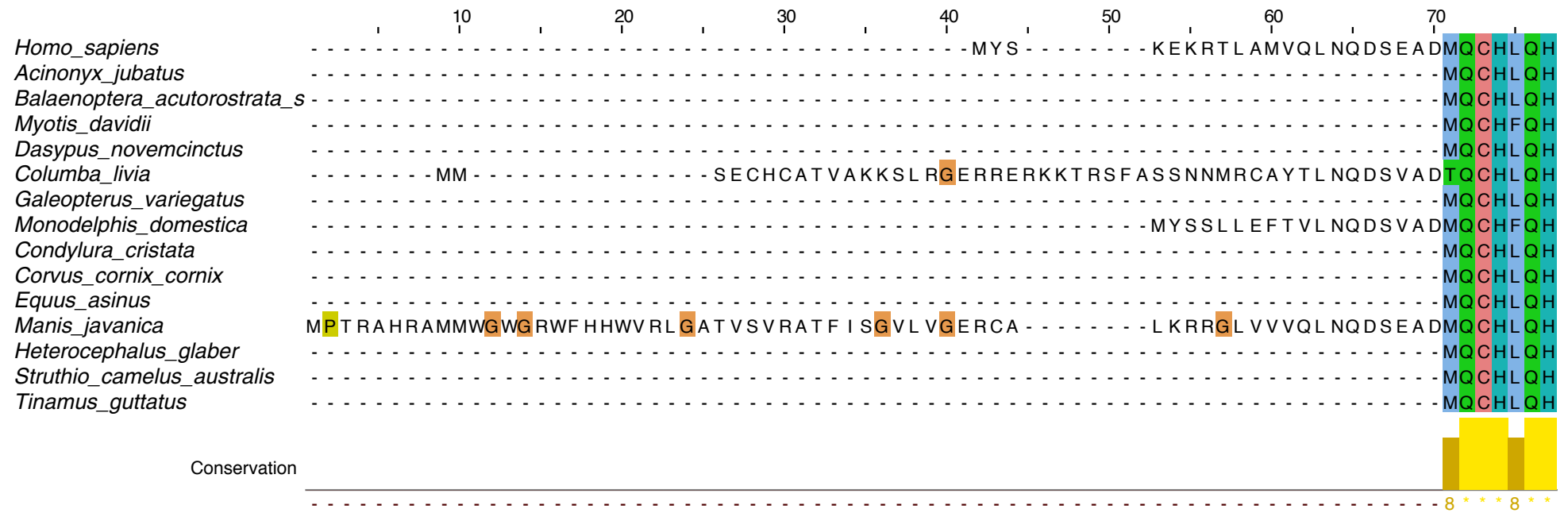
ENSG00000114933 (INO80D)



ENSG00000180530 (NRIP1)



ENSG00000177311 (ZBTB38)



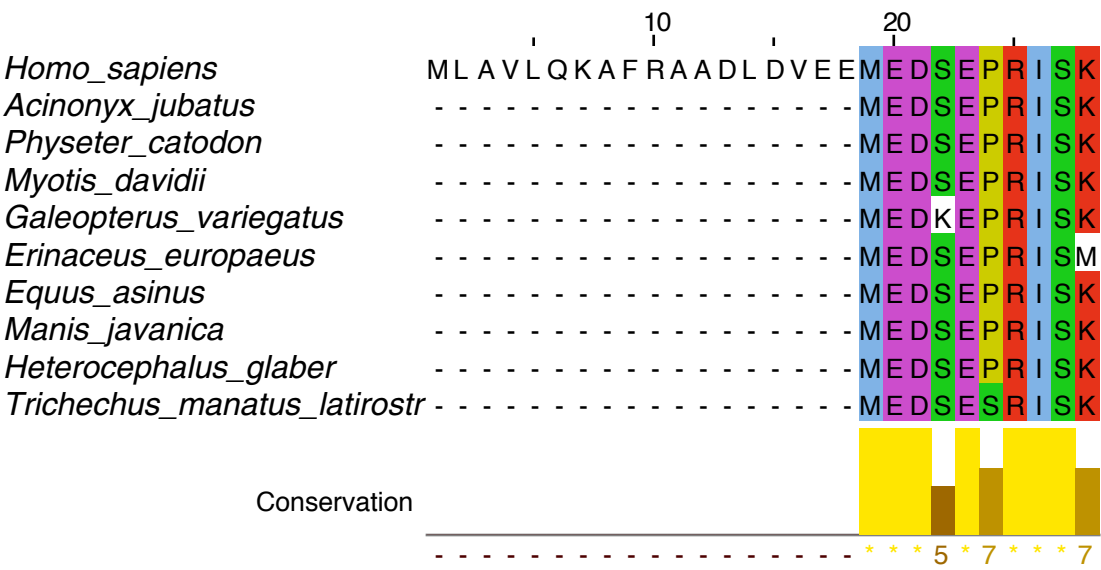
HG0171.2

ENSG00000177311 (ZBTB38)

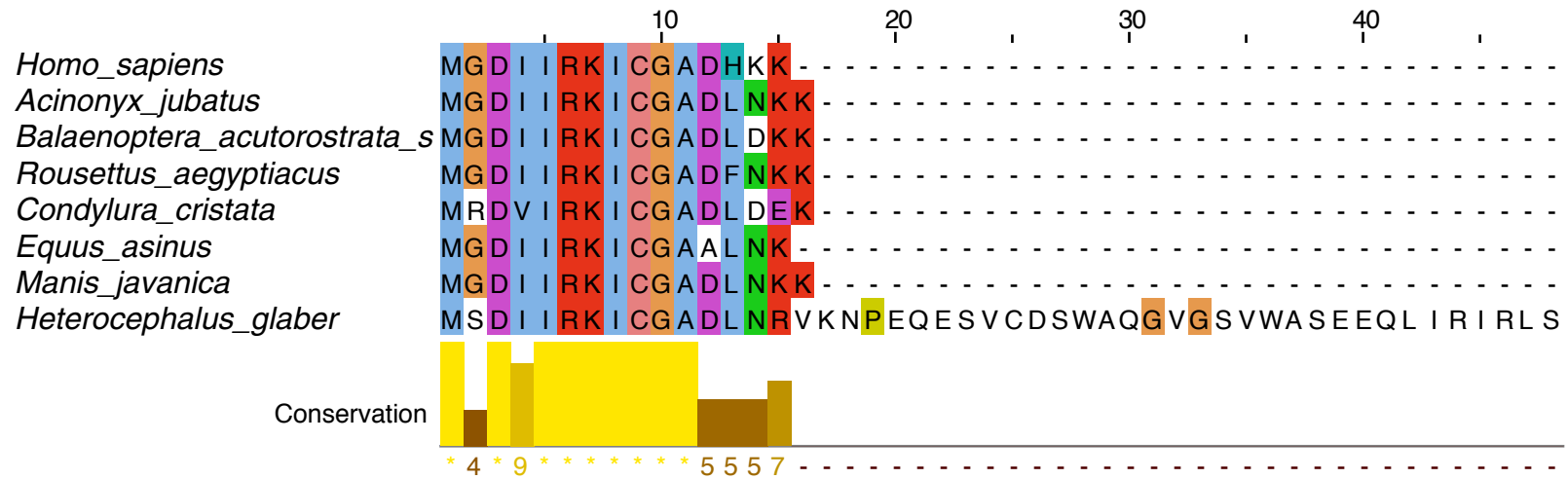


HG0171.3

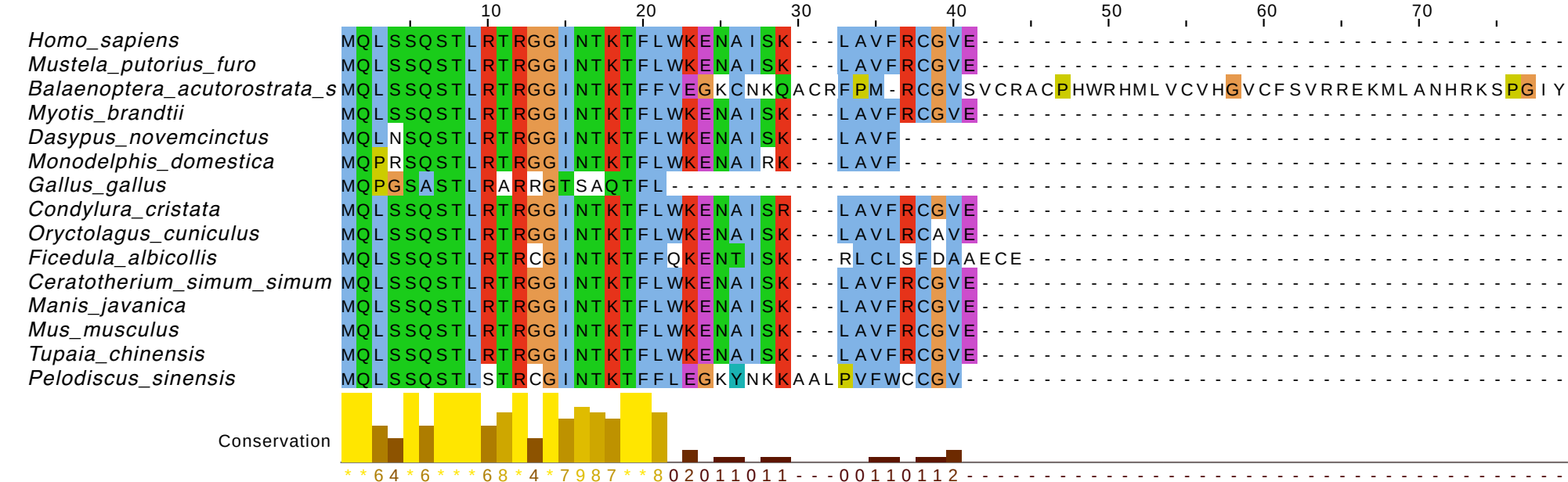
ENSG00000177311 (ZBTB38)



ENSG00000177311 (ZBTB38)

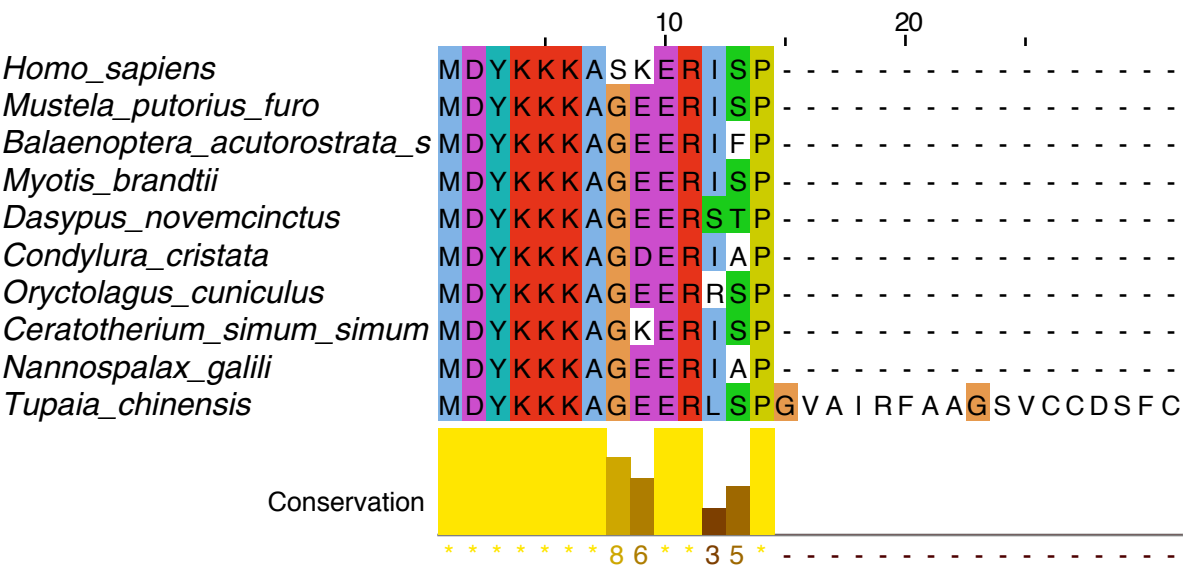


HG0172.1
ENSG00000196782 (MAML3)

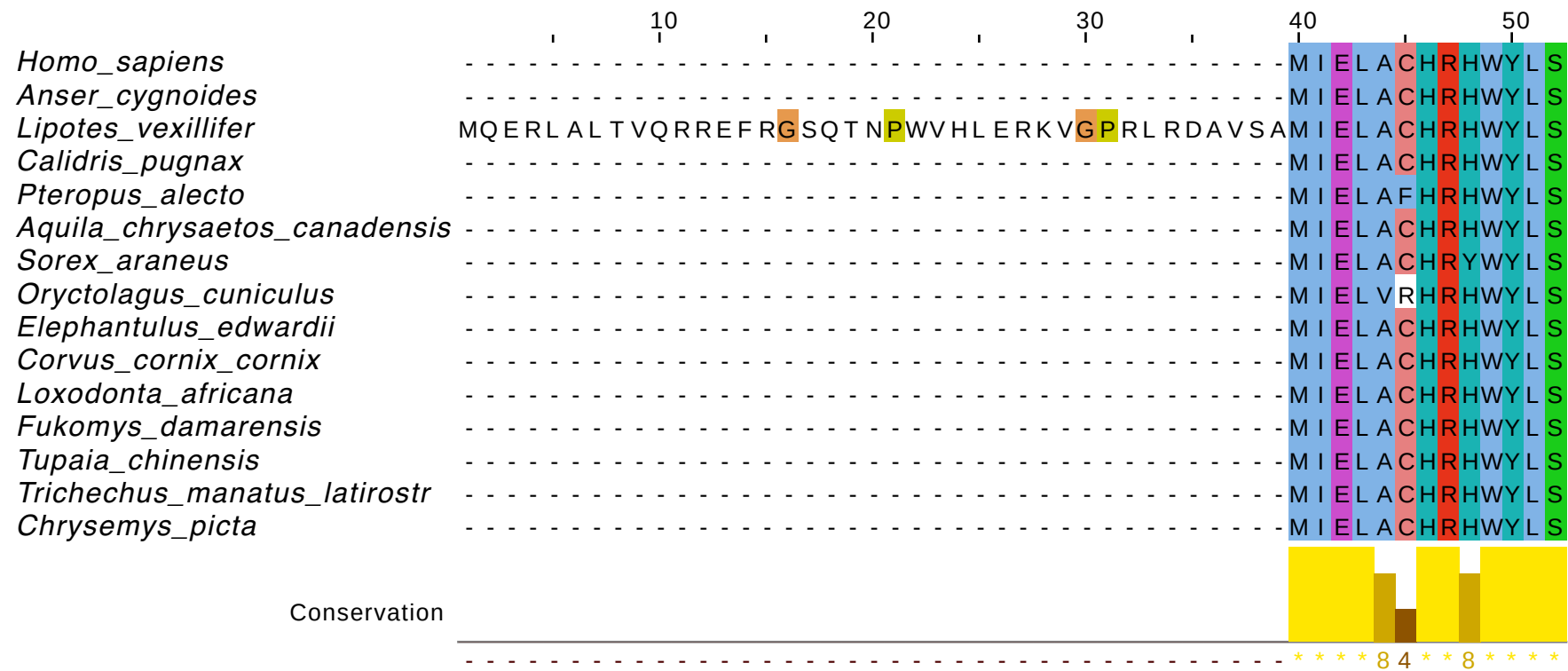


HG0172.2

ENSG00000196782 (MAML3)



HG0173
ENSG00000101746 (NOL4)



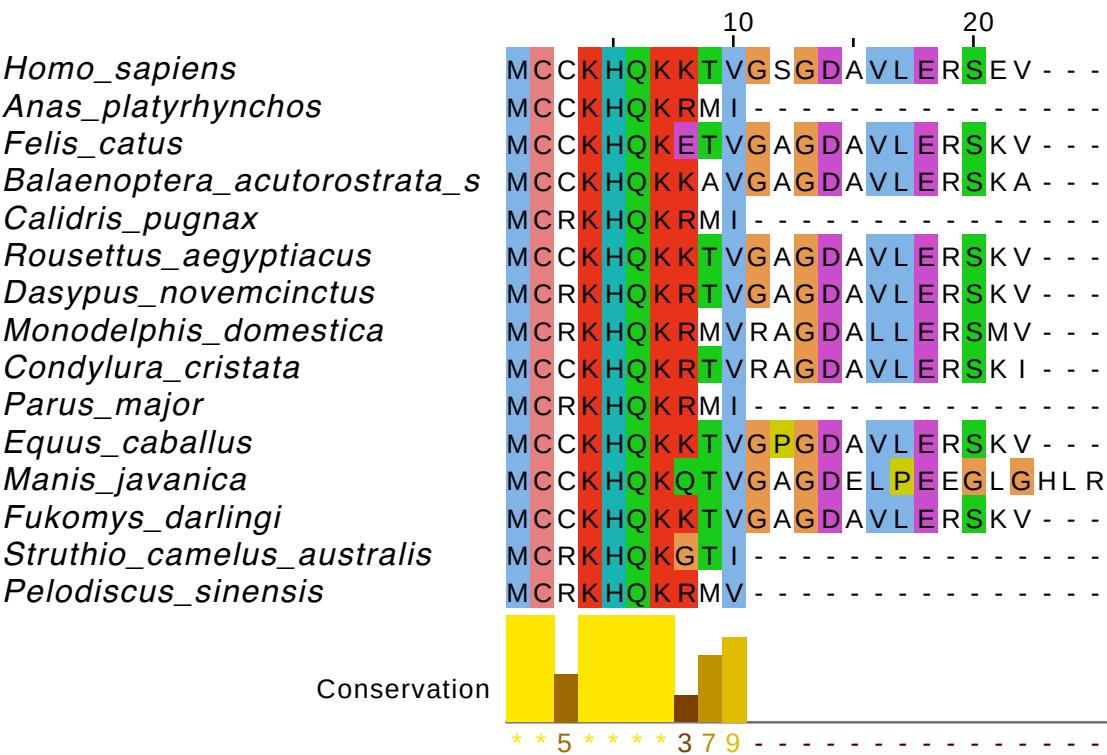
HG0174

ENSG00000144355 (DLX1)

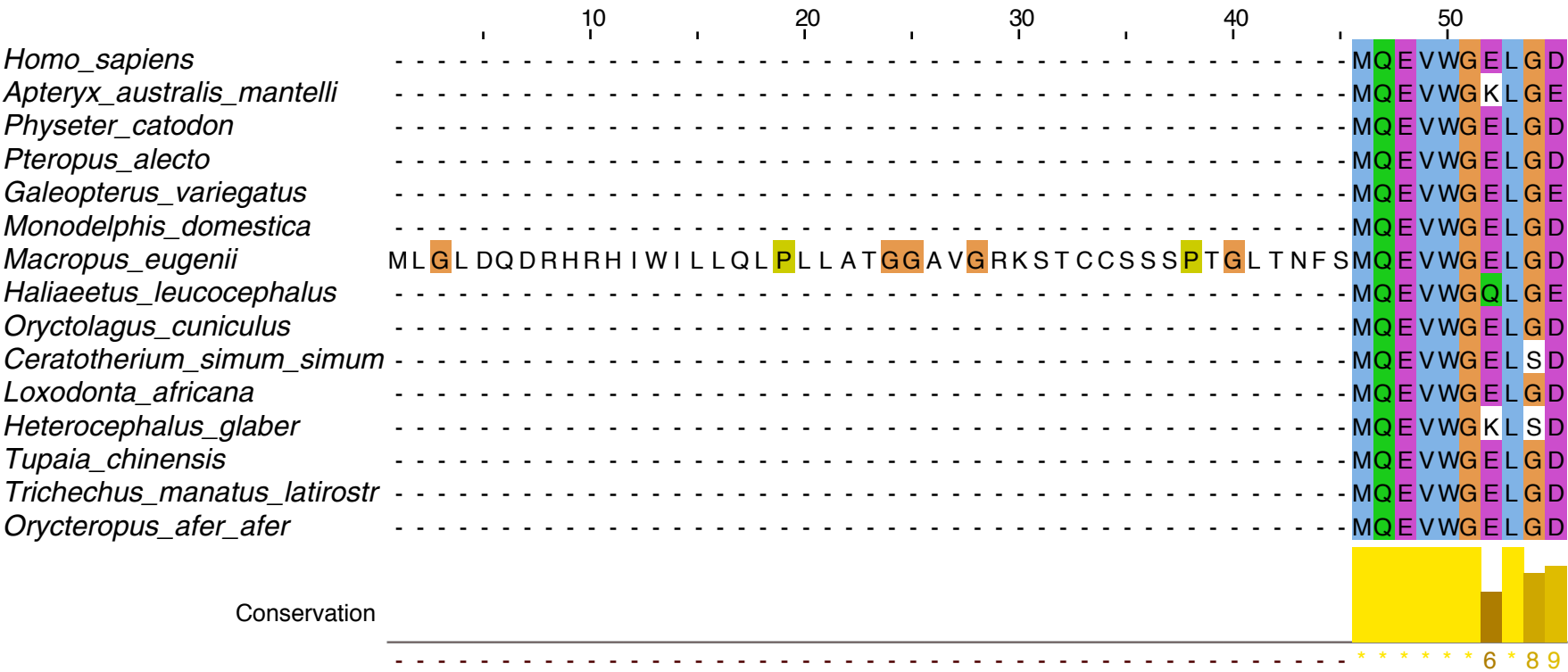


HG0175

ENSG00000151320 (AKAP6)



HG0176
ENSG00000170962 (PDGFD)

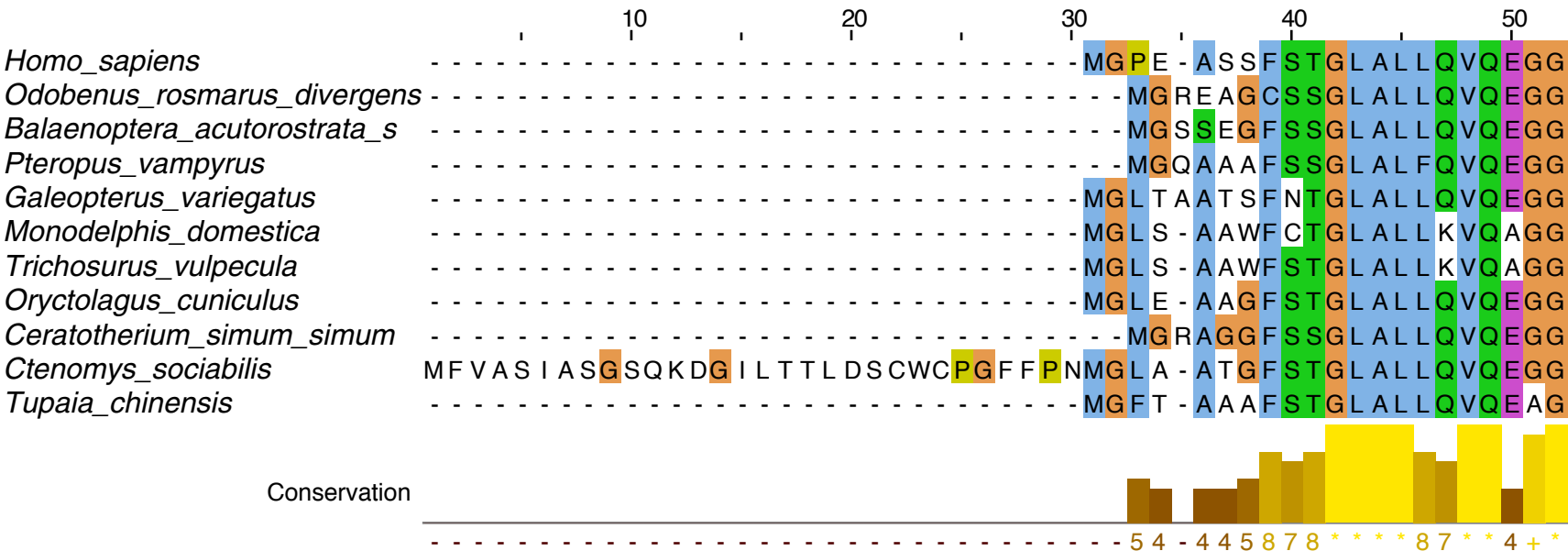


ENSG00000171843 (MLLT3)



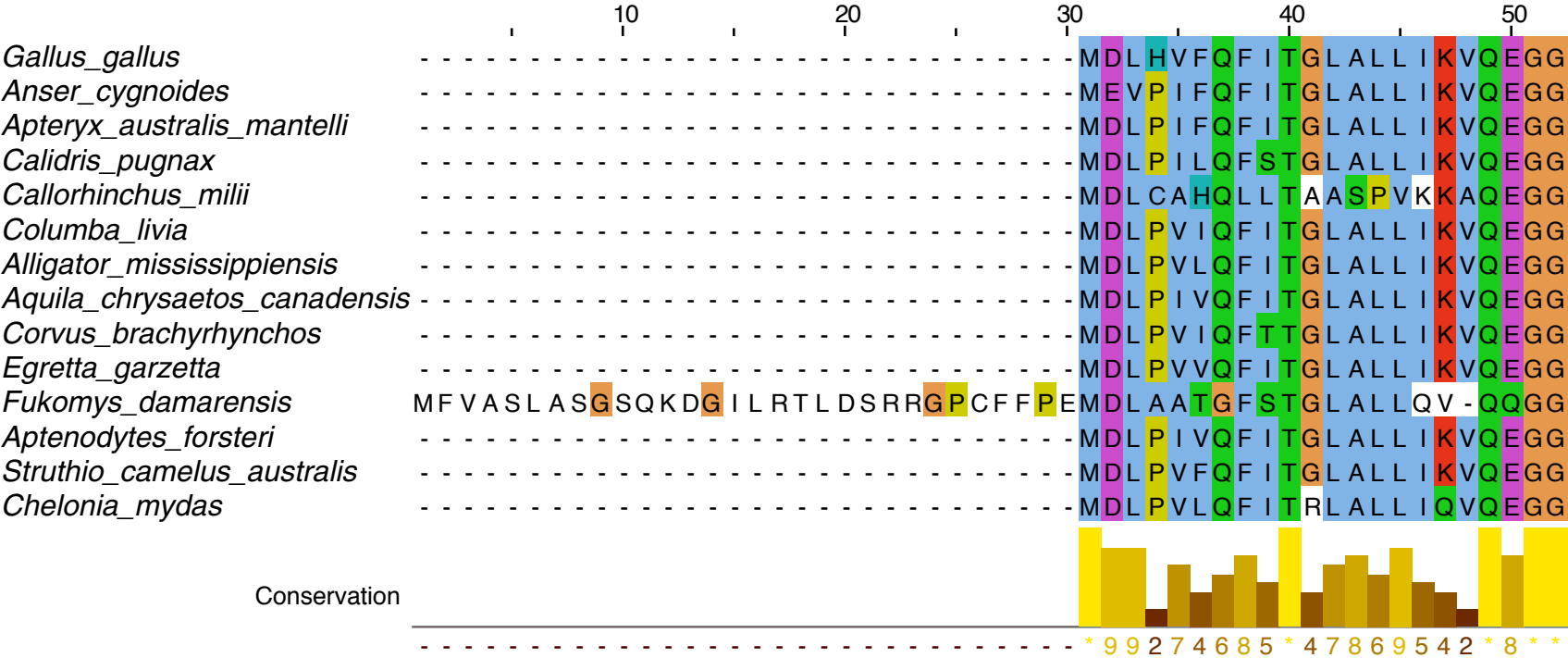
HG0178.1

ENSG00000131634 (TMEM204)



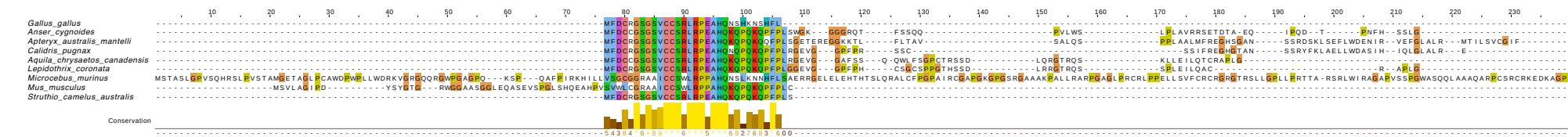
HG0178.1

ENSGALG00000029047 (TMEM204)

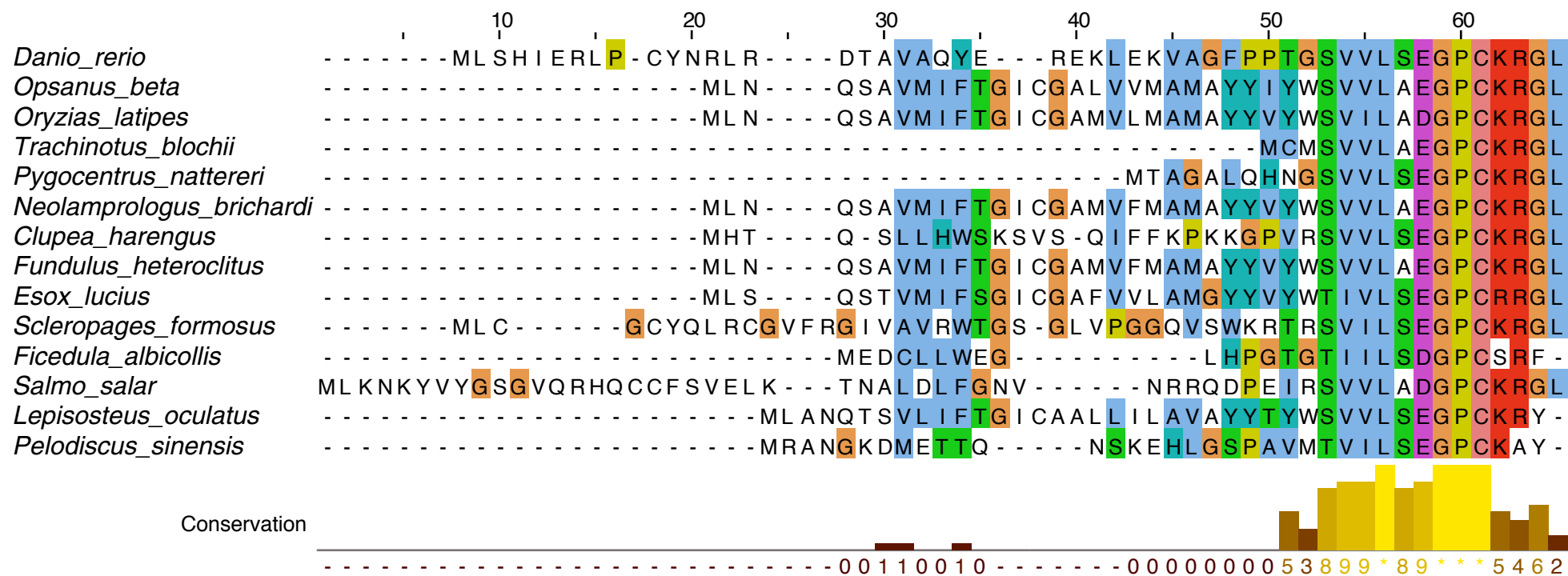


HG0178.2

ENSGALG00000029047 (TMEM204)

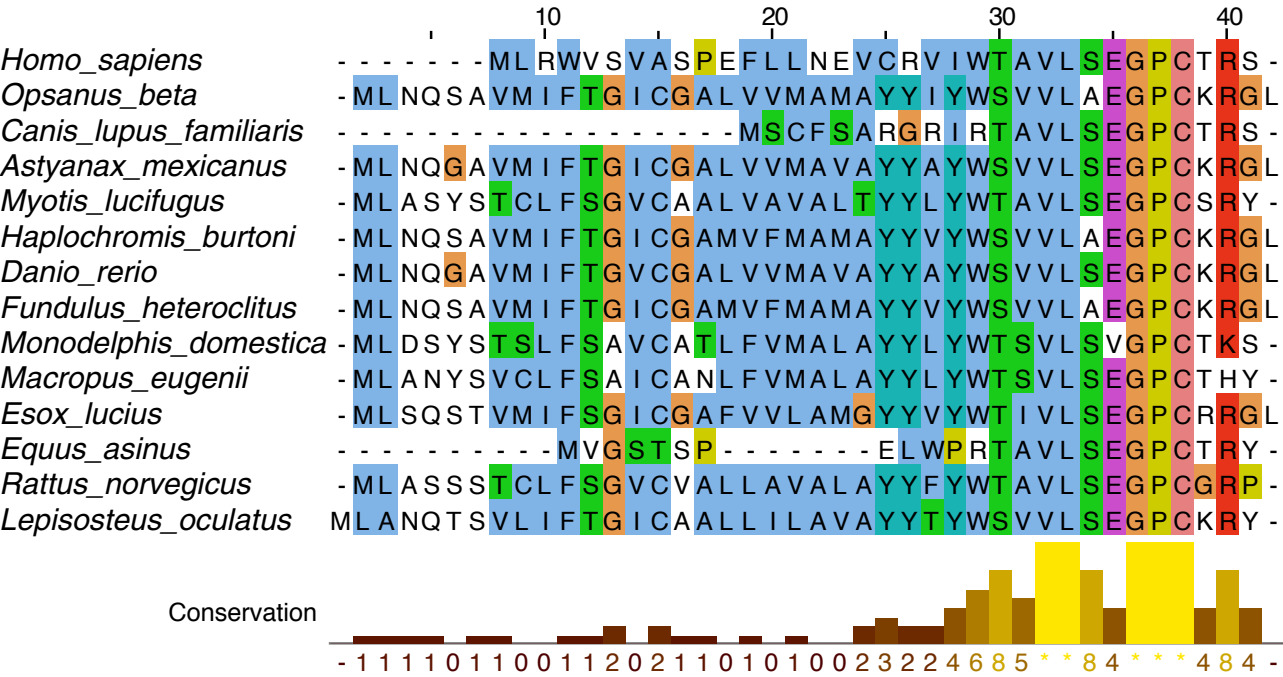


ENSDARG00000036549 (agpat3)



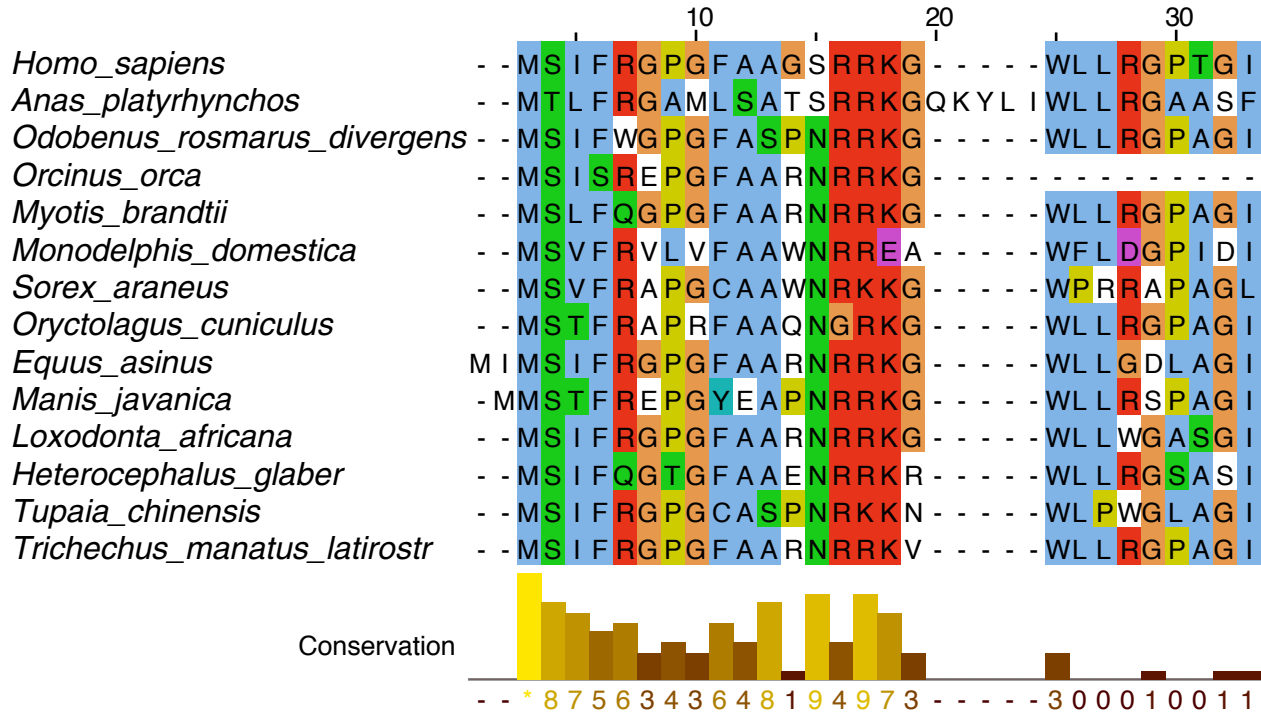
HG0179

ENSG00000160216 (AGPAT3)



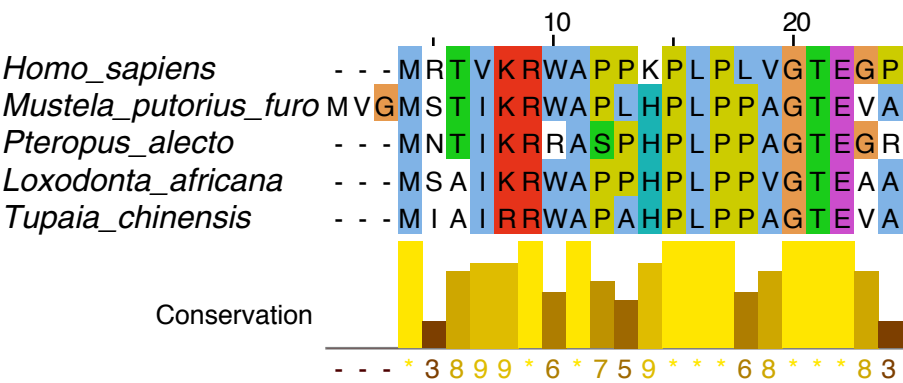
HG0180.1

ENSG00000112246 (SIM1)

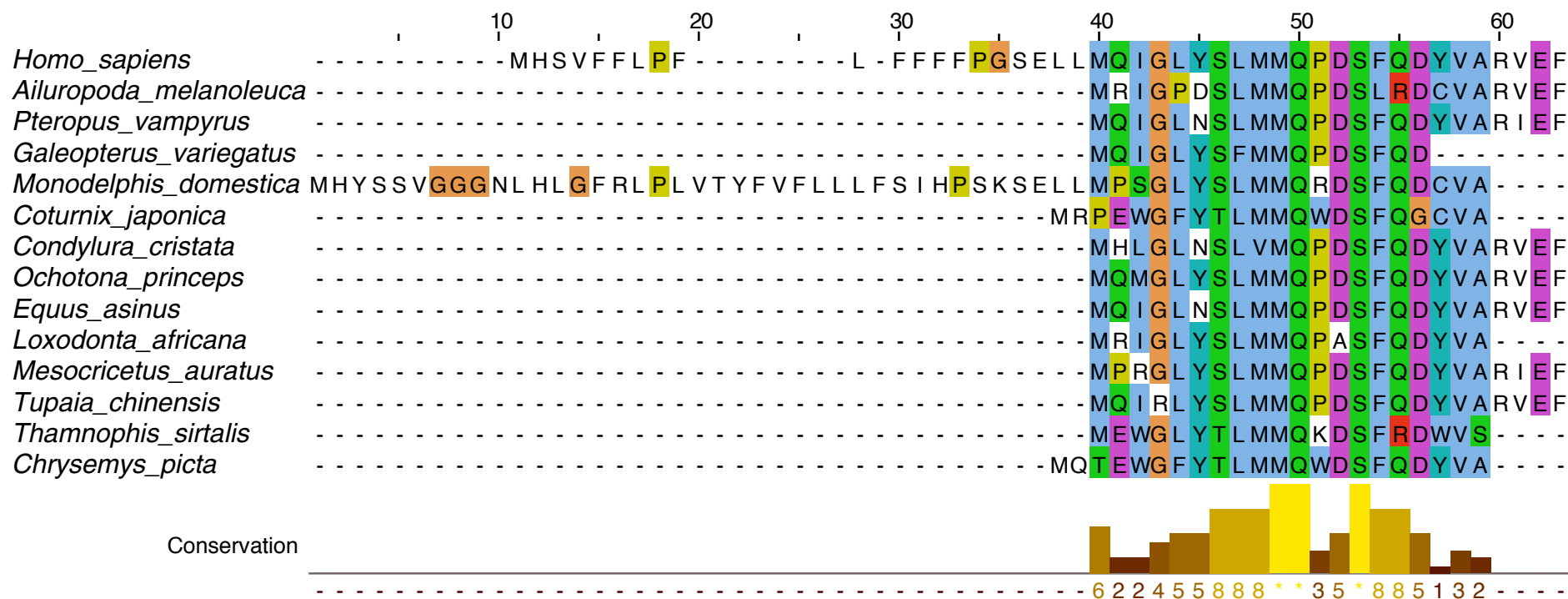


HG0180.2

ENSG00000112246 (SIM1)

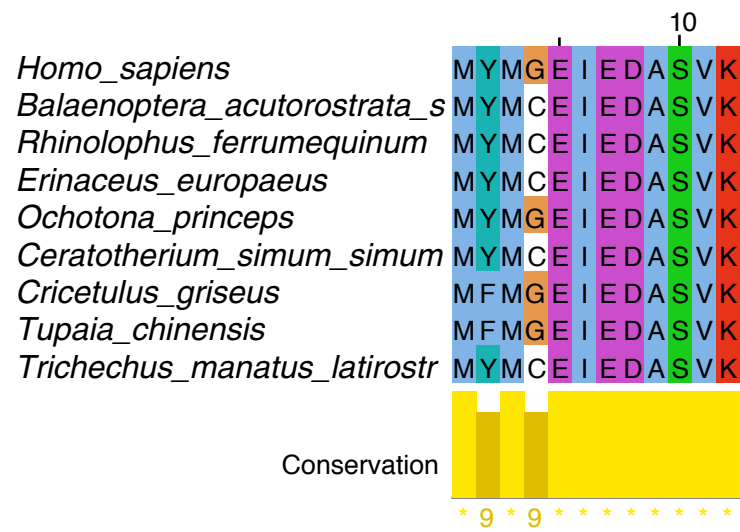


ENSG00000143776 (CDC42BPA)



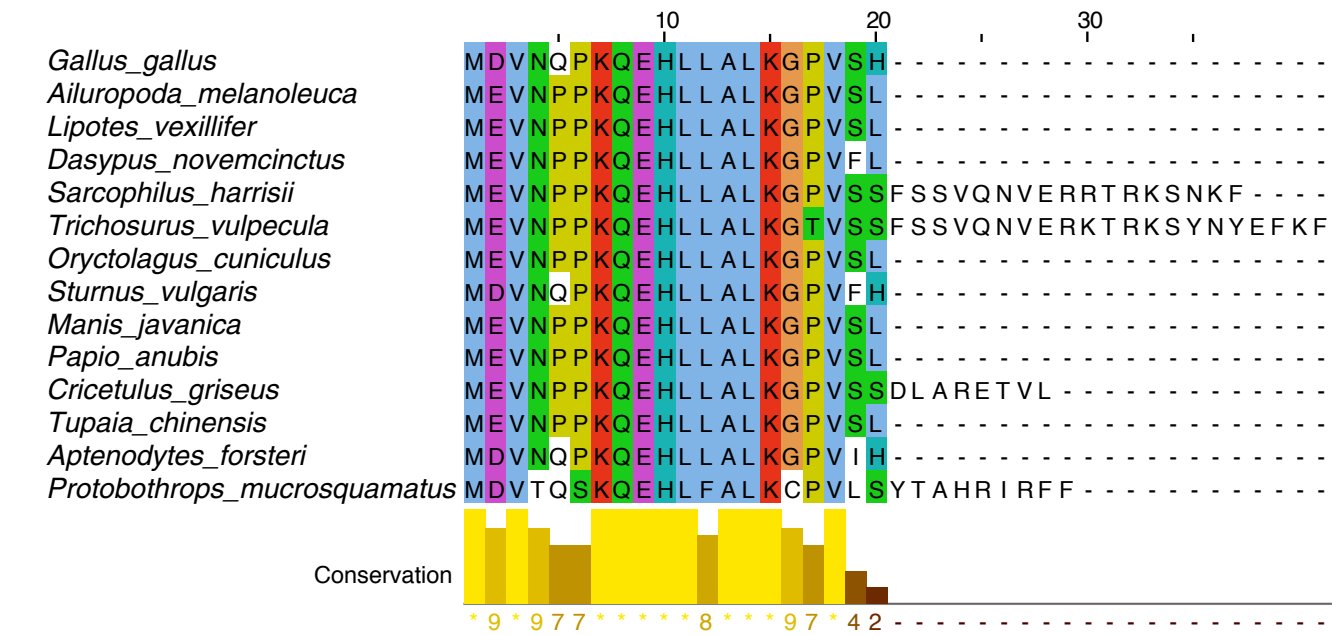
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ENSG00000143776 (CDC42BPA)

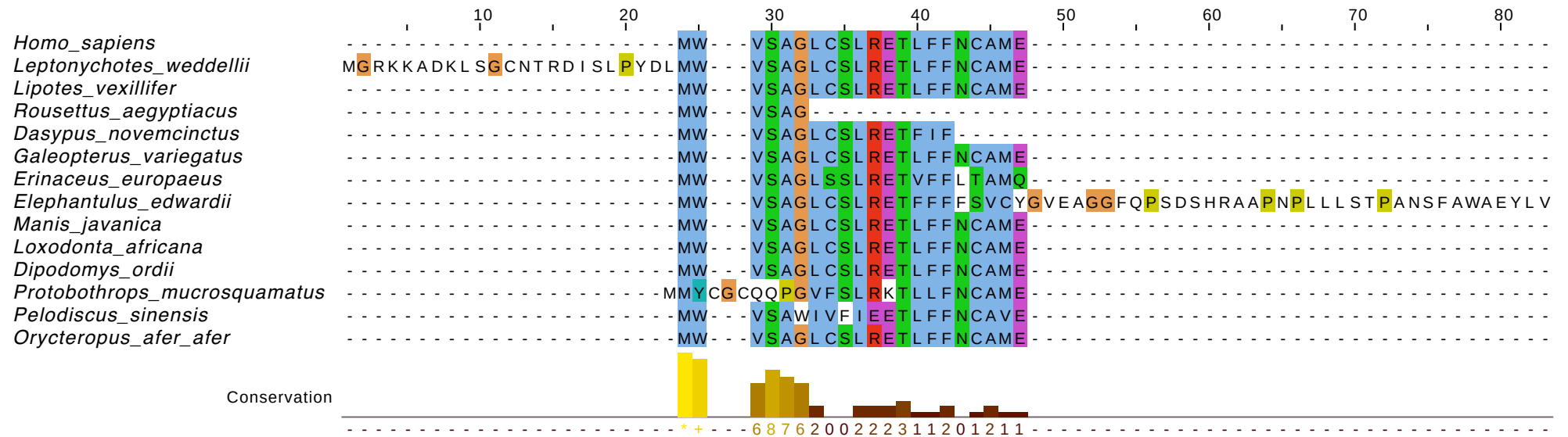


HG0182

ENSGALG00000031991

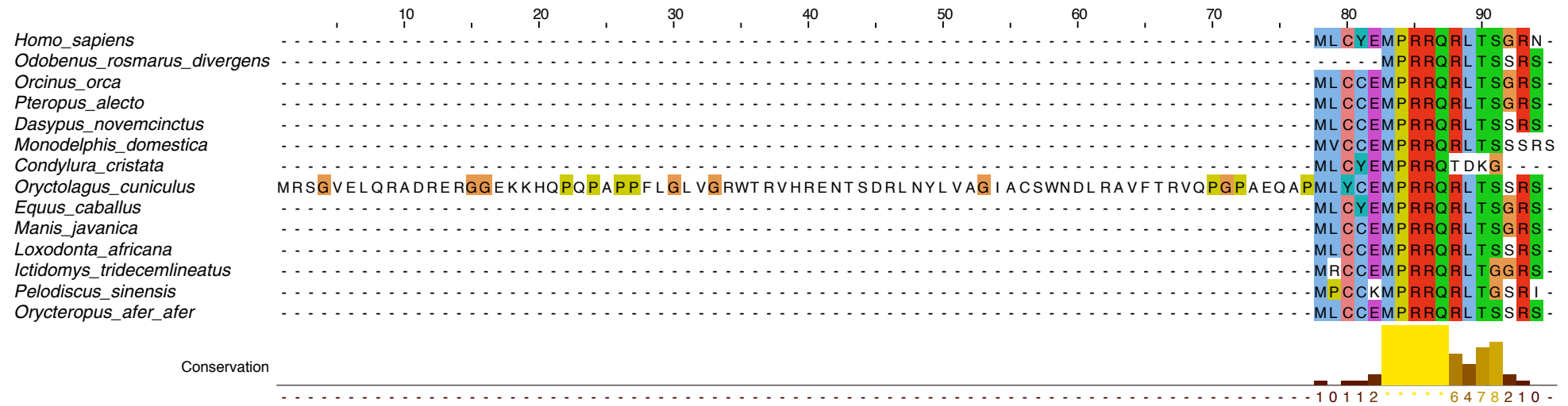


ENSG00000011465 (DCN)

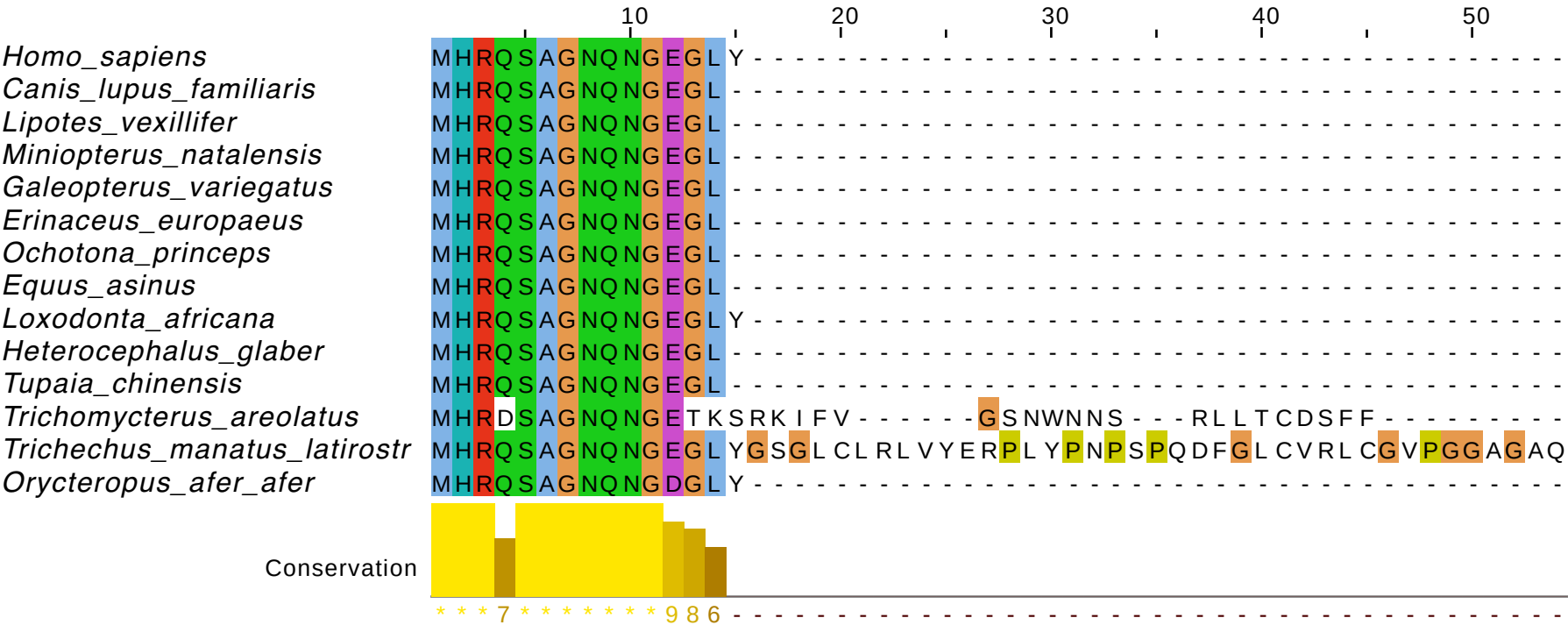


HG0184

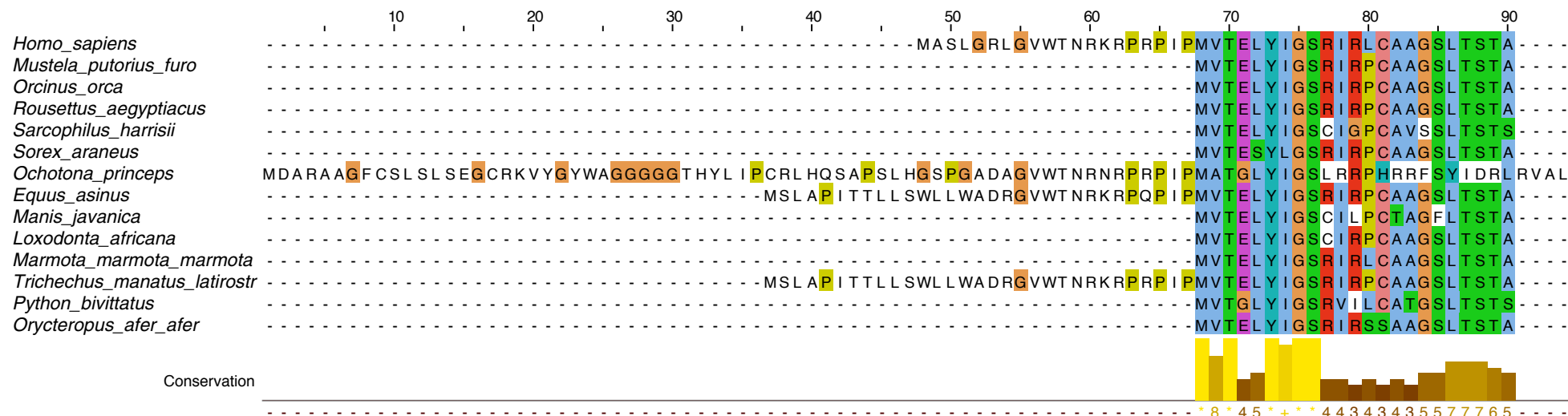
ENSG00000136542 (GALNT5)



HG0185
ENSG00000143033 (MTF2)

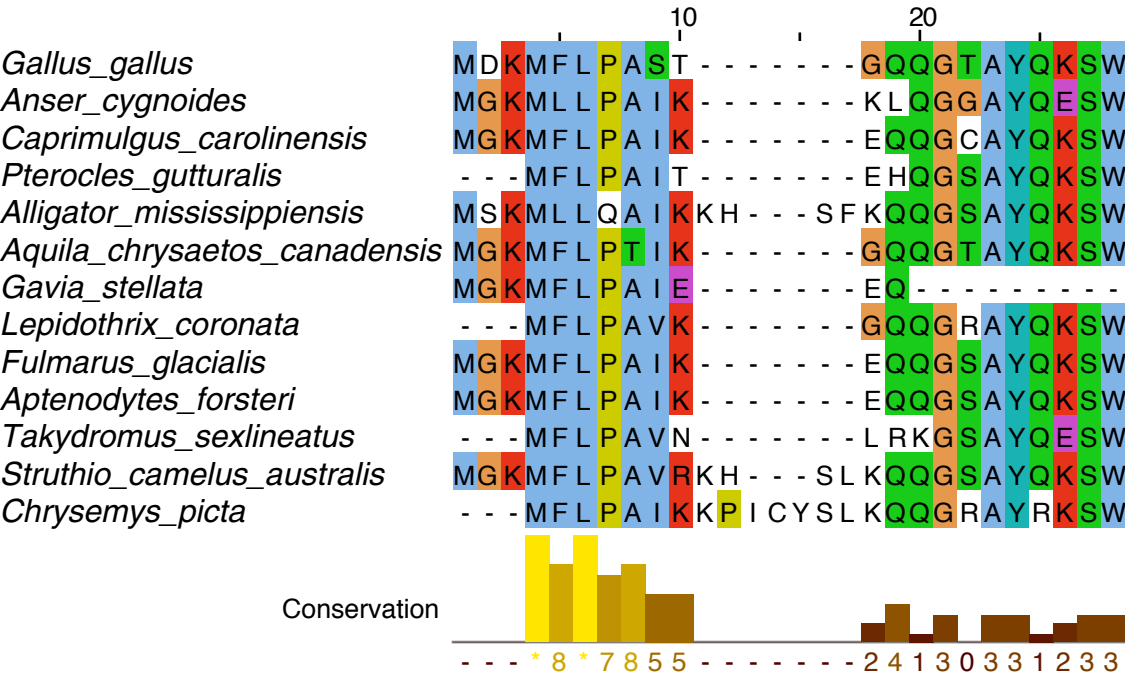


ENSG00000167552 (TUBA1A)



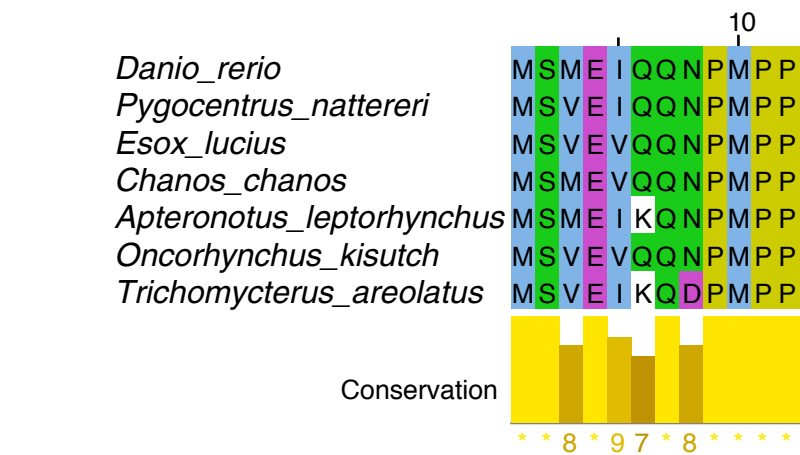
HG0187.1

ENSGALG00000004058 (GPR146)



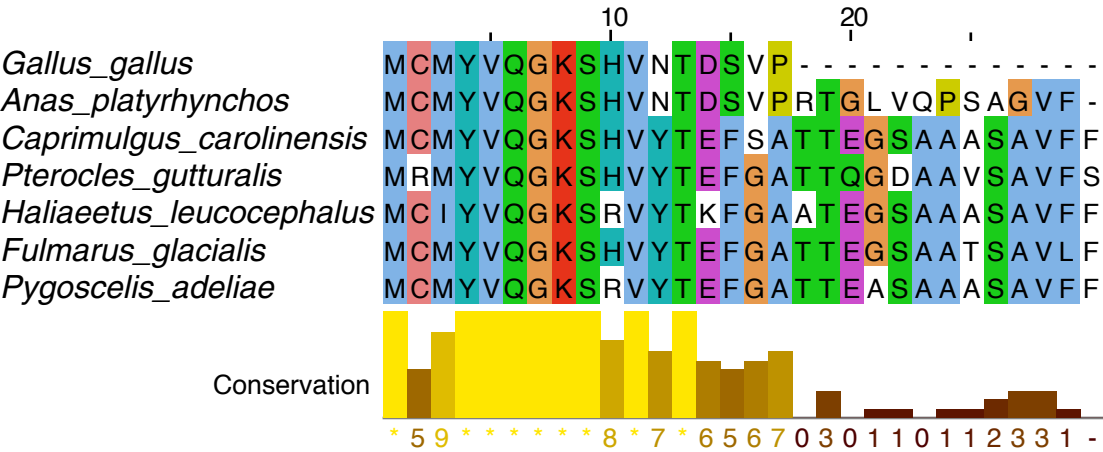
HG0187.2

ENSDARG00000059610 (gpr146)



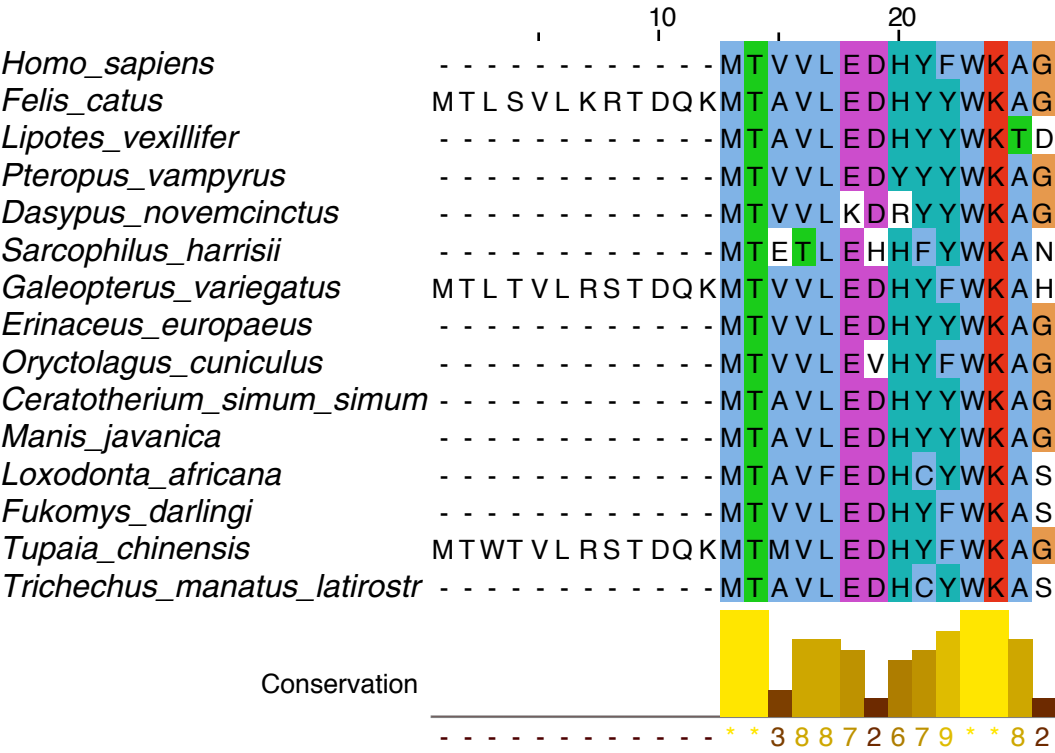
HG0187.3

ENSGALG00000004058 (GPR146)



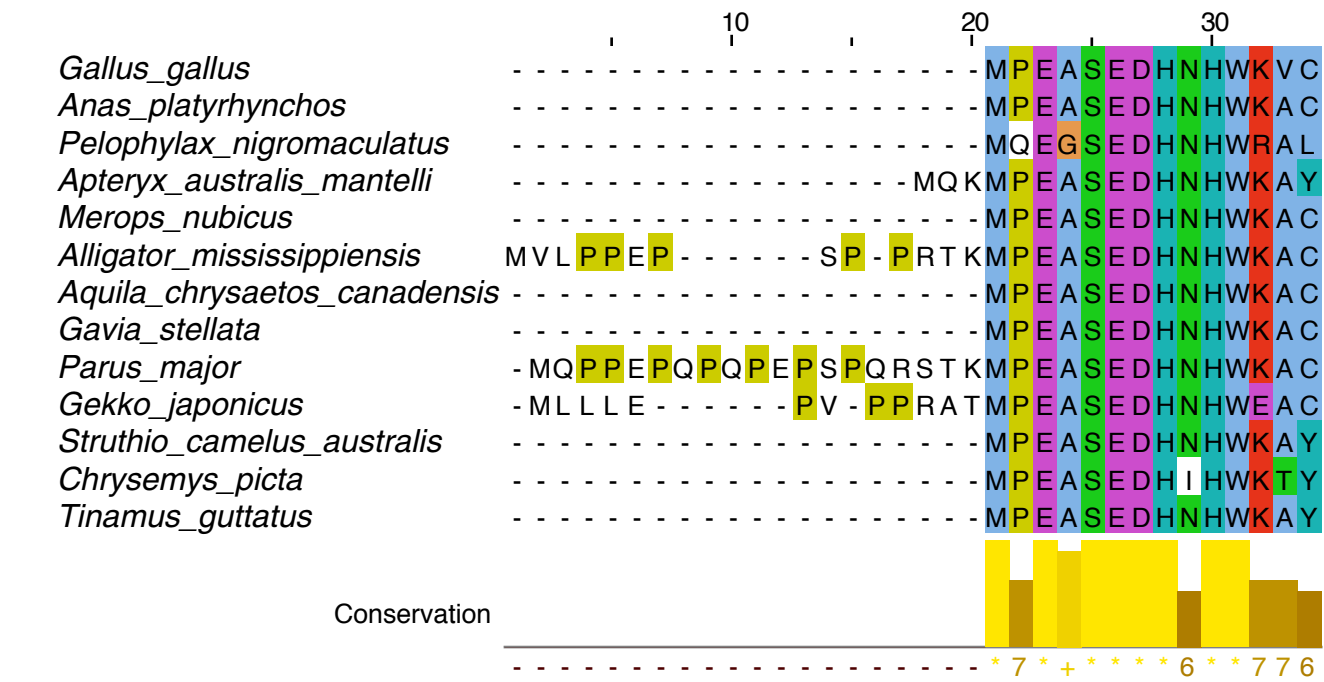
HG0188

ENSG00000157625 (TAB3)

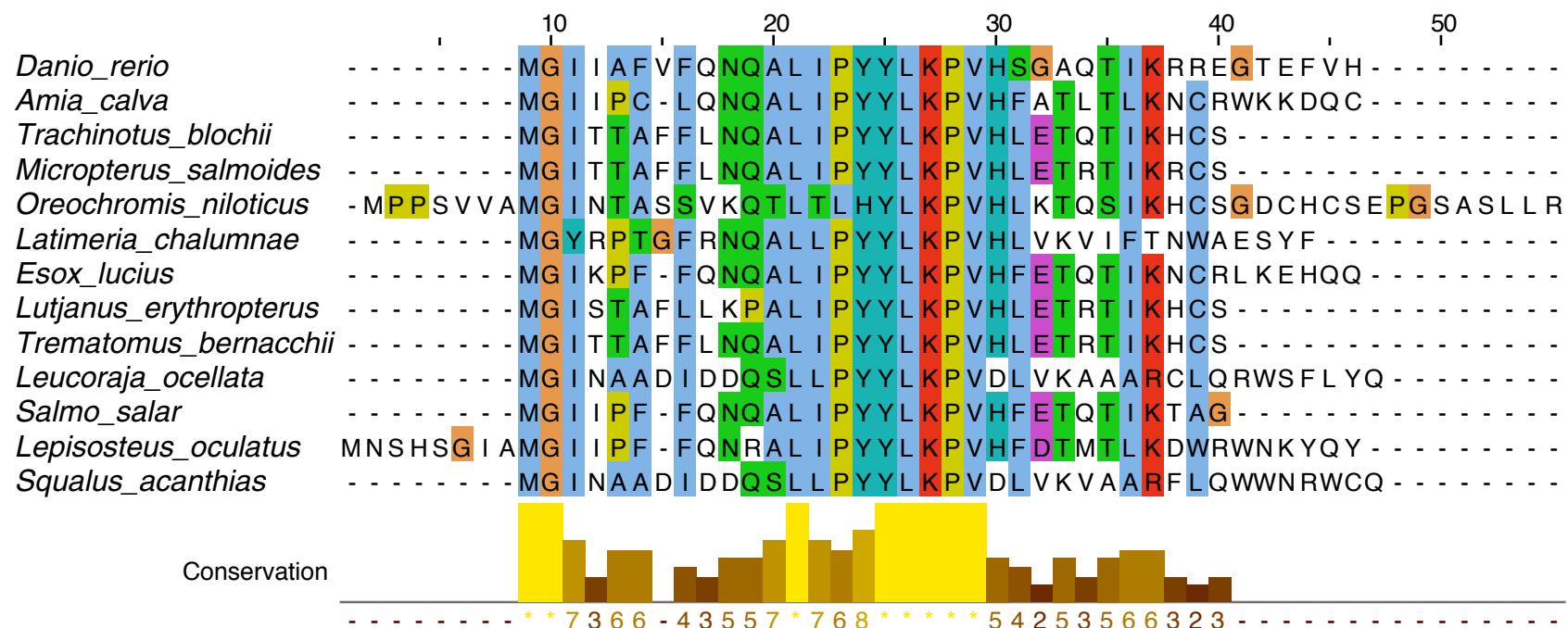


HG0188

ENSGALG00000016284 (TAB3)

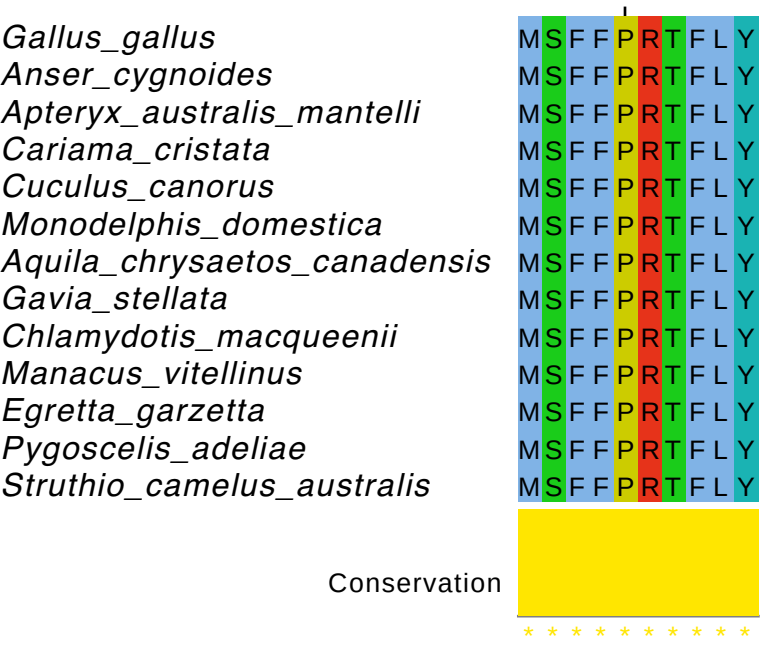


ENSDARG000000001807 (tnfrsf21)



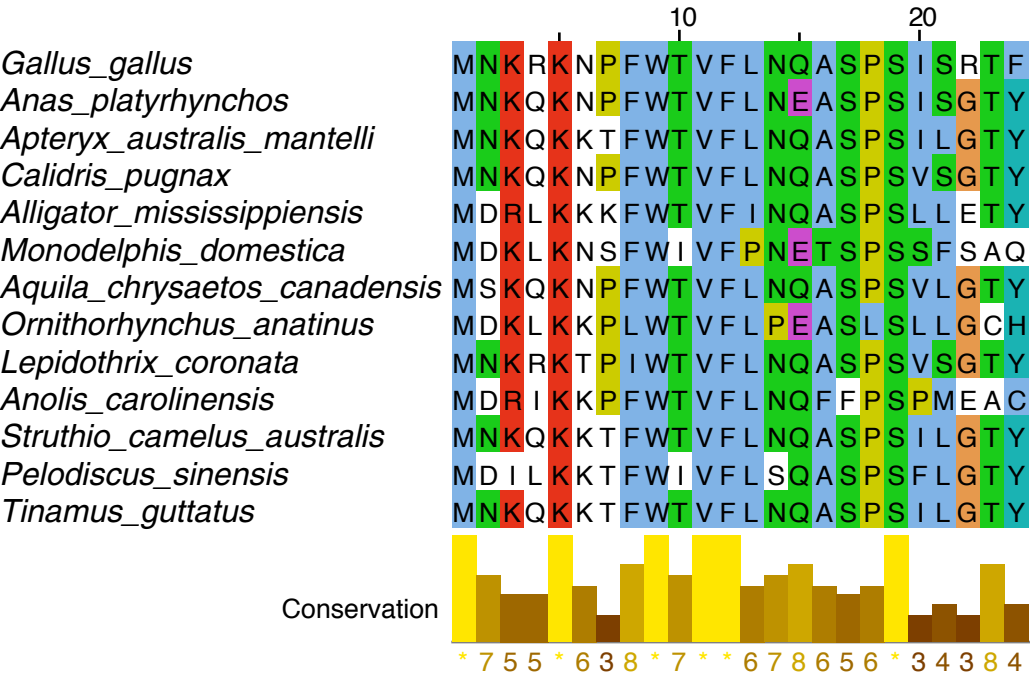
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ENSGALG00000006949 (CHD2)

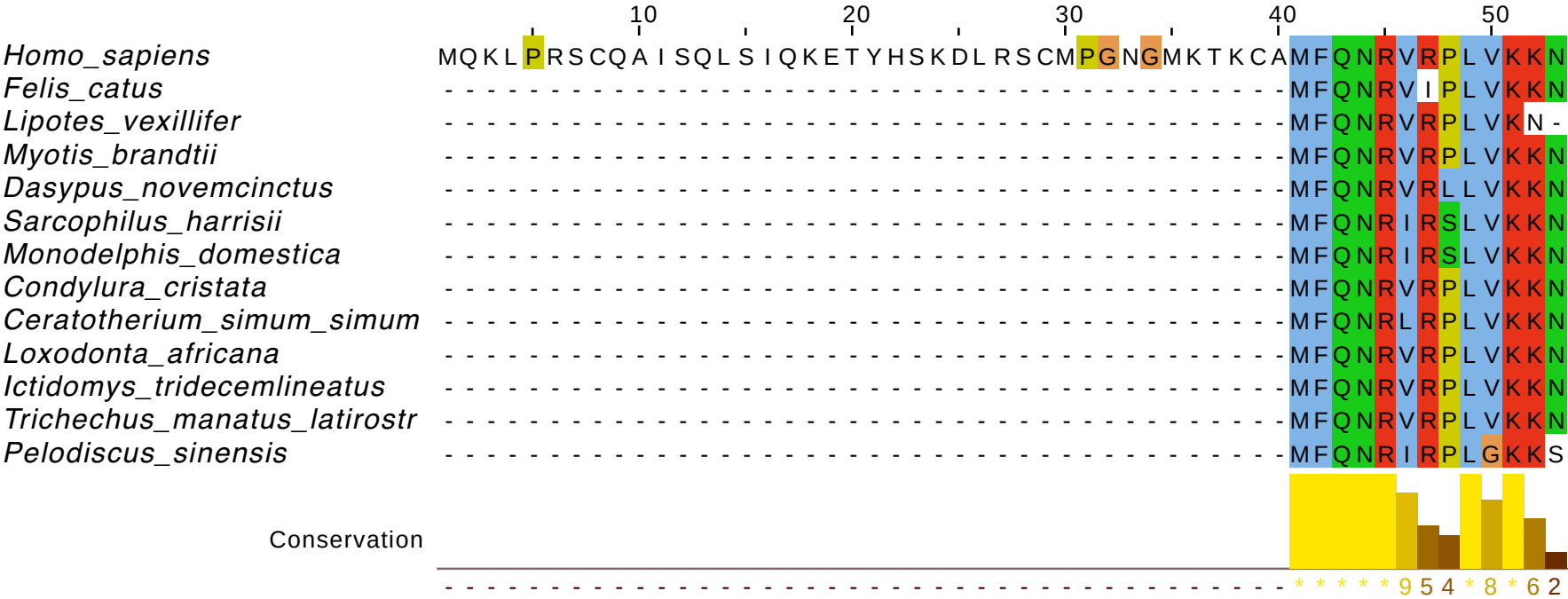


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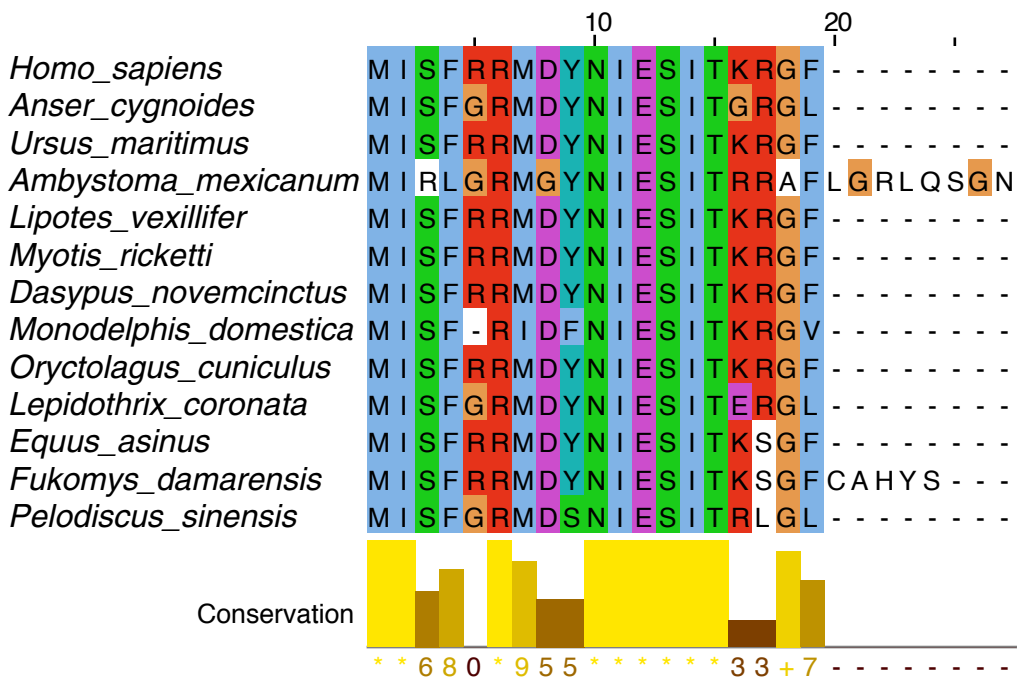


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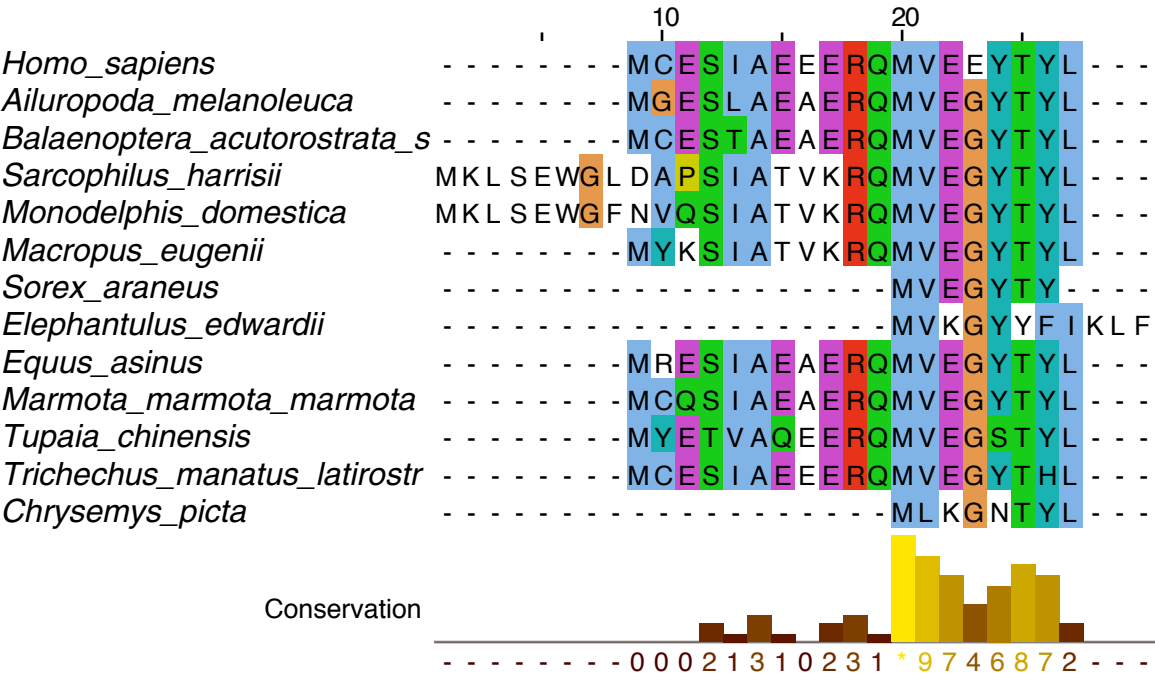
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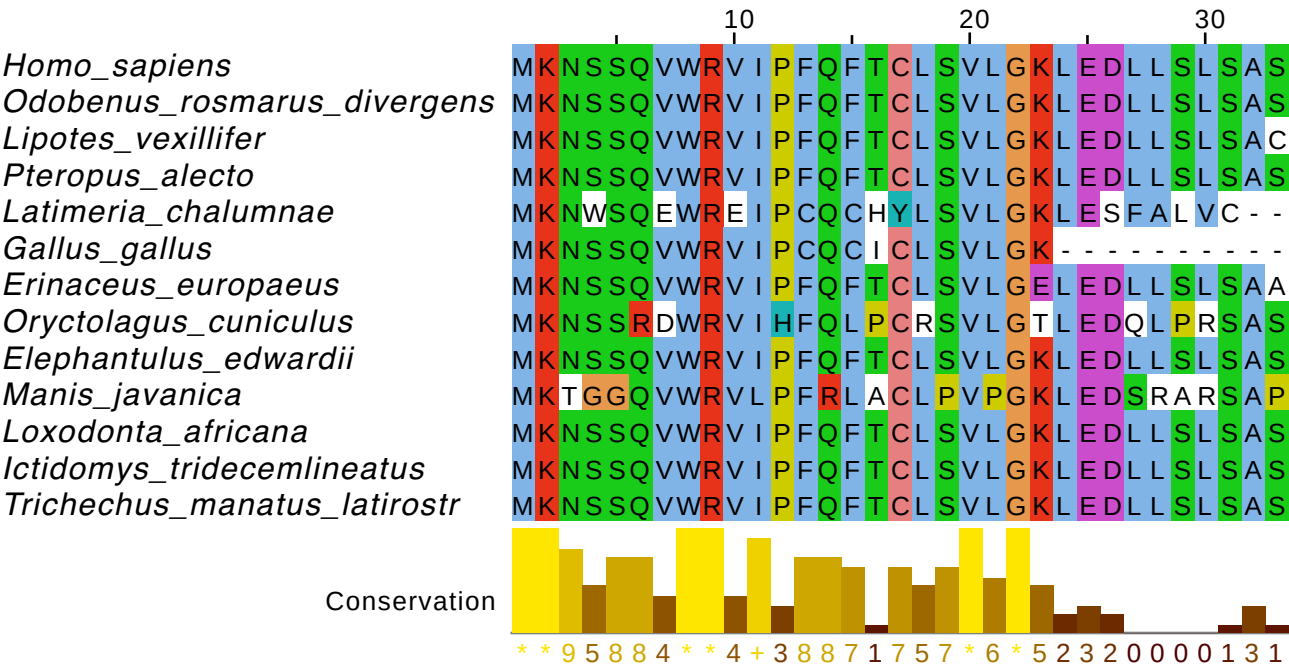
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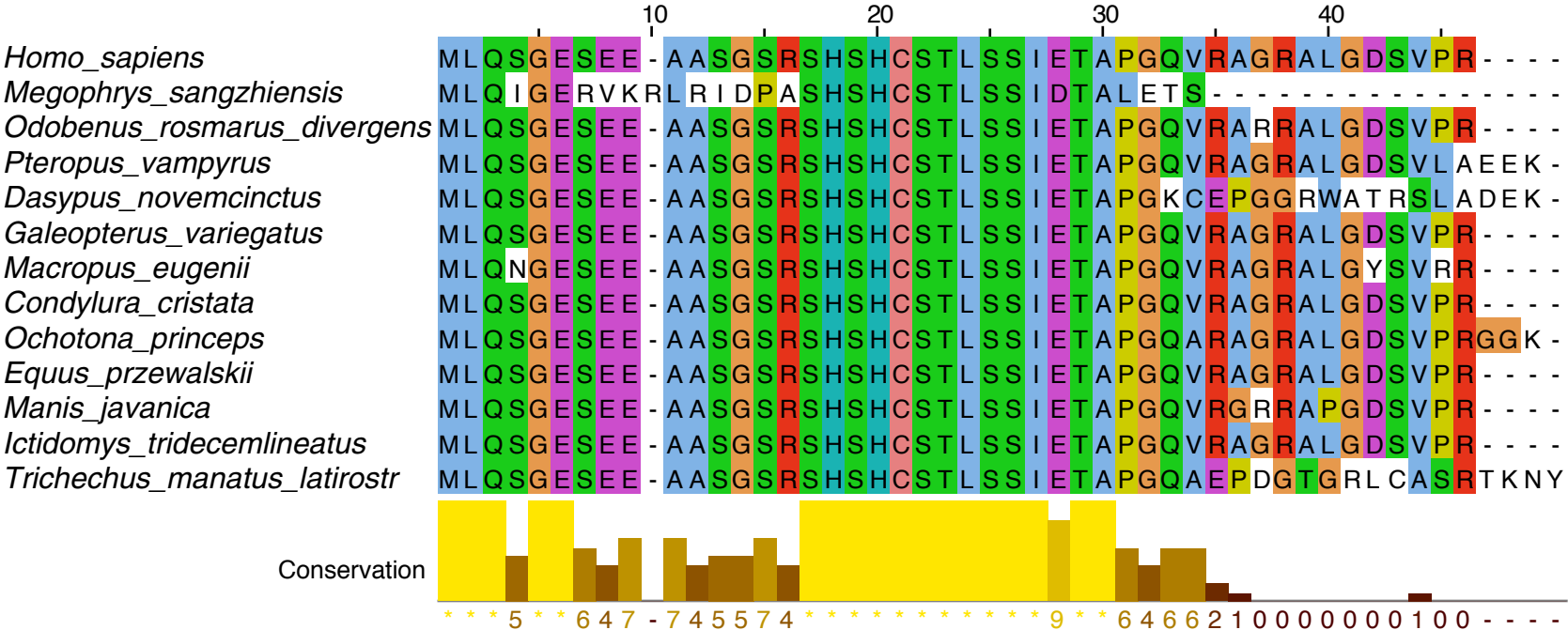
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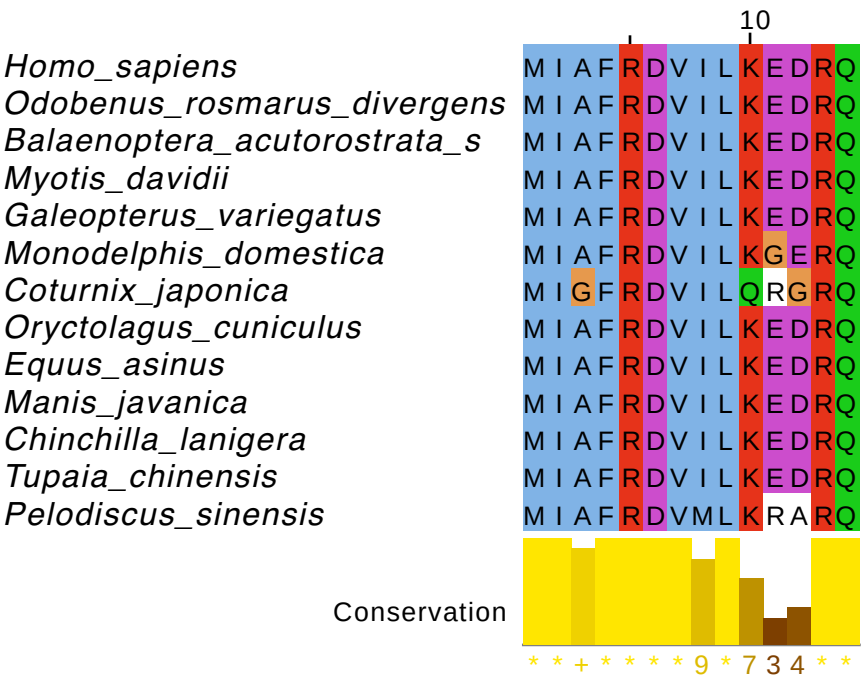
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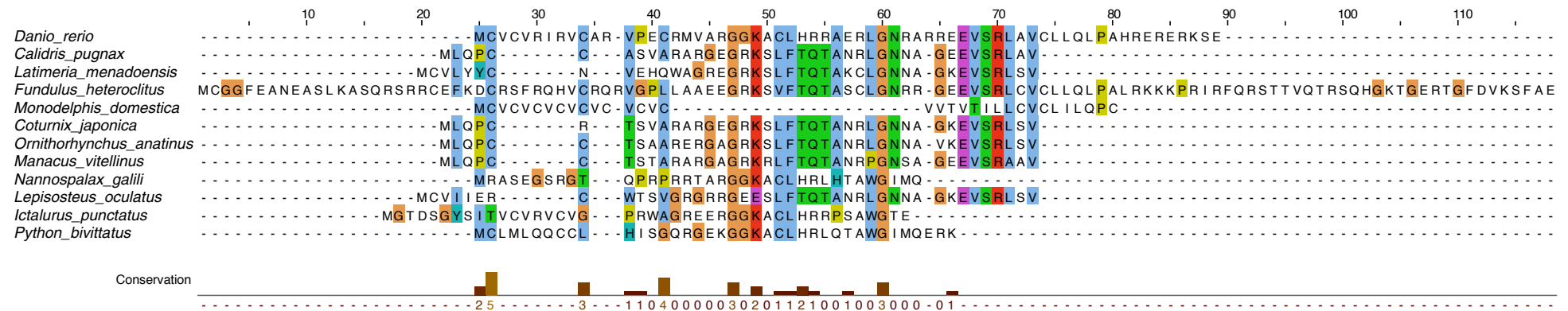


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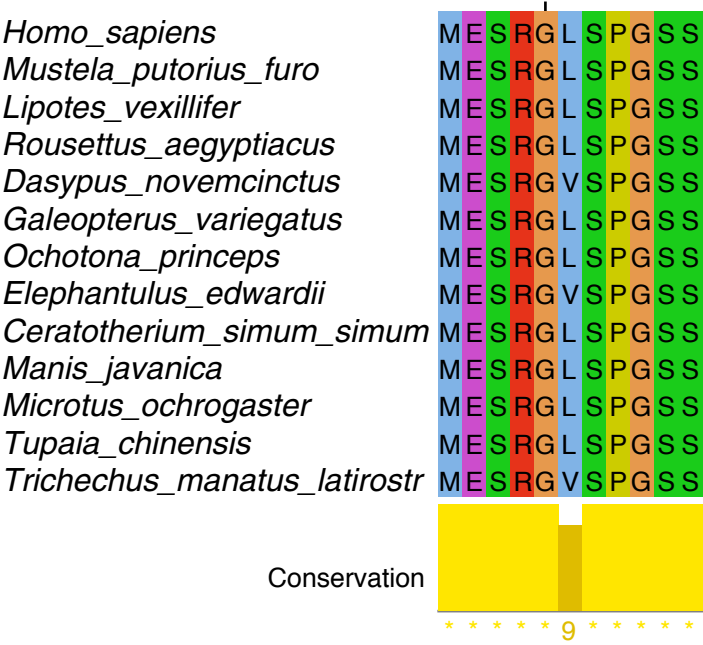


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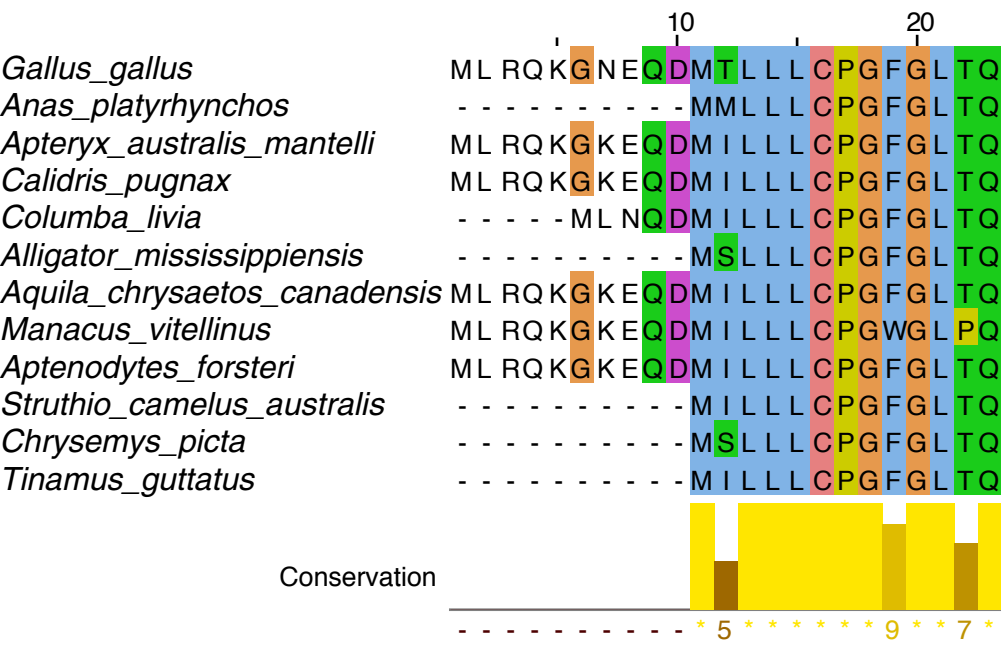
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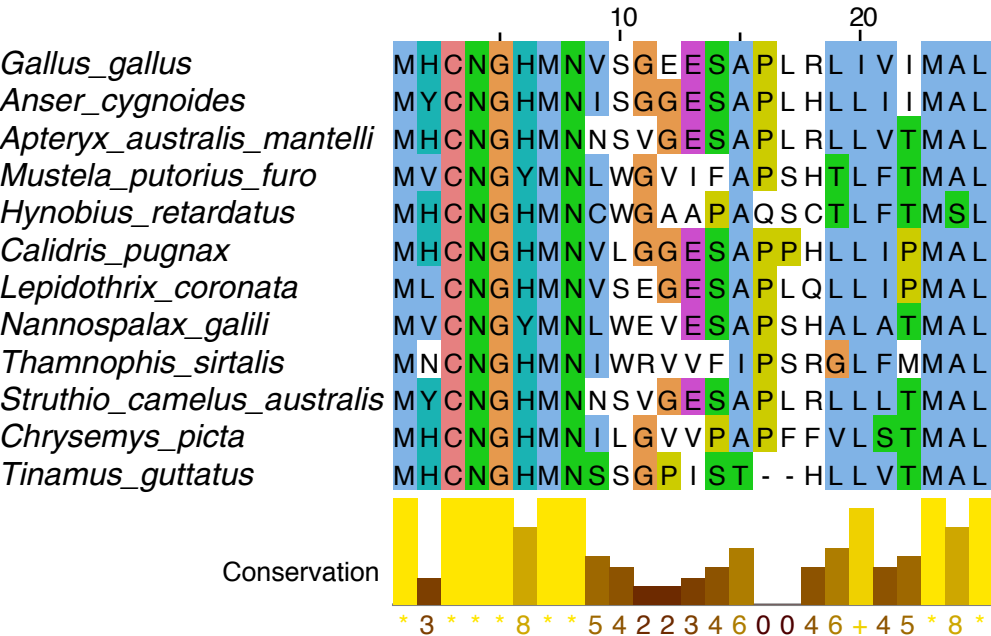
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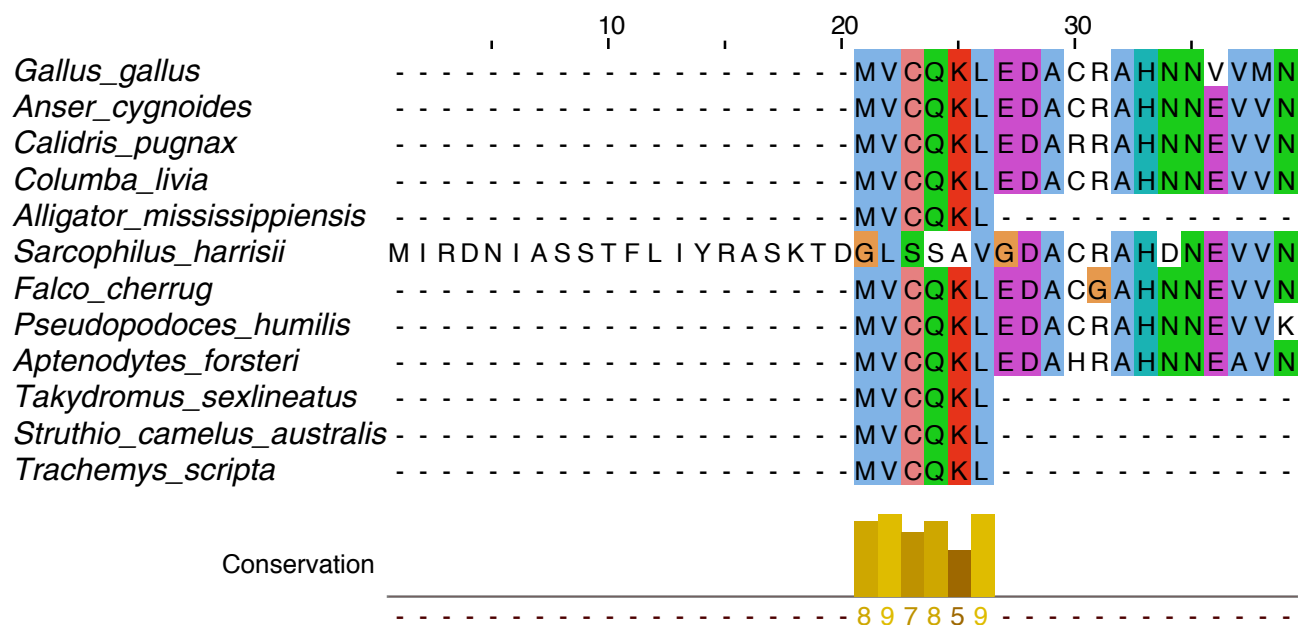
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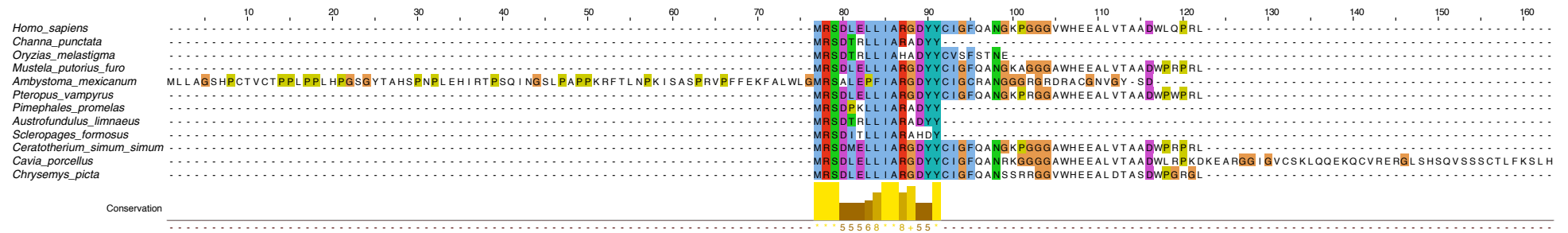


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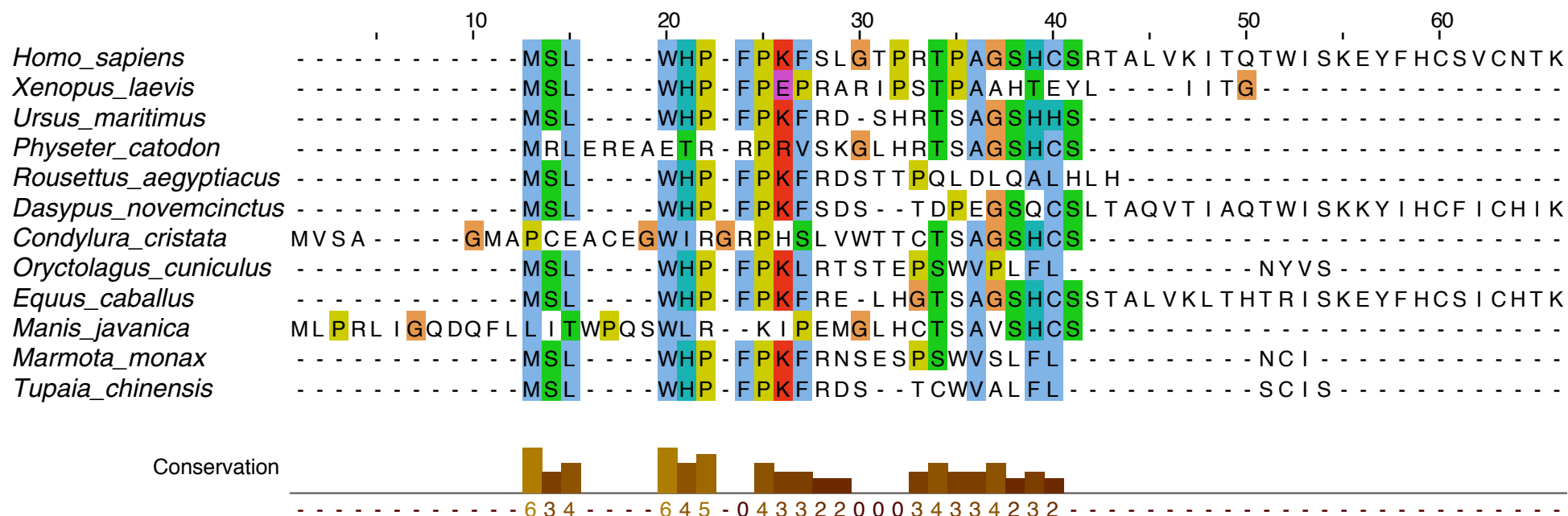
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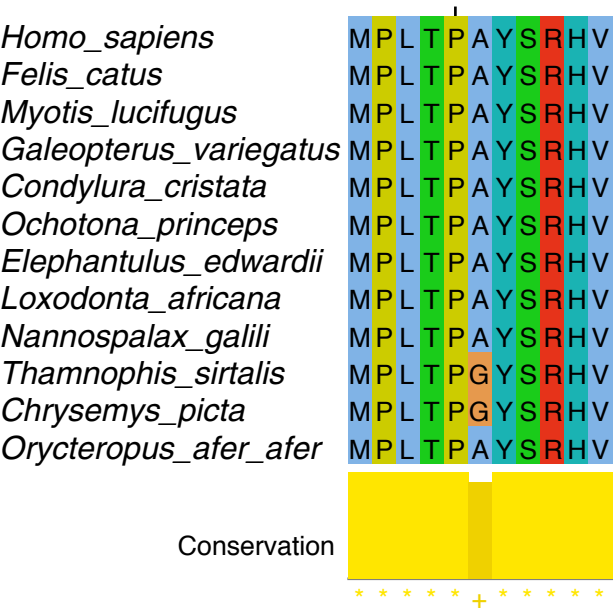


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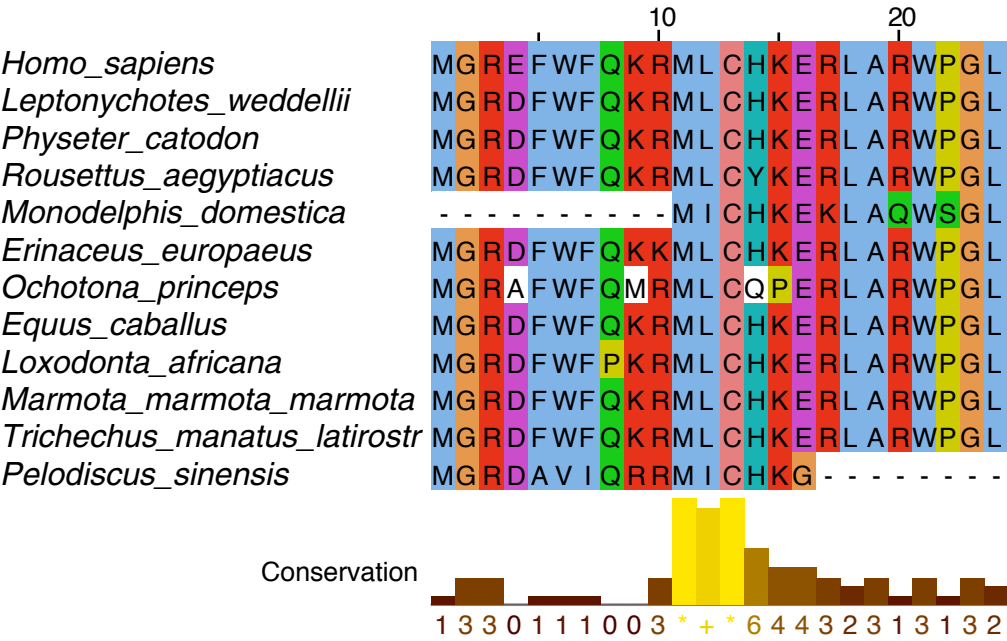
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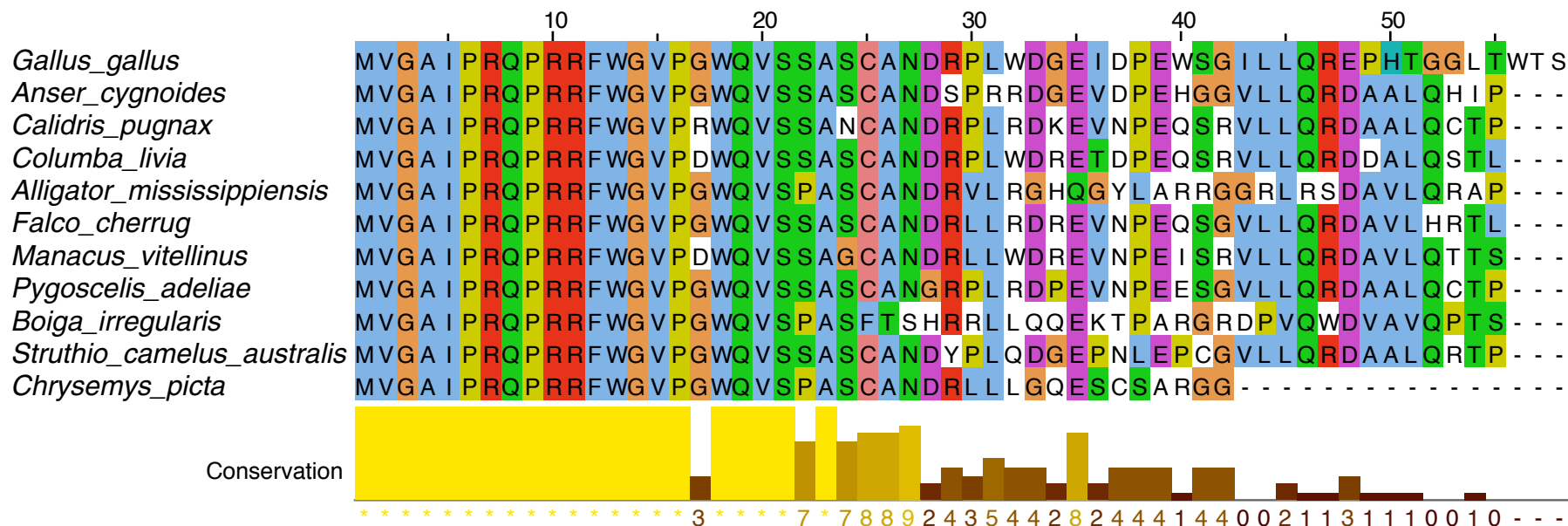
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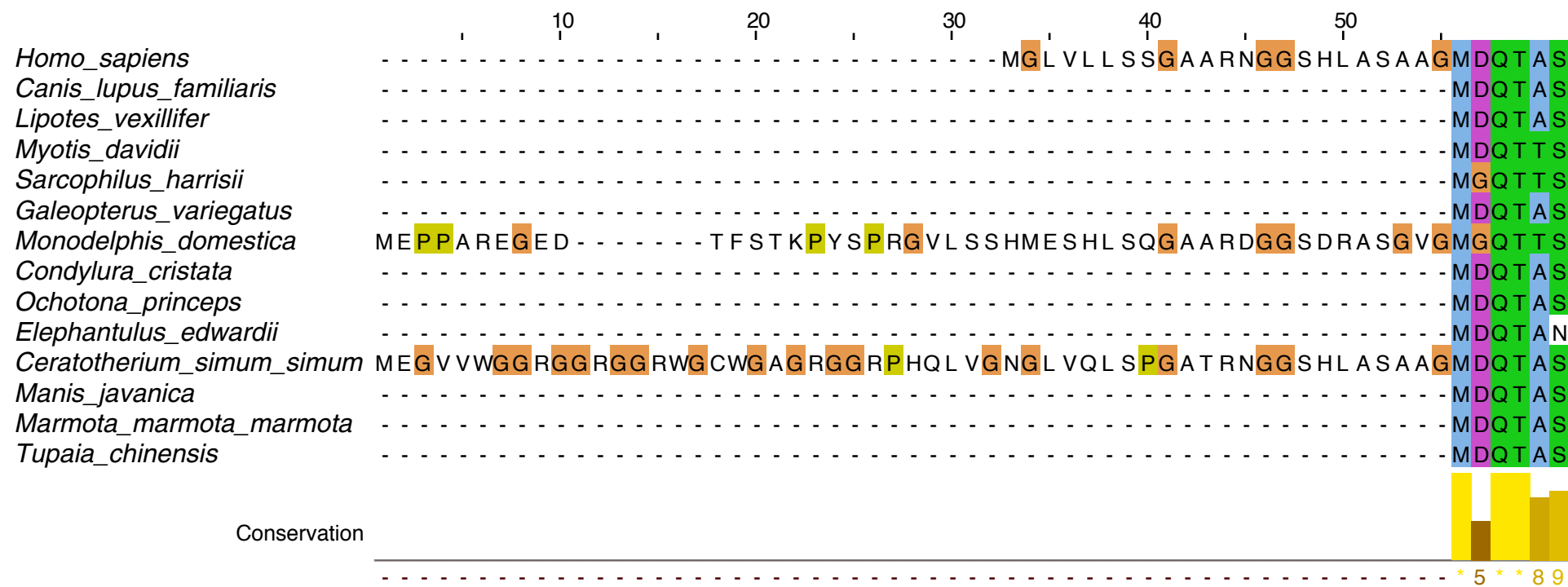


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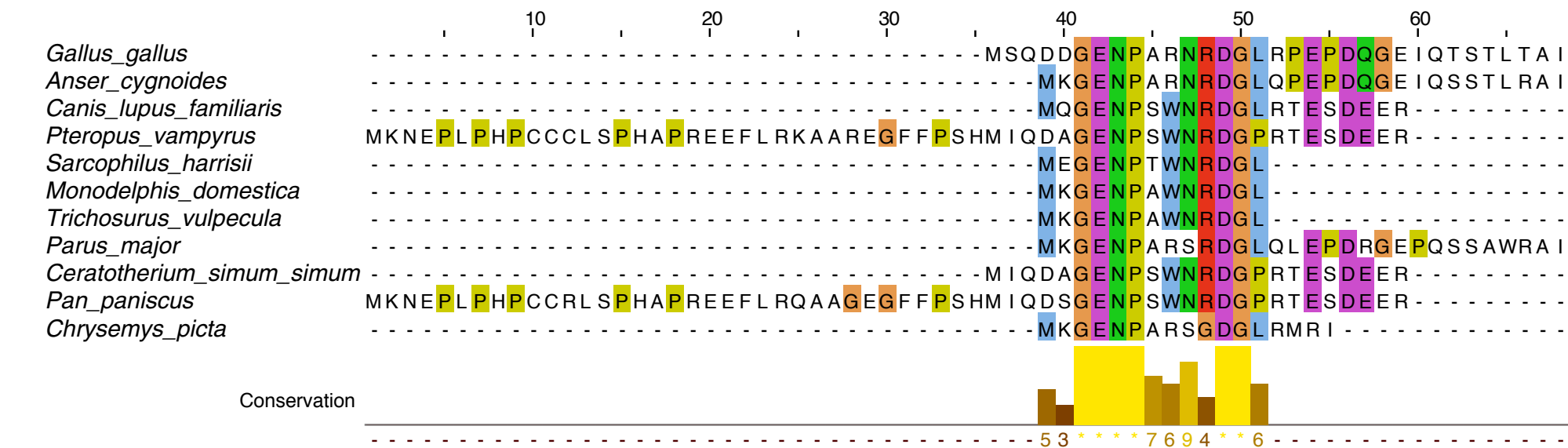


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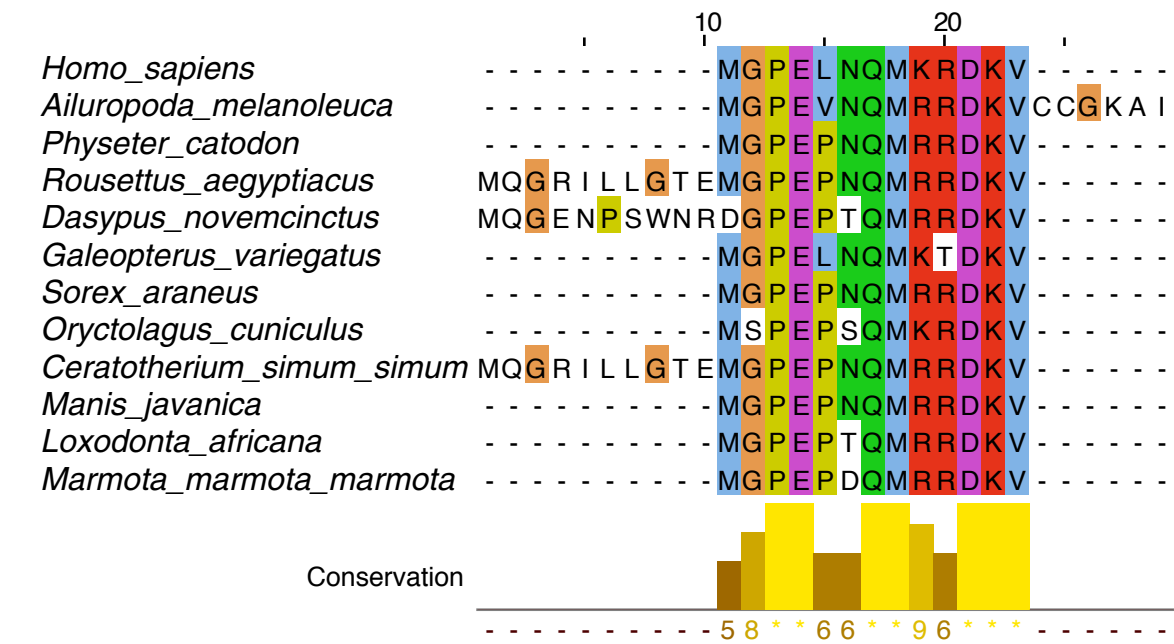
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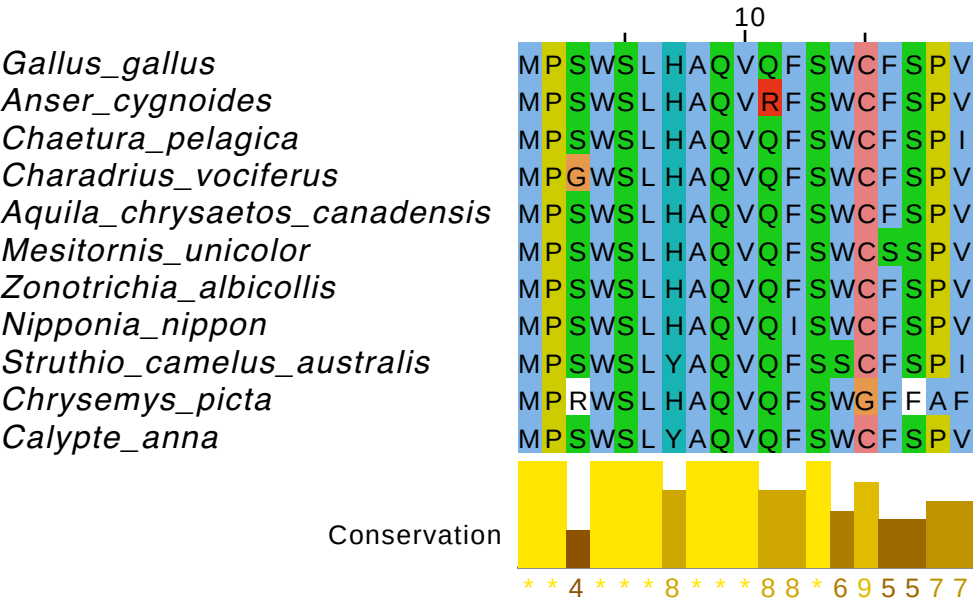
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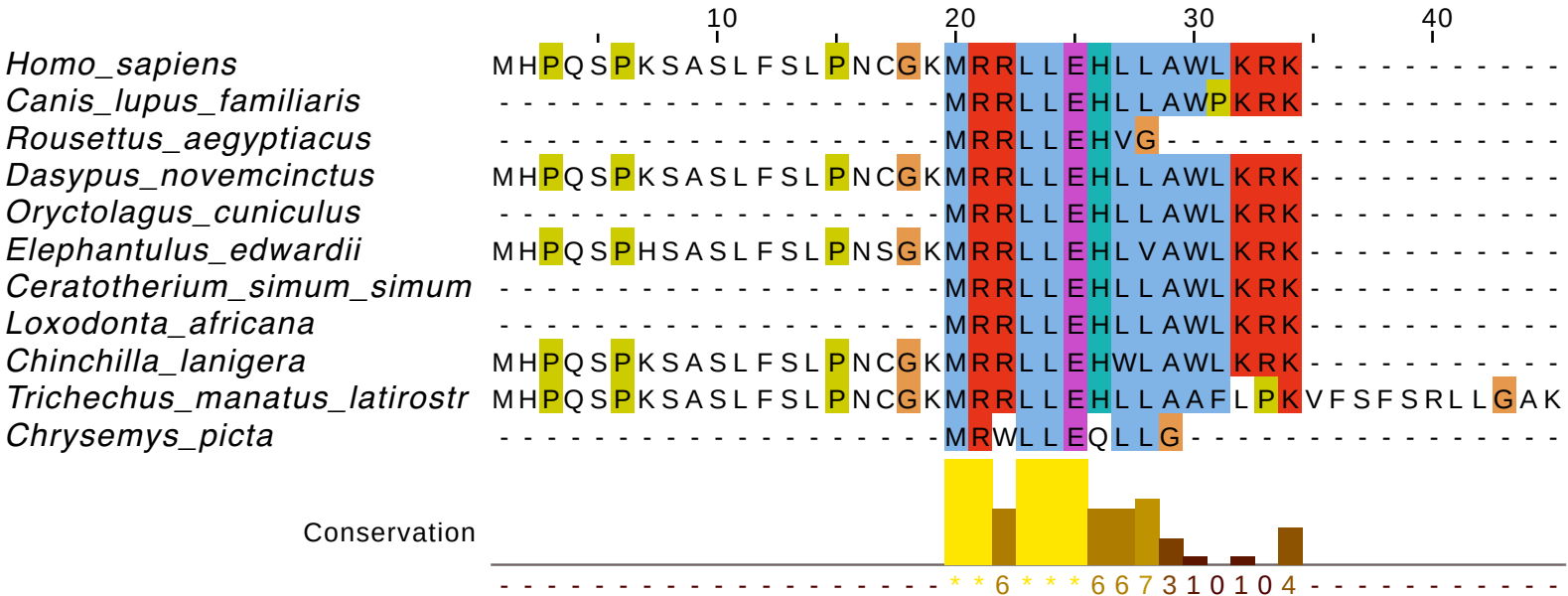


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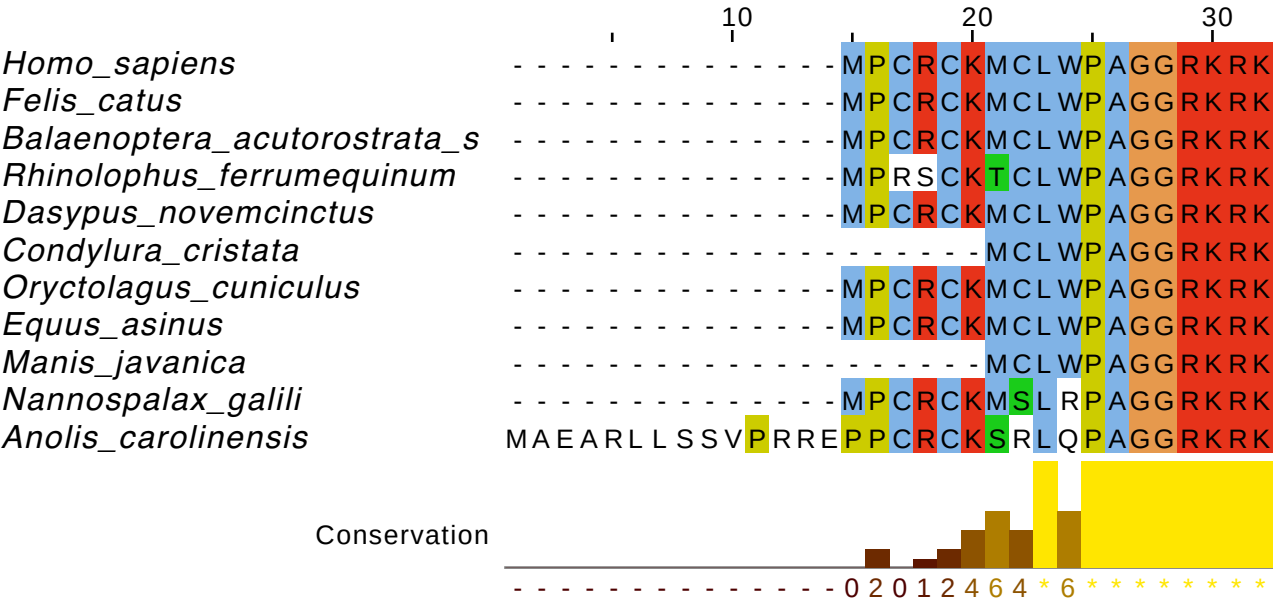


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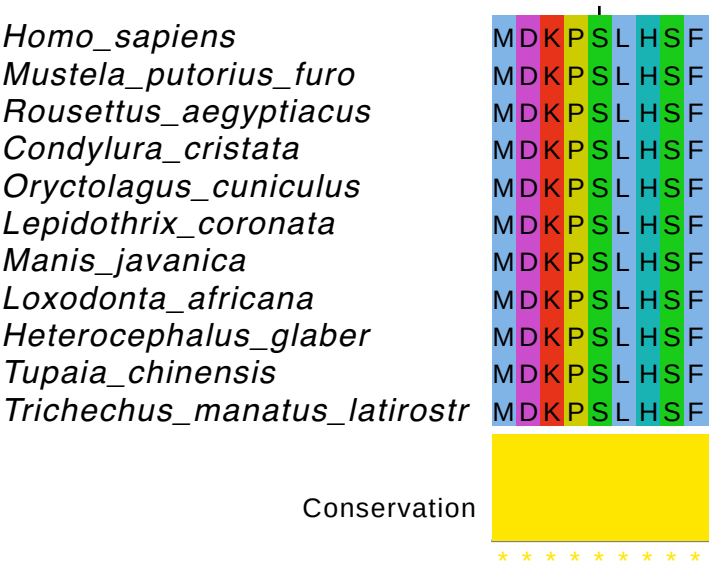
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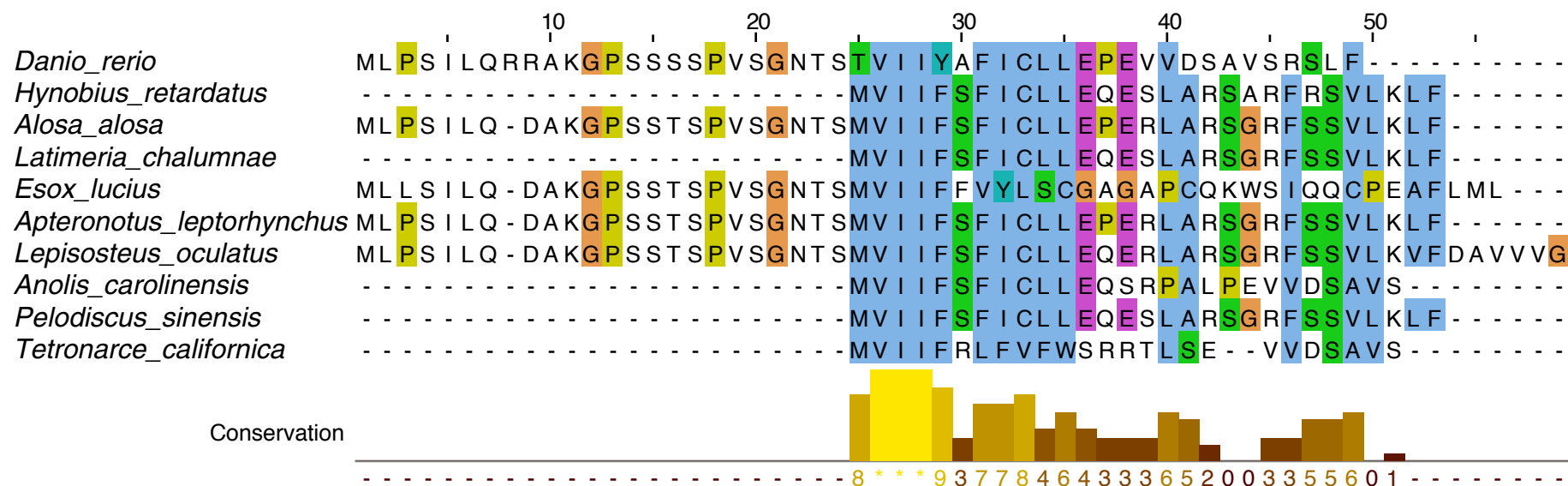
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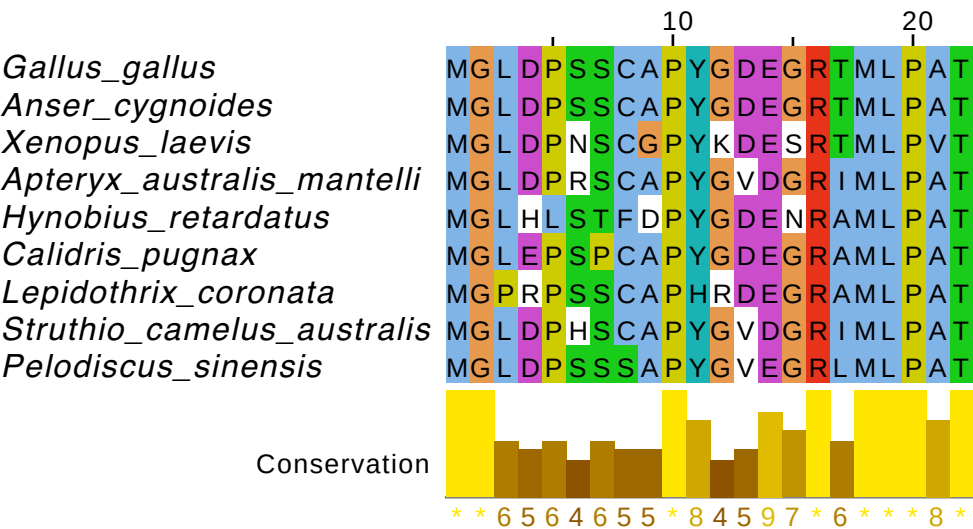
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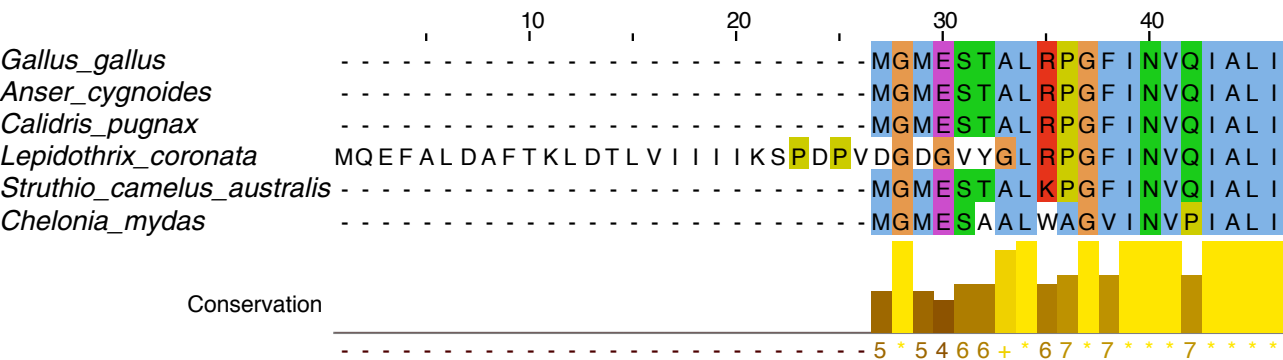
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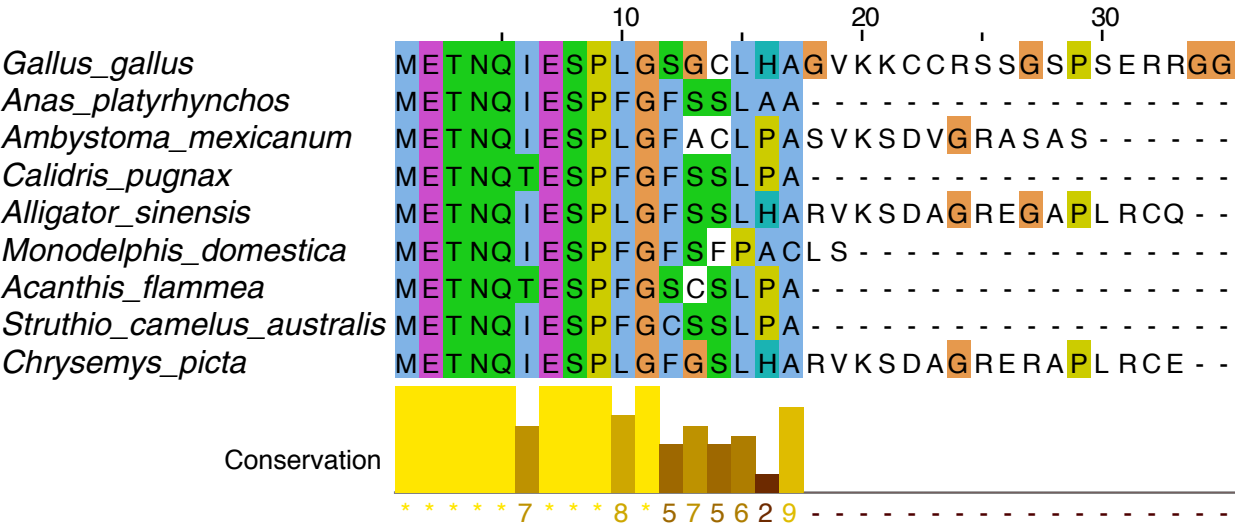
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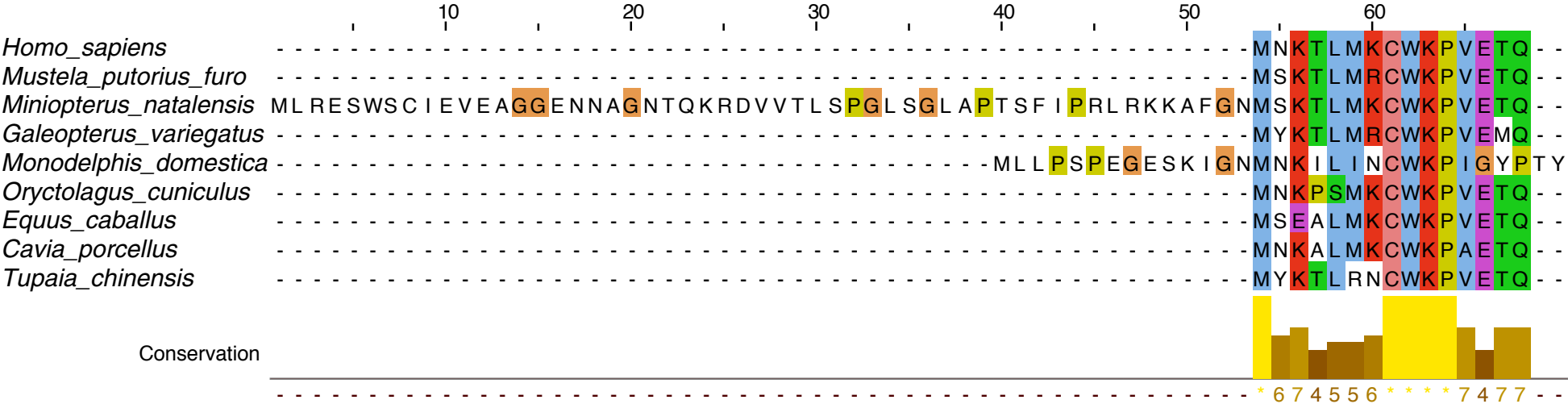
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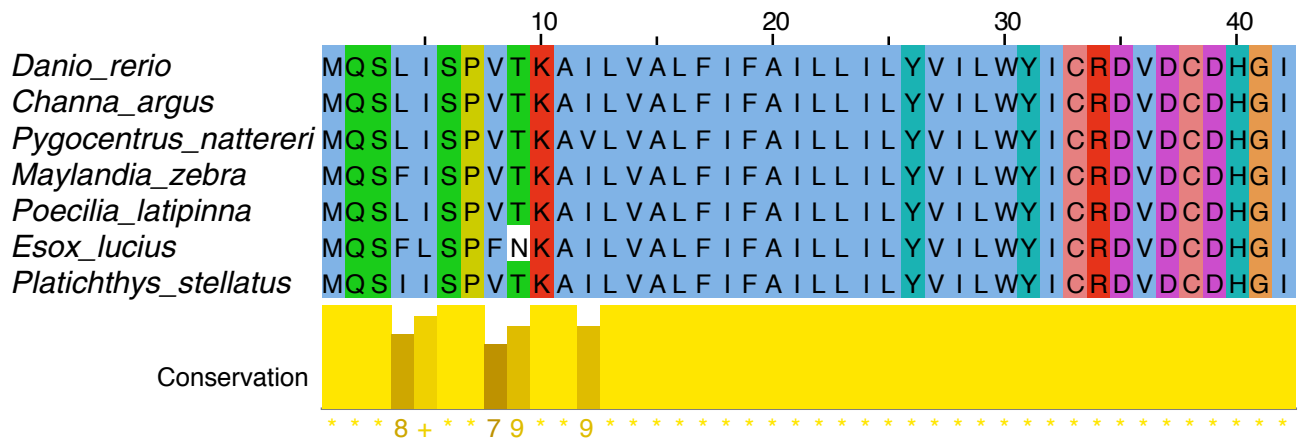
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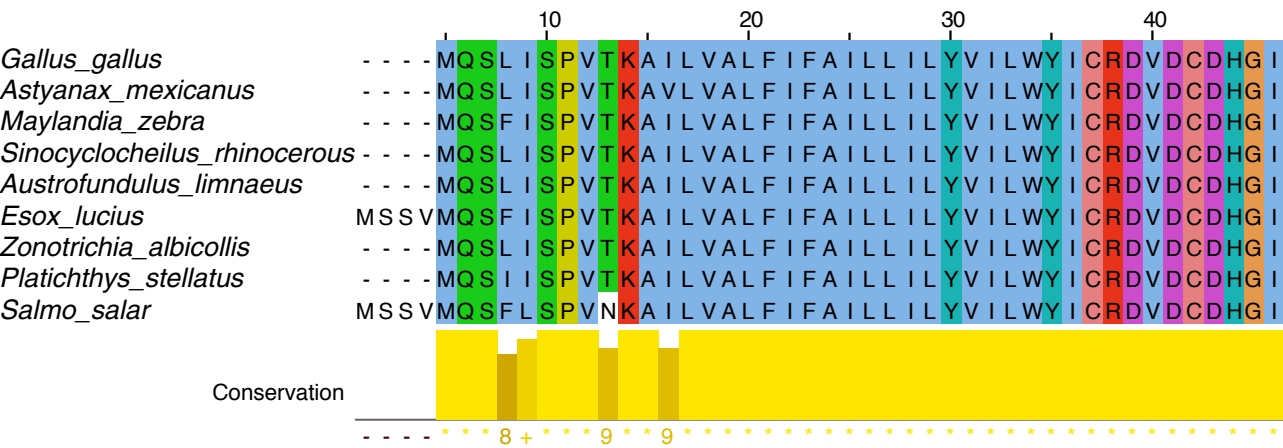
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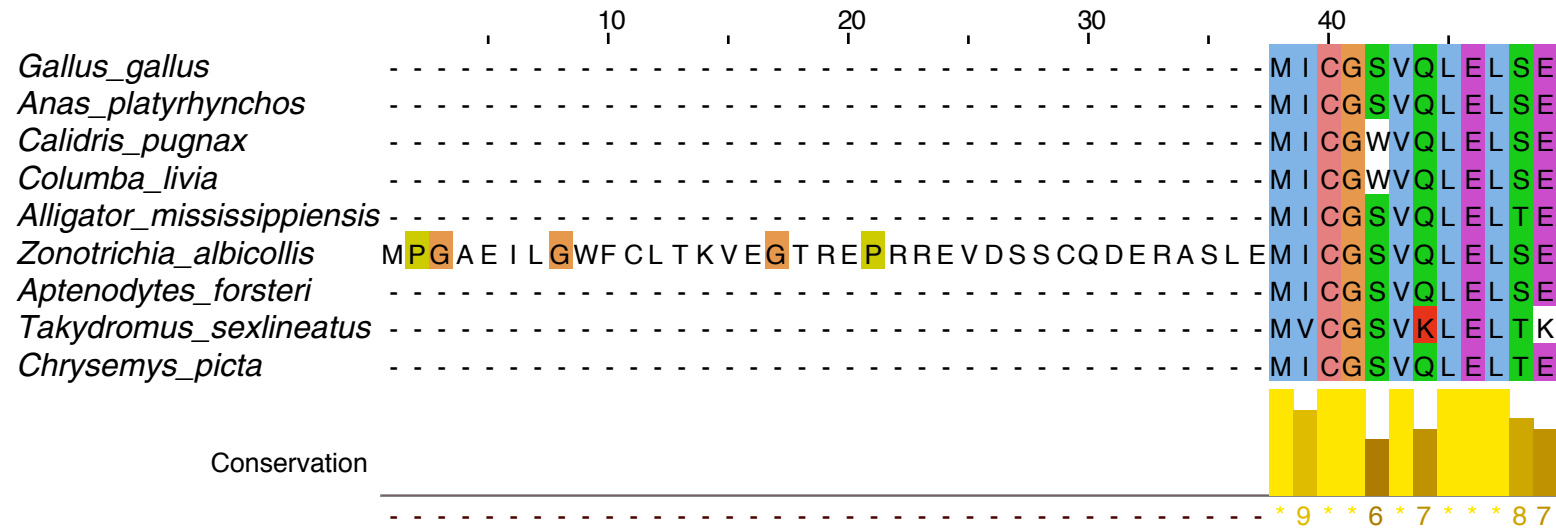


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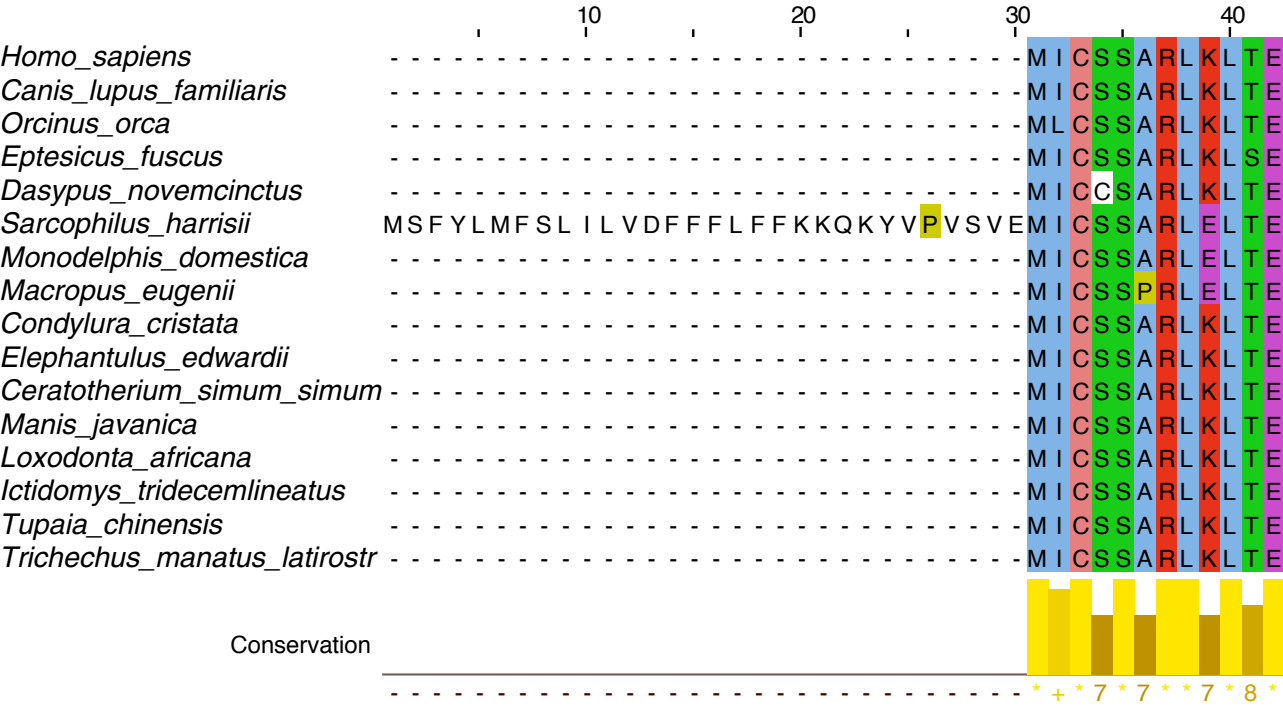


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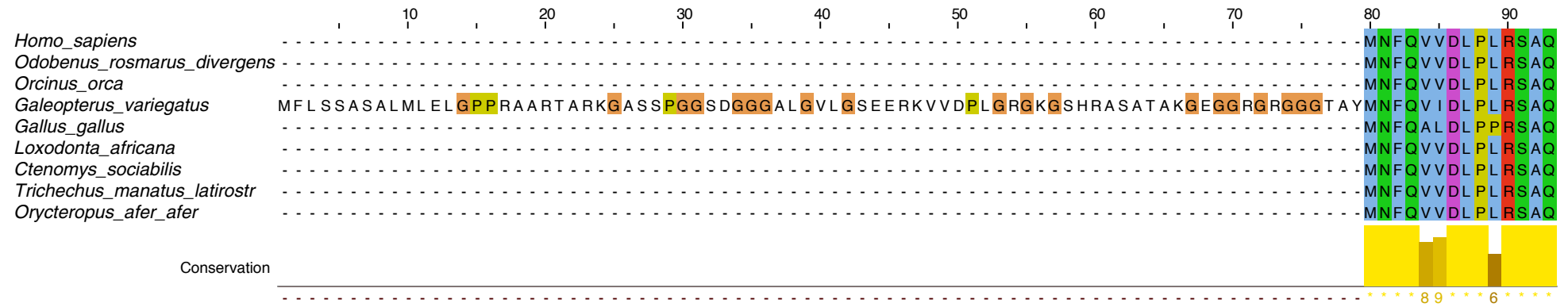
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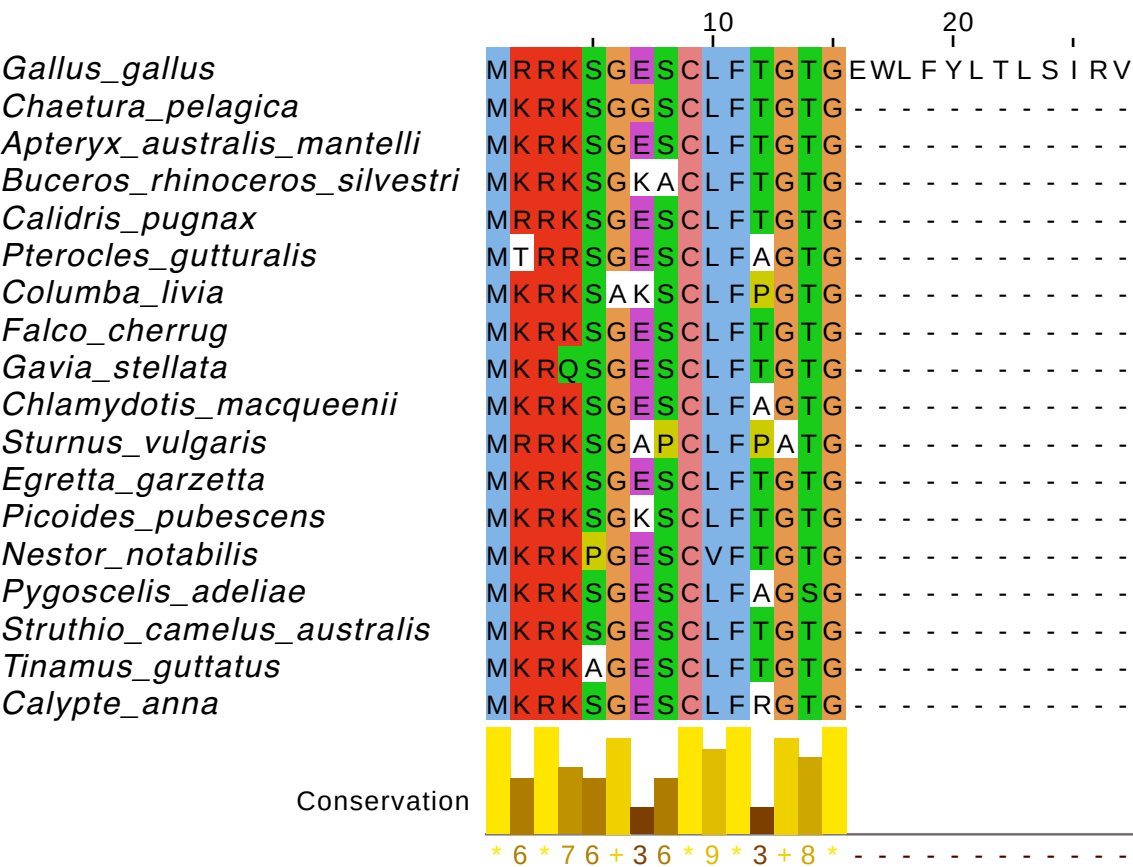
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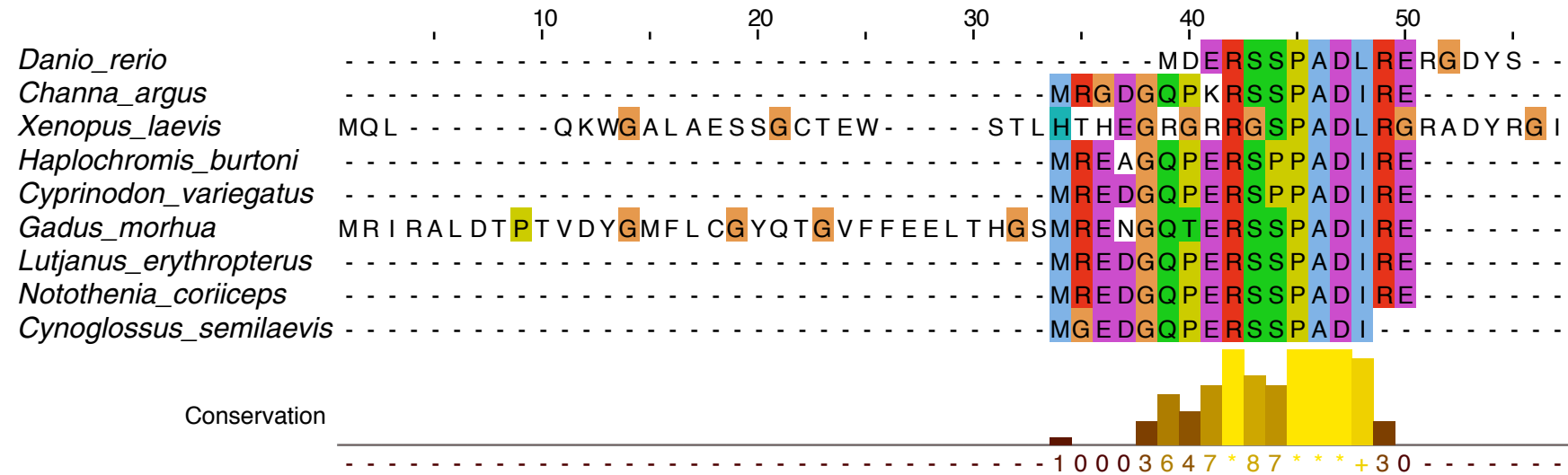
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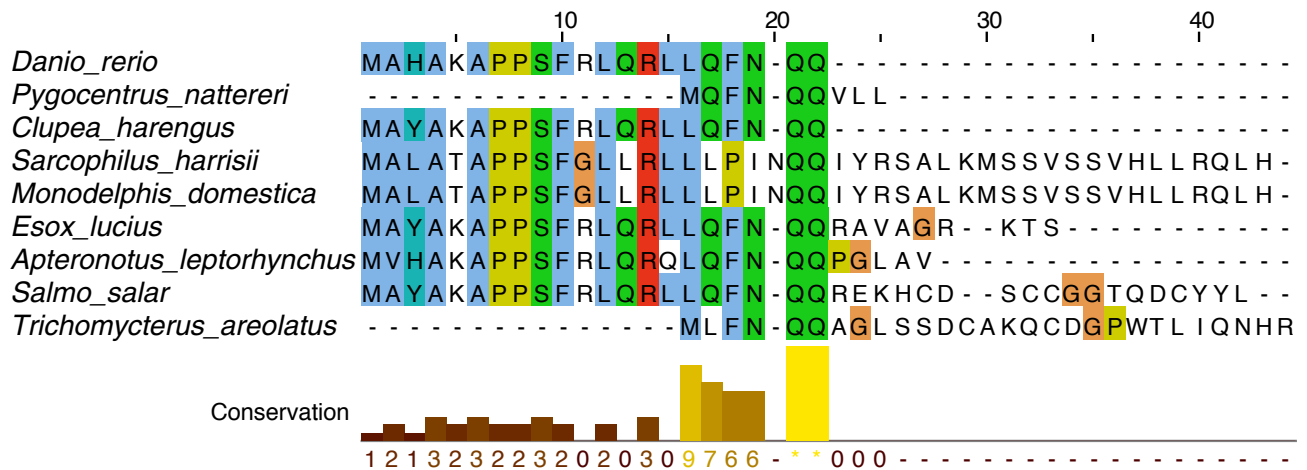
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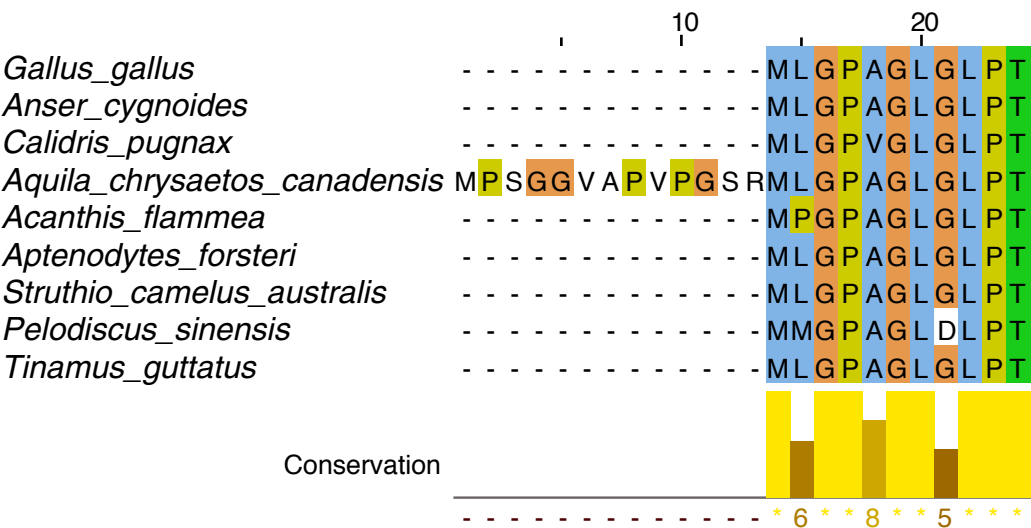
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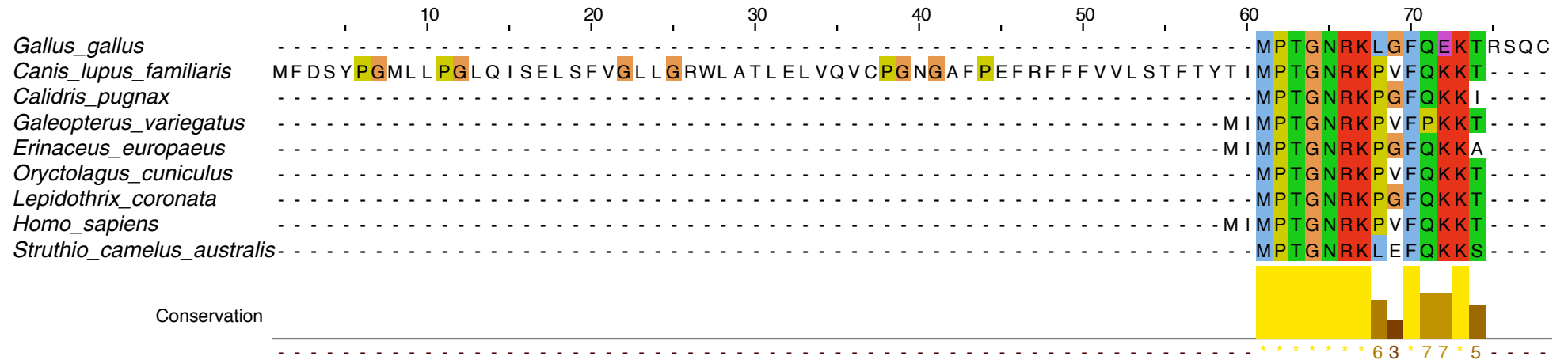
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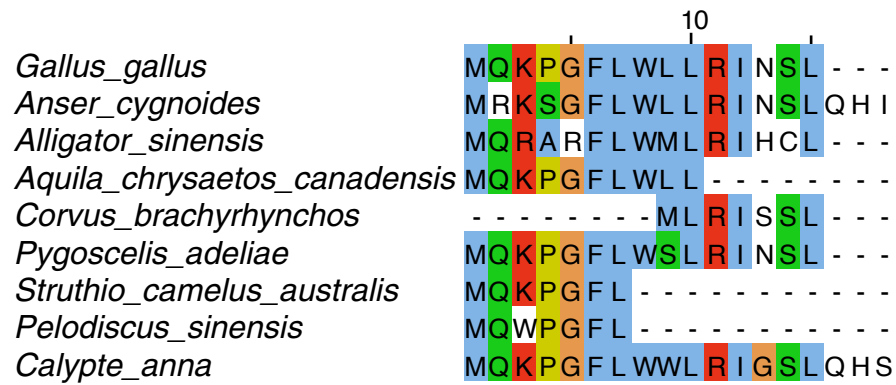
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HG0222

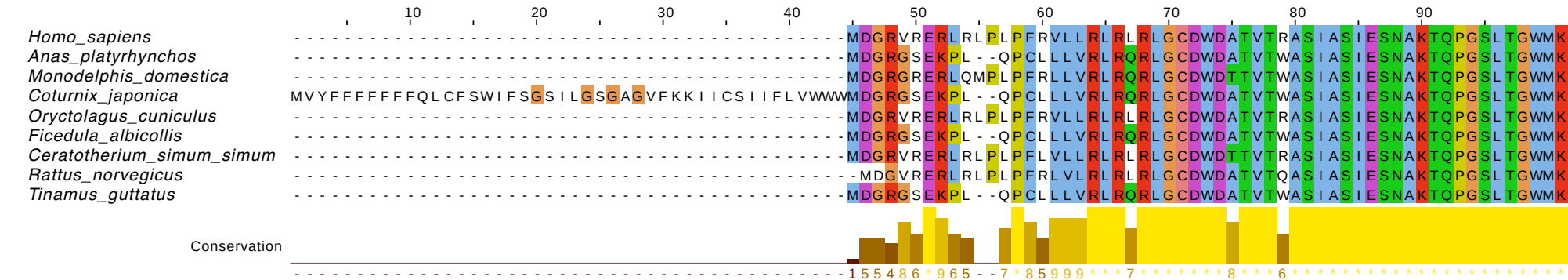
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Conservation

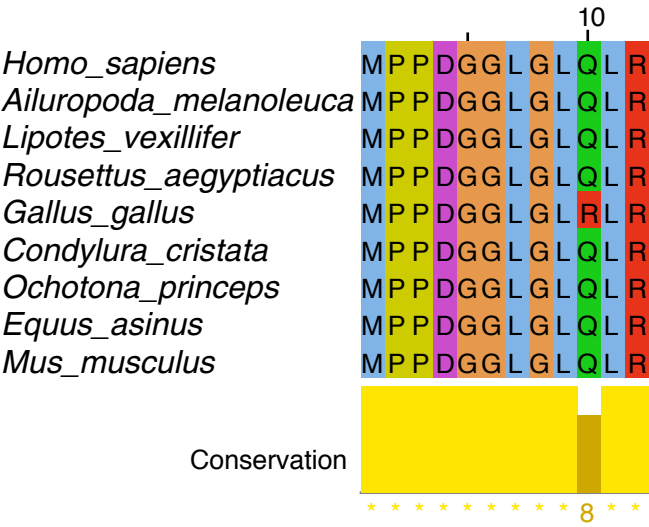


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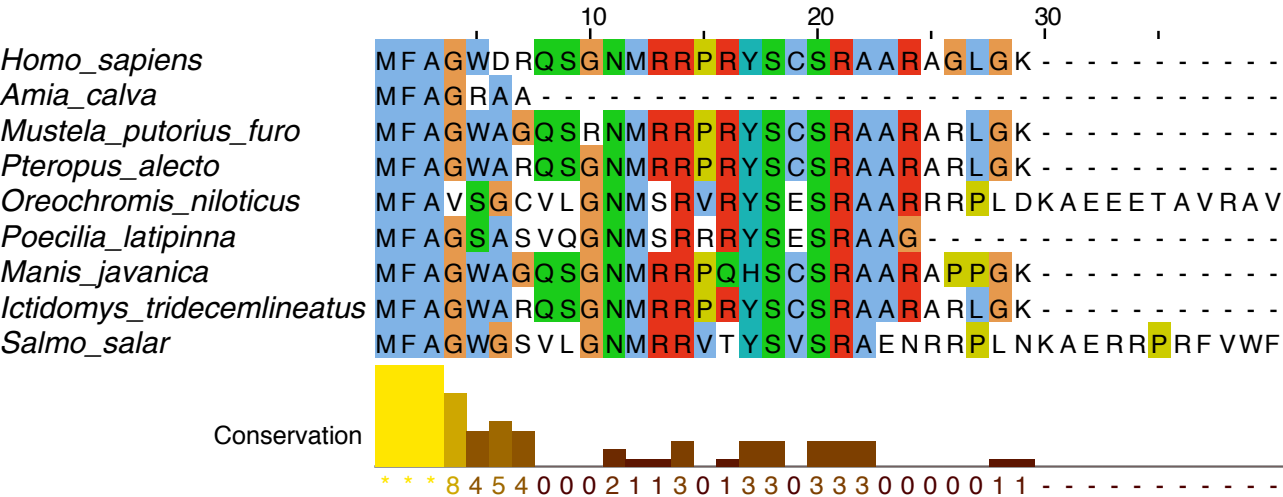
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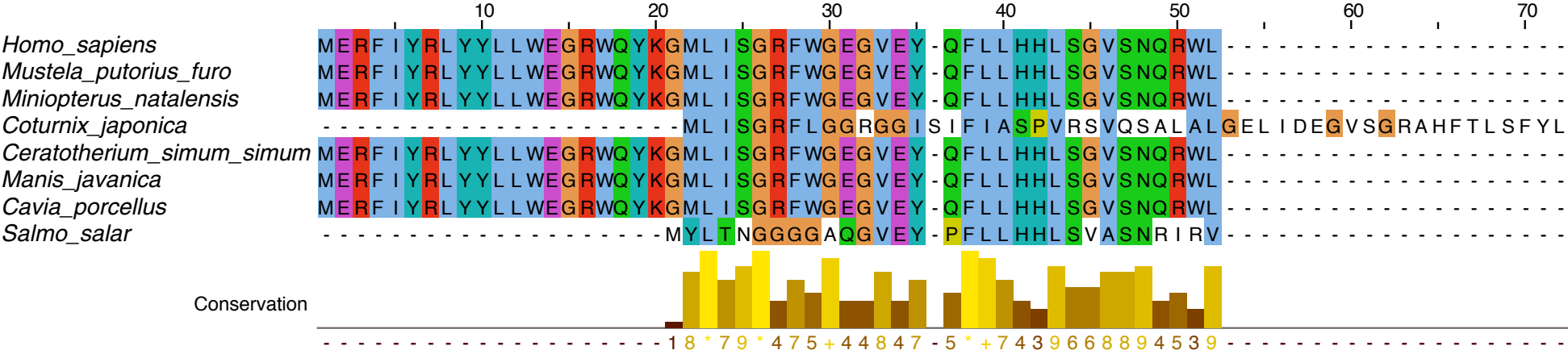
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HG0226.1

ENSG00000180592



ENSG00000180592

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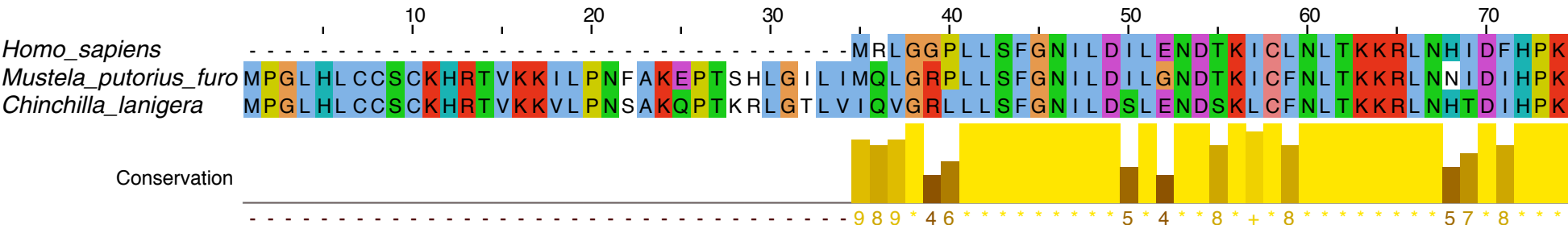
Conservation

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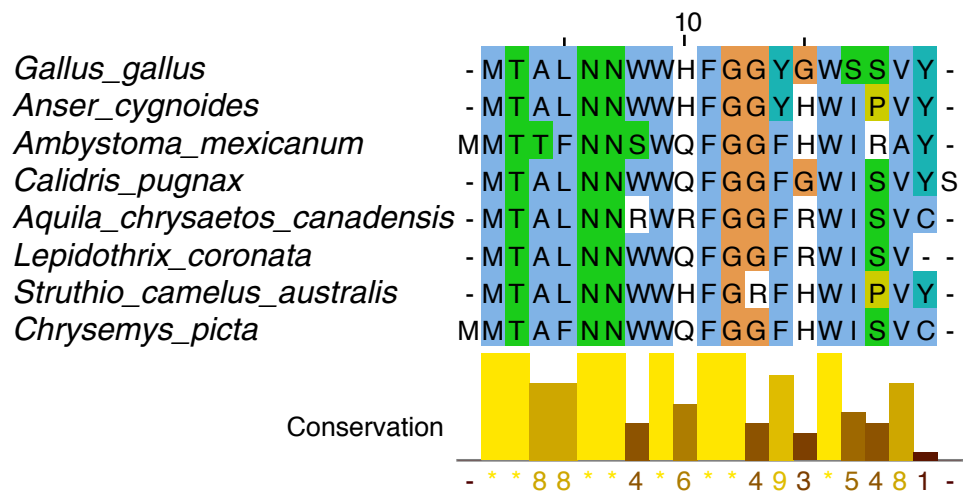
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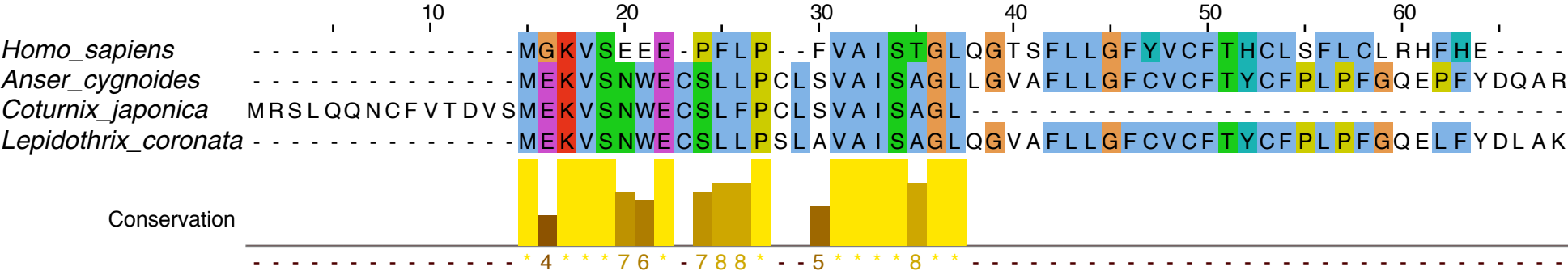
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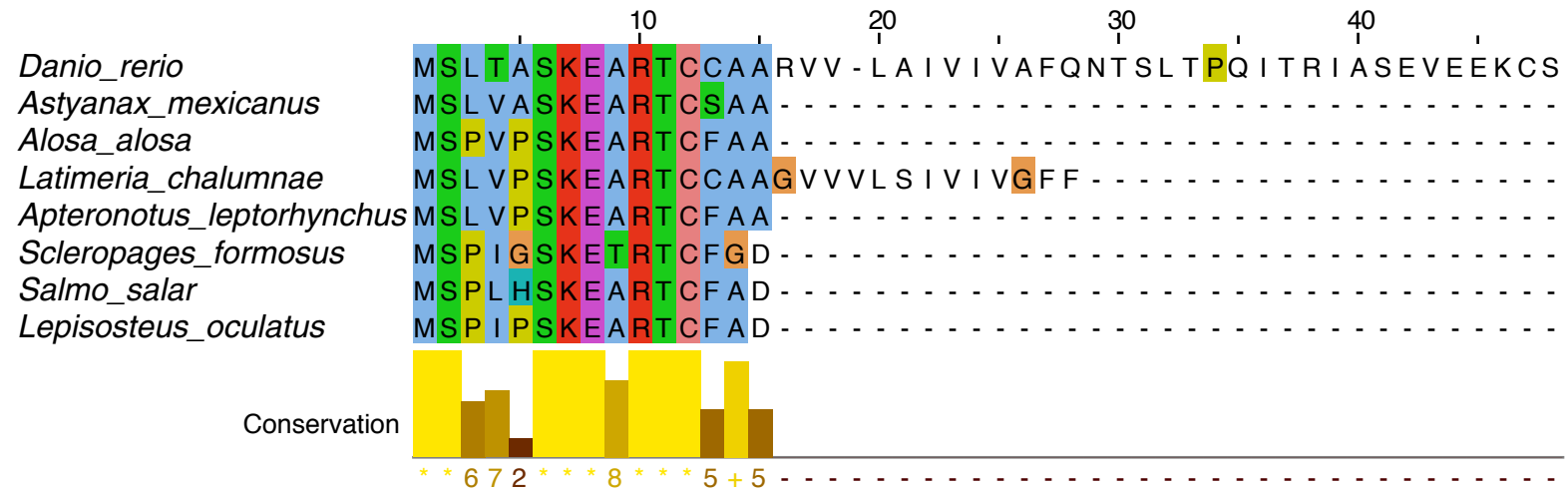
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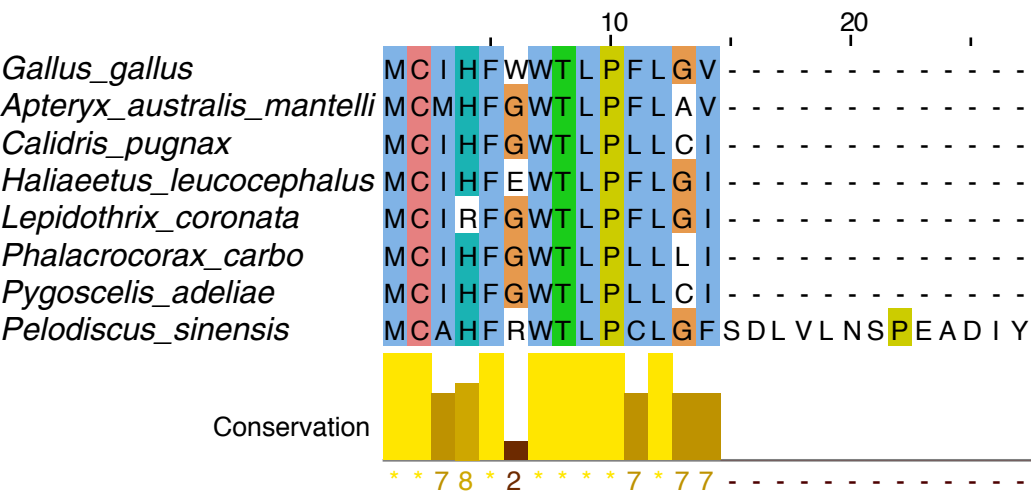
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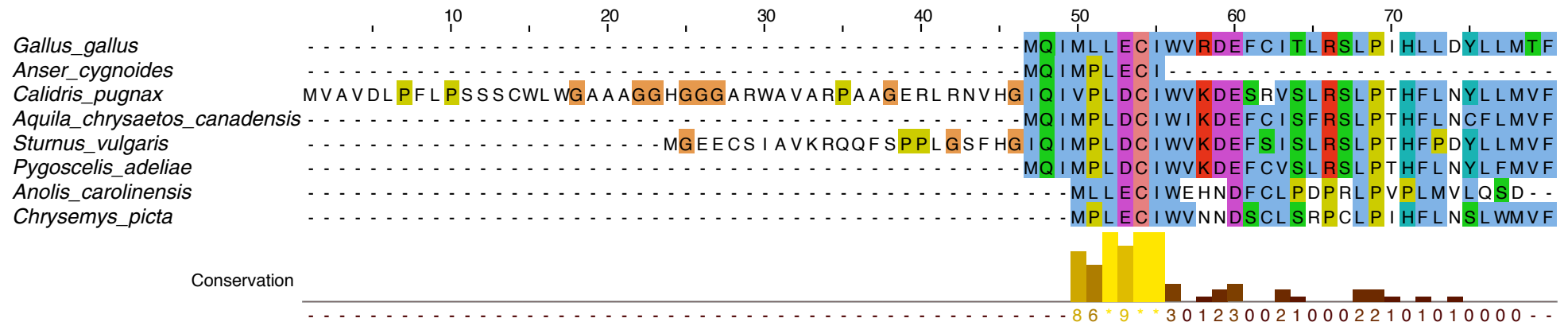


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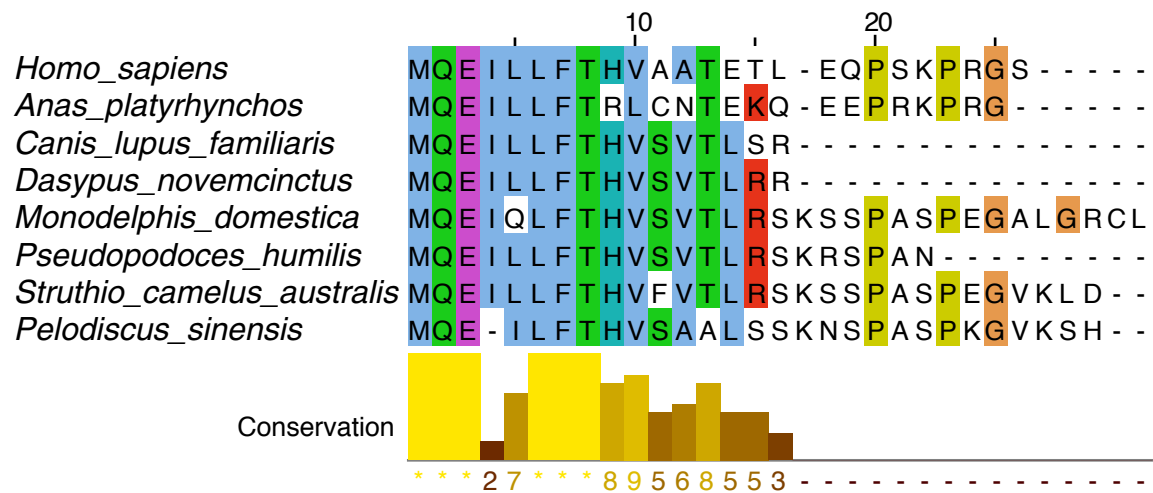


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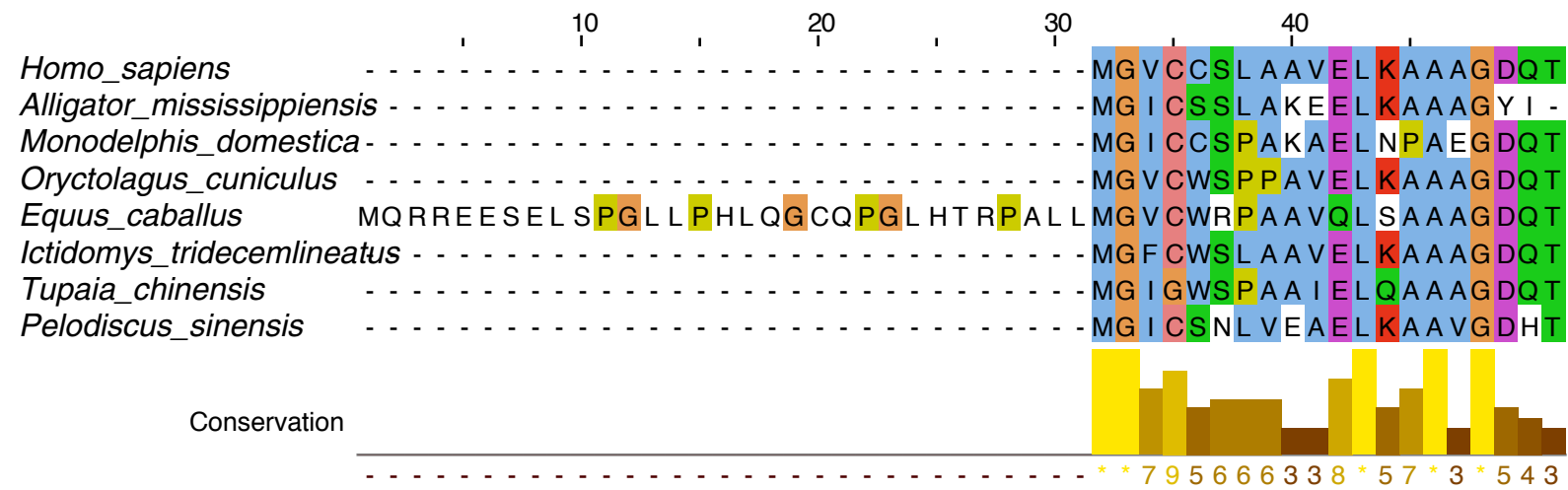


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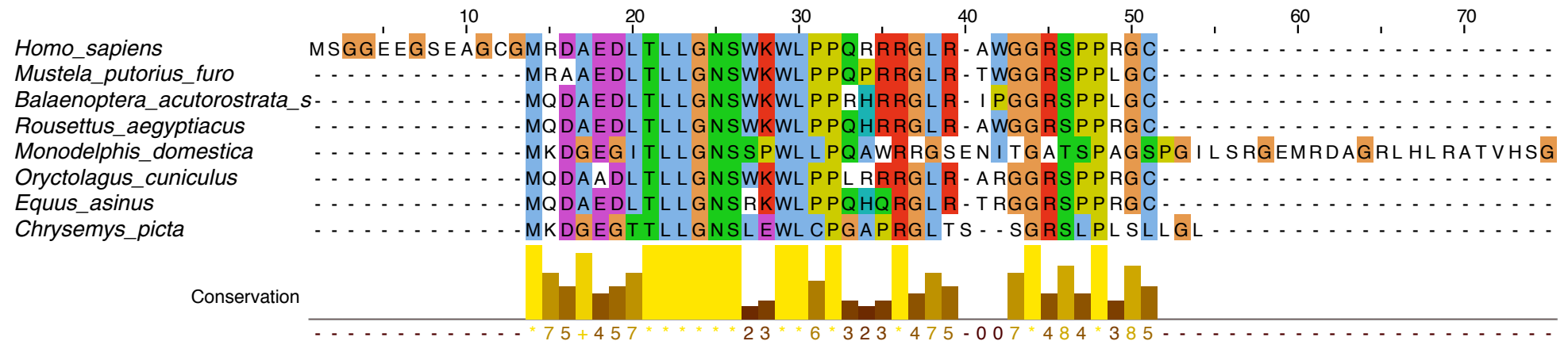
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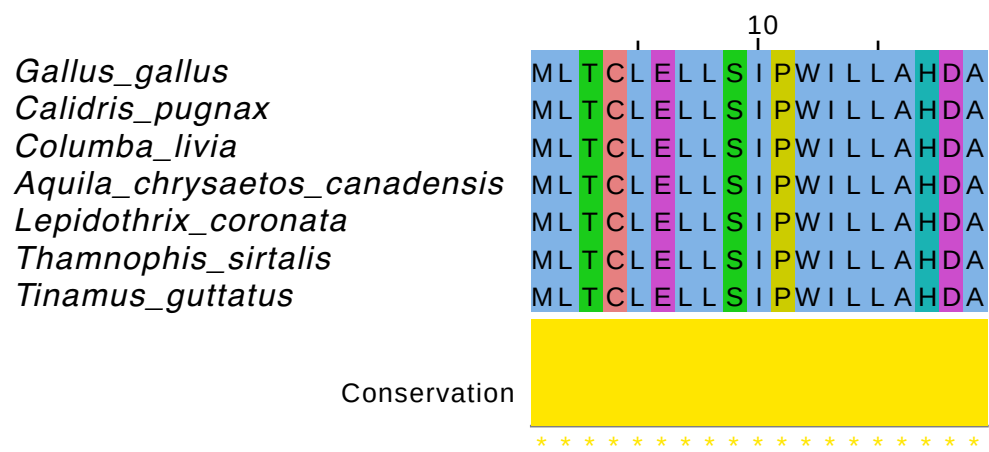


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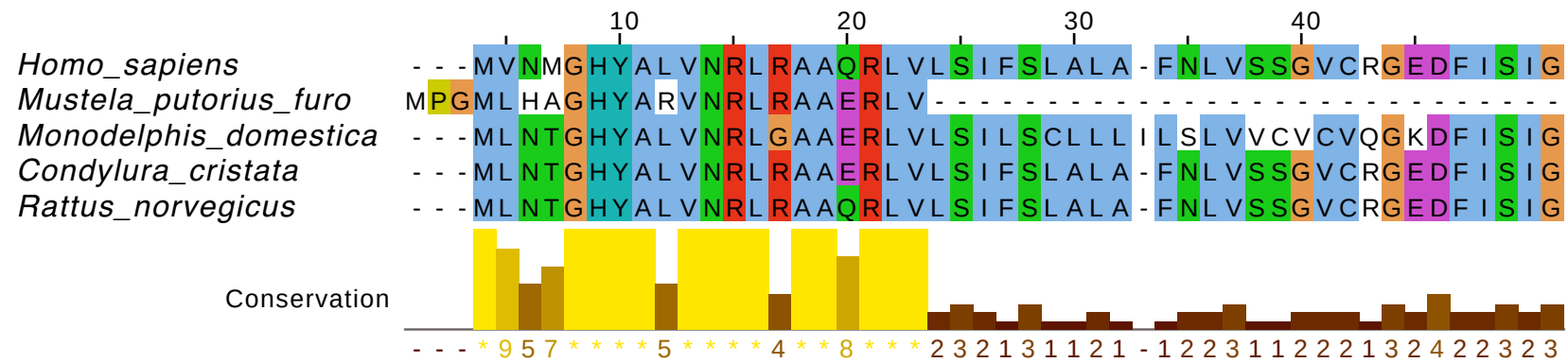


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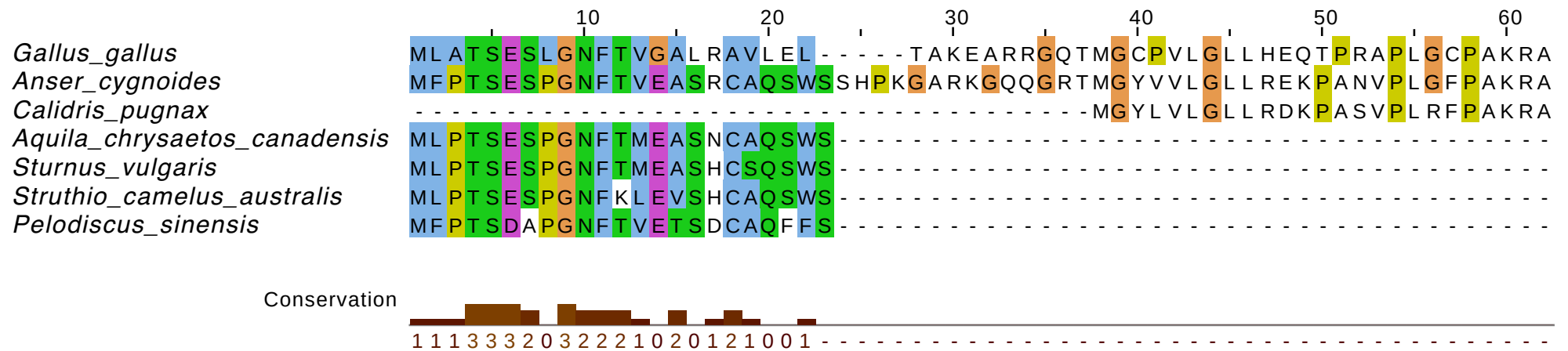
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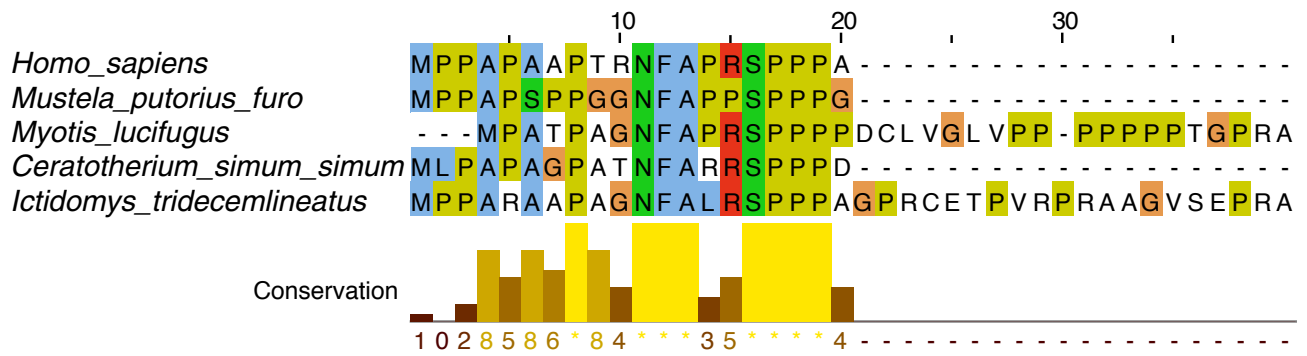


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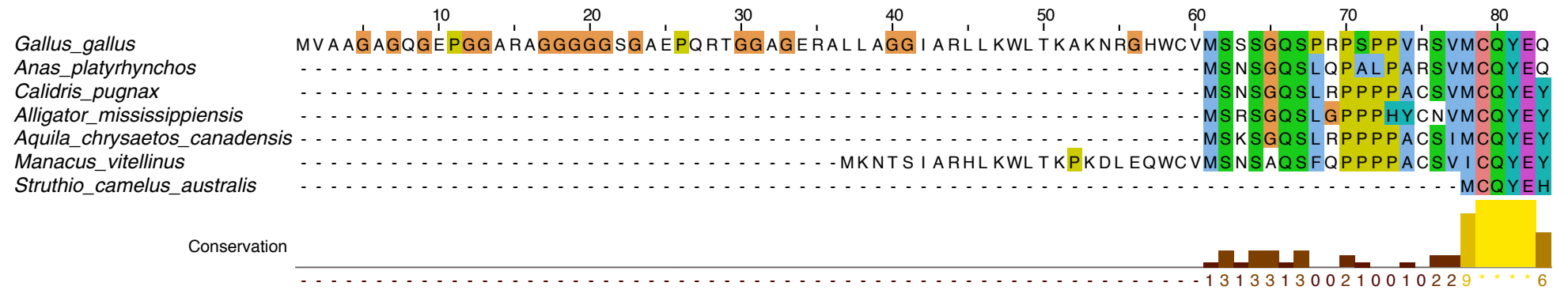
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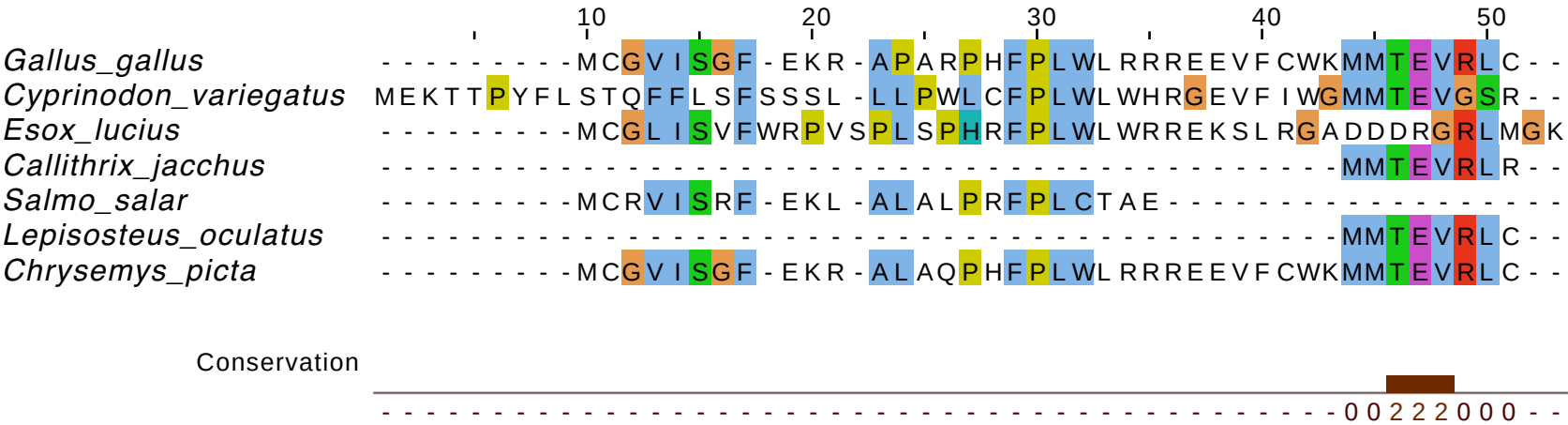


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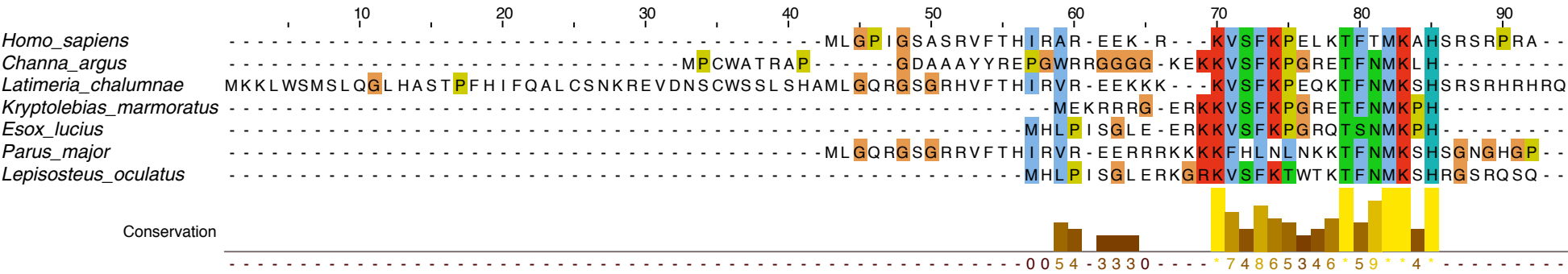
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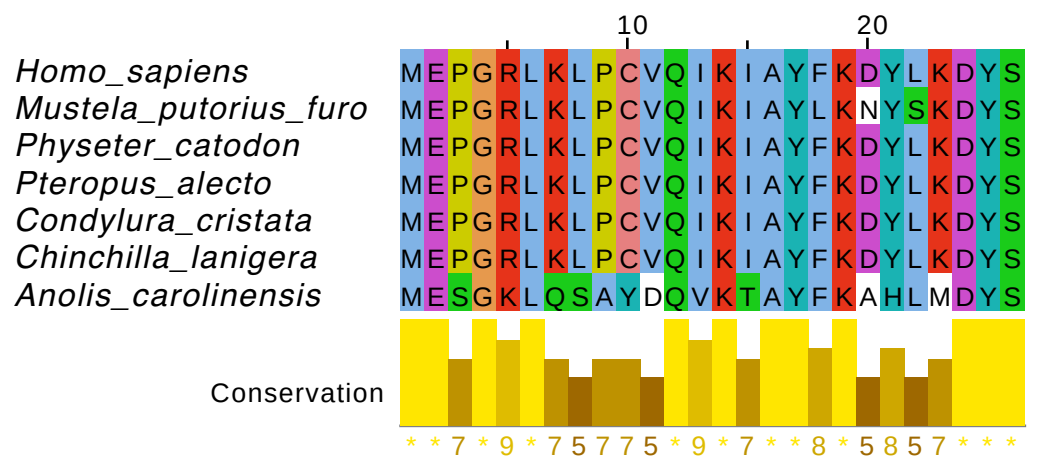


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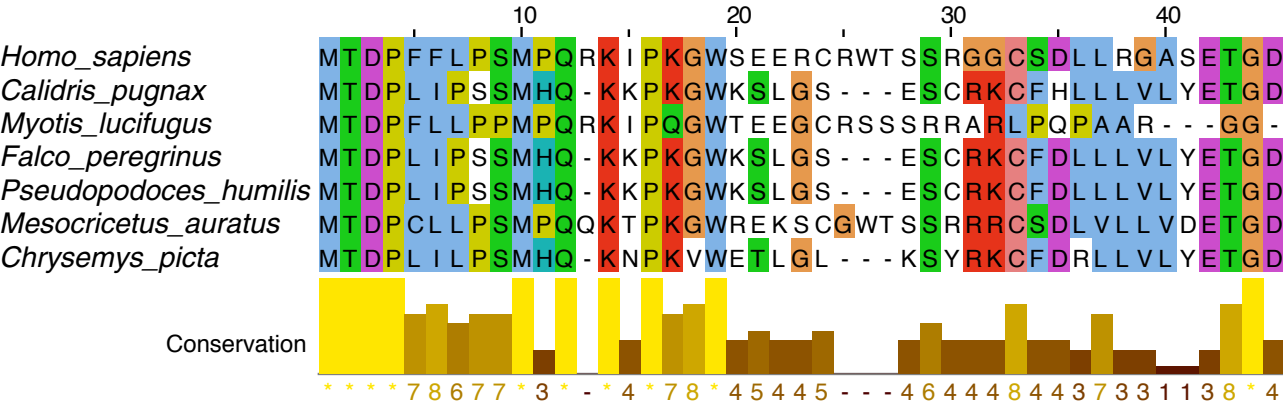
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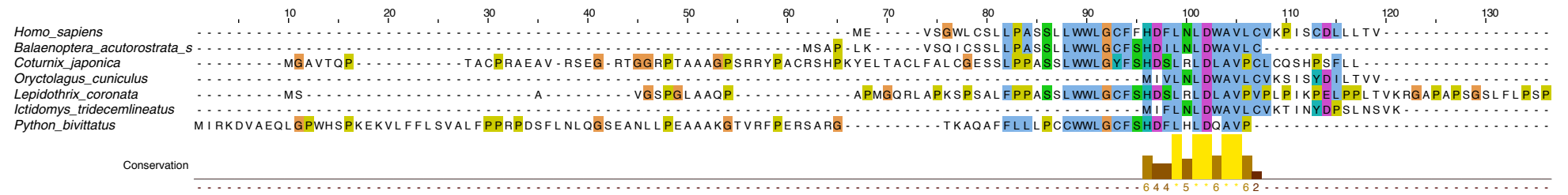


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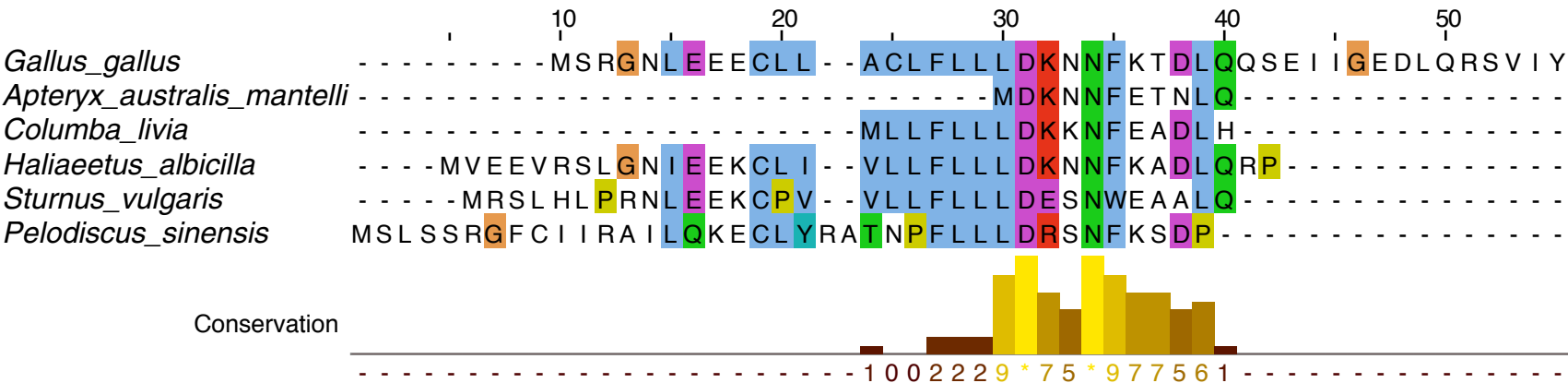


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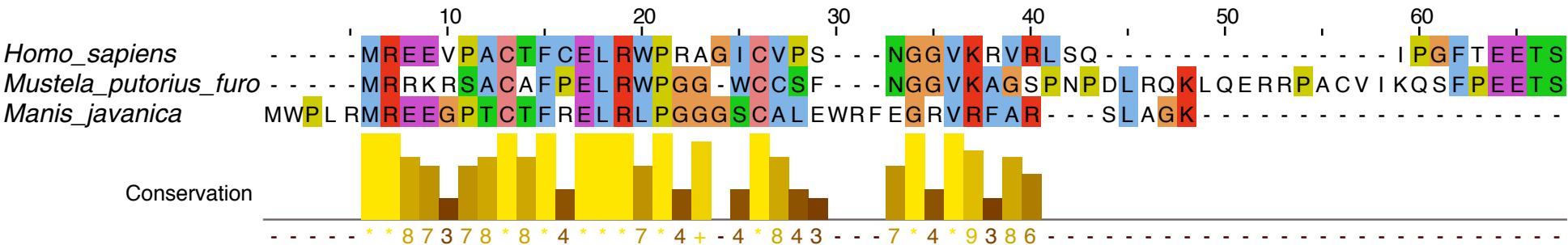
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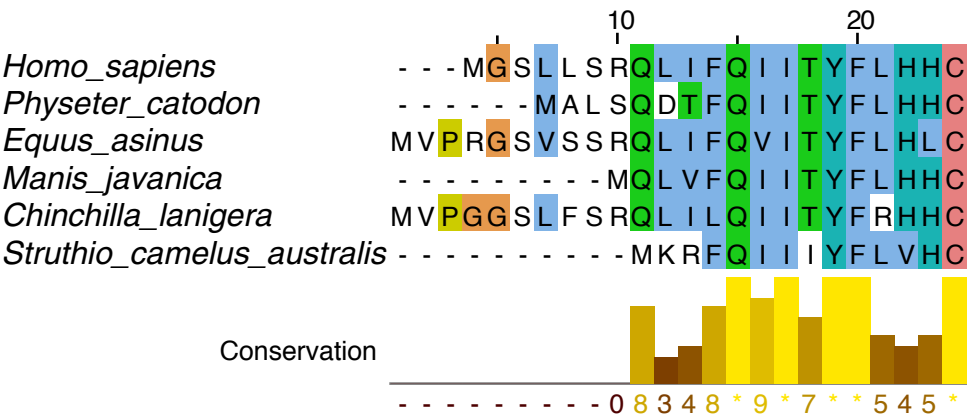
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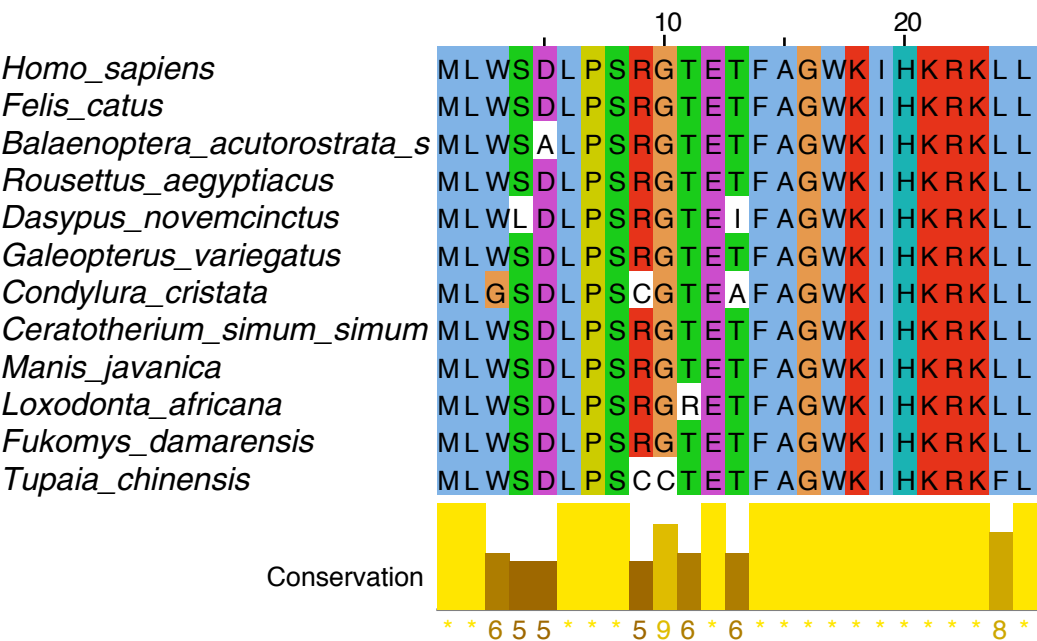
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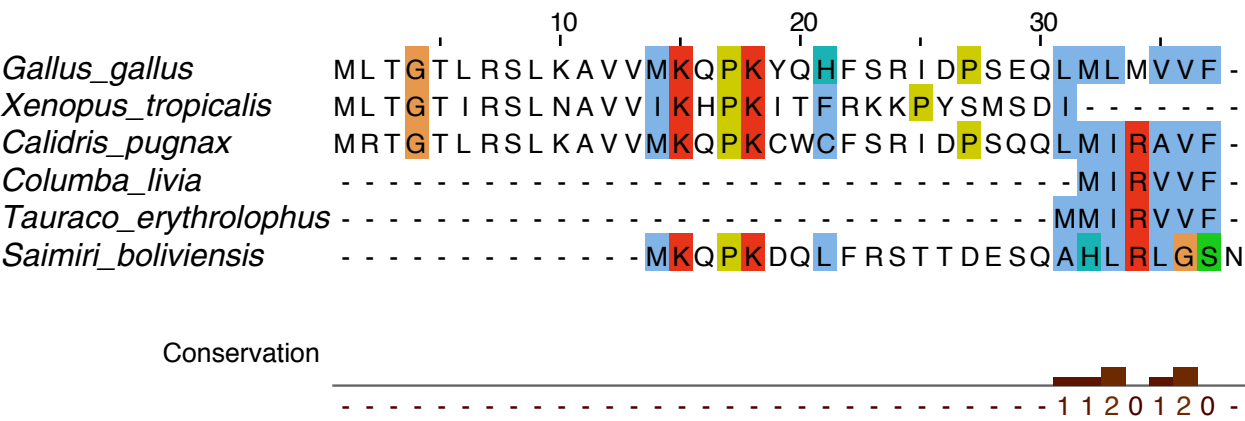
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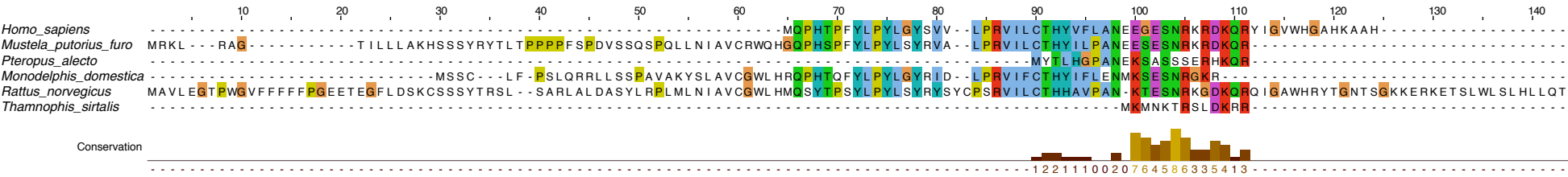
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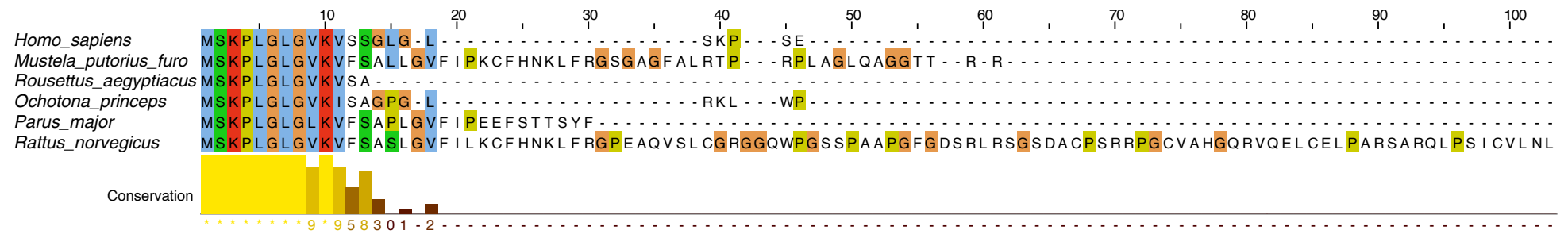


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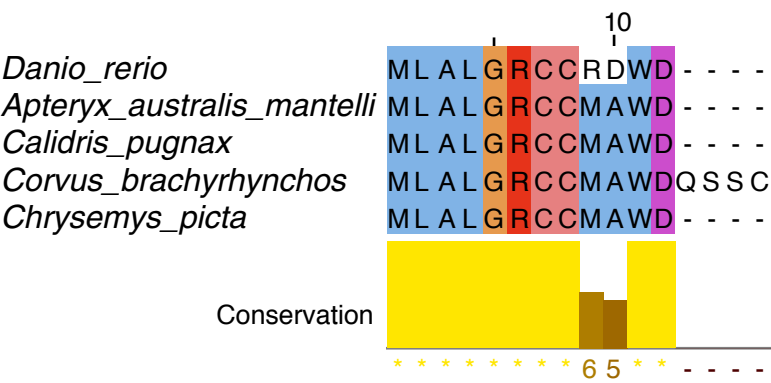


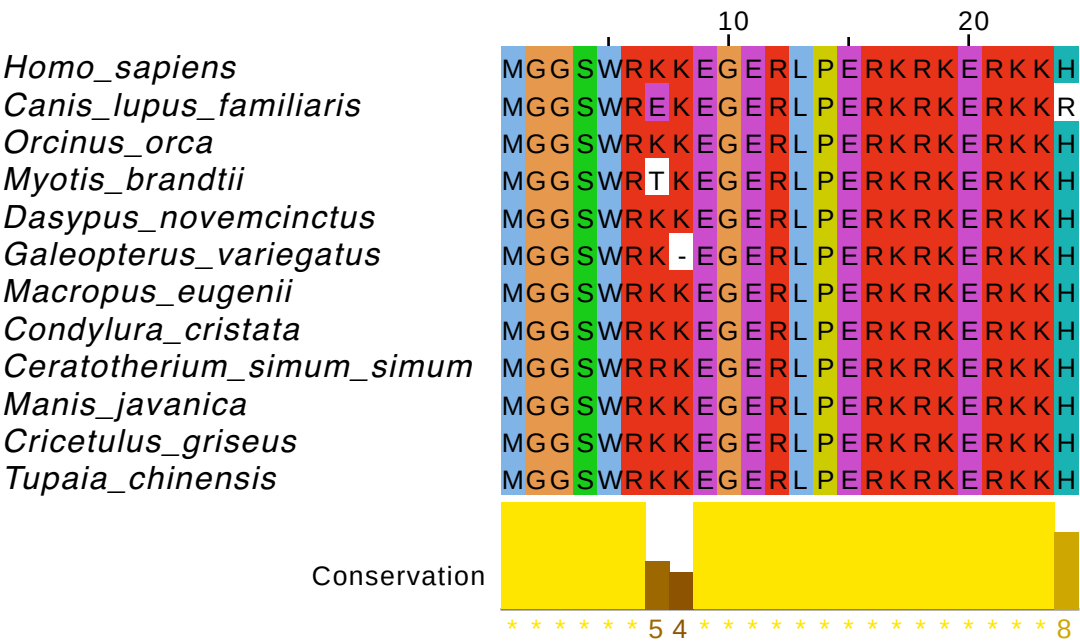
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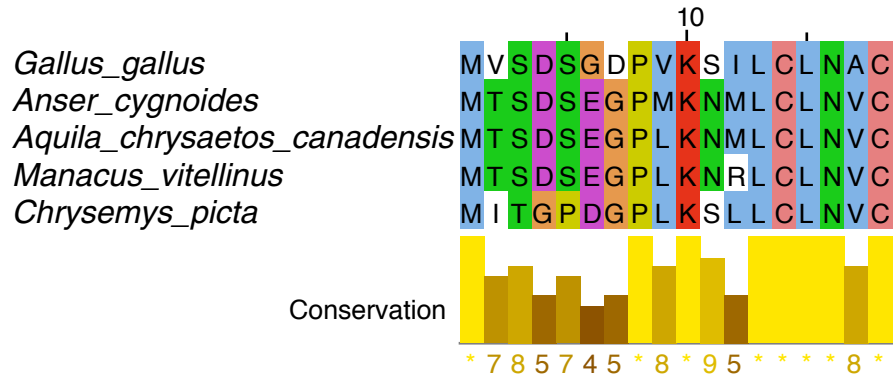
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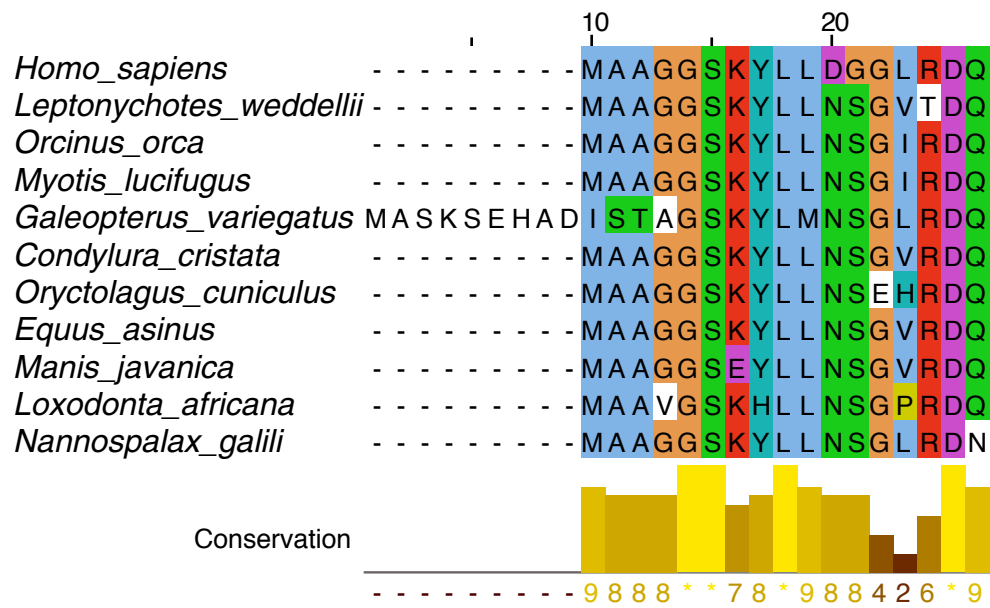
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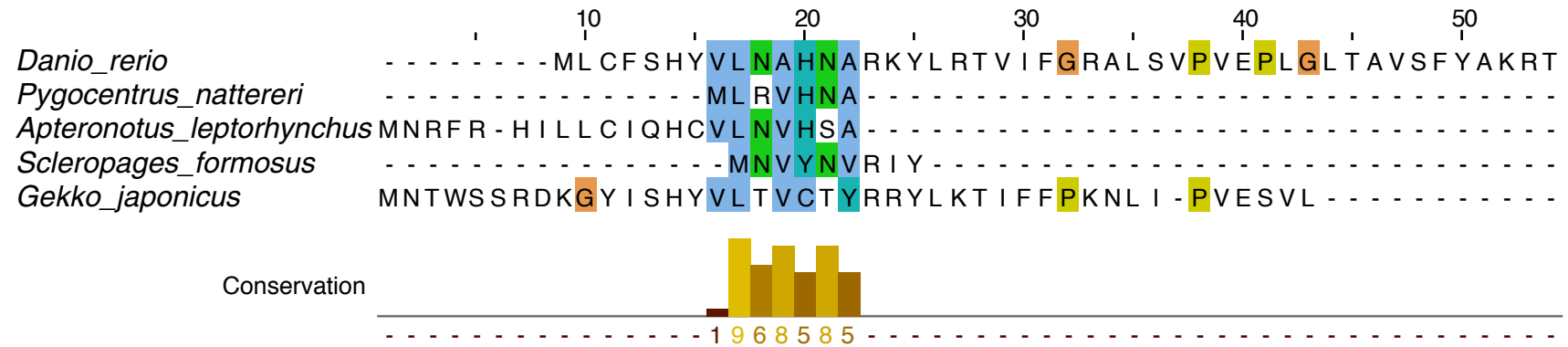
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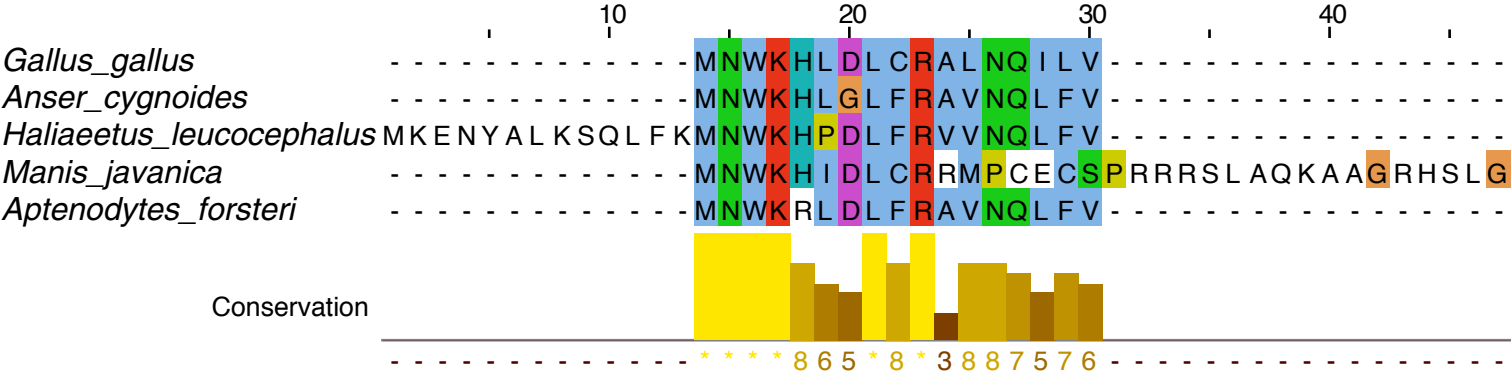


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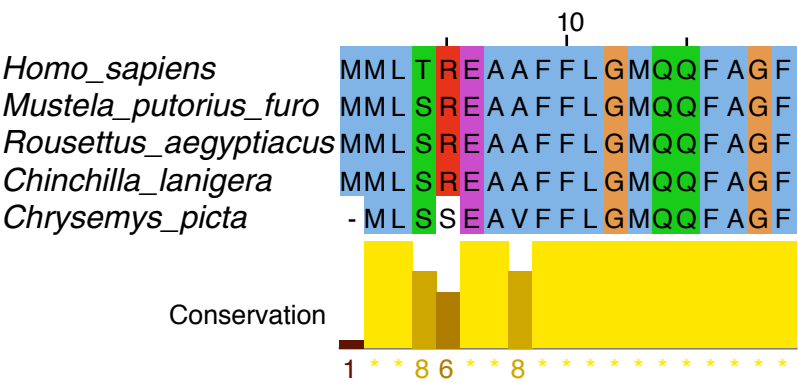


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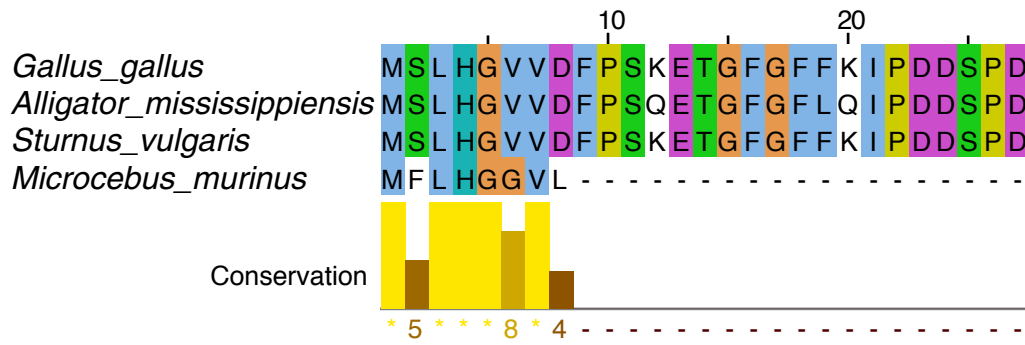
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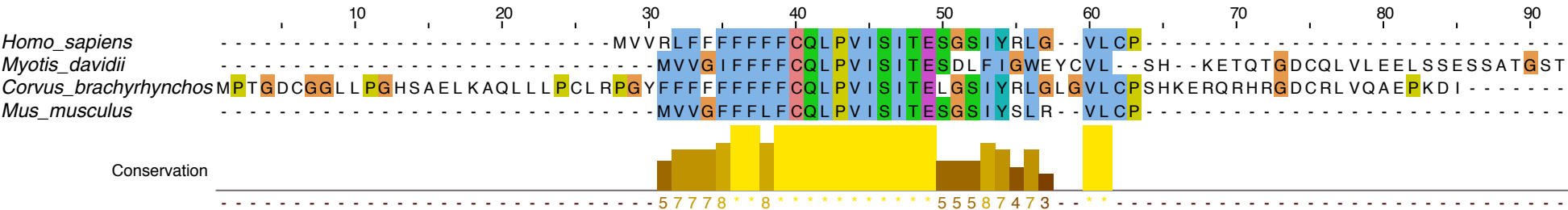
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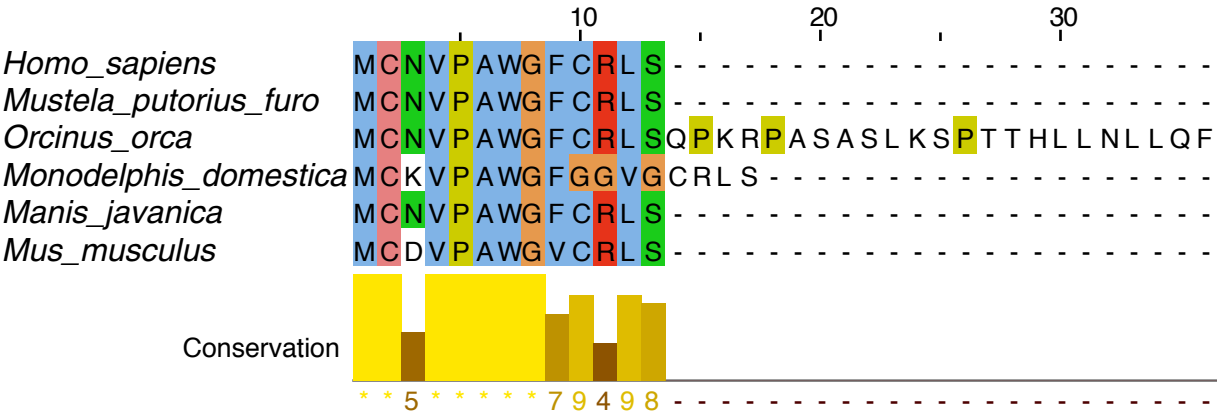
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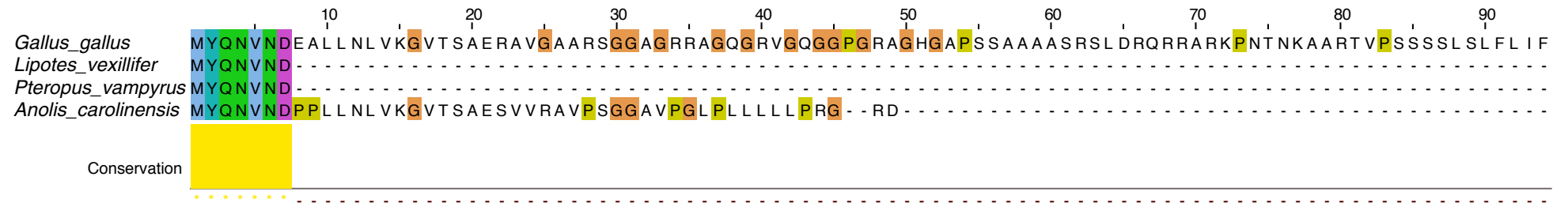
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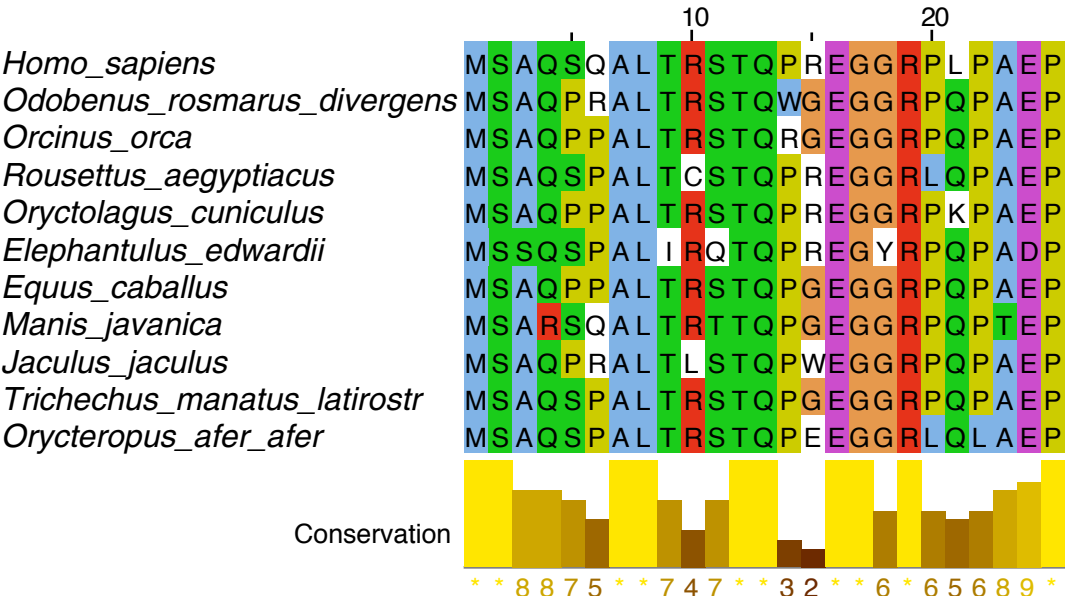
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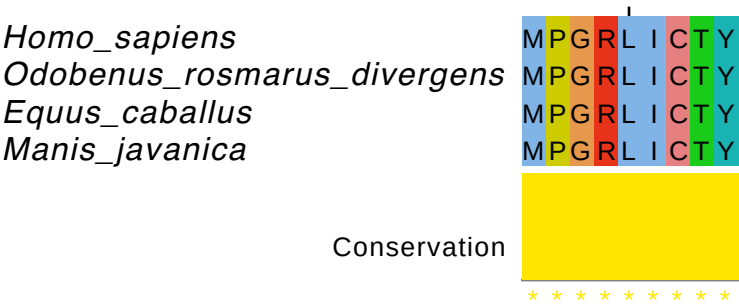
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ENSG00000140332 (TLE3)



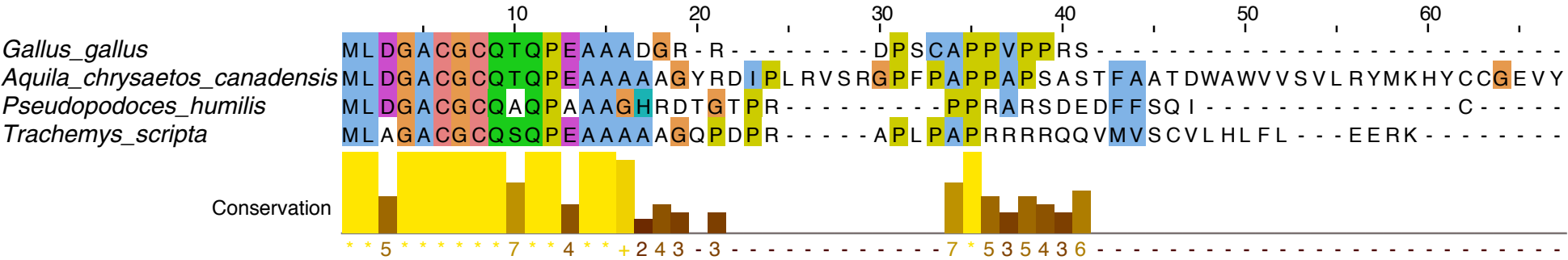
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ENSG00000140332 (TLE3)



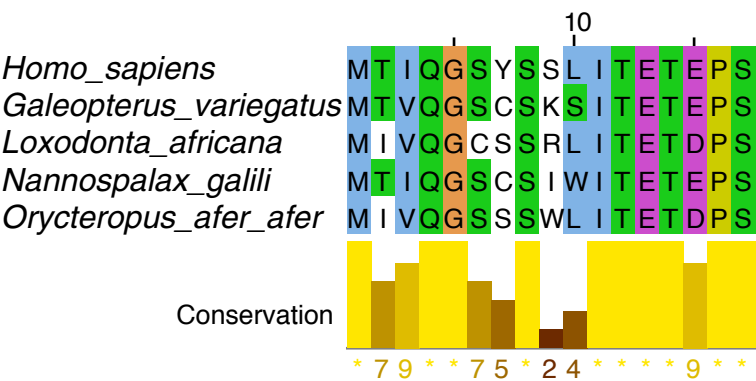
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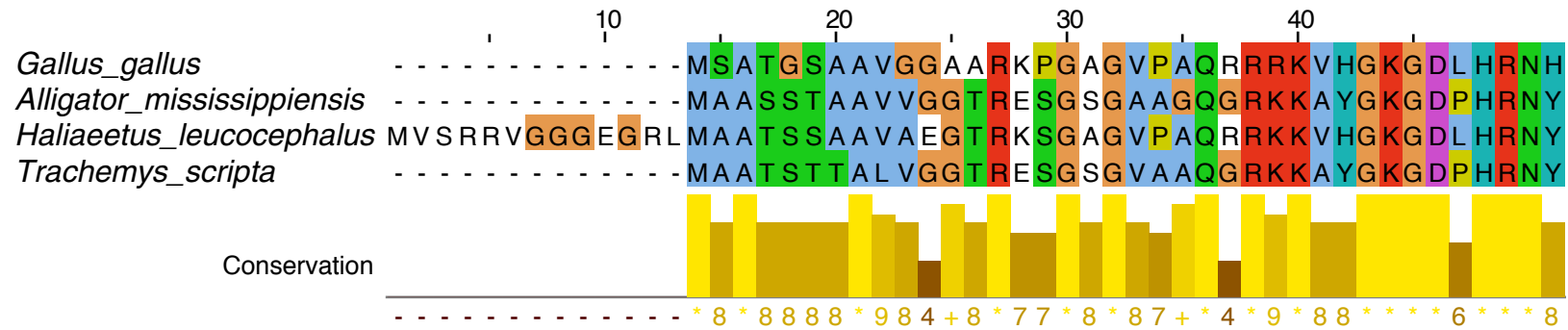
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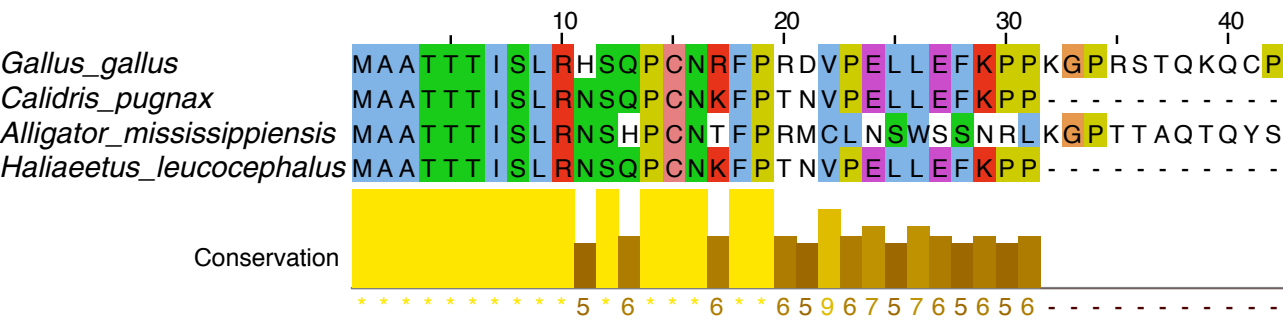
HG0255

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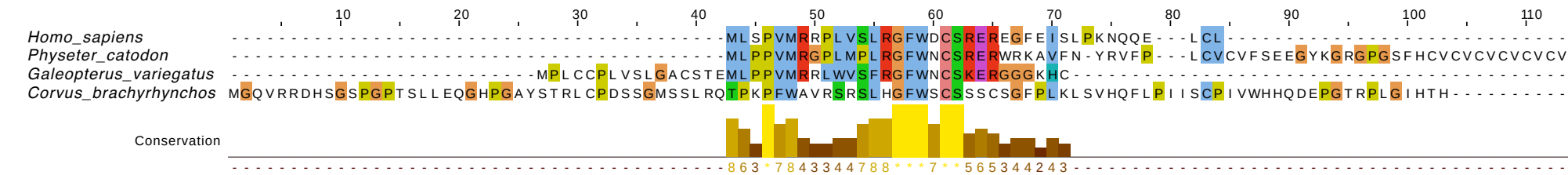


HG0256

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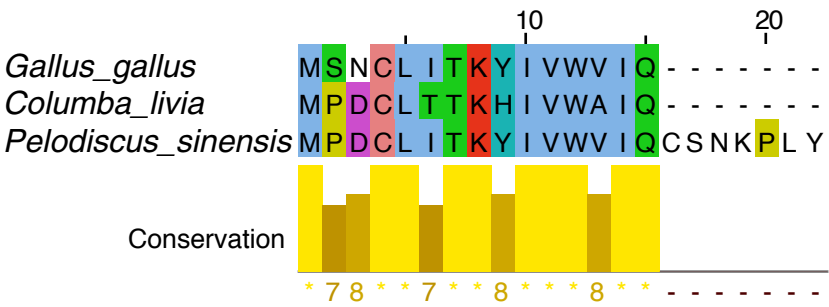


HG0257
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HG0258.1

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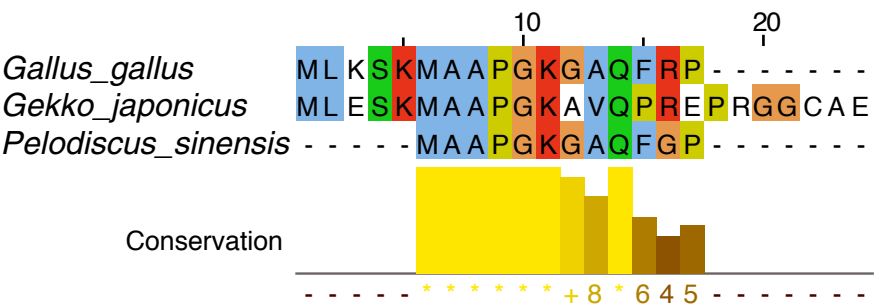


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Conservation

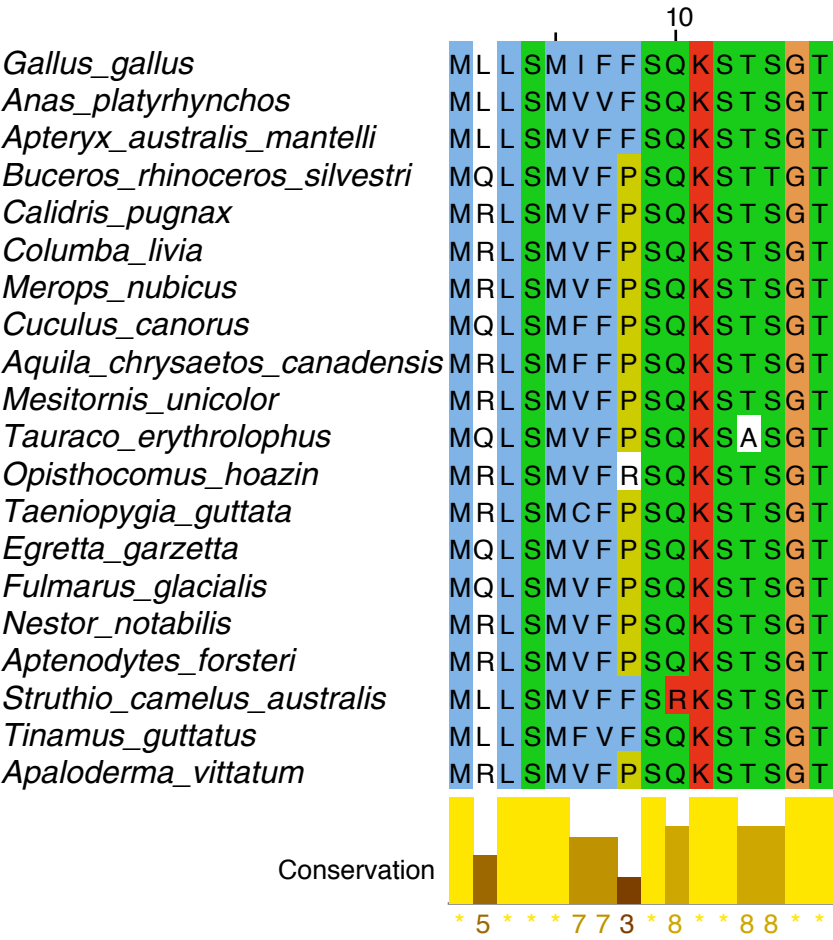
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ENSGALG00000009936 (AP4S1)



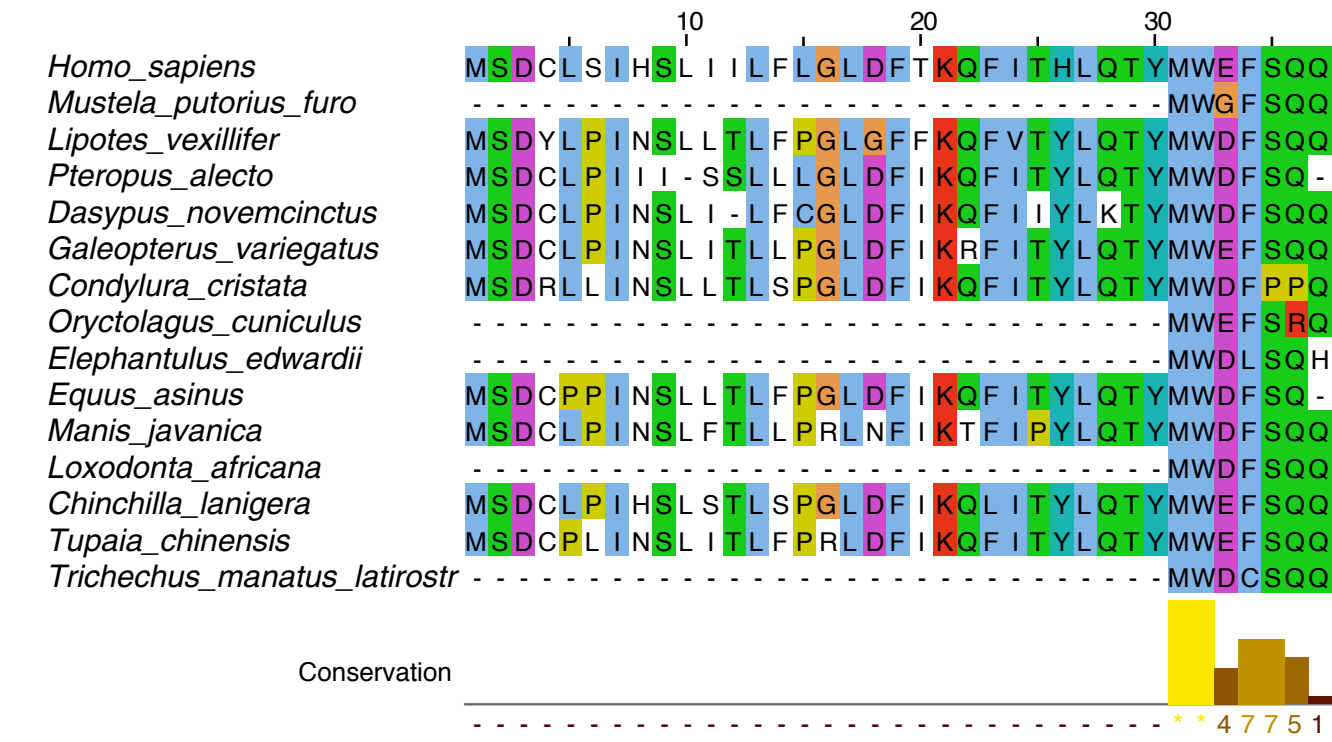
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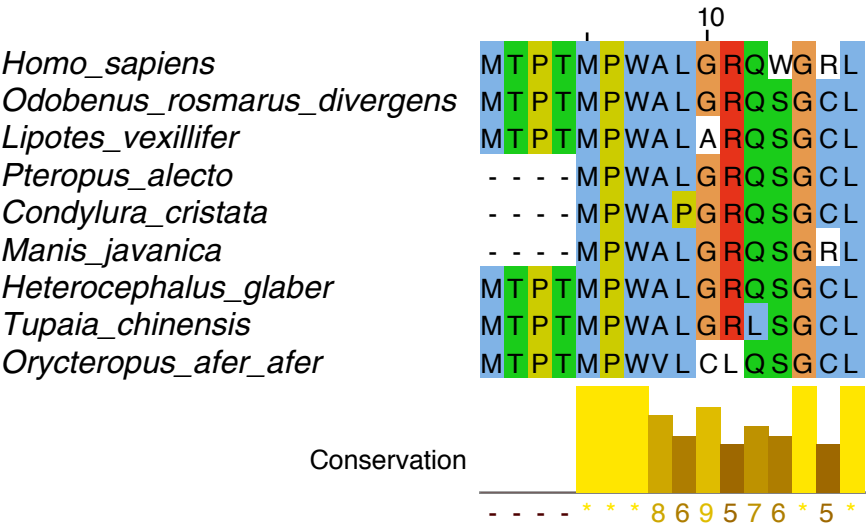
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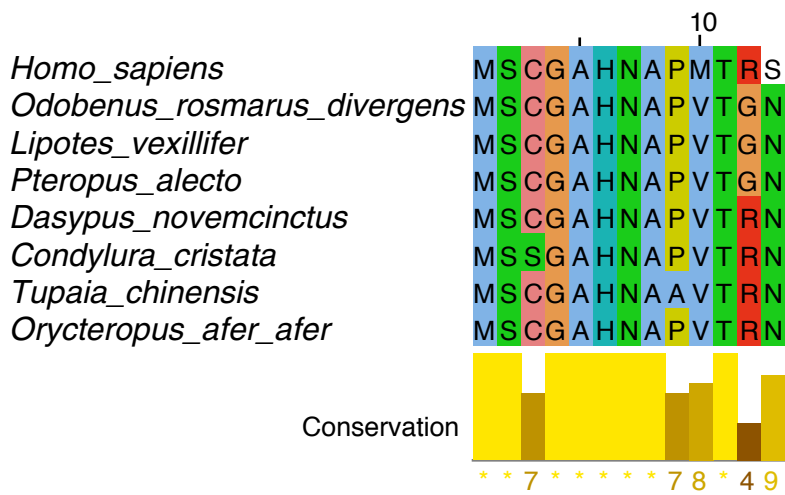
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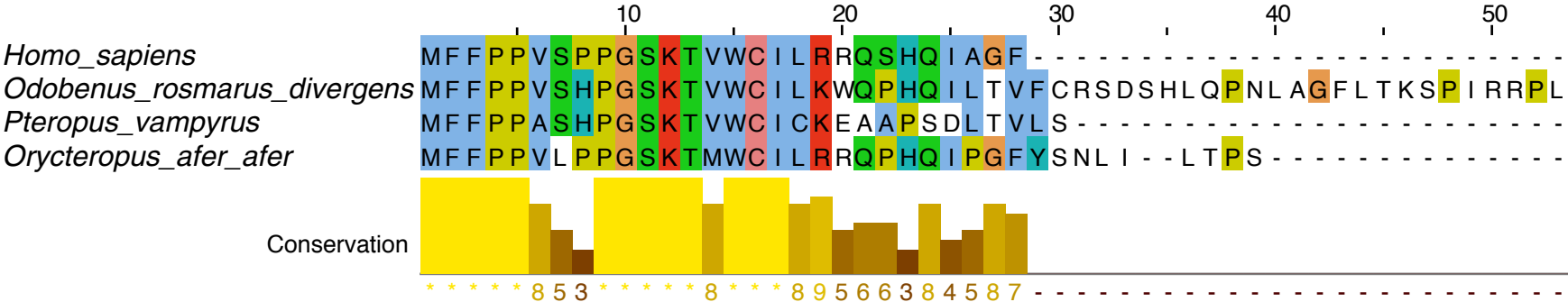
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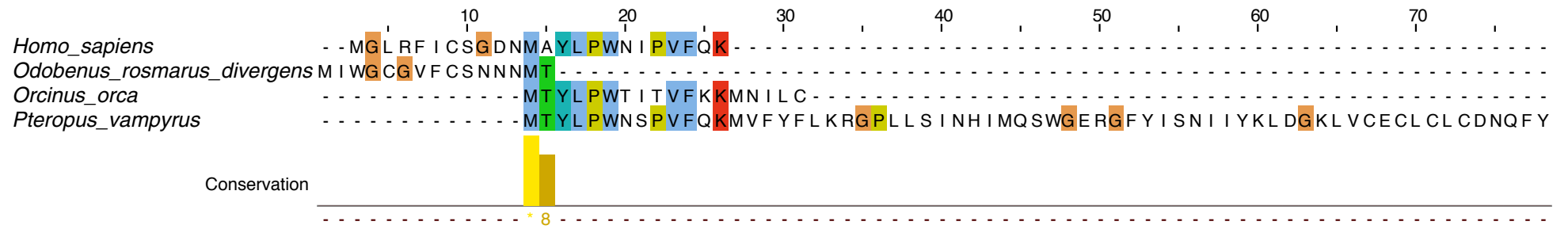
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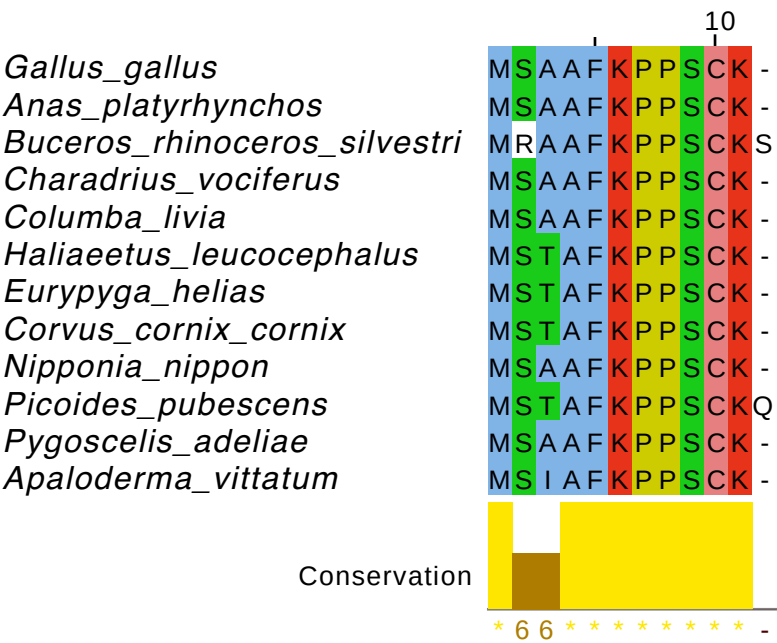
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HG0260.6

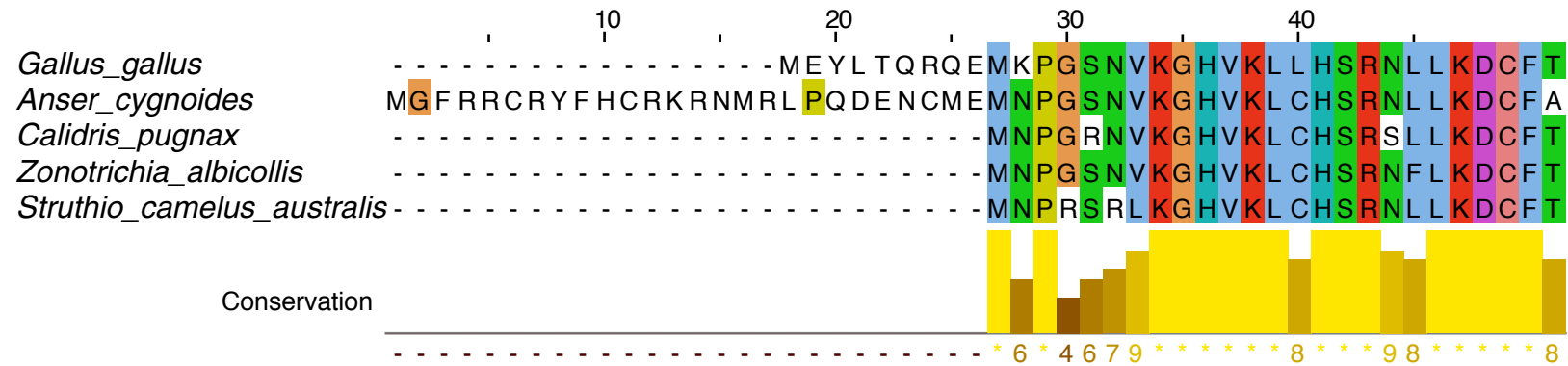
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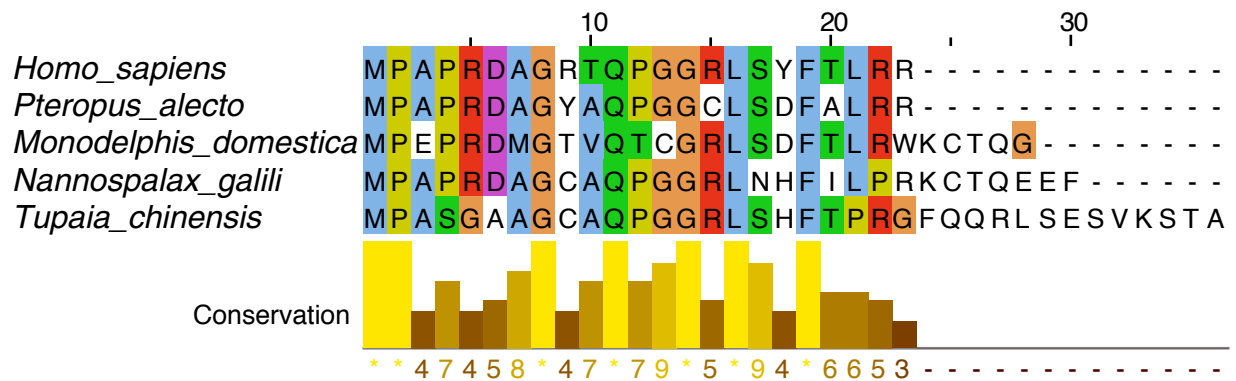
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ENSGALG00000009520 (1-Mar)



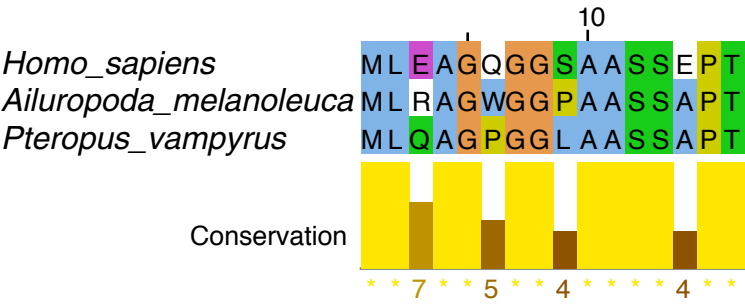
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ENSG00000145416 (1-Mar)



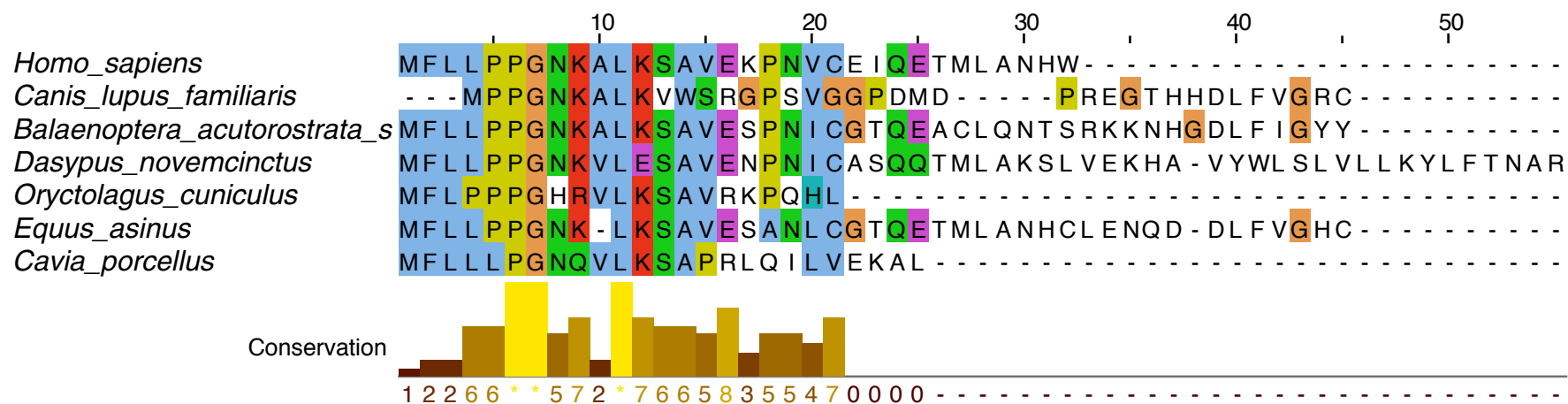
HG0261.4

ENSG00000165406 (8-Mar)



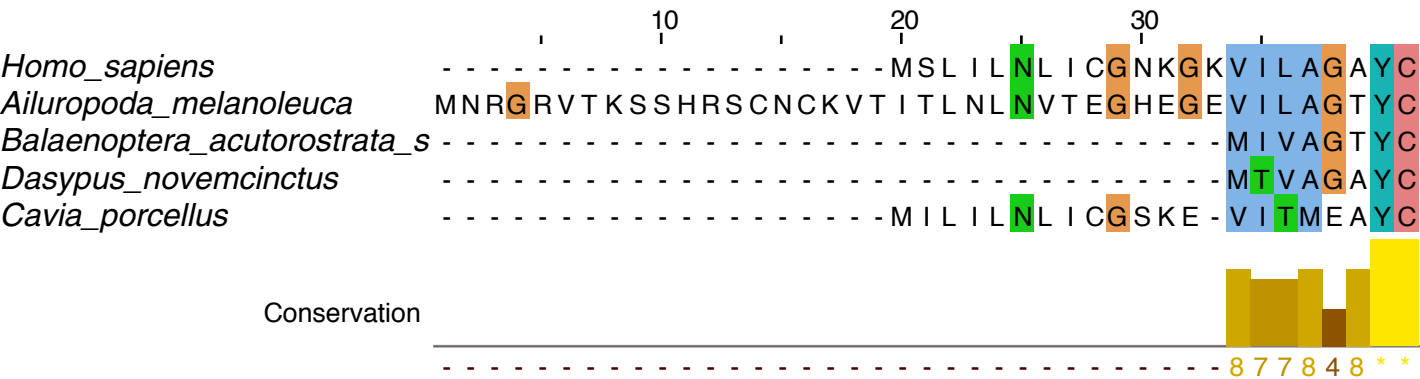
HG0262.1

ENSG00000023445 (BIRC3)

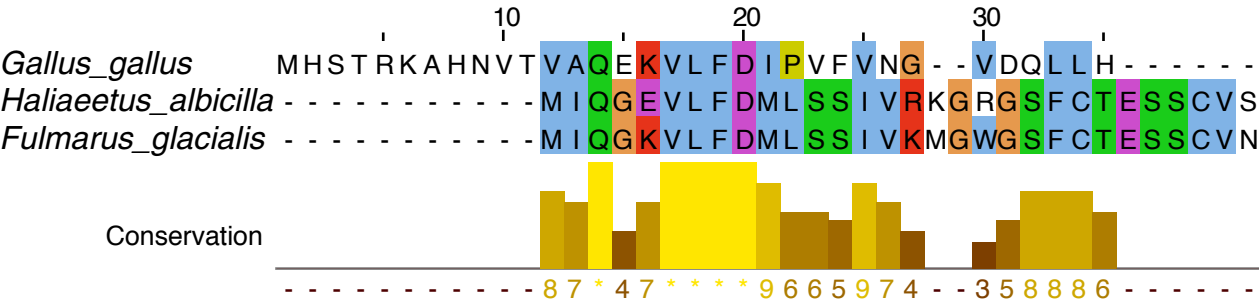


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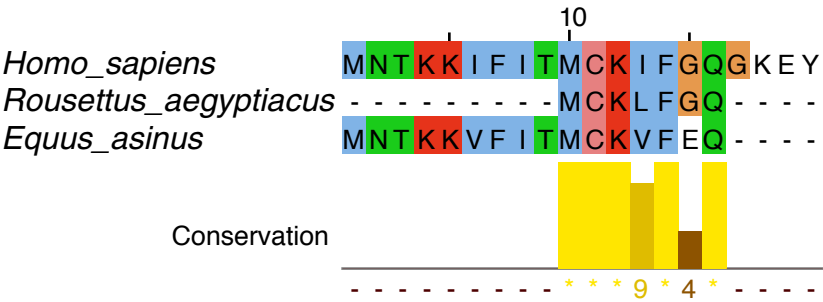


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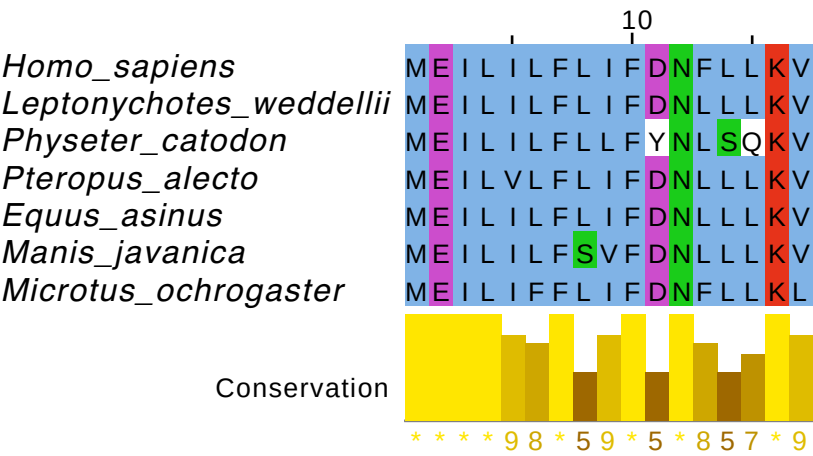
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ENSG00000023445 (BIRC3)



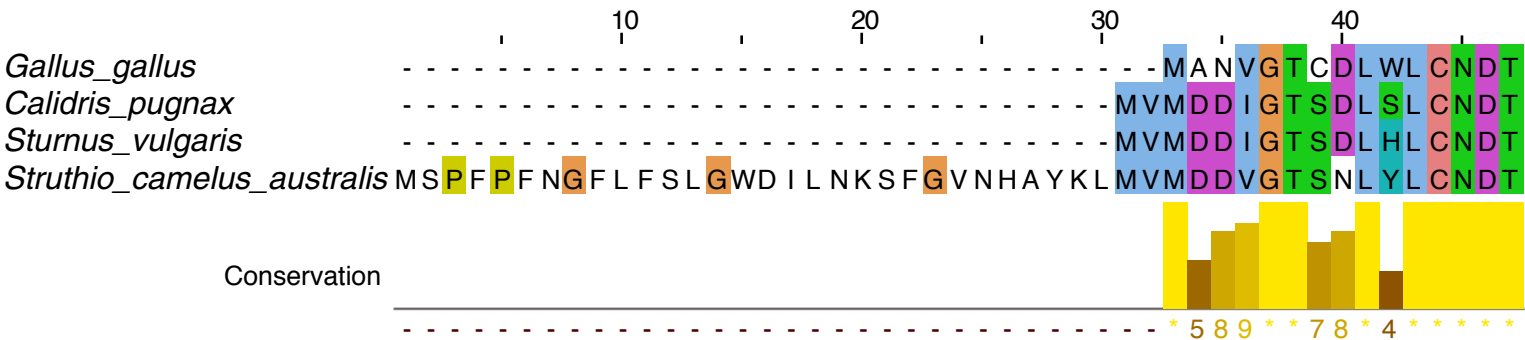
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ENSG00000169826 (CSGALNACT2)



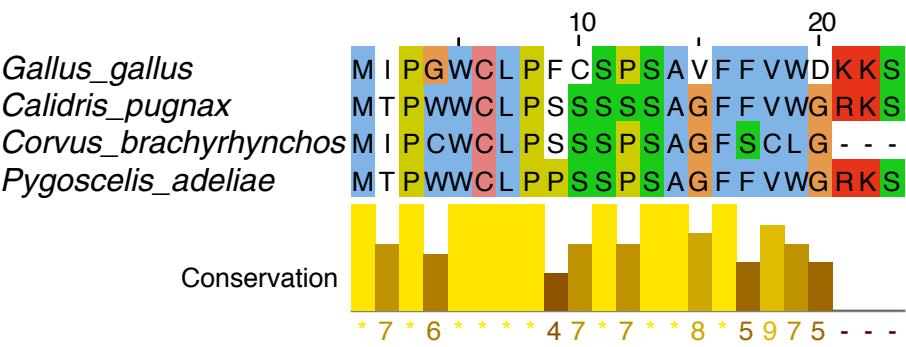
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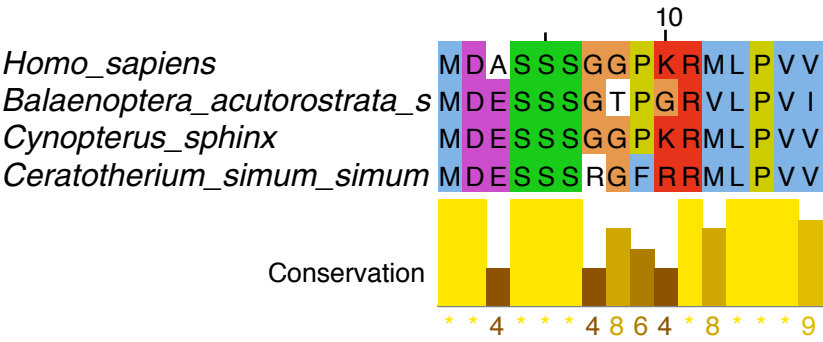
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ENSGALG00000002543 (CSGALNACT2)



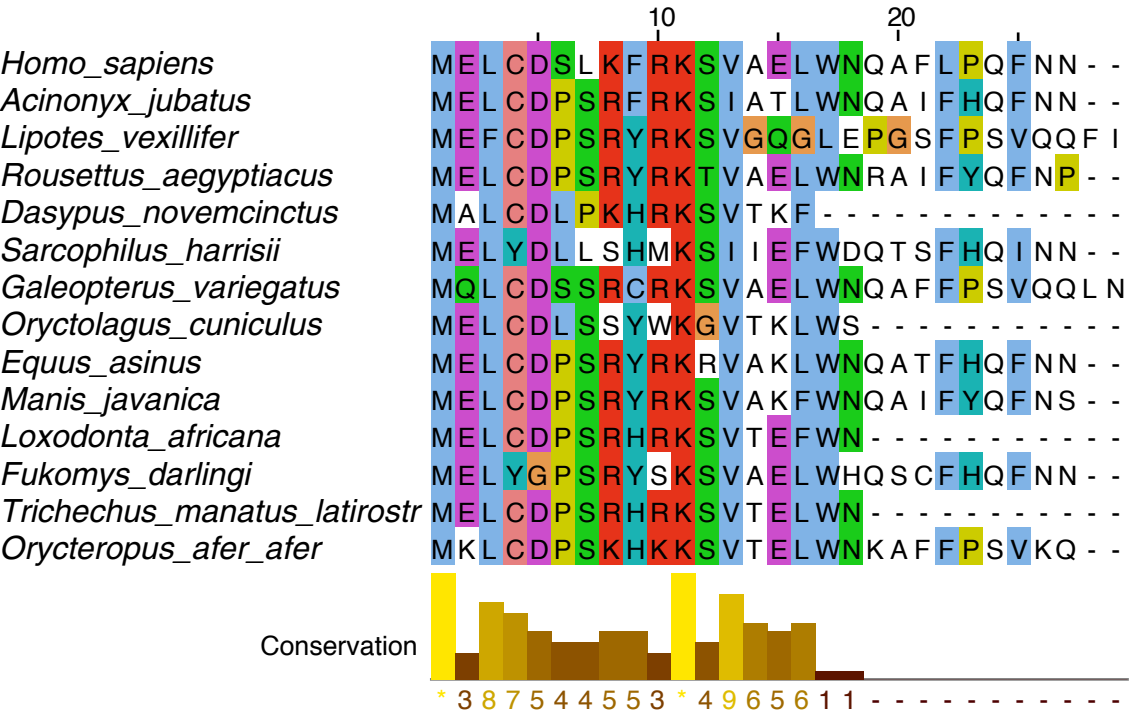
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ENSG00000147408 (CSGALNACT1)



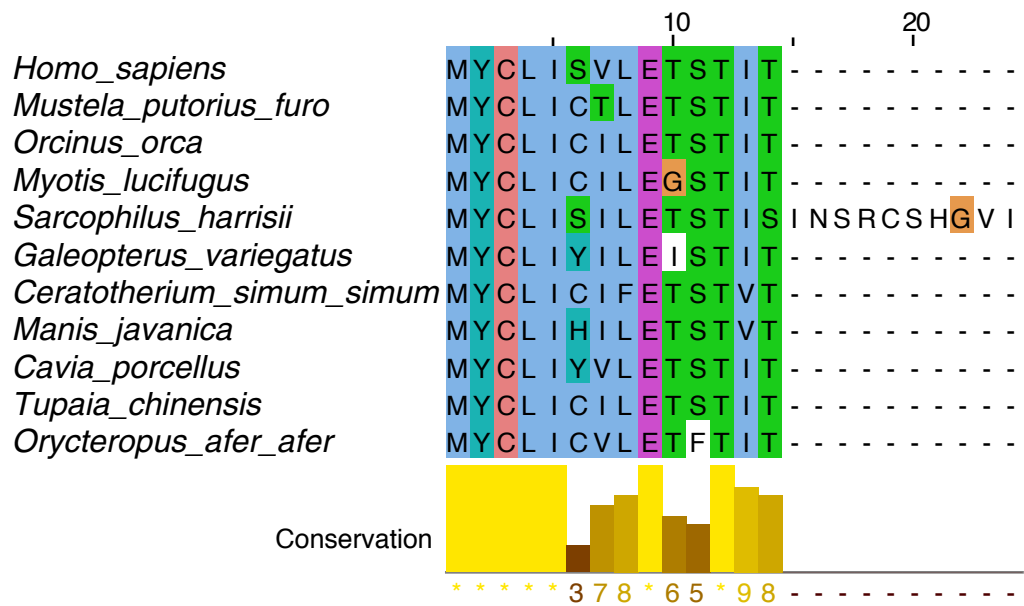
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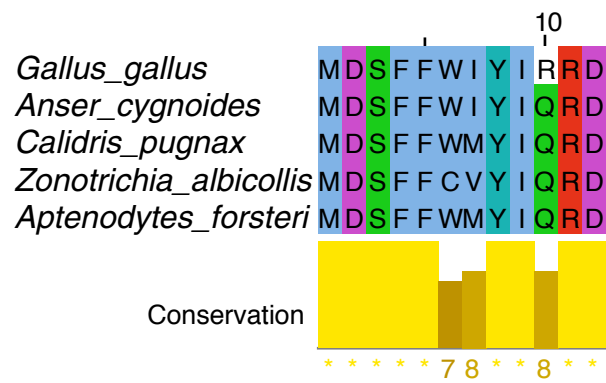
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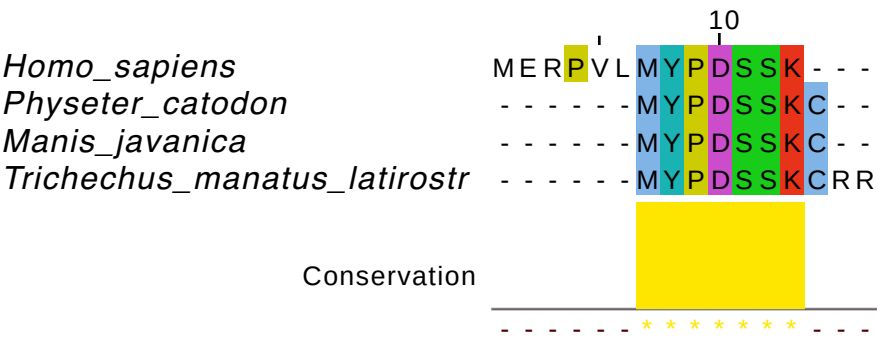
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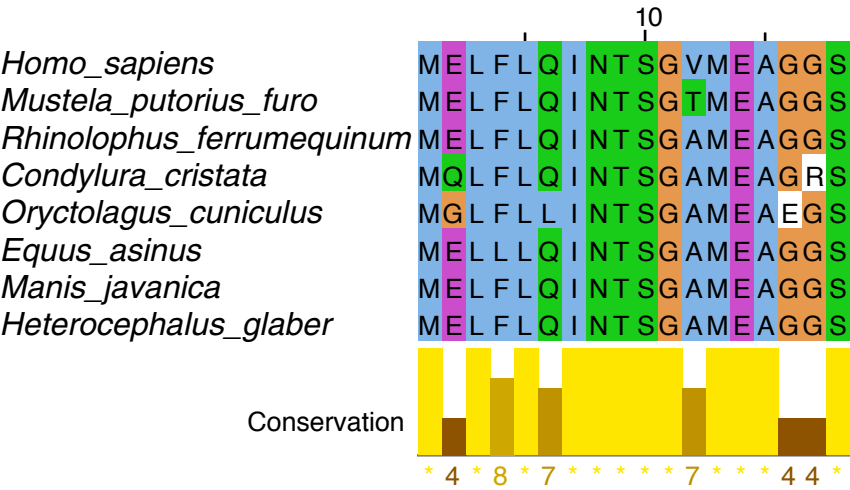
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ENSG00000151458 (ANKRD50)



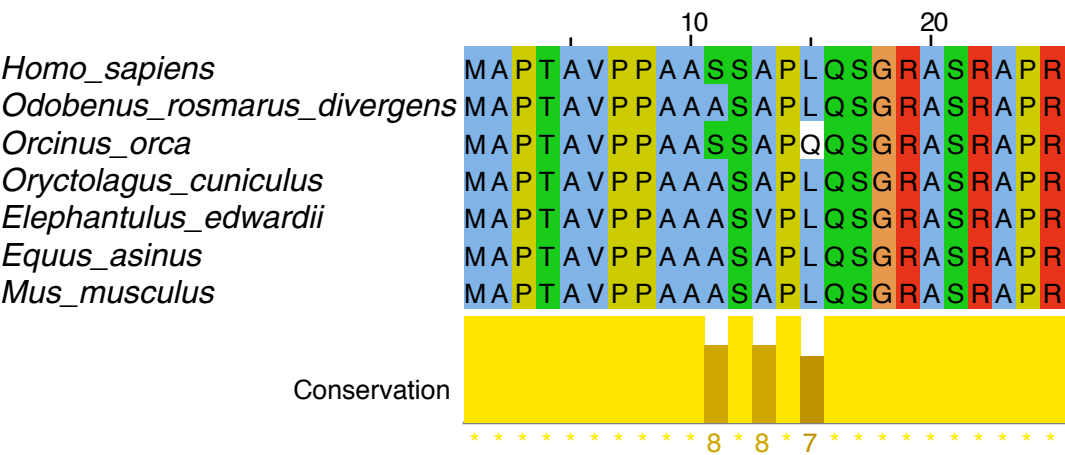
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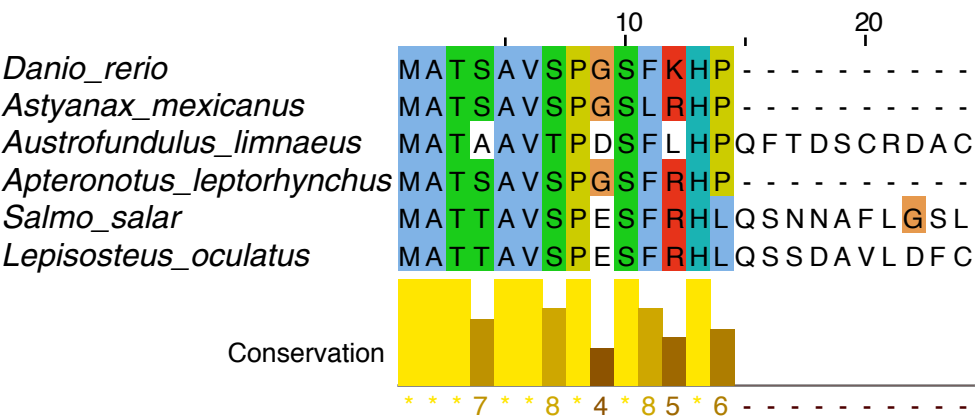
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ENSG00000196876 (SCN8A)



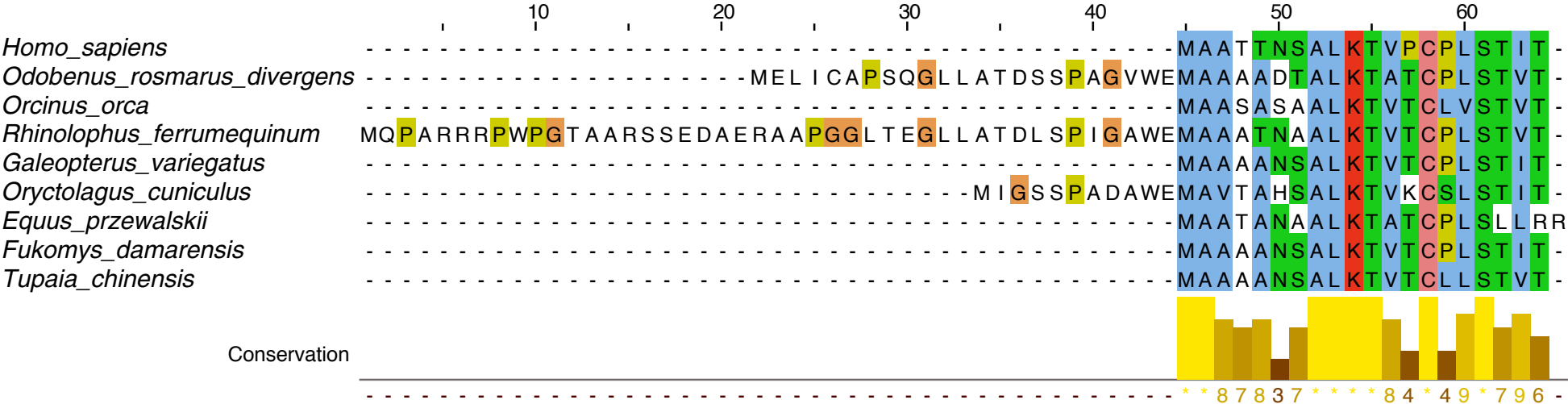
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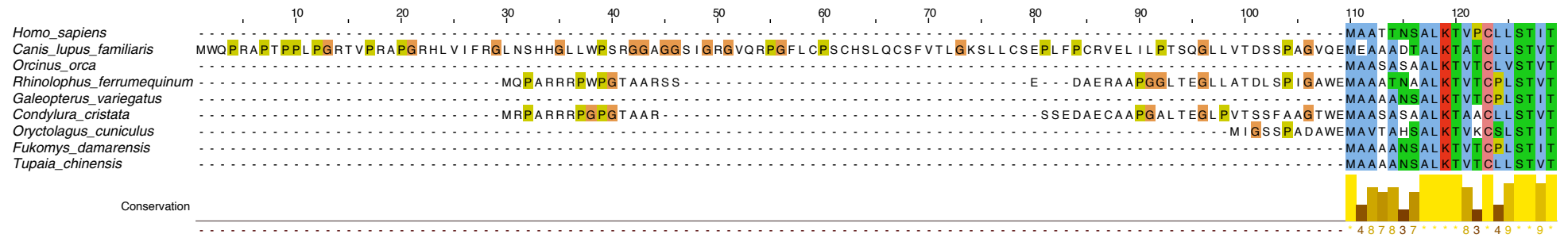


HG0266.1

ENSG00000184185 (KCNJ12)

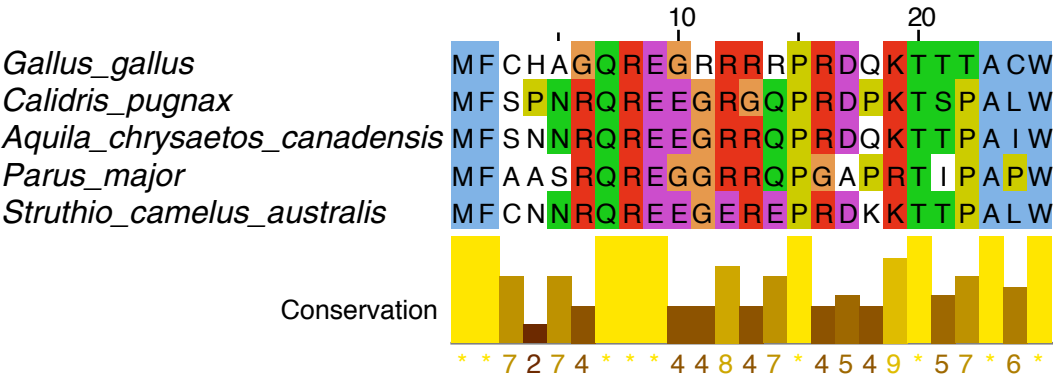


ENSG00000260458 (KCNJ18)



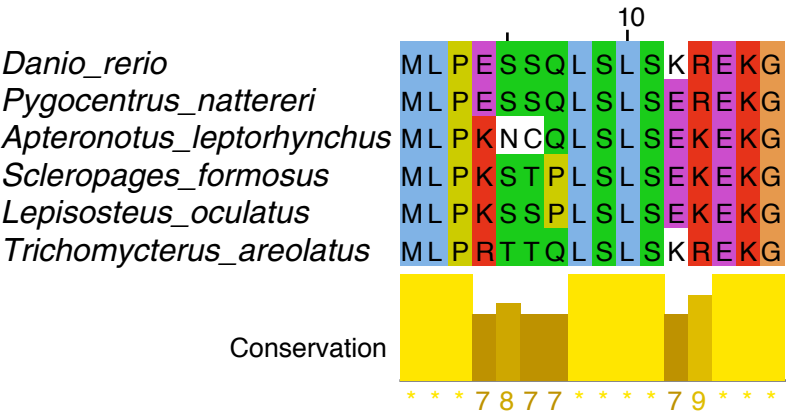
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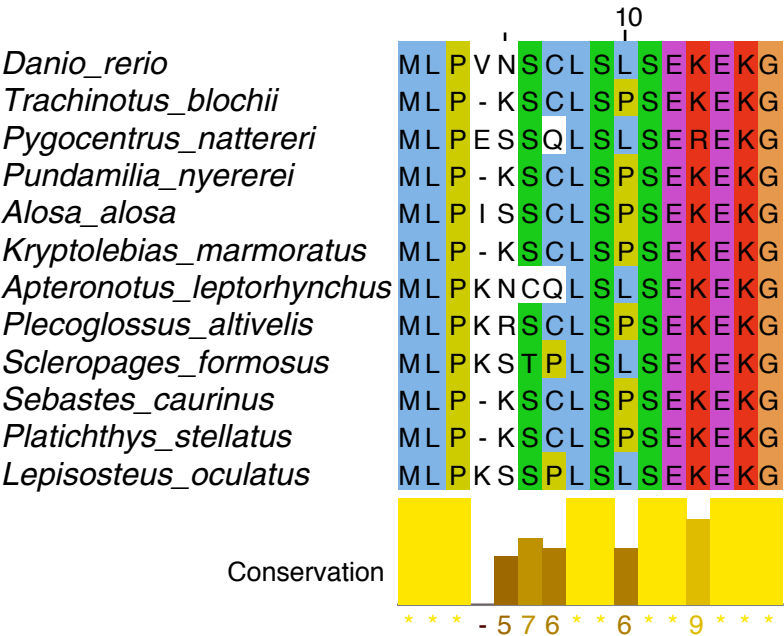
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ENSDARG00000028173 (slc4a2a)

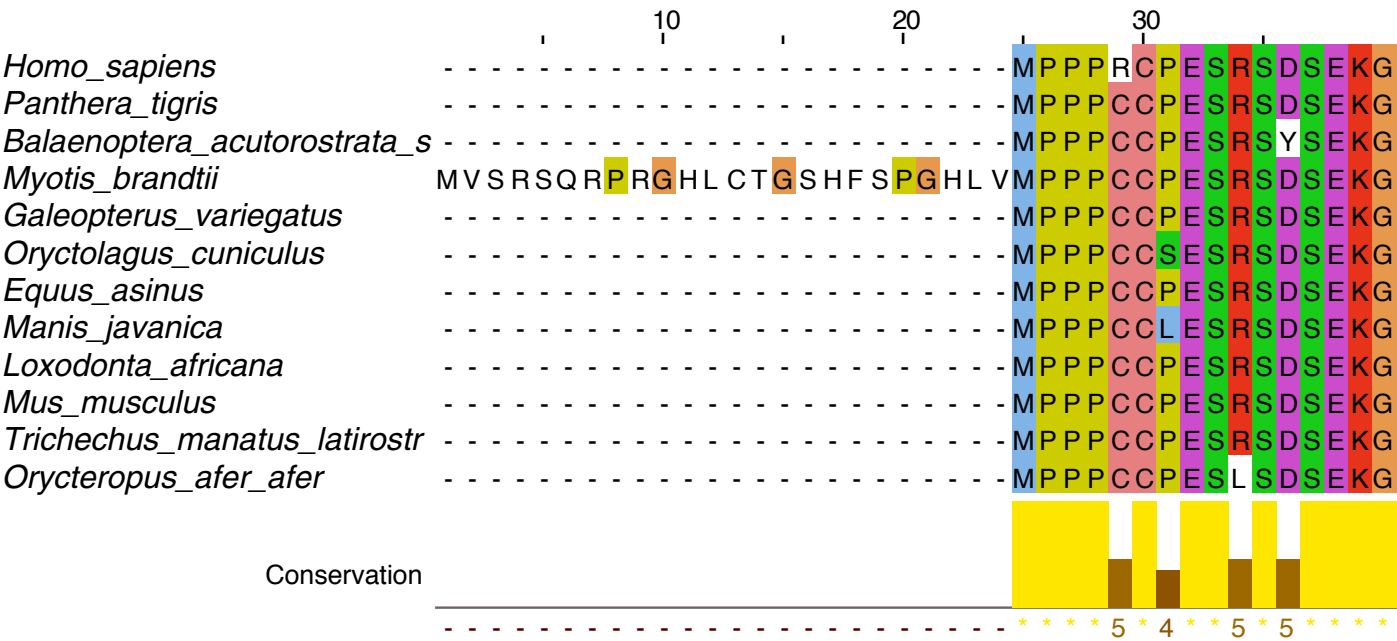


HG0267

ENSDARG00000052330 (slc4a2b)

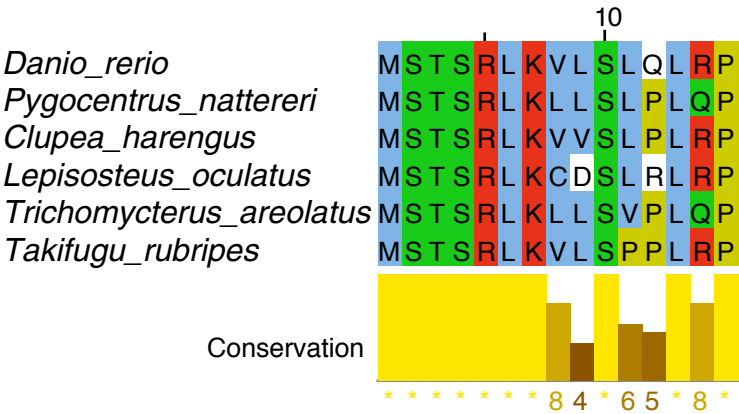


HG0267
ENSG00000164889 (SLC4A2)



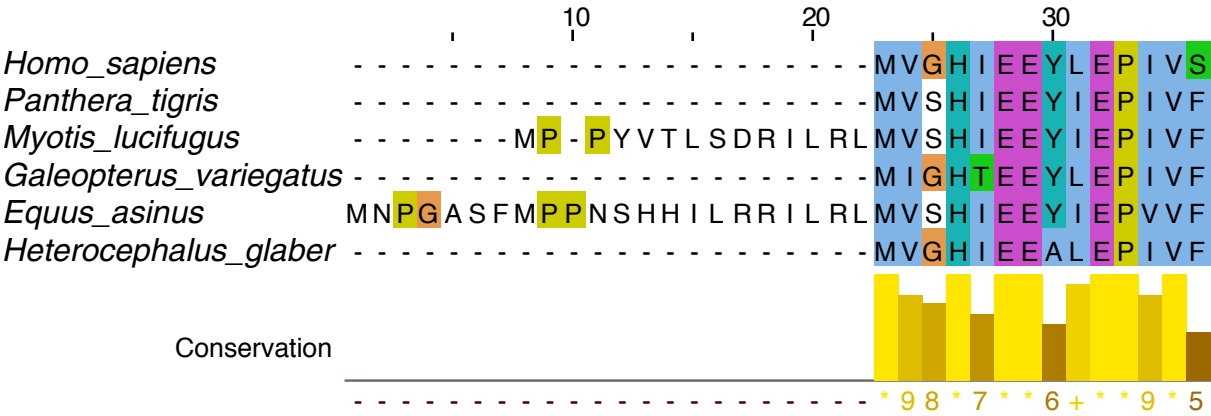
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ENSDARG000000011703 (clocka)

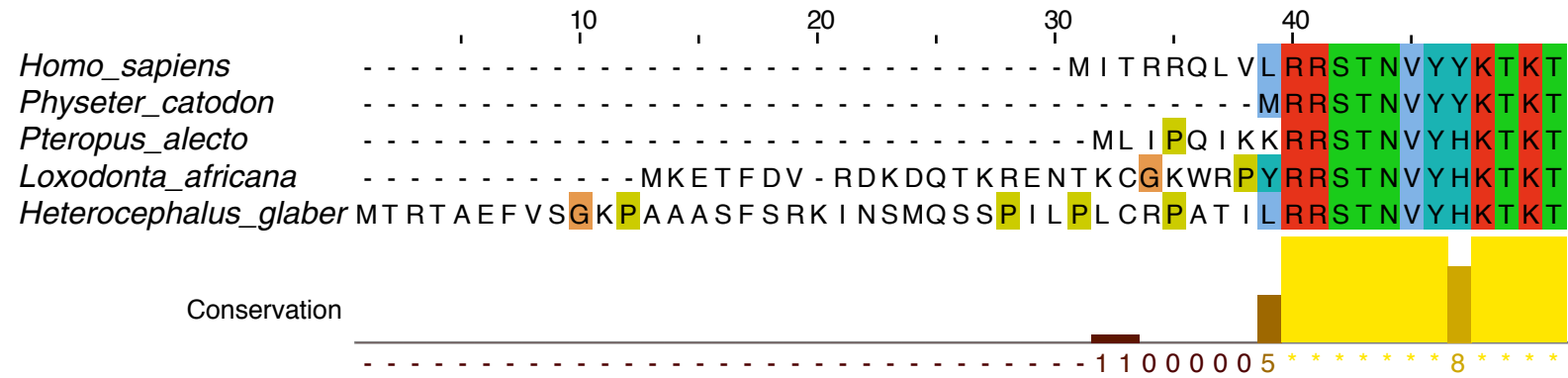


HG0268.2

ENSG00000134852 (CLOCK)

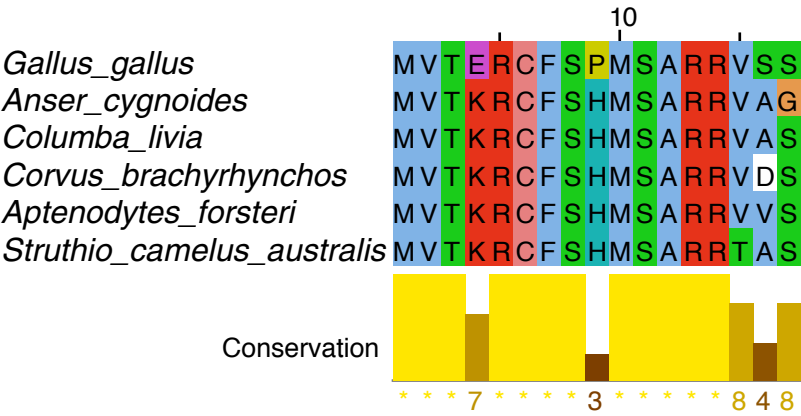


ENSG00000134852 (CLOCK)



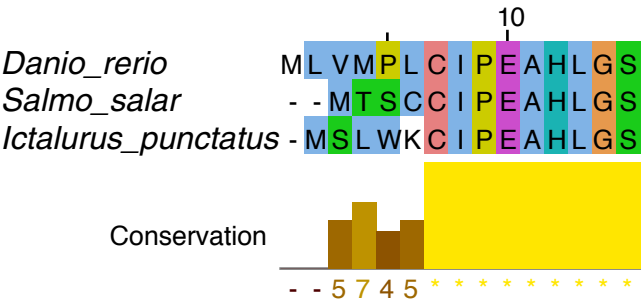
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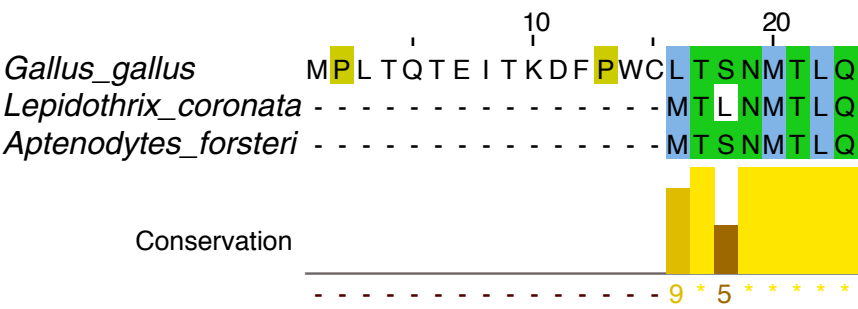
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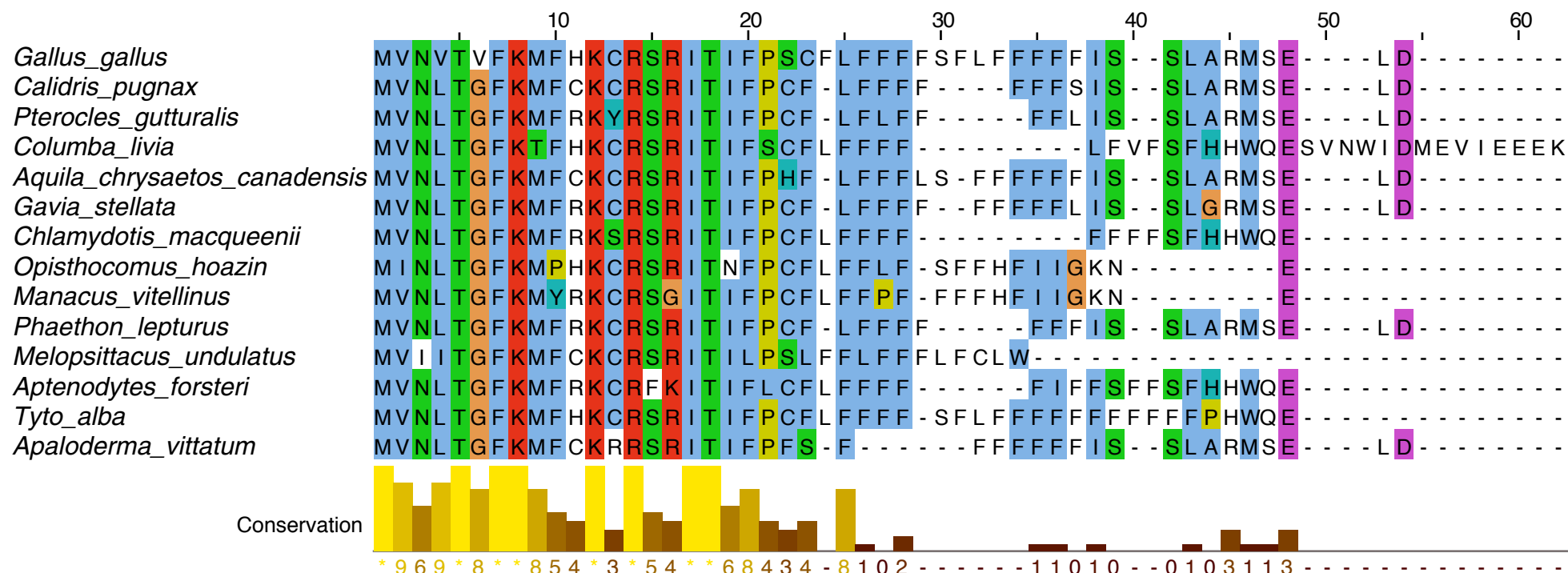
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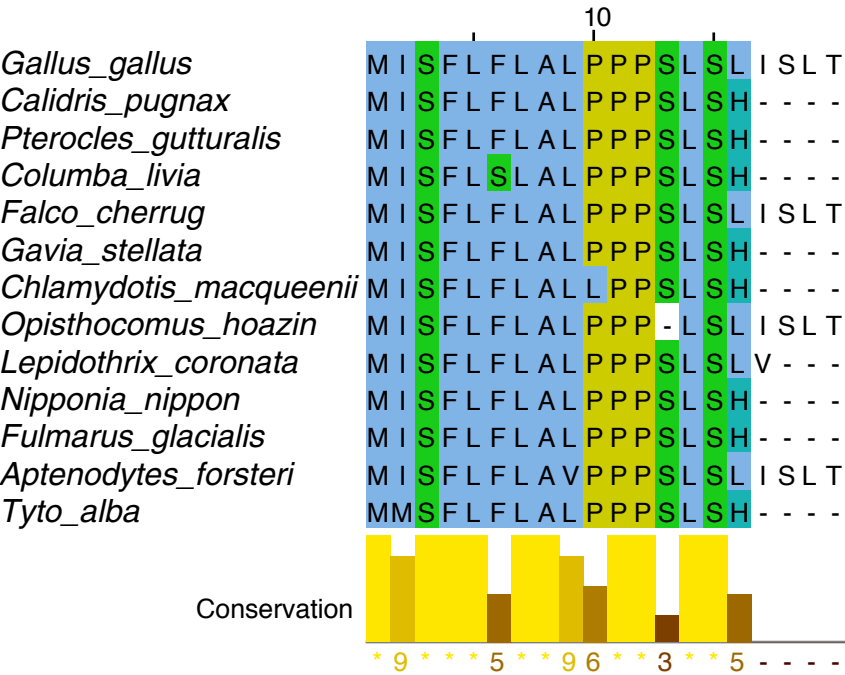
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ENSGALG00000015147 (ALDH1A1)



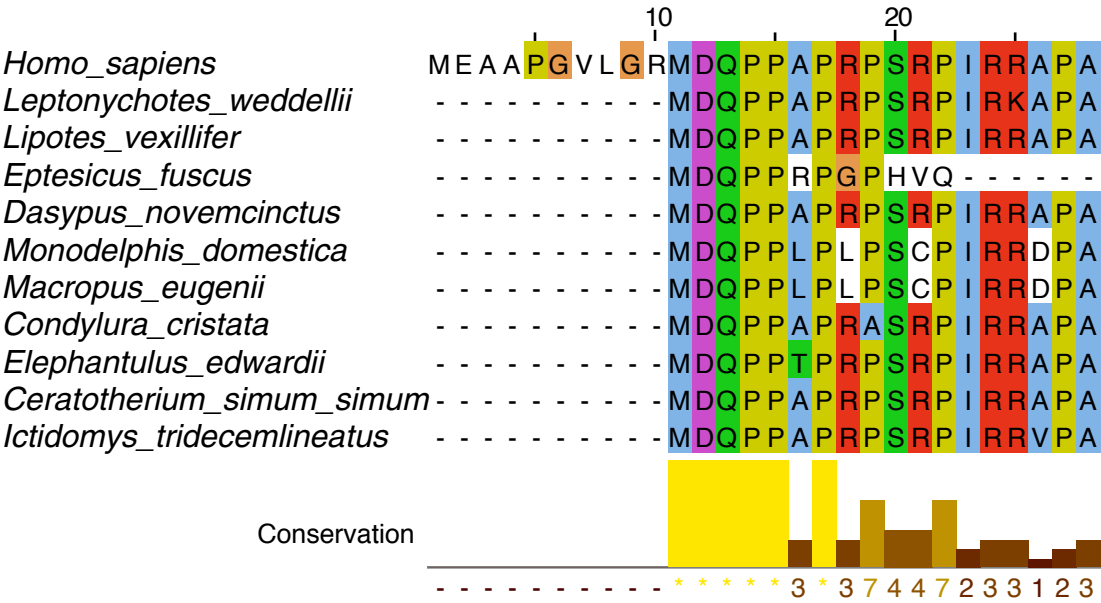
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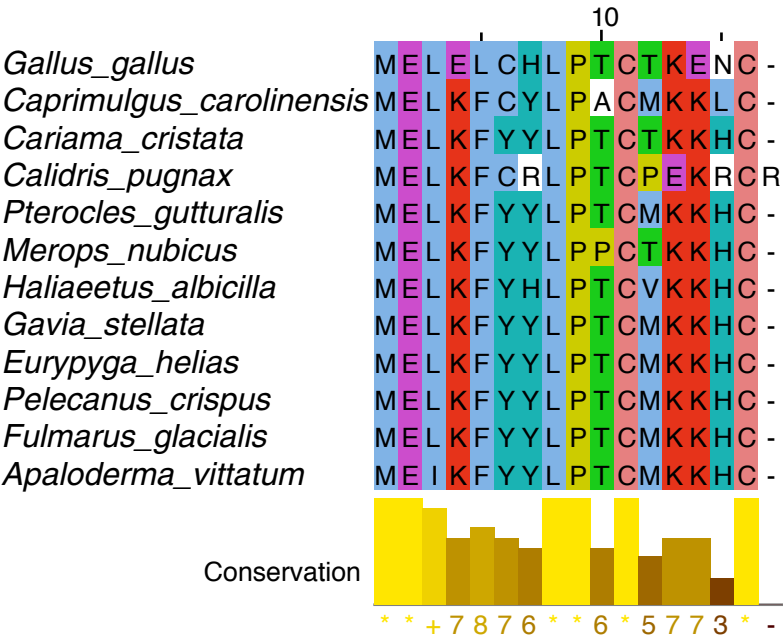
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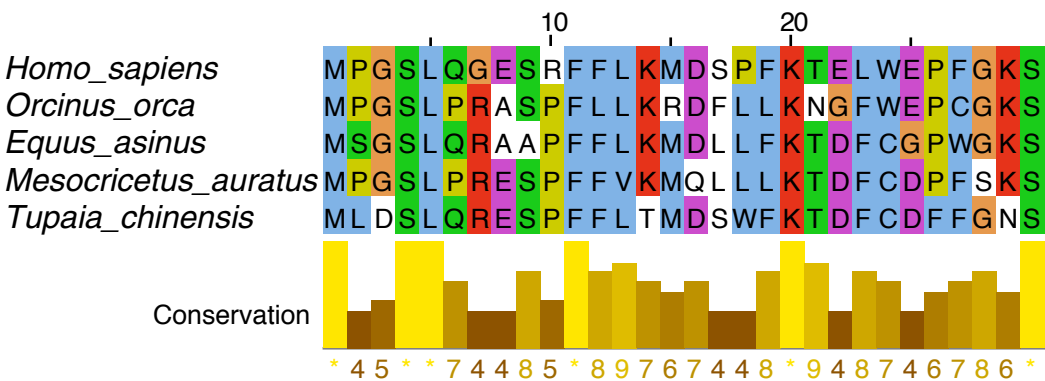
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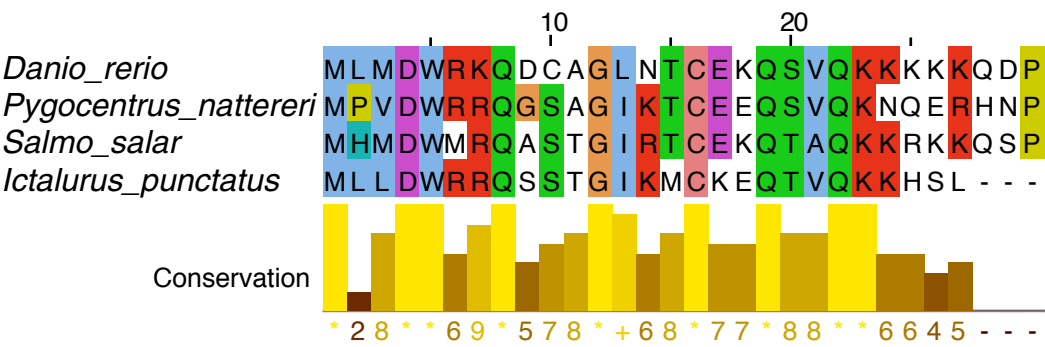
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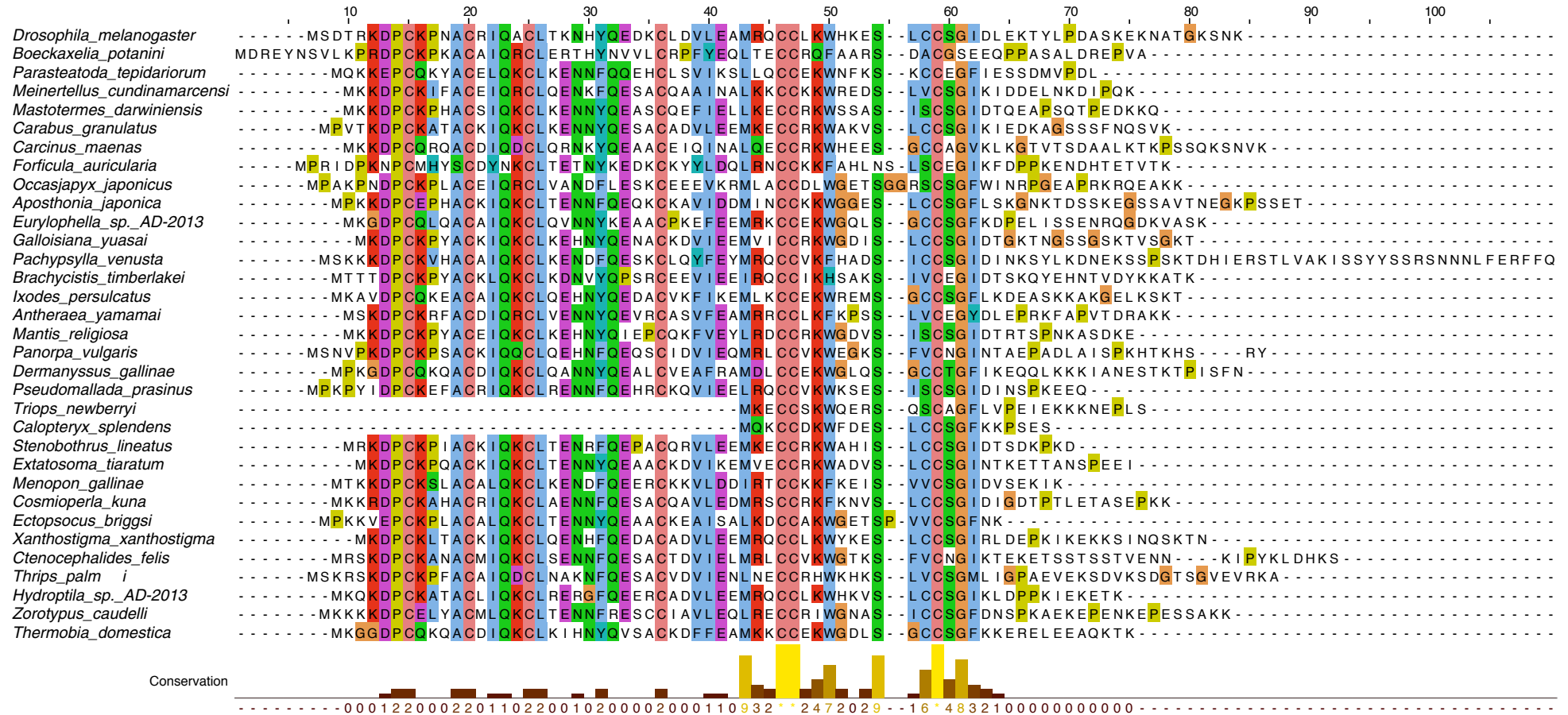
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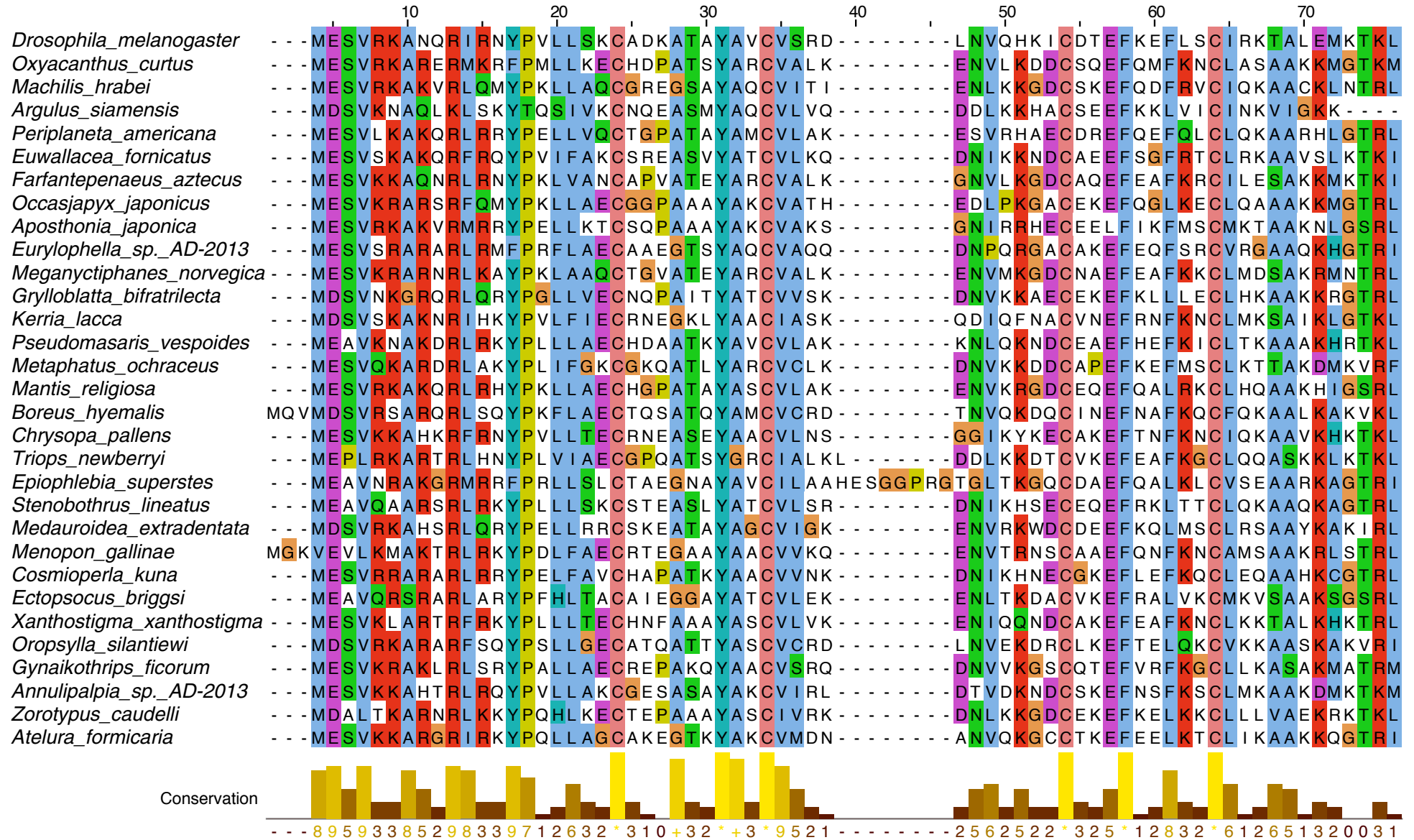
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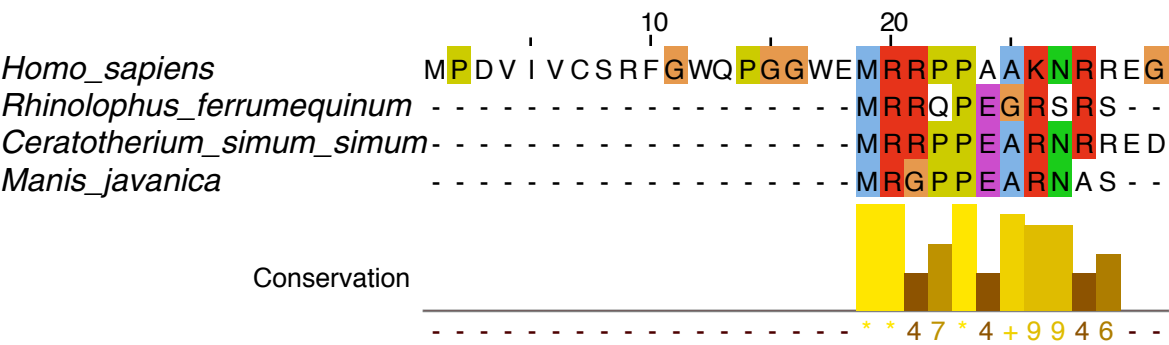
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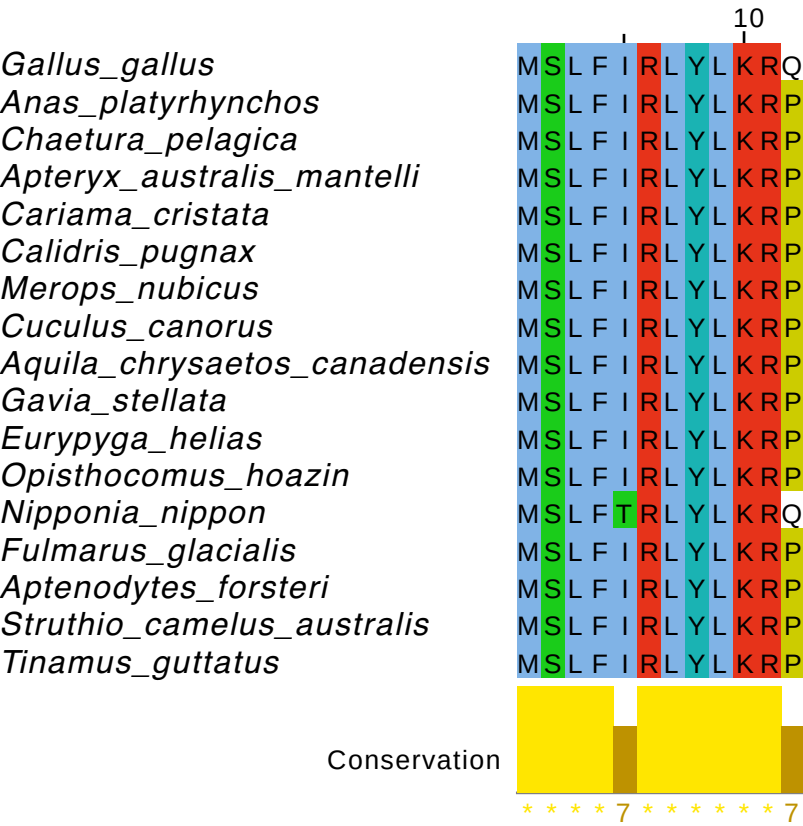
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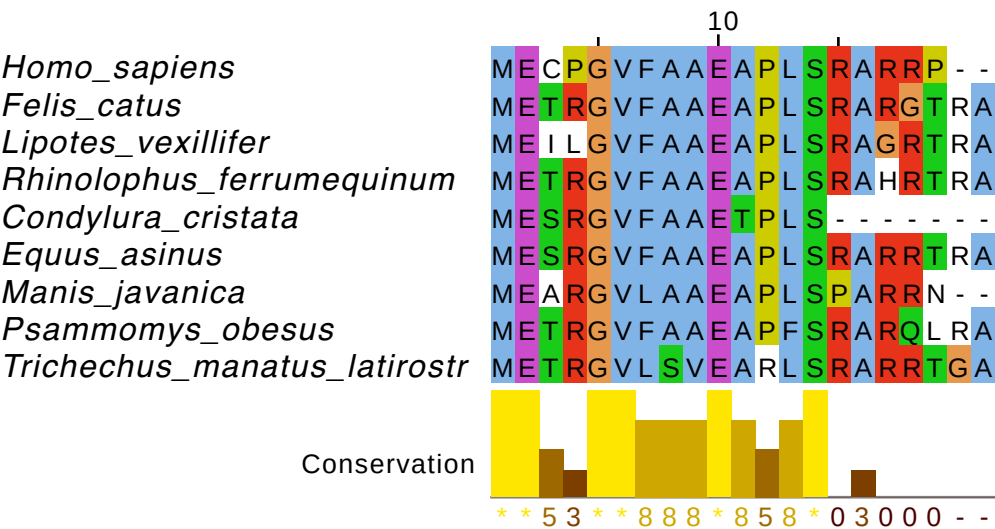
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HG0273.1

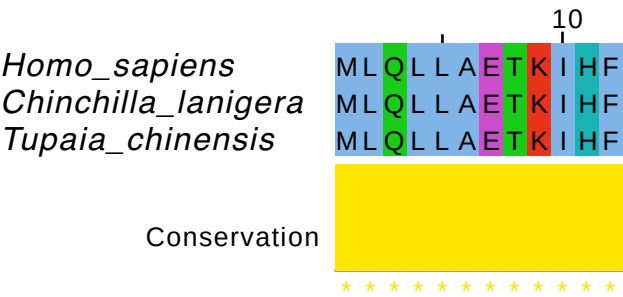
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HG0273.3

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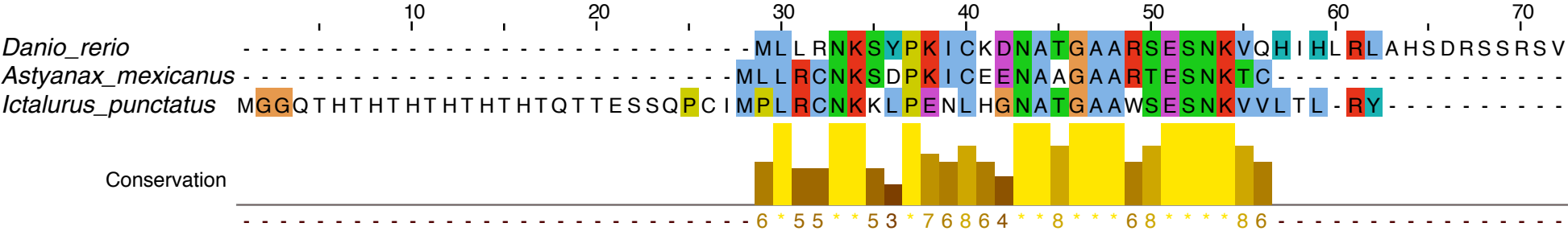


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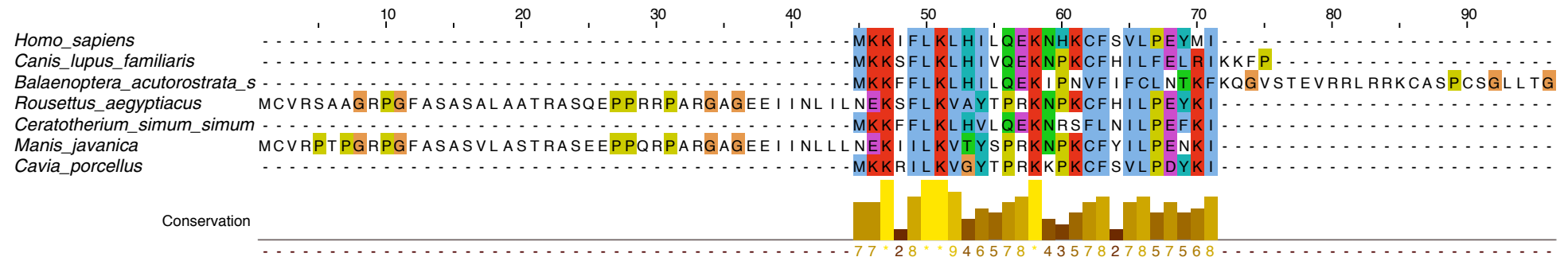
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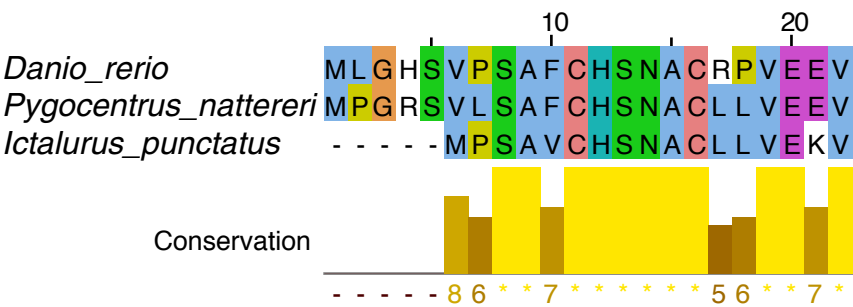
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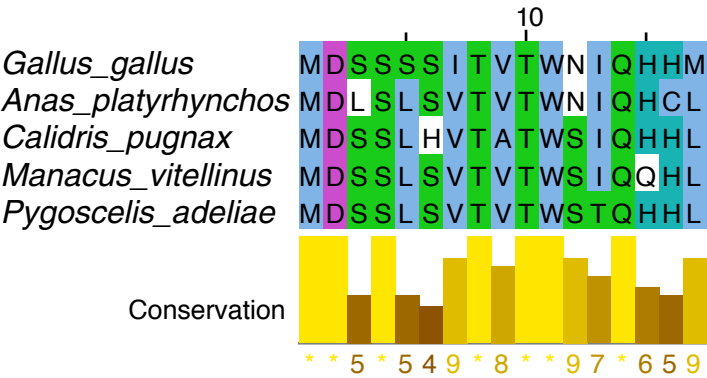


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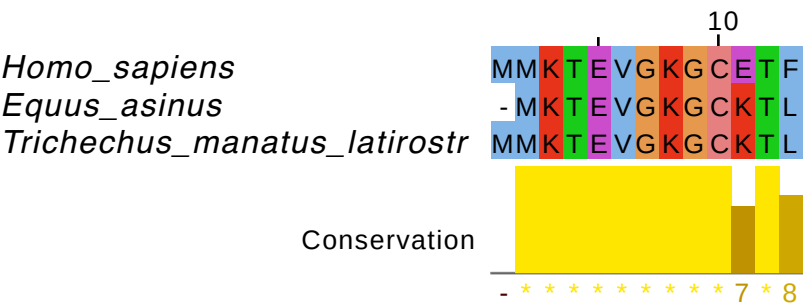


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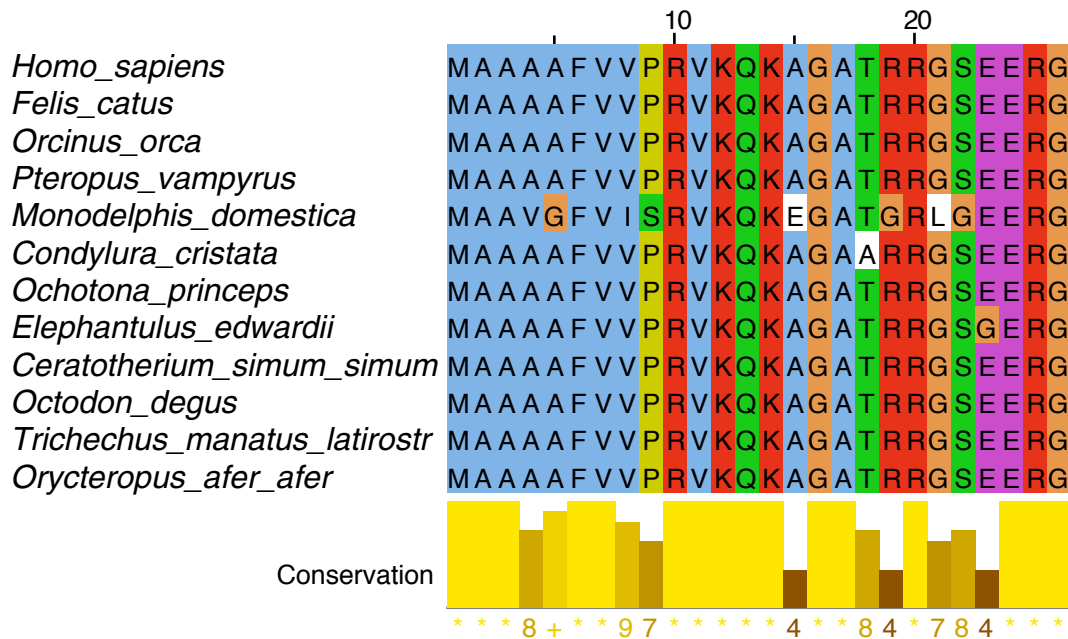
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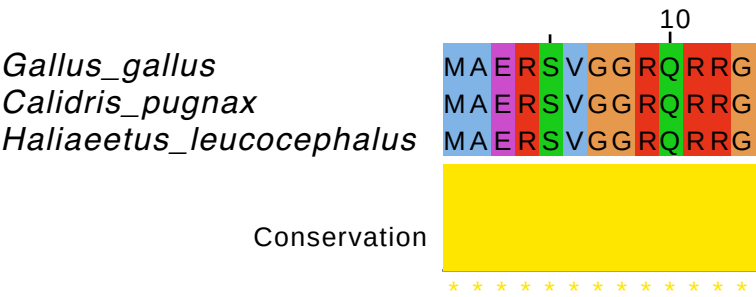


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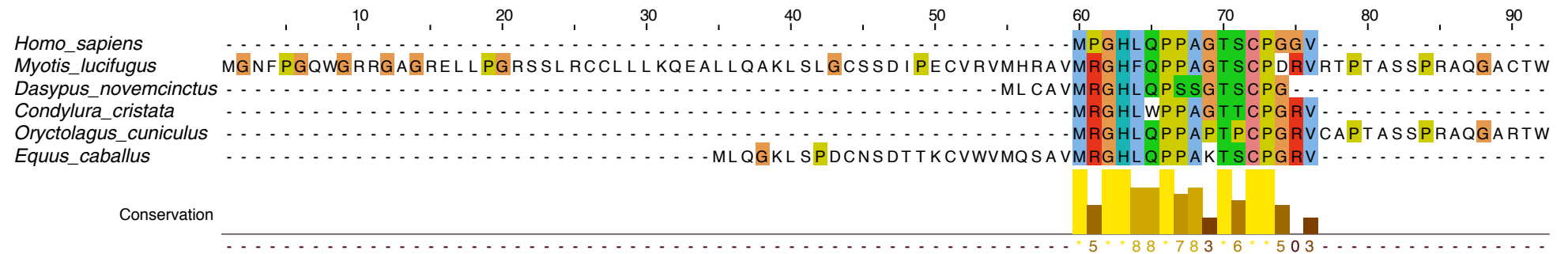
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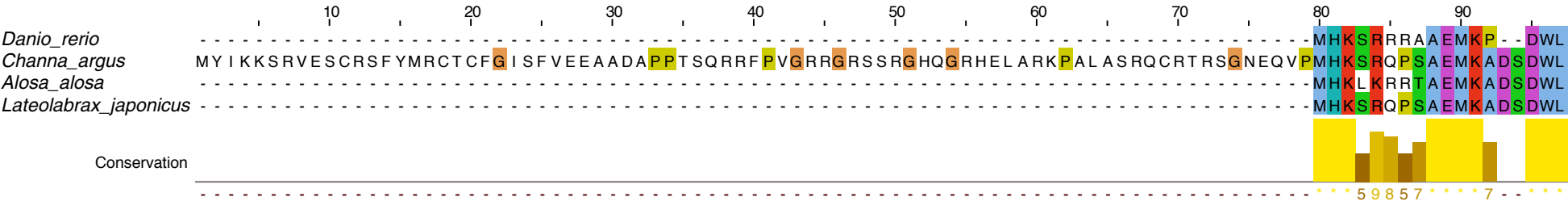


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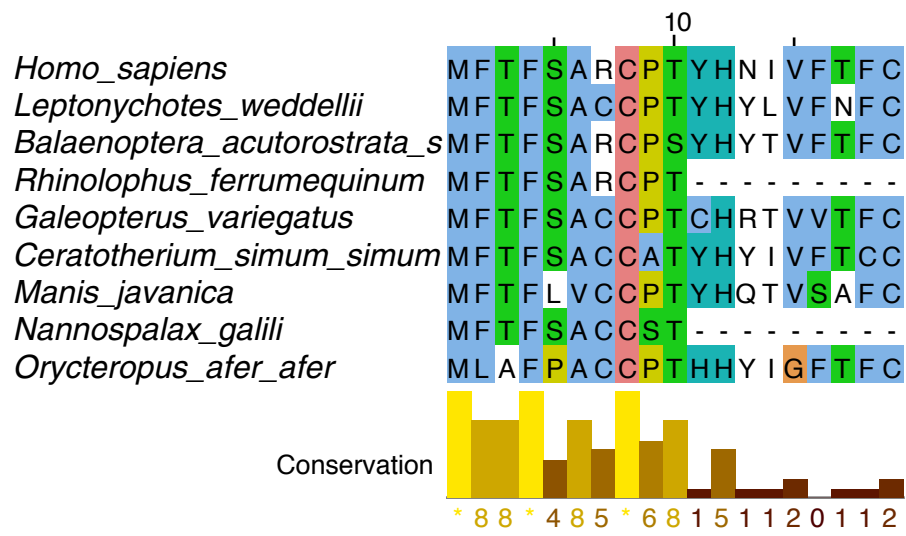
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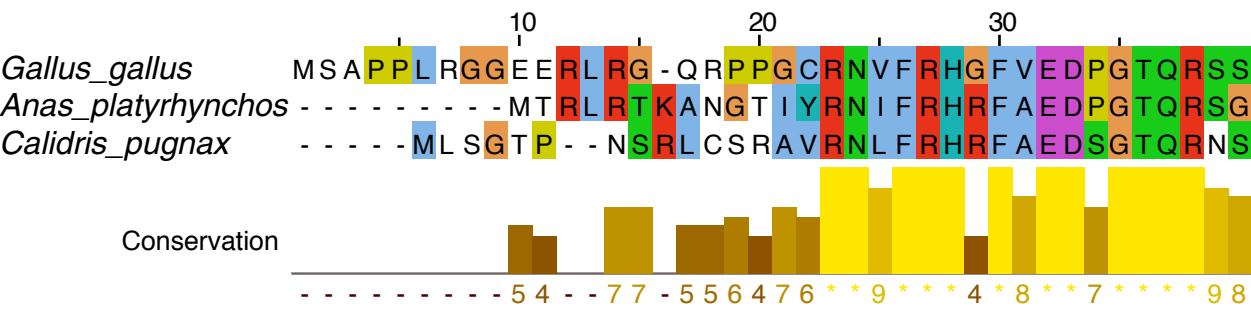
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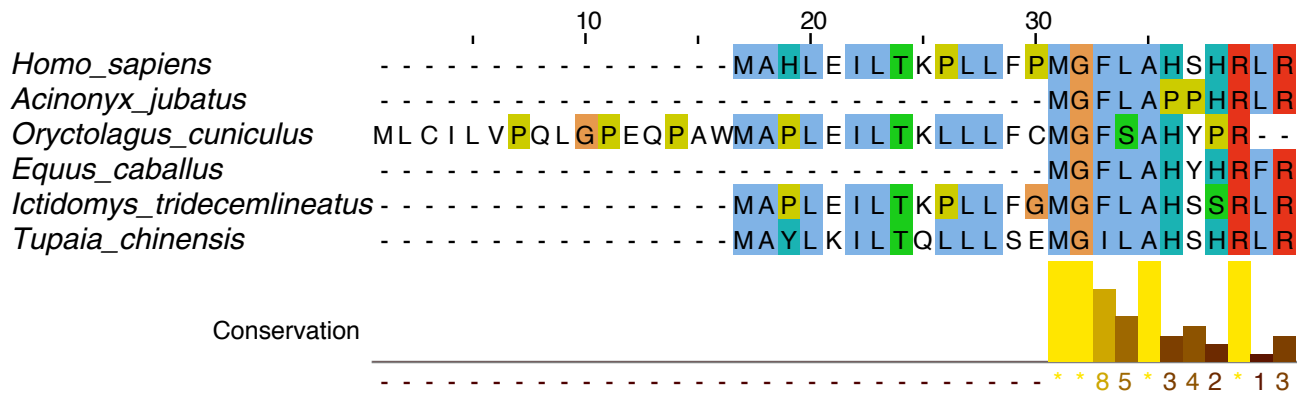
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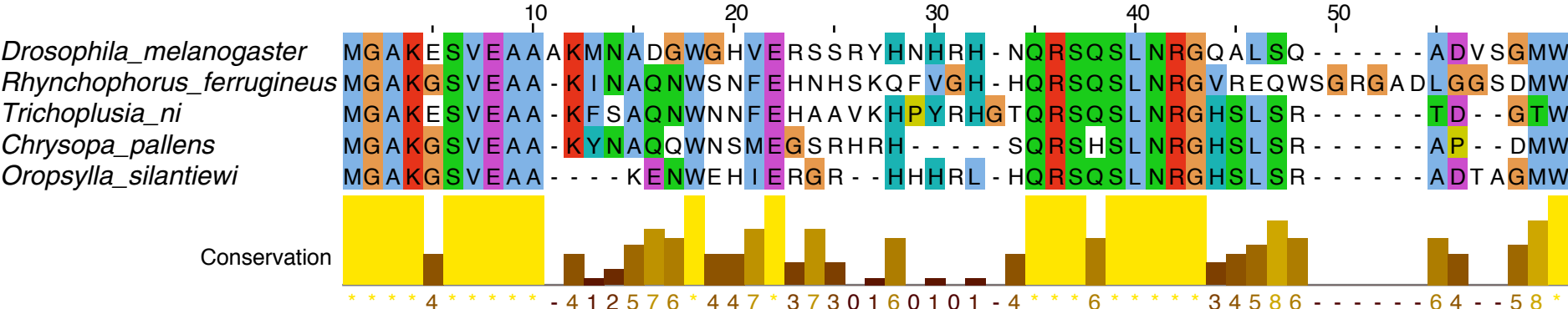
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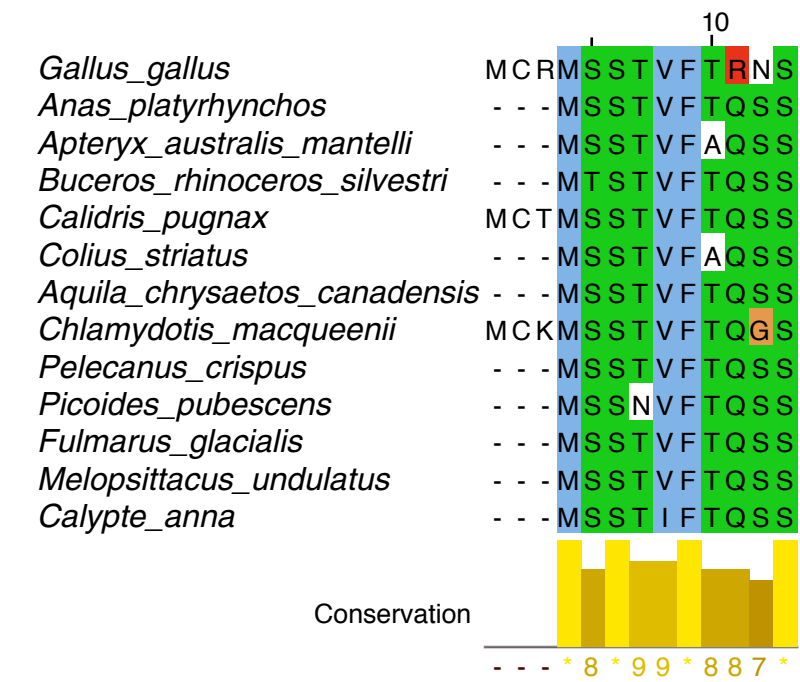
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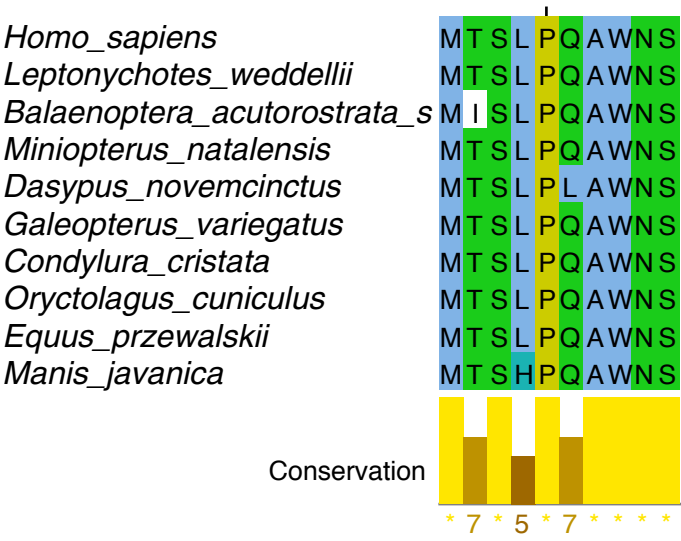
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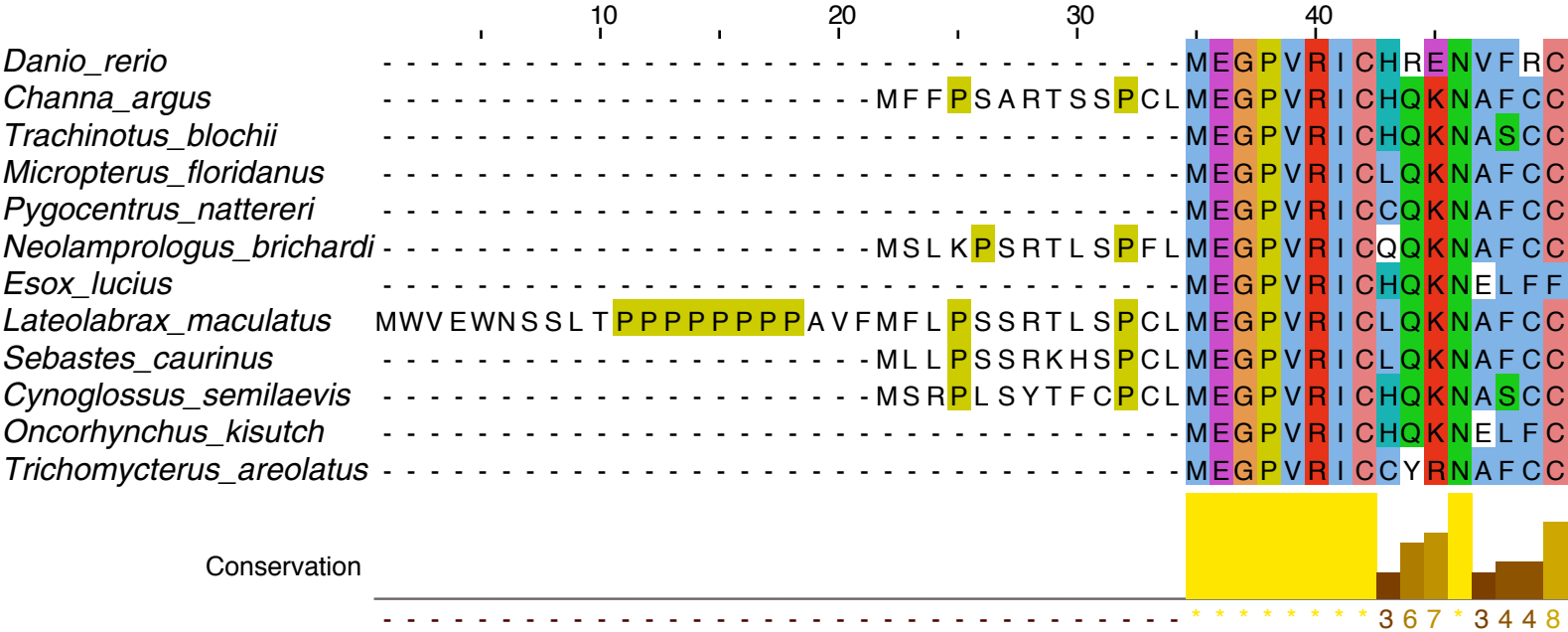
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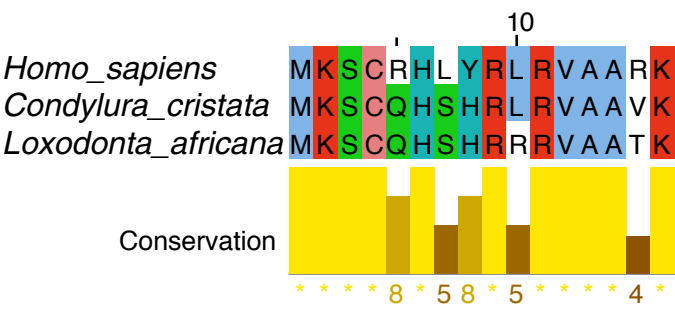
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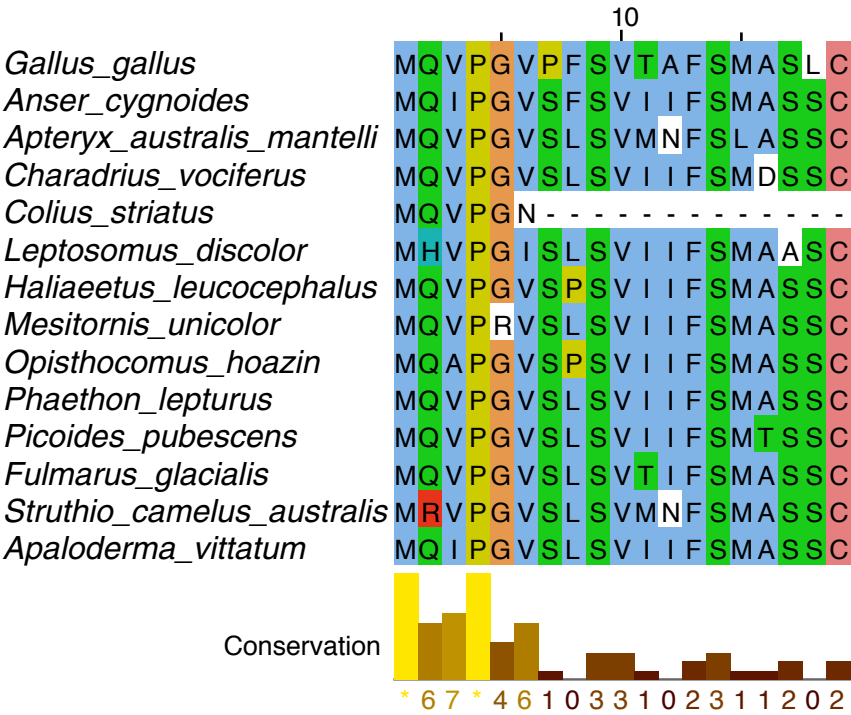
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ENSG00000144857 (BOC)



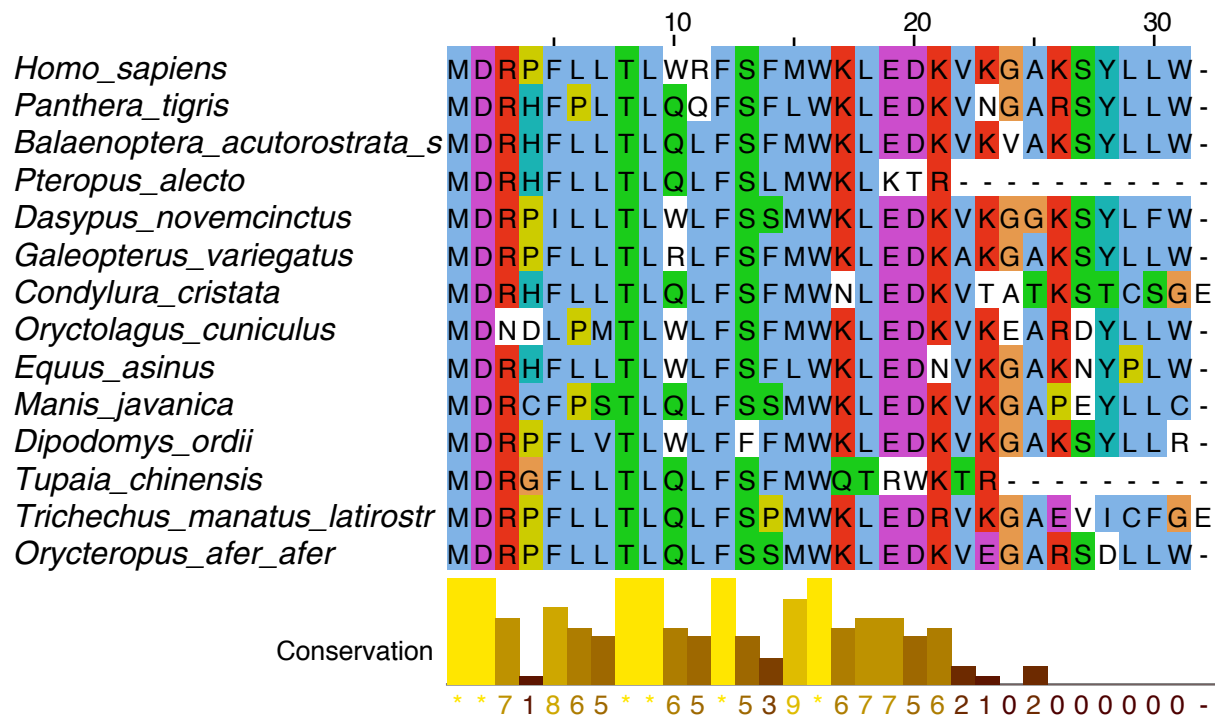
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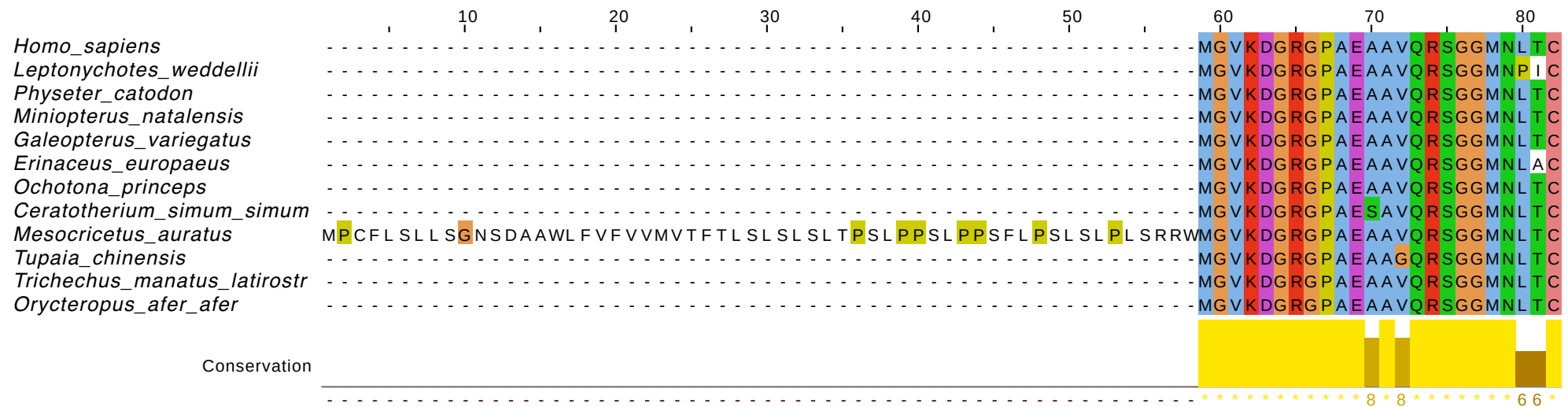
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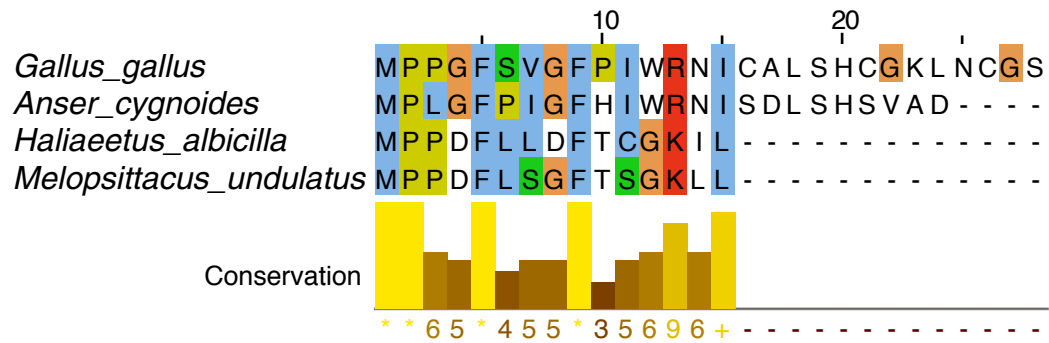
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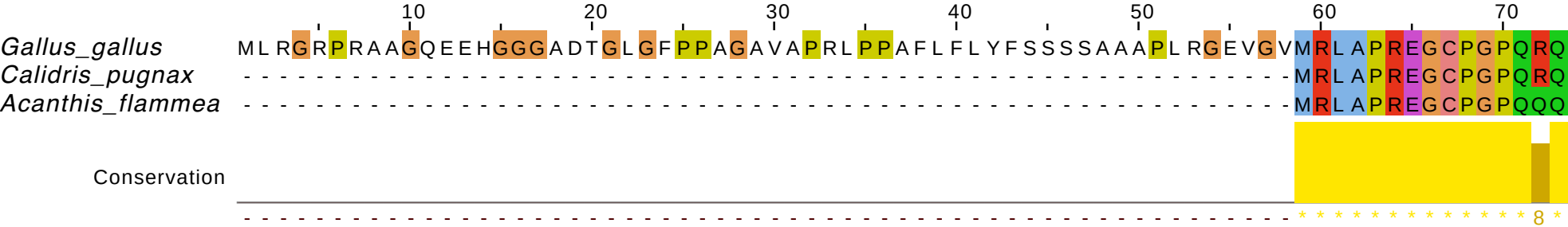


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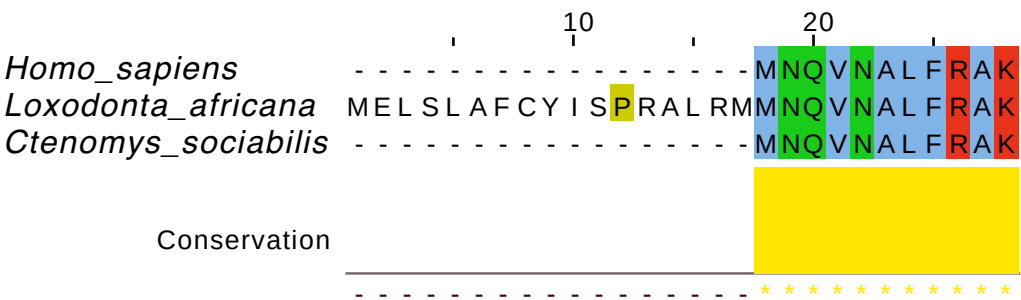


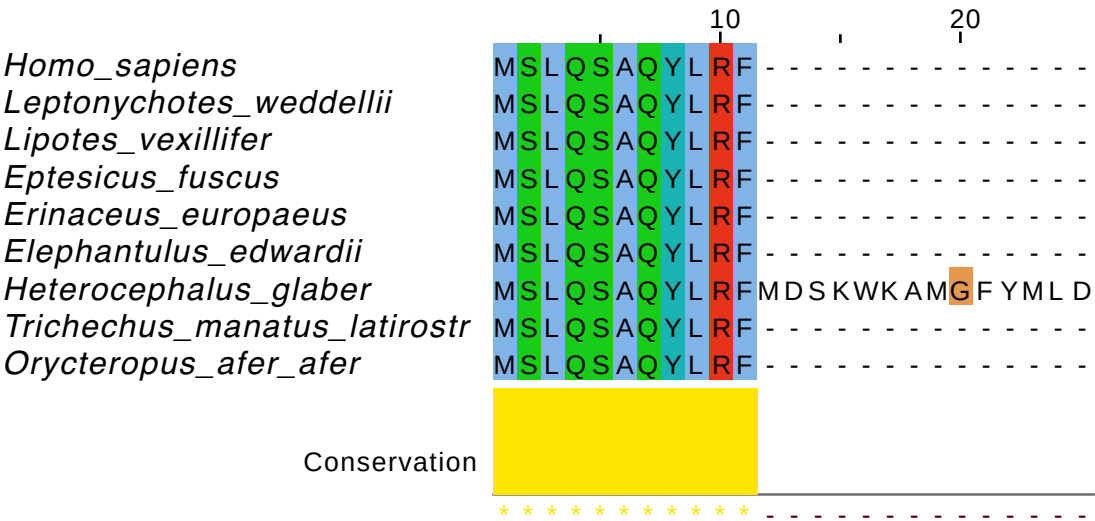
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HG0285.2

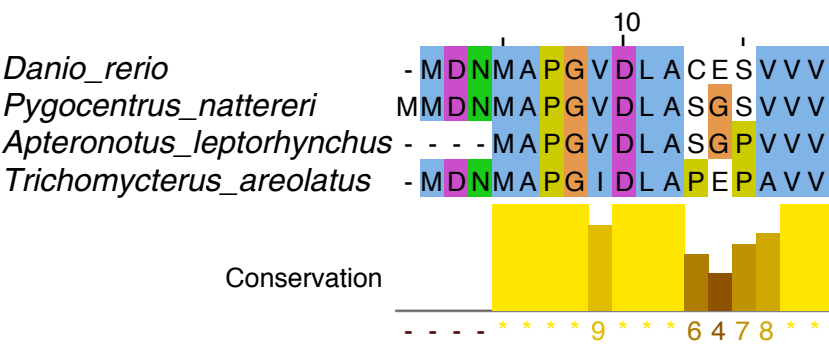
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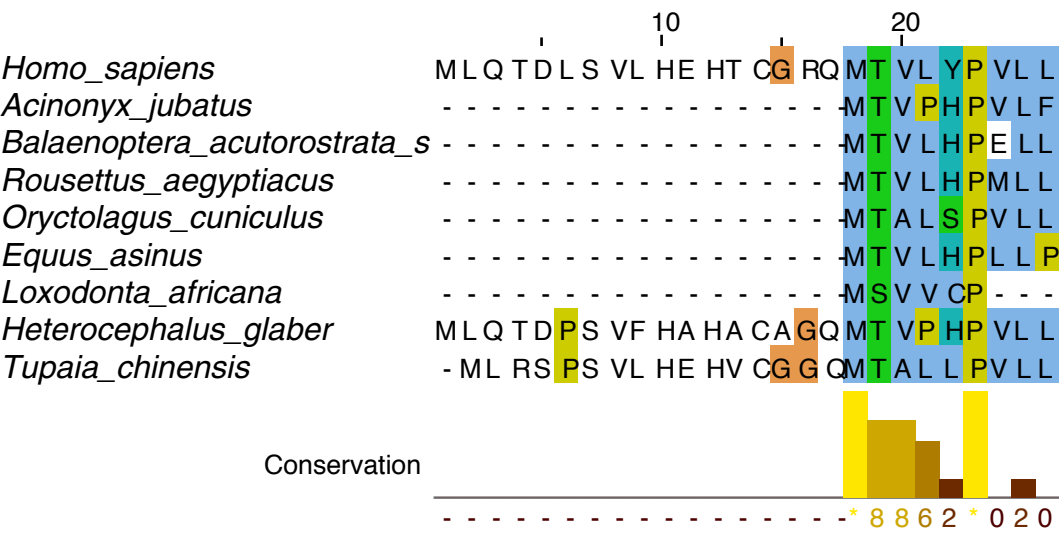
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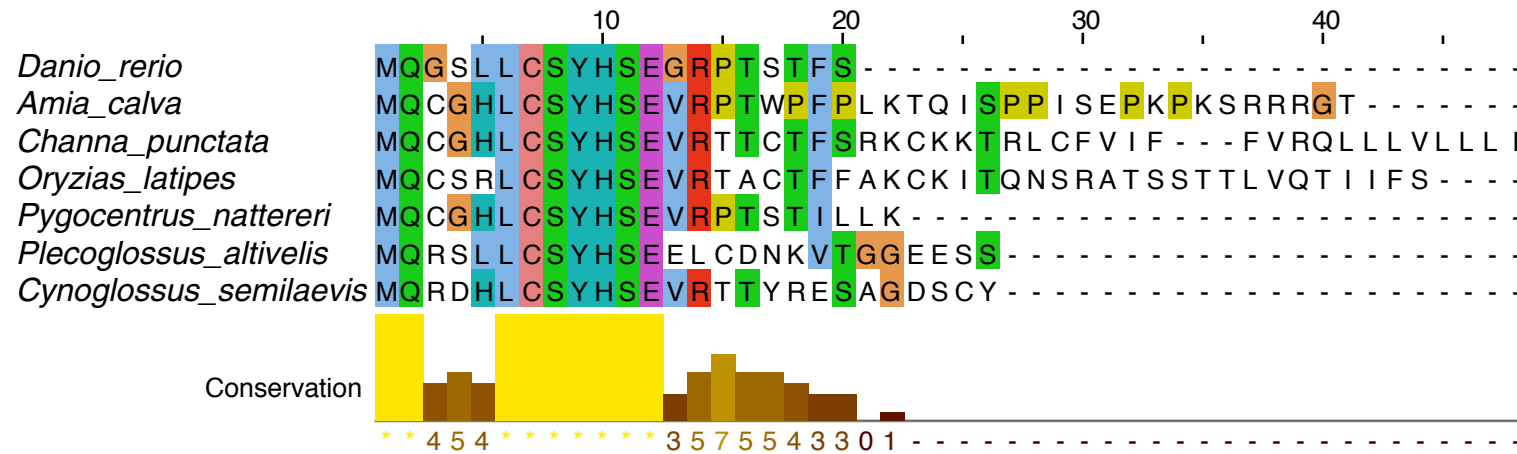
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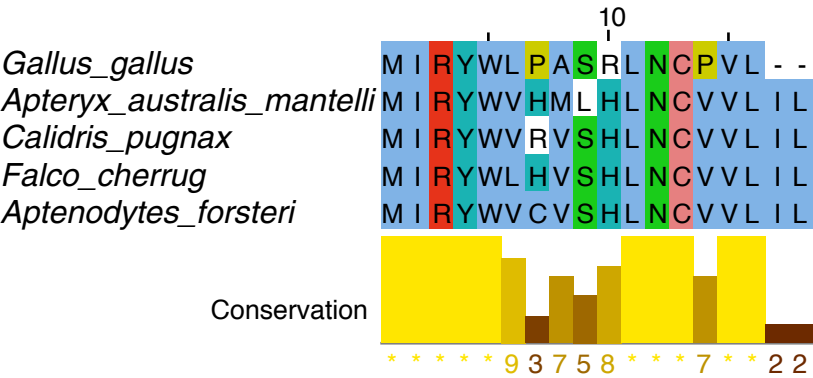
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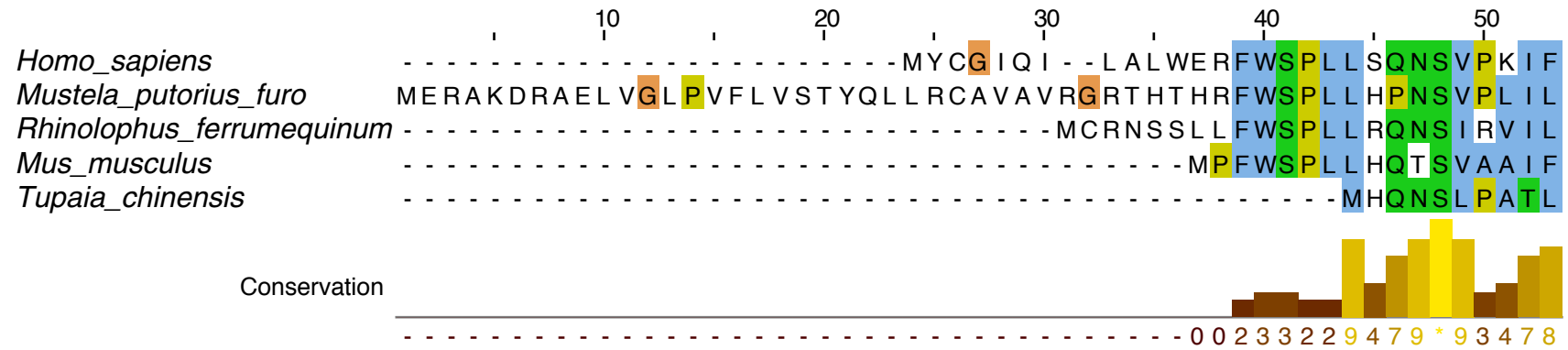
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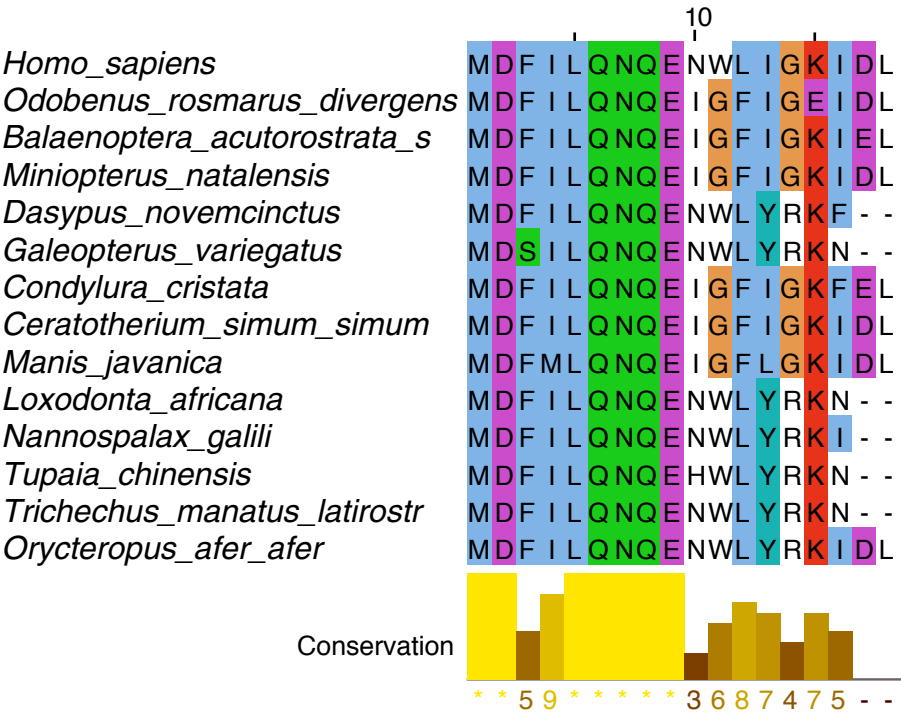
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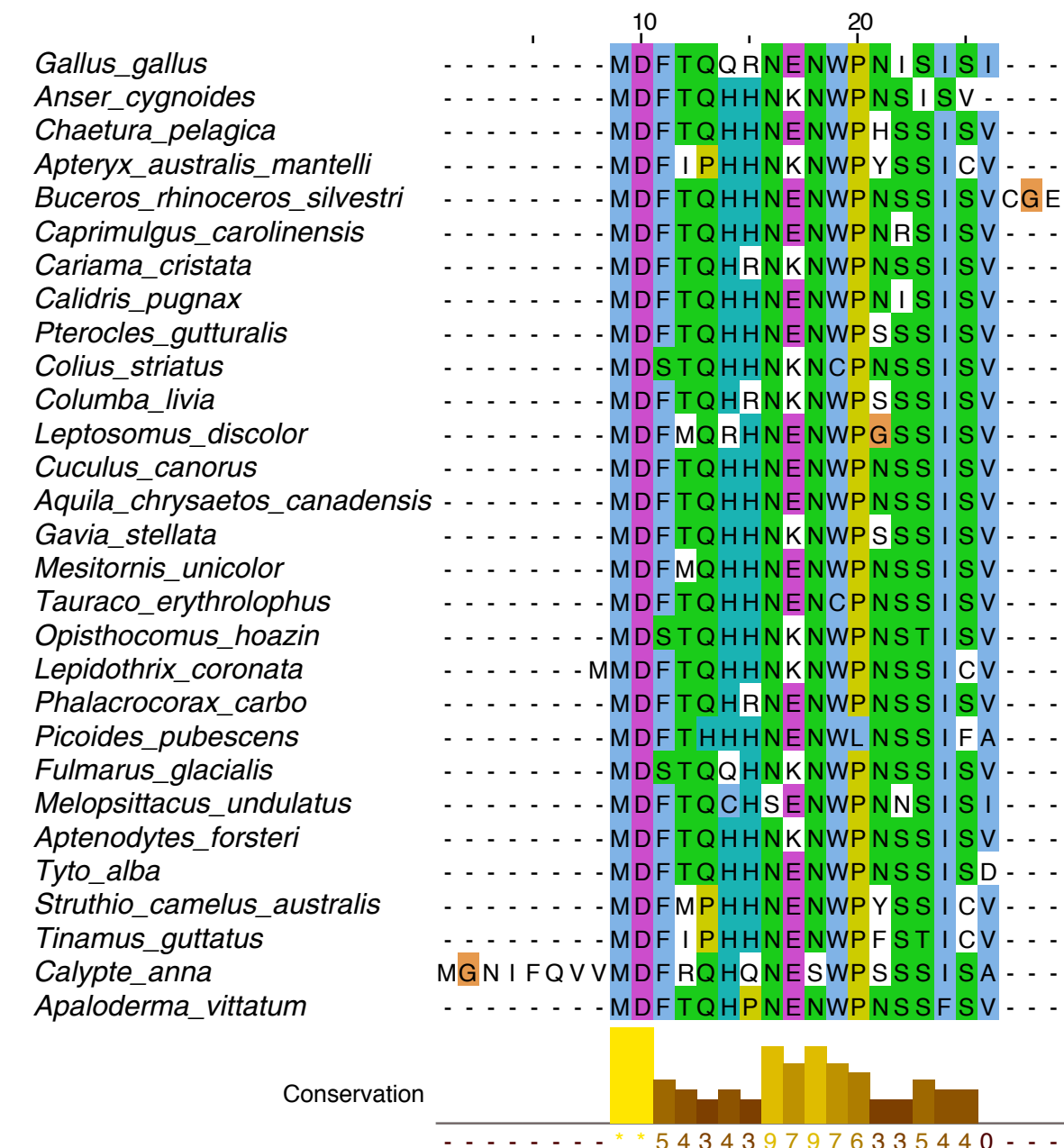


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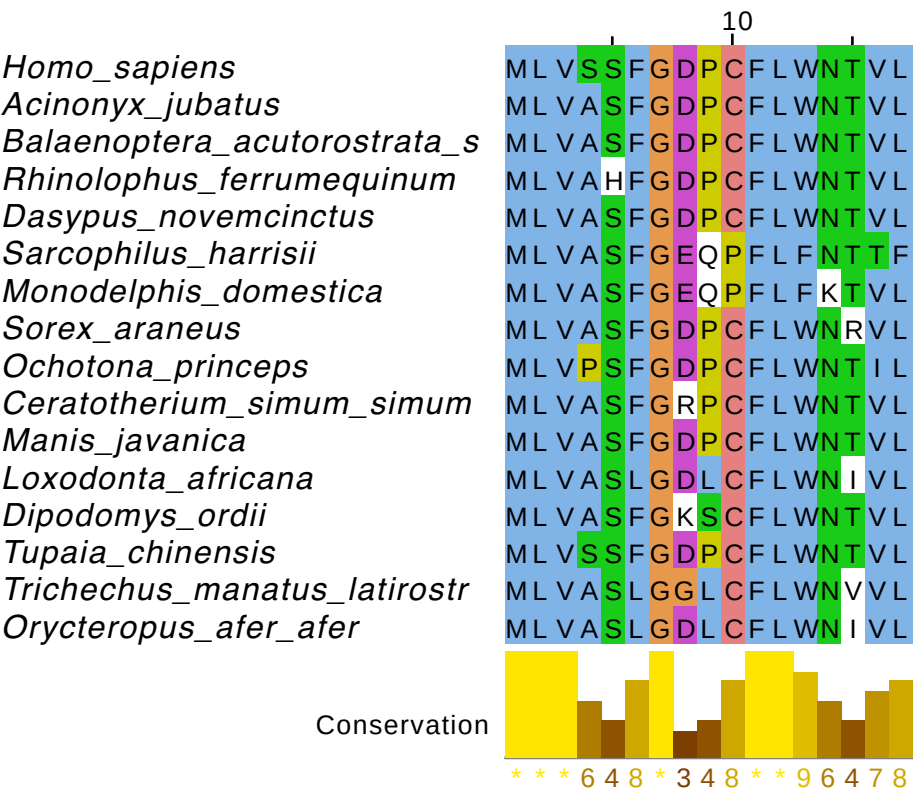


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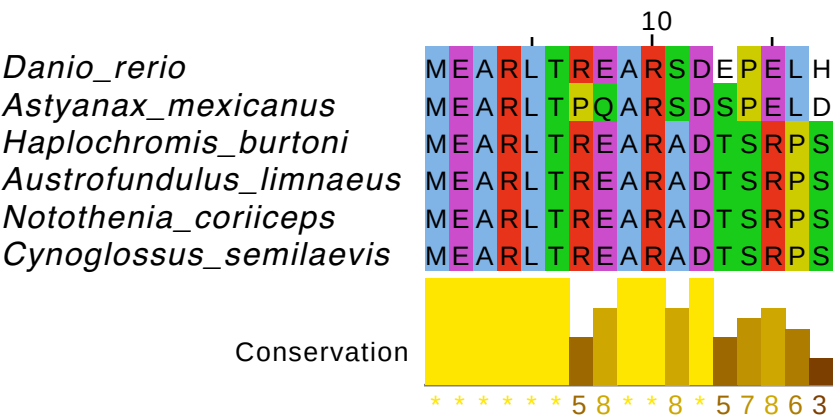
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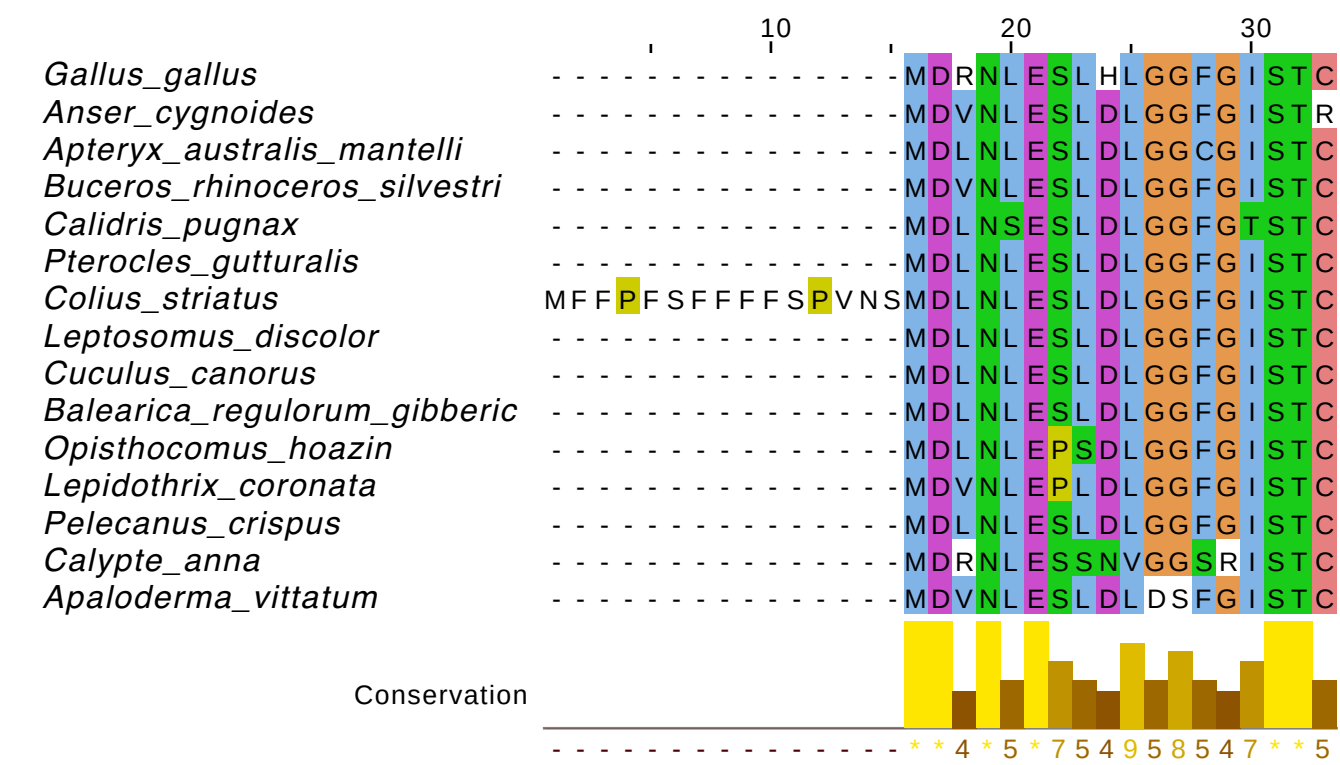
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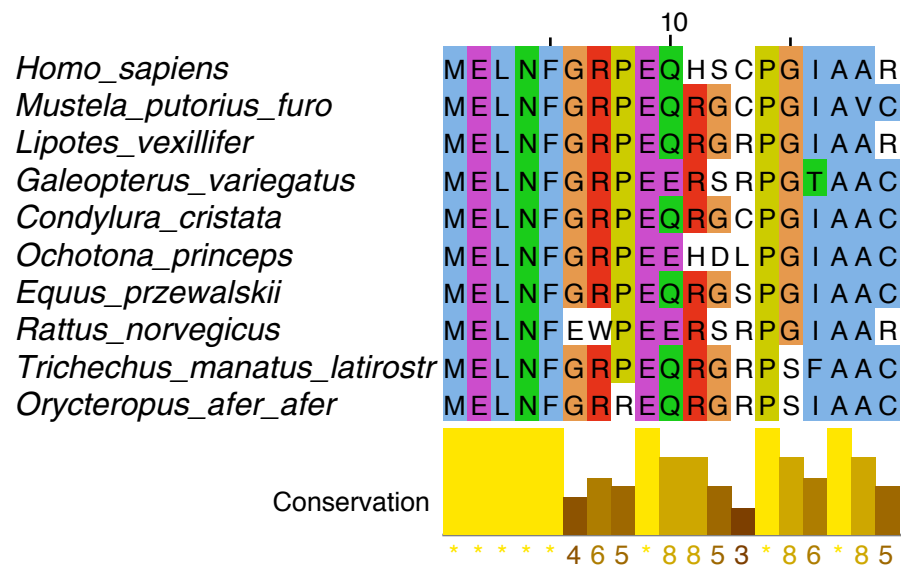
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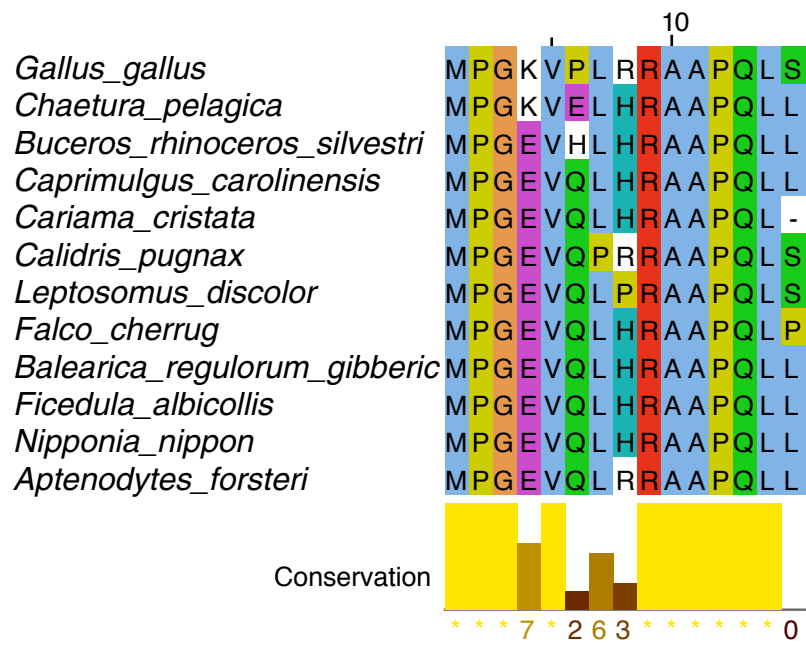
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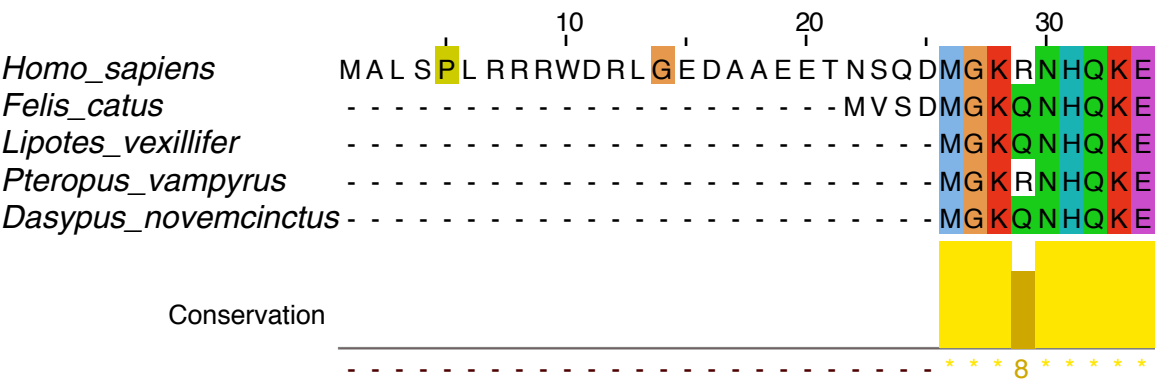
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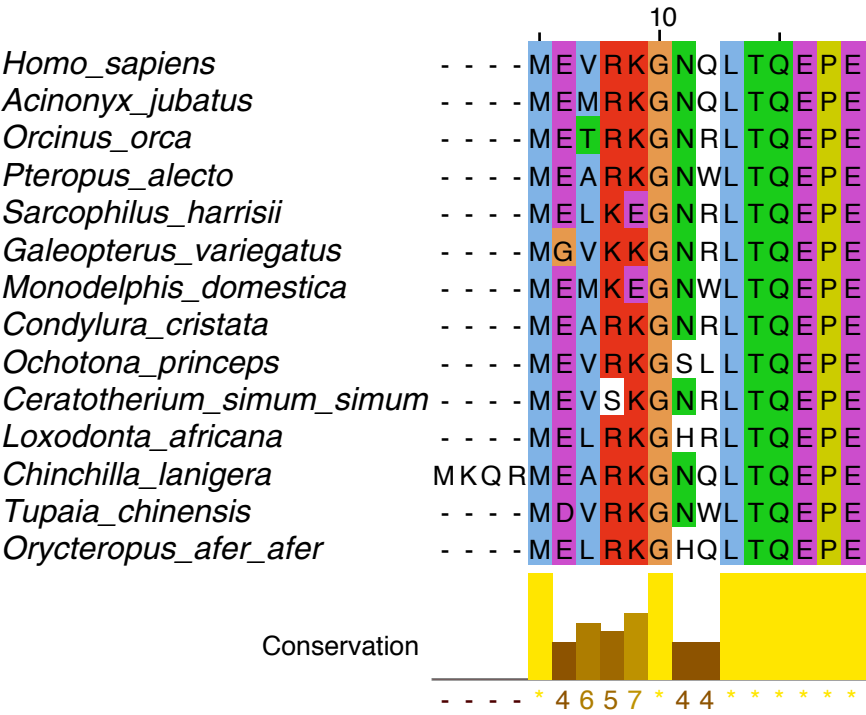
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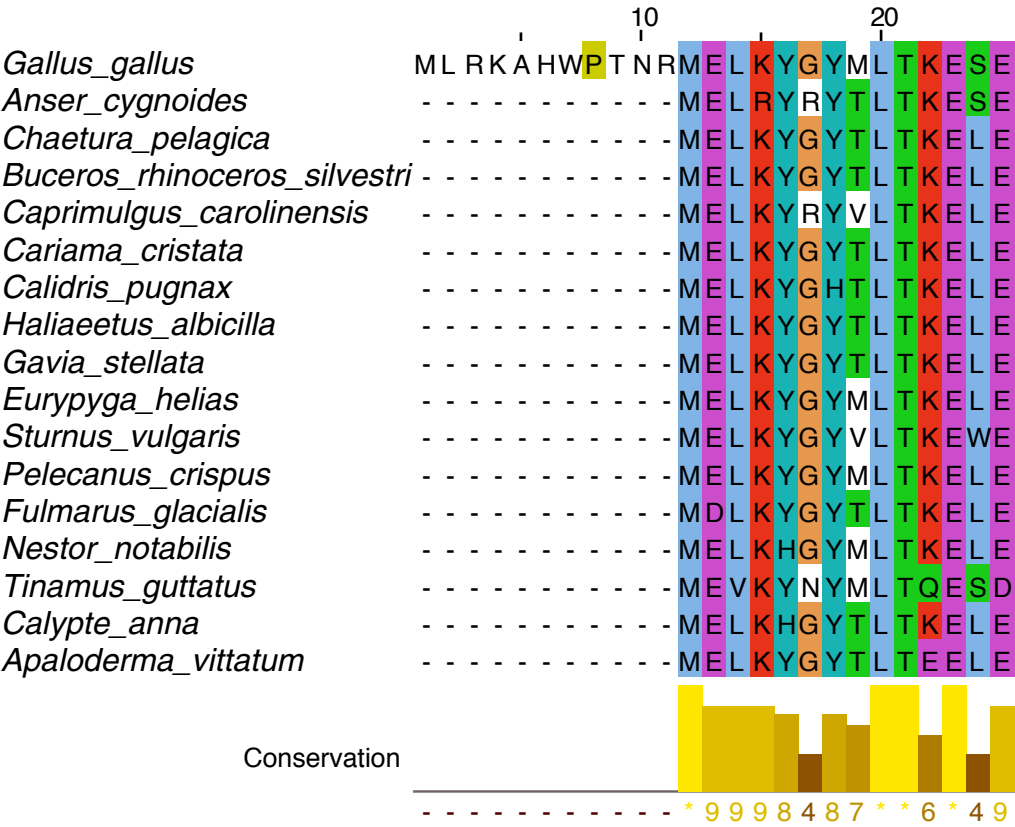
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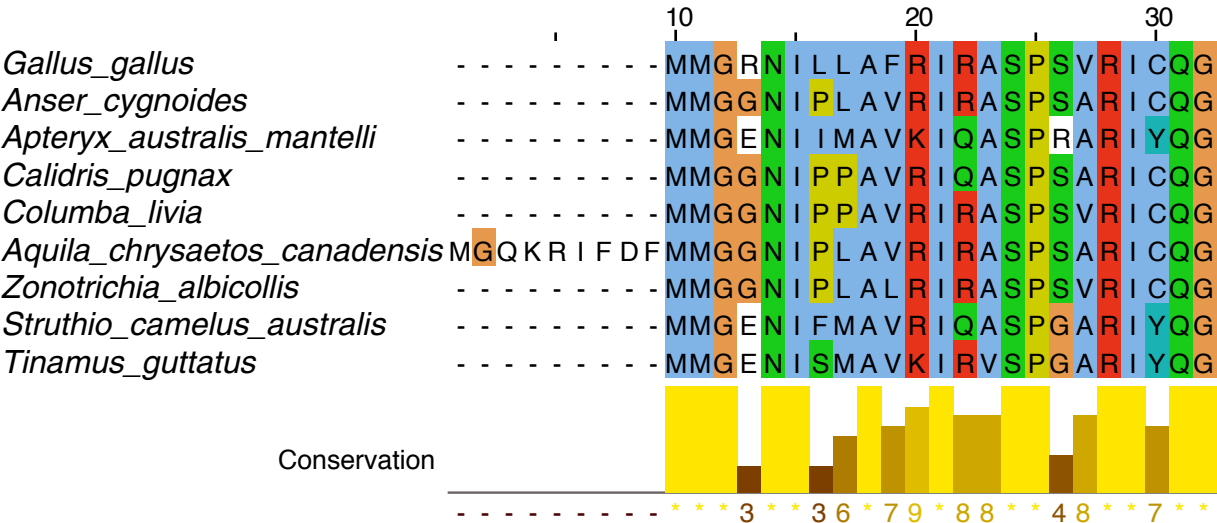
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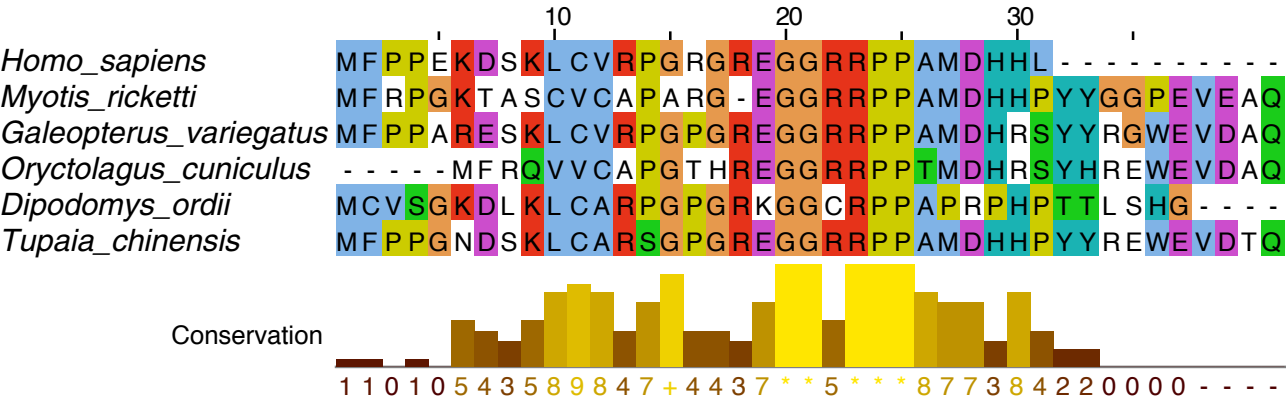
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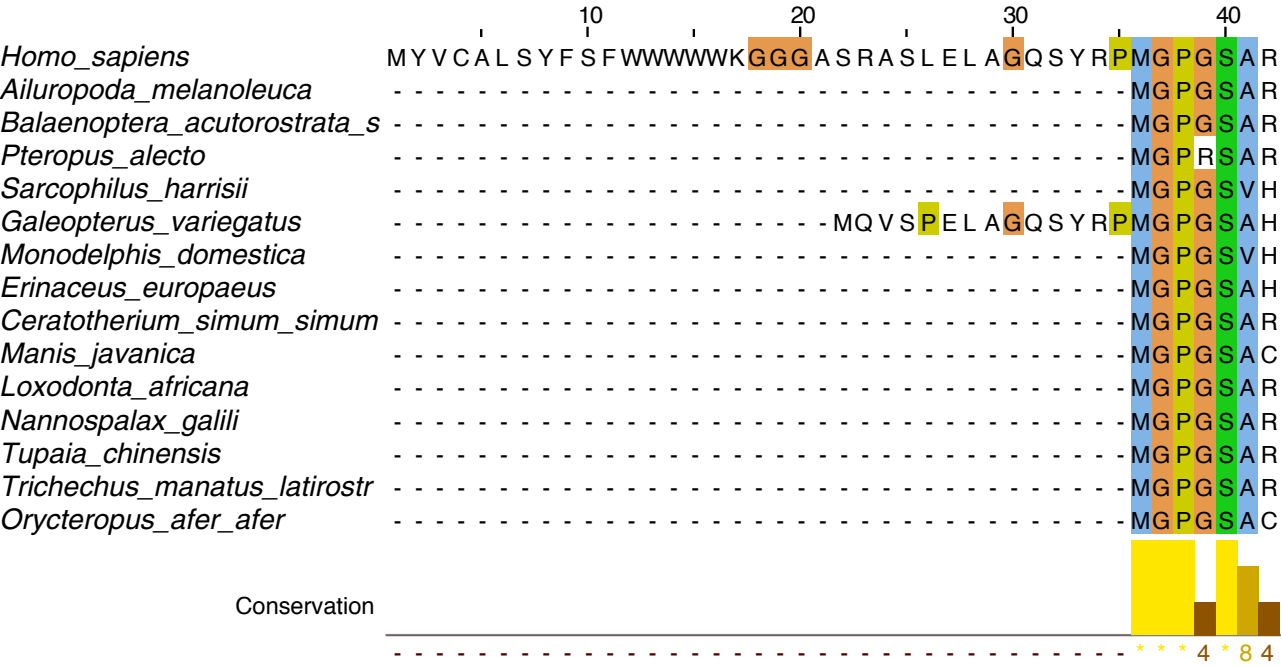
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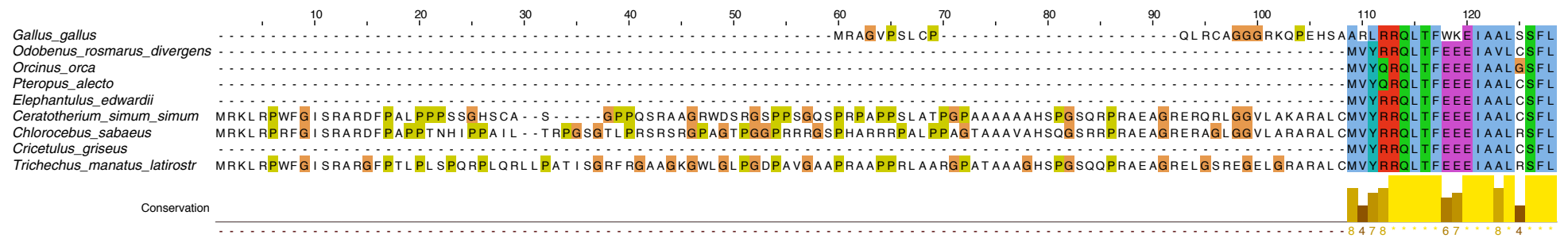


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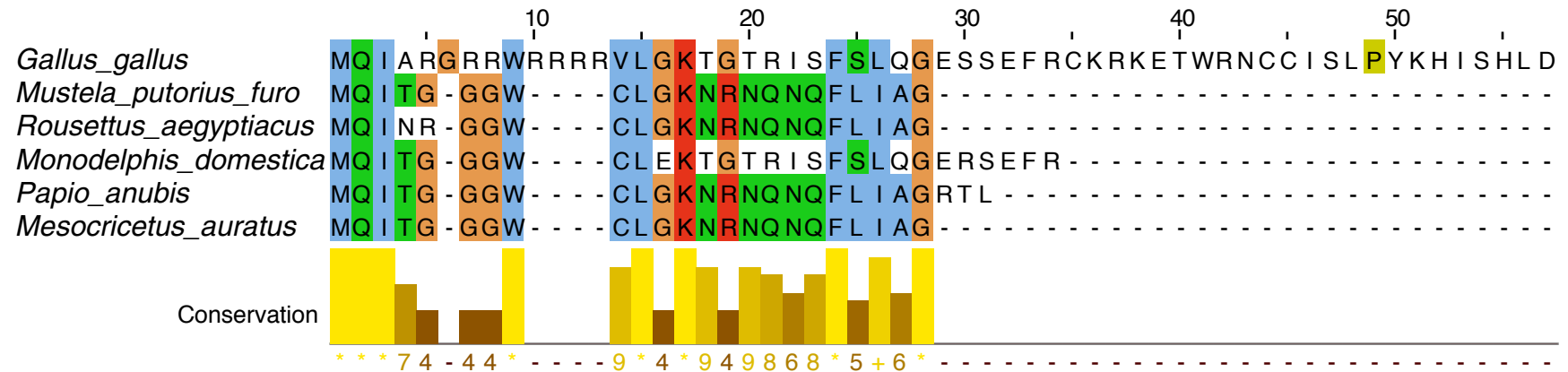


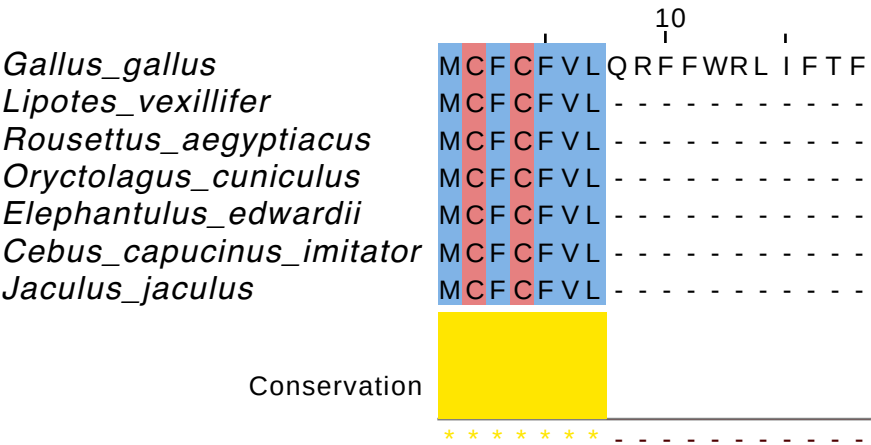
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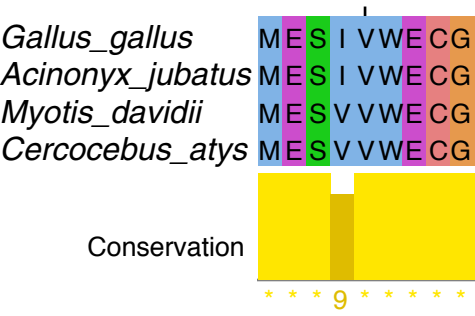
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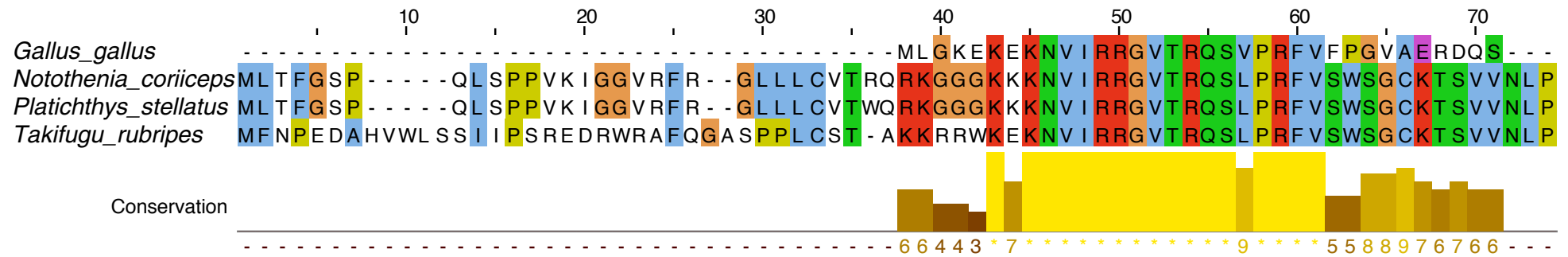


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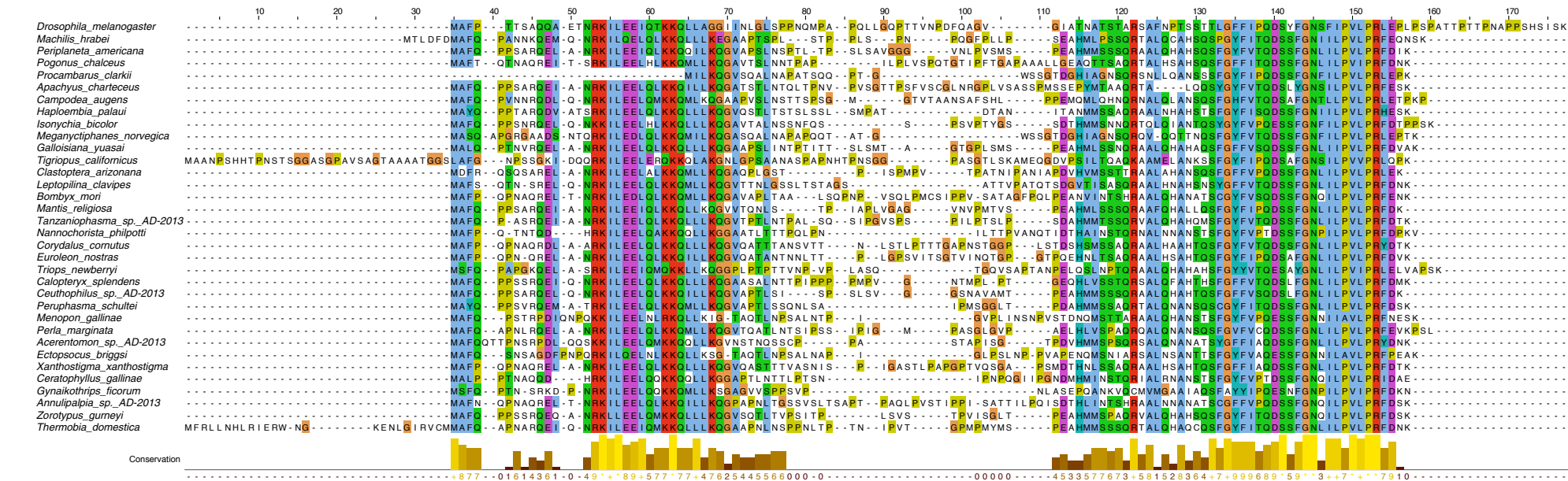
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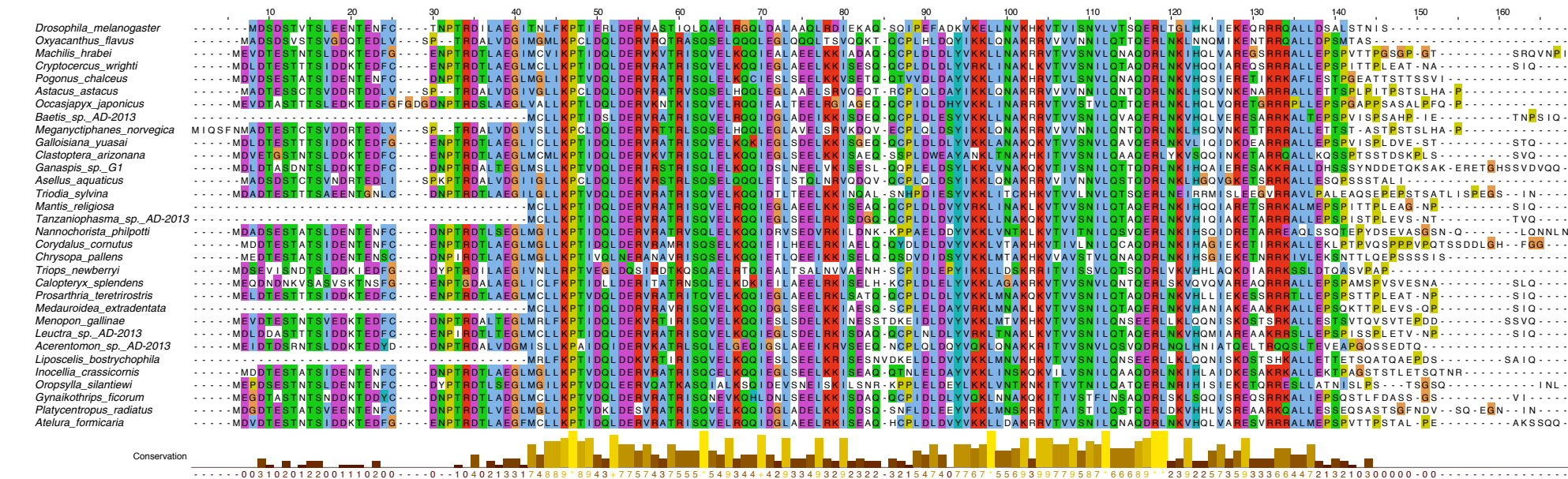
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<i>Drosophila_melanogaster</i>	-----	-----	MVNV	MVKGV	LV	ECD	PAM	KQ	FLL	HL	DE	KL	AL	GR	KFI	QDL	DE	NH	LF	ST	D	I	V	E	V	L	Q	A	R	V	D	D	L	M	D	R	I	S	F	P	L	H	D	K	D	A	-----																																										
<i>Eulimnogammarus_cruentus</i>	-----	-----	MVNV	IK	G	I	L	I	K	C	D	P	V	M	K	Q	L	L	L	H	L	D	E	T	L	A	L	G	S	K	F	V	L	A	N	L	D	D	C	H	L	F	V	A	Q	D	V	Y	E	Q	L	K	V	R	V	D	E	L	Y	E	K	V	Y	N	N	S	A	S	N	P	K	S	F	E	-----														
<i>Latrodectus_tredicimguttatus</i>	-----	-----	MVNV	Y	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	N	A	F	K	K	F	I	Q	D	L	E	T	H	L	F	I	A	P	D	M	L	E	I	L	Q	T	R	I	D	D	L	M	D	Q	I	S	F	P	L	A	E	K	-----																				
<i>Machilis_hrabei</i>	-----	-----	MVNV	K	K	G	I	L	V	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	G	L	G	K	F	I	Q	D	L	E	T	H	V	F	I	A	P	E	I	L	E	T	L	Q	S	R	I	D	D	L	M	D	Q	I	S	F	P	L	A	D	K	G	M	-----																			
<i>Argulus_siamensis</i>	-----	-----	MVNV	F	L	K	G	I	L	V	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	F	A	L	G	K	K	F	I	Q	D	L	D	N	H	L	F	I	S	S	D	I	E	T	L	K	A	R	I	D	D	L	M	D	Q	I	S	F	P	L	A	E	K	G	A	-----																		
<i>Mastotermes_darwiniensis</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	M	A	L	G	R	K	F	I	Q	D	L	E	T	H	L	F	I	S	A	D	I	L	E	T	L	Q	S	R	V	D	D	L	M	D	Q	I	S	F	P	L	A	D	R	G	L	-----
<i>Sitophilus_oryzae</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	K	L	G	R	K	F	I	Q	D	L	E	N	H	L	F	I	S	A	D	I	L	D	T	L	Q	A	K	I	D	D	L	M	D	Q	I	S	F	P	L	A	D	K	G	N	-----
<i>Eriocheir_sinensis</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	M	K	L	G	S	K	F	V	L	D	E	C	H	L	F	V	Q	P	E	V	Y	N	S	L	K	N	L	I	D	E	Q	Y	E	K	V	Y	N	Q	K	S	S	L	E	-----		
<i>Forficula_auricularia</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	S	A	L	G	R	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	P	L	A	D	R	G	L	-----
<i>Daphnia_magna</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	S	A	L	G	R	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	P	L	A	D	R	G	L	-----
<i>Occasjapyx_panicus</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	S	A	L	G	R	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	P	L	A	D	R	G	L	-----
<i>Haploembia_palau</i>	-----	-----	MVNV	H	V	T	K	G	I	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	A	D	I	L	T	L	Q	A	R	I	D	D	L	M	D	Q	I	S	F	P	L	A	D	K	G	F	-----																		
<i>Eurylophella_sp._AD-2013</i>	-----	-----	MVNV	H	V	T	K	G	I	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	I	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----																			
<i>Meganyctiphanes_norvegica</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Grylloblatta_bifratrilecta</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Cuerna_arida</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Copidosoma_floridanum</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Asellus_aquaticus</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Antheraea_assama</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Mantis religiosa</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
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<i>Boreus_hyemalis</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
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<i>Osmylus_fulvicephalus</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Triops_newberryi</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Epiophlebia_superstes</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S	T	E	I	M	V	N	V	M	K	G	V	L	E	C	D	P	A	M	K	Q	F	L	L	H	L	D	E	T	L	A	L	G	K	K	F	I	Q	D	L	E	T	H	L	F	I	S	S	D	I	L	E	T	L	Q	A	R	V	D	D	L	M	D	Q	I	S	F	T	D	K	Q	Q	-----		
<i>Platynocheilus_peltifer</i>	-----	-----	MVNV	M	K	Y	I	Q	Y	L	-	R	R	K	S</																																																																										

HG0301

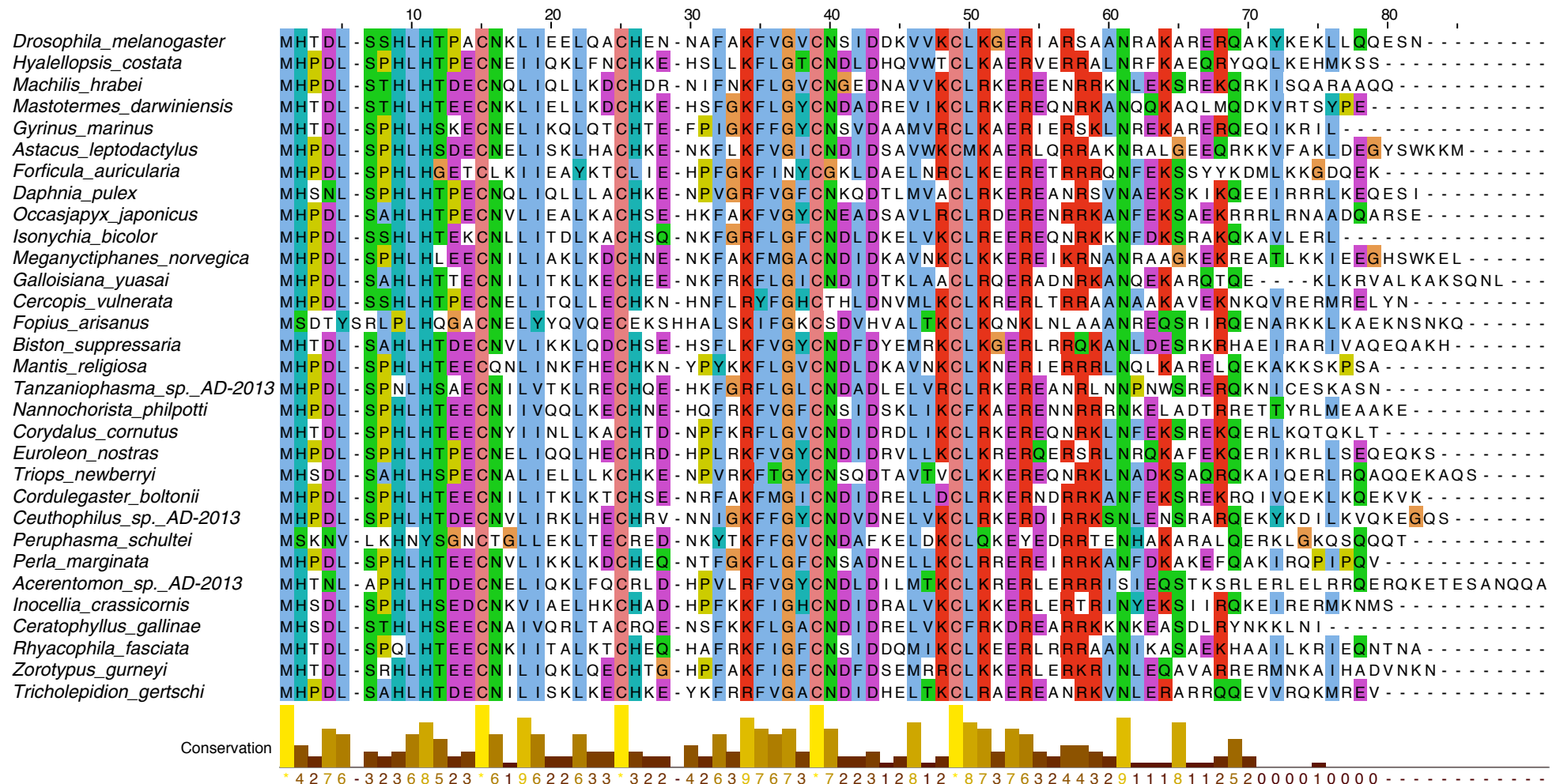
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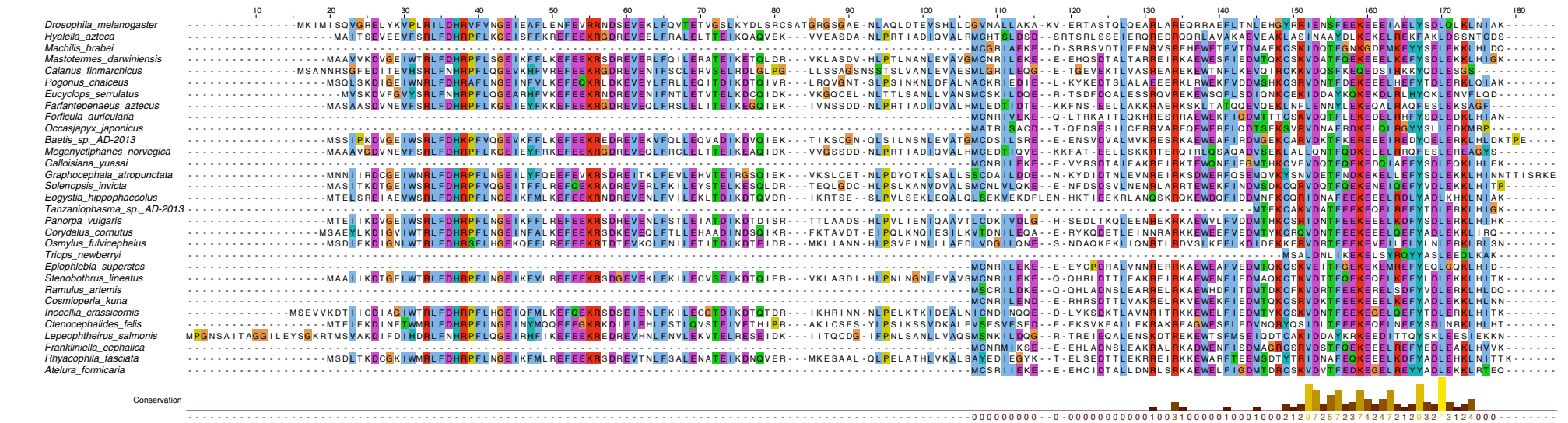
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HG0305

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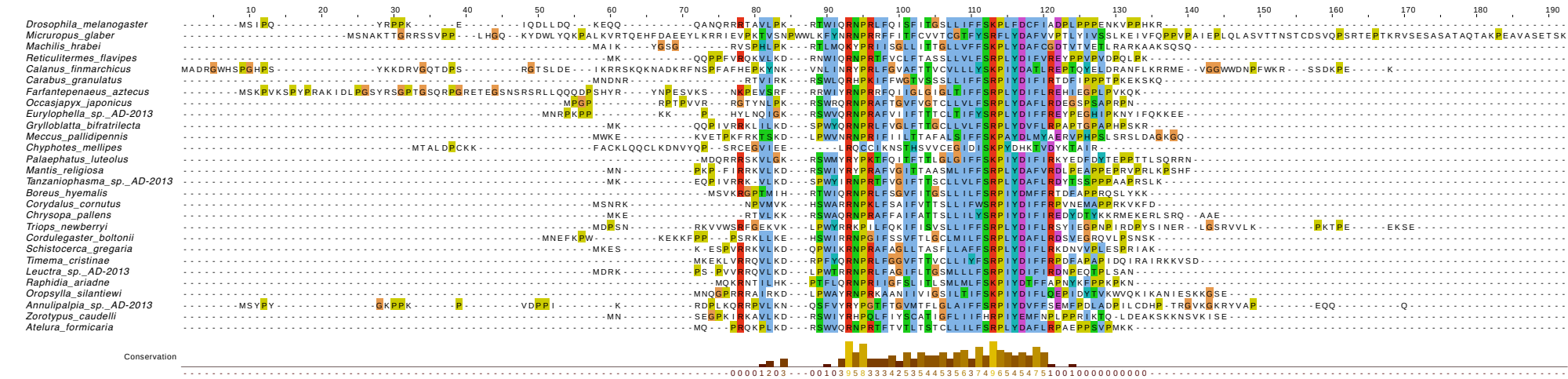
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<i>Asprogammarus_rhodophthalmus</i>	MGSMTLGT	RSFQPTTPPA	KGSFPLDHEGECK	TFMIKYMEC	MHQTTGGNN	SECREKARD	YLSCRM	EKGGLMAR	EEWSKLG	YADLASSAARDG	SE----							
<i>Meinertellus_cundinamarcensi</i>	MTTMTFGQ	KSFKPTTPPD	KGSFPLDHEGECK	RTMLKYMLC	LRENNNDNS	QCRVQAKD	YLCRMD	NNLMAK	EDWKT	LGLGDIVPEK	-----							
<i>Prorhinotermes_simplex</i>	MSSVTF	SQKFTPIPP	DKGSFPLDHEGQCK	KAMVKYMIC	LKTNNKND	SSPCREDAM	AYLDCR	MSNHLMA	KEEWSK	LGFSDVKT	KTSEK-----							
<i>Dastarcus_helophoroides</i>	MSAATFSQ	QRFVPTTPE	KGSFPLDHEGLCK	KFMVKYMG	CLRSNKNNS	ACREEARAY	LACRID	NNLMTKE	EWSKLG	FSDSEPK	EQH-----							
<i>Astacus_leptodactylus</i>	MASMTFSQ	KSFTPTTPP	KGSFPLDHEGECK	KFMIKYMLC	LRENQENNK	CREESREY	LGCRME	KGLMAKE	EWSKL	GYSDLT	TSAHHTS----							
<i>Forficula_auricularia</i>	MSAMTFSQ	KQFIPTAPD	KGSFPLDHEGICK	KVMLKYMIC	LNNNDKN	SNLCRQE	AKDYLS	CRMNNL	MAKEE	WETLGY	KDEKN-----							
<i>Daphnia_pulex</i>	MASNTFGQ	KNFTPTGPL	KGSFPLDHDGECK	INMLRYMIC	LRENSNQSS	ECRQLSKEY	LDCRM	QKQLMV	REEWT	KLGF	GDISEENK	Q-----						
<i>Occasjapyx_japonicus</i>	MSSTTFGQ	KFTFTPTTPE	KGSFPLDHEGLC	RRFMLRYLLC	IERQSHD	NSACRGE	ARDYLE	CRM	DRQLMAR	EDWGK	LGFSDSSA	PPAEPK	P----					
<i>Aposthonja_japonica</i>	MSSMTFGQ	KFTFTPTTP	KGSFPLDHEGLCK	RQMLKYMIC	LREYDNDG	AKCRAESK	DYLSCRM	ENLMAK	EDWSK	LGFDDNV	KMKNL-----							
<i>Meganyctiphanes_norvegica</i>	MSSMTFGQ	KSFTPTTPP	KGSFPLDHEGECK	KFMIKYMLC	LRESK	ENSLCRQ	SSKDYLE	CRM	EKGLMAK	EEWT	KLGLADV	GSAEP	SNSEQ----					
<i>Grylloblatia_bifratrilecta</i>	MSSVTFGQ	KSFTPTTPD	KGSFPLDHEGQCK	KEMLYMIC	LRRNRND	NSACREES	SMRYL	GCRMD	NNLMAR	EEWSK	LGFSDL	ELKPE	KNN-----					
<i>Halyomorpha_halys</i>	MSSLTFGQ	KFTPTTPE	KGSFPLDHDGQCK	RTMLKYMIC	LNTNSD	SSKCRQE	AKEYLA	CRMD	NNLMAK	EDWSK	LGFKEE	EVKQEN-----						
<i>Psytalia_concolor</i>	MSSYTFSQ	KIFTPIPP	DKGSFPLDHEGYCK	LPMIKYMR	CLHTNKN	DNTKCRD	DAREYL	GCRM	ENNLMS	REEWS	KLGFHDD	DKIEE	GEPK	NKT--				
<i>Armadillidium_vulgare</i>	MSSMTFGQ	KLFKPIPPE	EGSFPLDHEGLCK	KSMIN	YMQCLSKY	NNNS	ECRL	EAK	EYLCRM	RNNLM	ASEEWS	KLGFSD	KDK	QQSE	VEVKDN-			
<i>Metallyticus_splendidus</i>	MSTMTFGQ	KQFAPVPP	KGSFPLDHEGQCK	KAMLKYMIC	LNA	NSD	NSCRAE	AKVYL	QCRMD	NNLMAK	EEWSK	LGLSD	VEA	KLQKE-----				
<i>Boreus_hyemalis</i>	MSSMTFGQ	KFTIPTAPD	KGSFPLDHEGLCK	KMLKYMH	CLRMSK	NDNSLCRQE	AKEYL	GCRMD	NELMAK	EDWSK	LGFKE	SDVVK-----						
<i>Chrysopa_pallens</i>	MSTMTFGQ	KSFTPTTPD	KGSFPLDHEGICK	ETMYNYMR	CLRLNKN	NSACRIE	AKDYLA	CRMD	NNLMSKE	EWSKL	GFGNQ	NKST	INK-----					
<i>Gryllotalpa_sp._AD-2013</i>	MSSMTFGQ	KFTFTPVPPE	KGSFPLDHEGVCR	TLMKYMLC	LRRNDND	NSQCREE	AKSYL	GCRMD	NHLMAK	EEWSK	LGFKD	LD	MKDD	SKEN----				
<i>Medauroidea_extradentata</i>	MSSVTFGQ	KSFTPTTPD	KGSFPLDHEGQCK	REMLKYLLC	LBA	NNNDNS	ACRREA	KTYL	GCRMD	NNLMAK	EEWSK	LGFSDL	NL	DSK	GSDKSL---			
<i>Menopon_gallinae</i>	- - -MAY	QGGKVF	KVPVPP	MKGSFPLDHD	RSC	PEMLKYMK	CLMEN	KYDSE	FCRTE	IKTYL	E	CRMD	NNLMAK	ESWEAL	GLKDIAESN	SEYSS-----		
<i>Cosmioperla_kuna</i>	MSSMTFGQ	KSFKPTAPD	KGSFPLDHEGQCK	HEM	I	KYMLCLST	NNNS	ACRE	EAKSYL	GCRMD	NQLMAK	EDWSK	LGFDDL	RS	DSNR	VEH-----		
<i>Acerentomon_sp._AD-2013</i>	MGTRSFQ	QKPLQSI	PPEKGSFPLDH	ENECKRSML	EYMIC	LQ	QNKNDNS	ACRM	KA	KGYL	KCRMD	NGLMA	I	EDW	PSL	GFKDGN	VEAS	VSAKL----
<i>Ectopsocus_briggsi</i>	MSSMTF	NQKFTPTAPD	KGSFPLDHENL	CKQMMKYMQ	CLRV	SKADNSK	CRLES	KDYLA	CRME	HQLMTKE	PWSK	LGL	ED	L	EDQ	TVQ-----		
<i>Inocellia_crassicornis</i>	MSAMNF	-QRTFIPTTP	DKGSFPLDHEGLCK	DQMIRYMT	CLRQNR	NDNS	CCRIE	AKDYLA	CRMD	NNLMLK	EDWSK	LGYSD	NKNN	V	KD-----			
<i>Ceratophyllus_gallinae</i>	MSSMTFSQ	KSFTPTAPQ	KGSFPLDHEGQCK	KFMIKYMS	CLRQHK	NDNS	SCRNEA	QAYL	GCRMD	NELMAK	EDFSK	LGFNS	NE	INK-----				
<i>Caligus_rogercresseyi</i>	MASNVFGA	KNFKPV	PEKGSFPLDYEG	KCKEYLFK	MI	CLKDNKY	VVEN	CREES	KNYL	VCRMD	HGLMAK	ETLP	N	L	G	FKEE	EN	KKADK-----
<i>Mengenilla_moldrzyki</i>	MSNPLLRQ	KVSKPIPP	QKGSFPLDHNA	I	CKKEMKYI	ICL	RNNENG	GSN	CRELA	KSYL	KCRMD	NNLM	ASEEWS	H	LGF-----			
<i>Frankliniella_cephalica</i>	- -MAQ	FAKSRFVPTTPE	KGSFPLDHDGVCK	DLMRKYMT	CLSSN	KQD	NTKCRKE	I	KTYL	DCRM	NNLMAR	EEWSK	LL	GL	EDV	G	AKSE	VVQK-----
<i>Zorotypus_gurneyi</i>	MSSATFGK	KIFTPTTPD	KGSFPLDHEGQCK	RVMLQYMS	CLTKNN	NDNS	F	CRLEAK	KNYL	ACRME	NNLMAK	EEWSK	LGFQ	D-----				

Conservation

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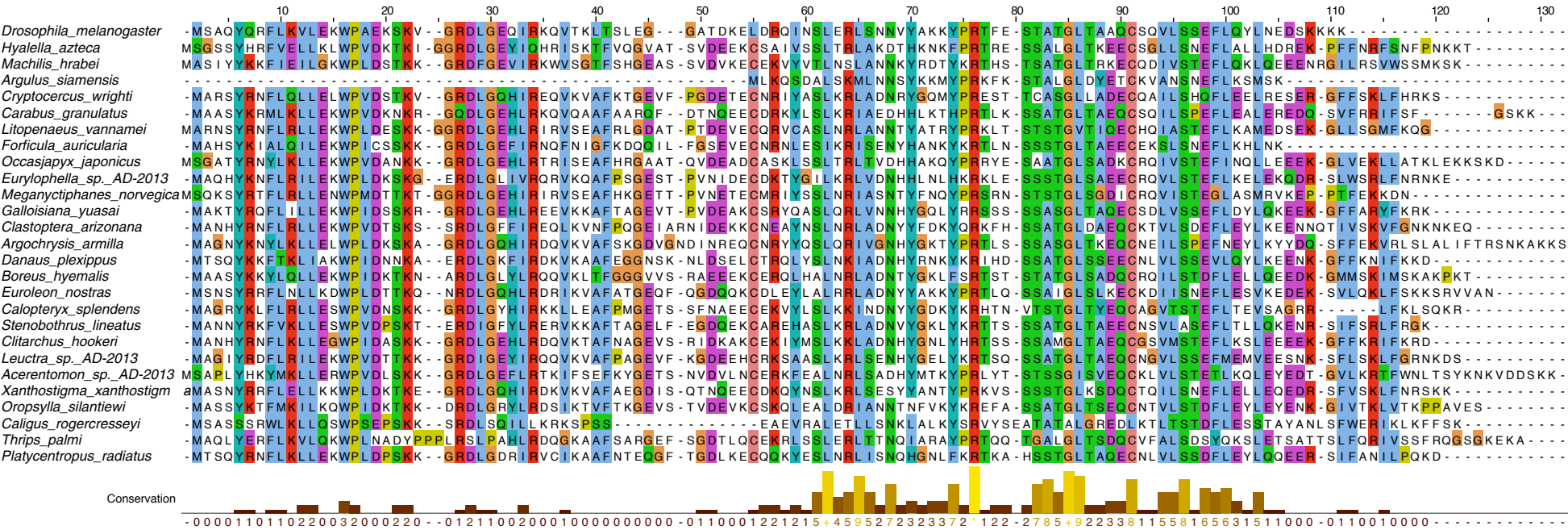
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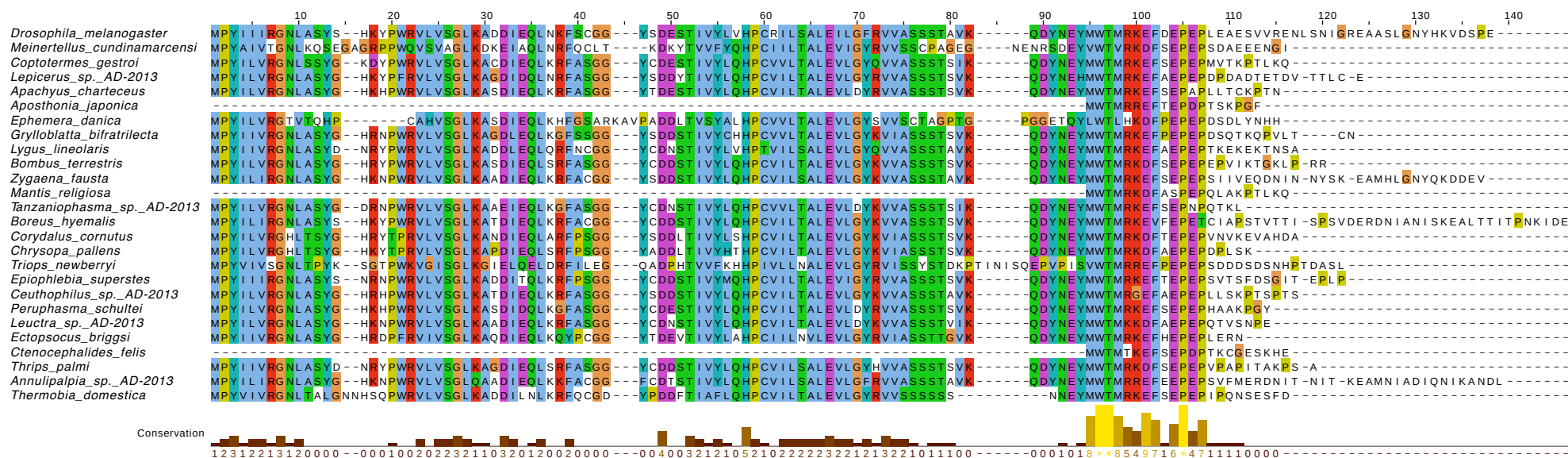


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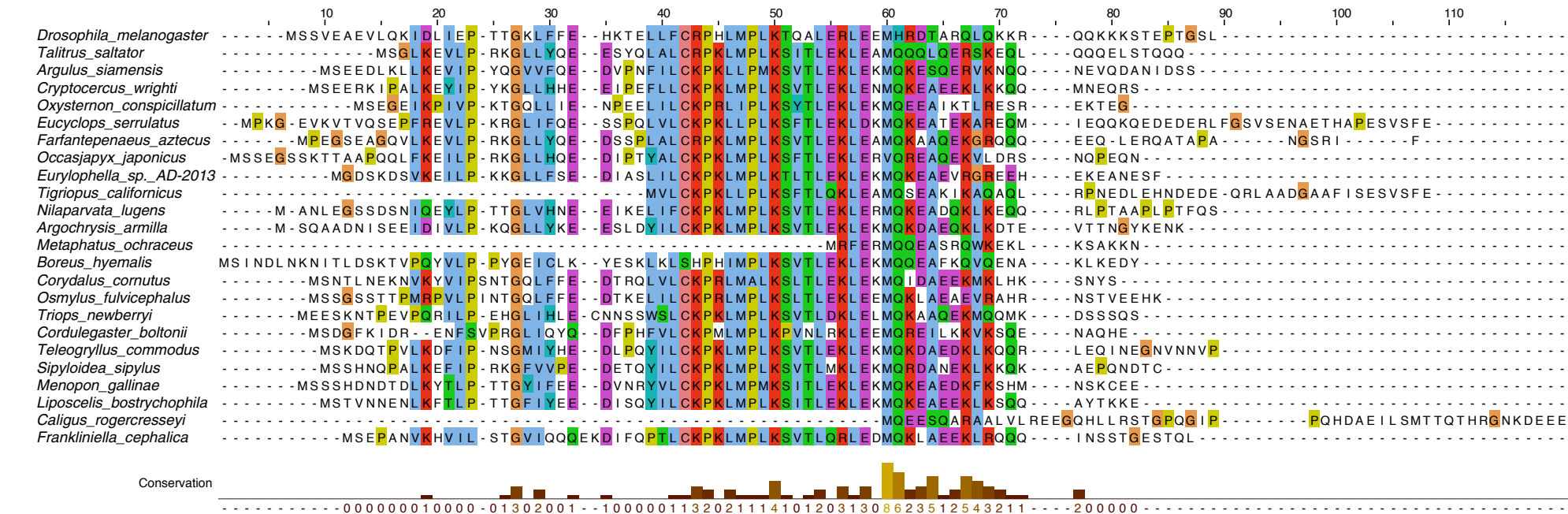


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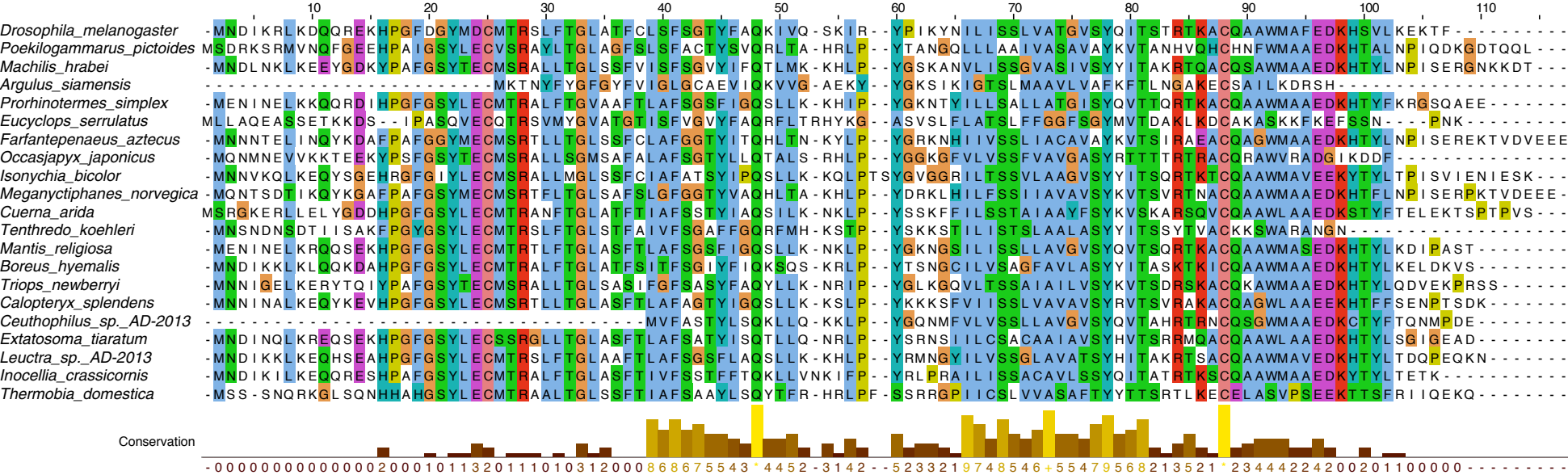
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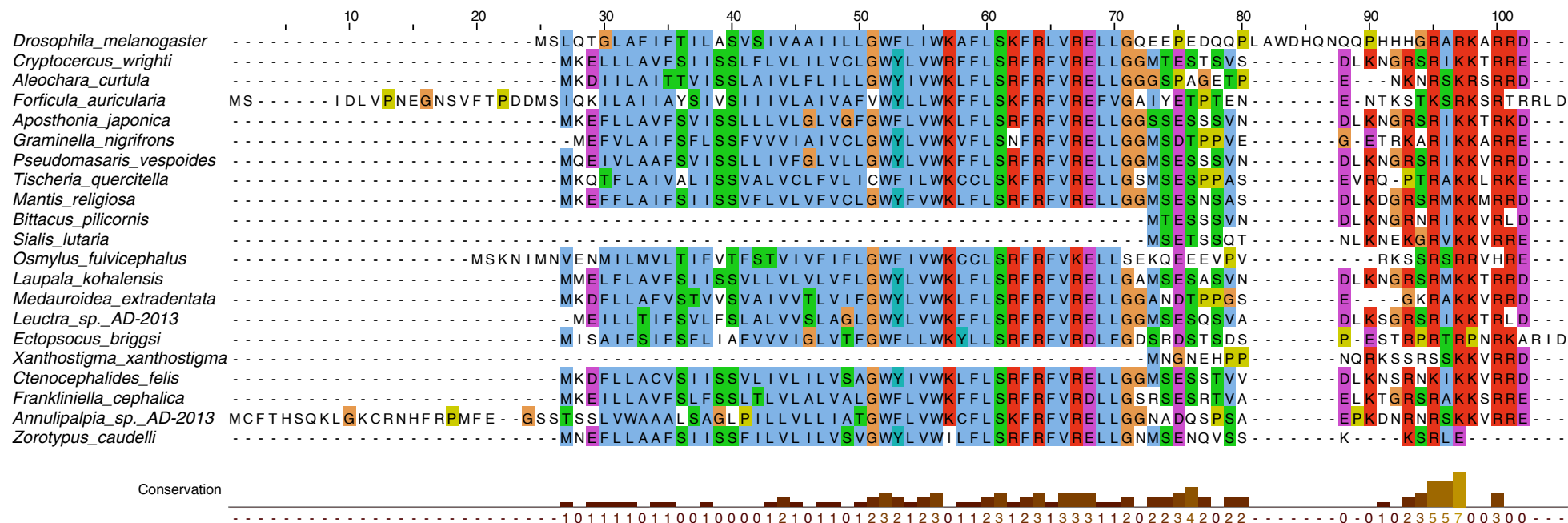


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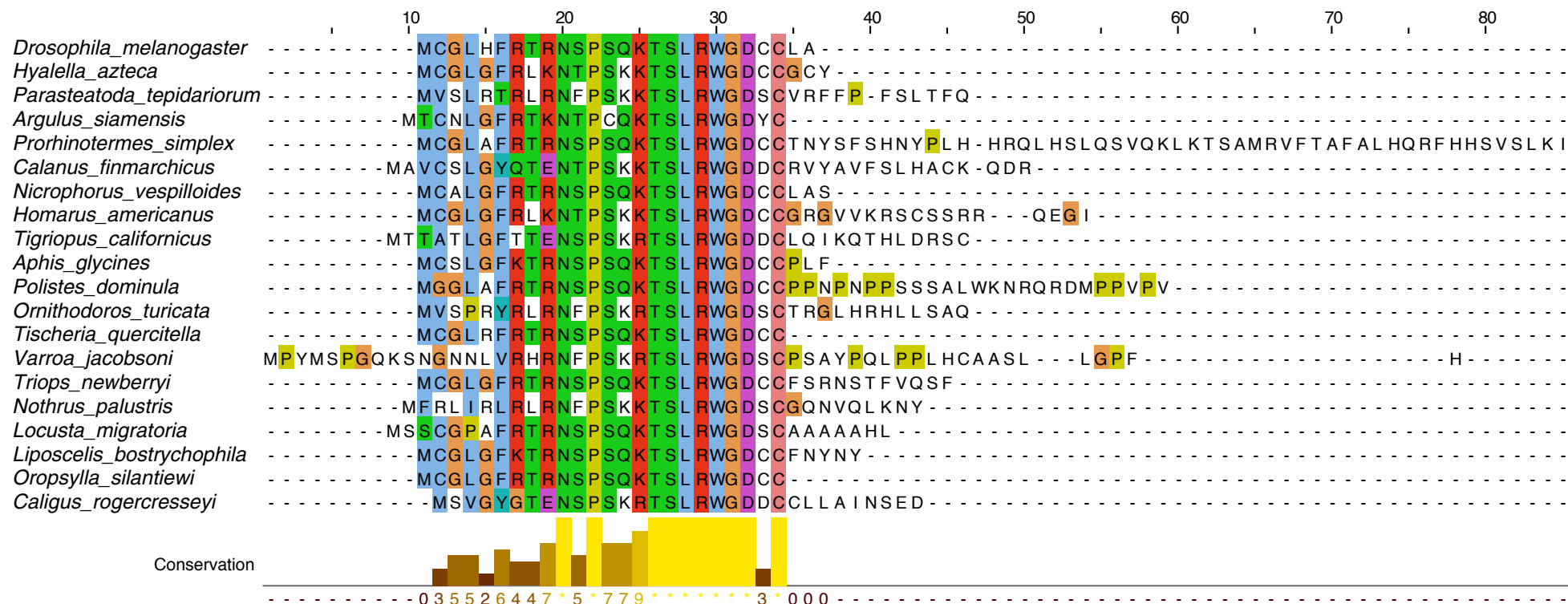
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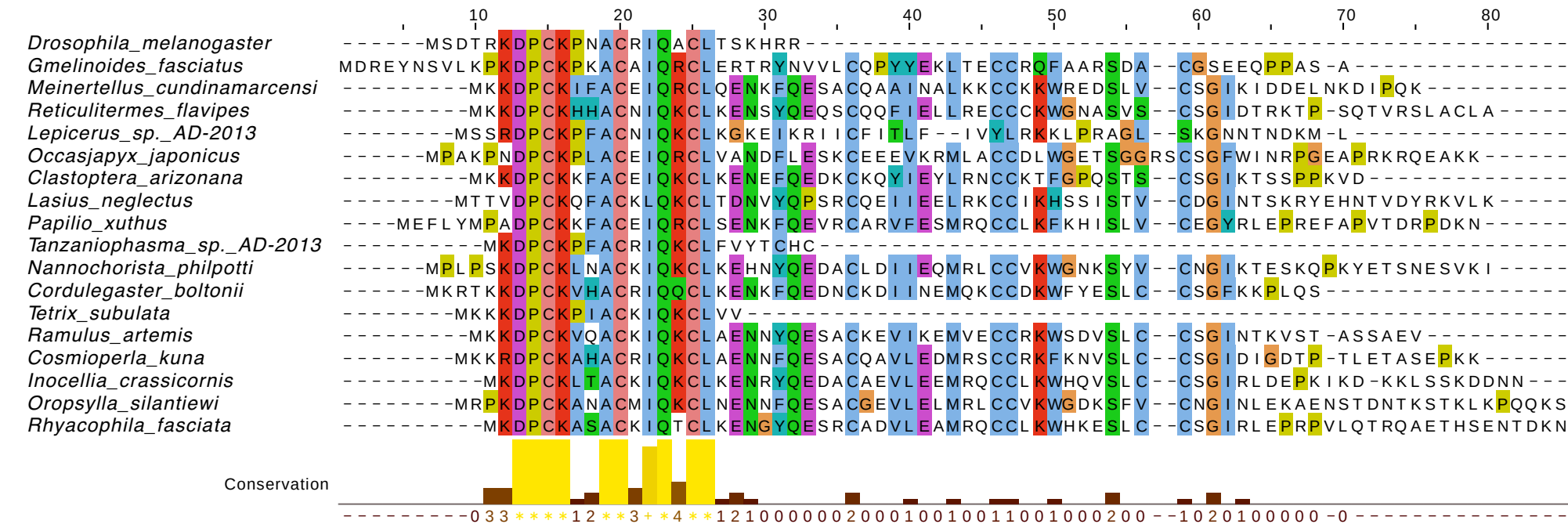
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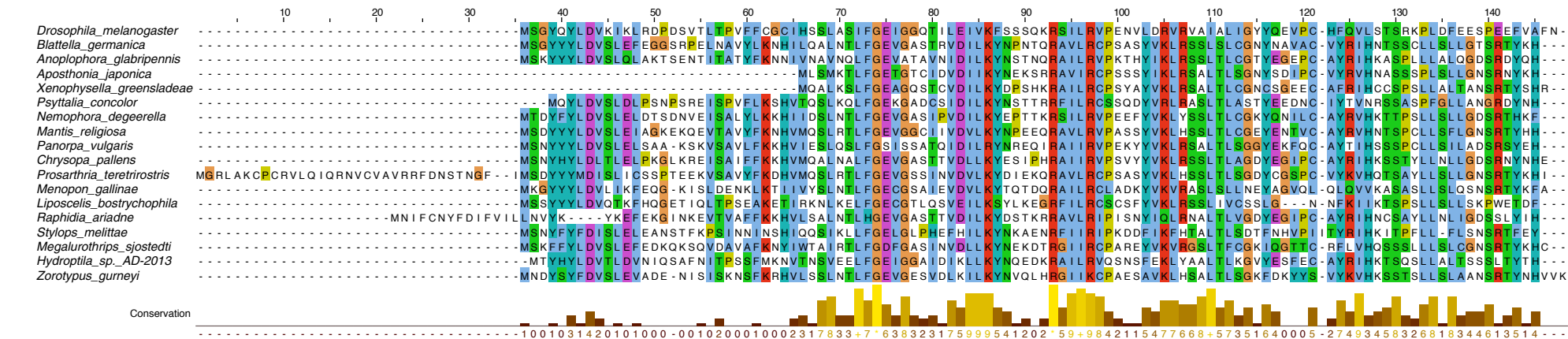


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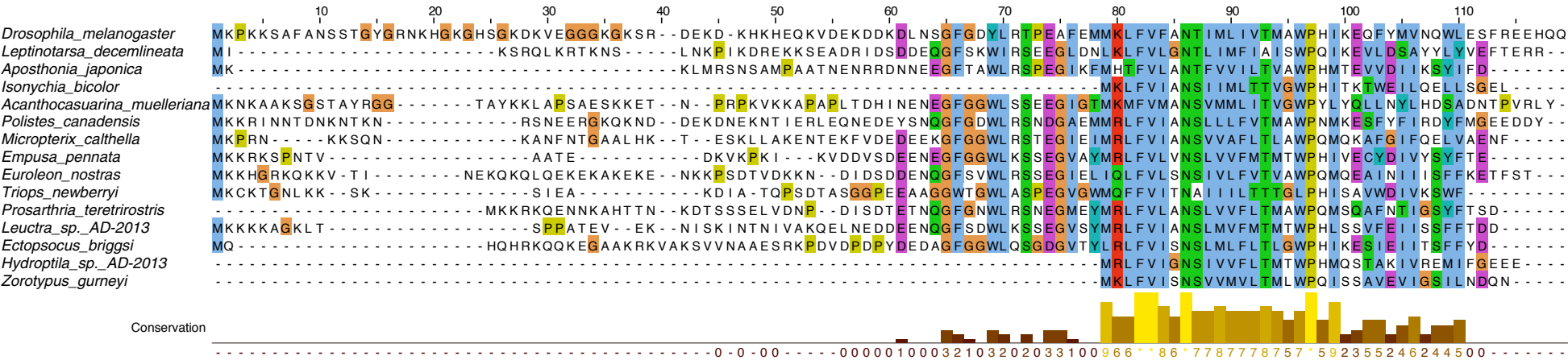
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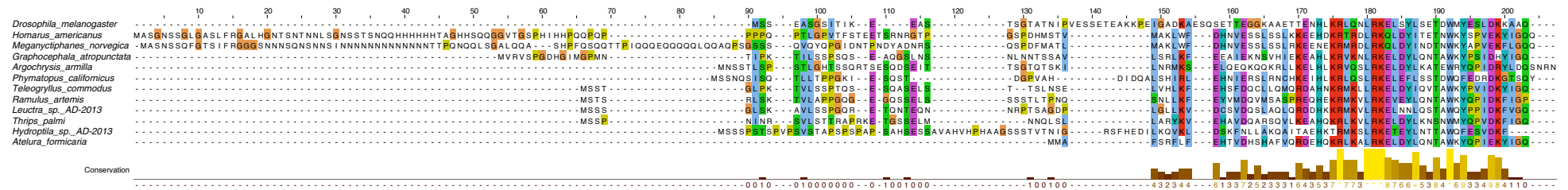


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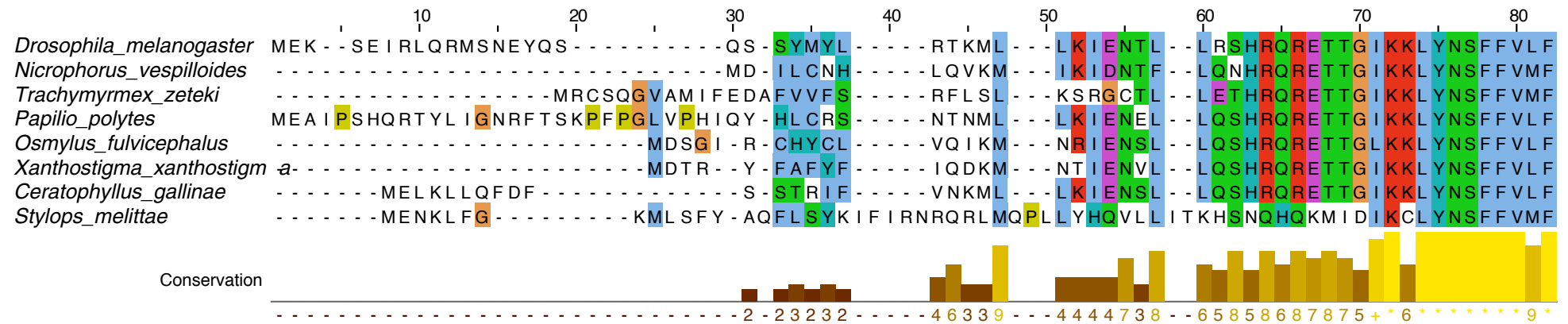
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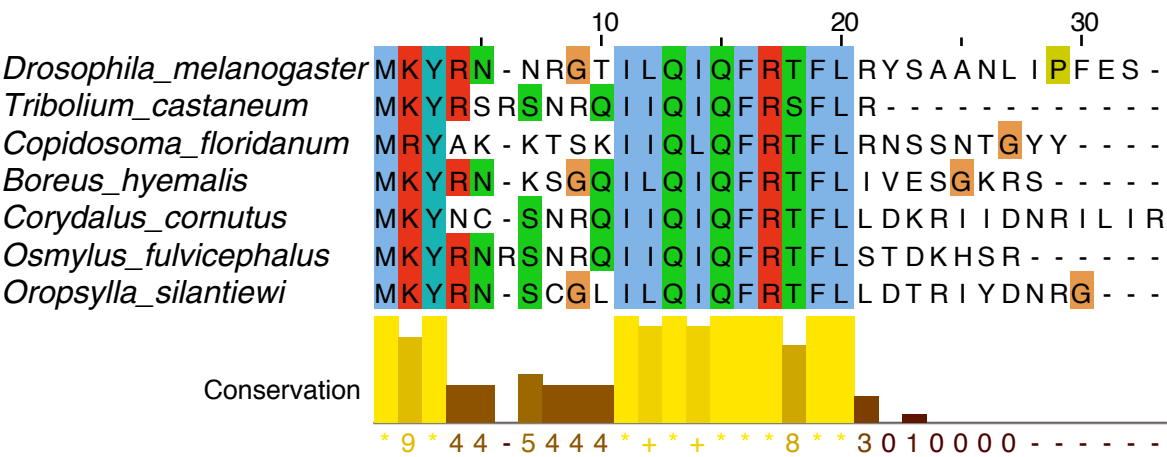


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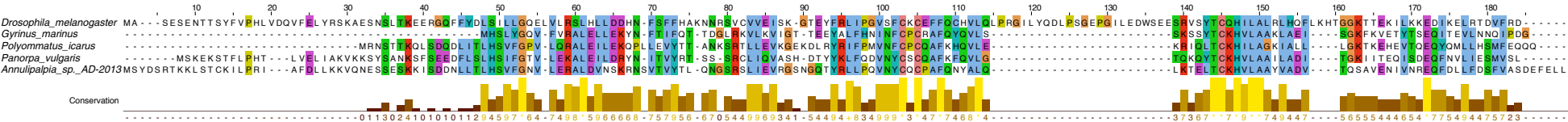
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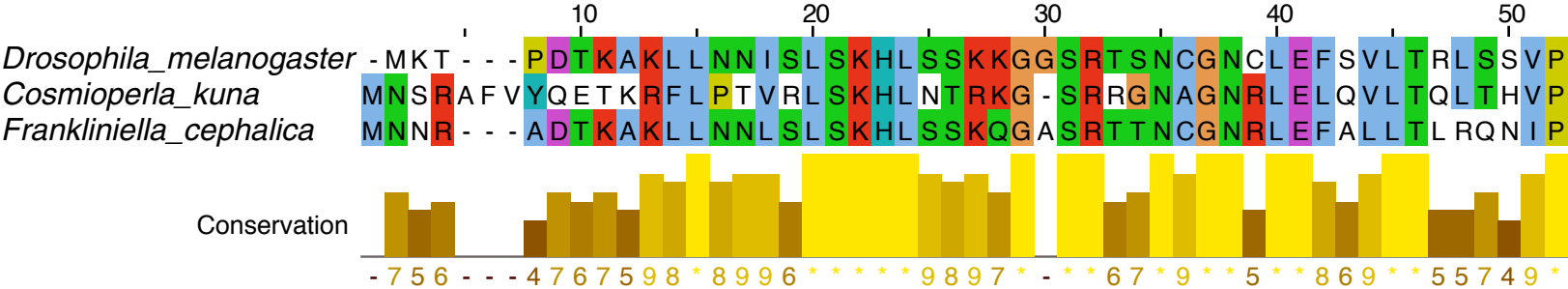


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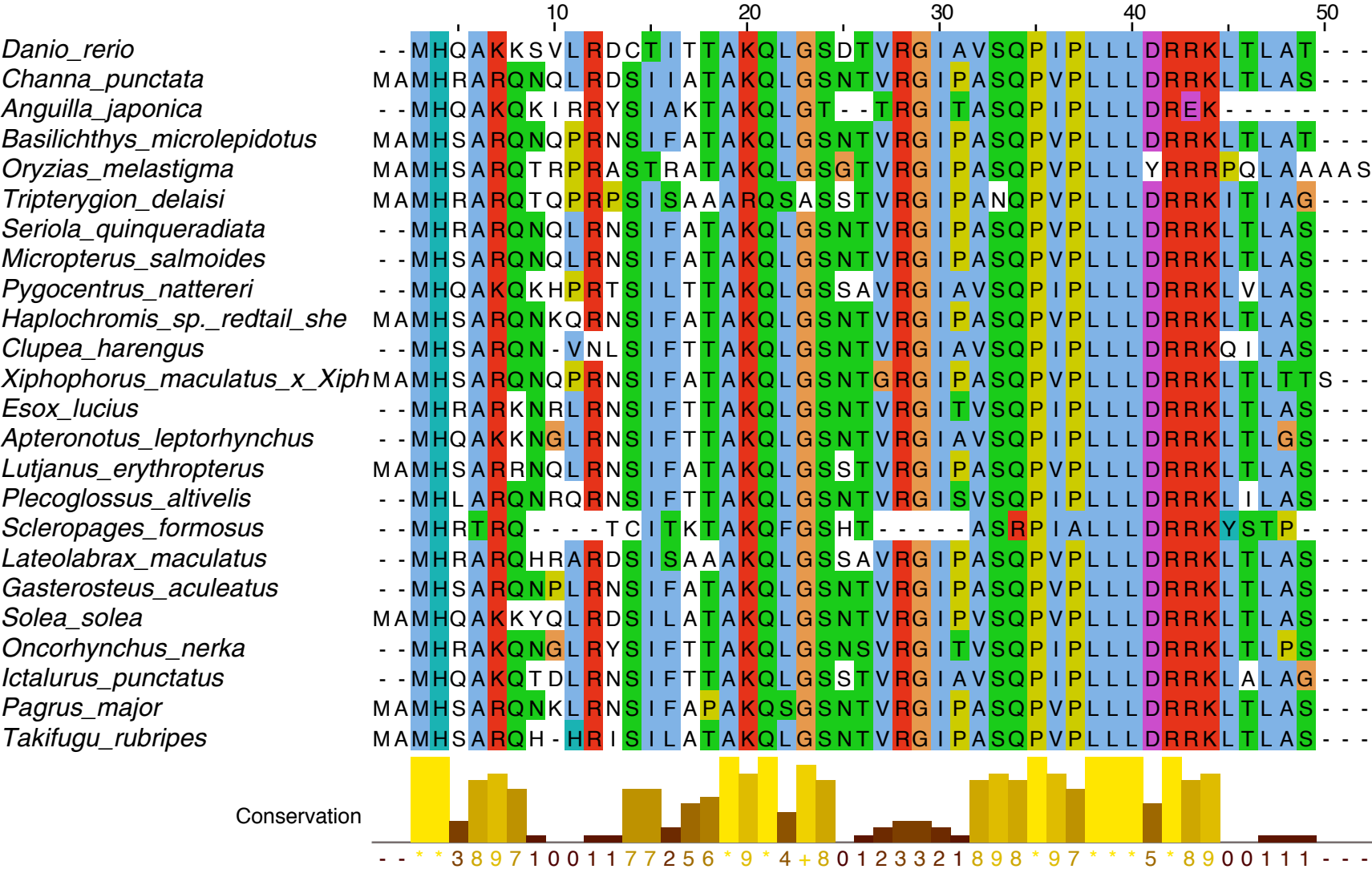


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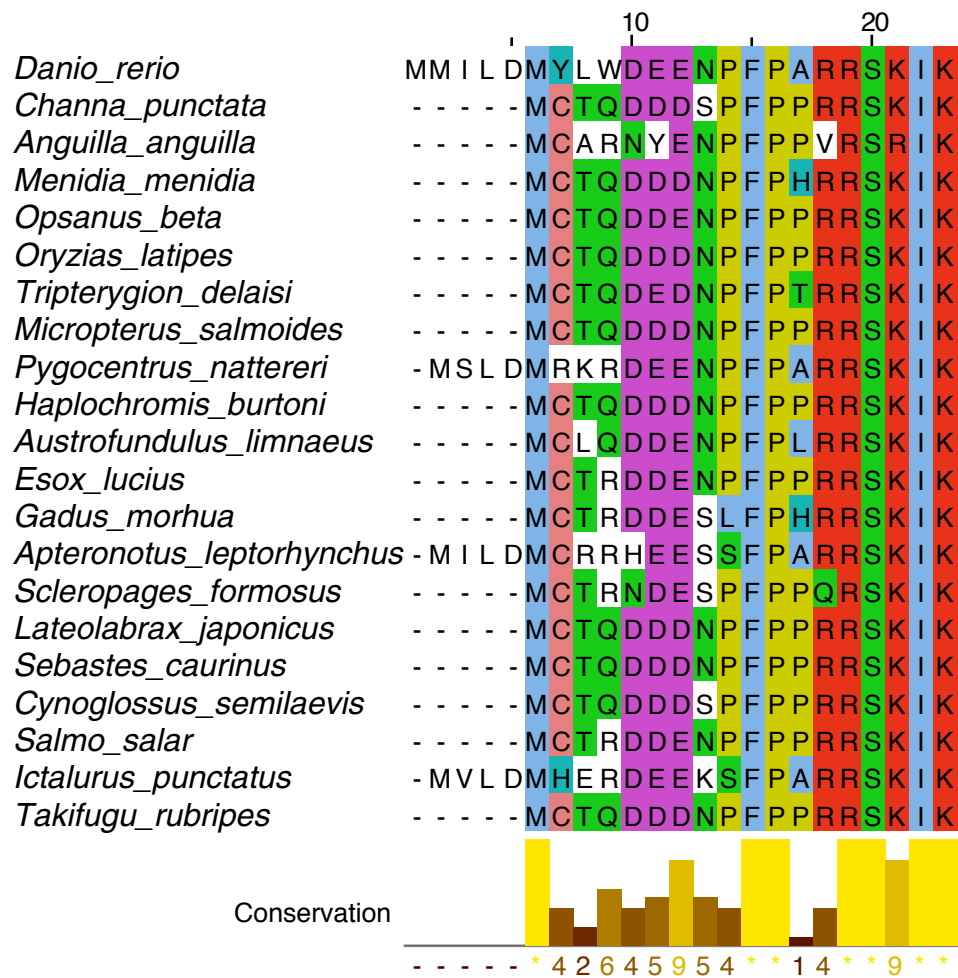
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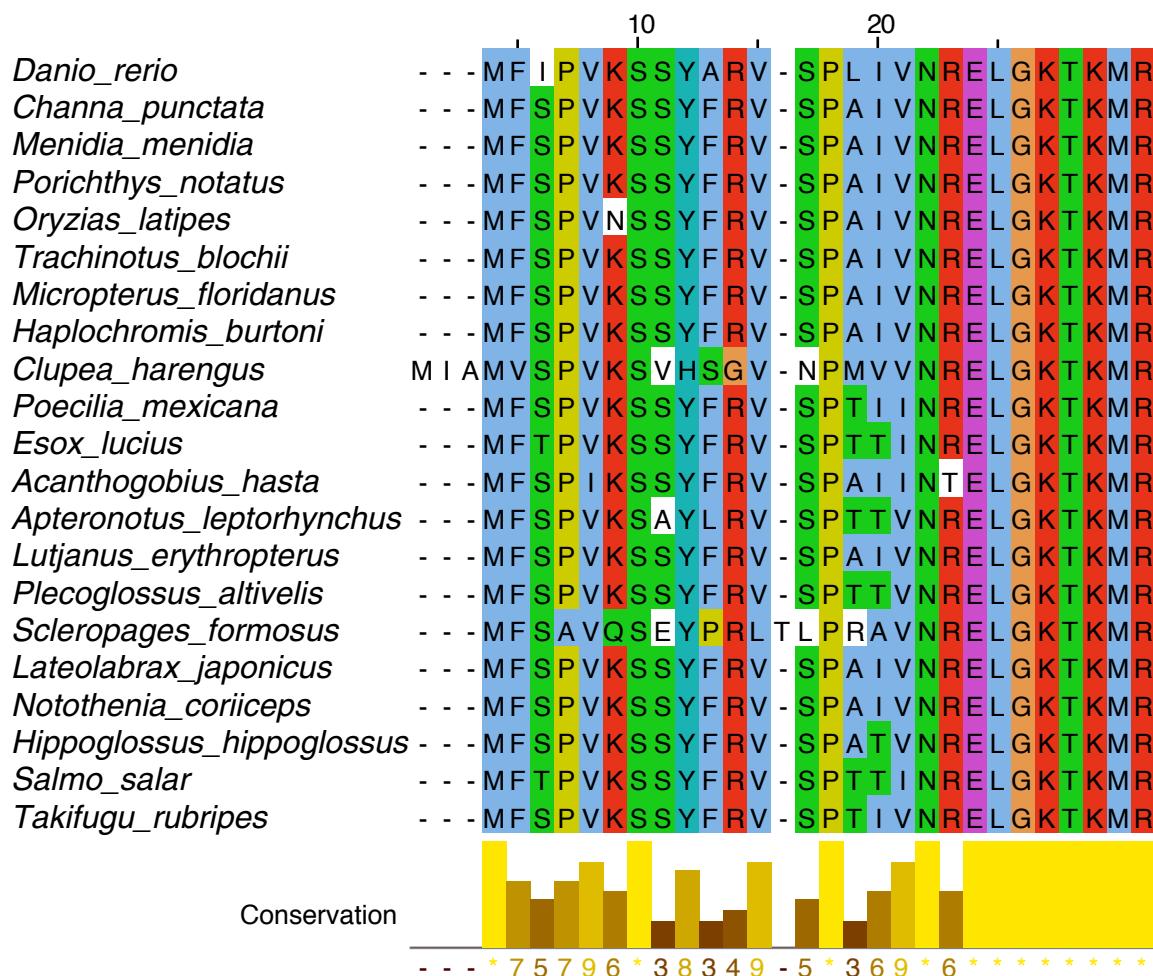


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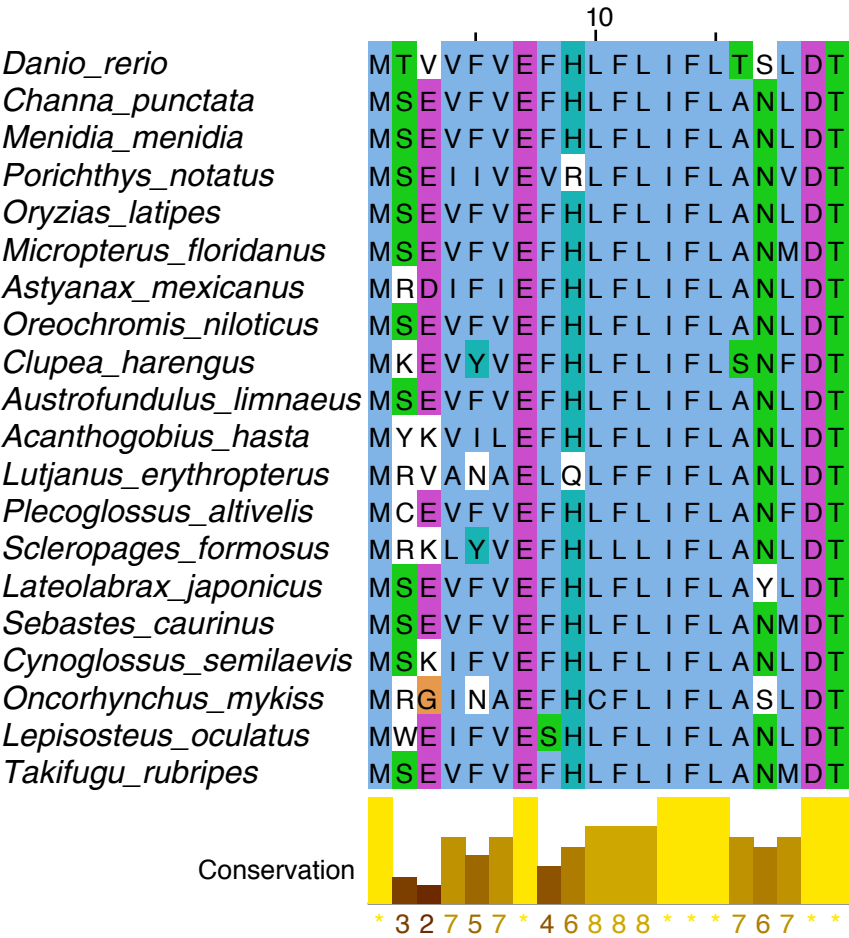


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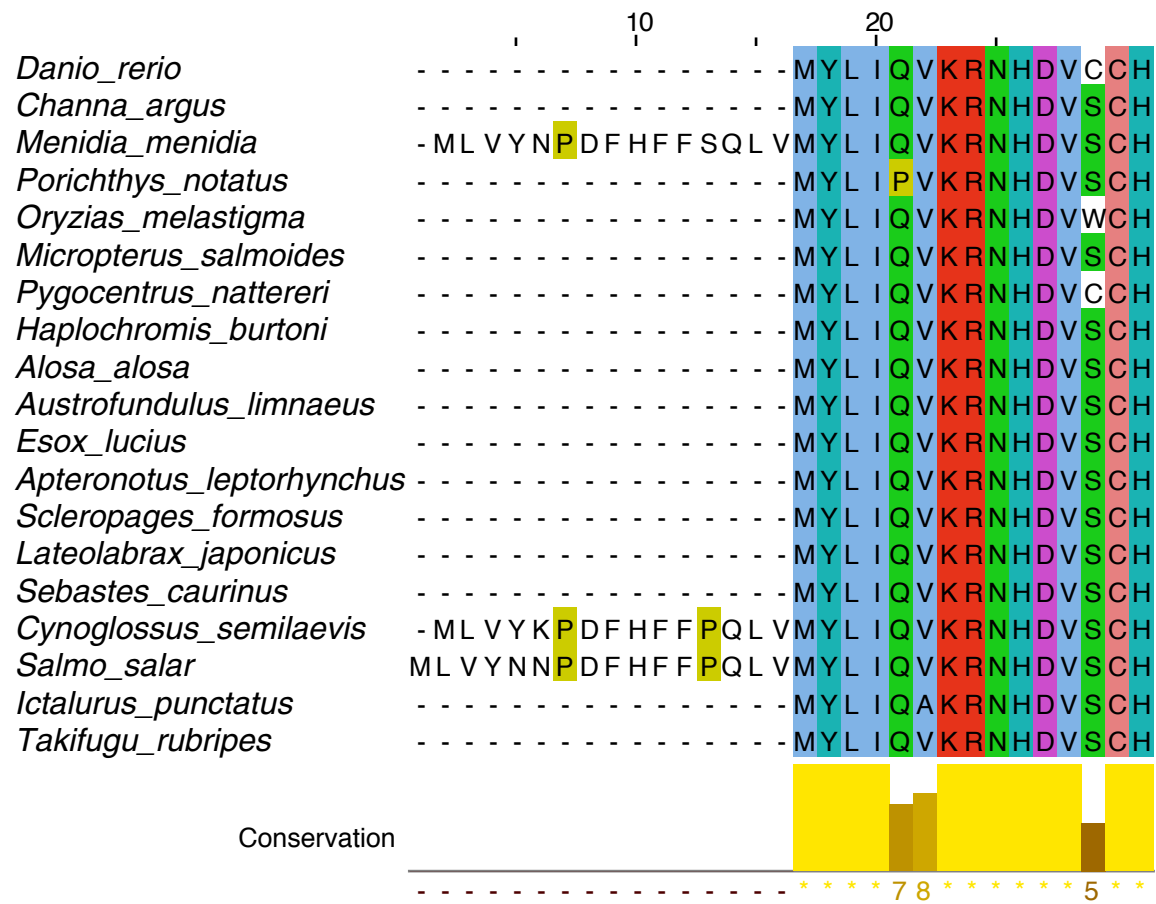
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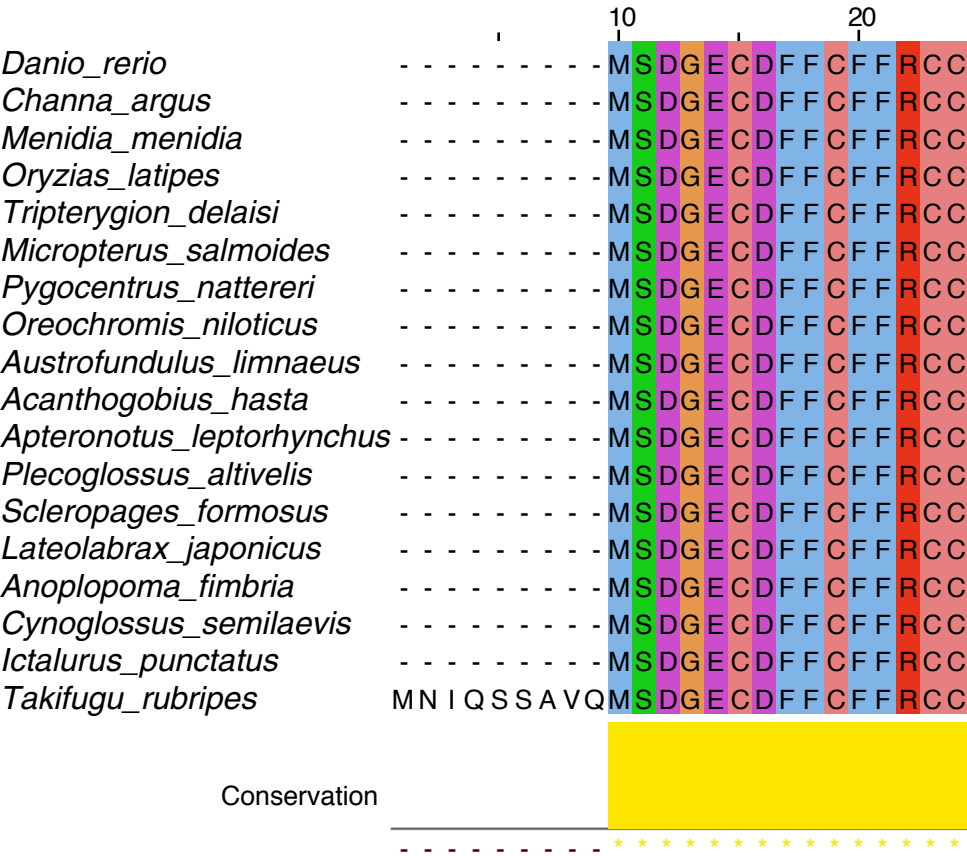
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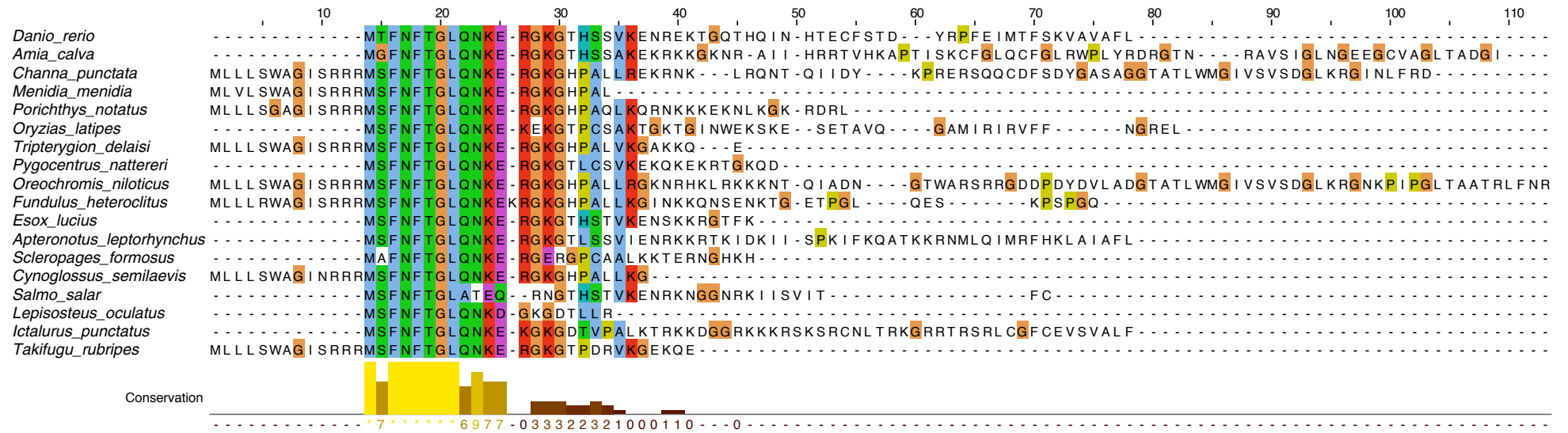


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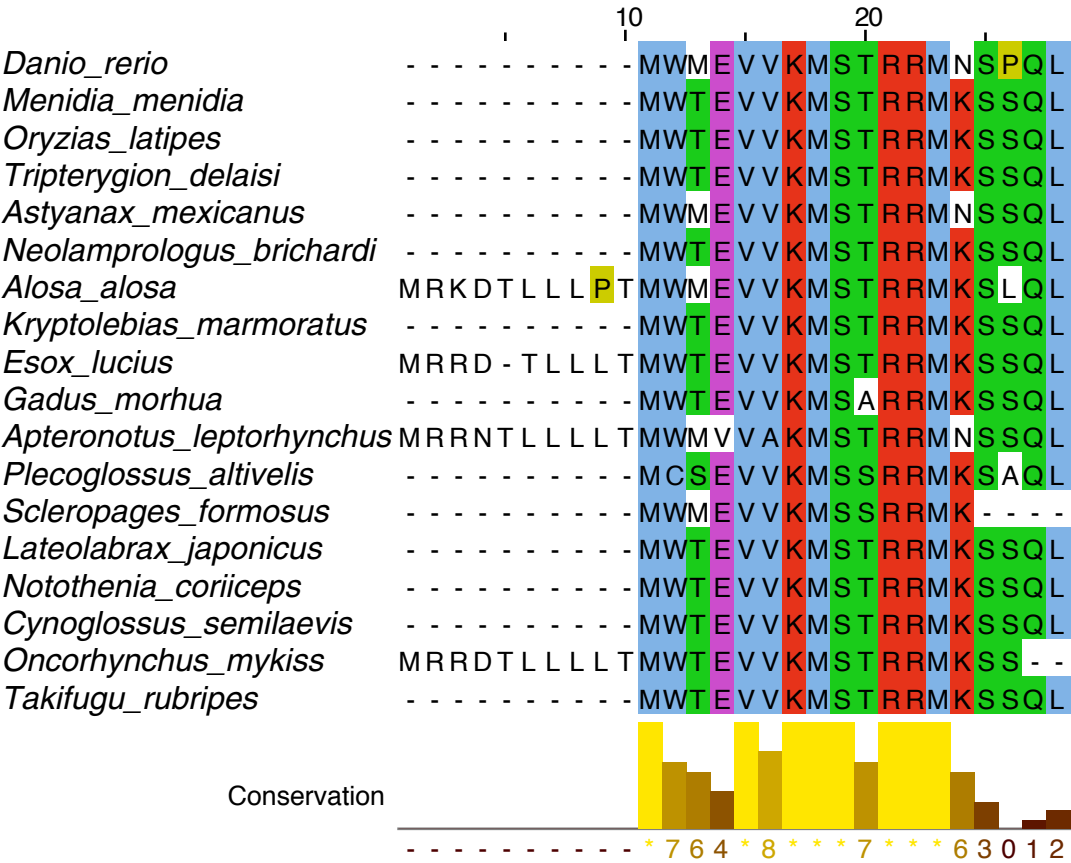


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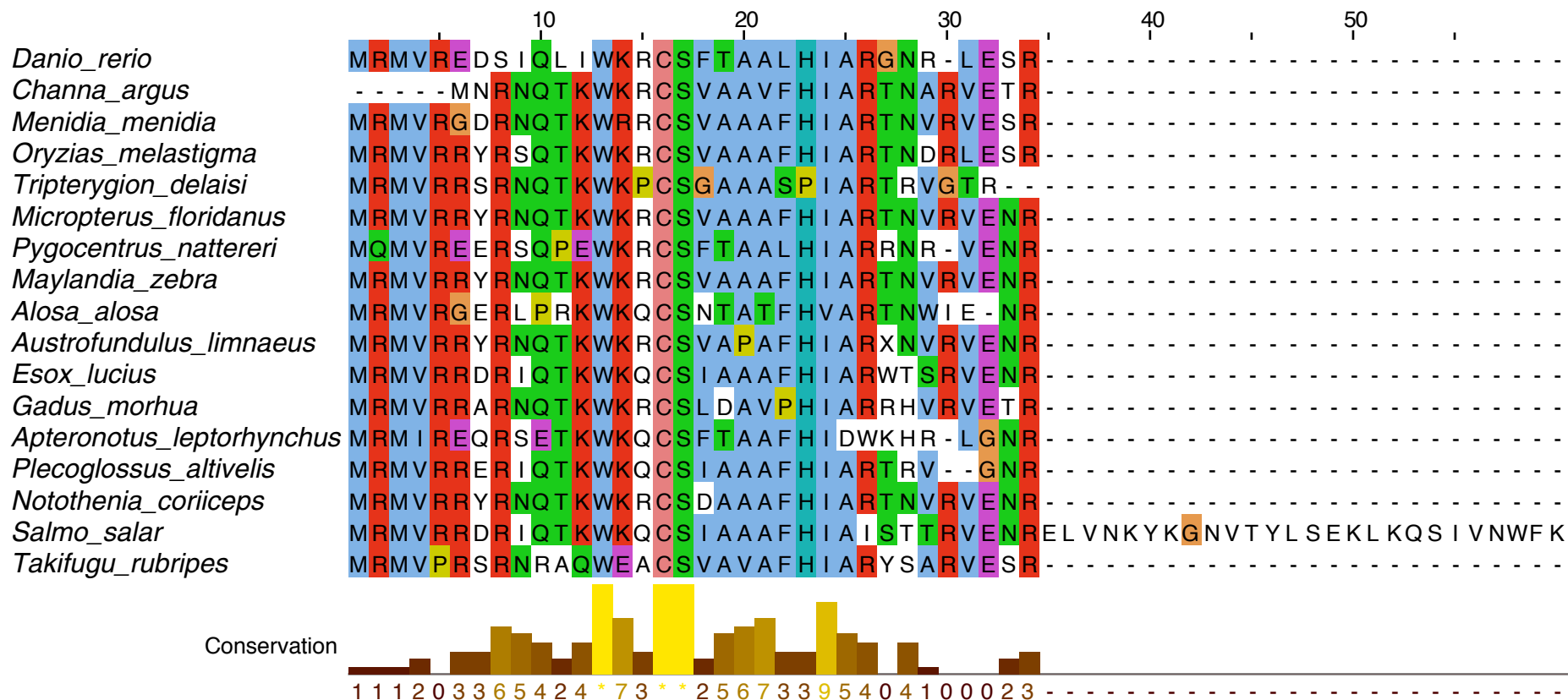


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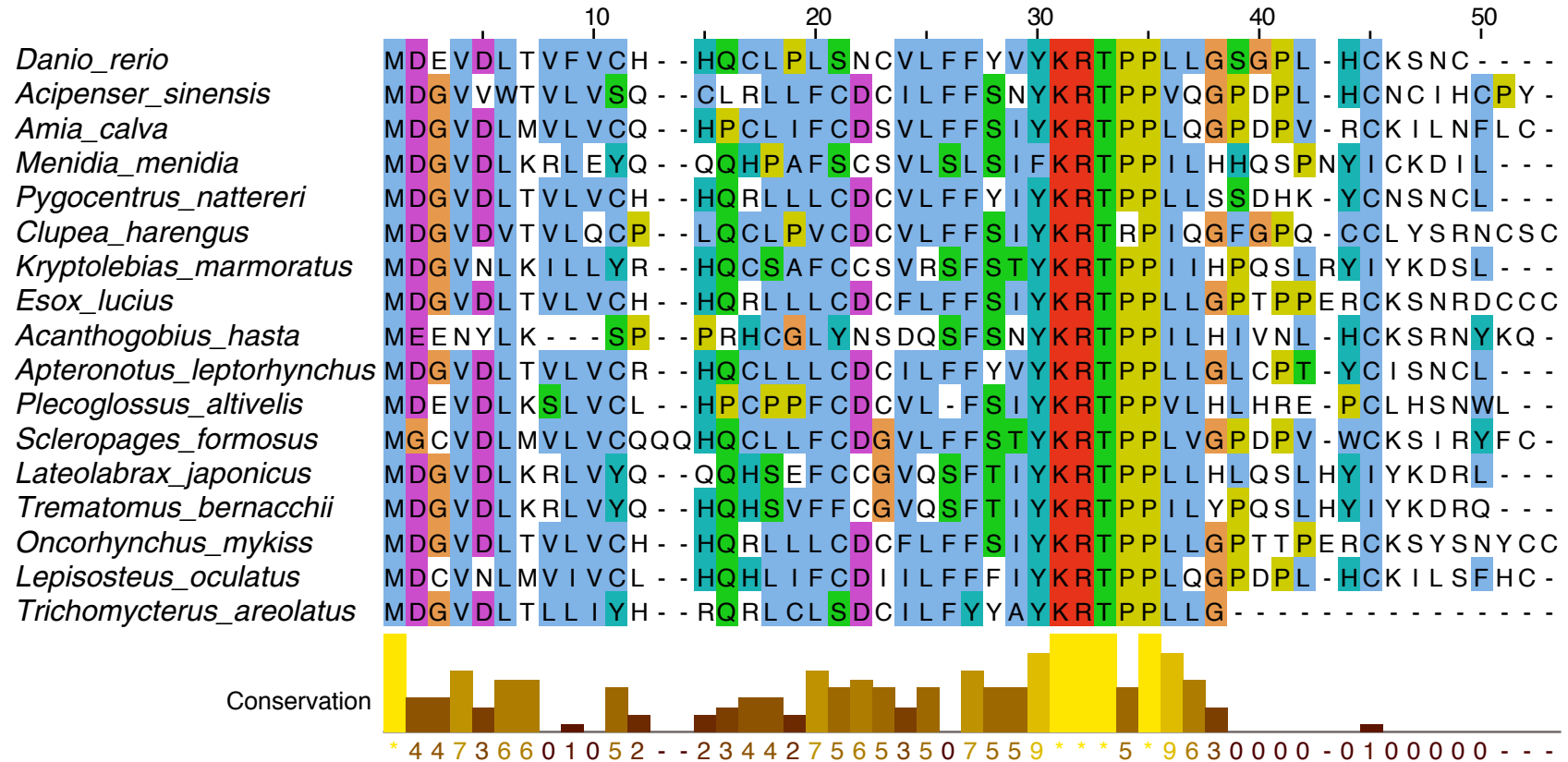


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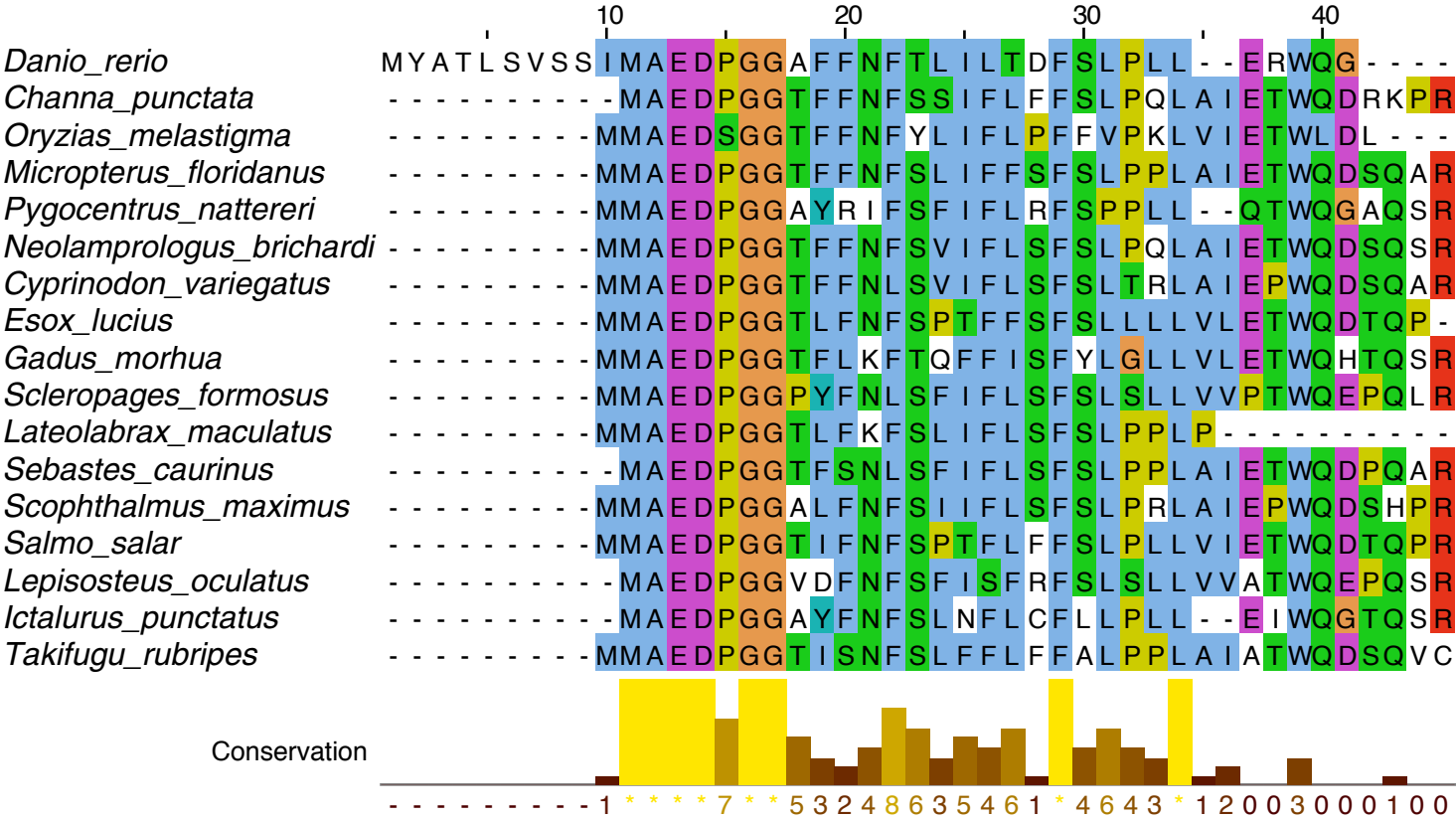
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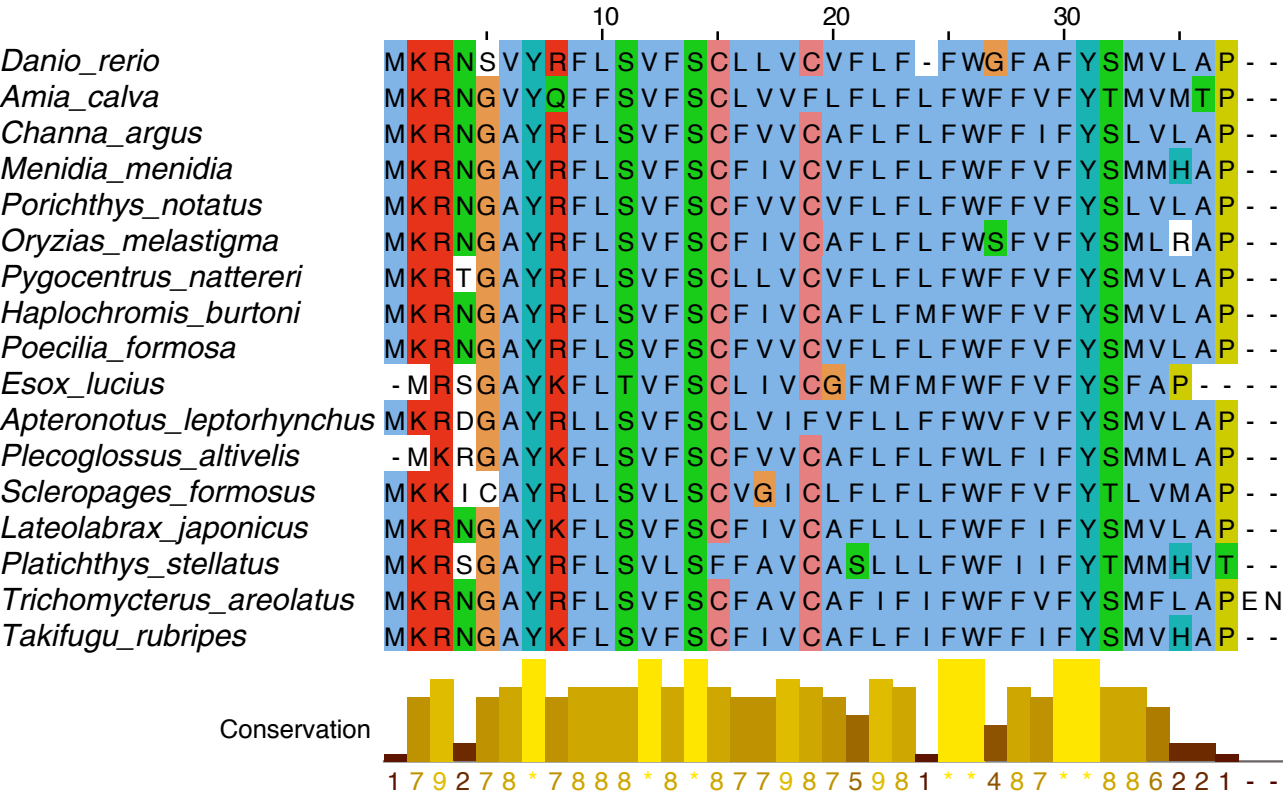
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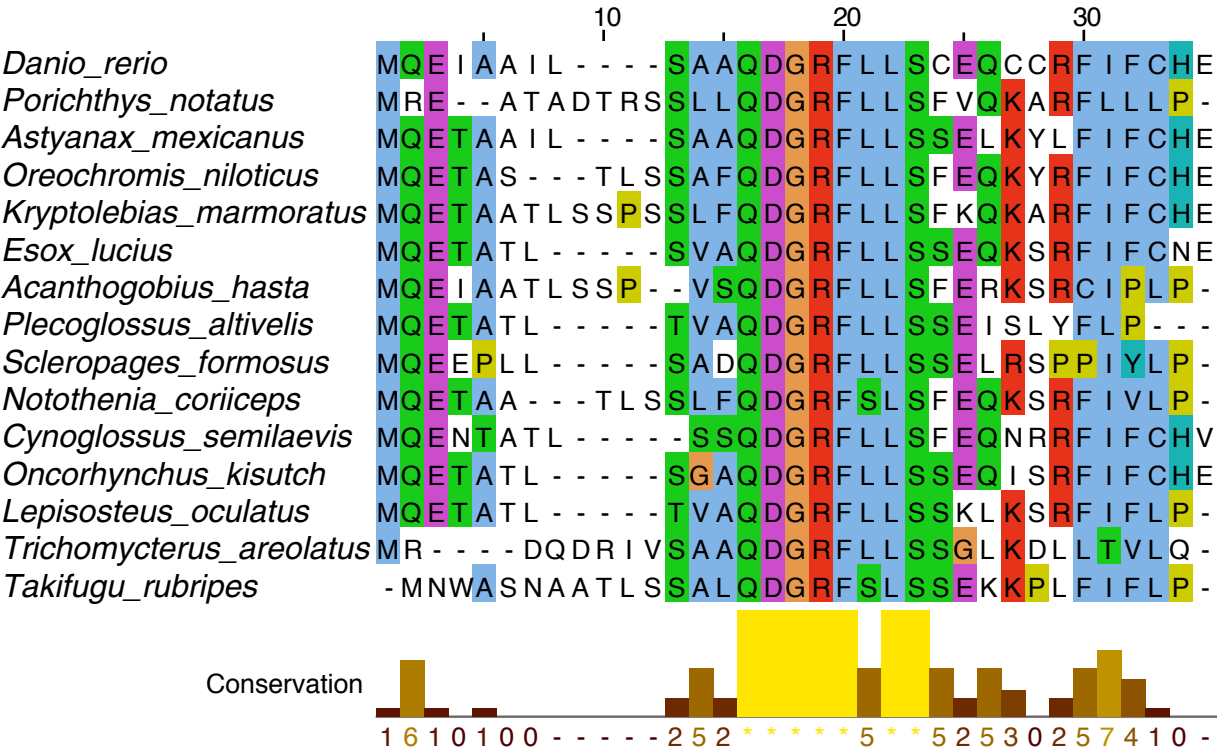
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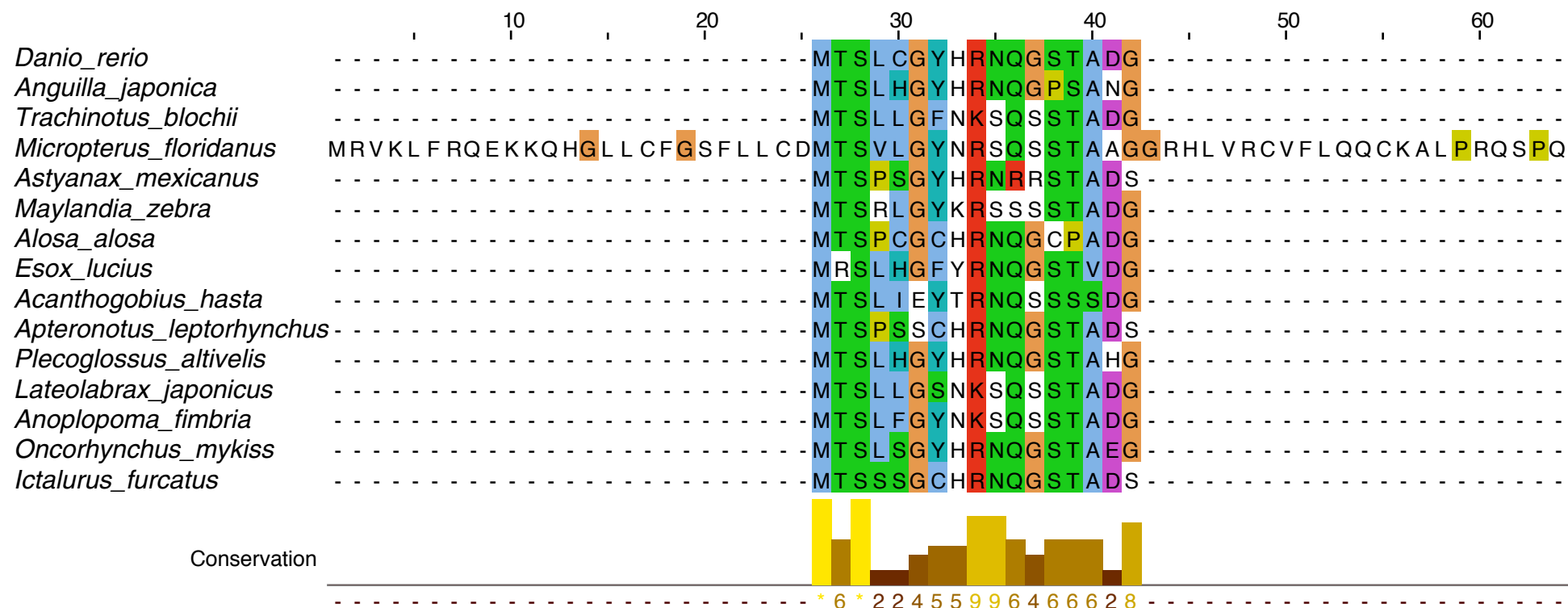
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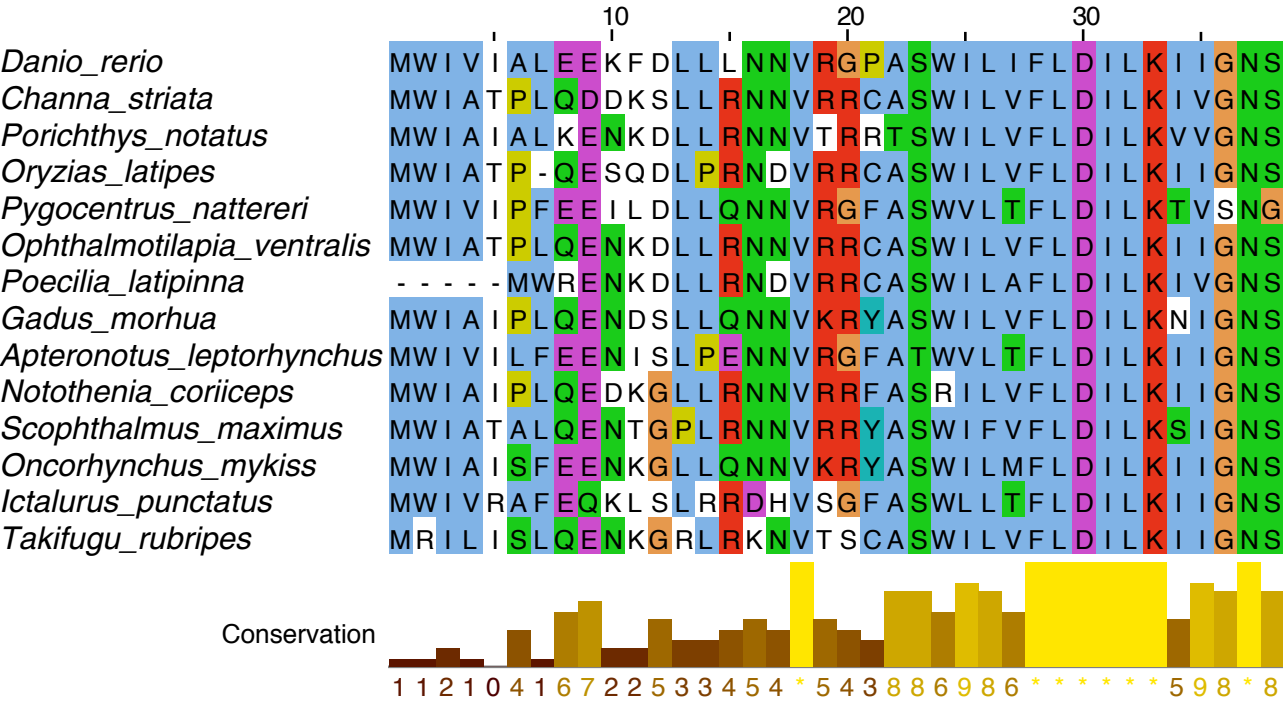
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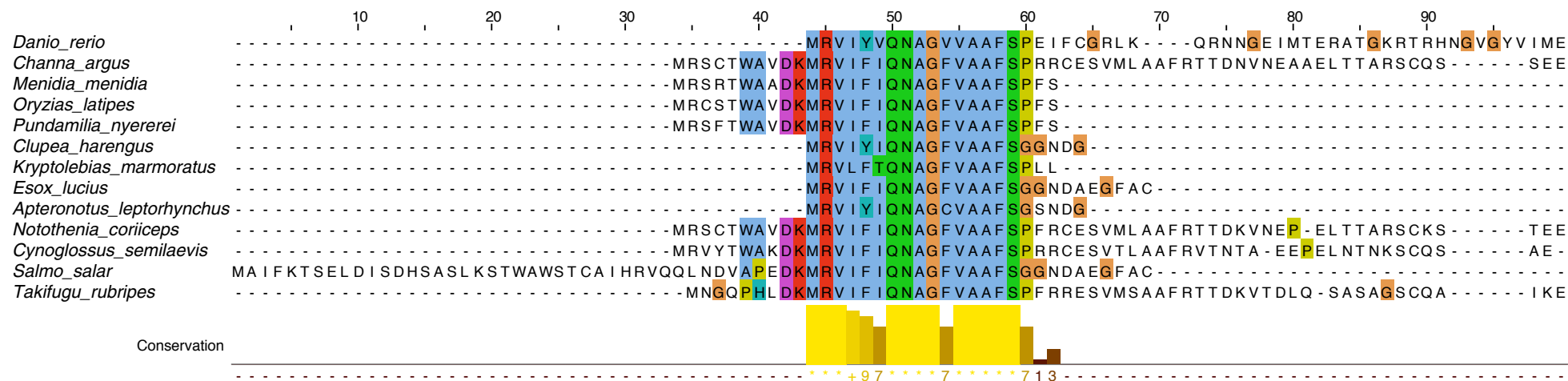
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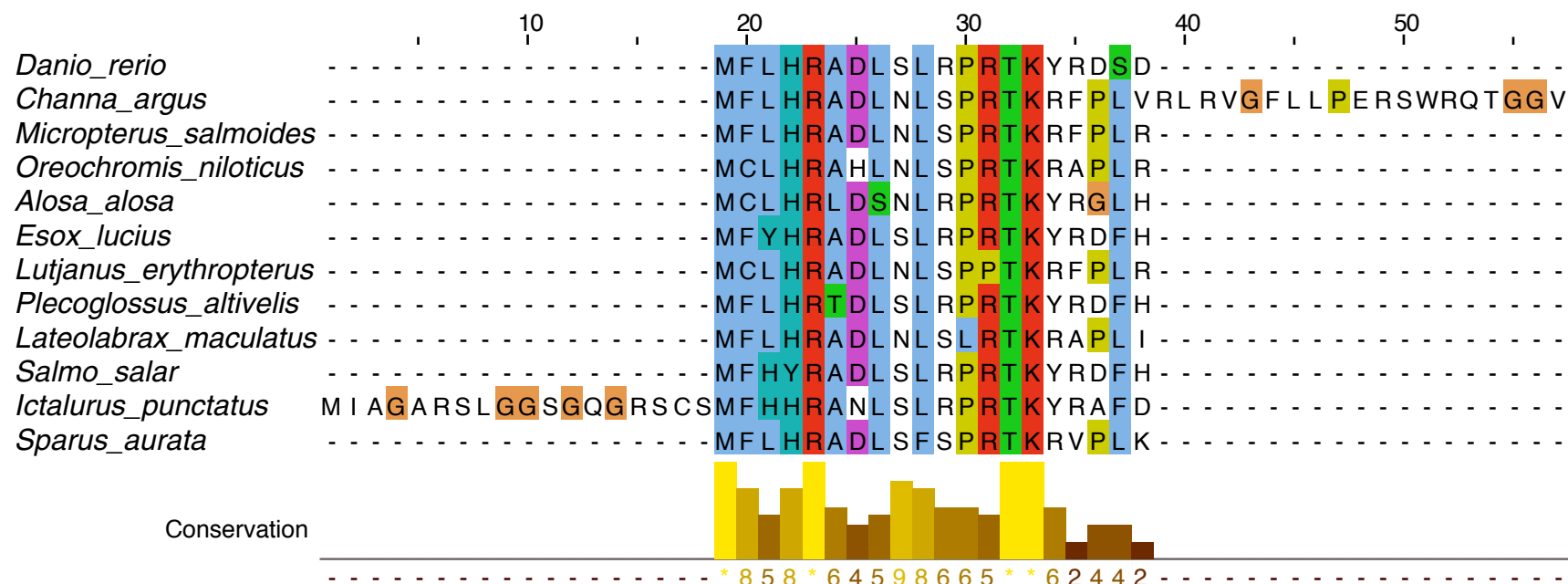


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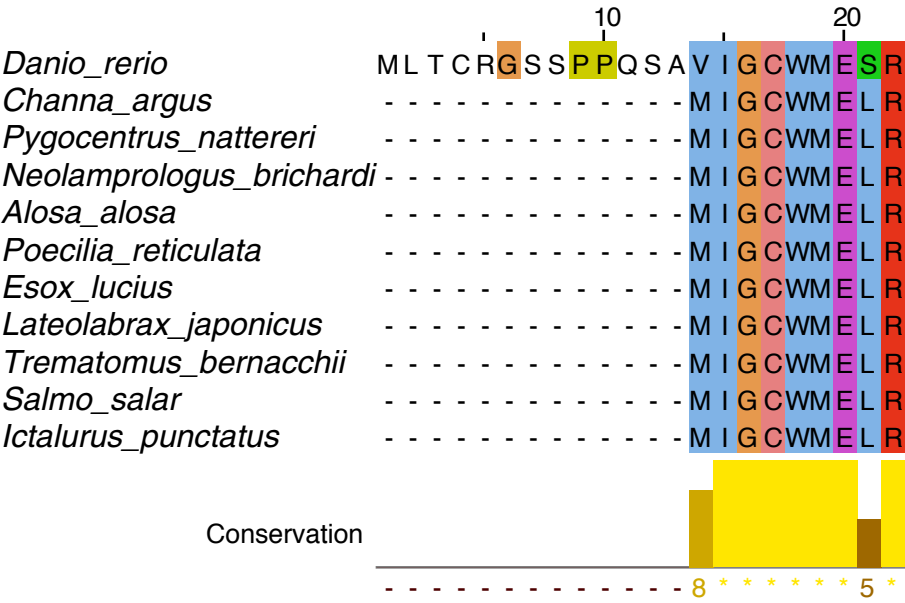


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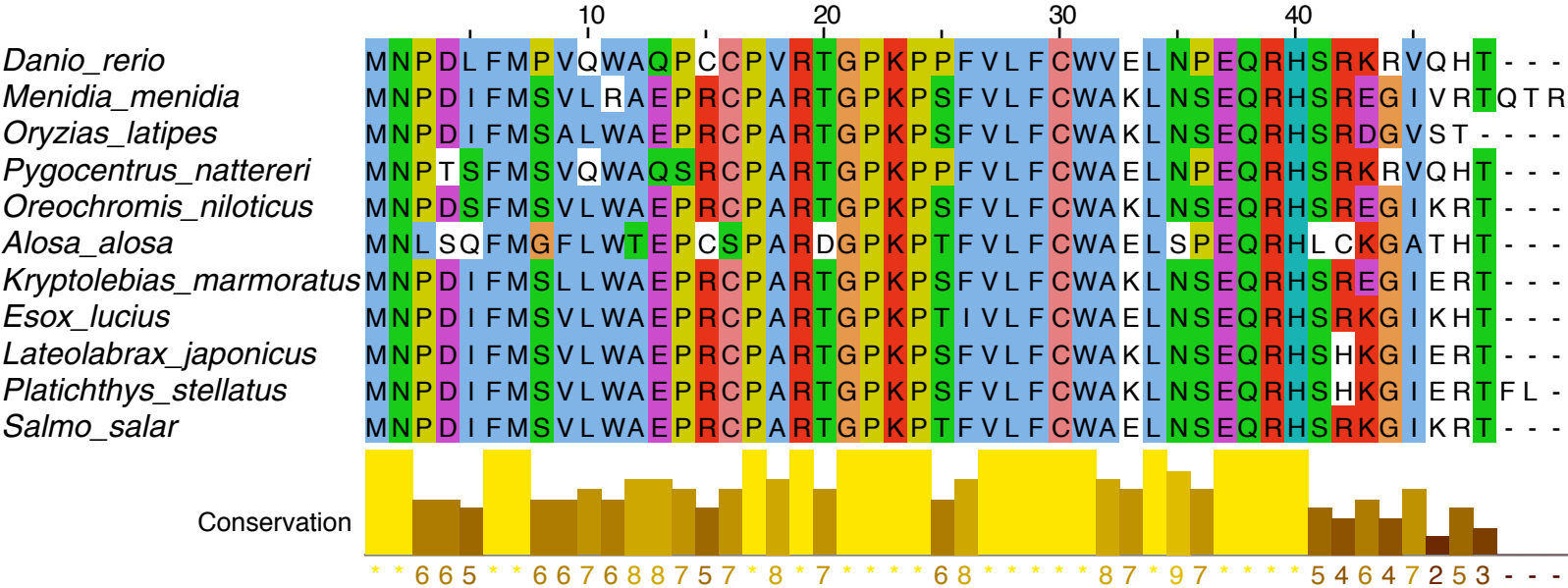
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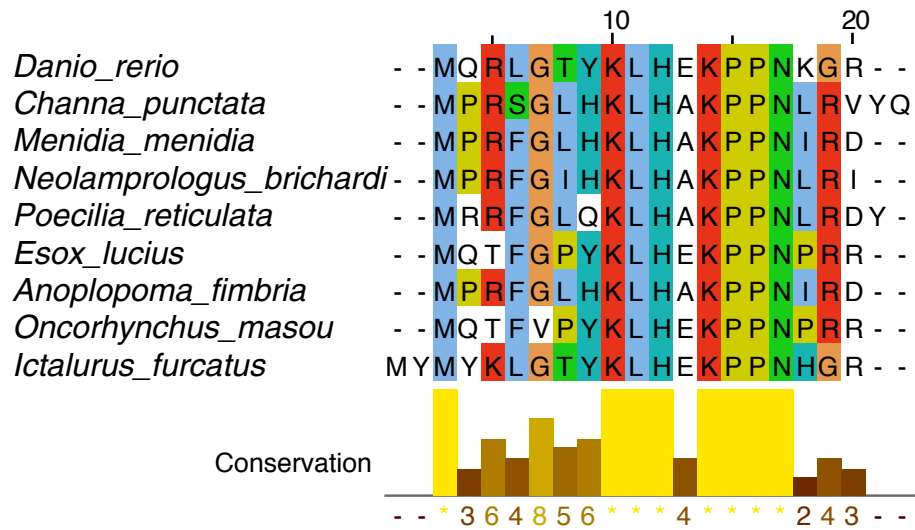


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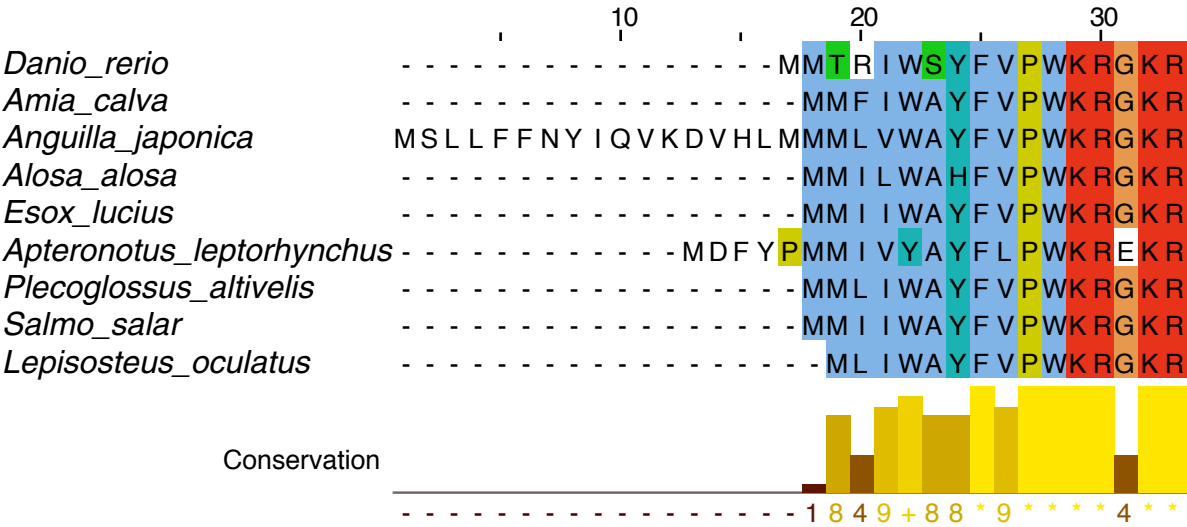


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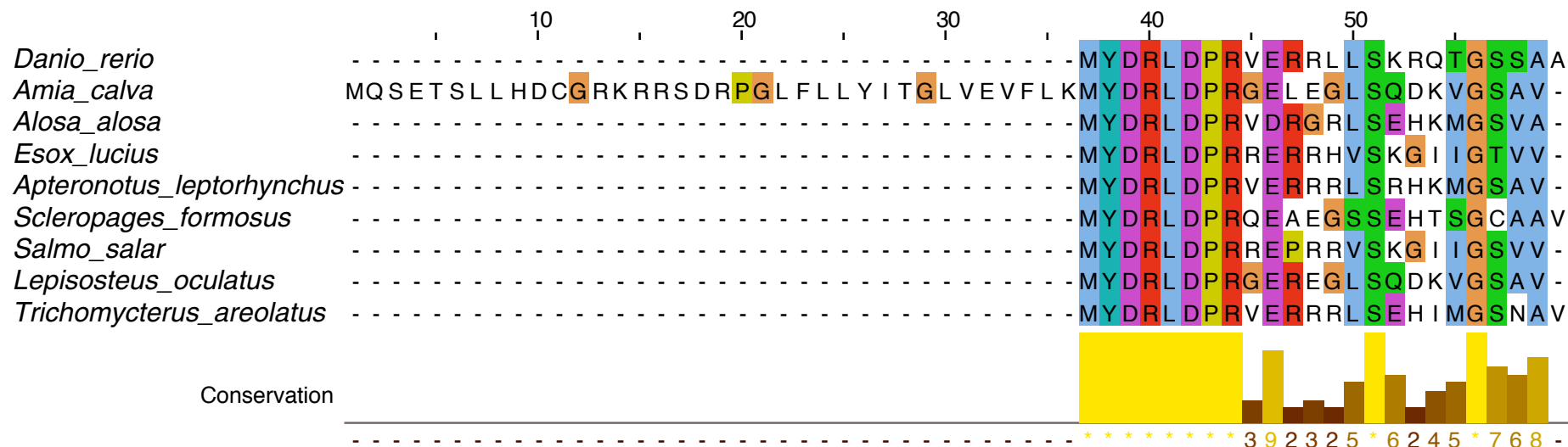
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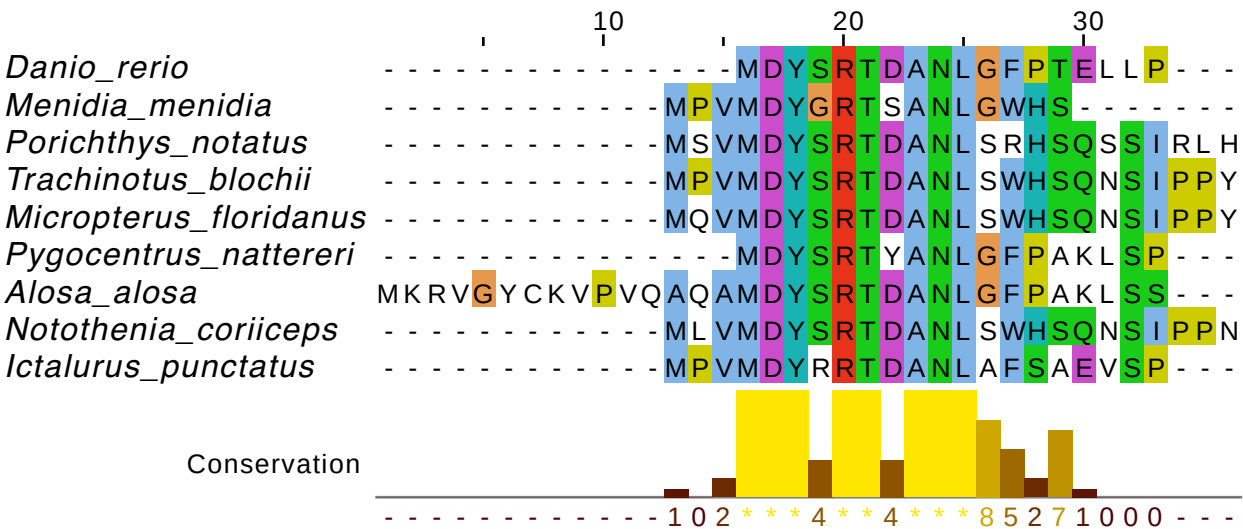
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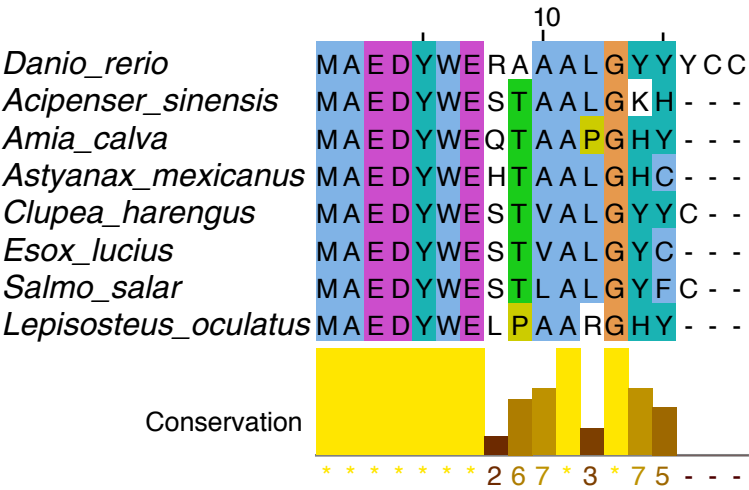
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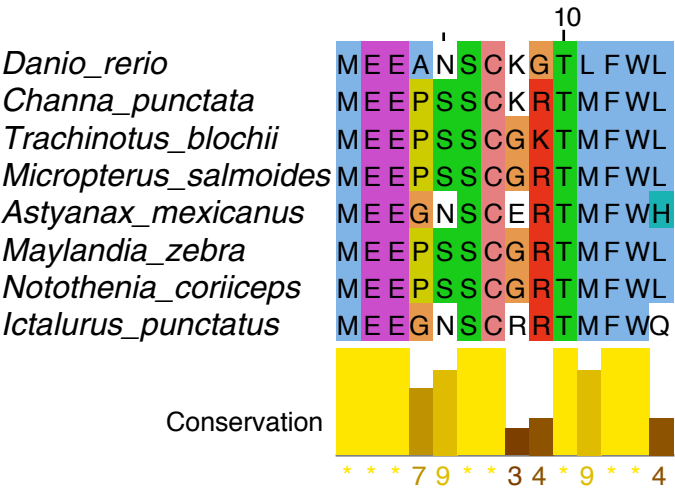
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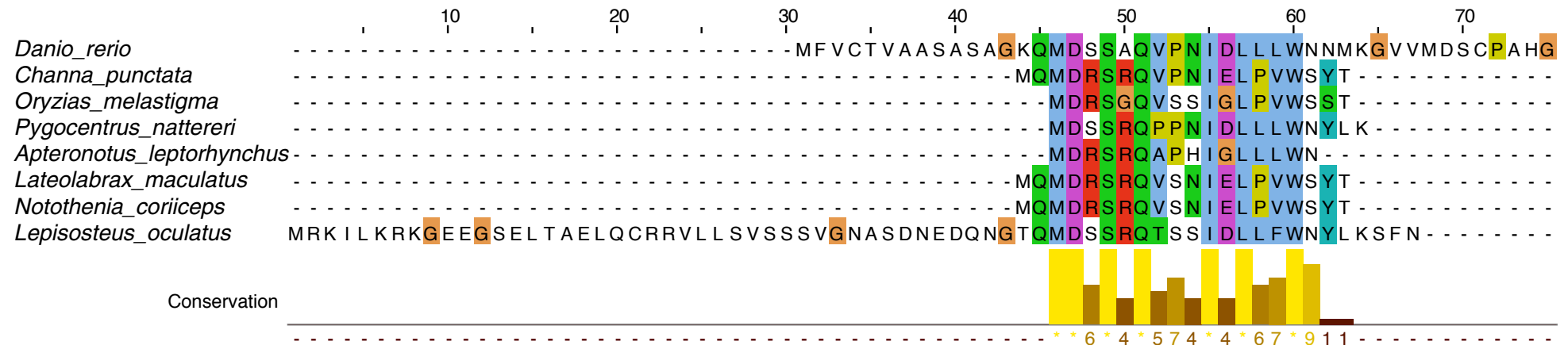
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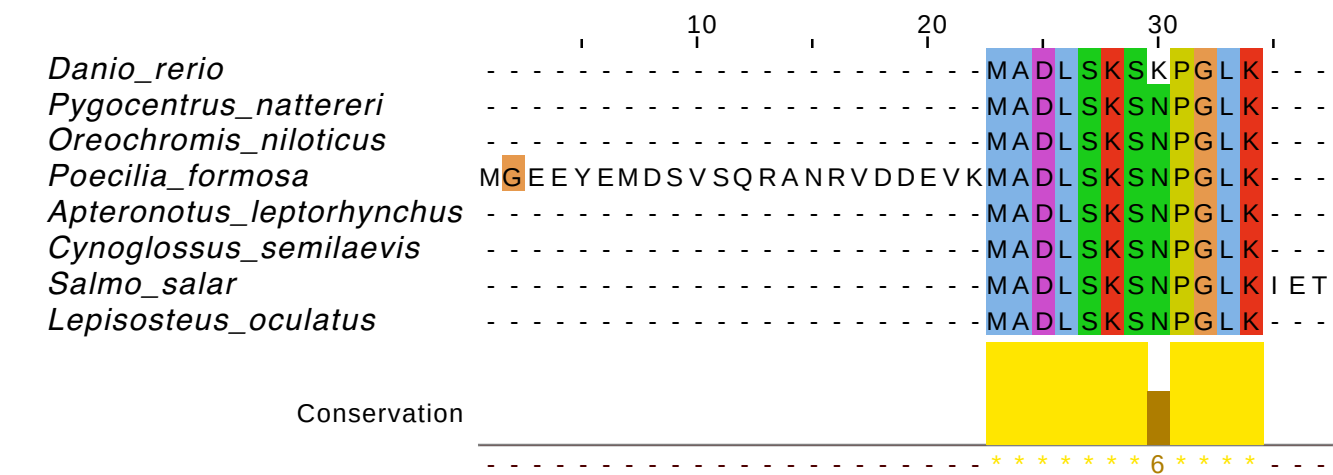
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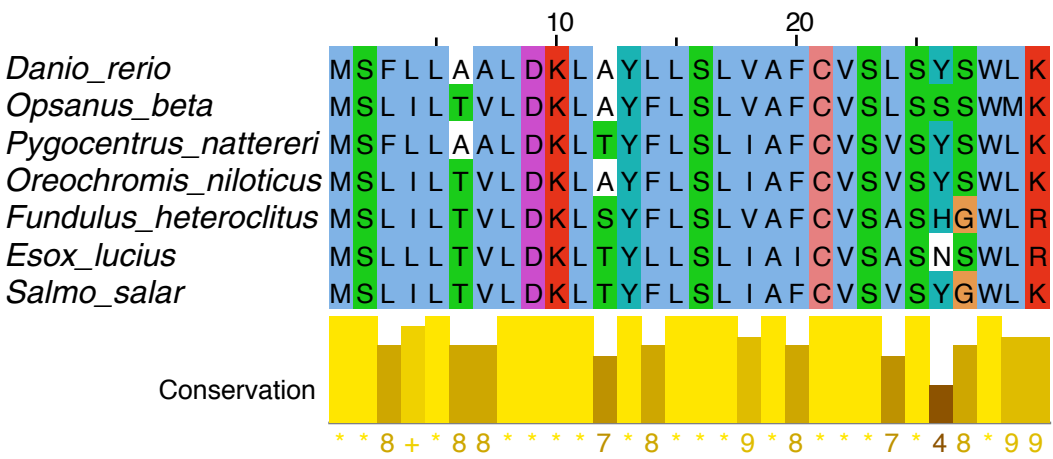
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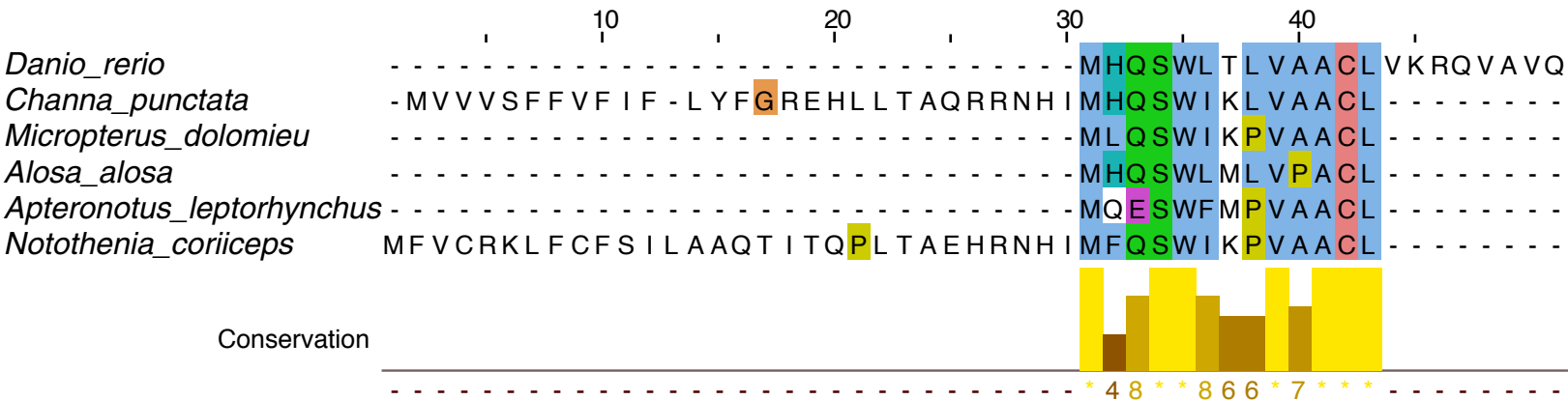
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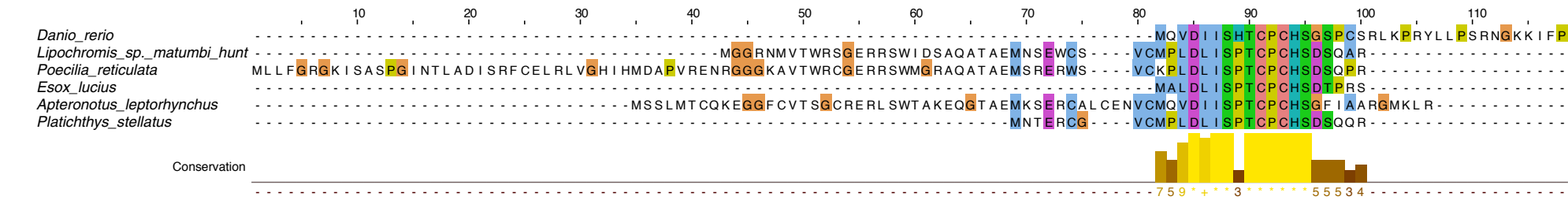
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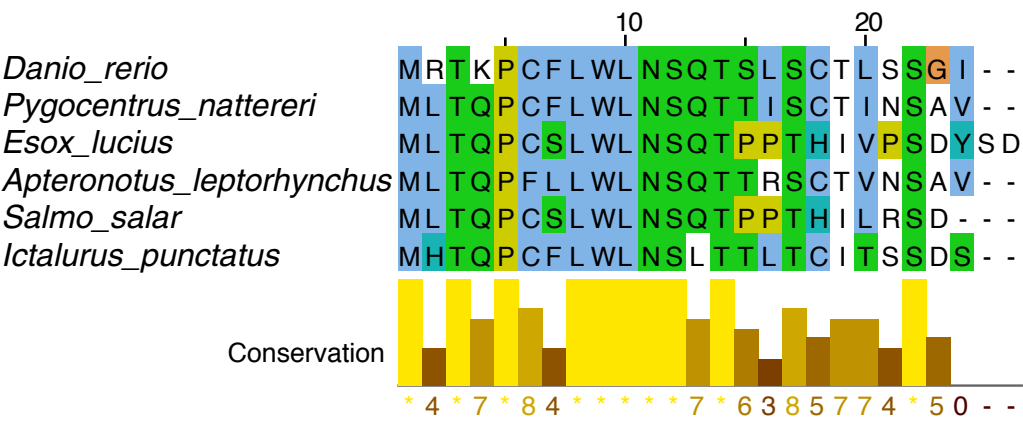
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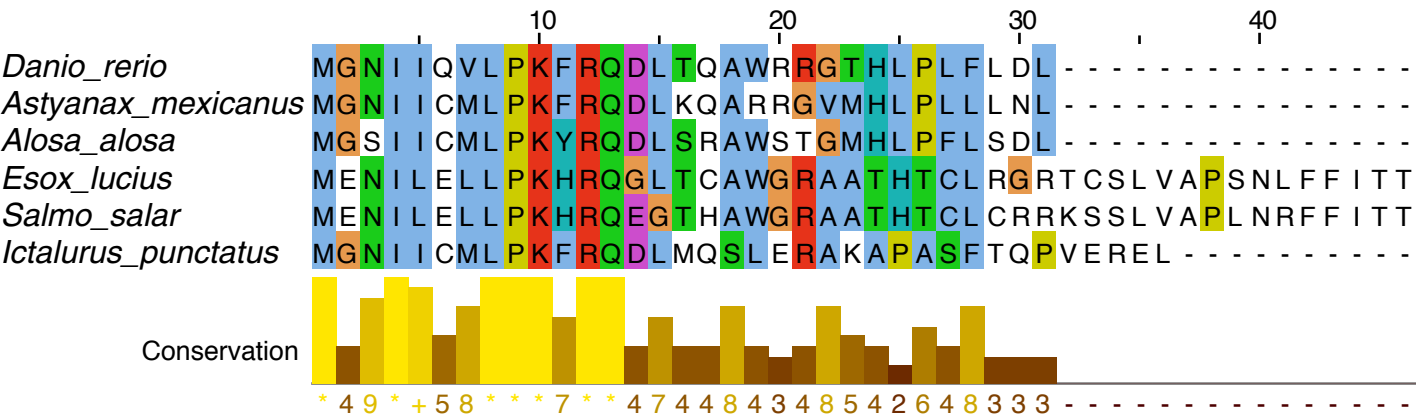
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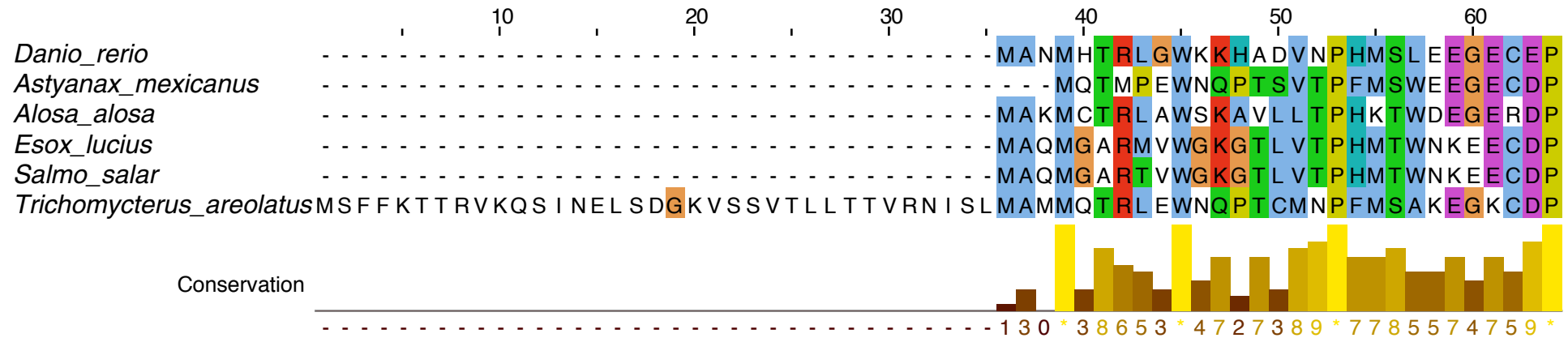
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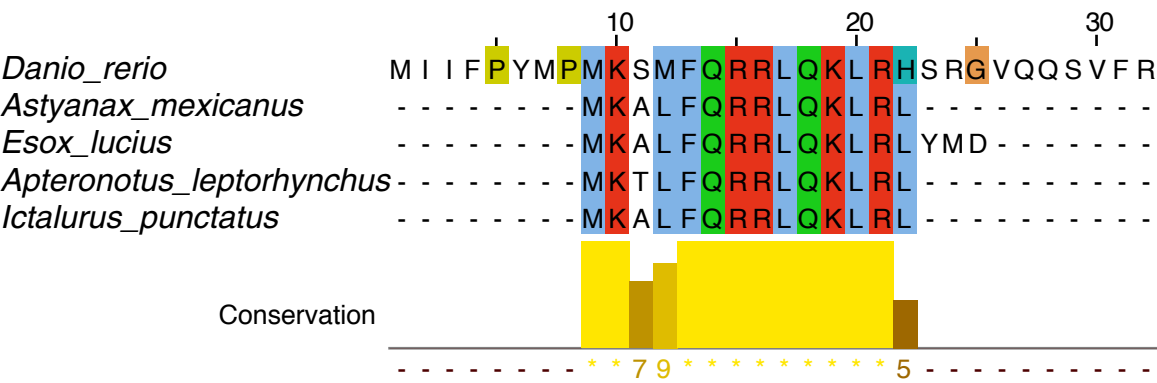
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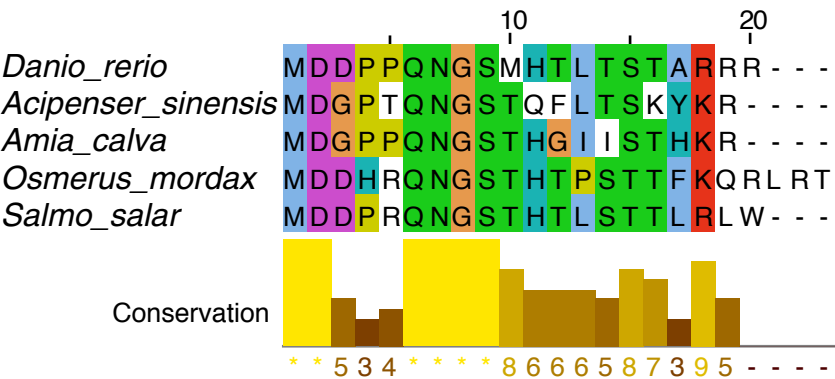
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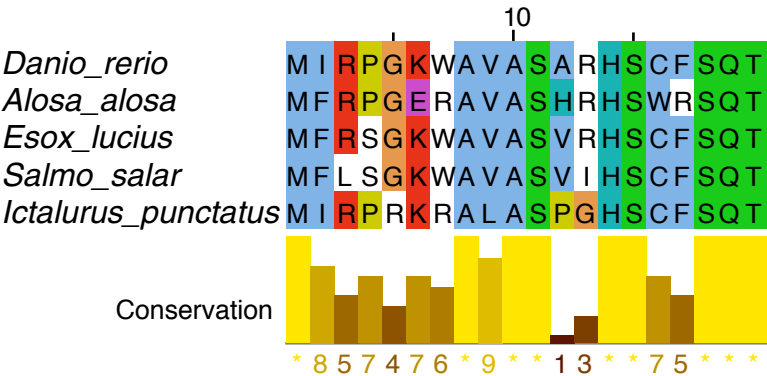
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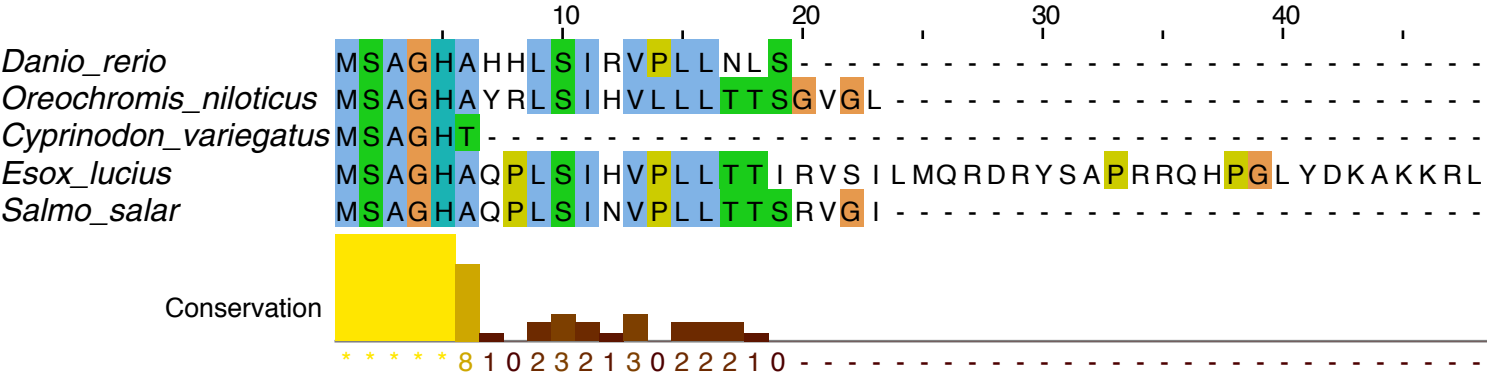
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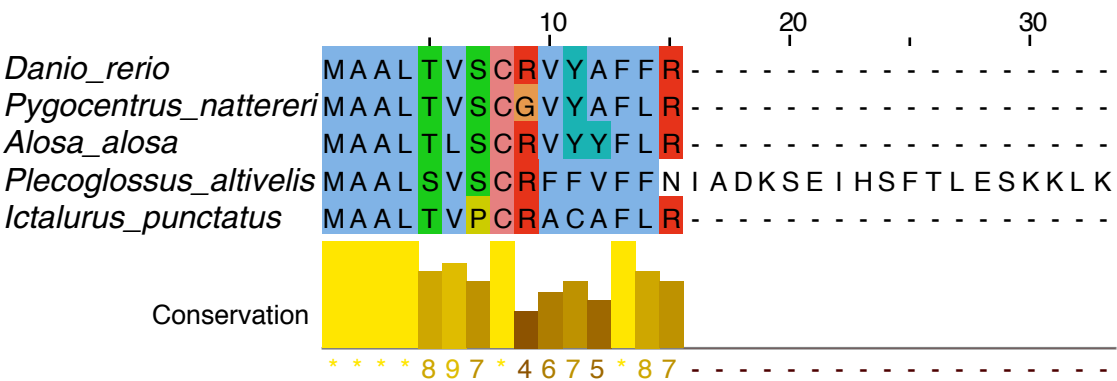
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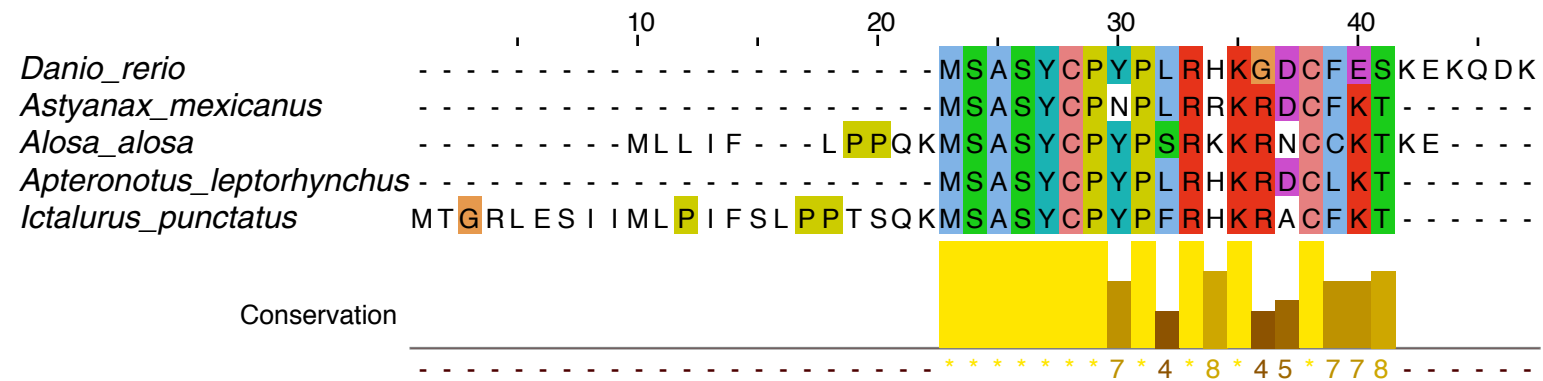
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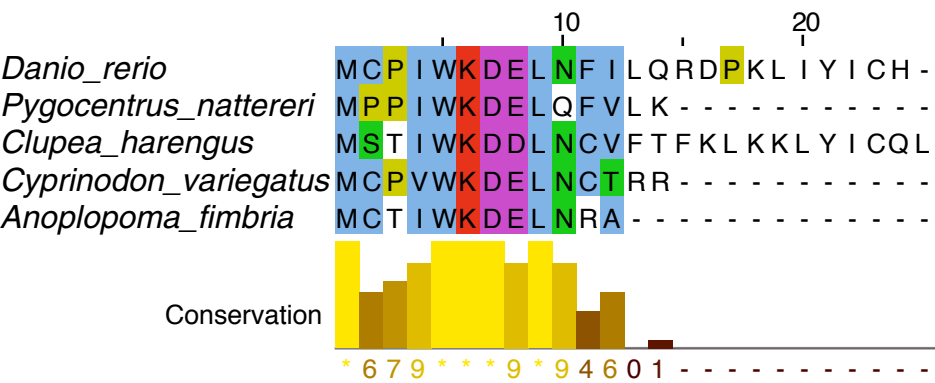
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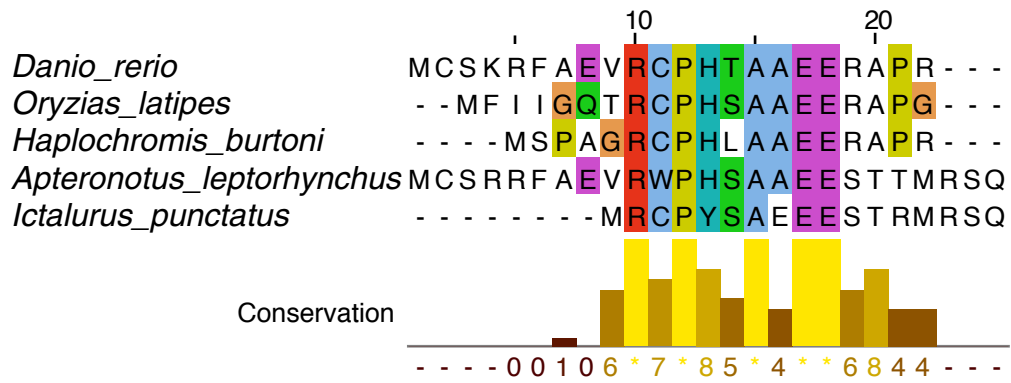
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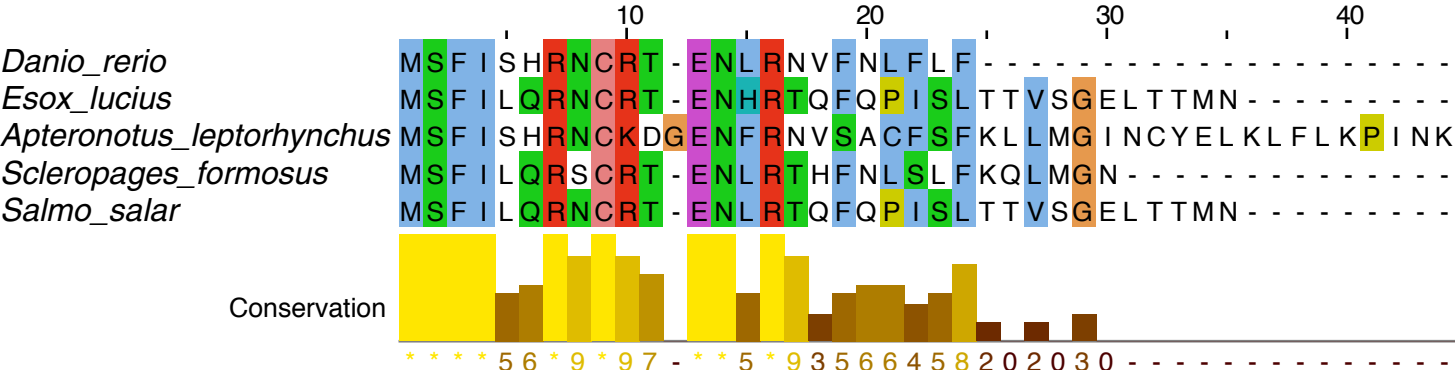
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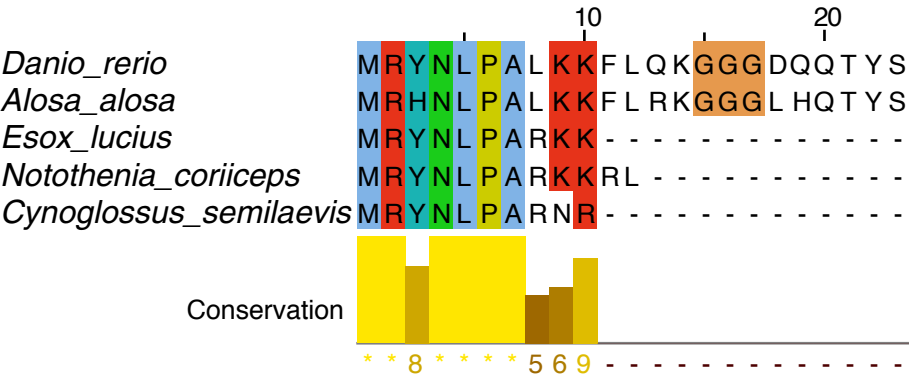
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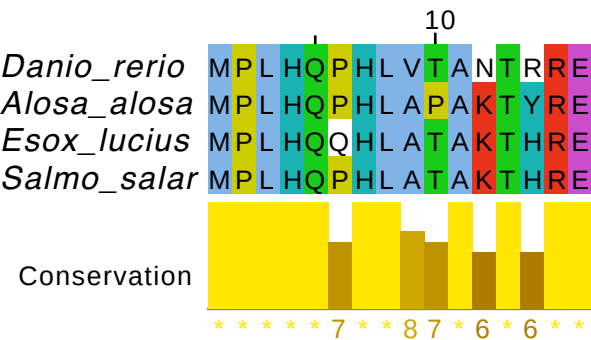
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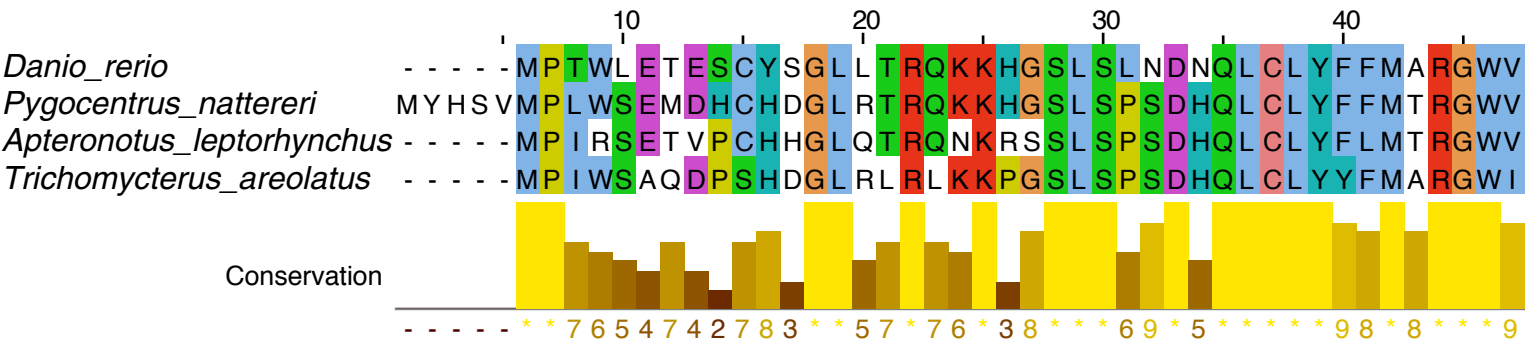
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ENSDARG000000004988 (ppp3ca)



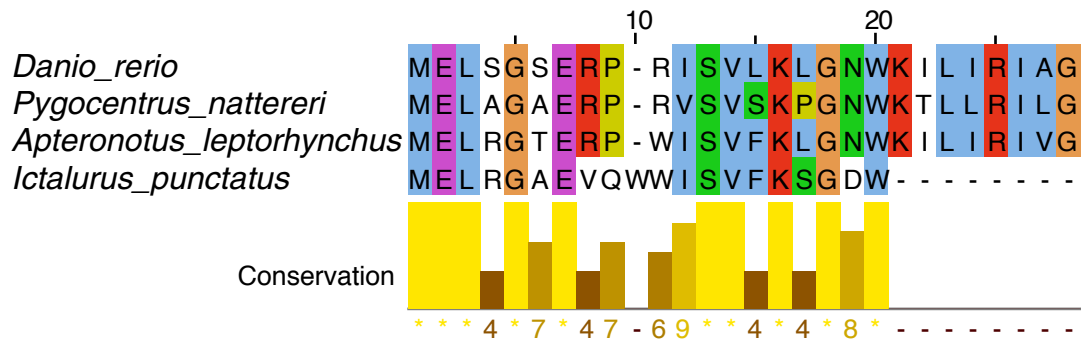
HG0365

ENSDARG00000016132 (keap1a)



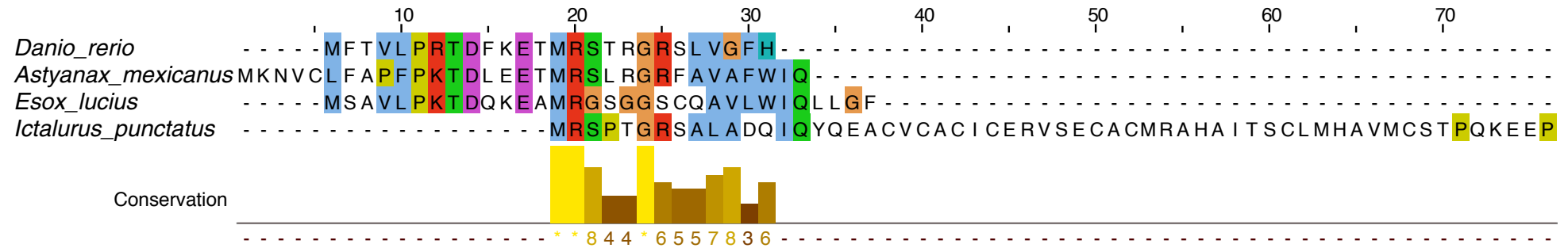
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ENSDARG00000017803 (gsk3b)



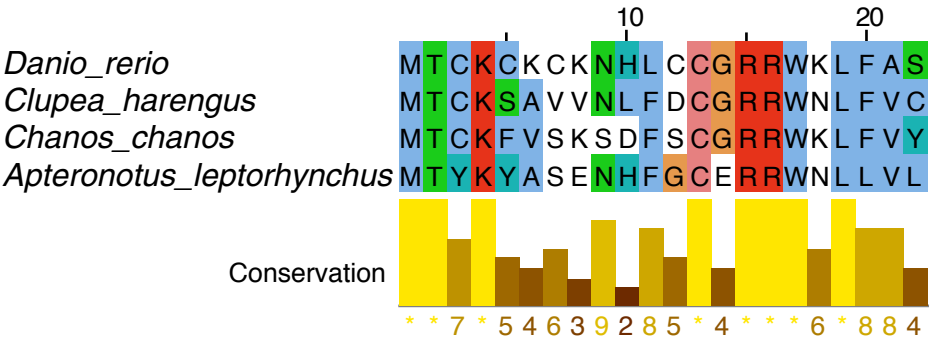
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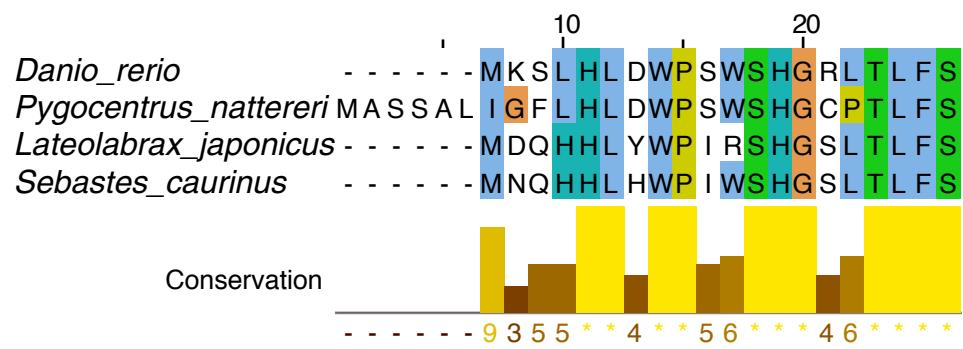
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ENSDARG00000058606 (sik1)



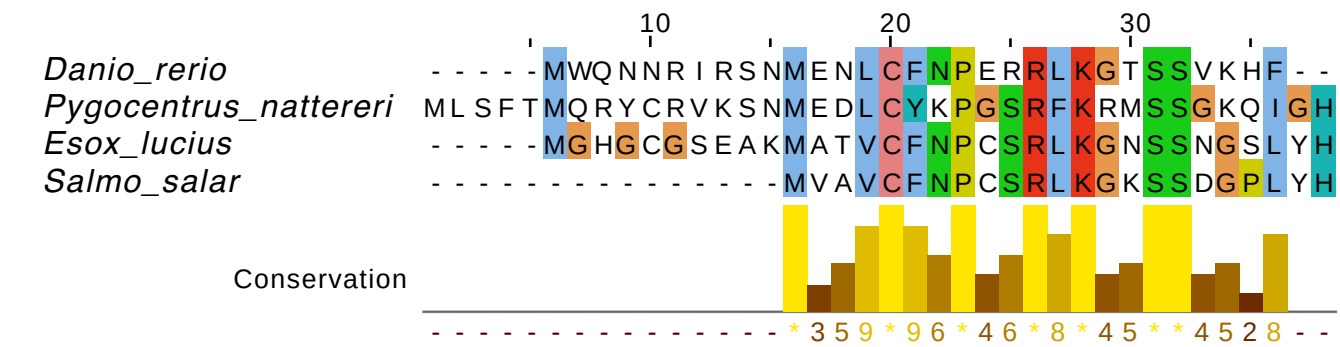
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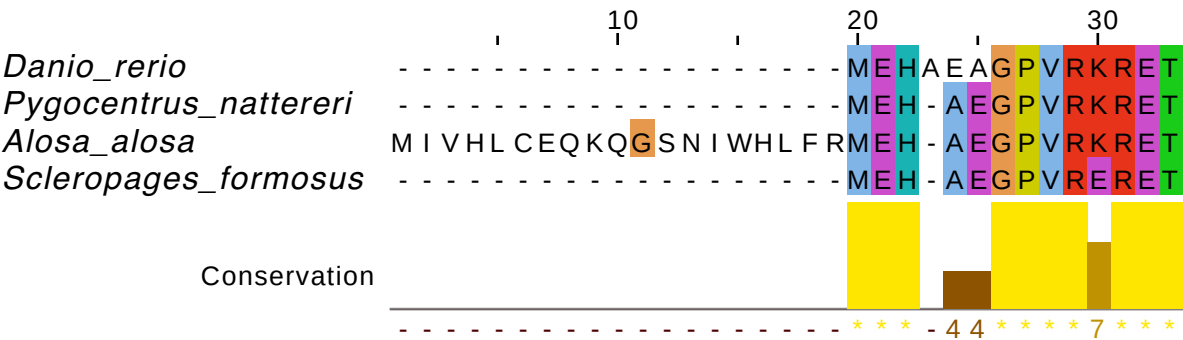
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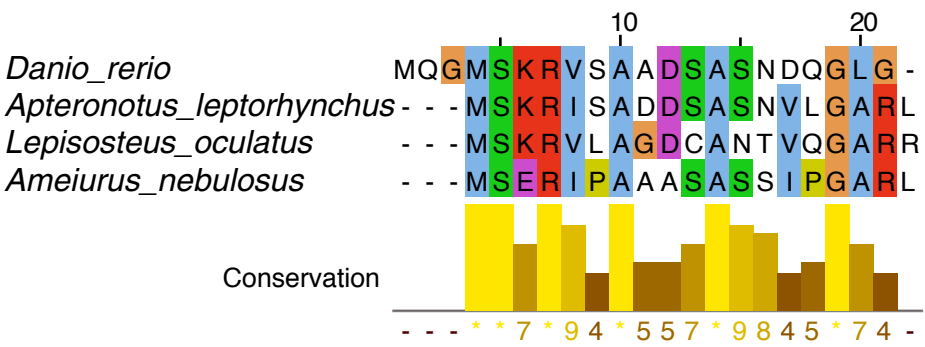
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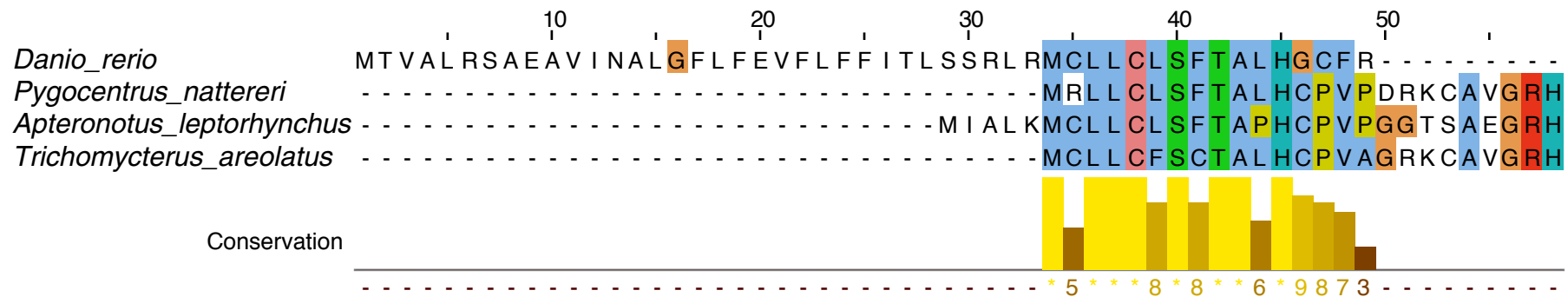
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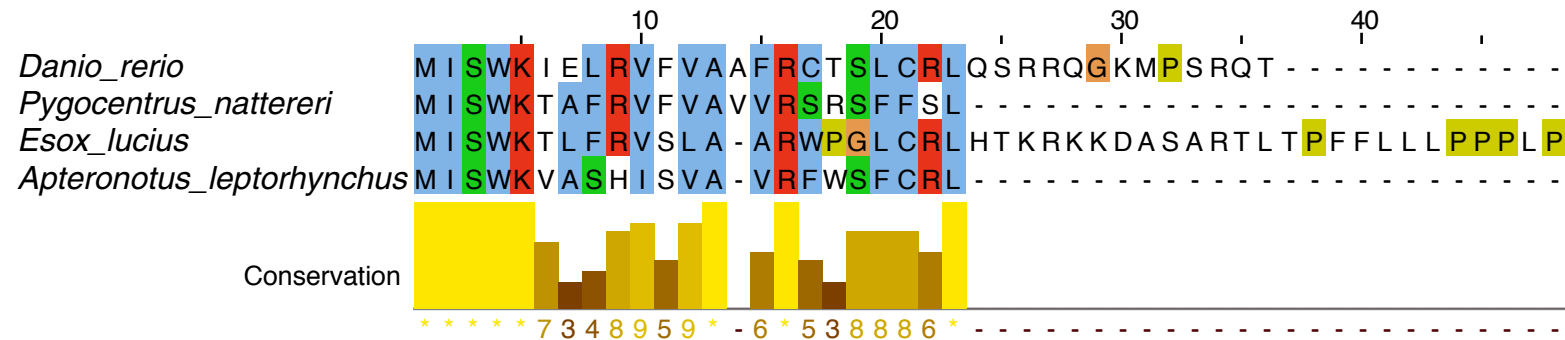
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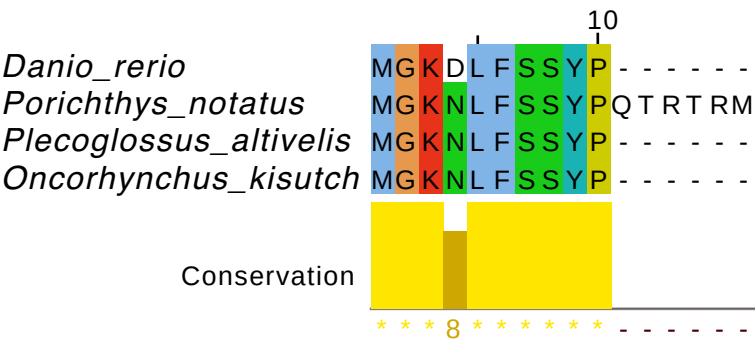
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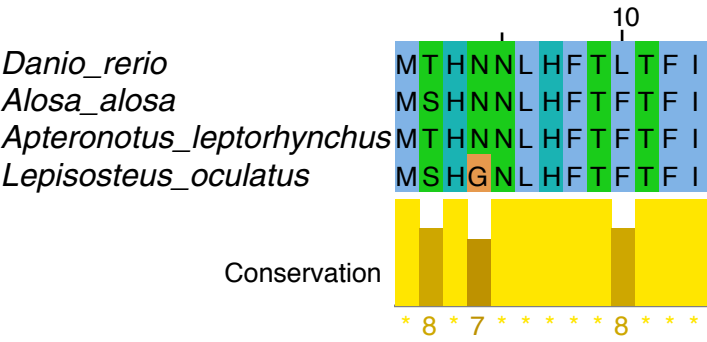
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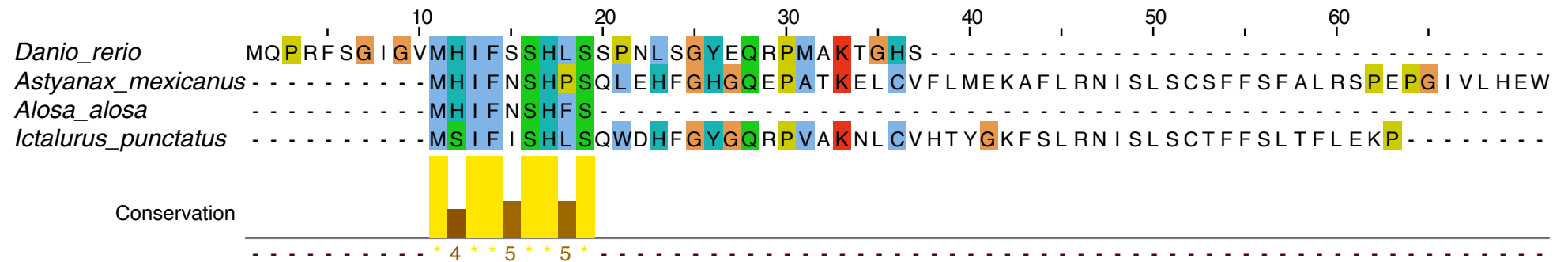
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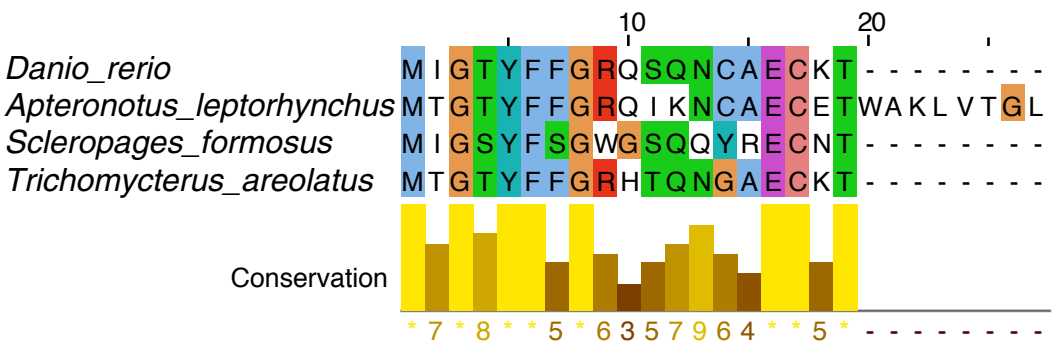
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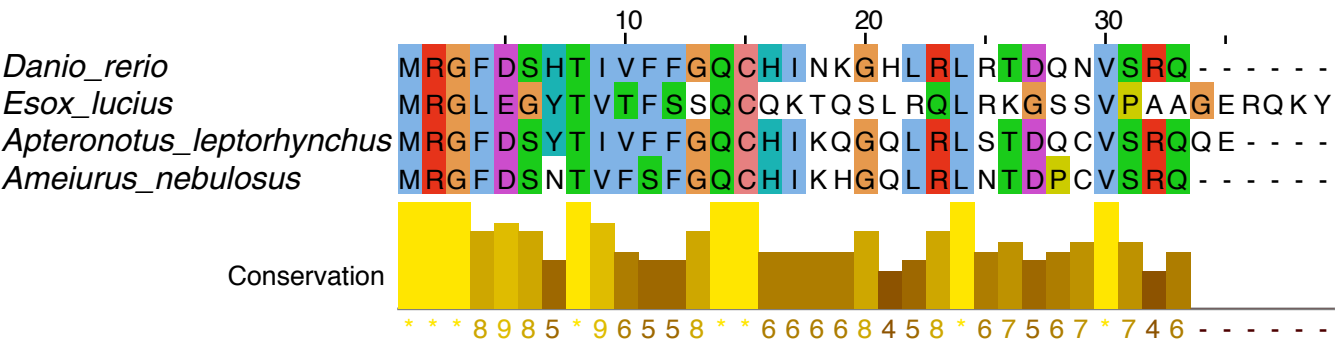
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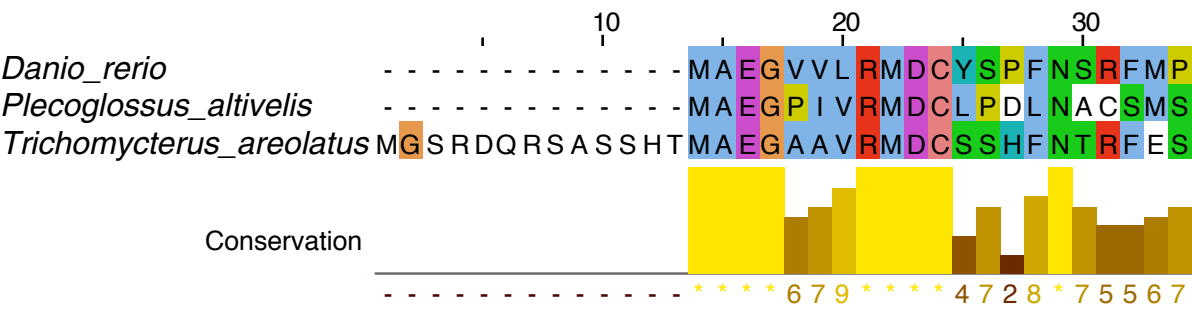
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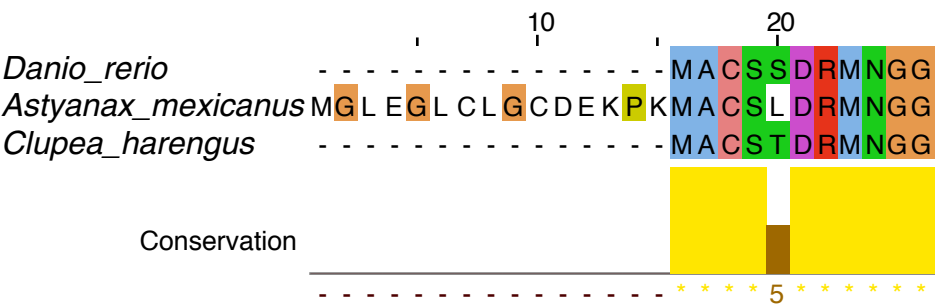
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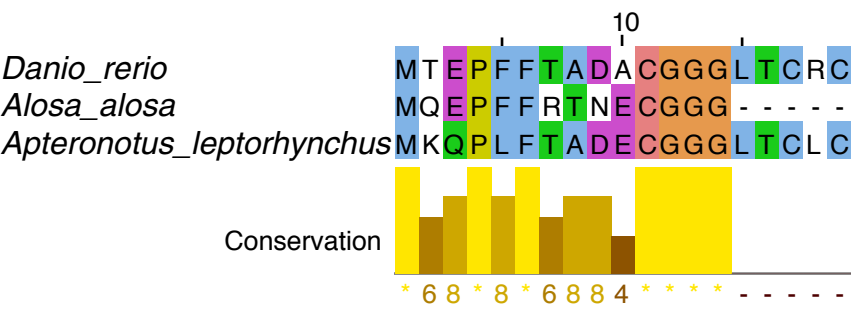
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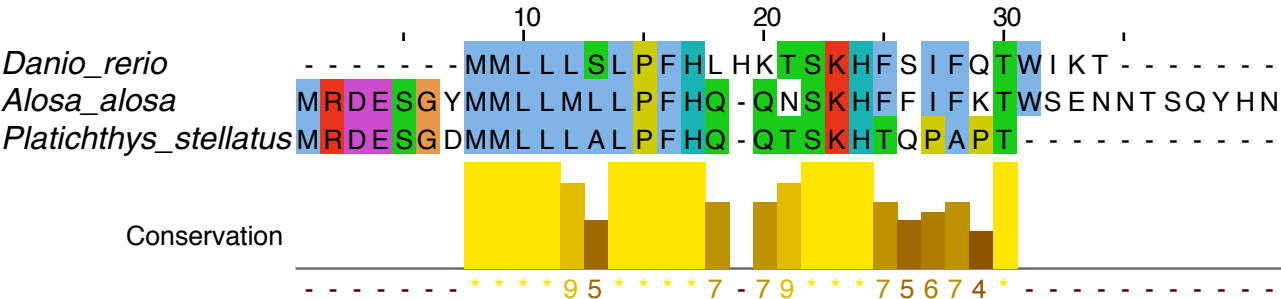
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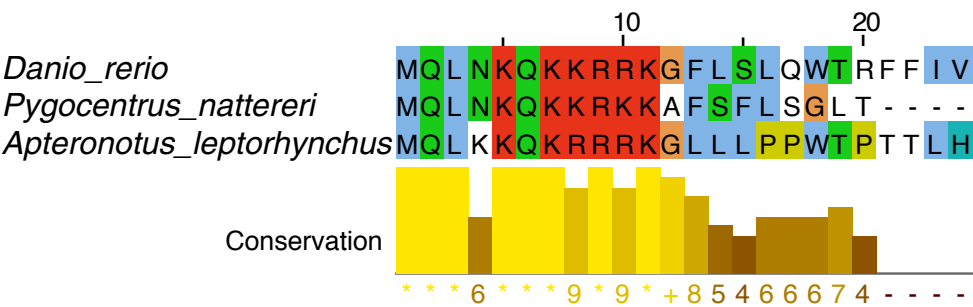
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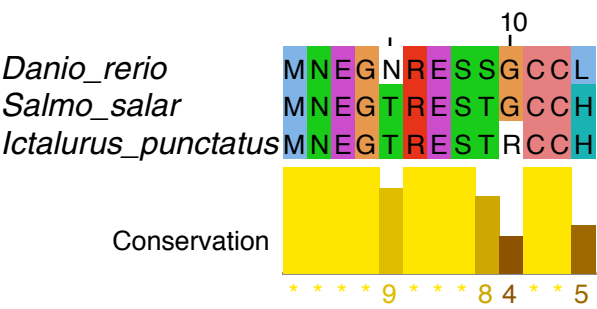
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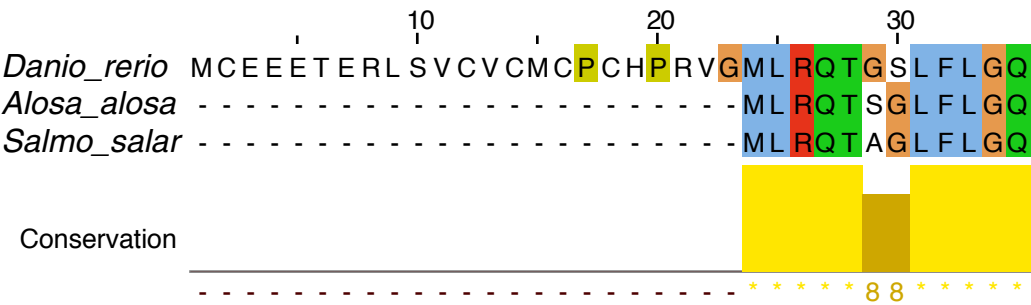
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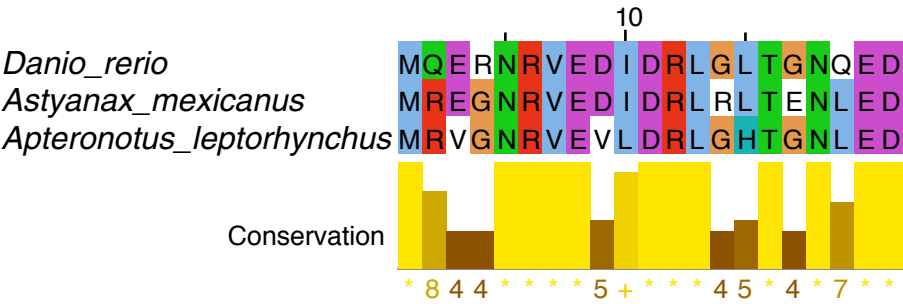
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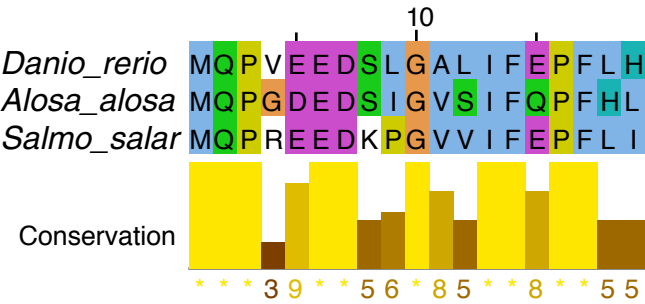
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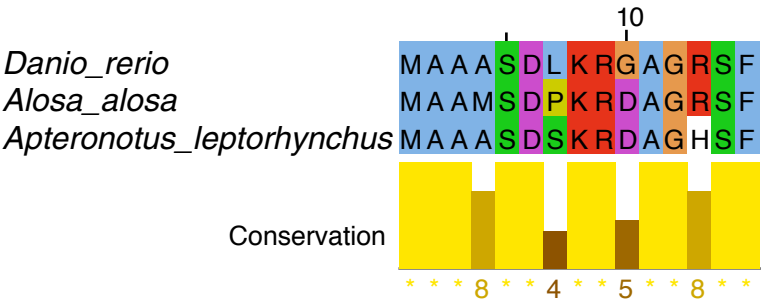
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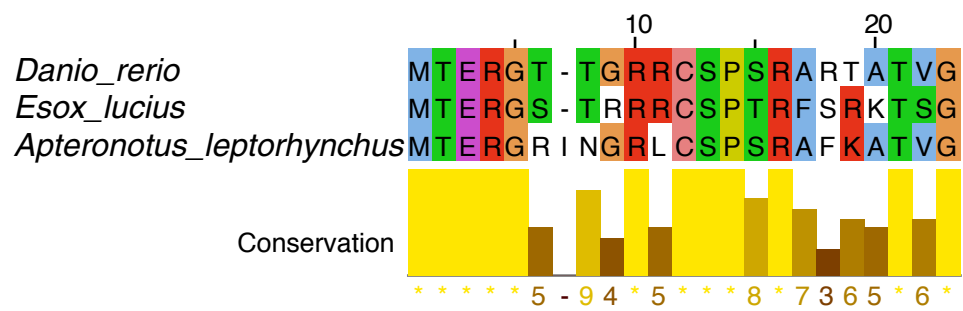
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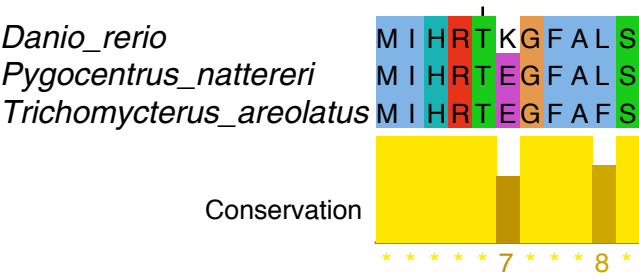
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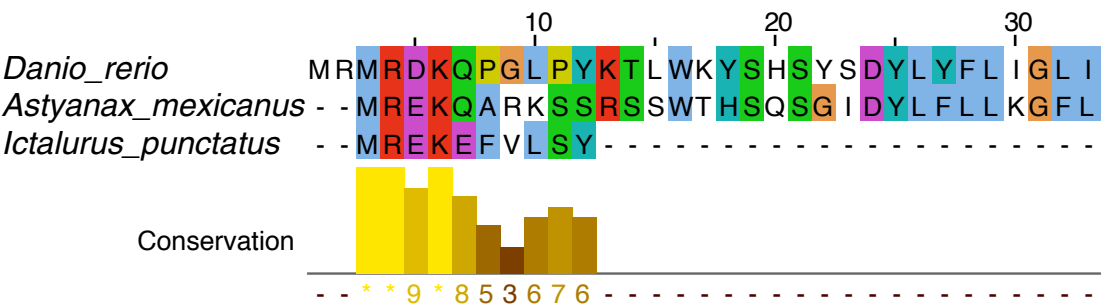
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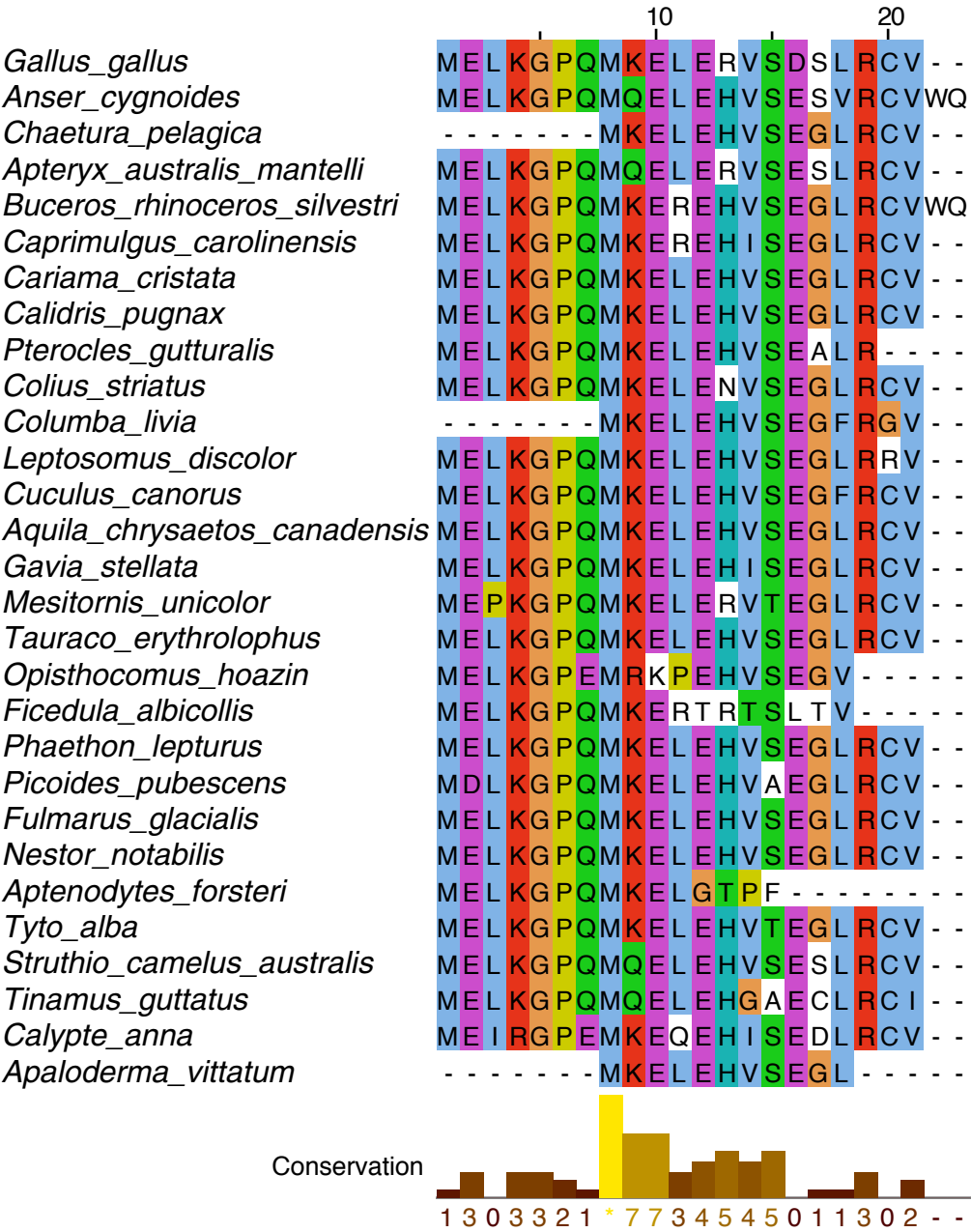
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HG0393

ENSGALG00000002090 (GPSM2)



HG0394

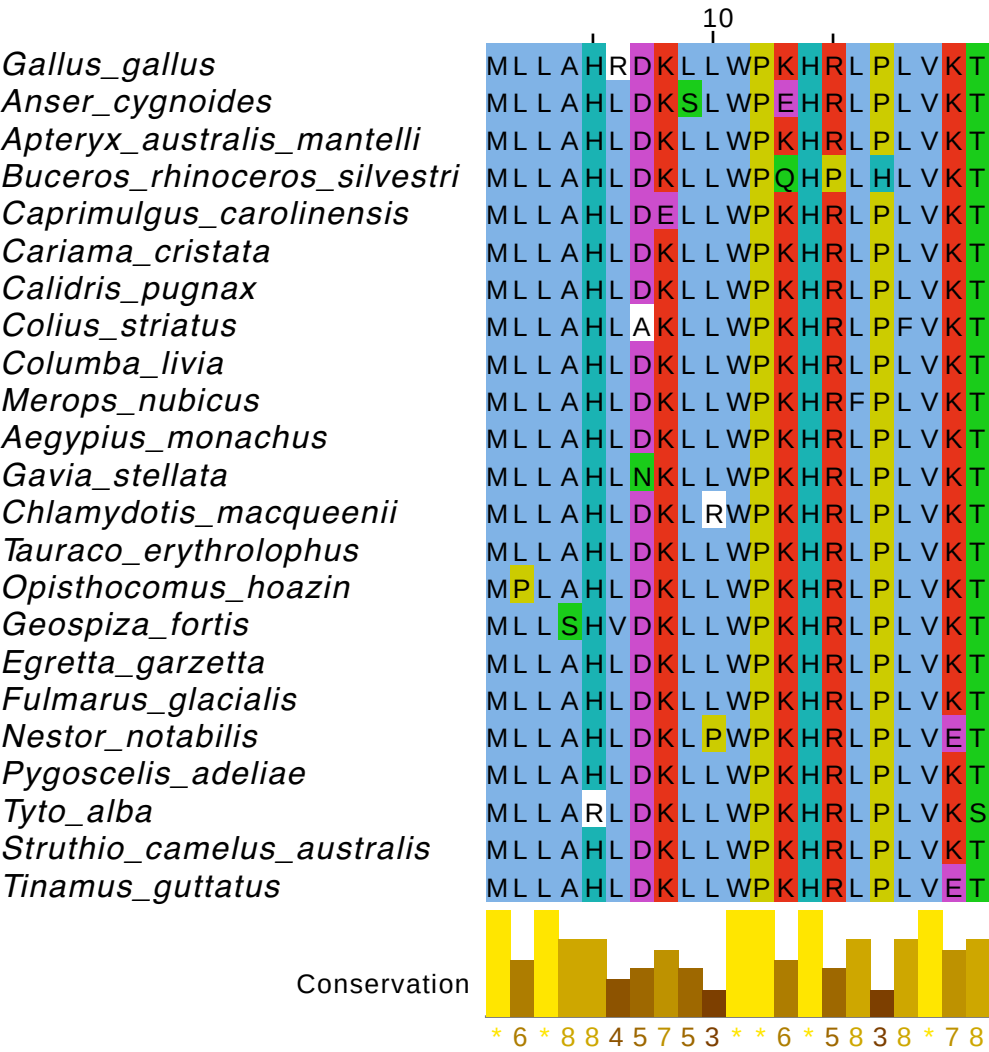
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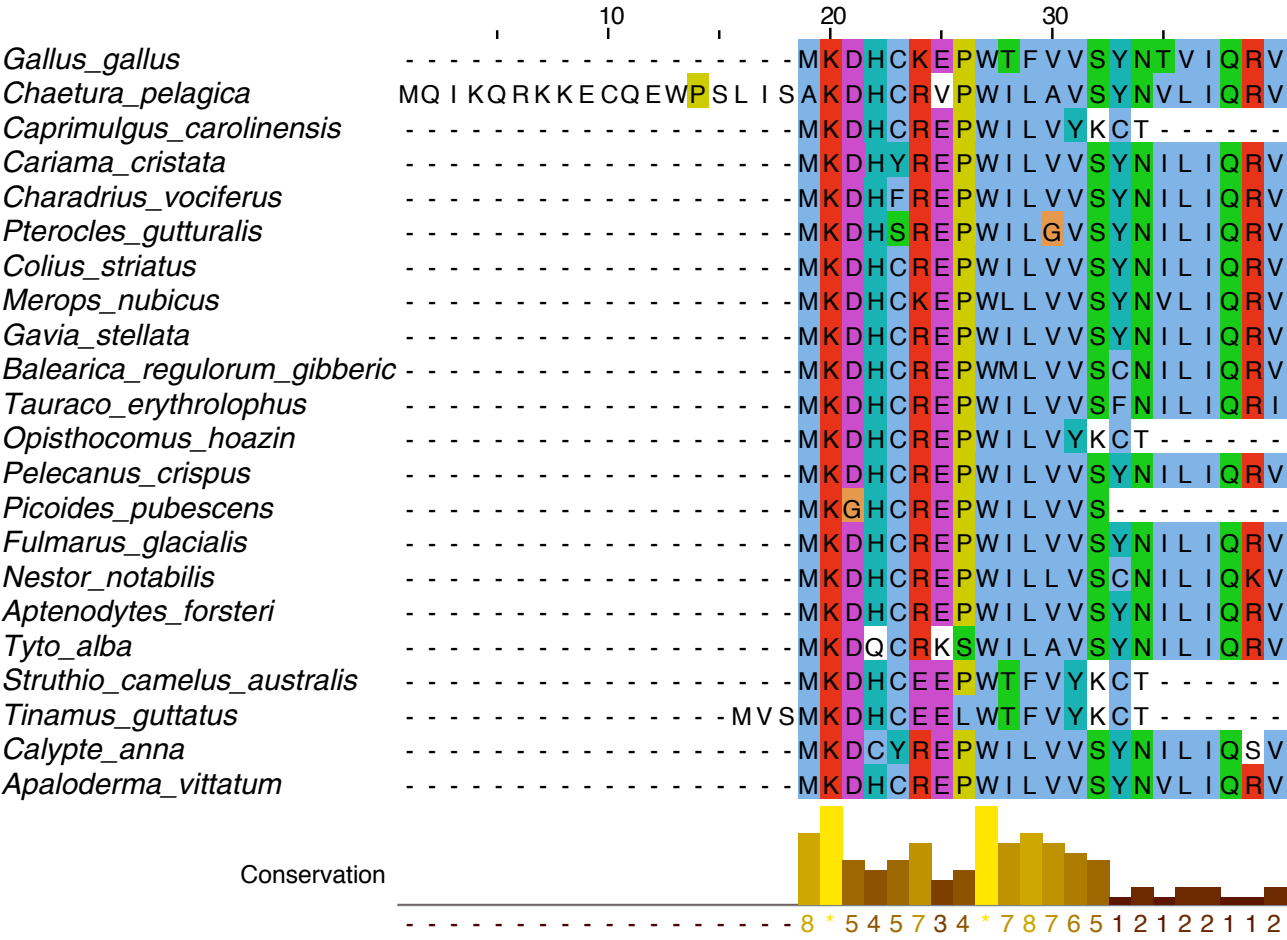
										10										20				
<i>Gallus_gallus</i>	M	R	S	P	C	M	H	T	Q	I	Q	A	H	A	D	F	T	D	-	-	-	-	-	-
<i>Anser_cygnoides</i>	M	H	T	P	C	V	H	A	Q	I	Q	A	H	A	E	F	T	R	-	-	-	-	-	-
<i>Chaetura_pelagica</i>	M	H	S	P	C	M	C	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Apteryx_australis_mantelli</i>	M	H	T	P	C	T	H	T	Q	I	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Caprimulgus_carolinensis</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Cariama_cristata</i>	M	H	A	P	C	M	R	T	Q	M	Q	A	H	A	E	F	T	H	-	-	-	-	-	-
<i>Charadrius_vociferus</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	R	A	D	F	T	Y	-	-	-	-	-	-
<i>Pterocles_gutturalis</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Colius_striatus</i>	M	H	T	P	C	M	H	A	Q	M	Q	A	H	A	G	F	T	H	-	-	-	-	-	-
<i>Columba_livia</i>	M	H	T	P	C	M	C	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Merops_nubicus</i>	-	-	-	-	-	-	-	-	-	M	Q	A	H	A	E	F	T	H	S	N	L	S	-	-
<i>Aquila_chrysaetos_canadensis</i>	M	H	A	P	C	M	H	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Gavia_stellata</i>	M	H	T	A	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Chlamydotis_macqueenii</i>	M	H	A	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	R	-	-	-	-	-	-
<i>Tauraco_erythrolophus</i>	M	H	T	P	C	M	C	T	R	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Manacus_vitellinus</i>	M	R	S	P	C	V	H	A	Q	M	Q	A	Y	A	A	F	T	H	-	-	-	-	-	-
<i>Egretta_garzetta</i>	M	H	T	P	C	M	C	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Fulmarus_glacialis</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Nestor_notabilis</i>	M	H	T	P	C	M	C	T	Q	M	Q	A	H	A	V	F	T	H	-	-	-	-	-	-
<i>Pygoscelis_adeliae</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Tyto_alba</i>	M	H	T	P	C	M	R	T	Q	M	Q	A	H	A	D	F	T	H	-	-	-	-	-	-
<i>Struthio_camelus_australis</i>	M	H	A	P	C	T	H	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>Tinamus_guttatus</i>	M	H	T	A	C	T	H	S	Q	L	Q	A	R	A	D	F	T	H	-	-	-	-	-	-
<i>Calypte_anna</i>	M	H	A	P	C	M	C	T	Q	M	K	A	H	A	D	F	I	H	-	-	-	-	-	-
<i>Apaloderma_vittatum</i>	M	H	T	P	C	V	C	T	Q	M	Q	T	H	A	D	F	T	H	-	-	-	-	-	-



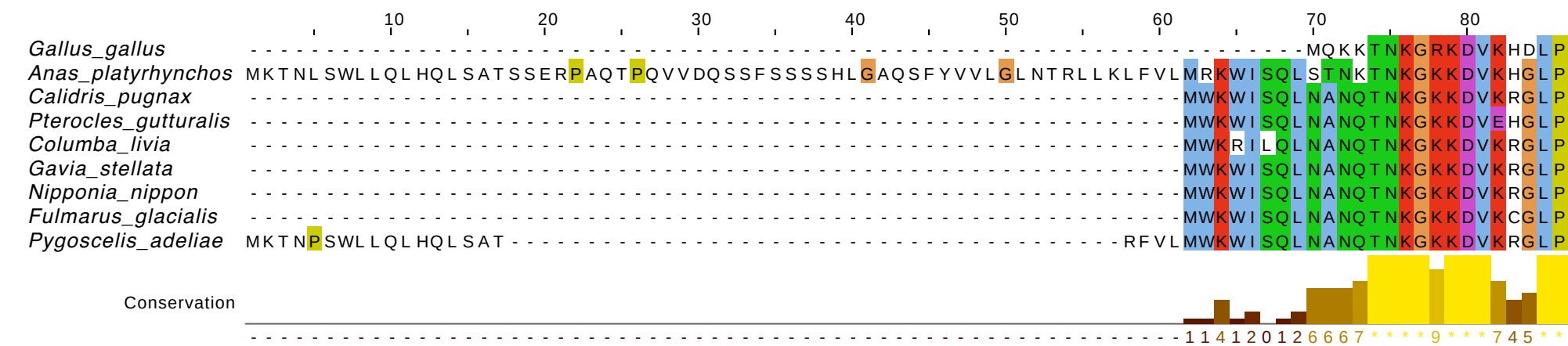
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ENSGALG00000014936 (ESCO1)



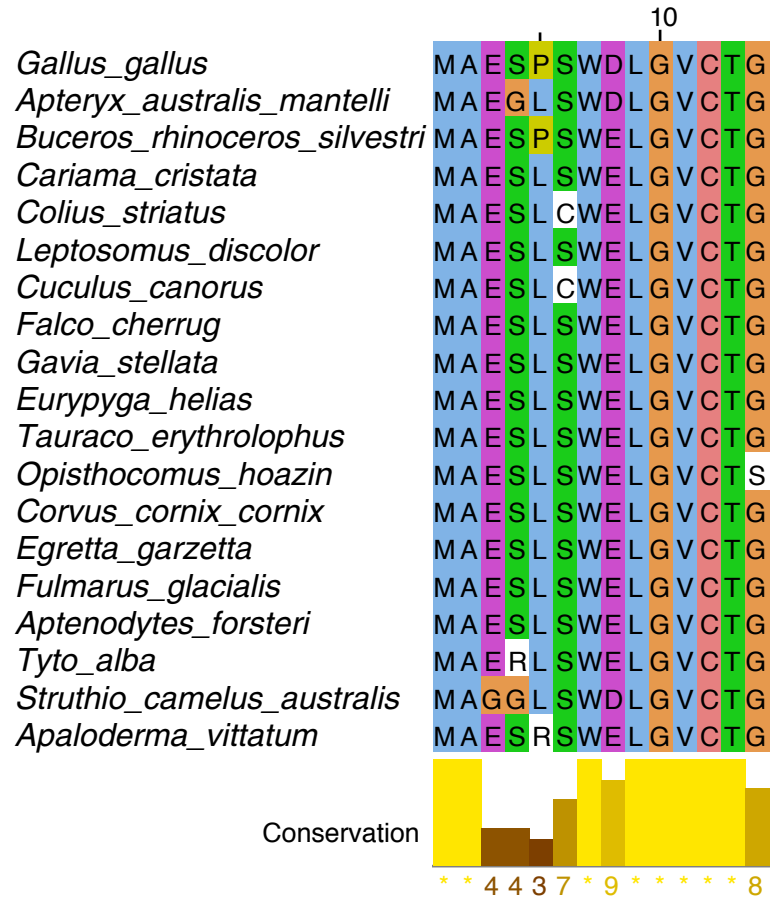


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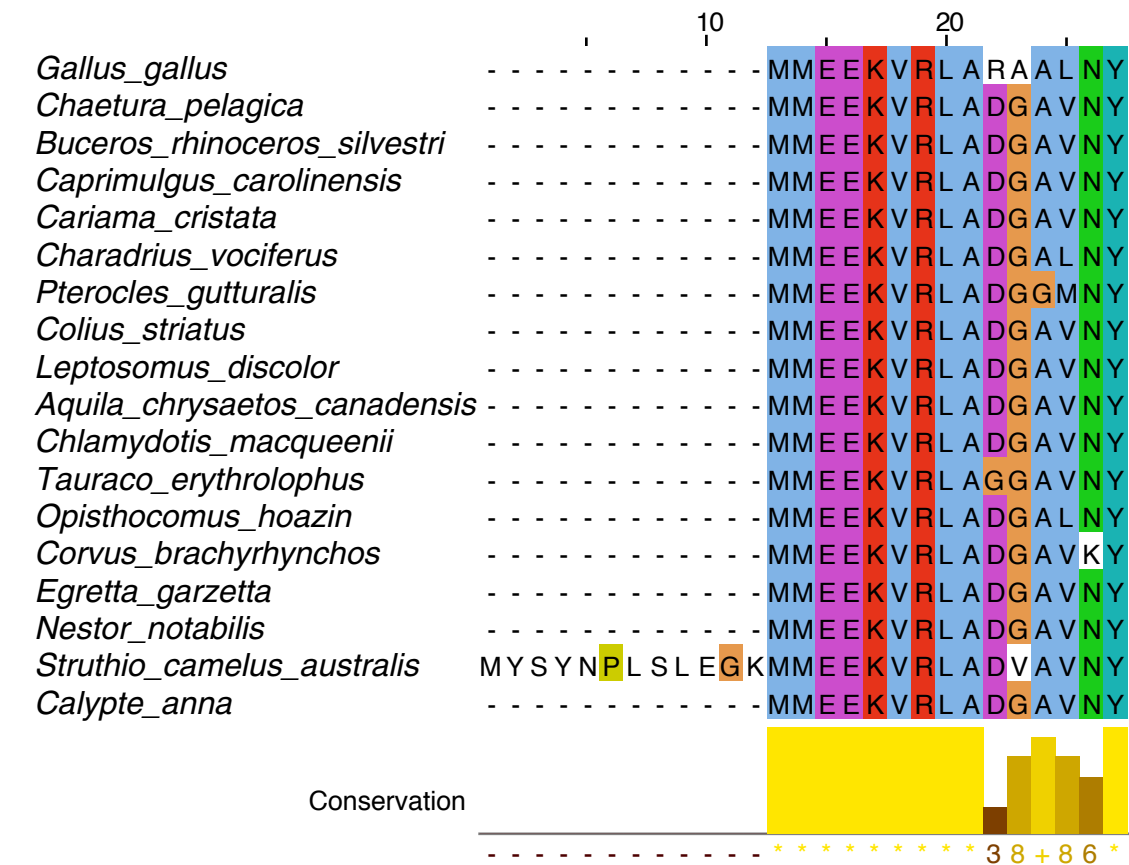
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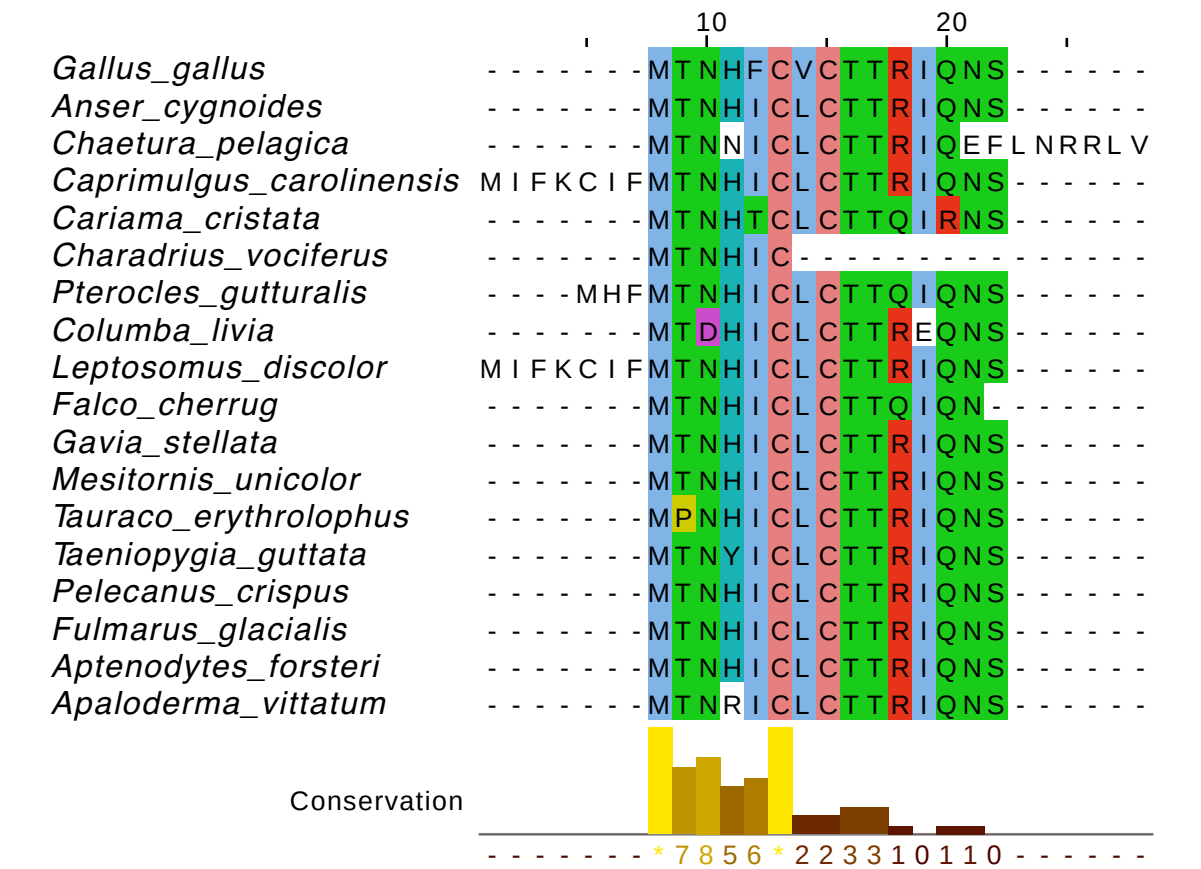
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HG0398

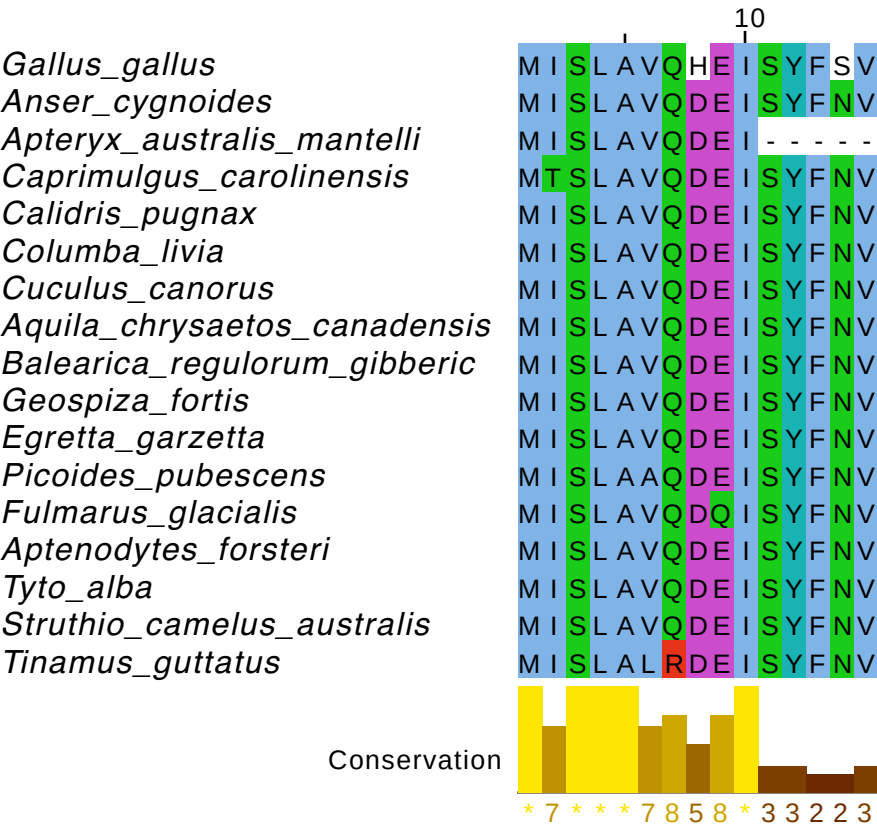
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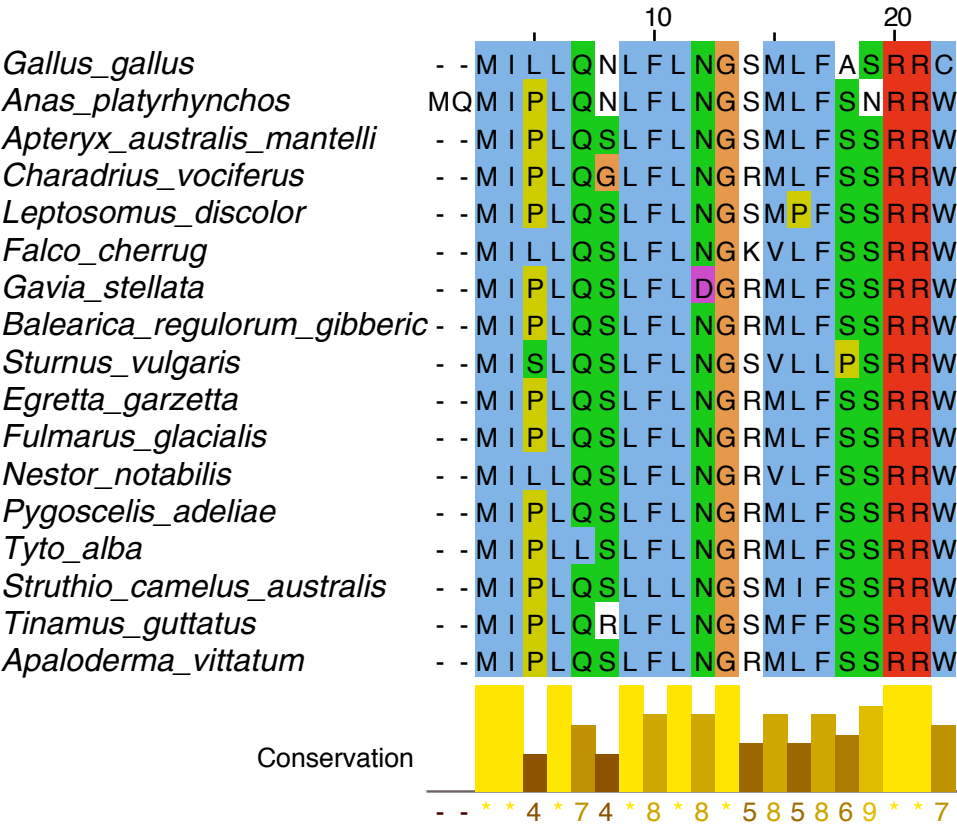
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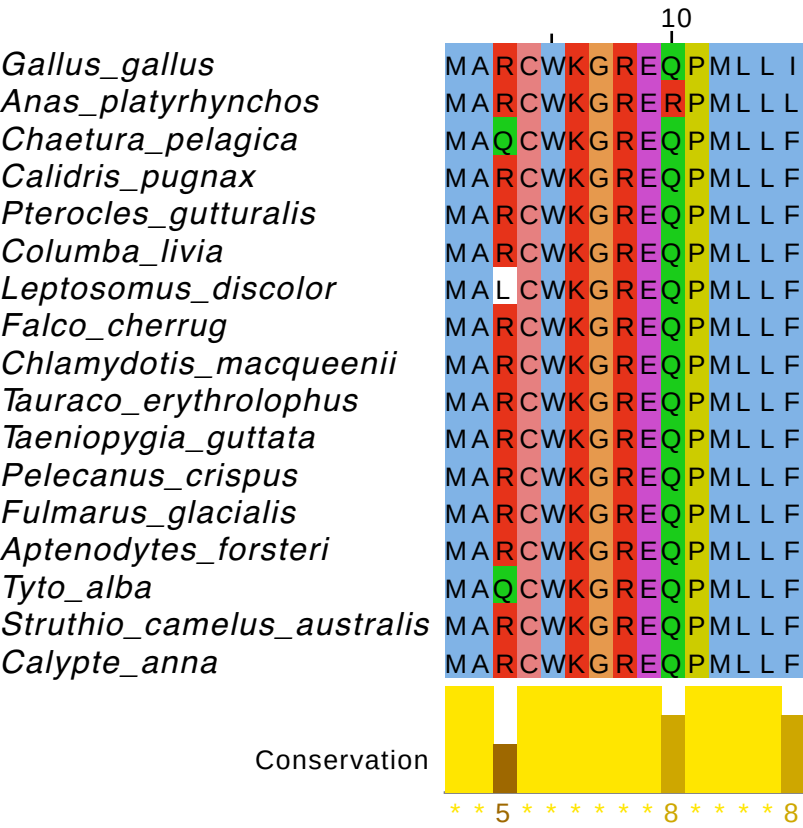
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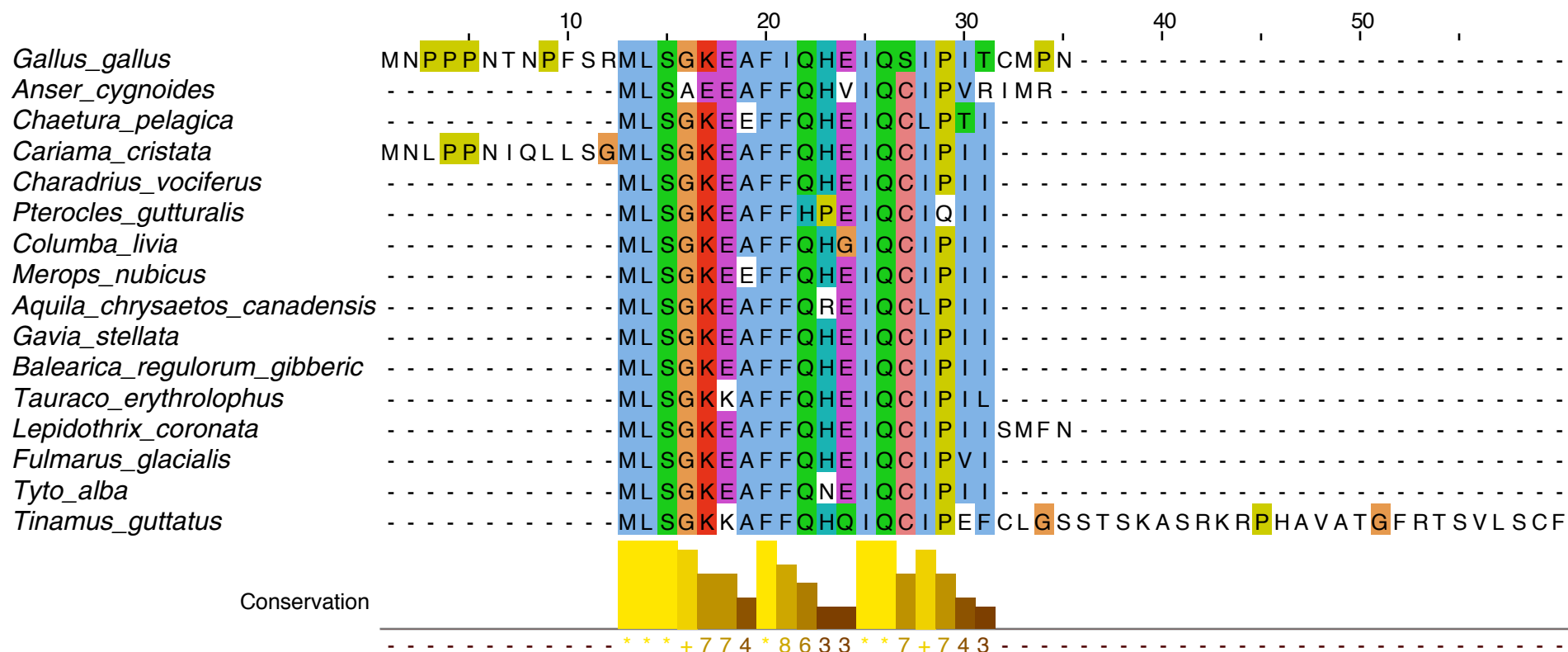
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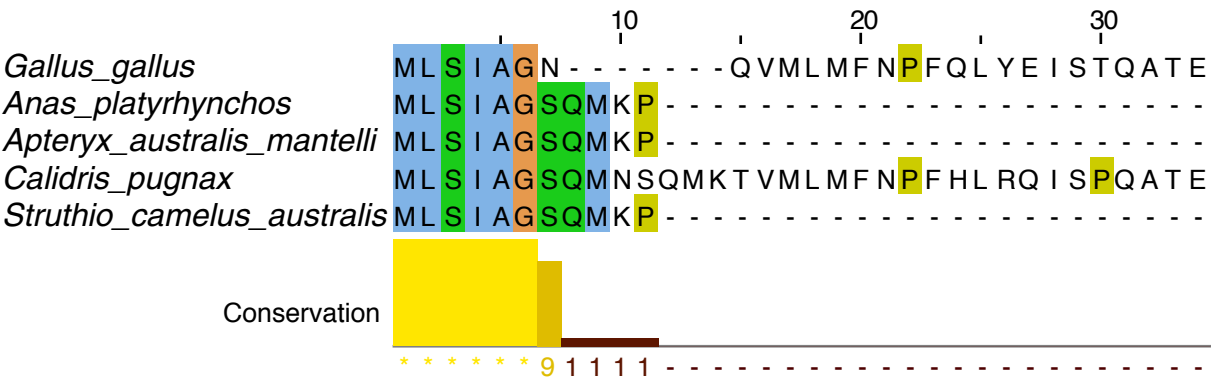
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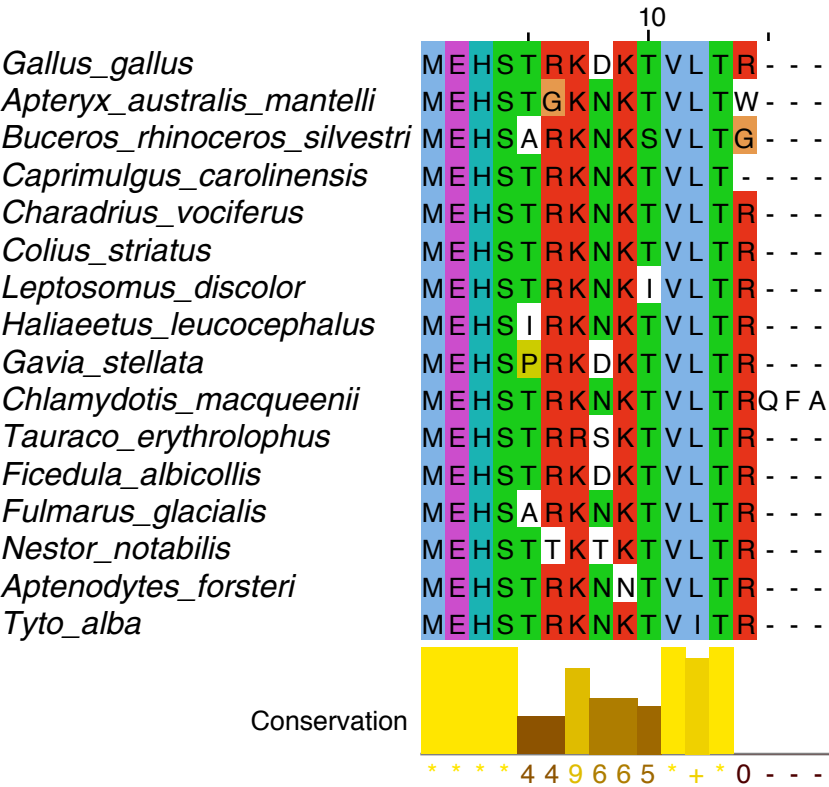
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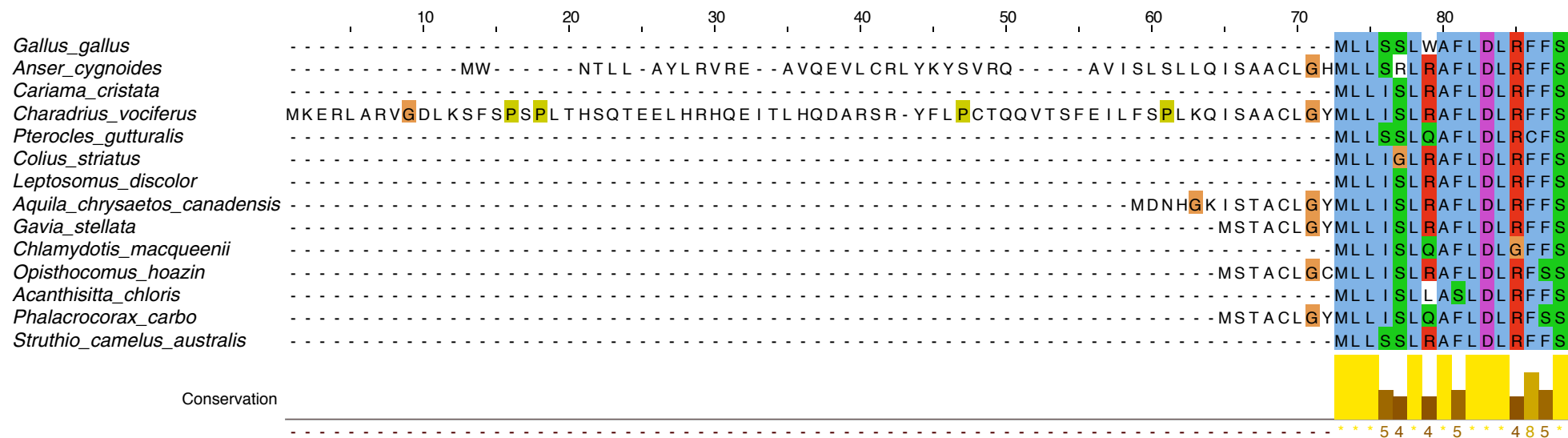


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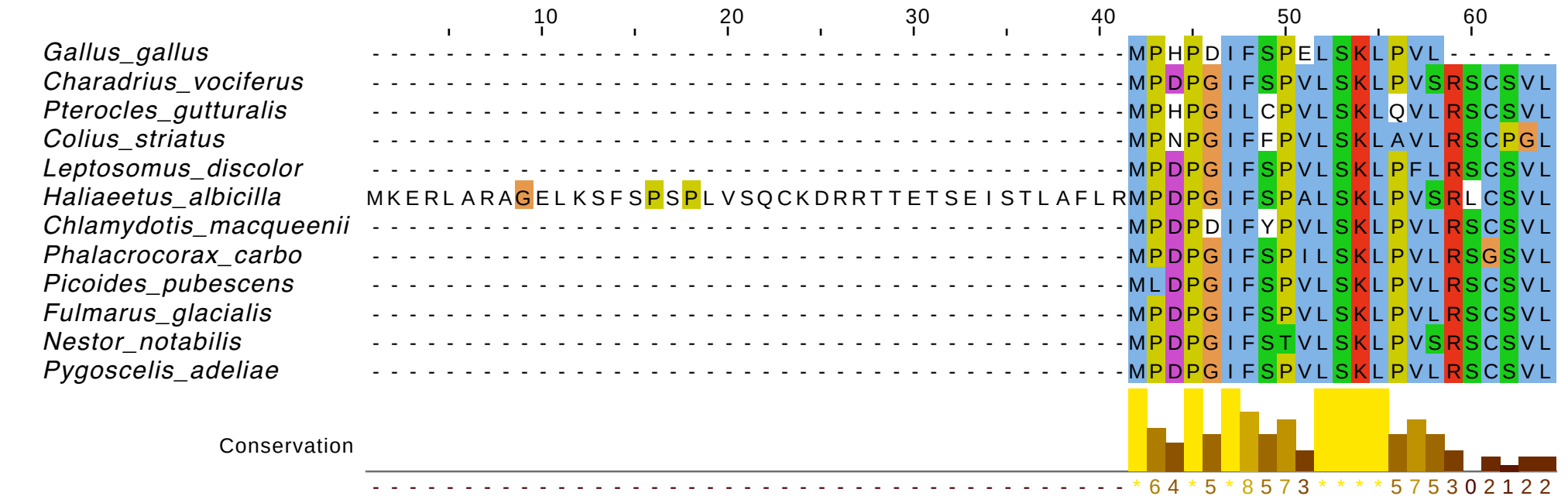
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ENSGALG00000009185

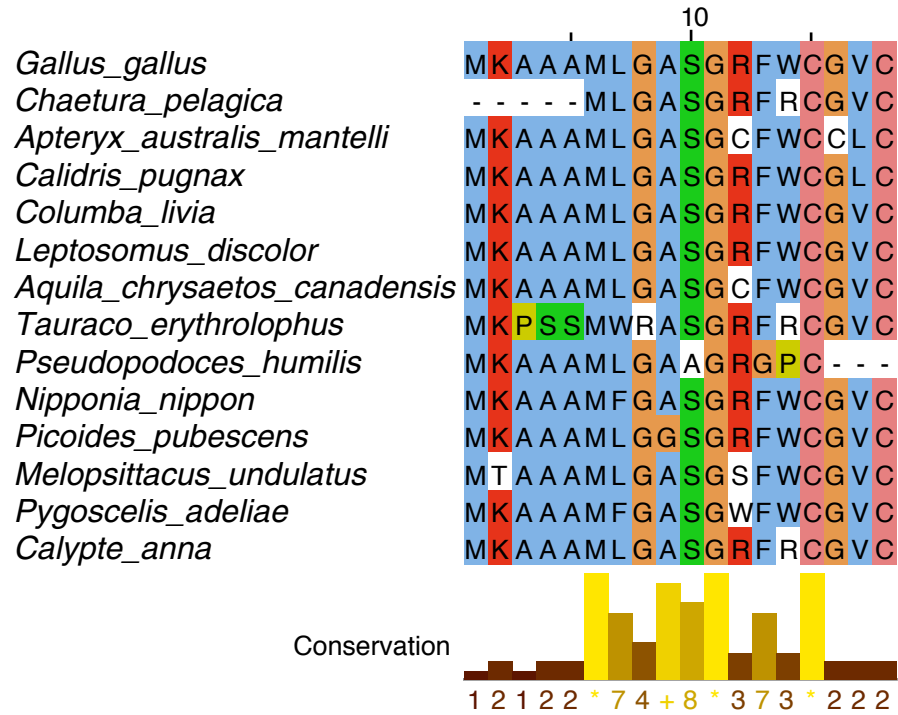


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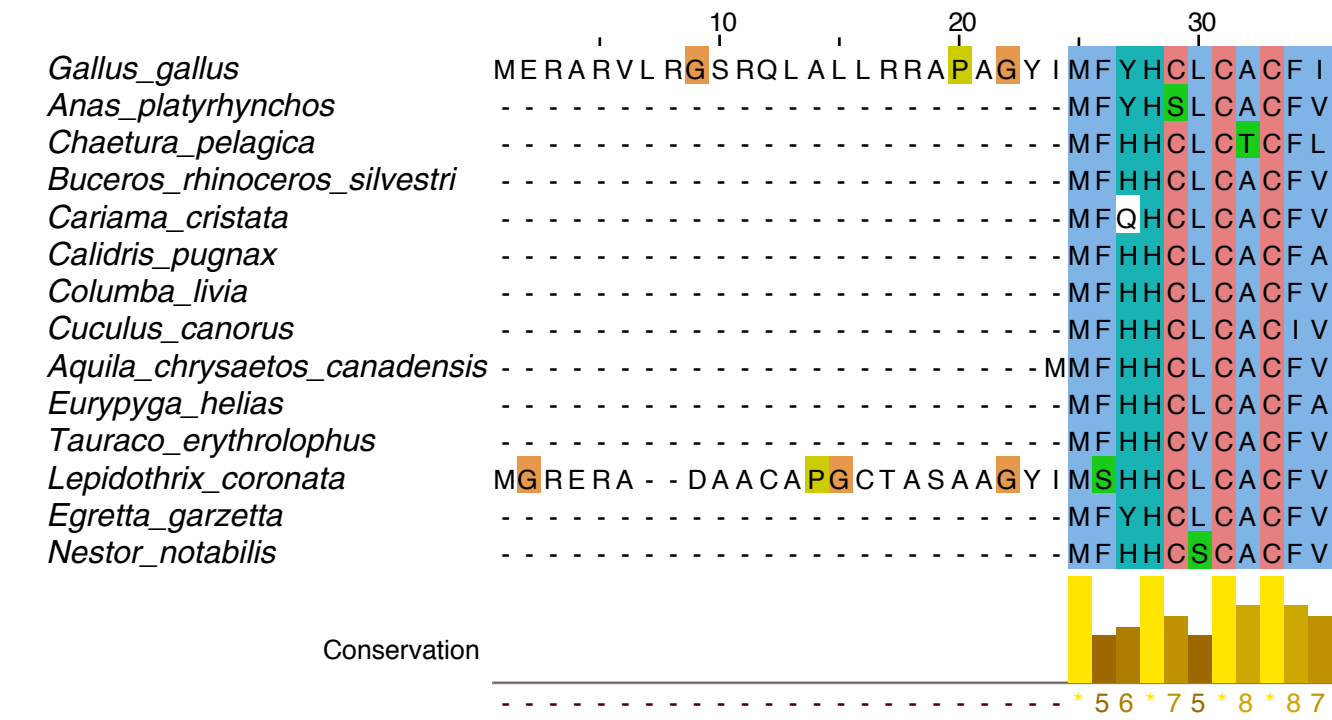
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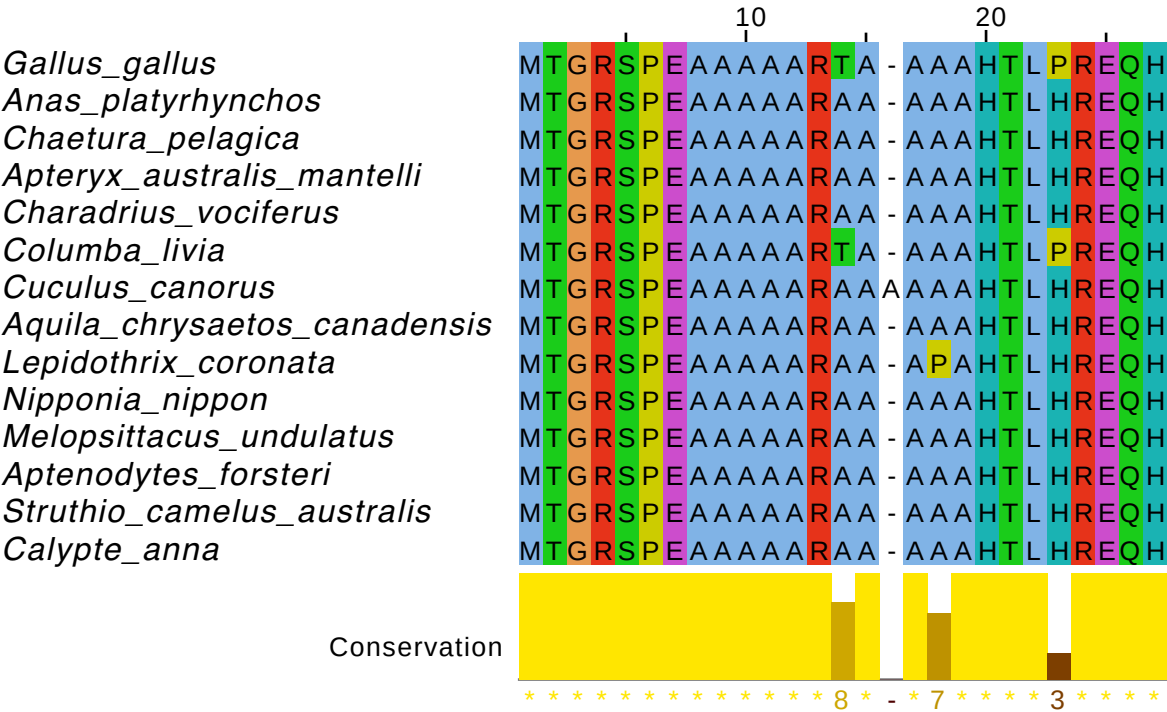
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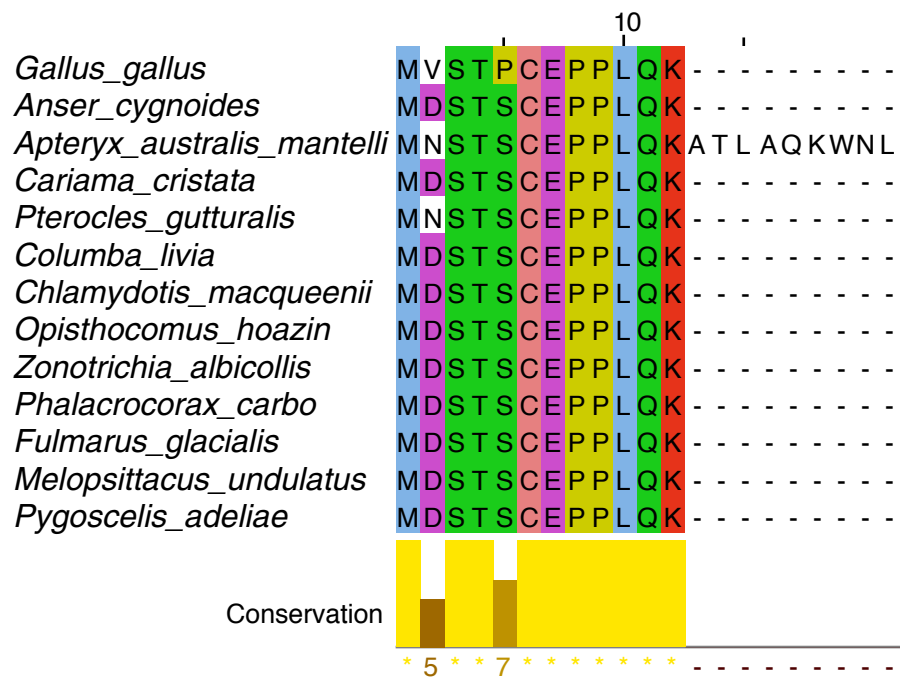
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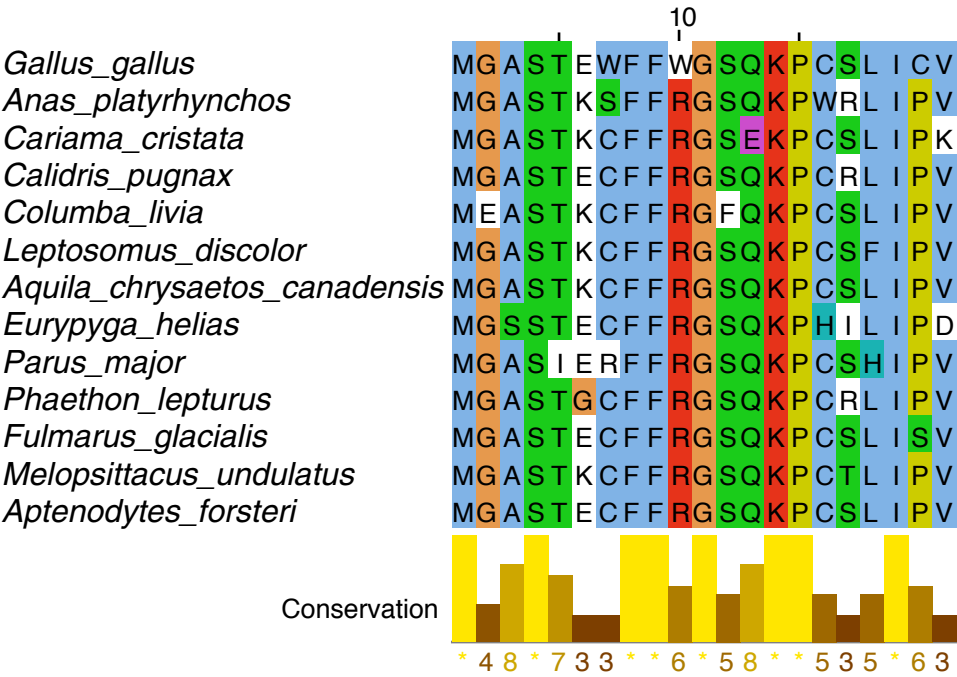
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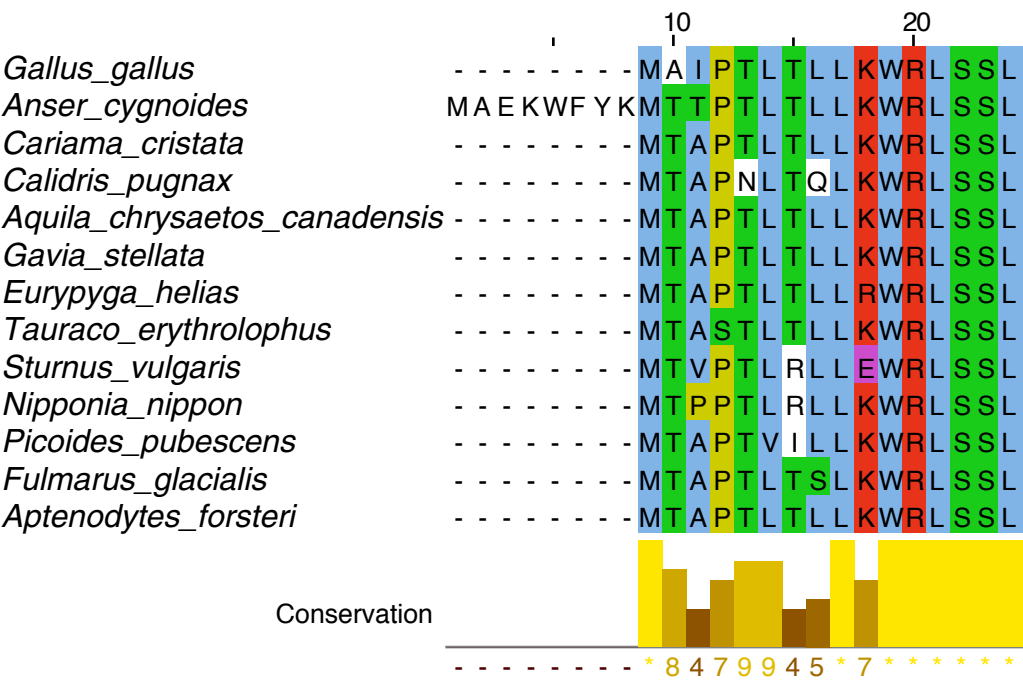
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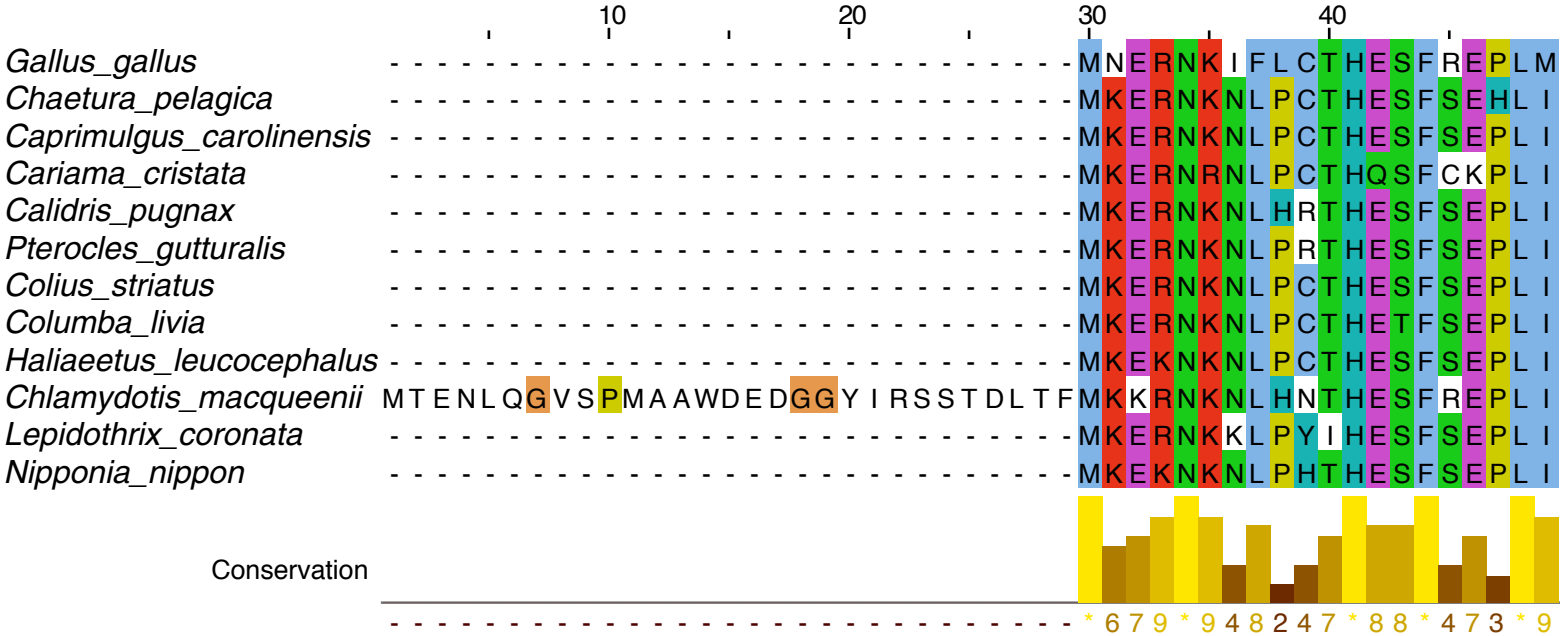


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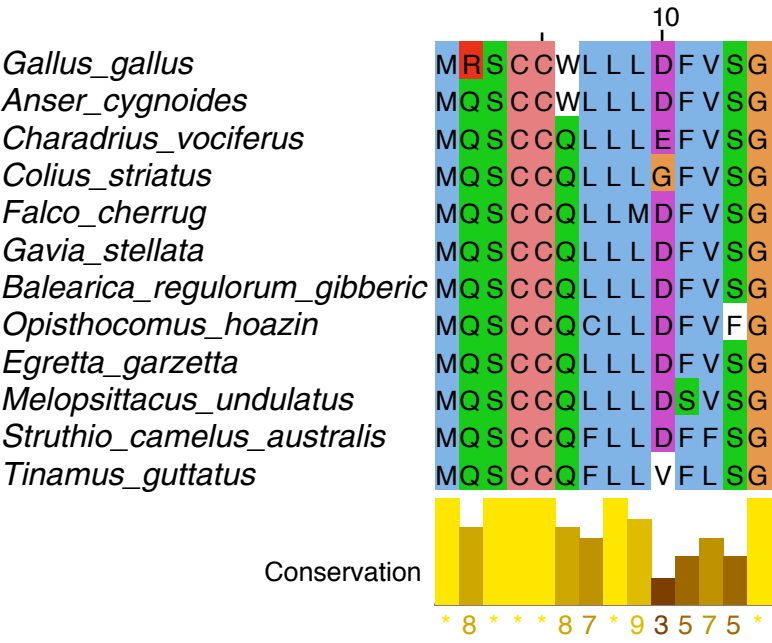


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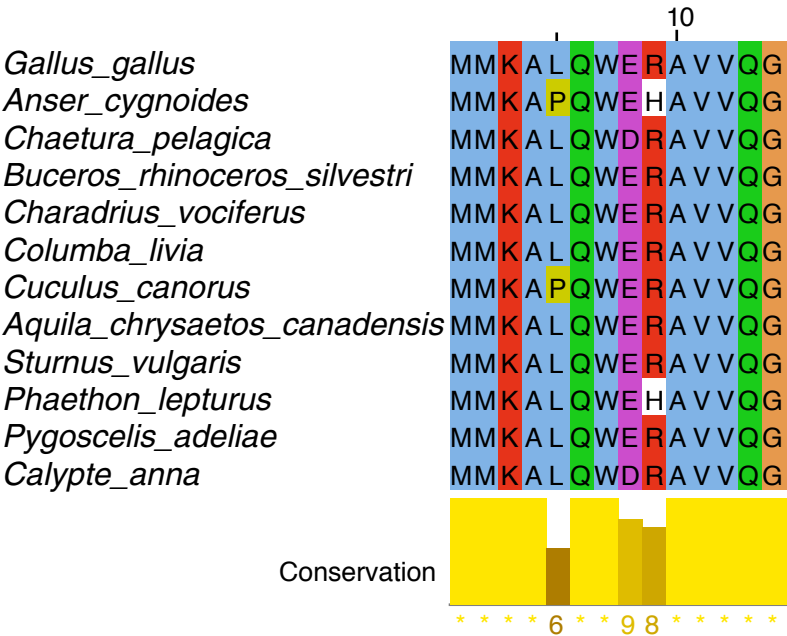
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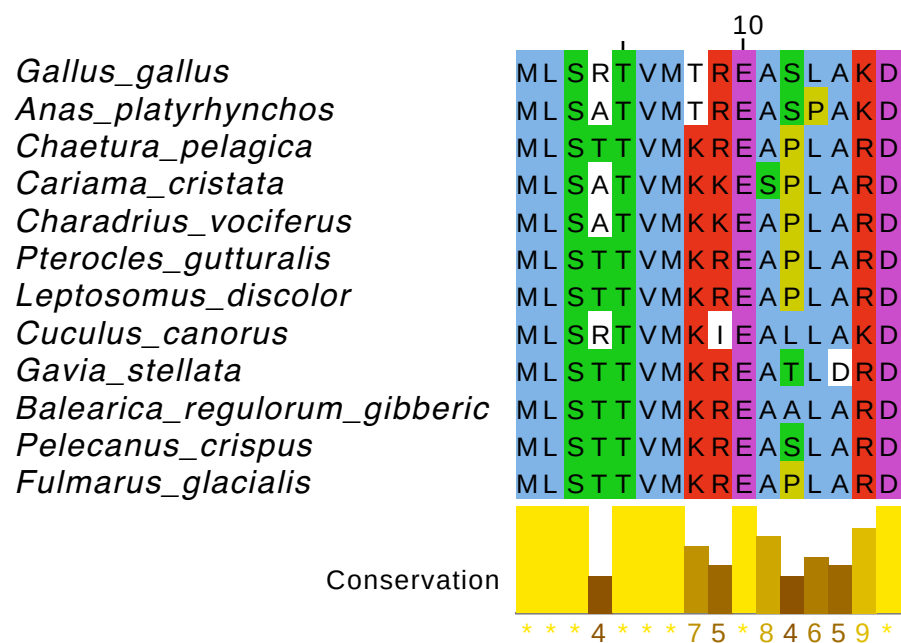
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HG0414

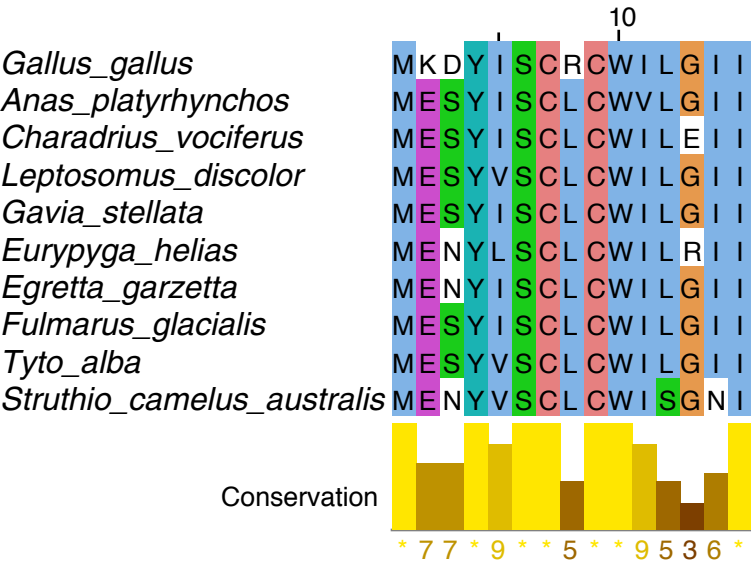
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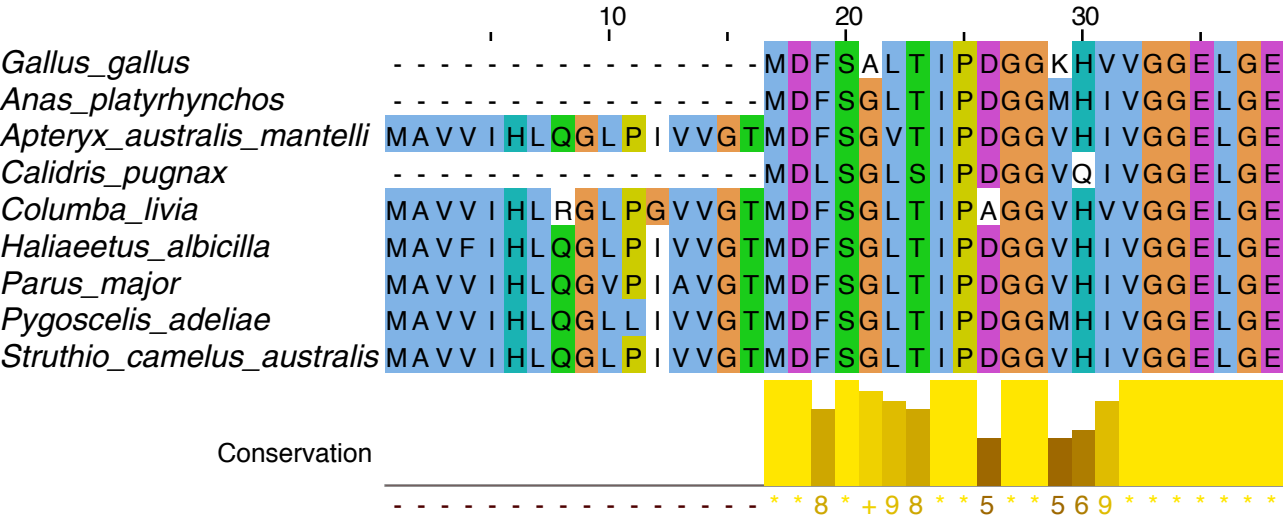
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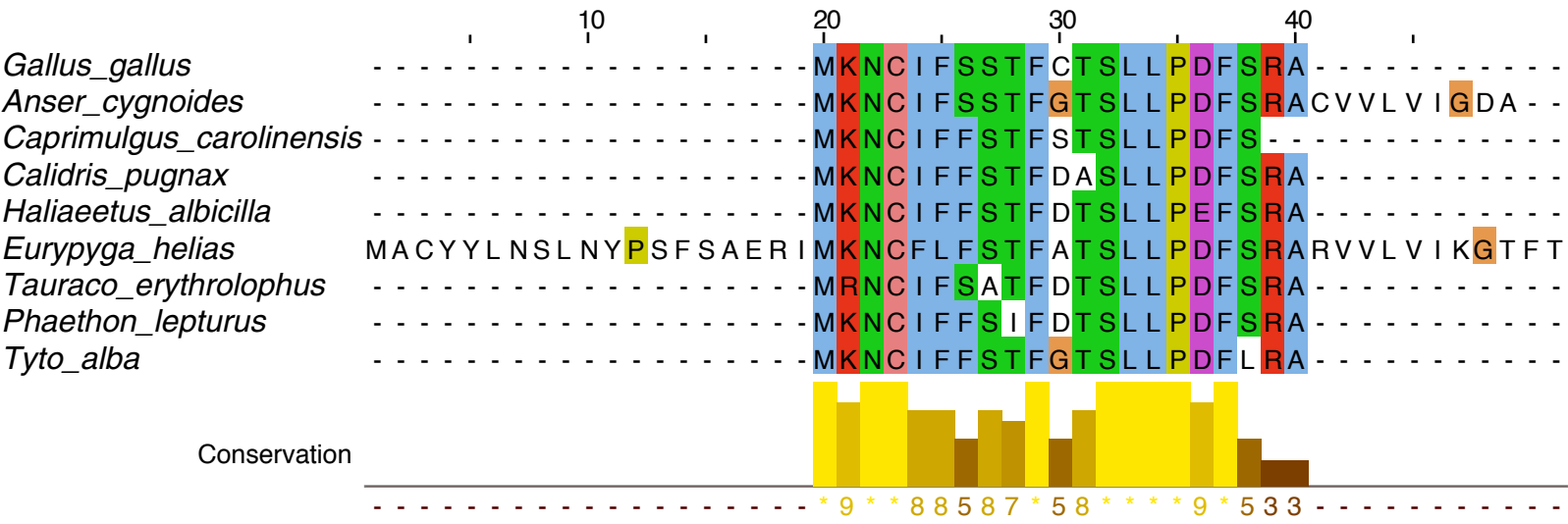


HG0417

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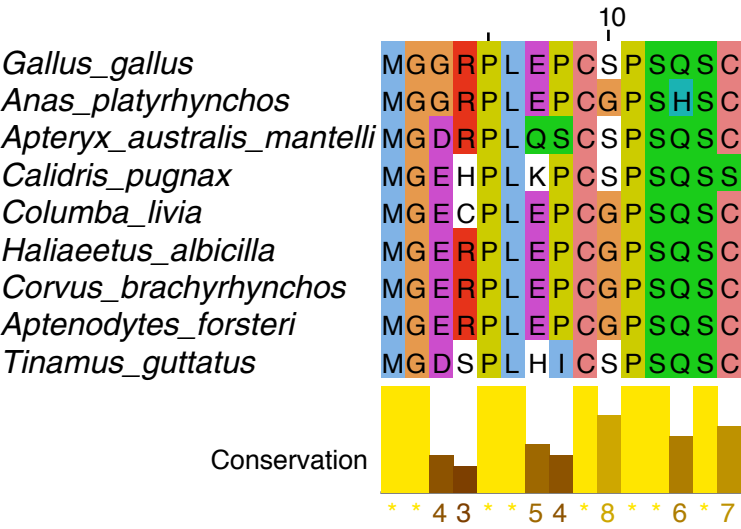


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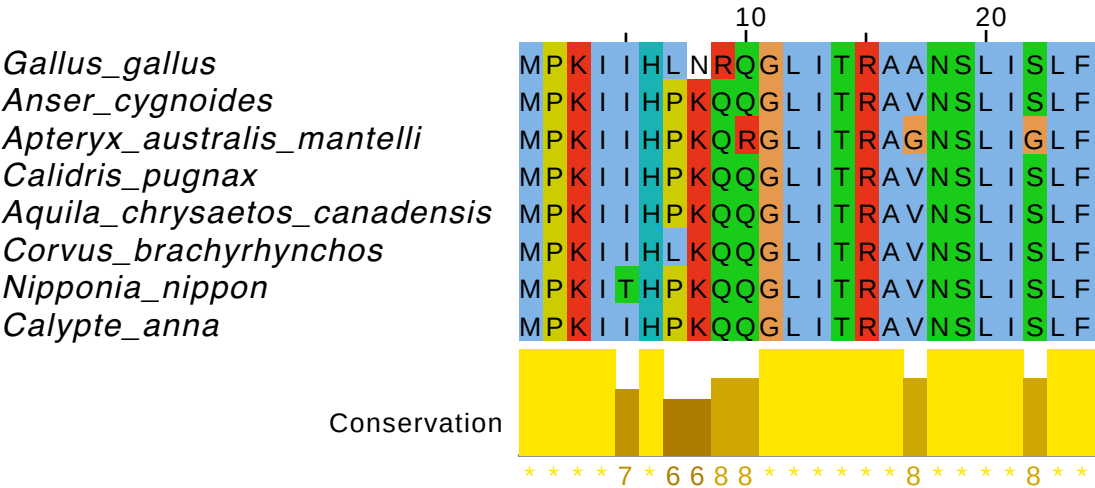
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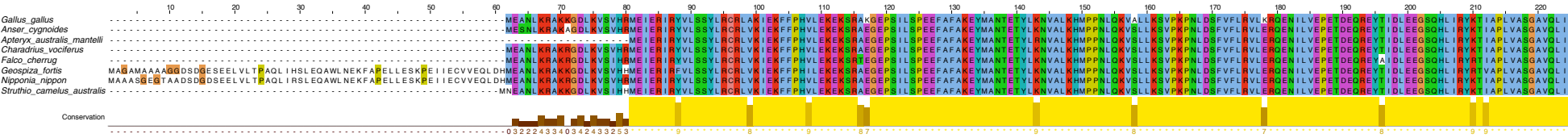
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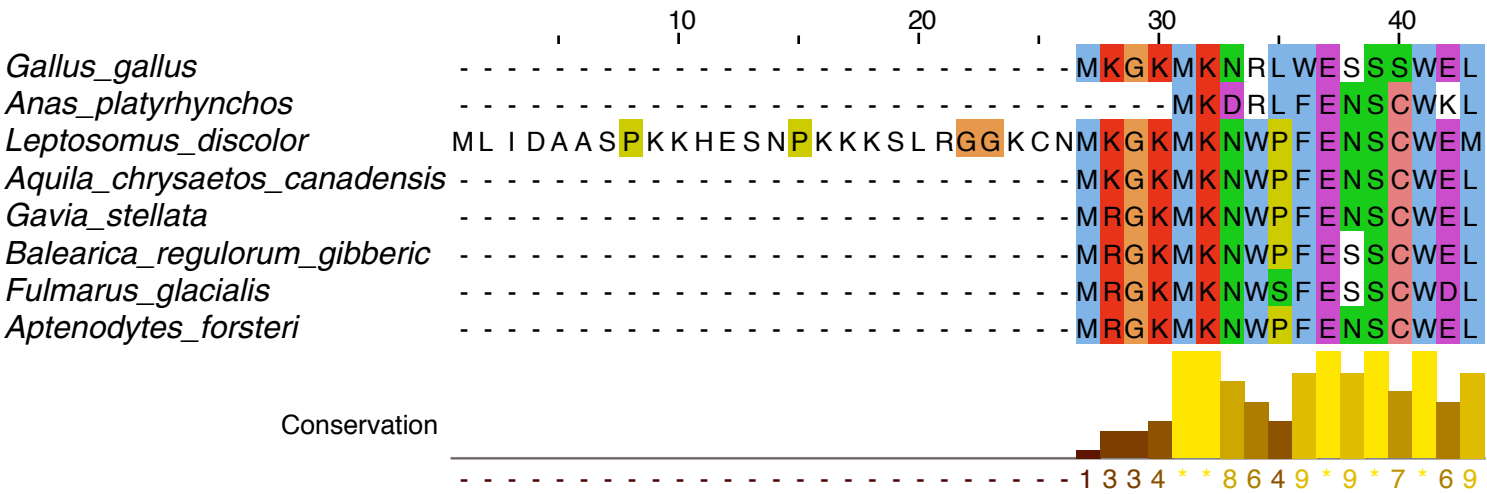


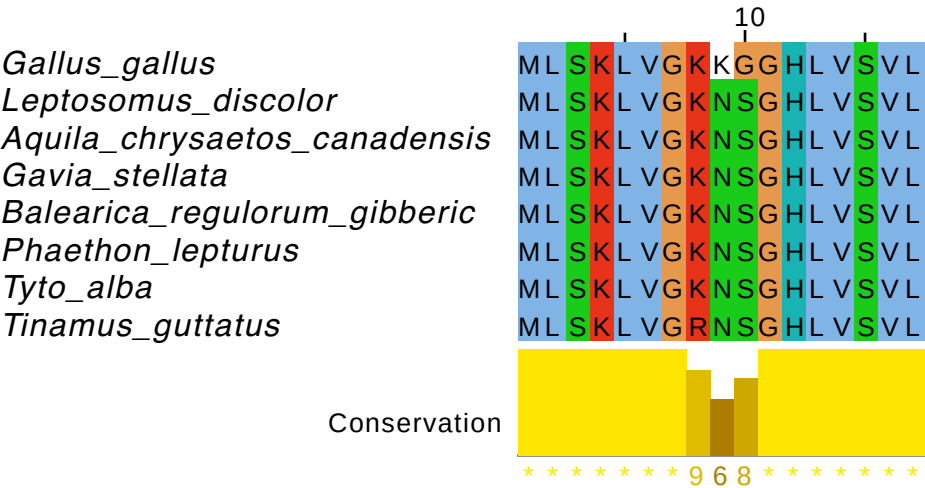
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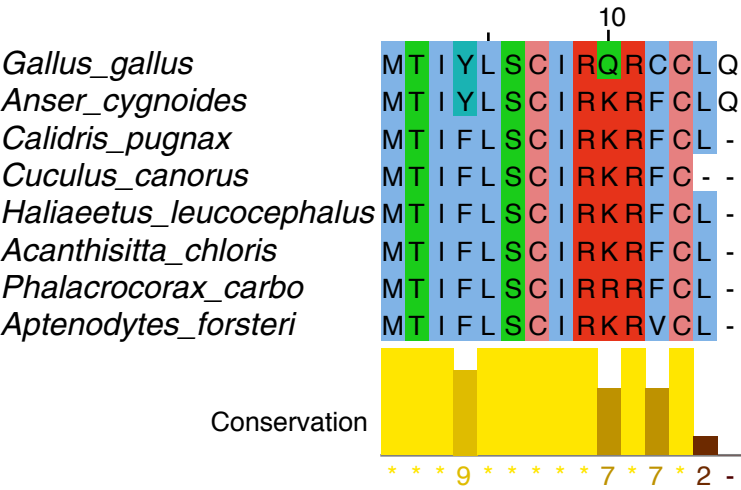
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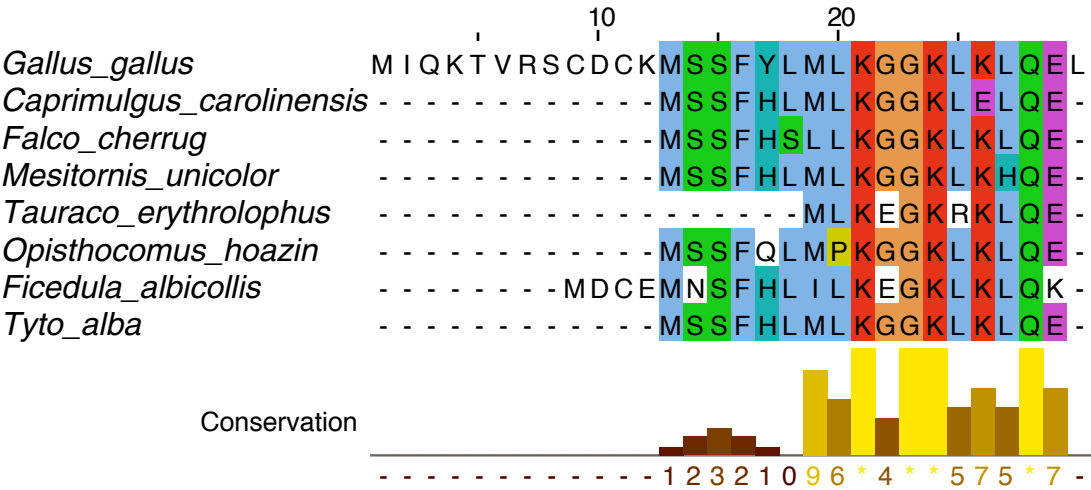
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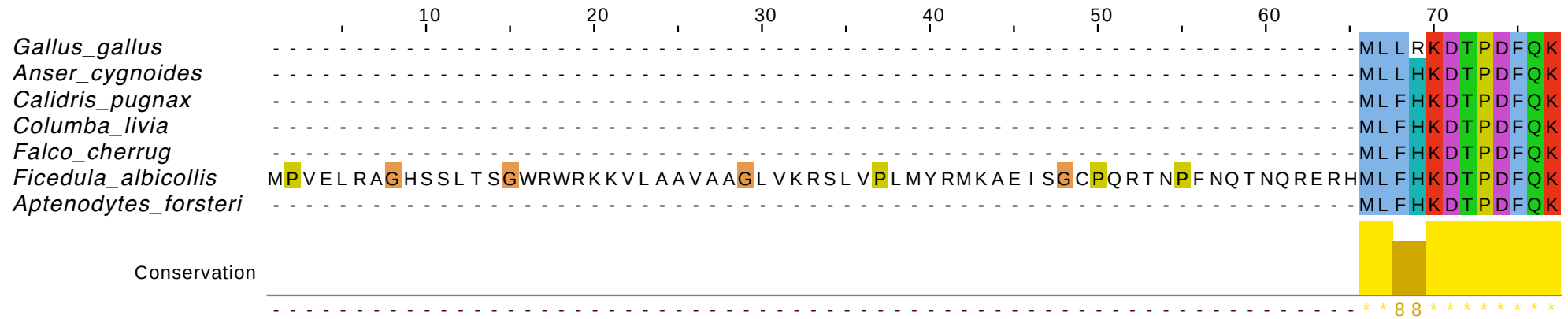
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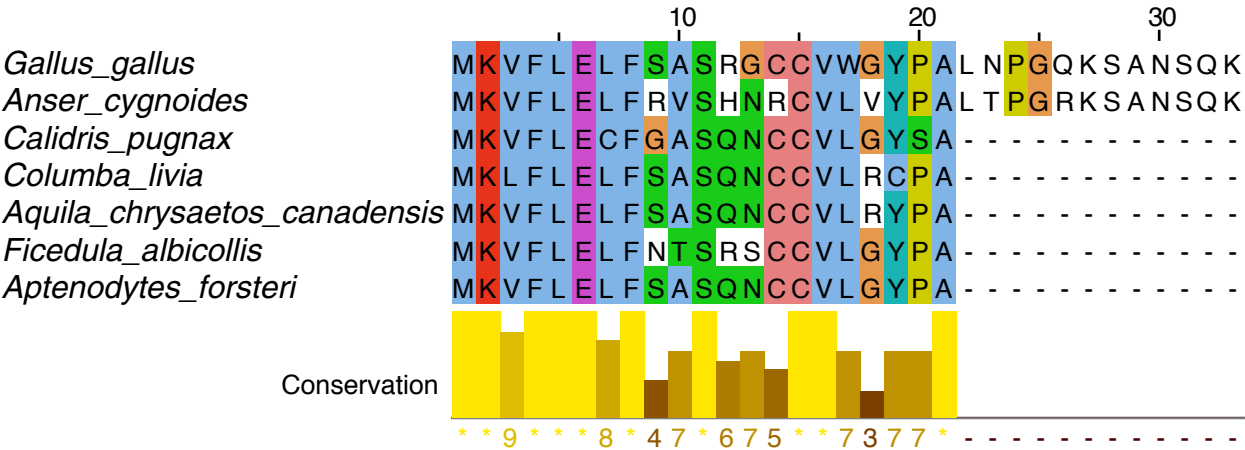
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ENSGALG00000002192 (PTPRC)



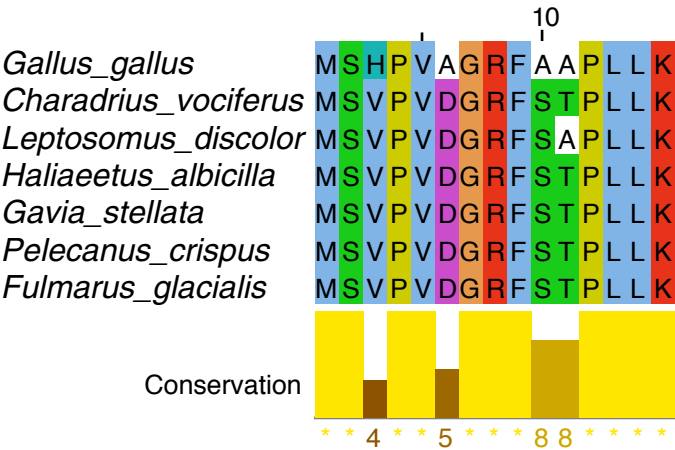
HG0427

ENSGALG00000005550 (ST6GAL1)



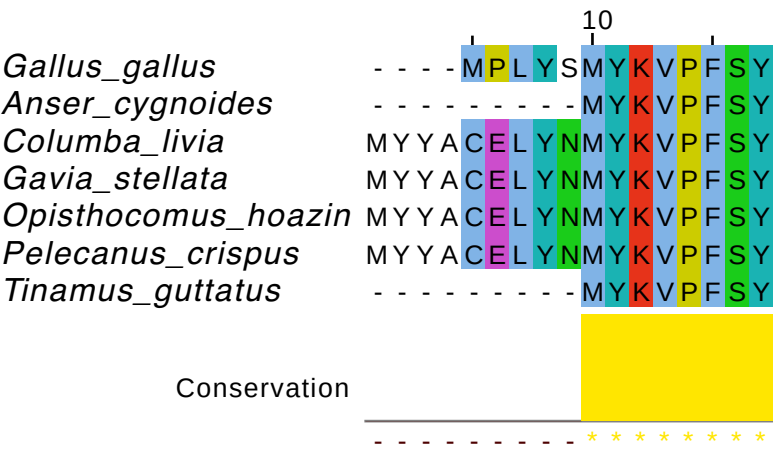
HG0428

ENSGALG00000005976 (TCEA2)

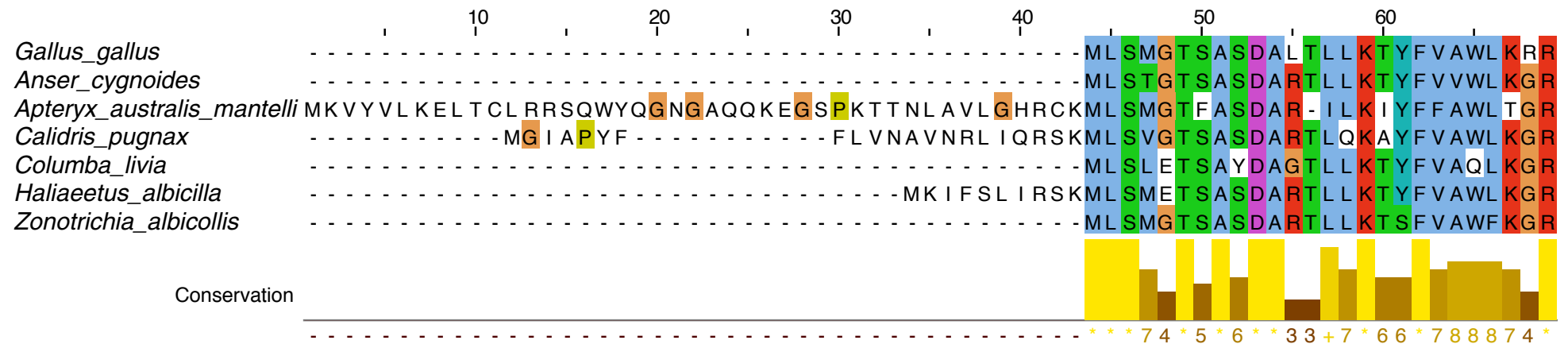


HG0429

ENSGALG00000006626 (PDE6C)

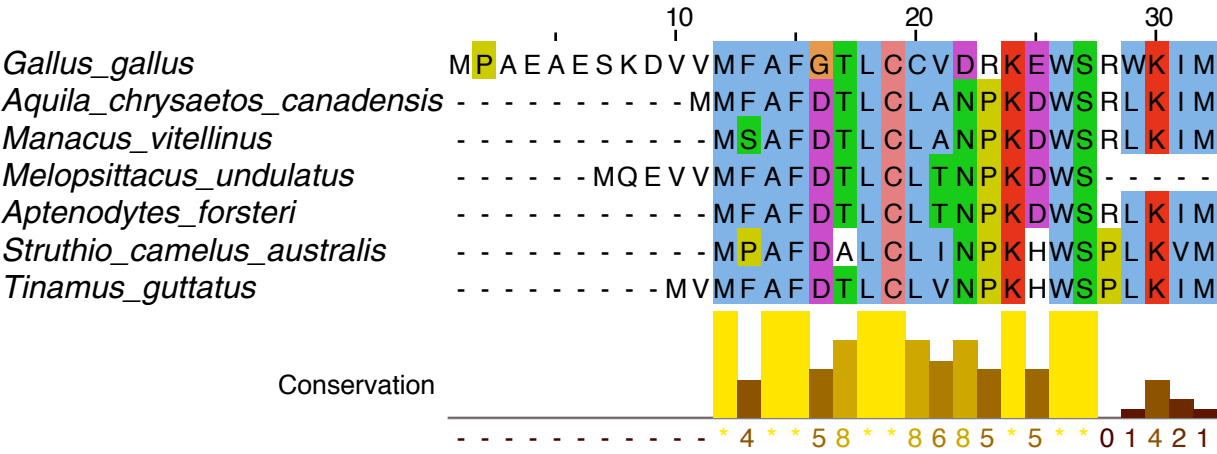


ENSGALG00000015490



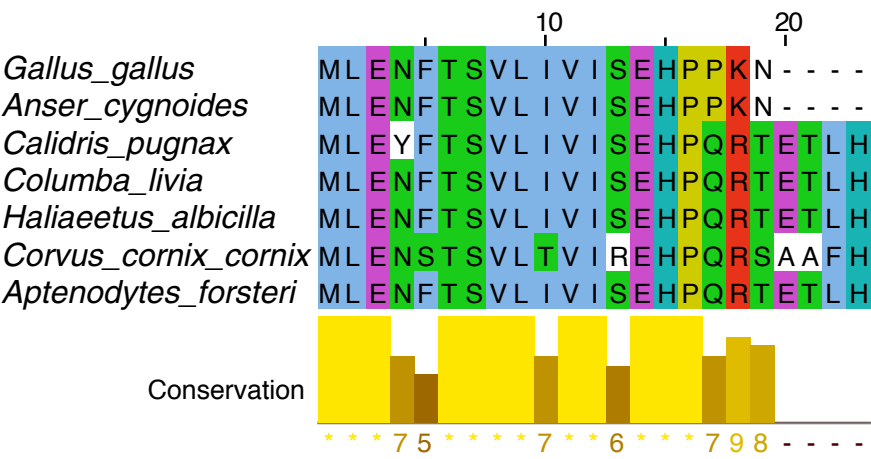
HG0431

ENSGALG00000026542 (FAM217B)



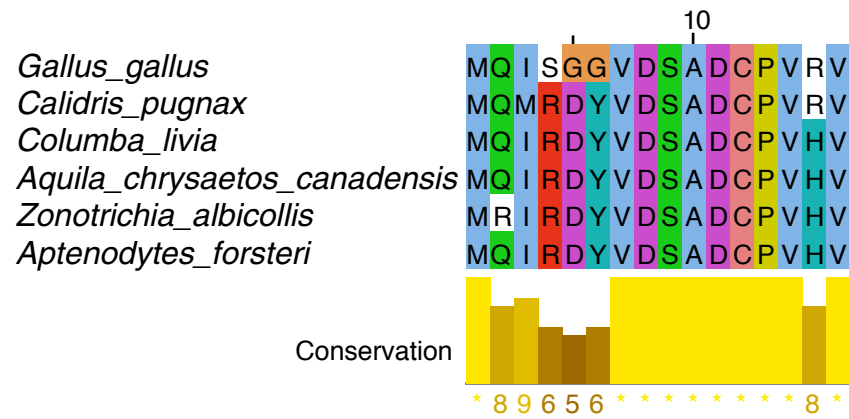
HG0432

ENSGALG00000040546



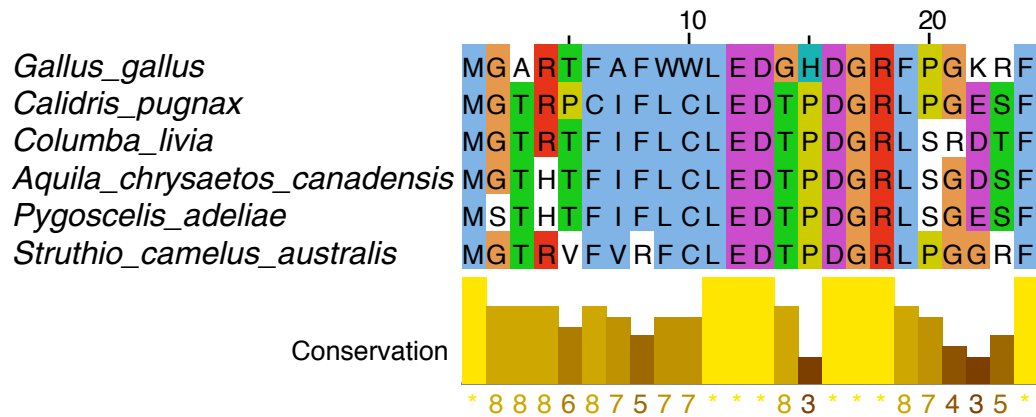
HG0433

ENSGALG00000002952 (NRG4)



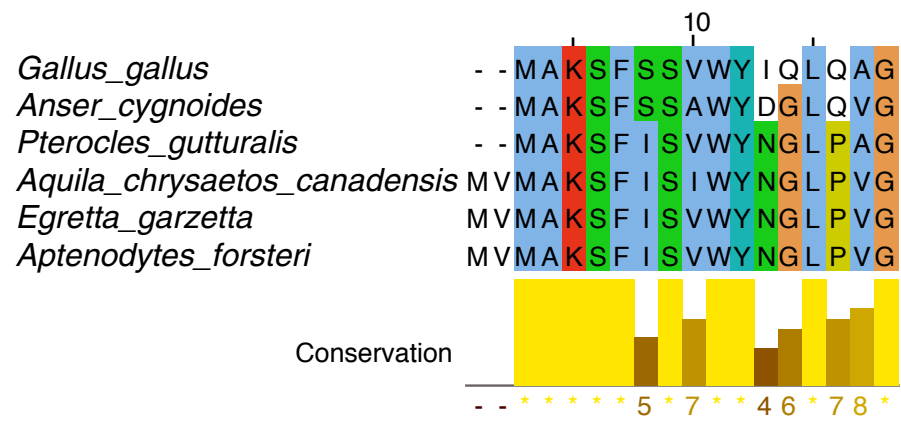
HG0434

ENSGALG00000008357 (TPCN1)

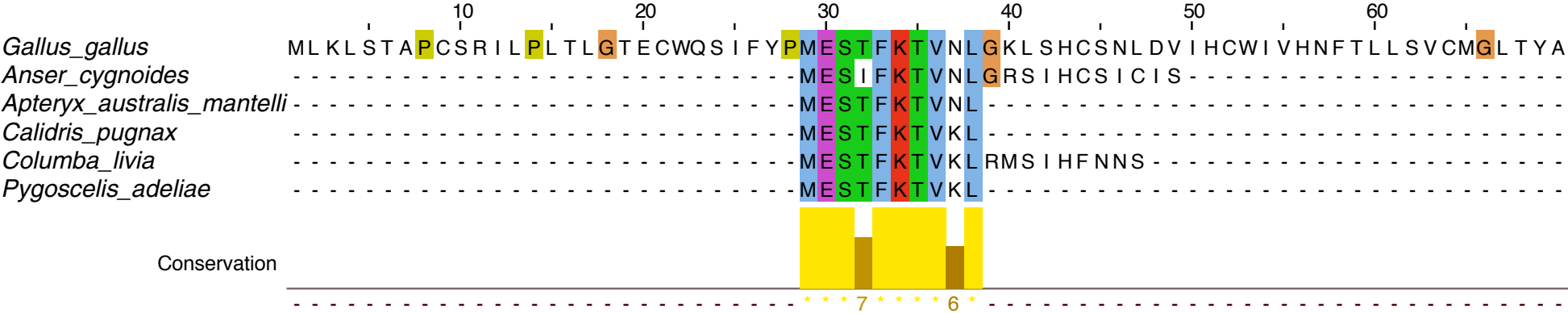


HG0435

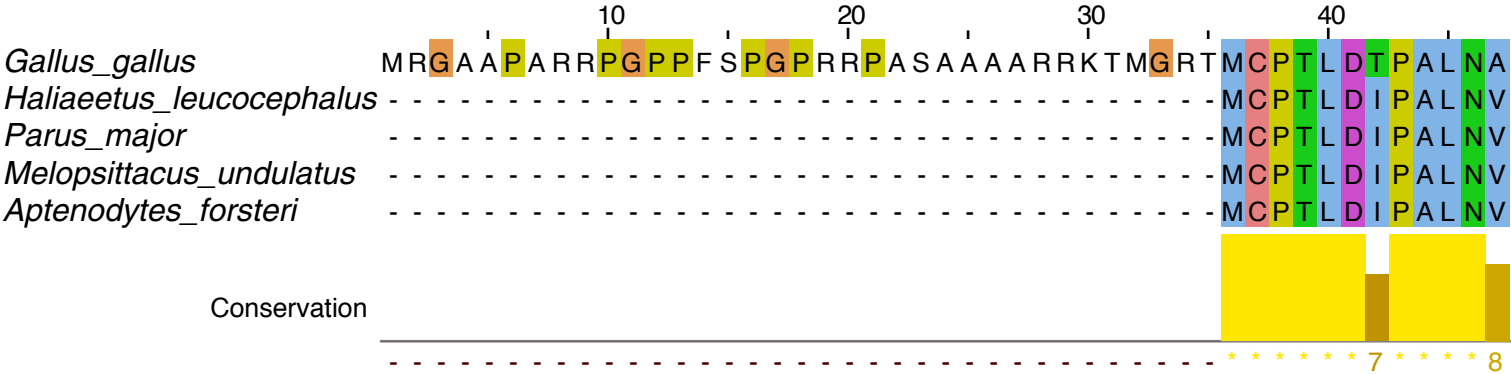
ENSGALG00000010778 (CHRM3)



HG0436
ENSGALG00000026736 (OGN)

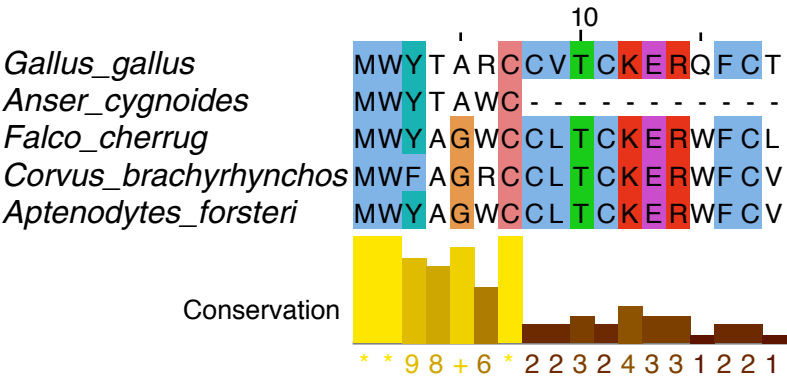


HG0437
ENSGALG00000001728 (NACC2)



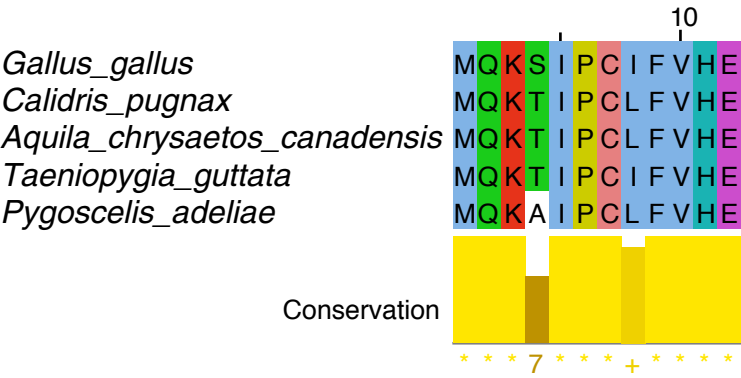
HG0438

ENSGALG00000008545 (SENP5)



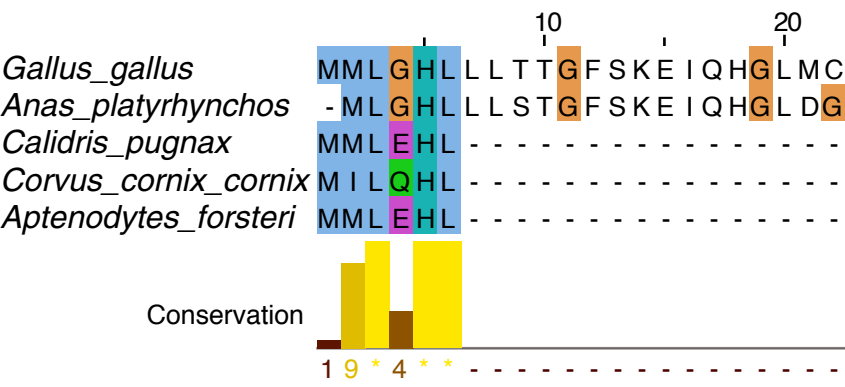
HG0439

ENSGALG00000009172 (OSBPL6)



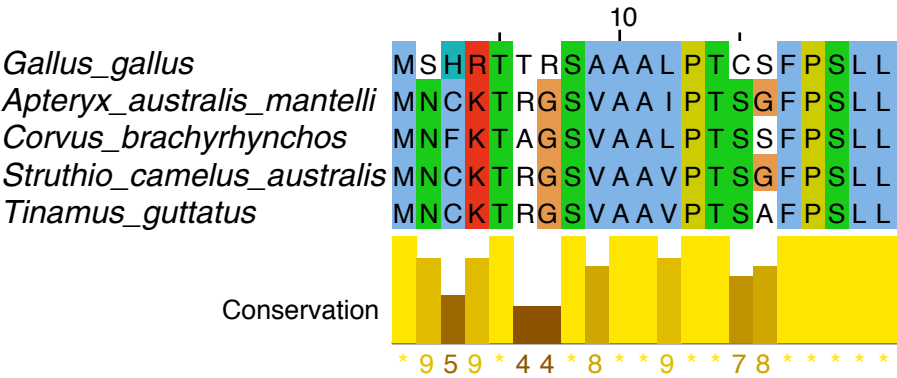
HG0440

ENSGALG00000010090



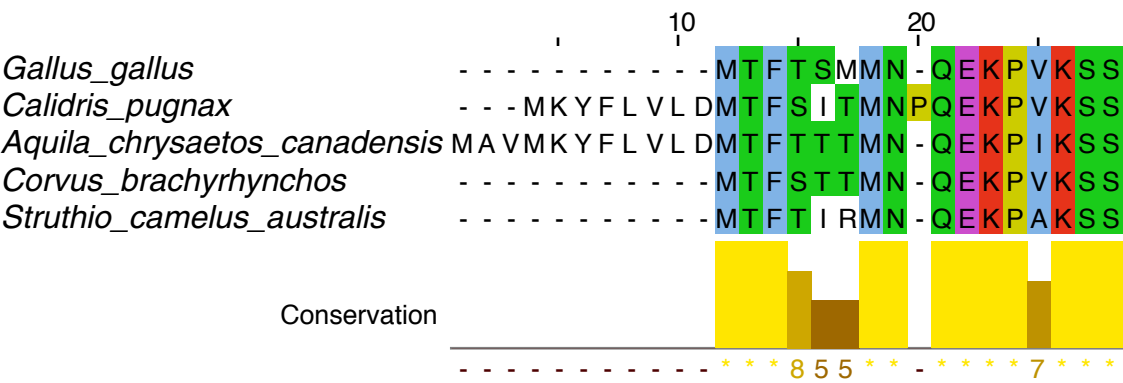
HG0441

ENSGALG00000015069 (B4GALT4)

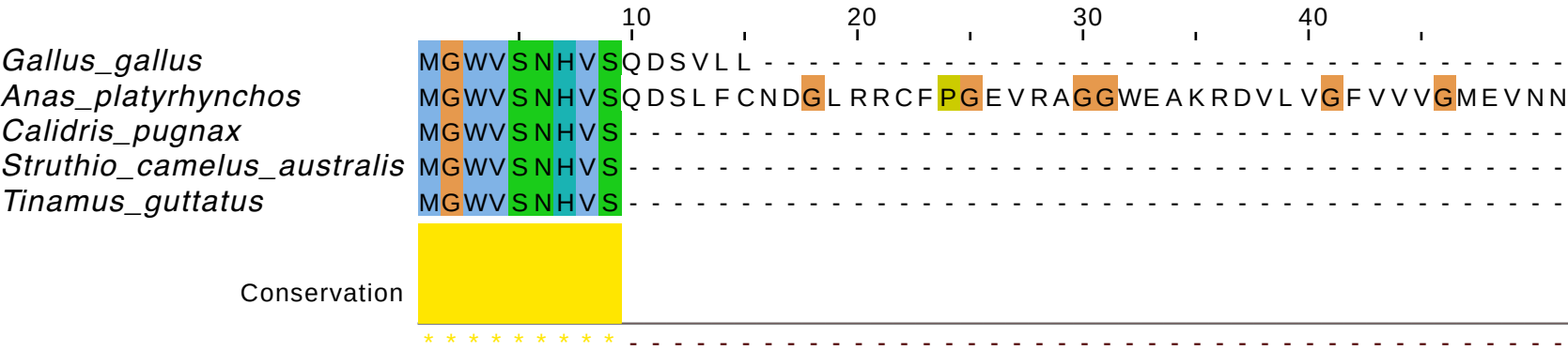


HG0442

ENSGALG00000030250

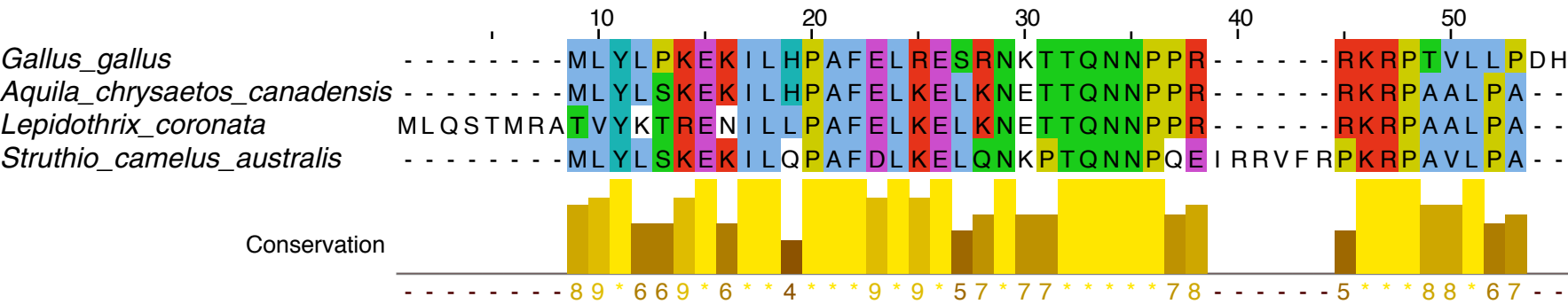


HG0443
ENSGALG00000039454



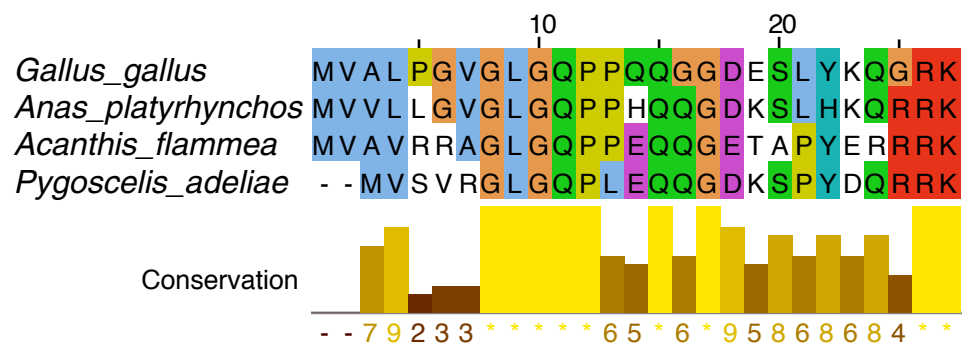
HG0444

ENSGALG00000000558 (SLC1A6)

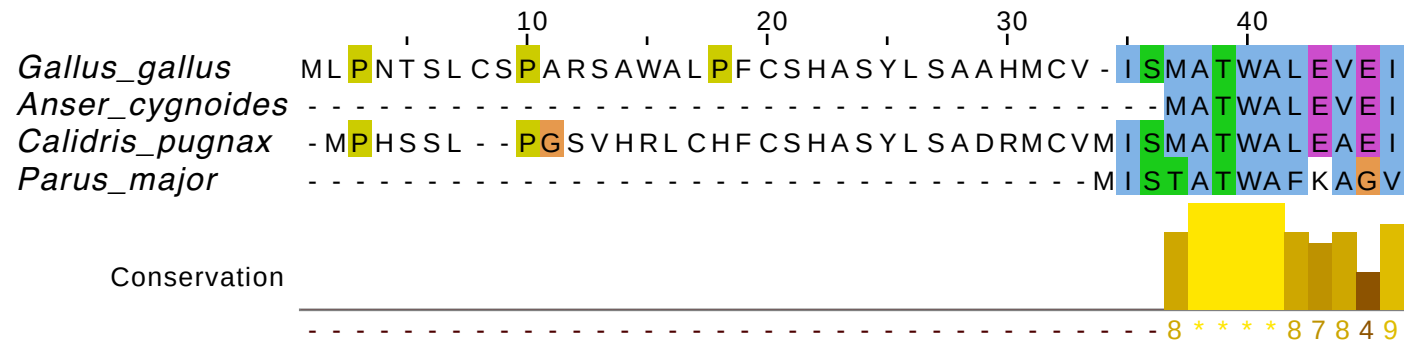


HG0445

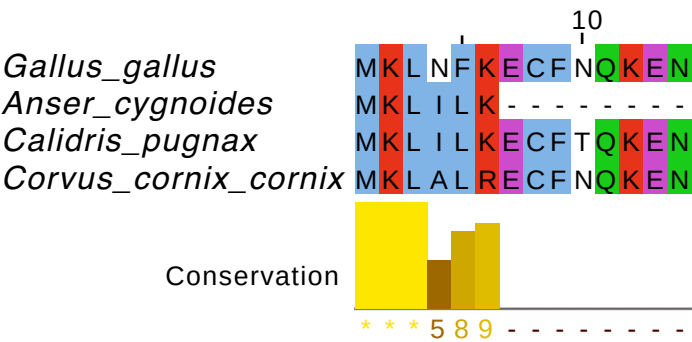
ENSGALG00000004017



ENSGALG00000006807 (PLSCR5)

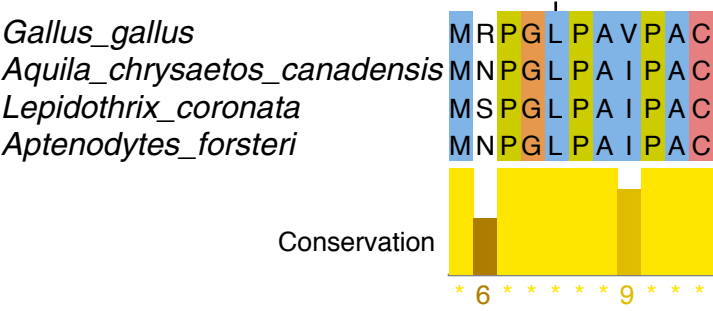


HG0447
ENSGALG00000008784



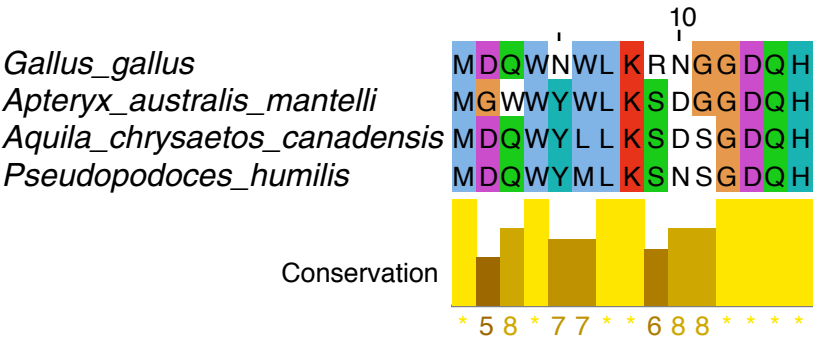
HG0448

ENSGALG00000011762 (UBA6)



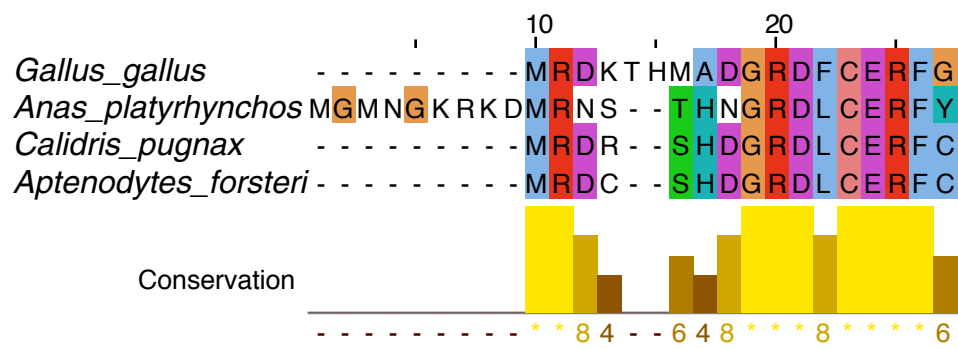
HG0449

ENSGALG00000014106 (PPFIBP1)



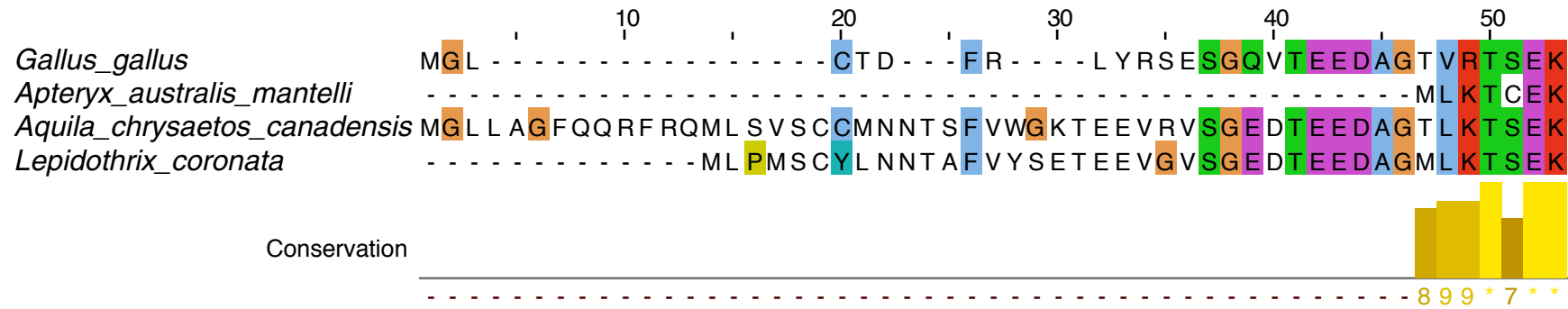
HG0450

ENSGALG00000015528 (JAKMIP1)



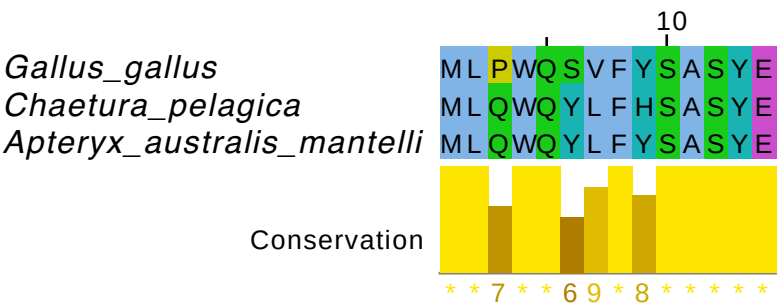
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ENSGALG00000019489 (CHST9)



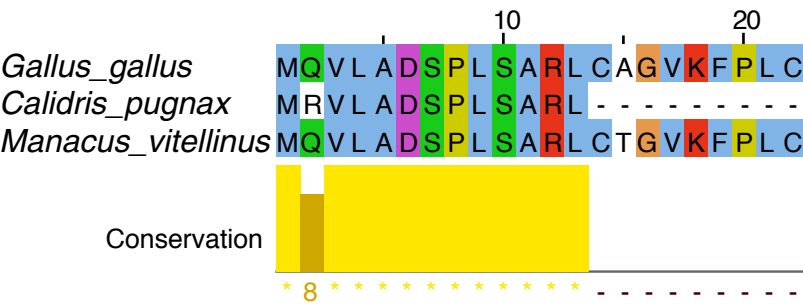
HG0452

ENSGALG00000004227 (FAM20B)



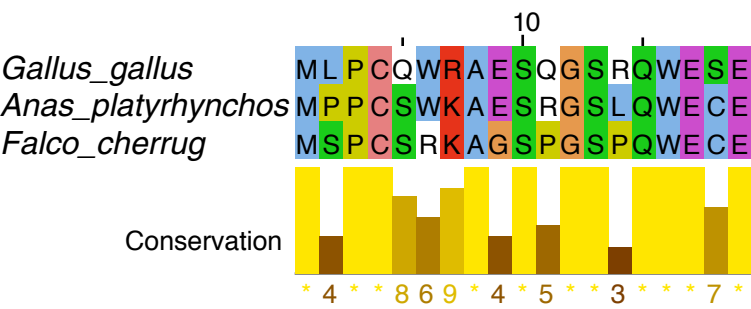
HG0453

ENSGALG00000005995 (SLC13A5)



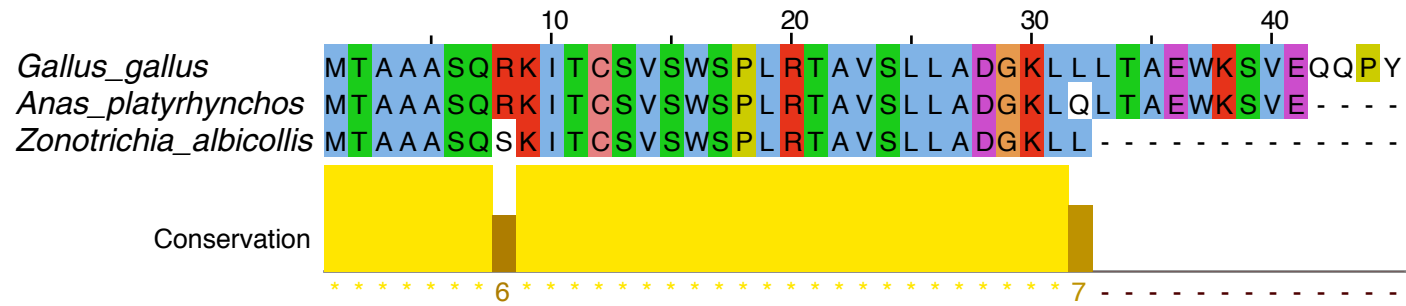
HG0454

ENSGALG00000007186 (TMEM268)



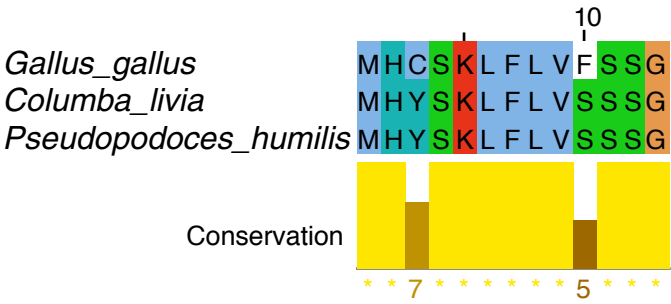
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ENSGALG00000010718 (THSD7A)



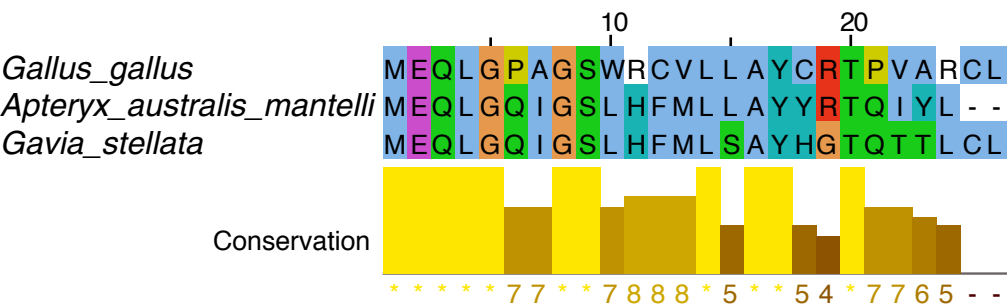
HG0456

ENSGALG00000033256

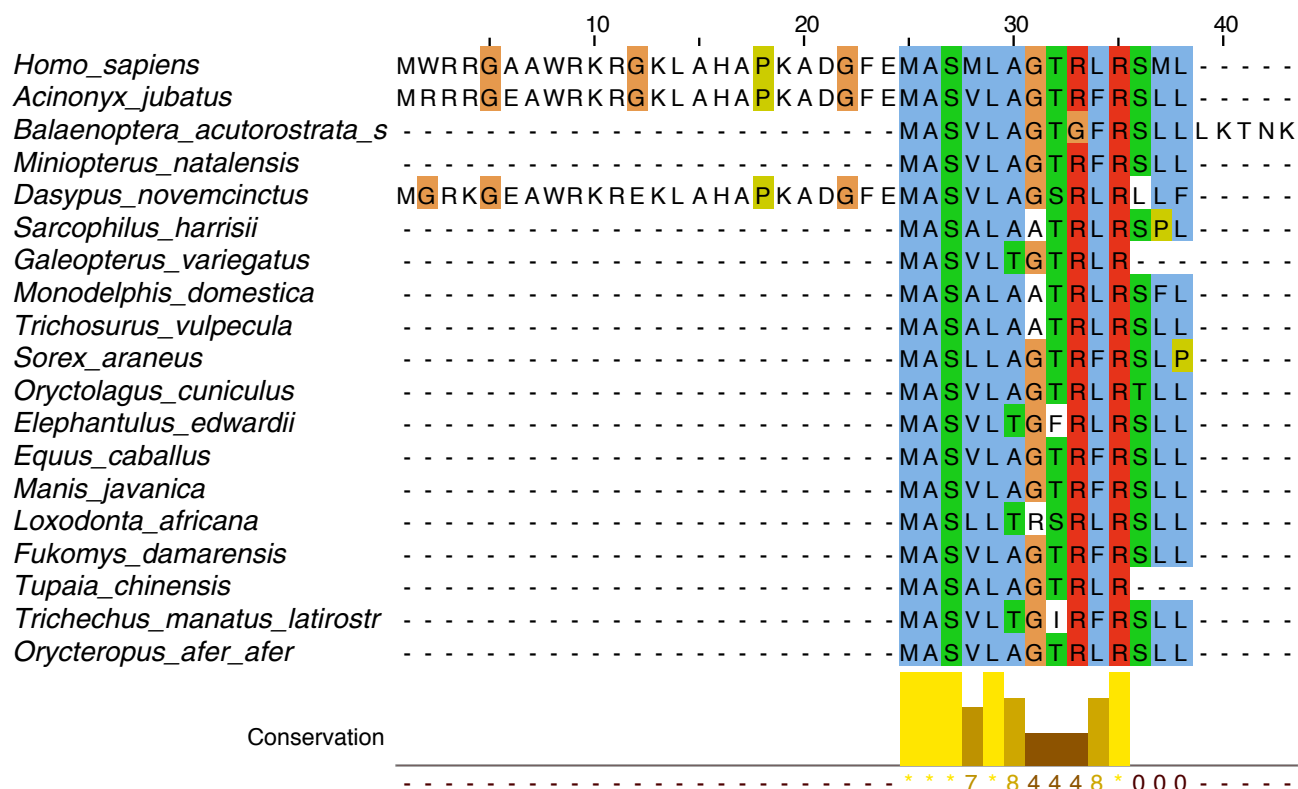


HG0457

ENSGALG00000039538 (CLDND1)

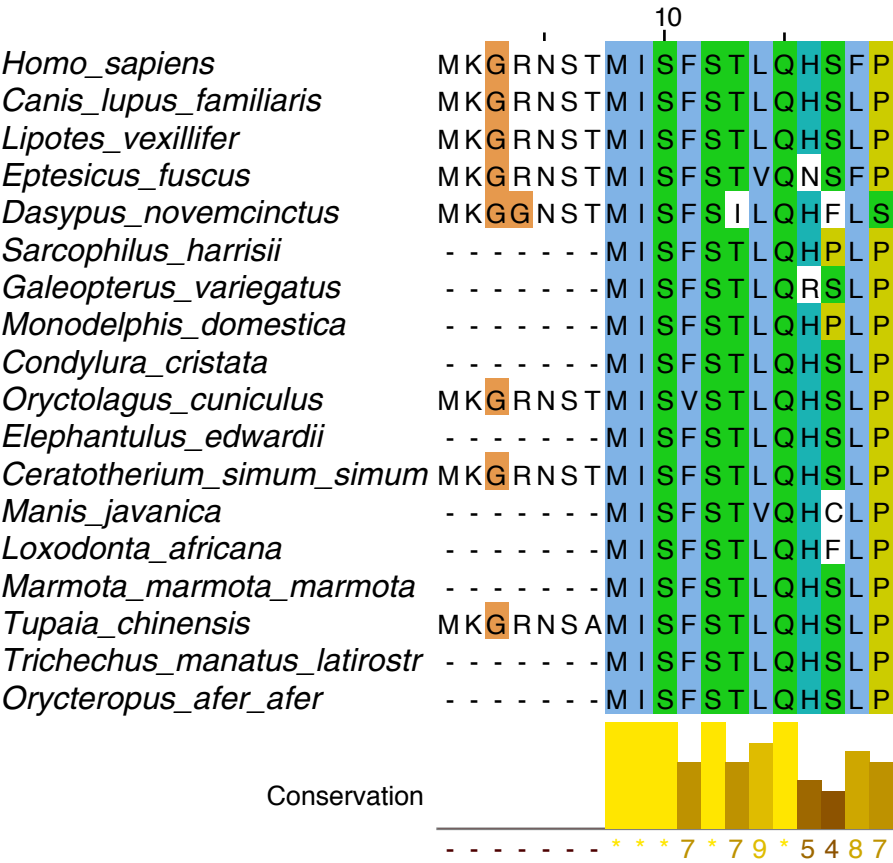


ENSG00000060339 (CCAR1)



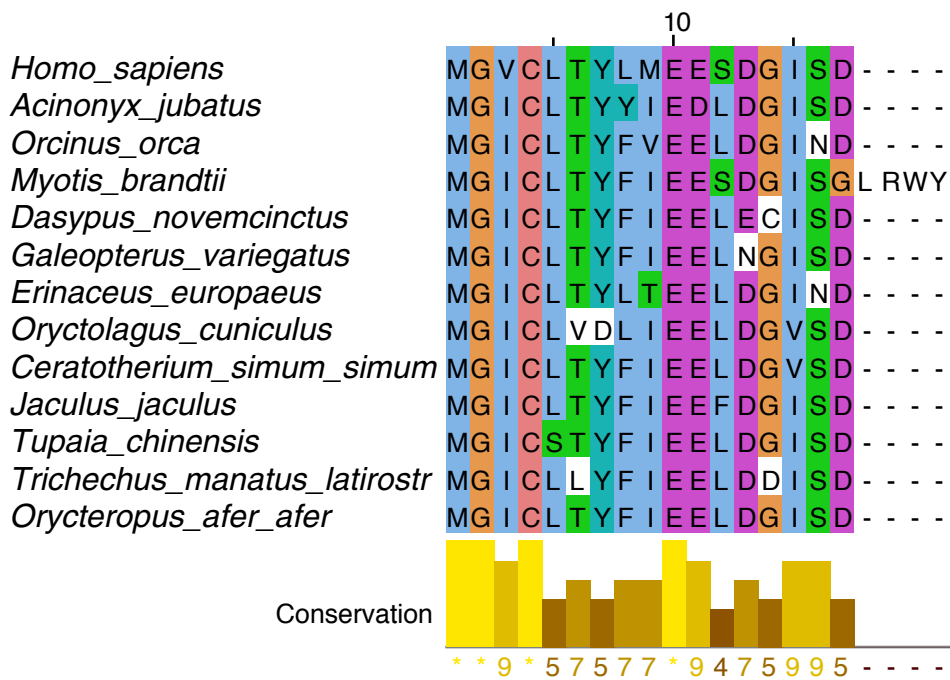
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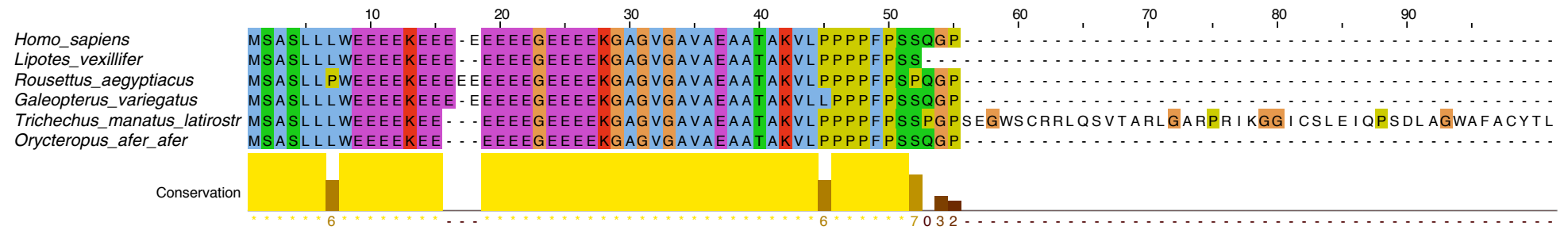


HG0459.2

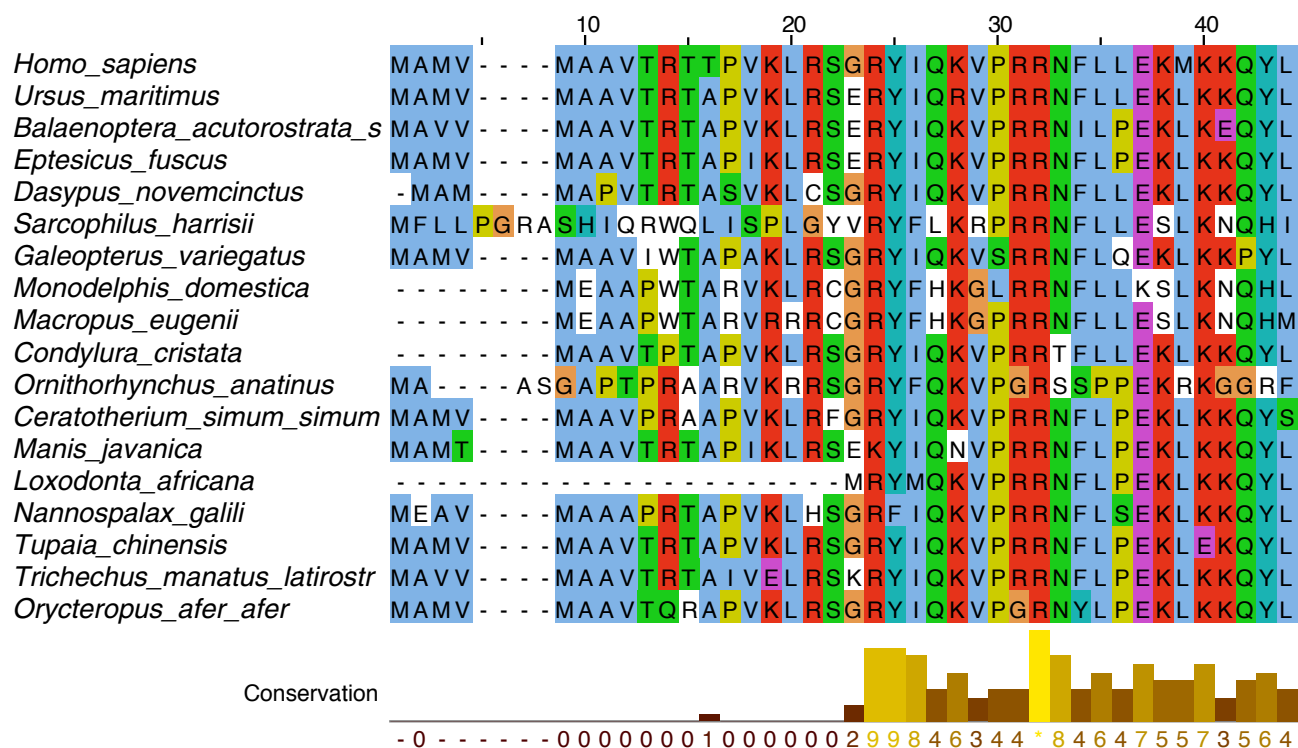
ENSG00000163848 (ZNF148)



ENSG00000163848 (ZNF148)

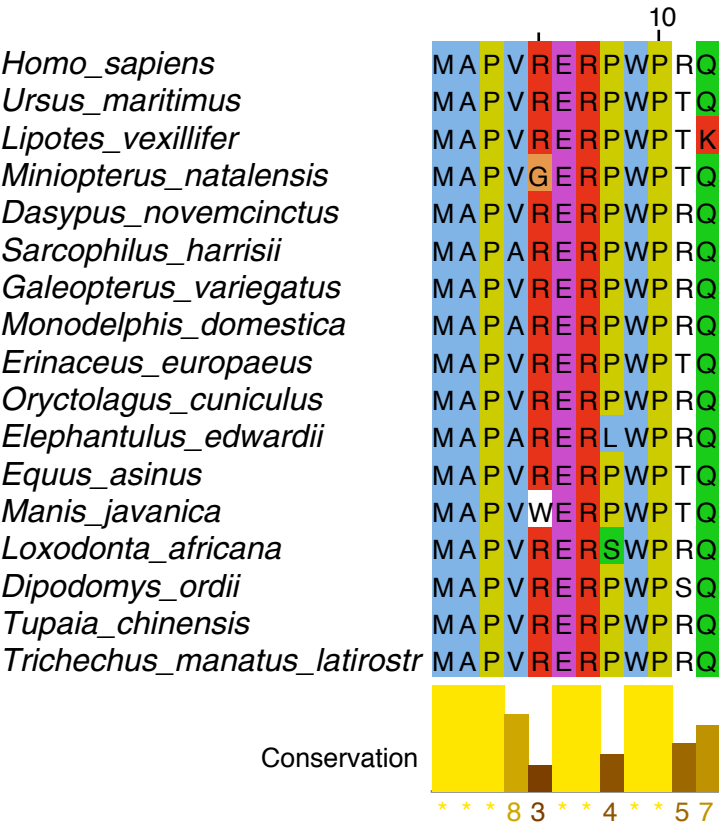


ENSG00000180008 (SOCS4)



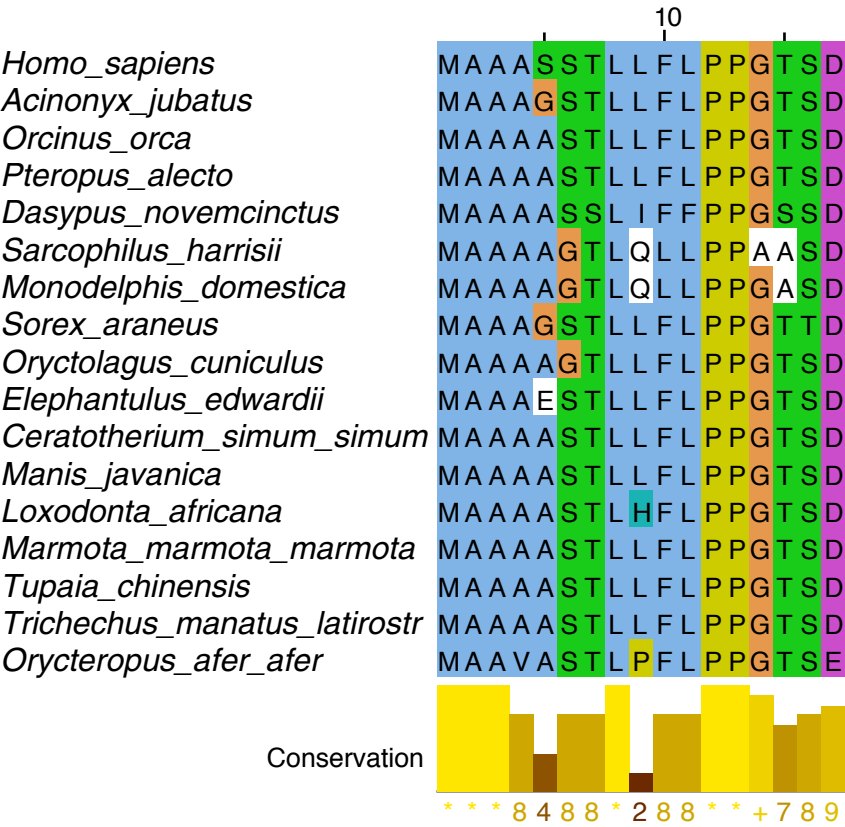
HG0461

ENSG00000064419 (TNPO3)



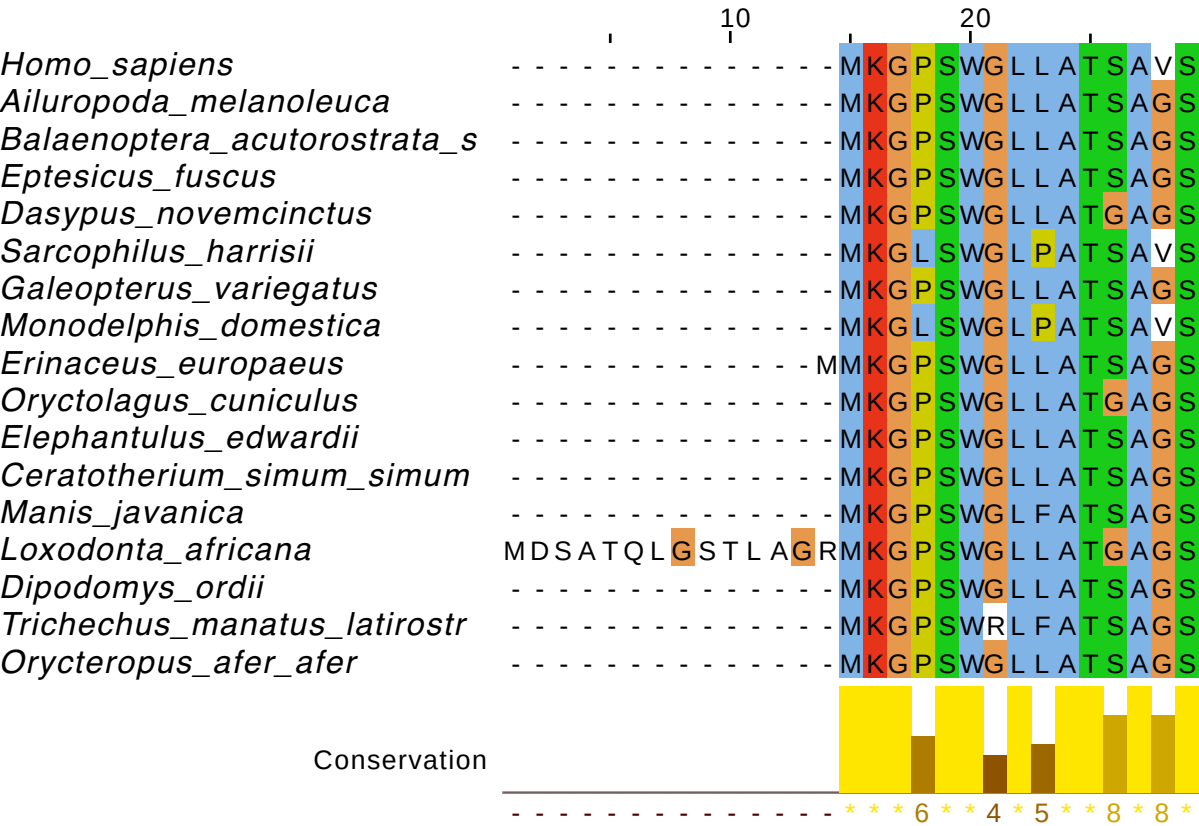
HG0462

ENSG00000125686 (MED1)



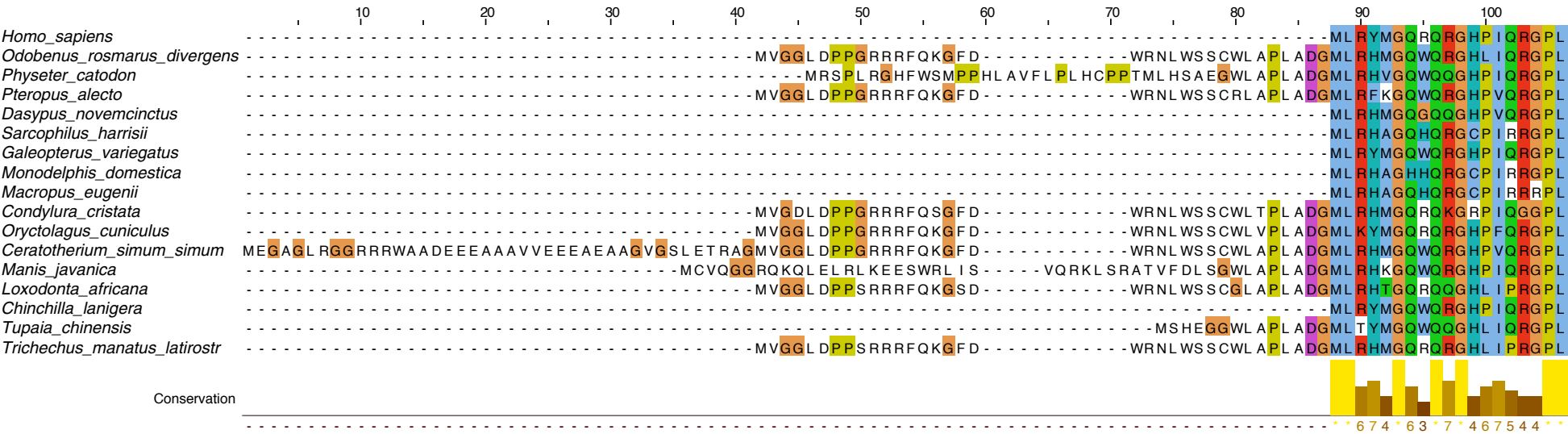
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ENSG00000129473 (BCL2L2)



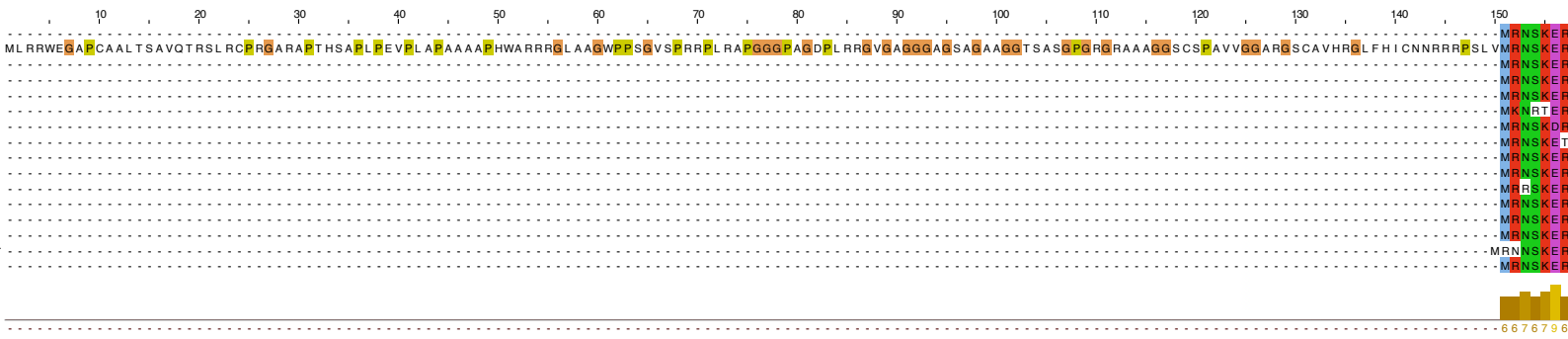
HG0464

ENSG00000188215 (DCUN1D3)

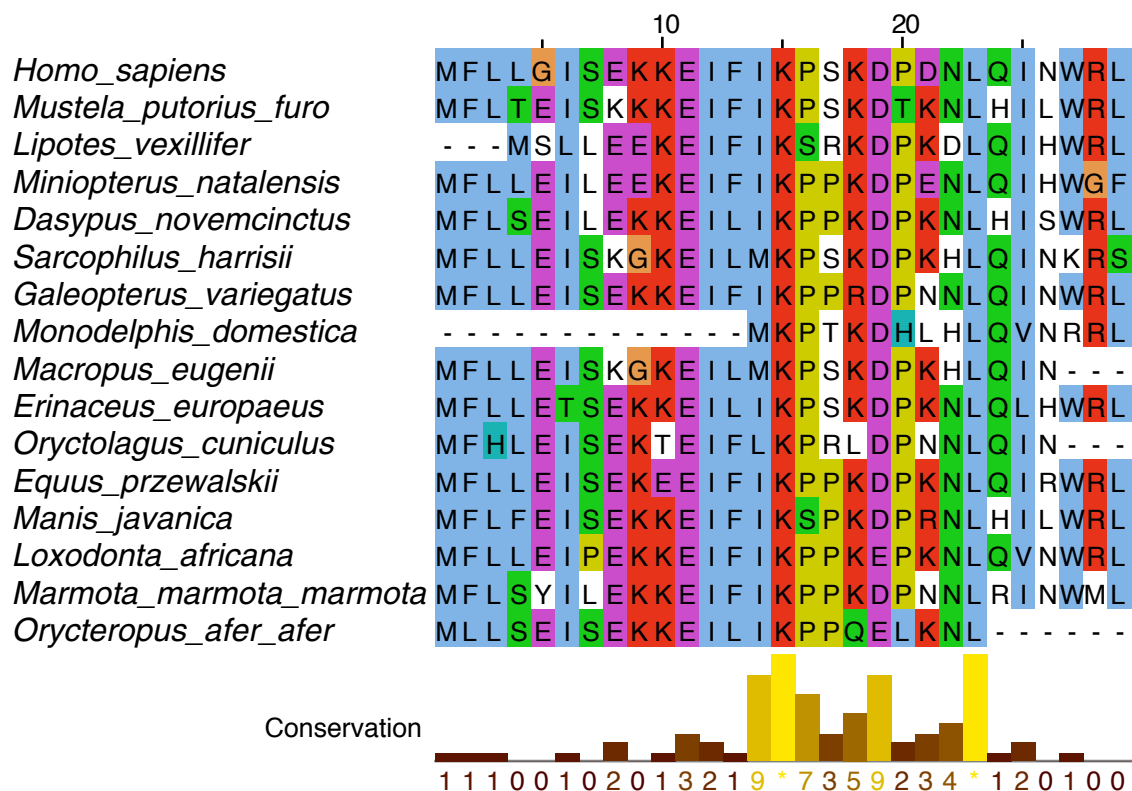


HG0465

ENSG00000132153 (DHX30)

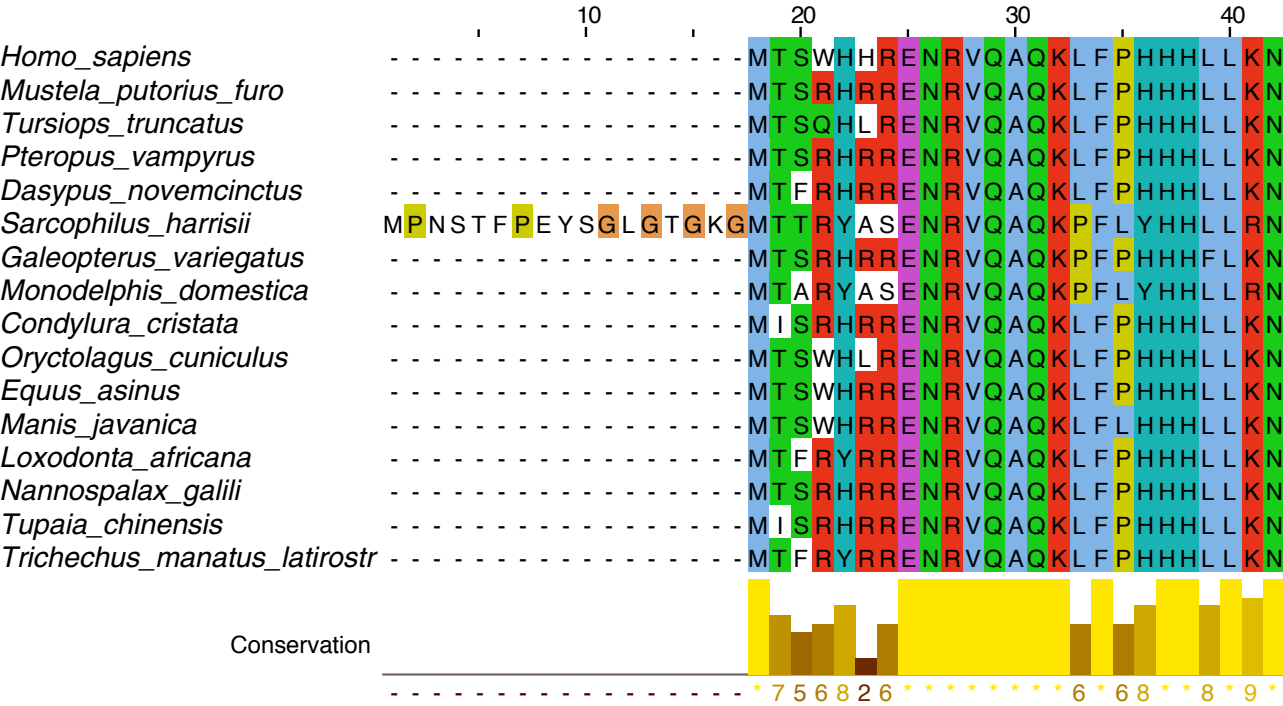


ENSG00000139679 (LPAR6)



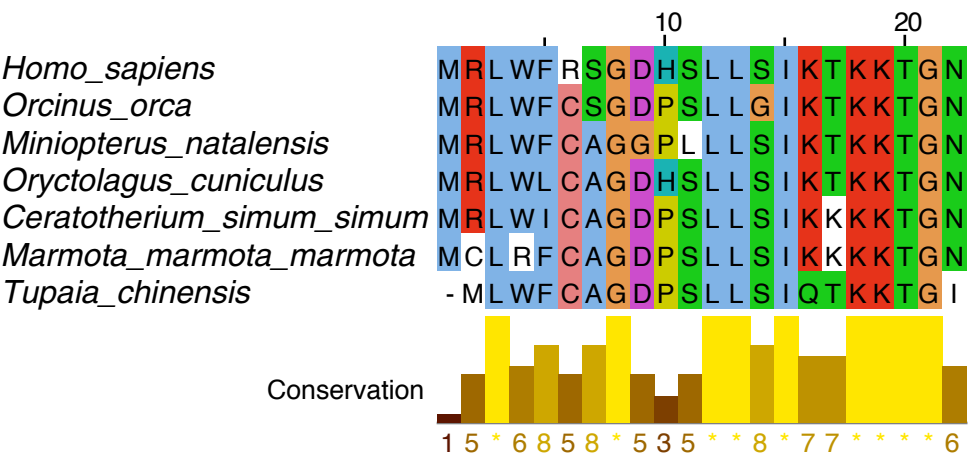
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ENSG00000163320 (CGGBP1)

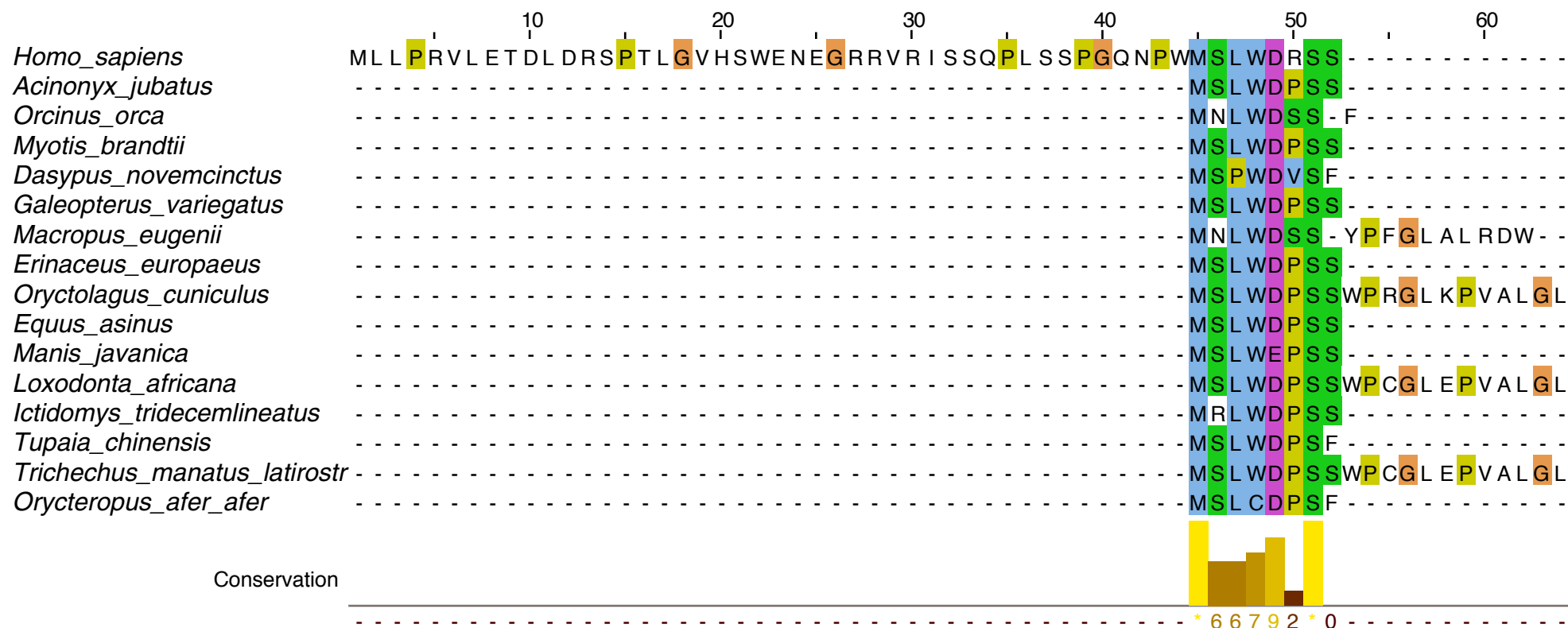


HG0467.2

ENSG00000163320 (CGGBP1)

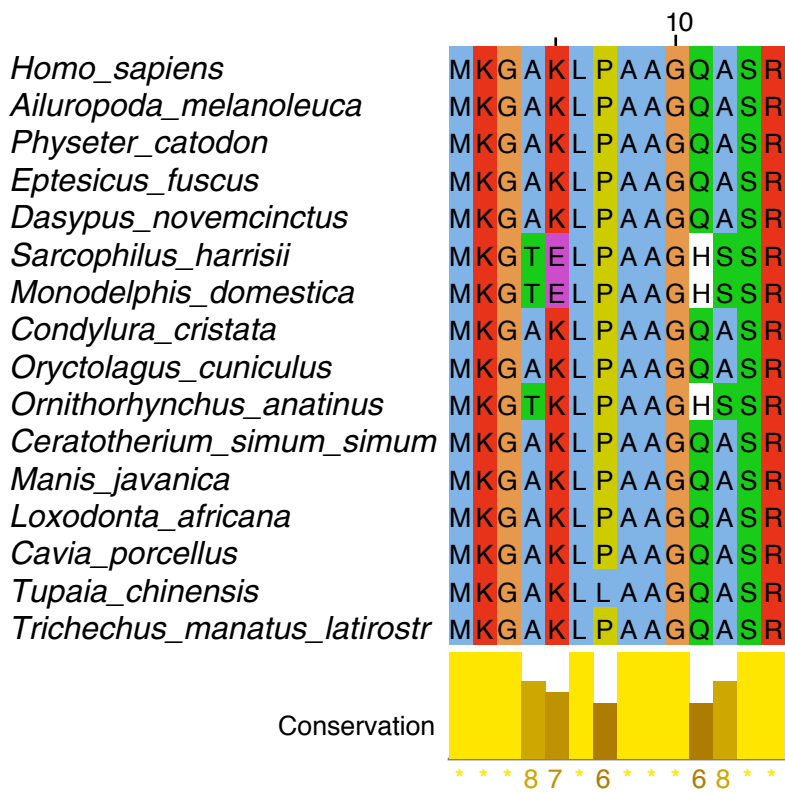


ENSG00000187778 (MCRS1)



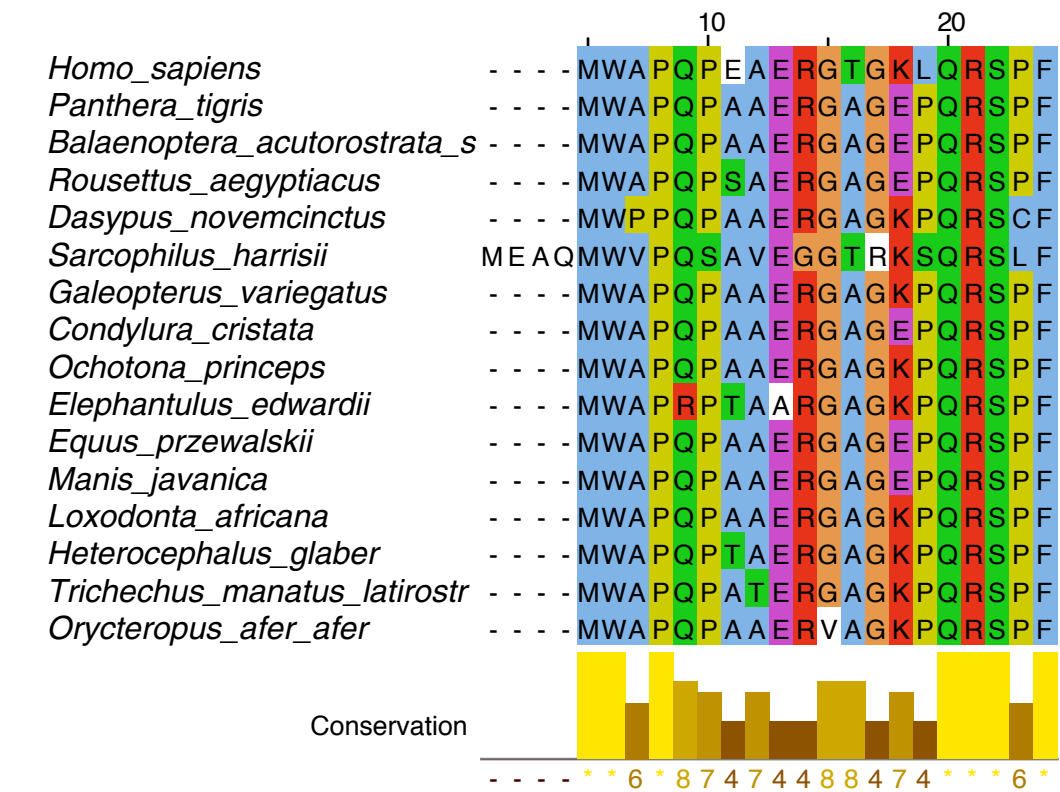
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ENSG00000198369 (SPRED2)

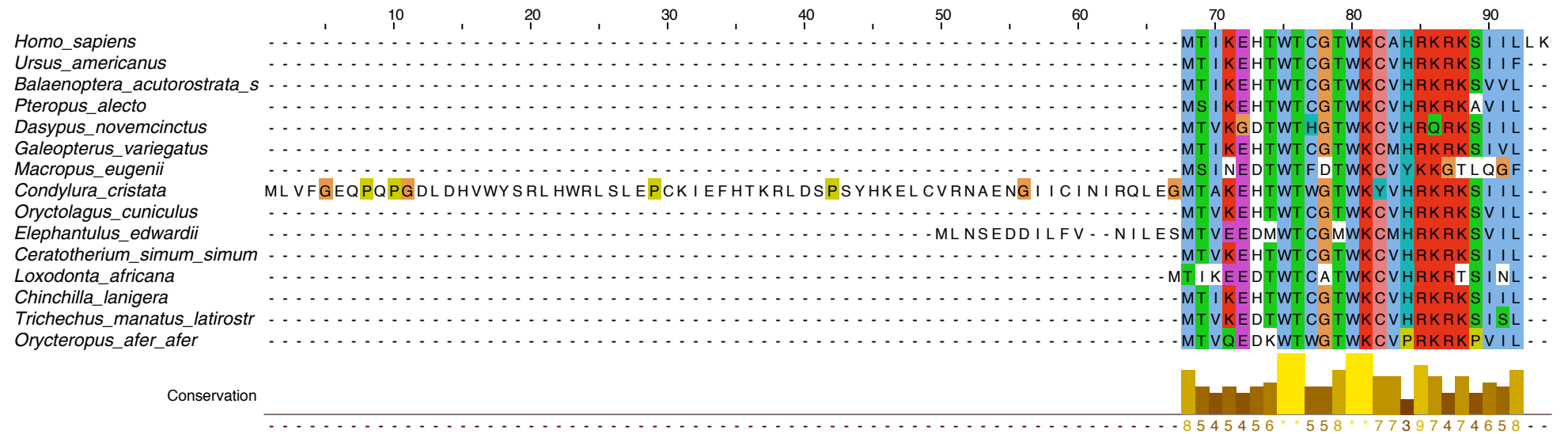


HG0470

ENSG00000224470 (ATXN1L)

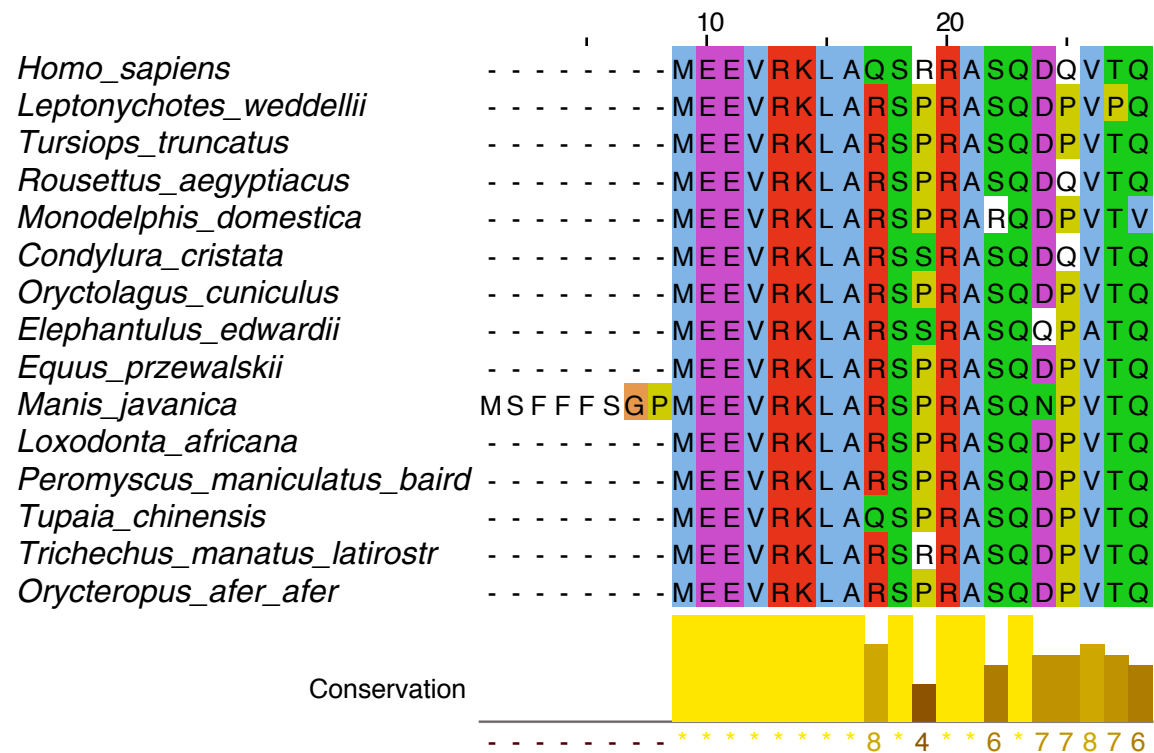


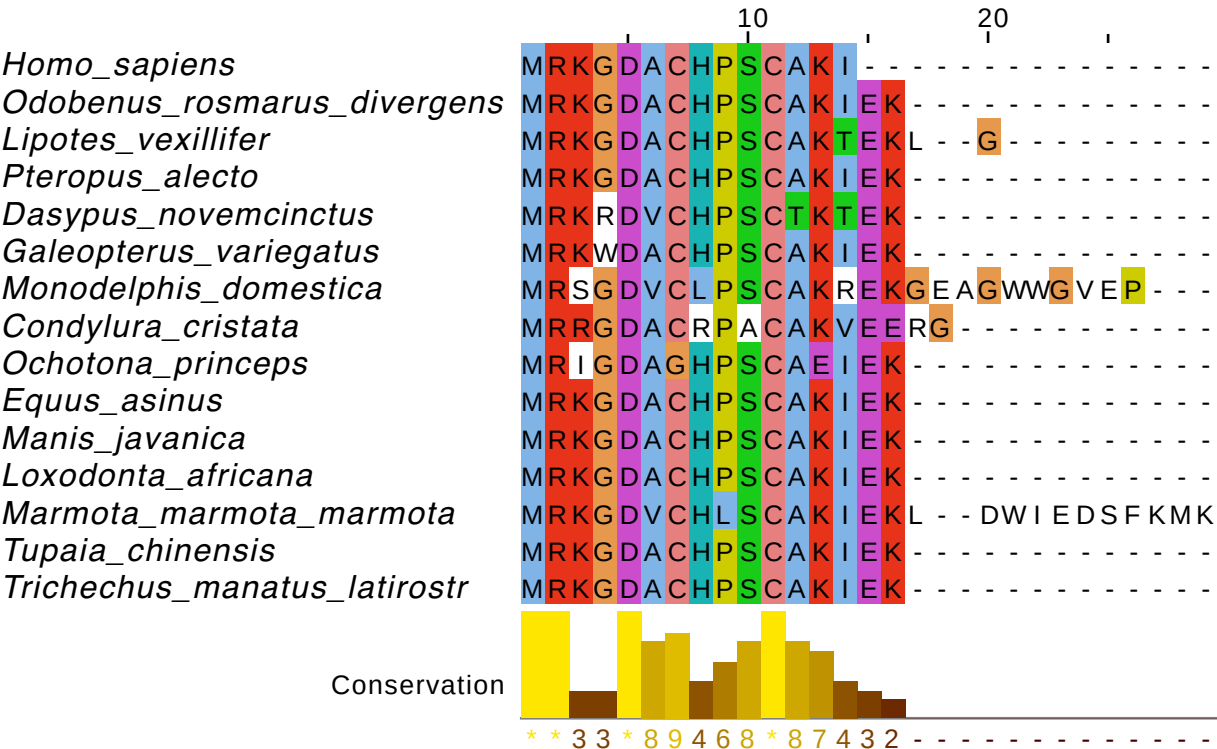
ENSG00000023041 (ZDHHC6)



HG0472

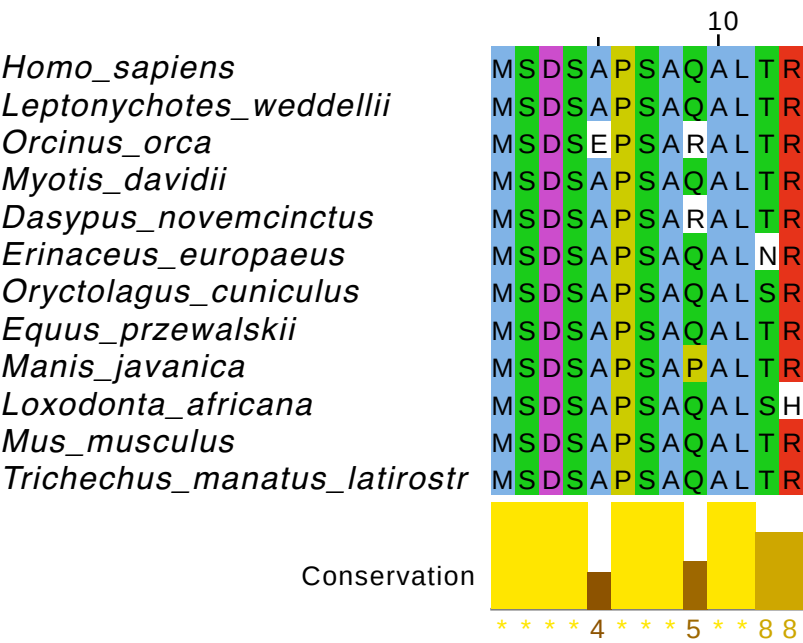
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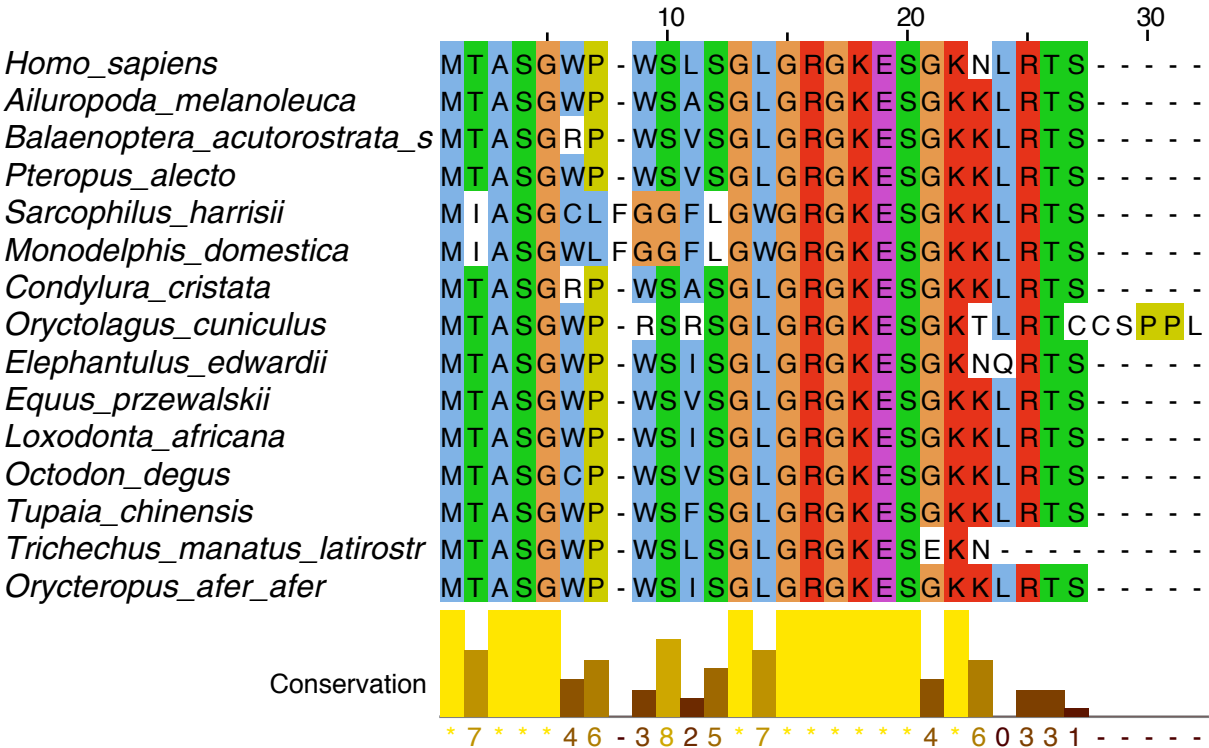
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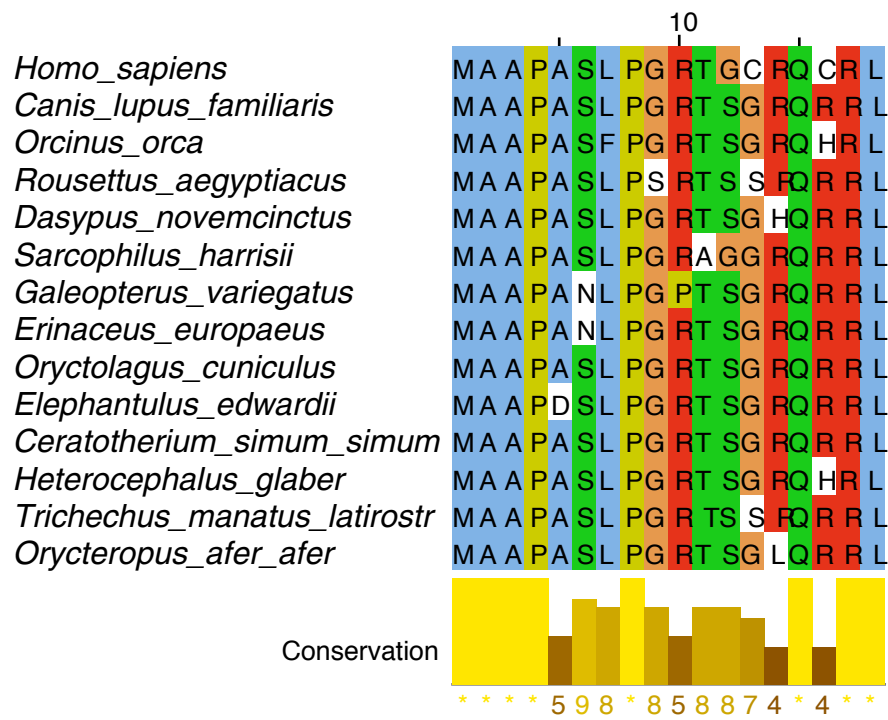
HG0474

ENSG00000139083 (ETV6)

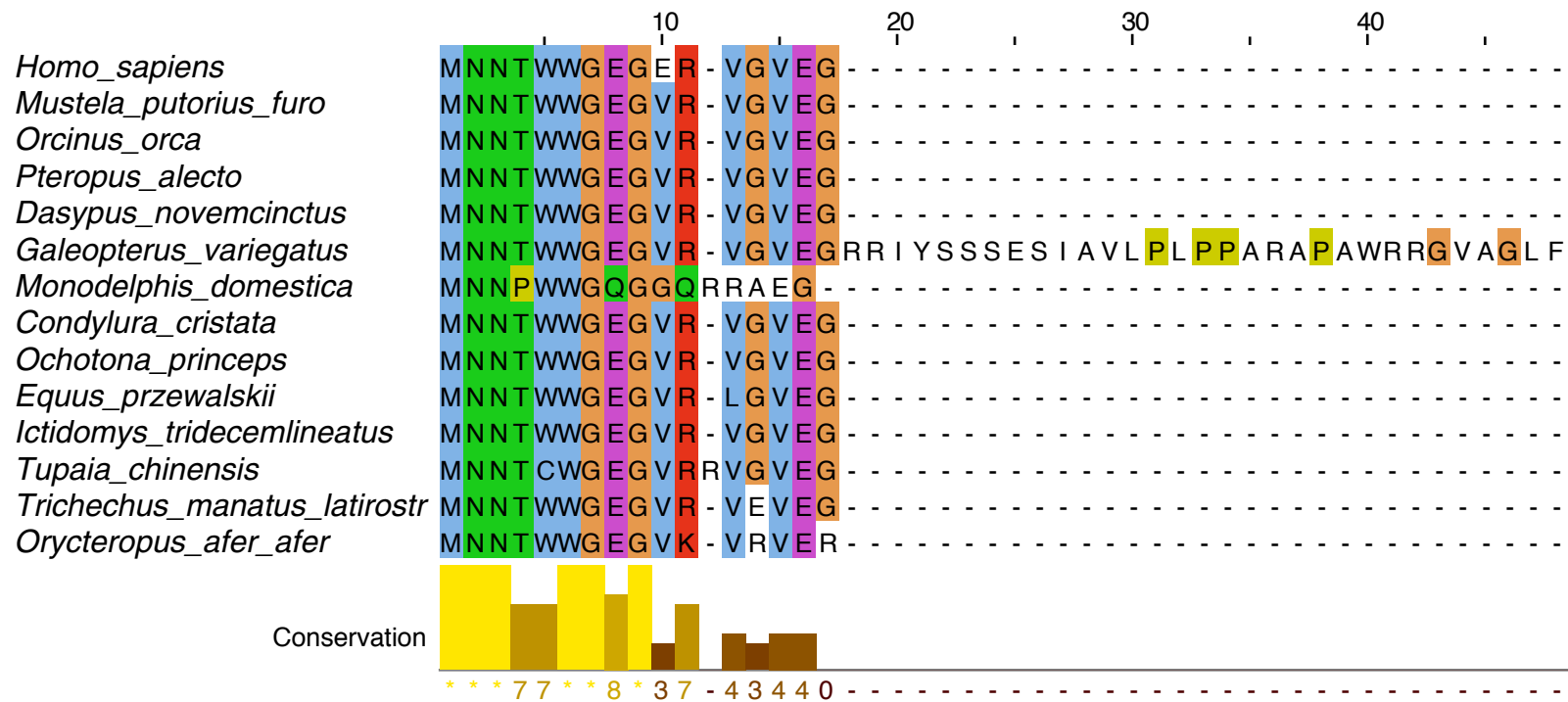


HG0475

ENSG00000109118 (PHF12)

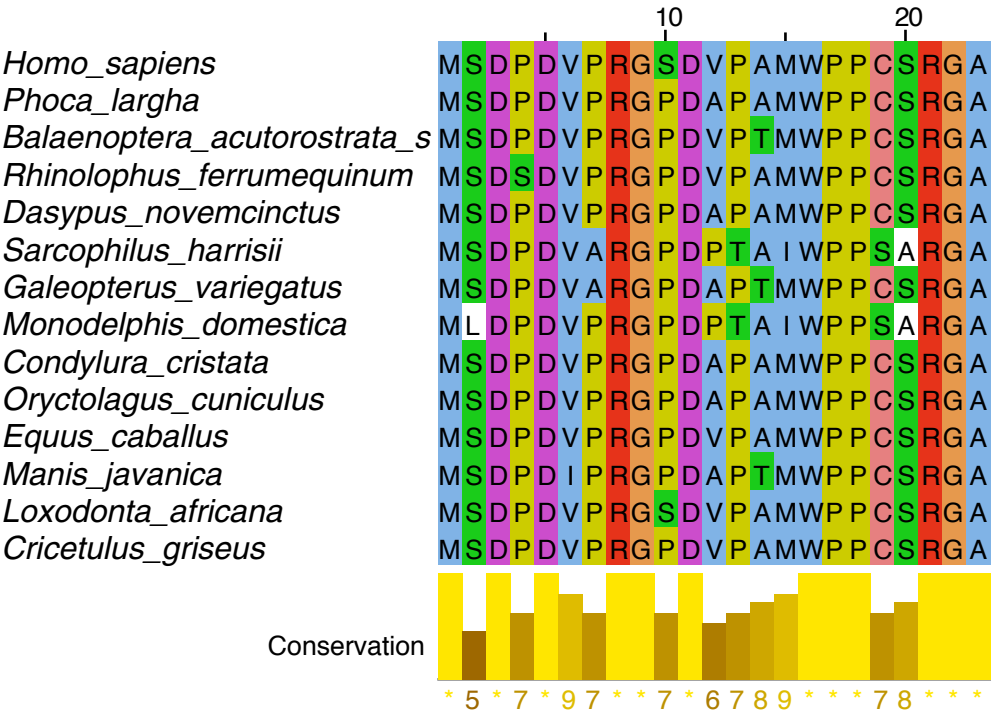


ENSG00000130939 (UBE4B)

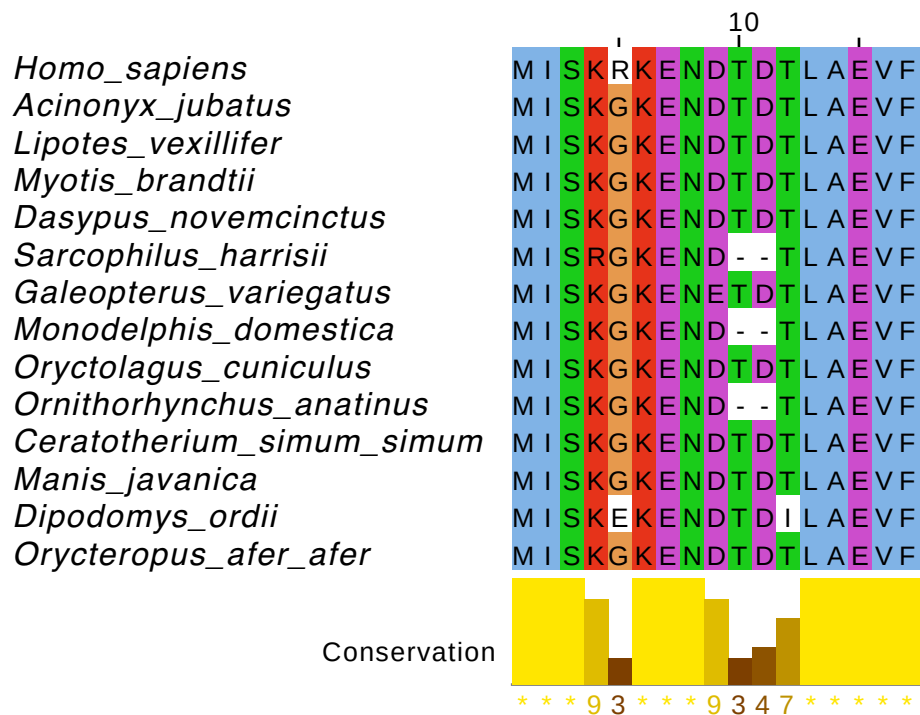


HG0477

ENSG00000166925 (TSC22D4)

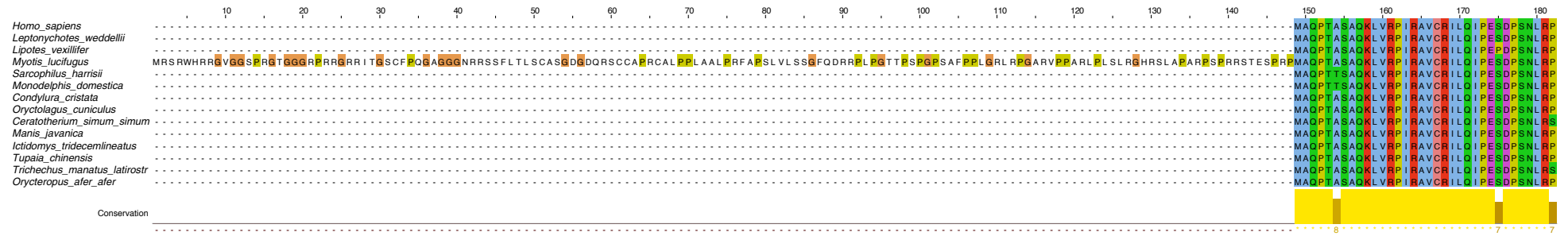


ENSG00000168214 (RBPJ)



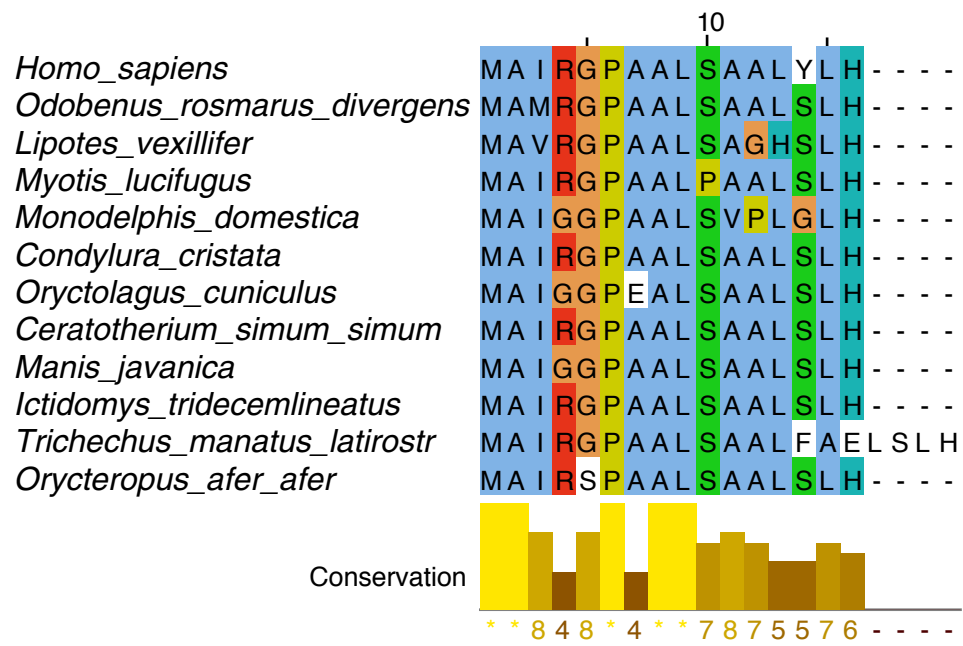
HG0479.1

ENSG00000168453 (HR)



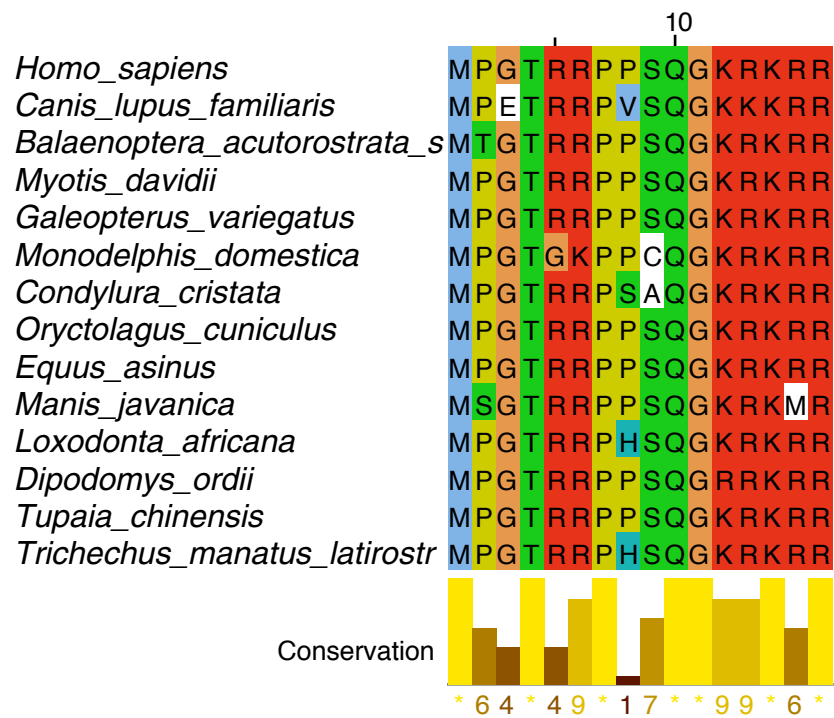
HG0479.2

ENSG00000168453 (HR)



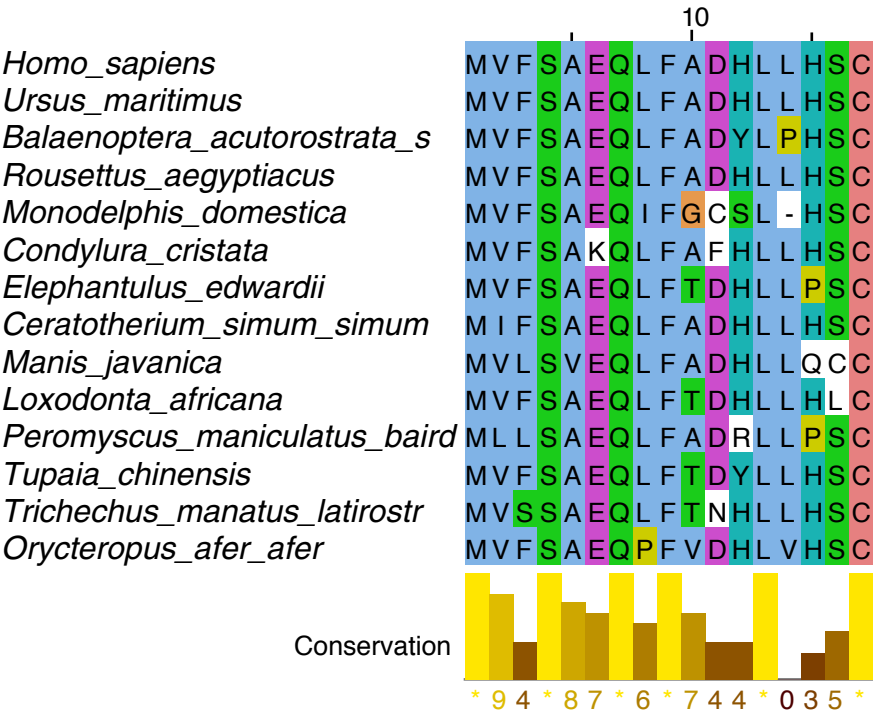
HG0480

ENSG00000198018 (ENTPD7)



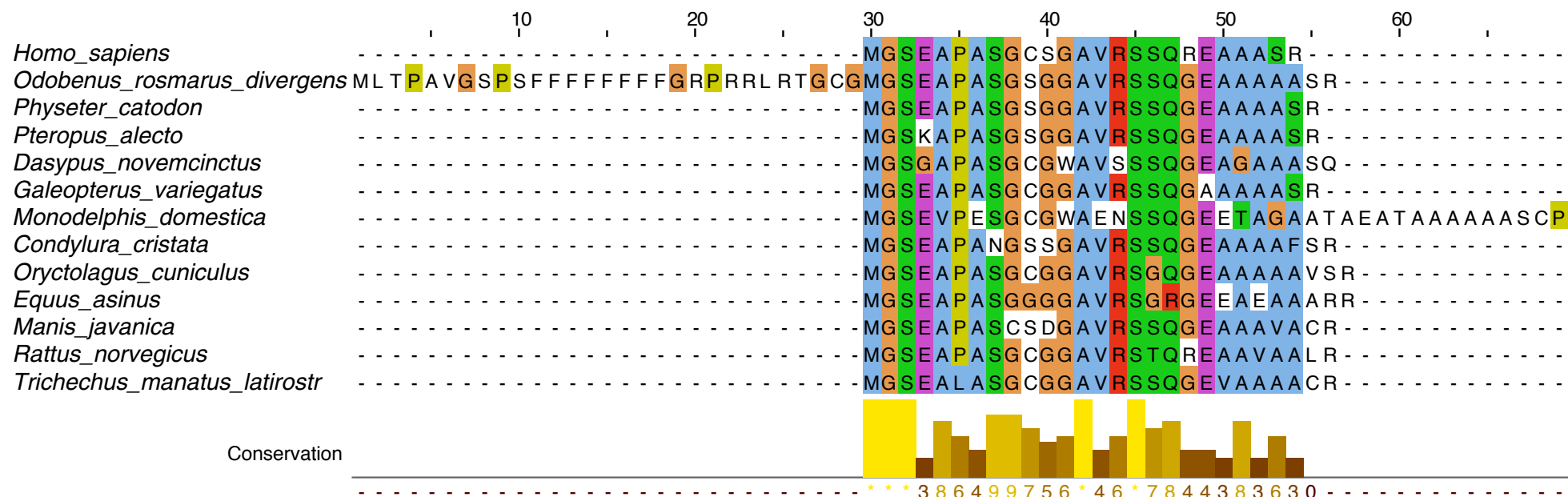
HG0481

ENSG00000198963 (RORB)



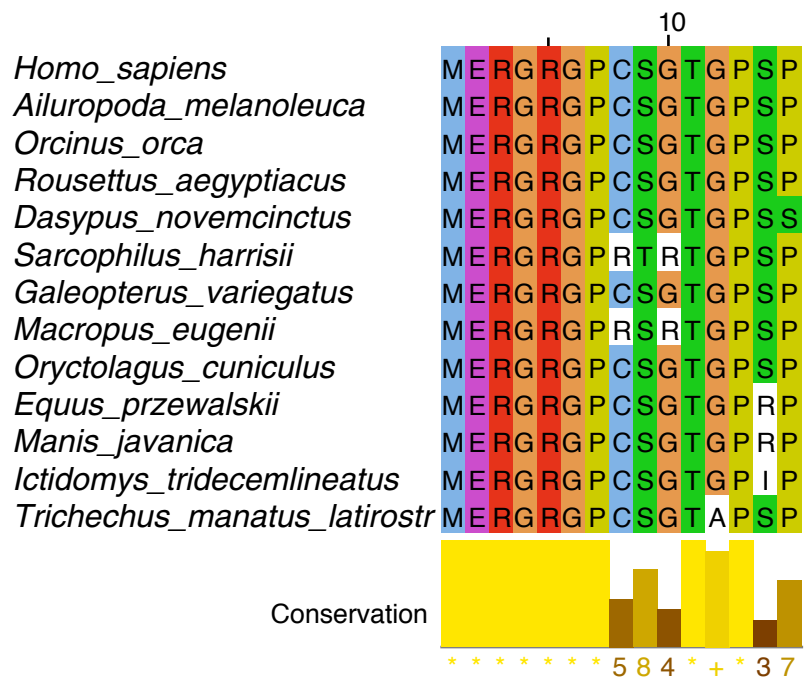
HG0482

ENSG00000067167 (TRAM1)



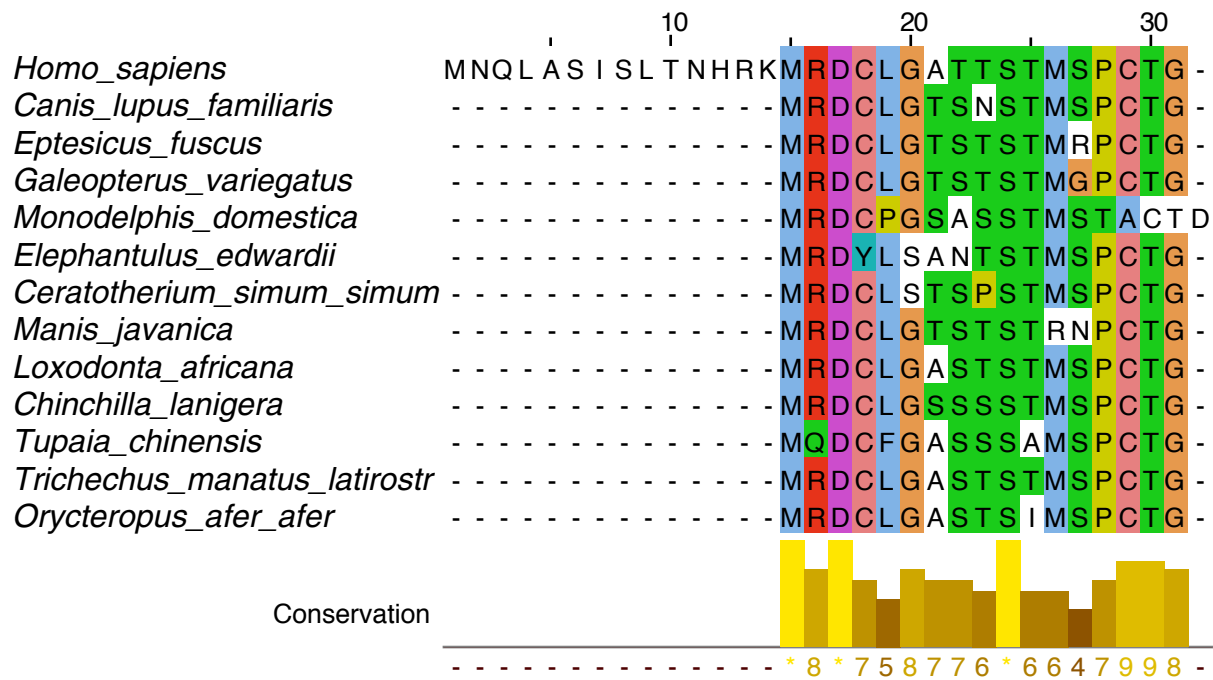
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ENSG00000164463 (CREBRF)



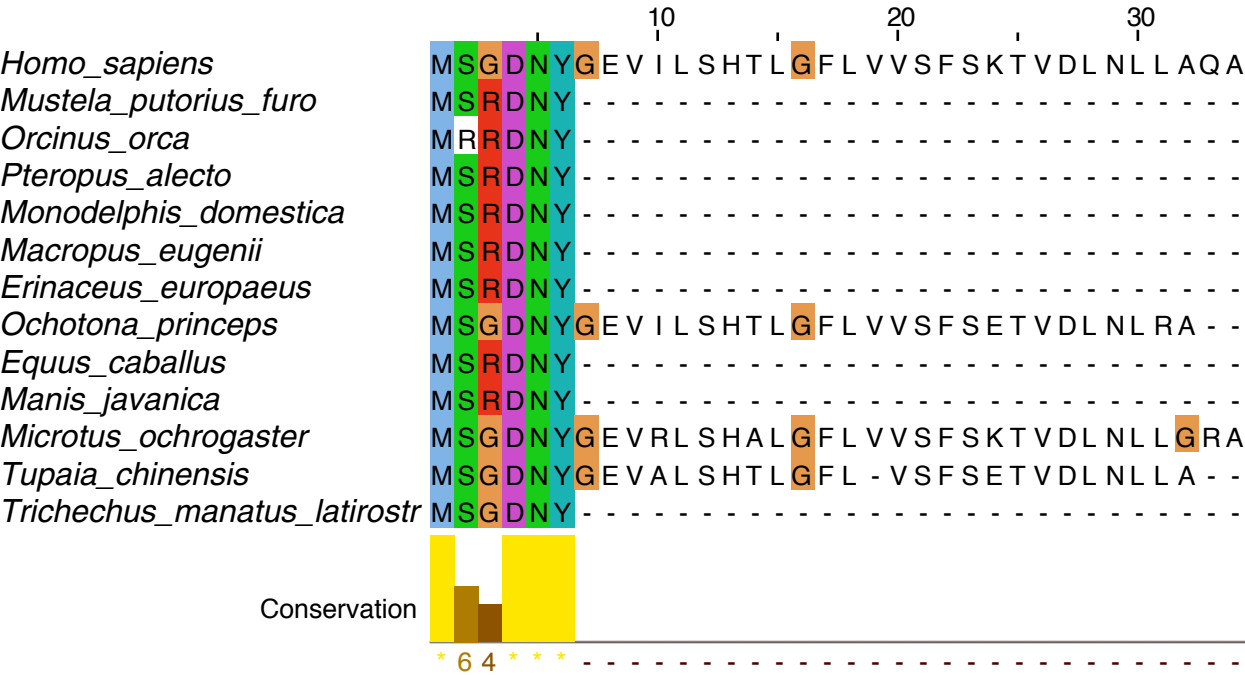
HG0484

ENSG00000166444 (ST5)



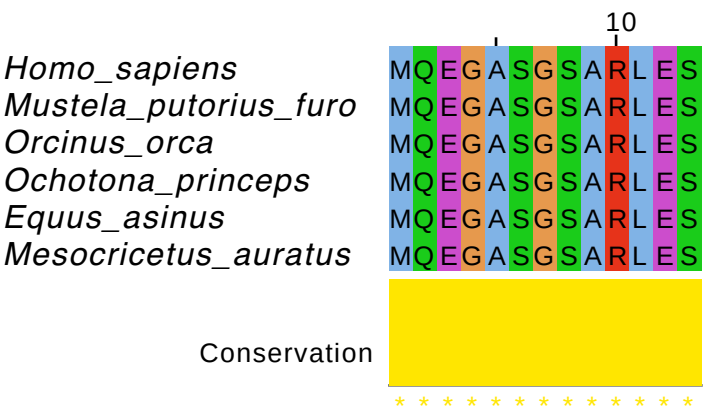
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ENSG00000182667 (NTM)



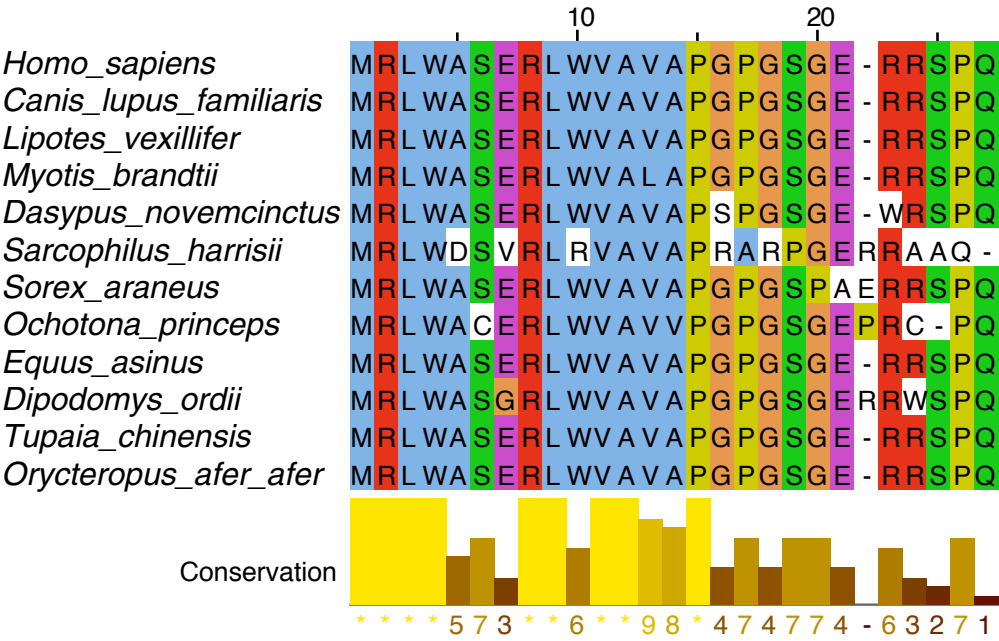
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ENSG00000183715 (OPCML)



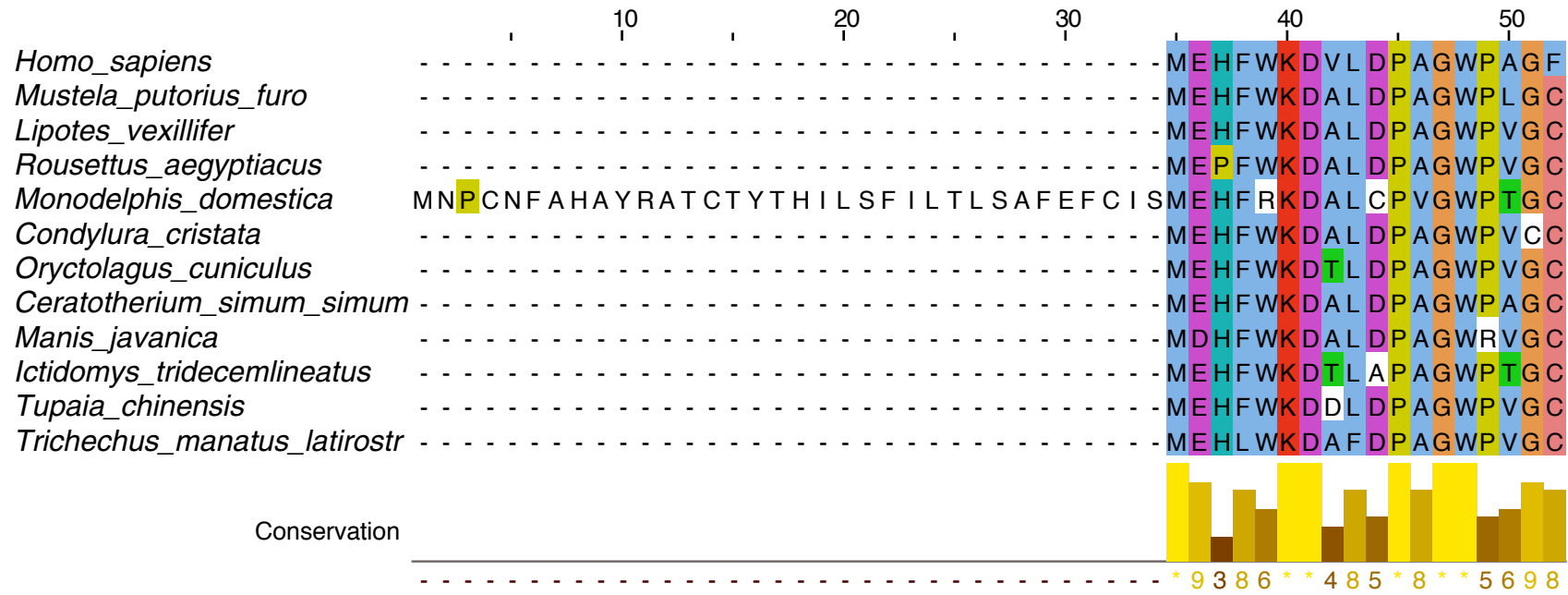
HG0486

ENSG00000067900 (ROCK1)

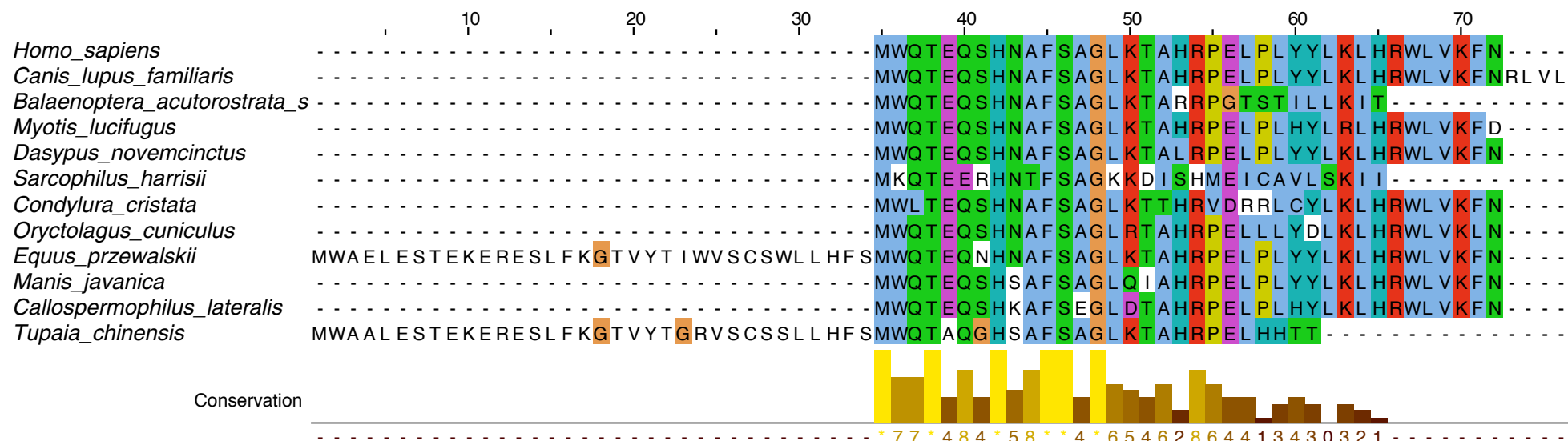


HG0487

ENSG00000091831 (ESR1)

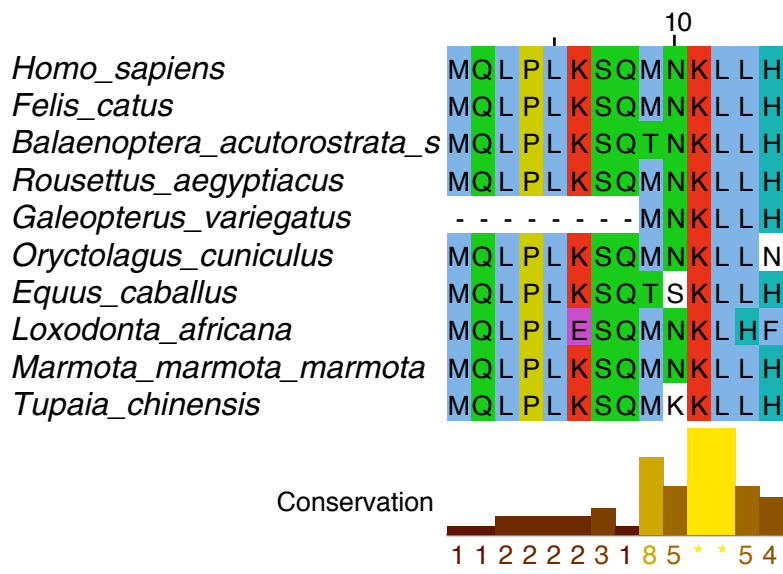


ENSG00000116194 (ANGPTL1)

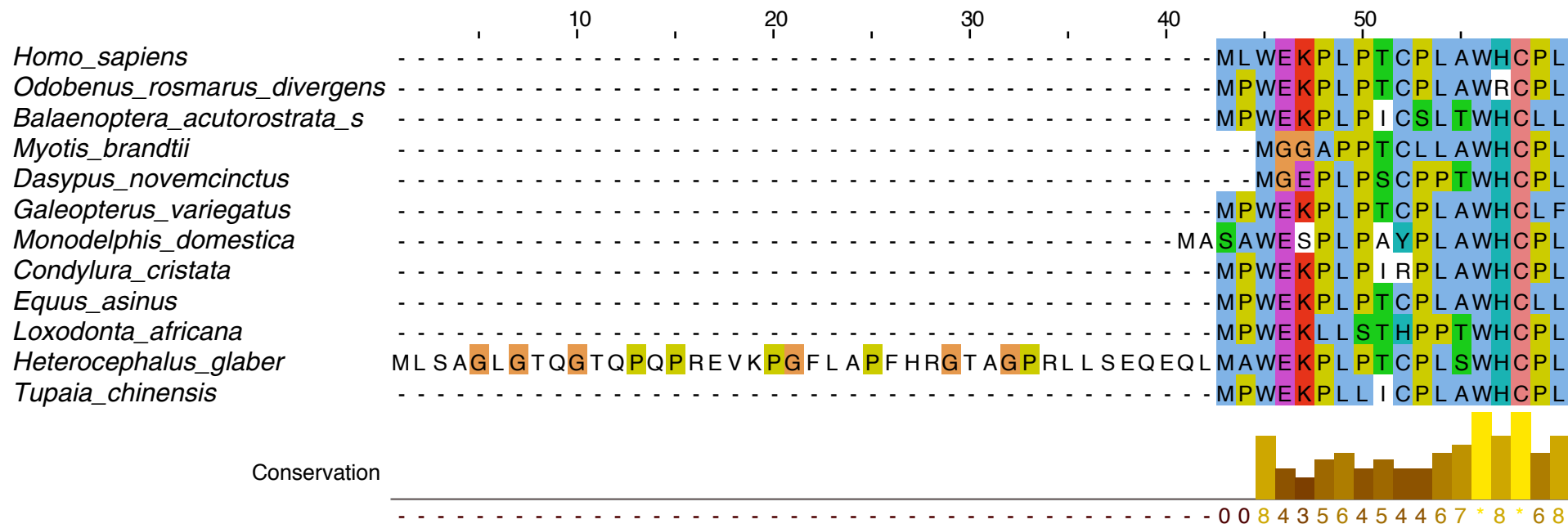


HG0488.2

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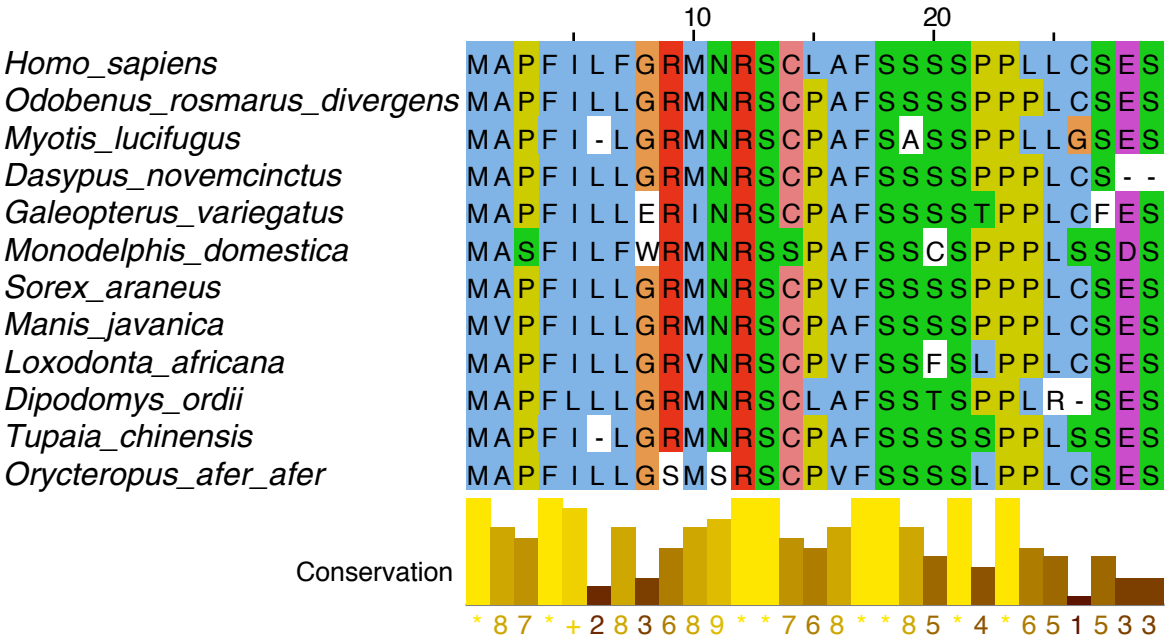


ENSG00000143847 (PPFIA4)



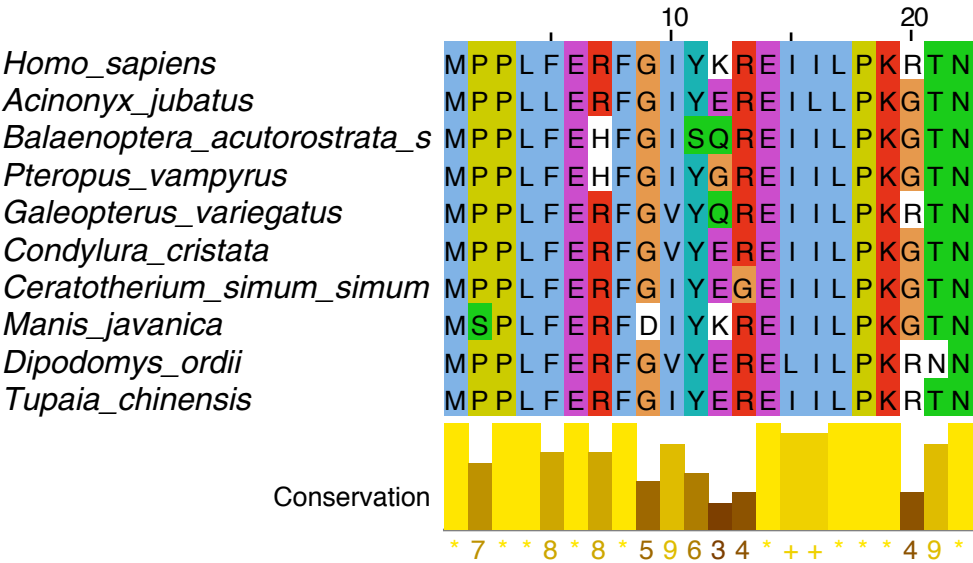
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ENSG00000152413 (HOMER1)



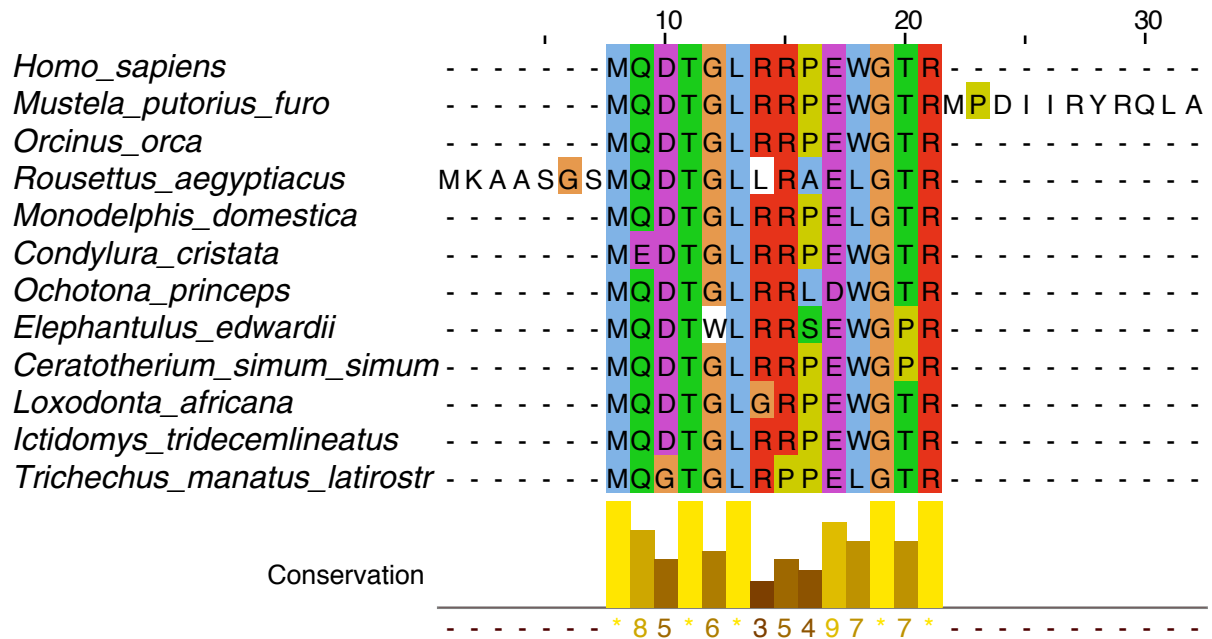
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ENSG00000152413 (HOMER1)

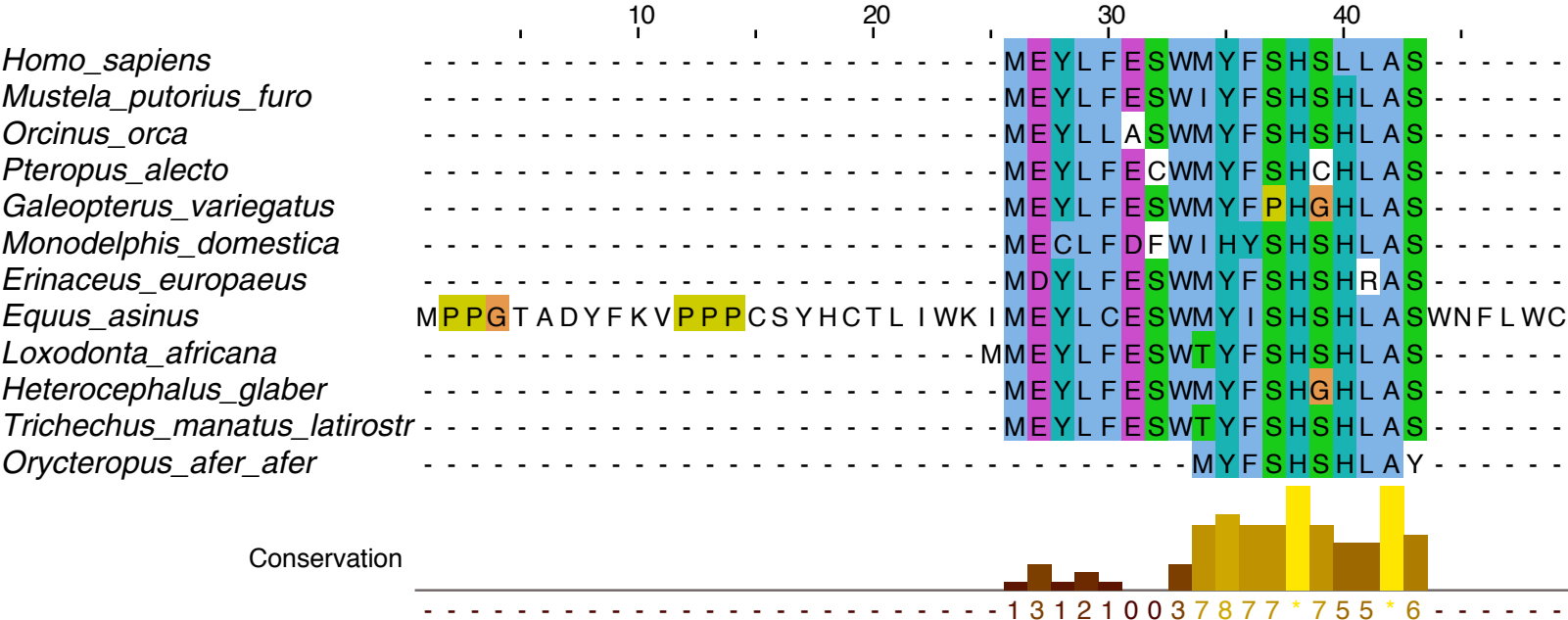


HG0491

ENSG00000154114 (TBCEL)

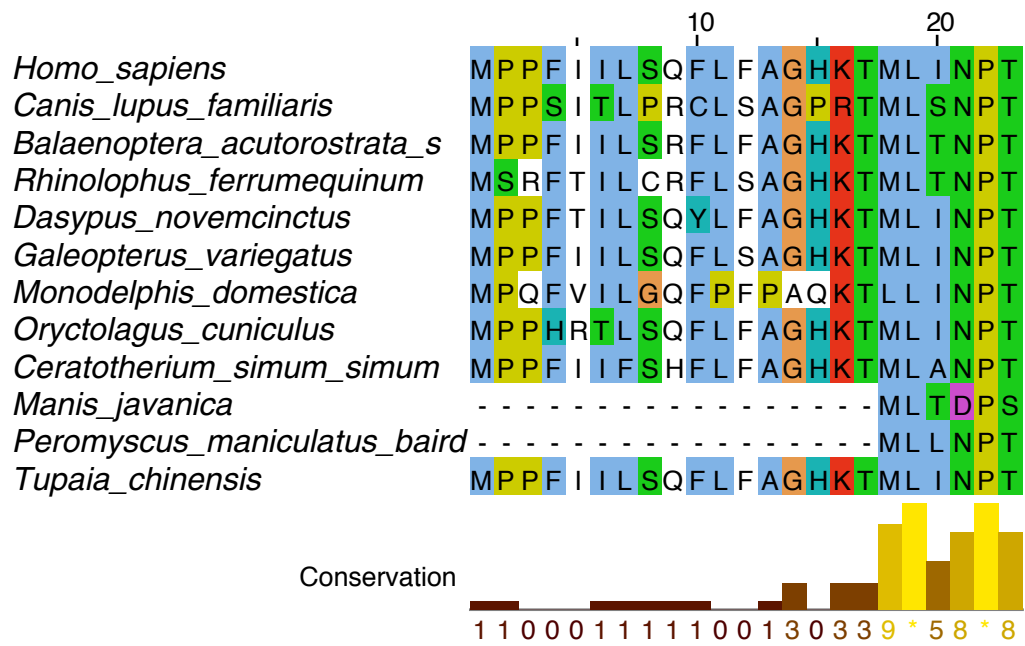


HG0492
ENSG00000162670 (BRINP3)



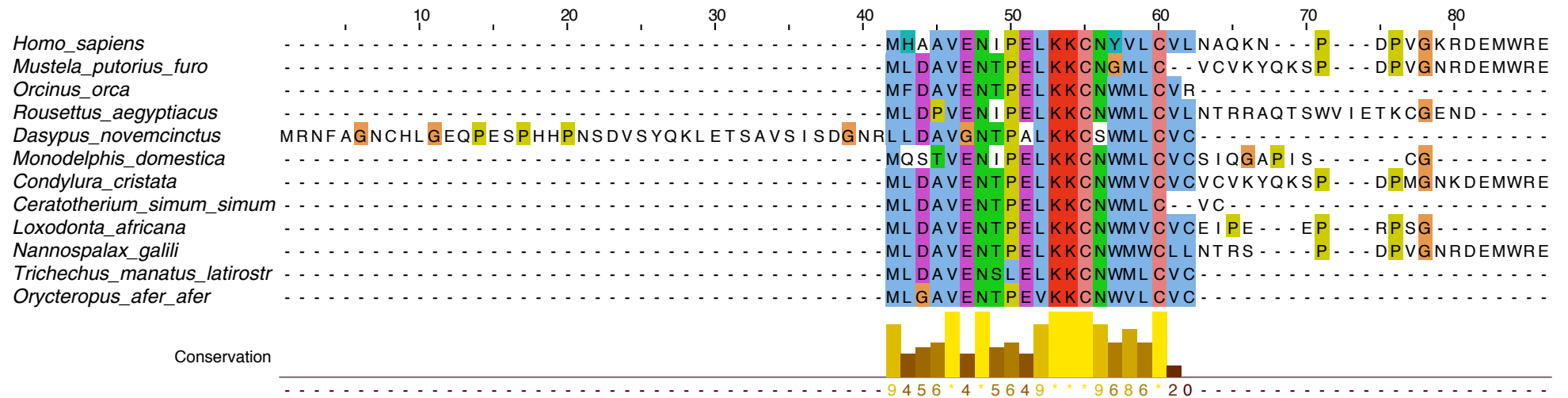
HG0493

ENSG00000164707 (SLC13A4)



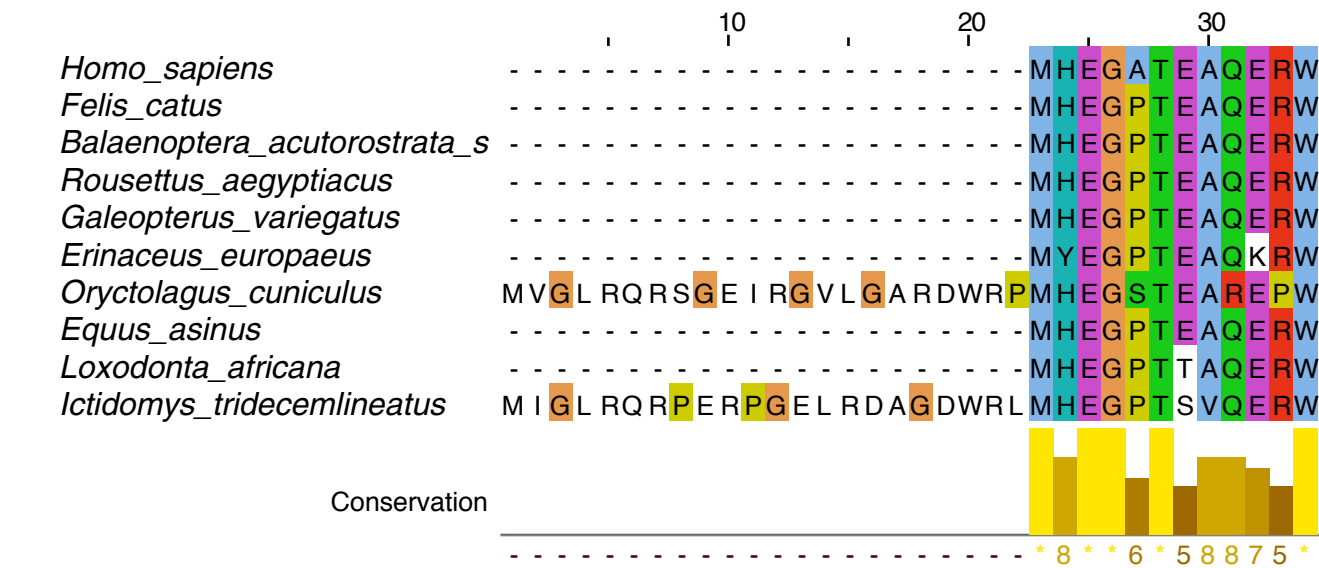
HG0494

ENSG00000184226 (PCDH9)



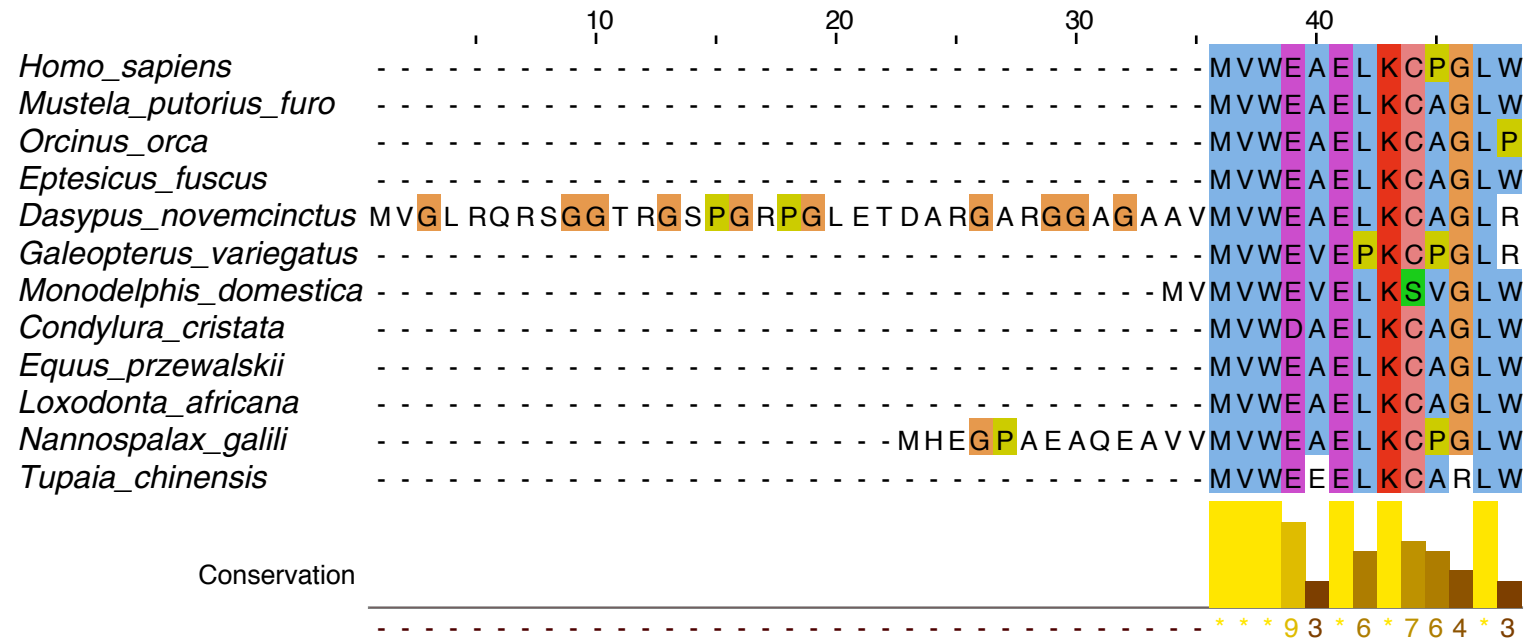
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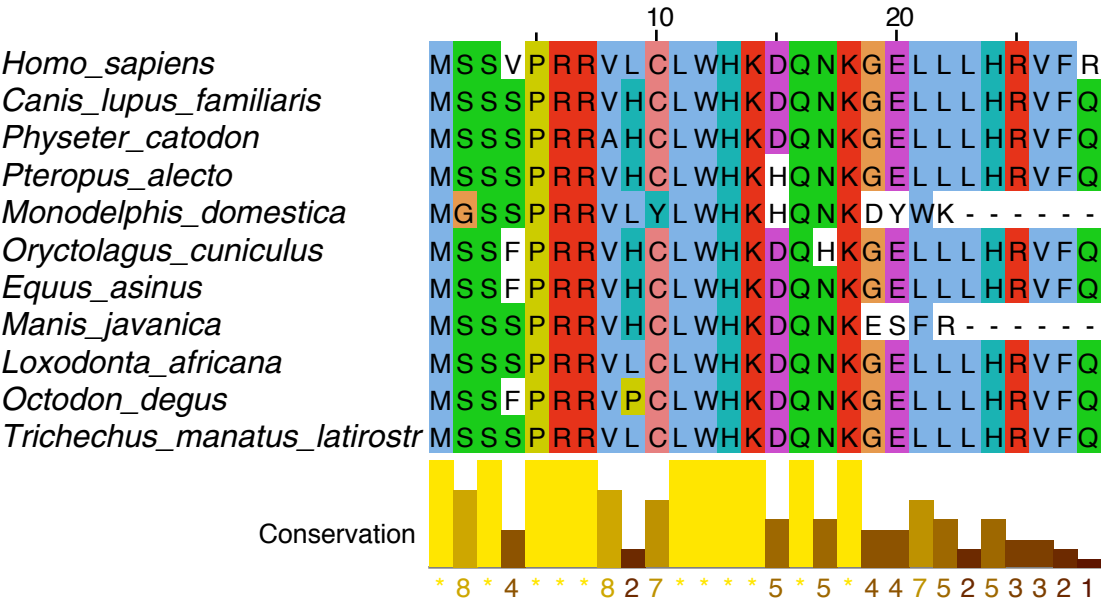
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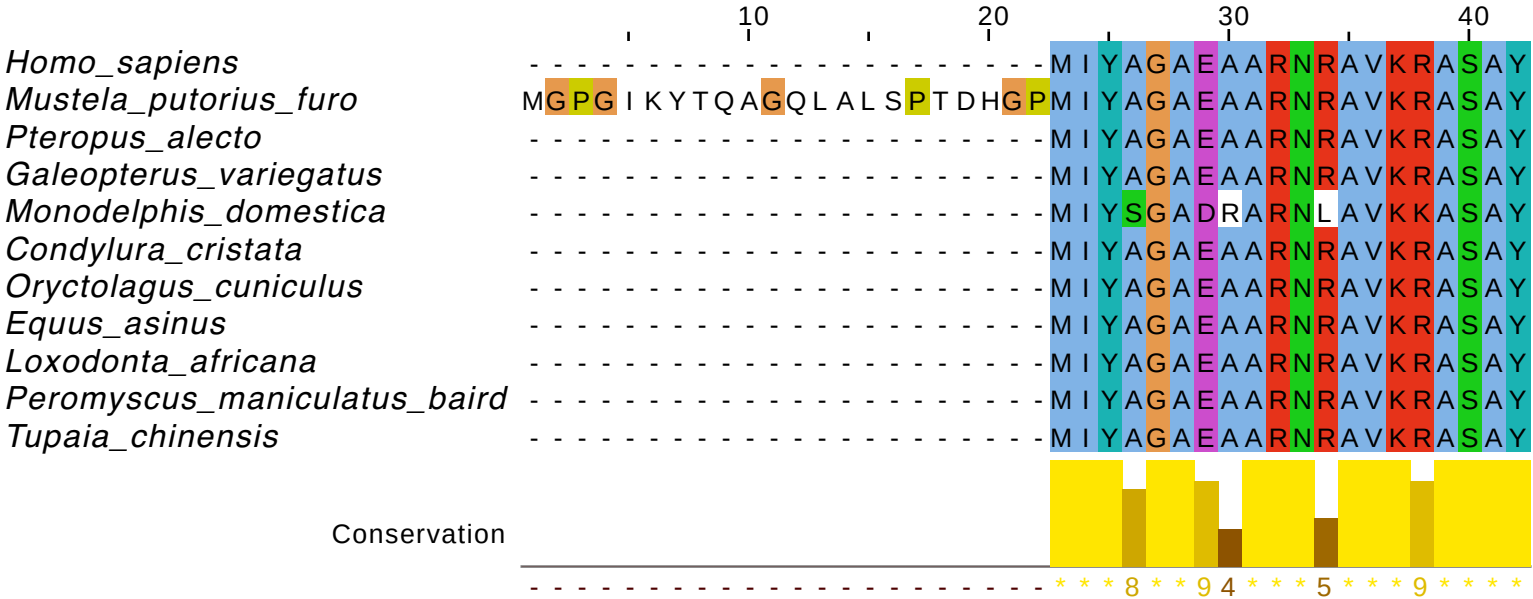


HG0496

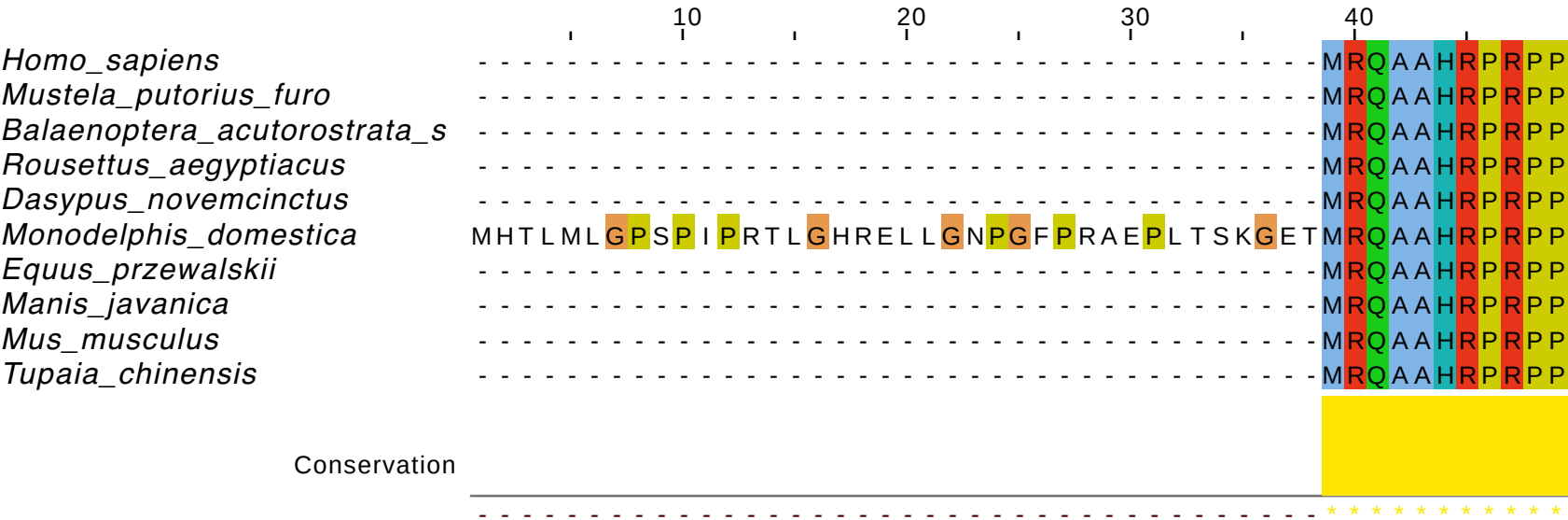
ENSG00000135913 (USP37)



HG0497
ENSG00000147571 (CRH)

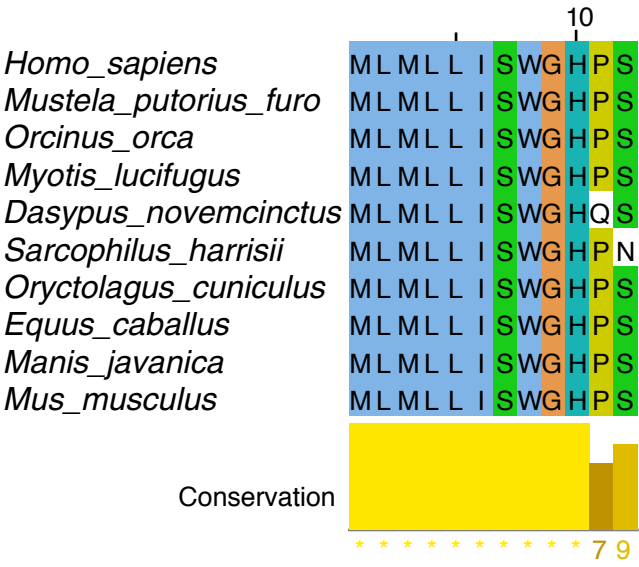


HG0498
ENSG00000005379 (TSPOAP1)



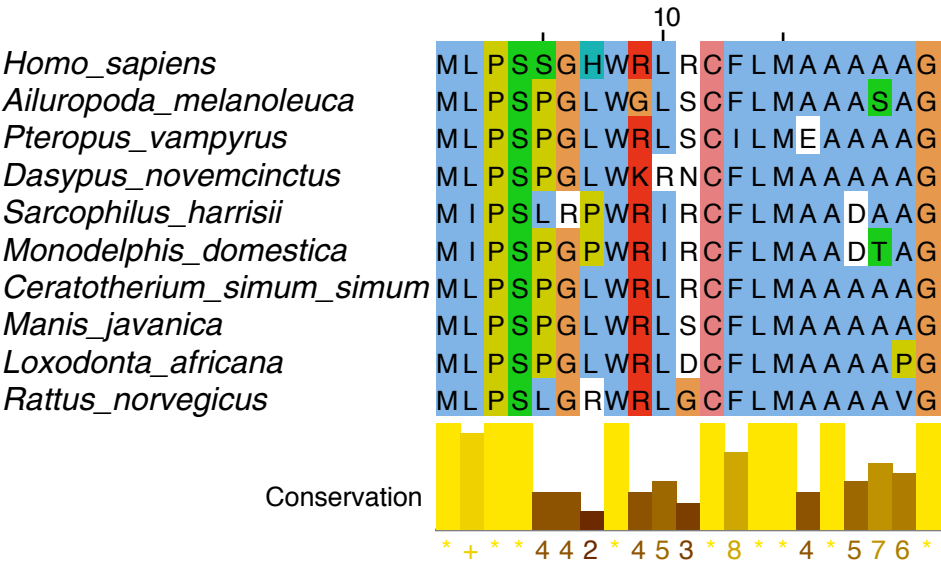
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ENSG00000011258 (MBTD1)



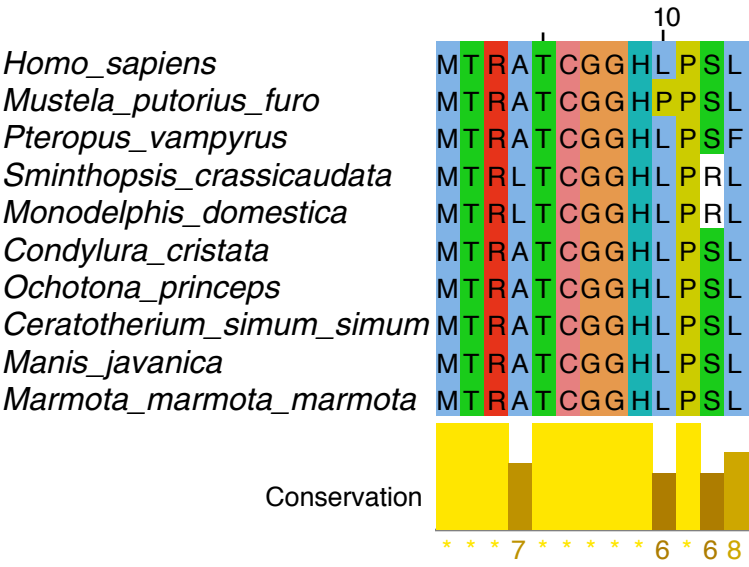
HG0500

ENSG00000070778 (PTPN21)

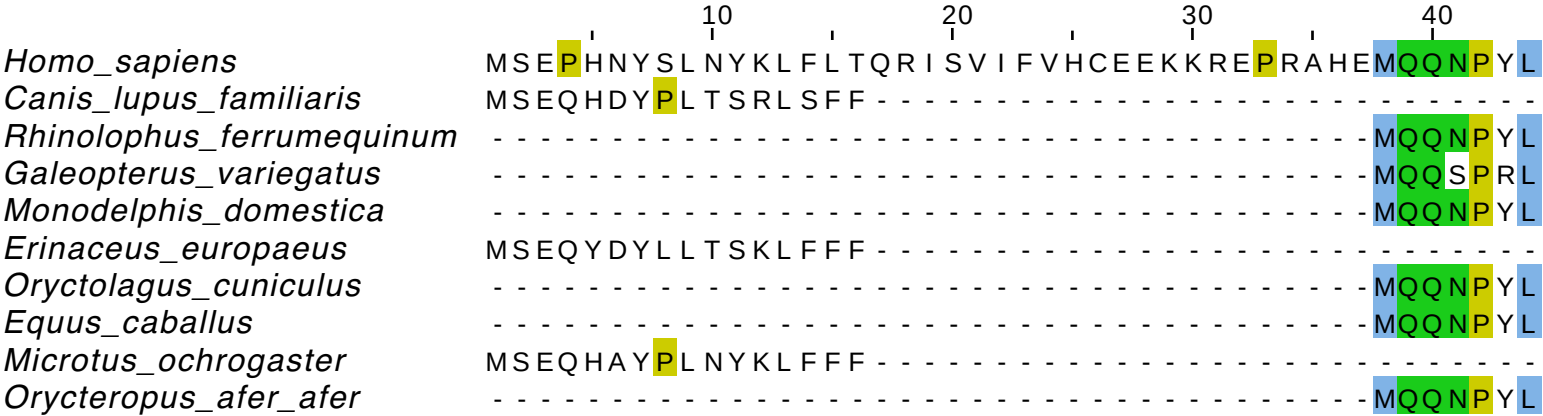


HG0501

ENSG00000110400 (NECTIN1)

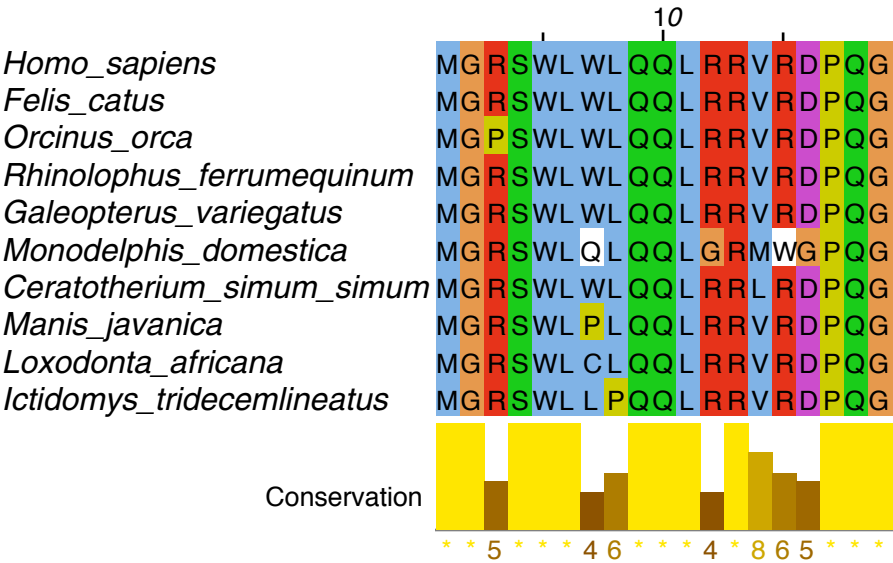


HG0502
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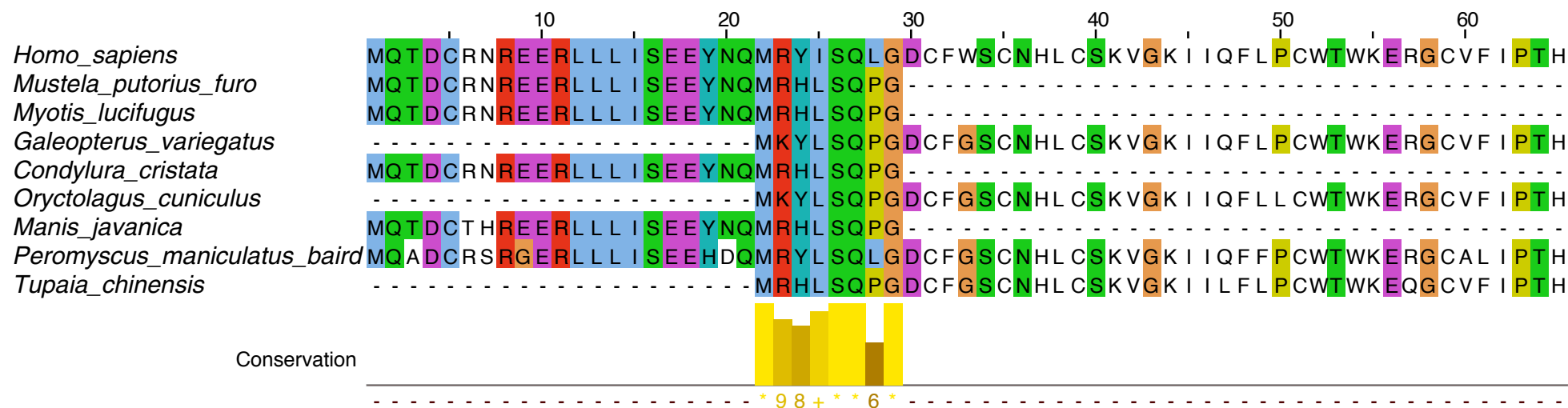
HG0503

ENSG00000141564 (RPTOR)

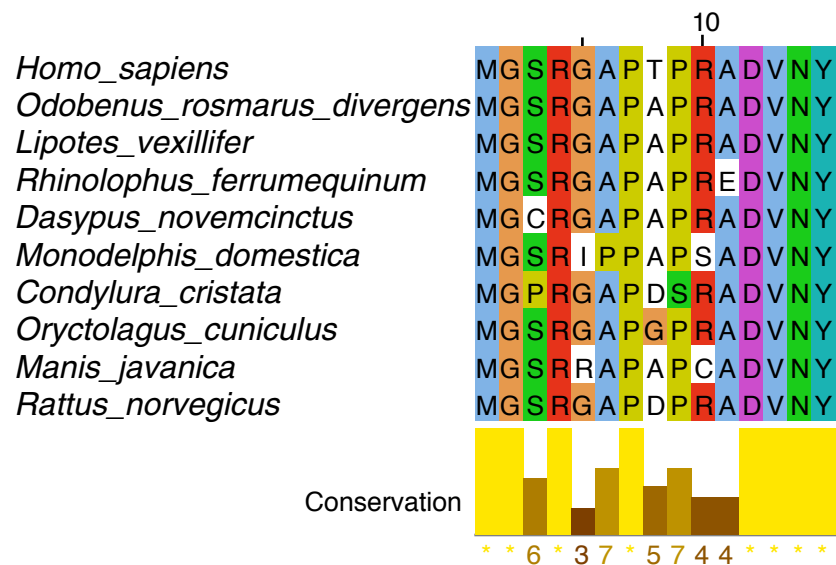


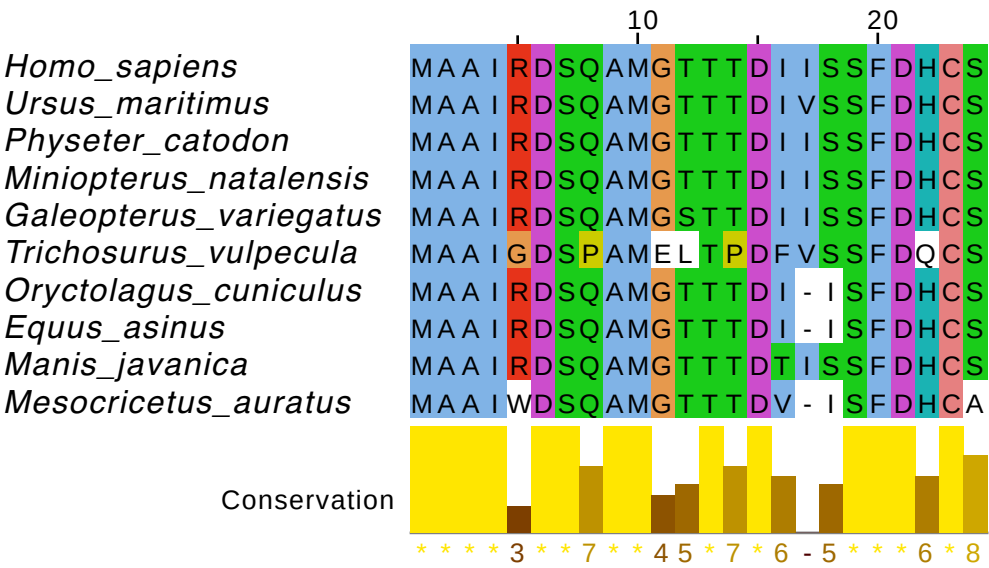
HG0504

ENSG00000144460 (NYAP2)



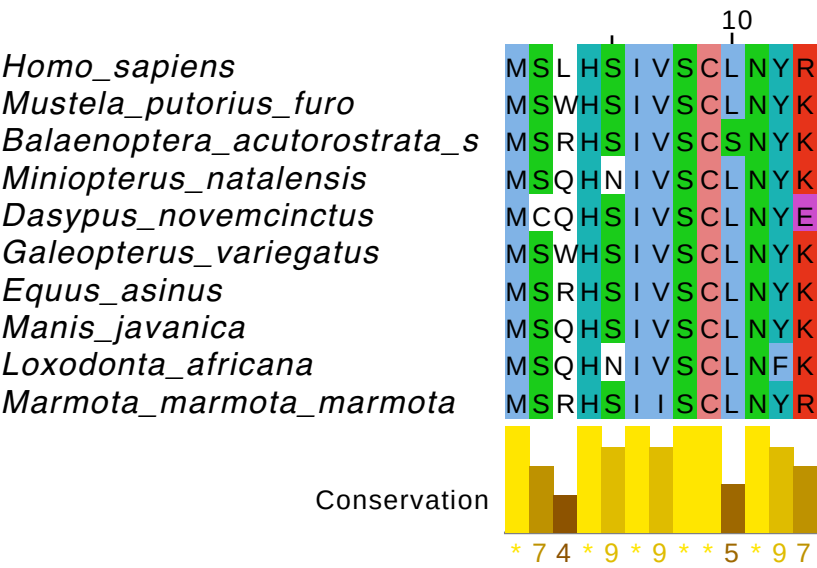
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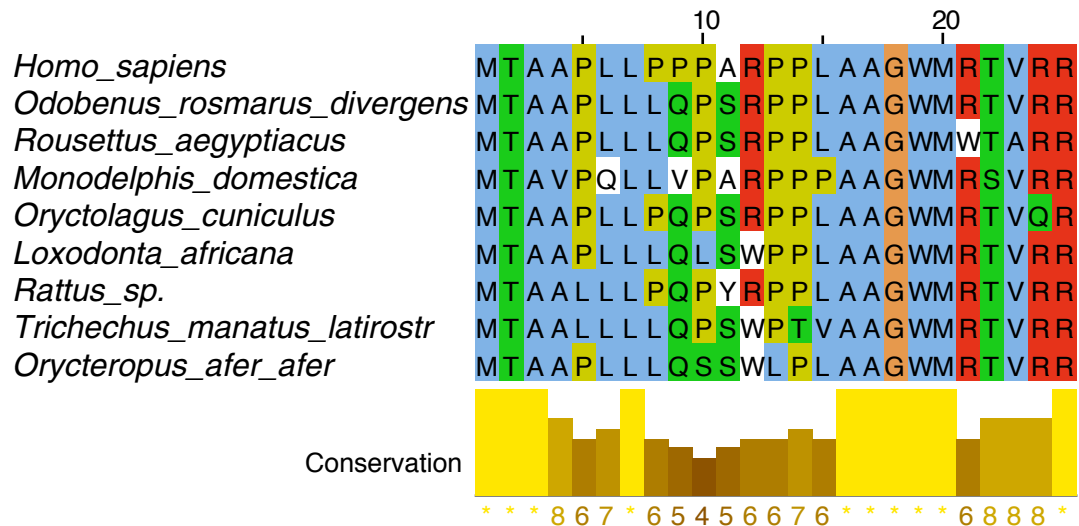
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ENSG00000177853 (ZNF518A)



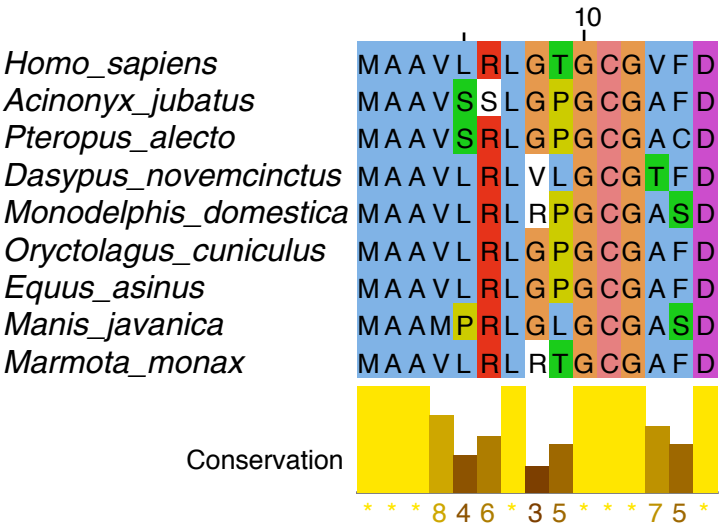
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ENSG00000060237 (WNK1)



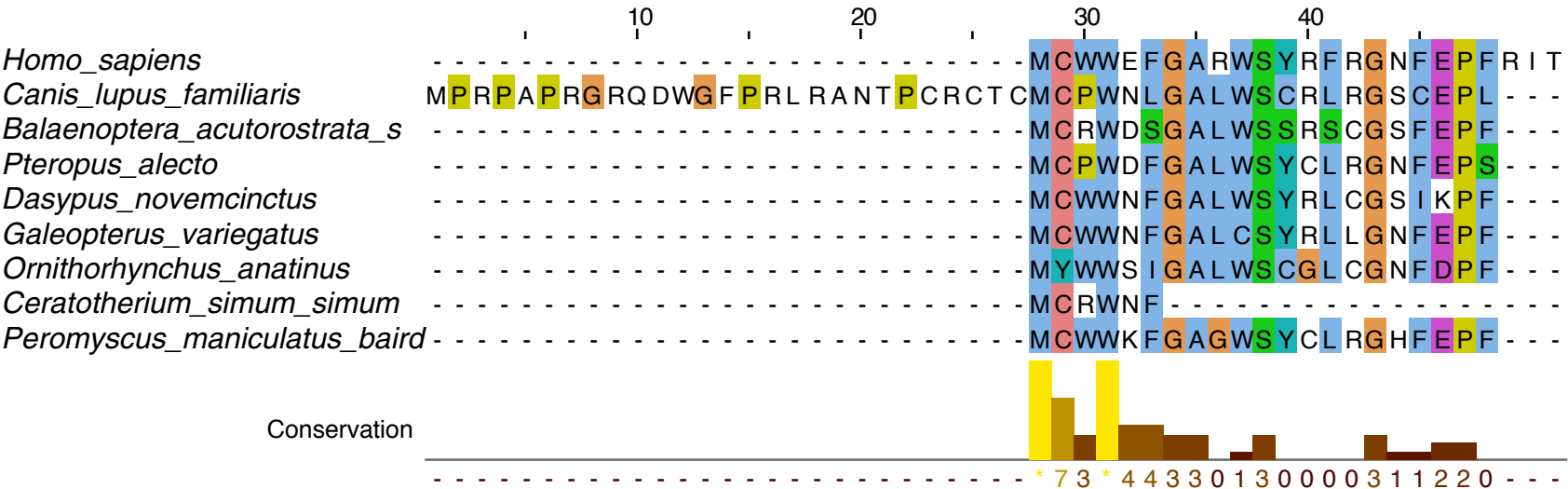
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ENSG000000061936 (SFSWAP)



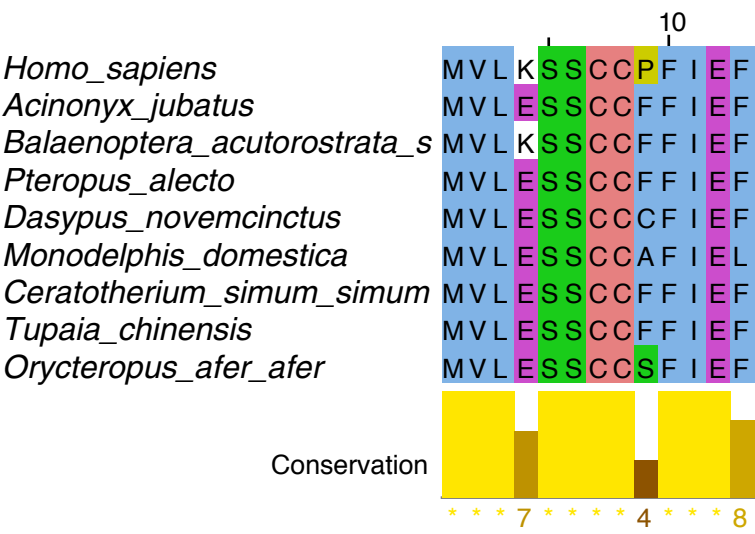
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ENSG00000068024 (HDAC4)



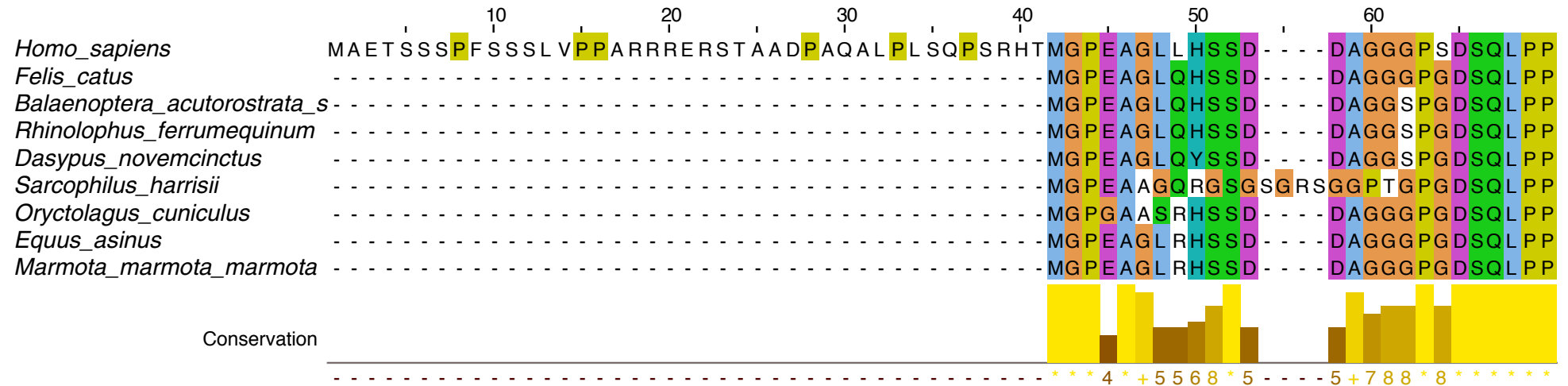
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ENSG00000134769 (DTNA)



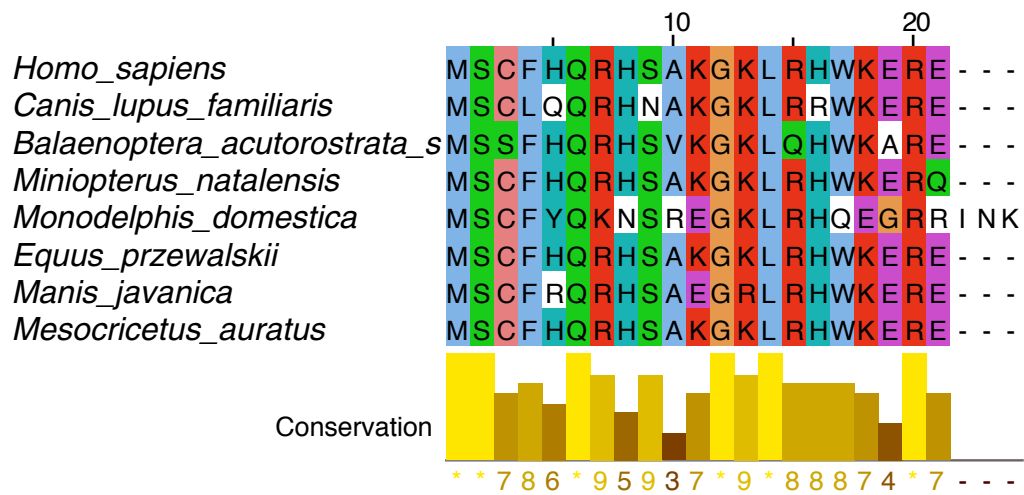
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ENSG00000143337 (TOR1AIP1)



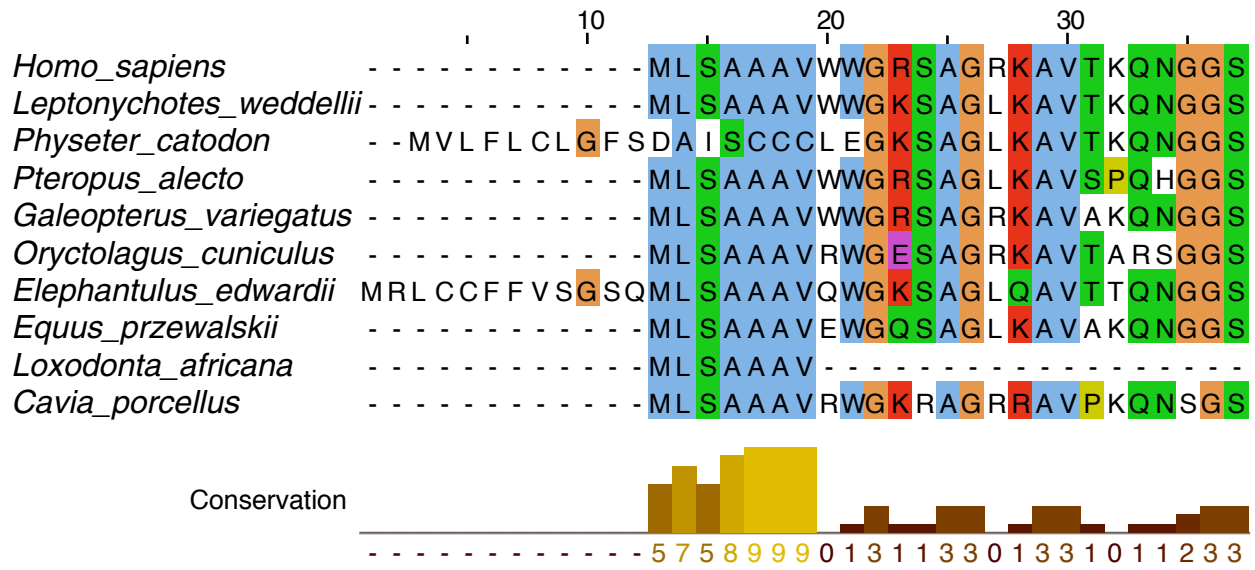
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ENSG00000112319 (EYA4)



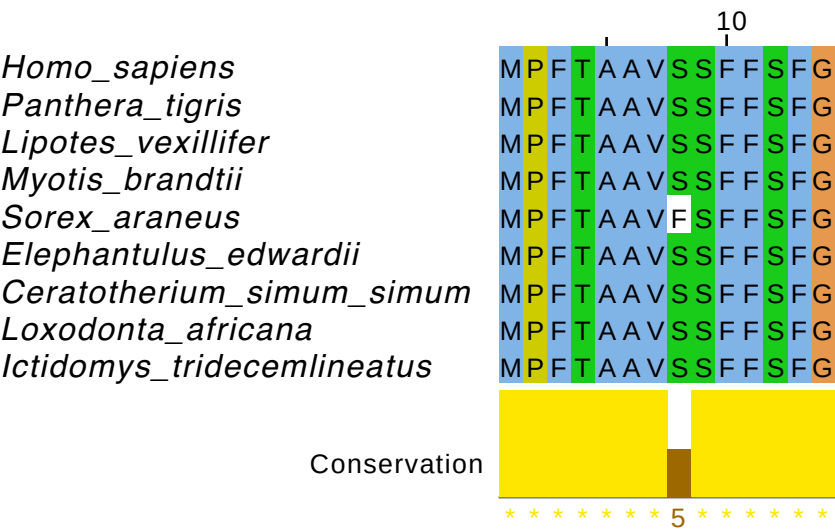
HG0512.2

ENSG00000104313 (EYA1)



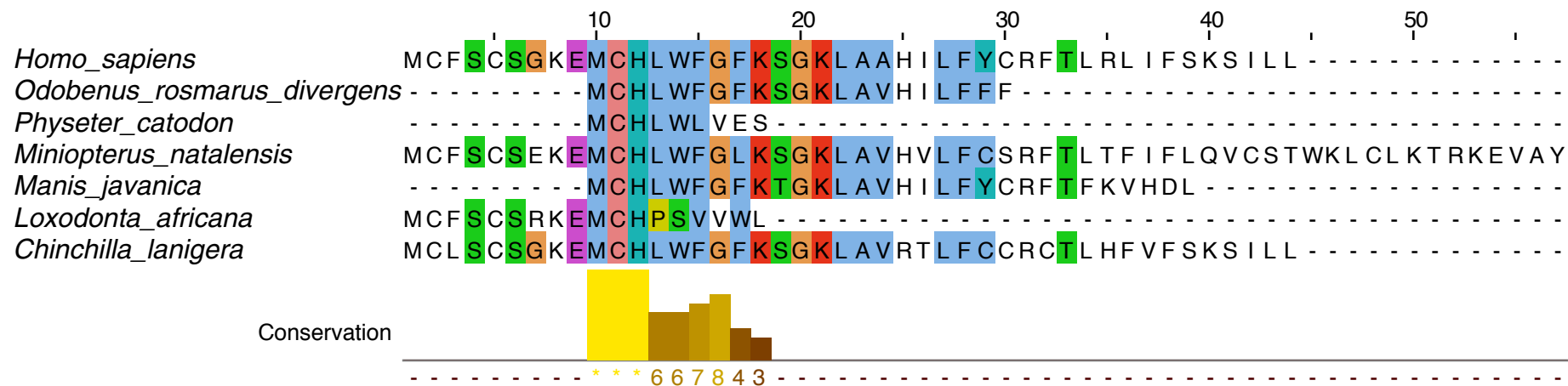
HG0512.3

ENSG00000104313 (EYA1)



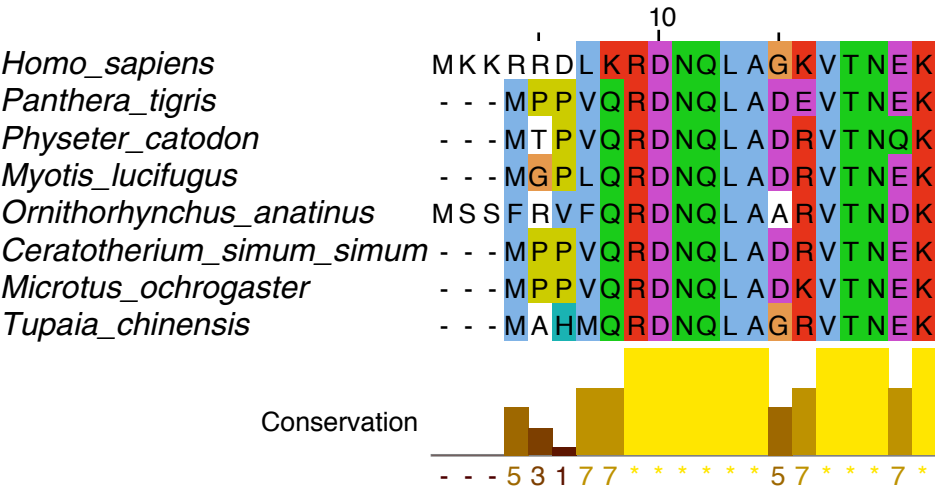
HG0513

ENSG00000126860 (EVI2A)



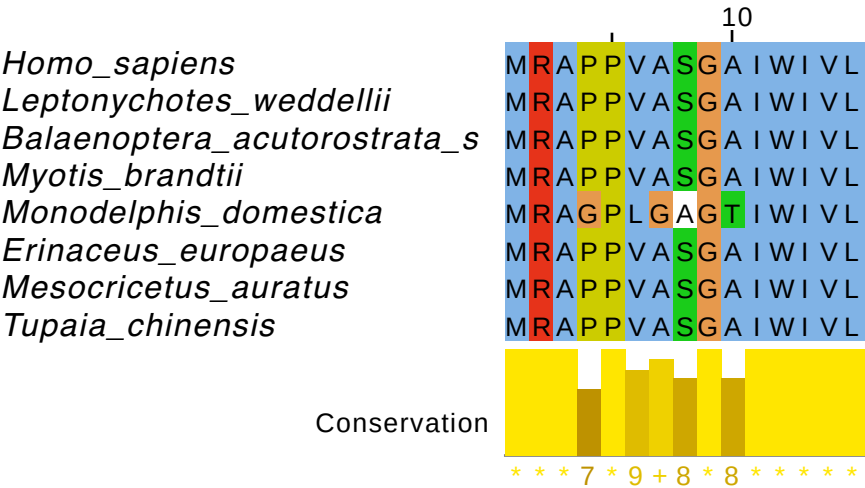
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ENSG00000147570 (DNAJC5B)



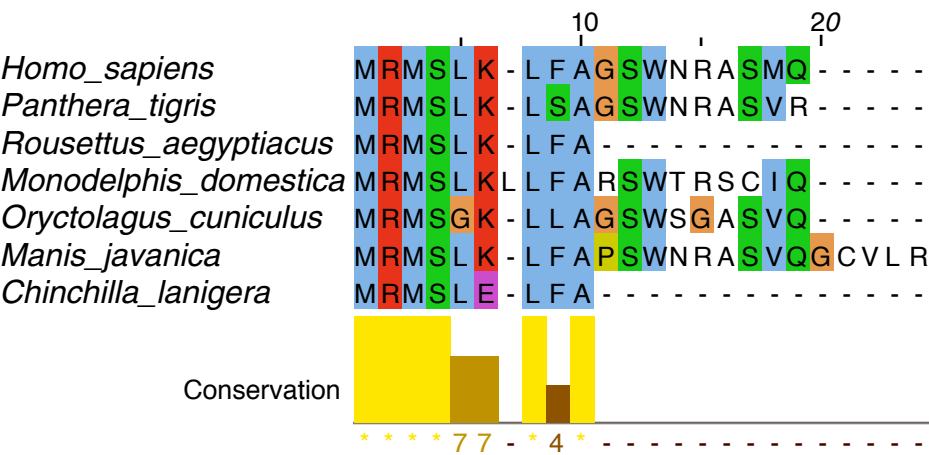
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ENSG00000170471 (RALGAPB)



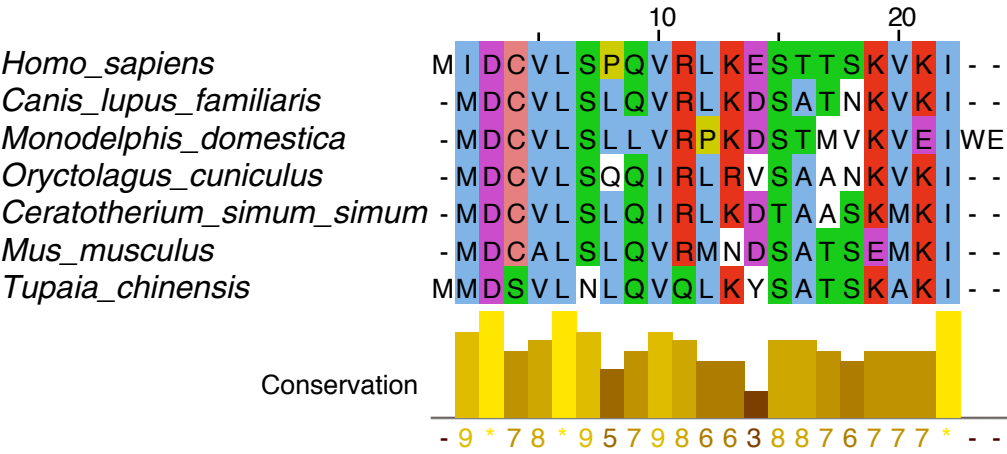
HG0516

ENSG00000041515 (MYO16)



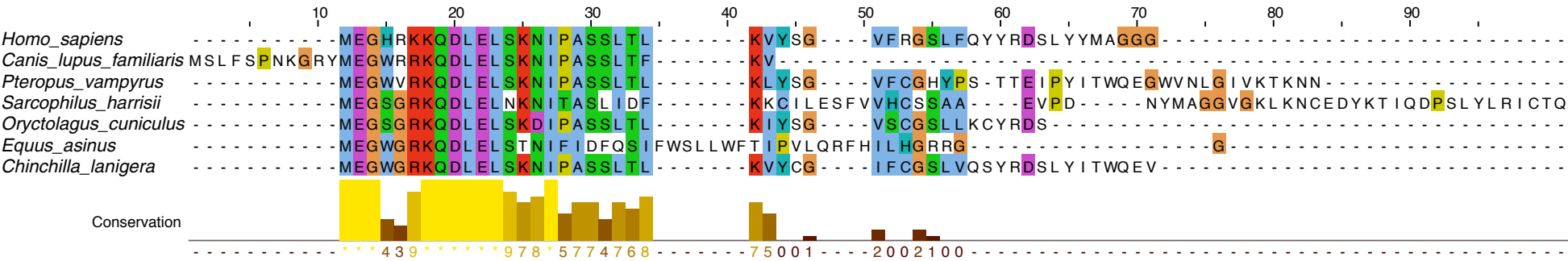
HG0517

ENSG00000086717 (PPEF1)



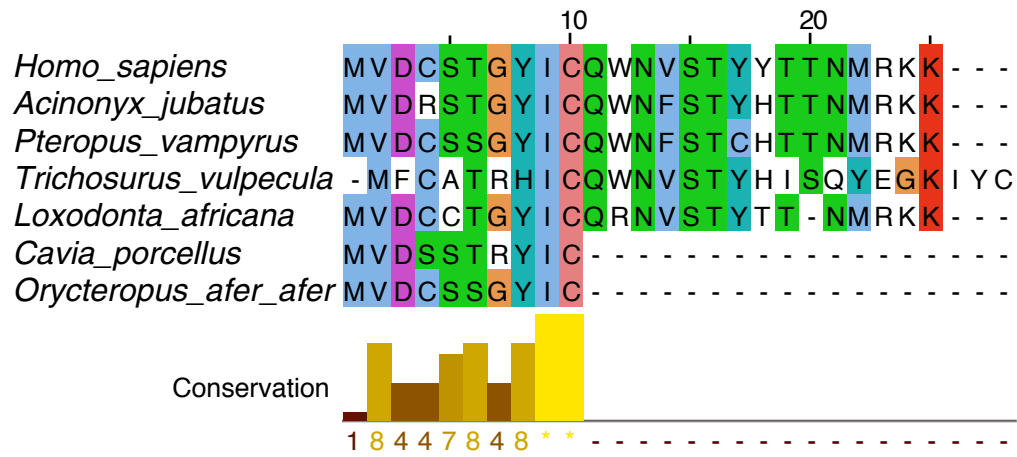
HG0518

ENSG00000111254 (AKAP3)



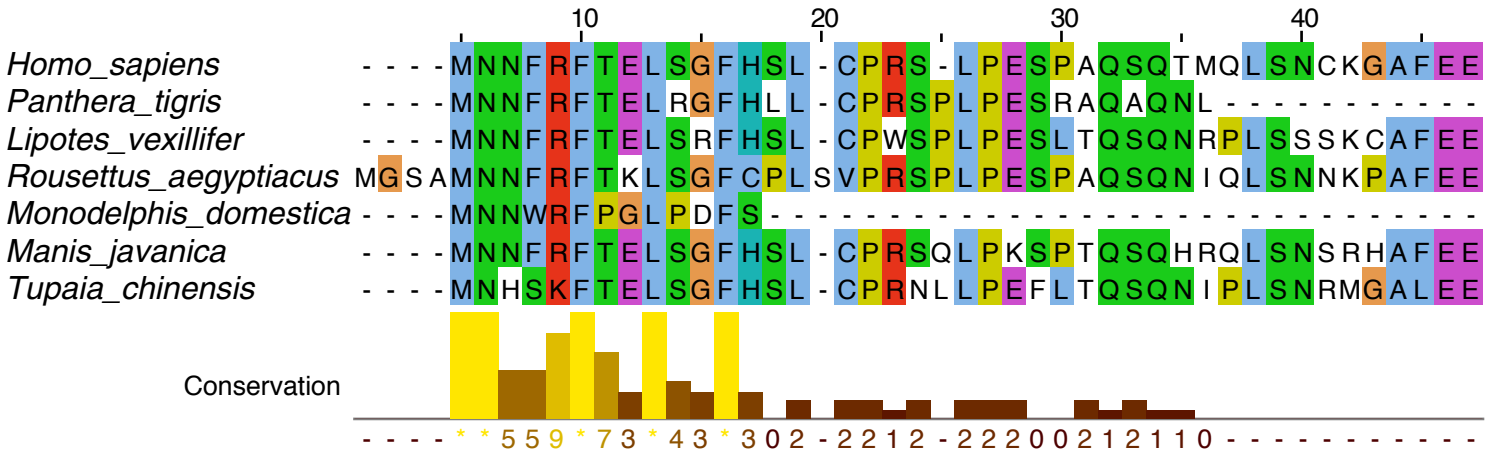
HG0519

ENSG00000127074 (RGS13)



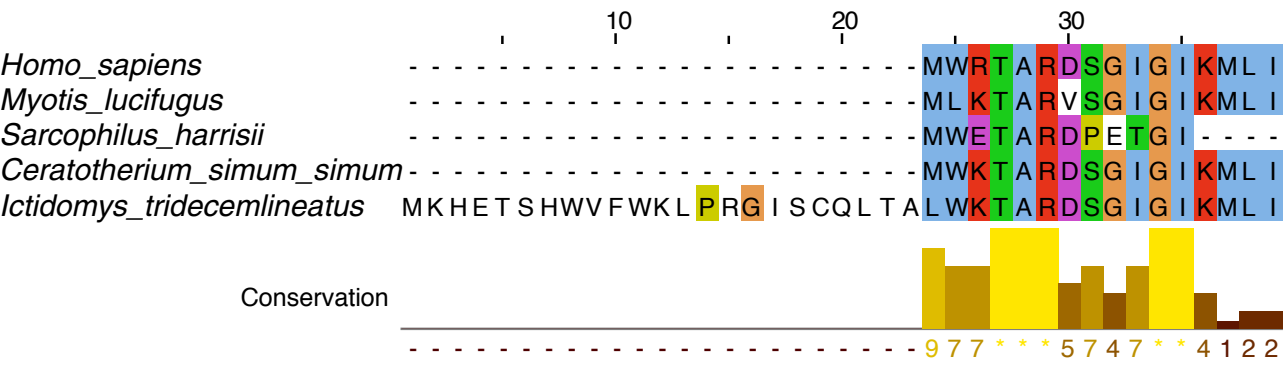
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ENSG00000197415 (VEPH1)



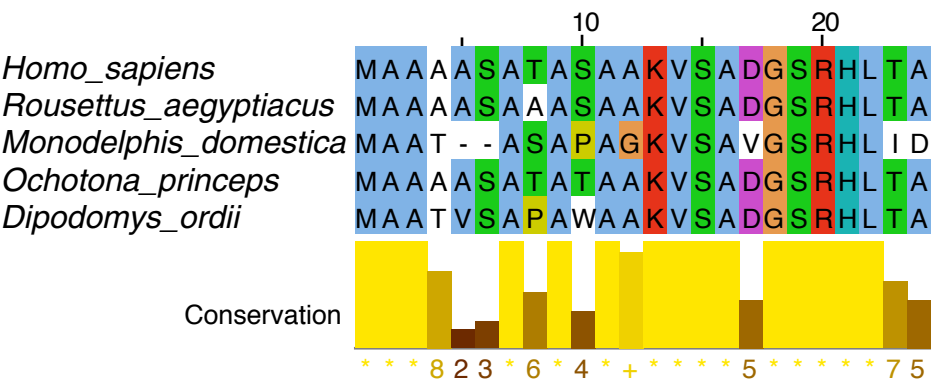
HG0521

ENSG00000038274 (MAT2B)



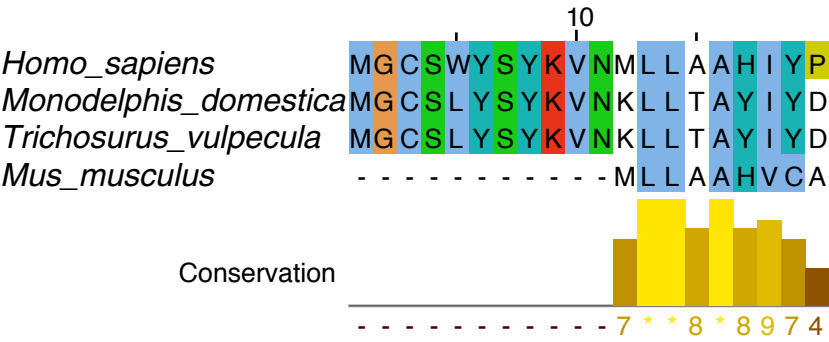
HG0522

ENSG00000140396 (NCOA2)



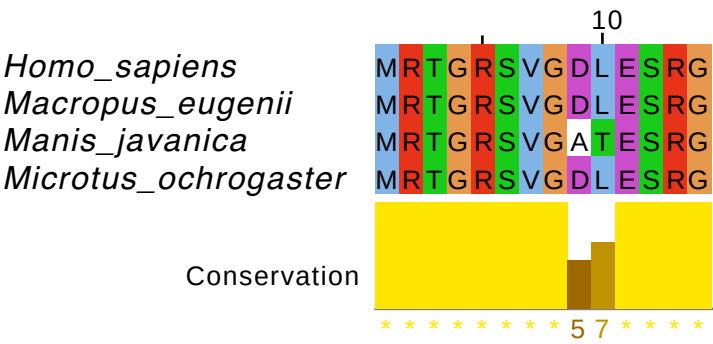
HG0523

ENSG00000075213 (SEMA3A)



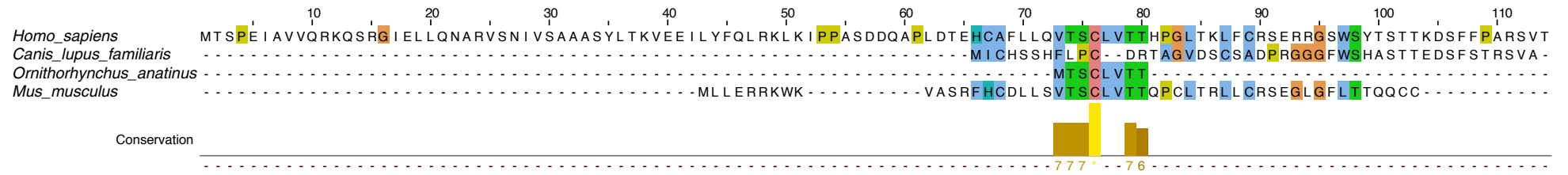
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ENSG00000107929 (LARP4B)



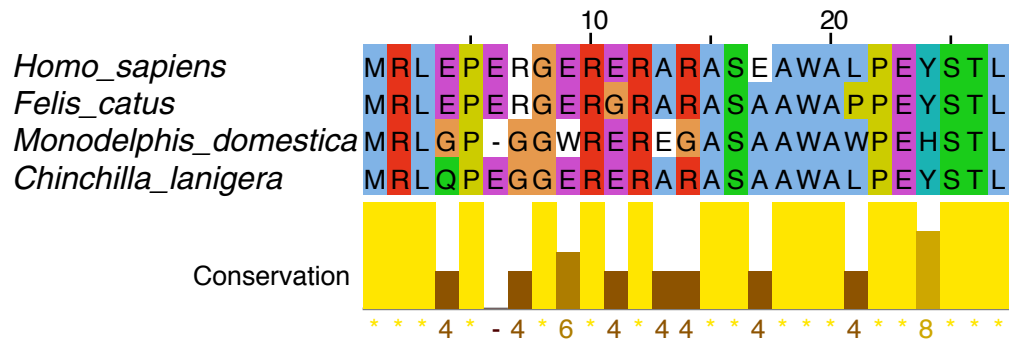
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ENSG00000136167 (LCP1)



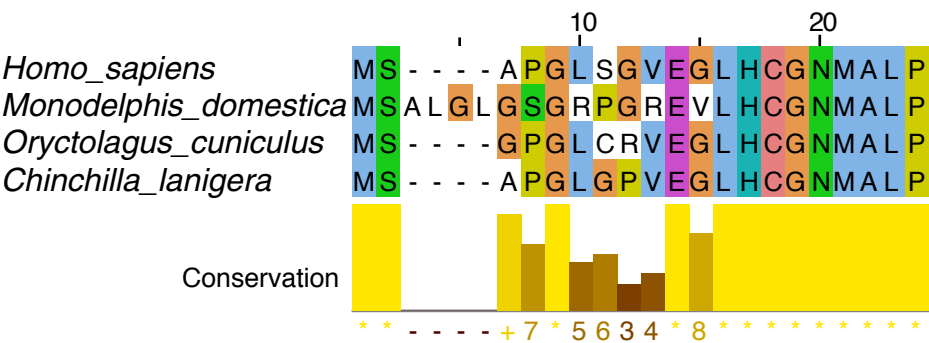
HG0526

ENSG00000143569 (UBAP2L)



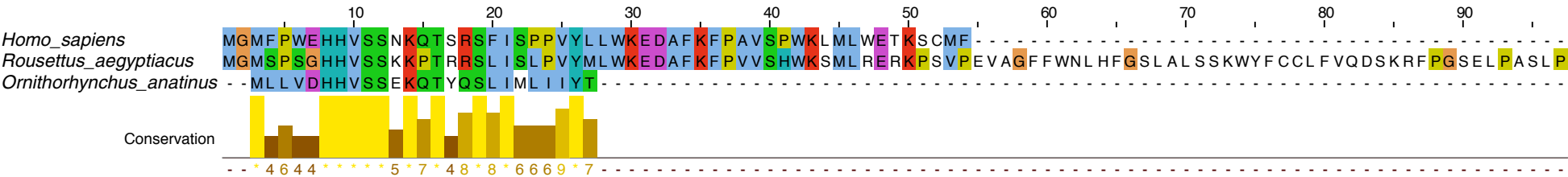
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ENSG00000198382 (UVRAG)



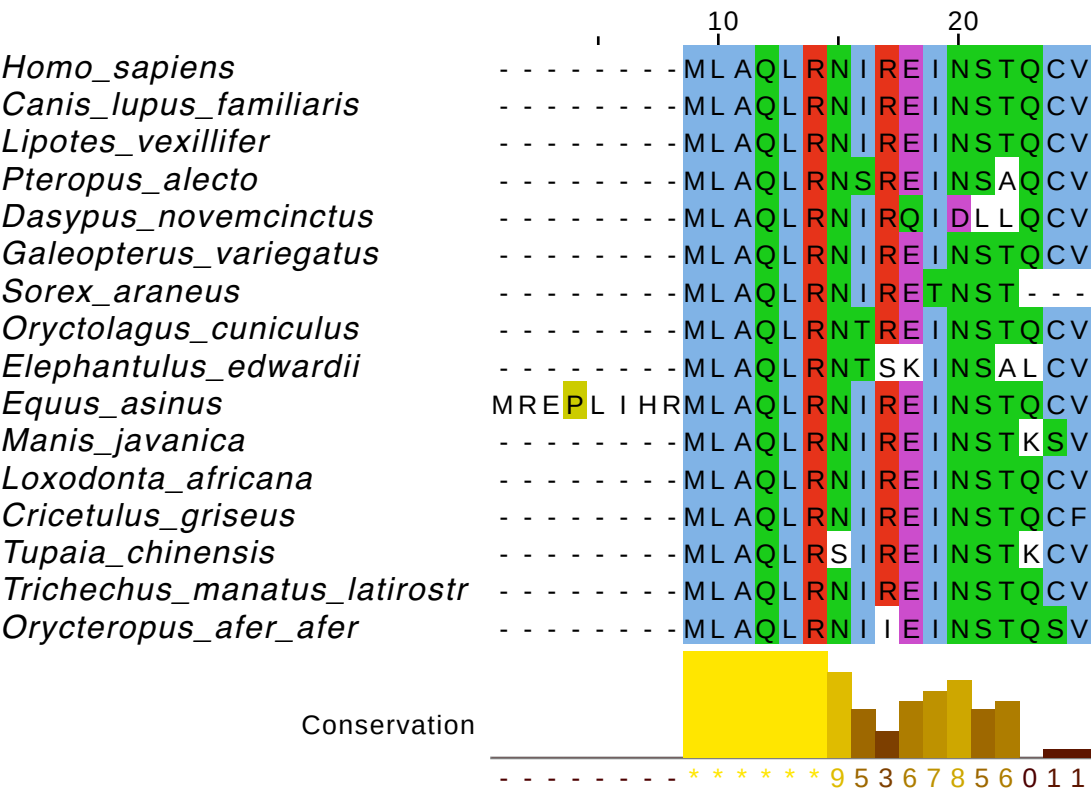
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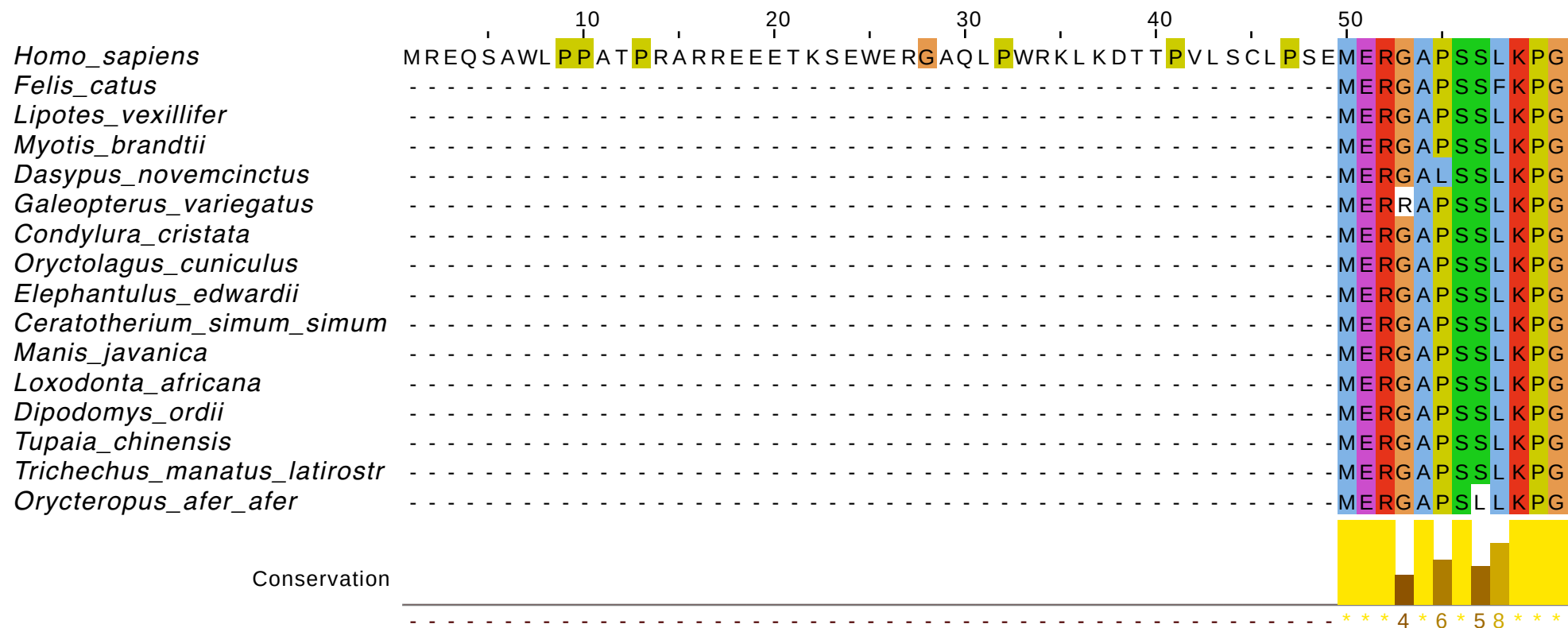


HG0529

ENSG00000112851 (ERBIN)

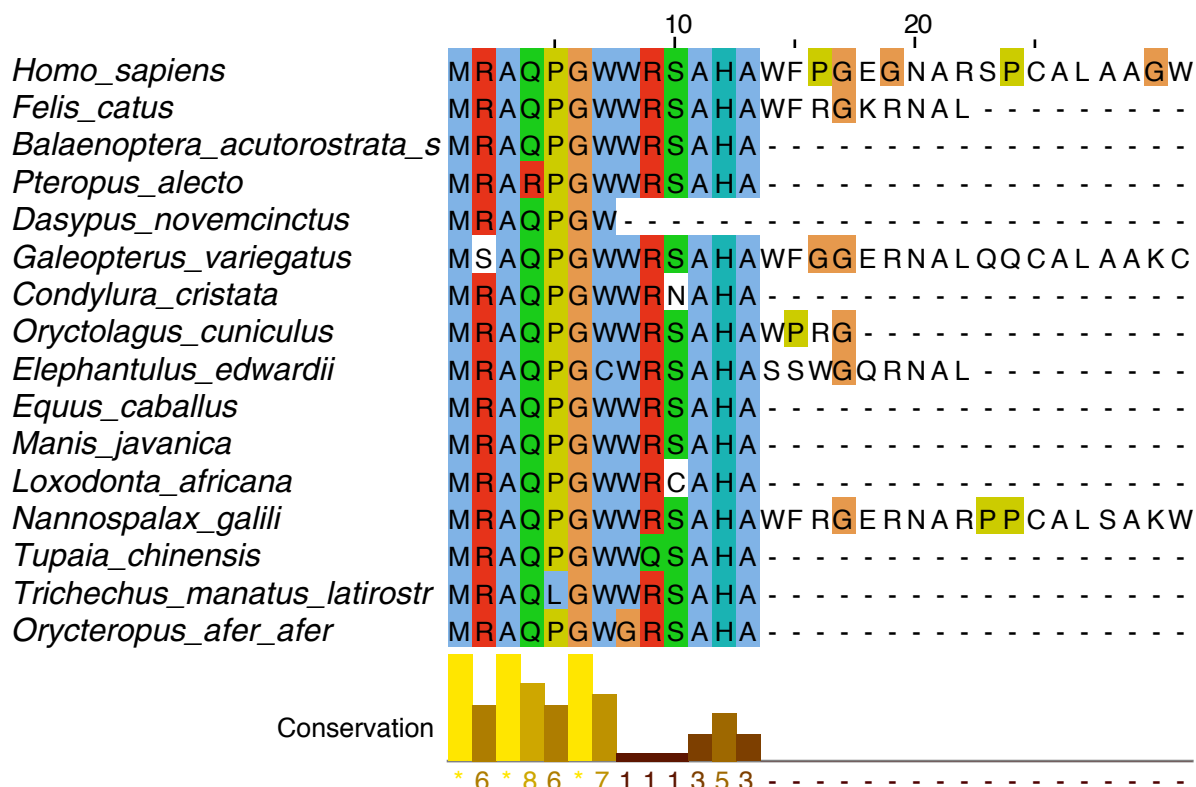


ENSG00000128594 (LRRC4)

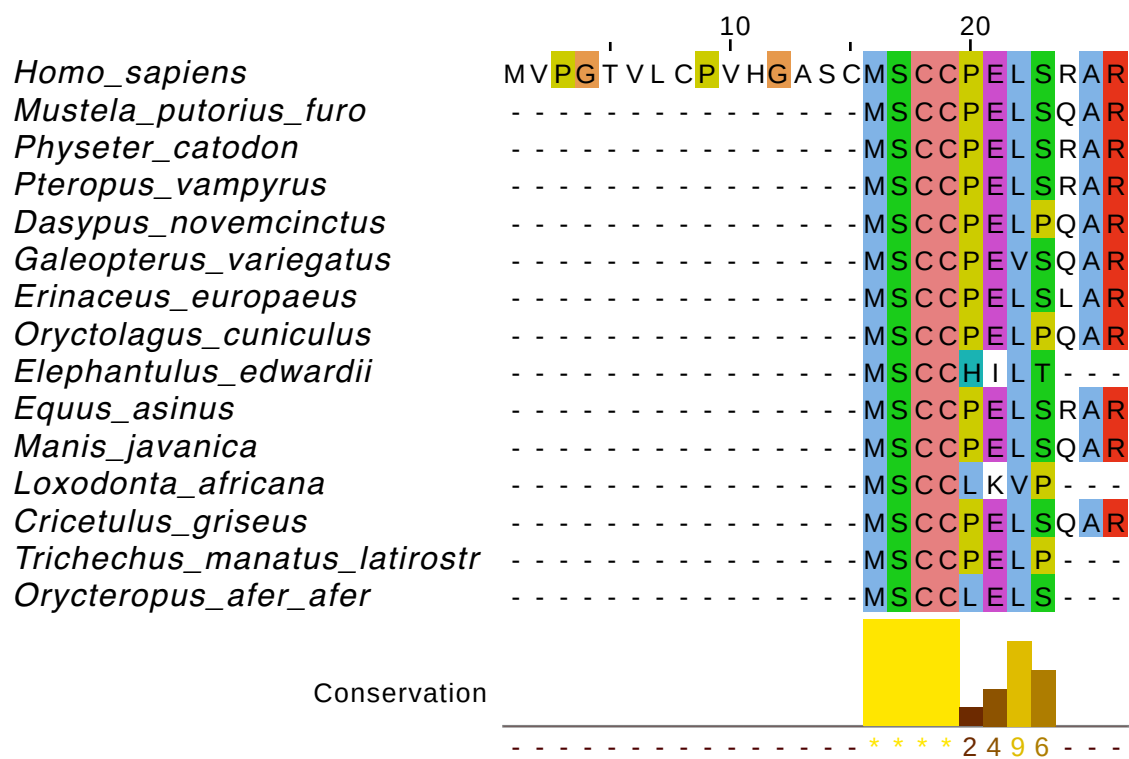


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ENSG00000146834 (MEPCE)

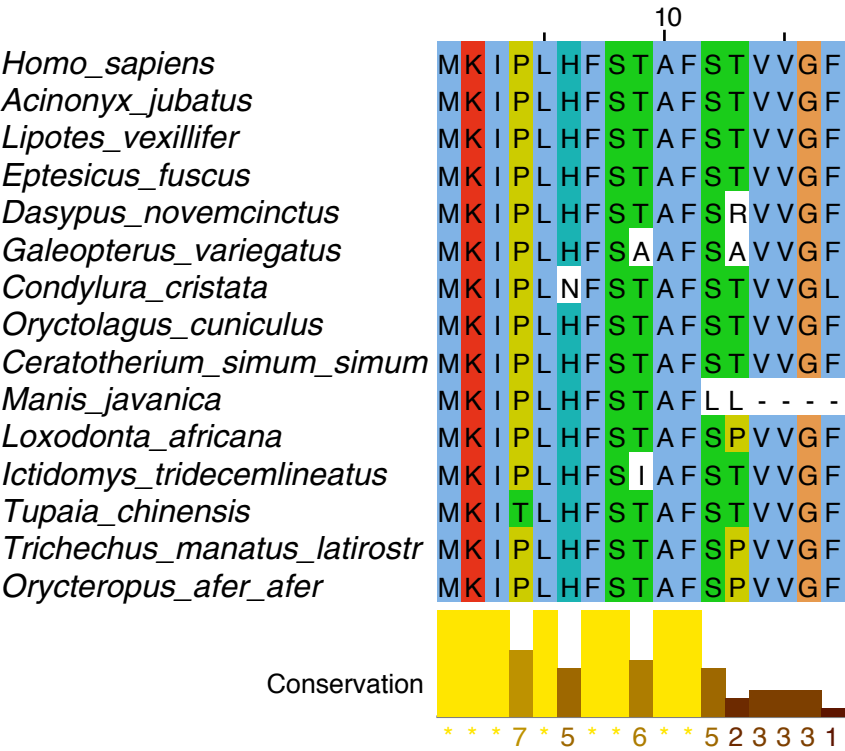


ENSG00000105221 (AKT2)



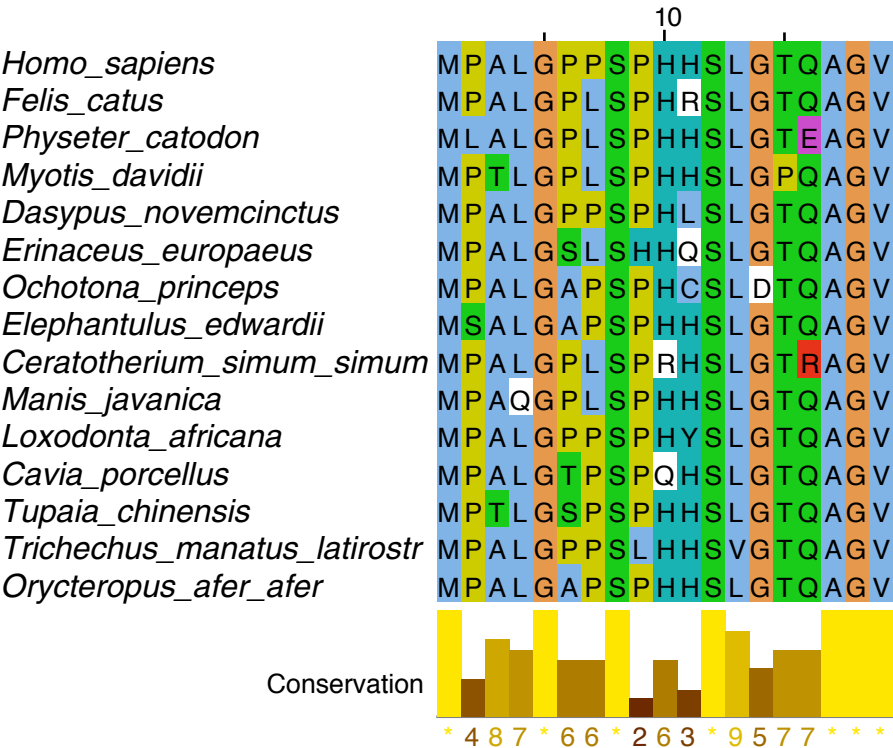
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ENSG00000114209 (PDCD10)



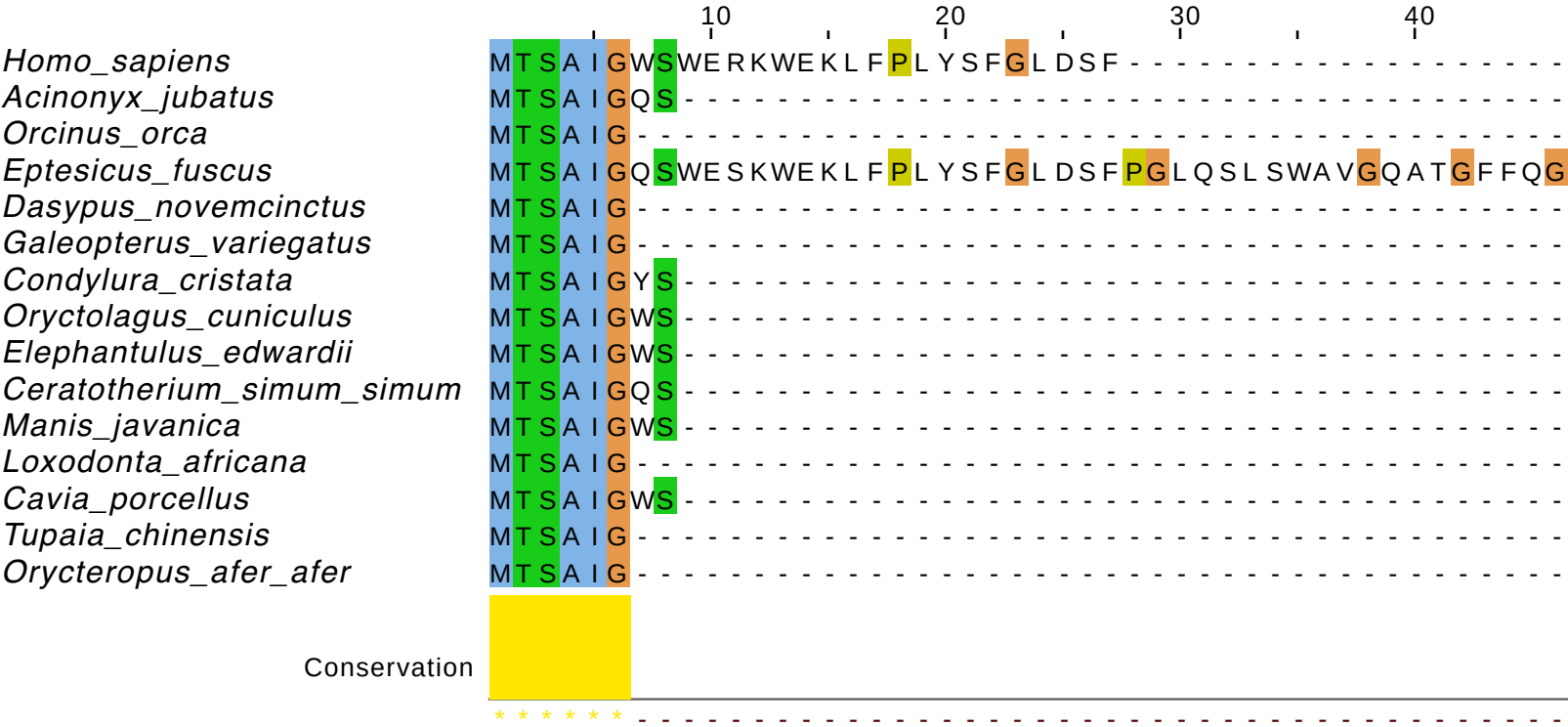
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ENSG00000117408 (IPO13)



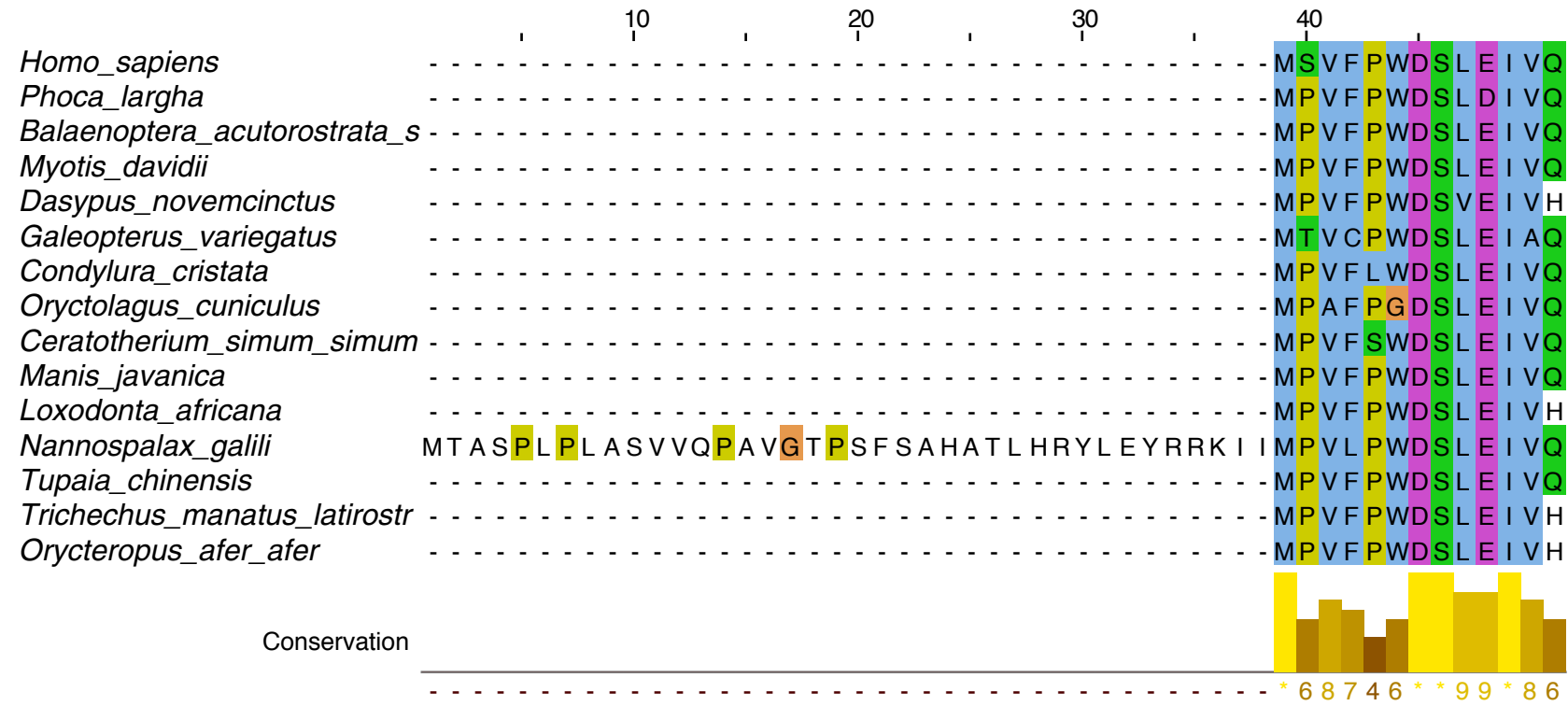
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ENSG00000118407 (FILIP1)



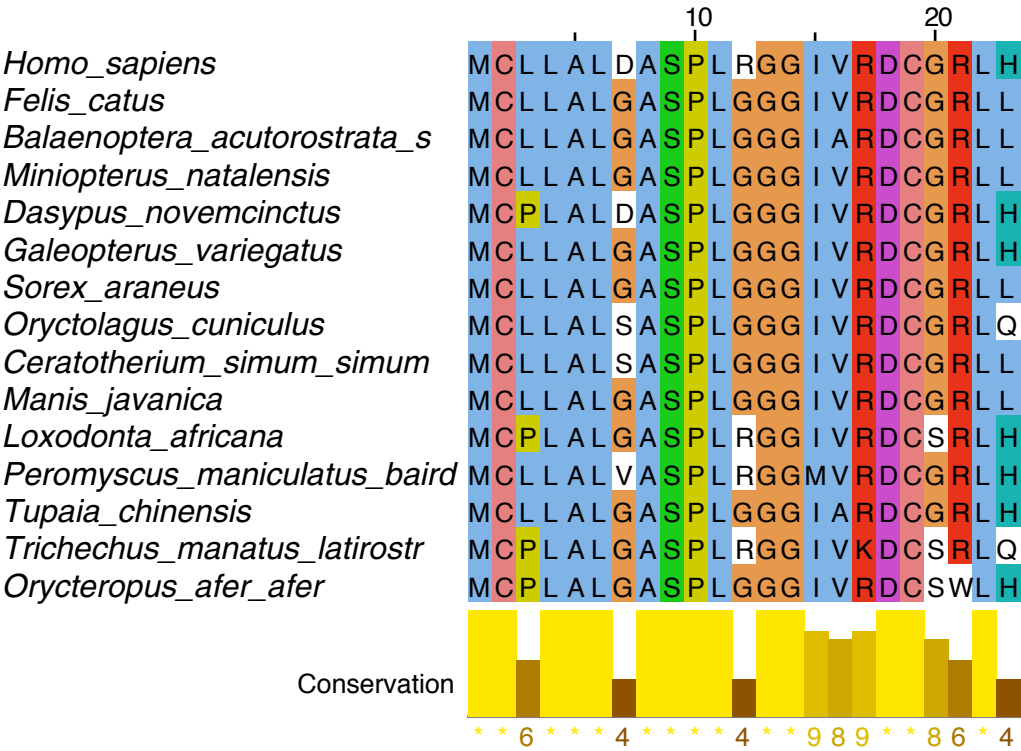
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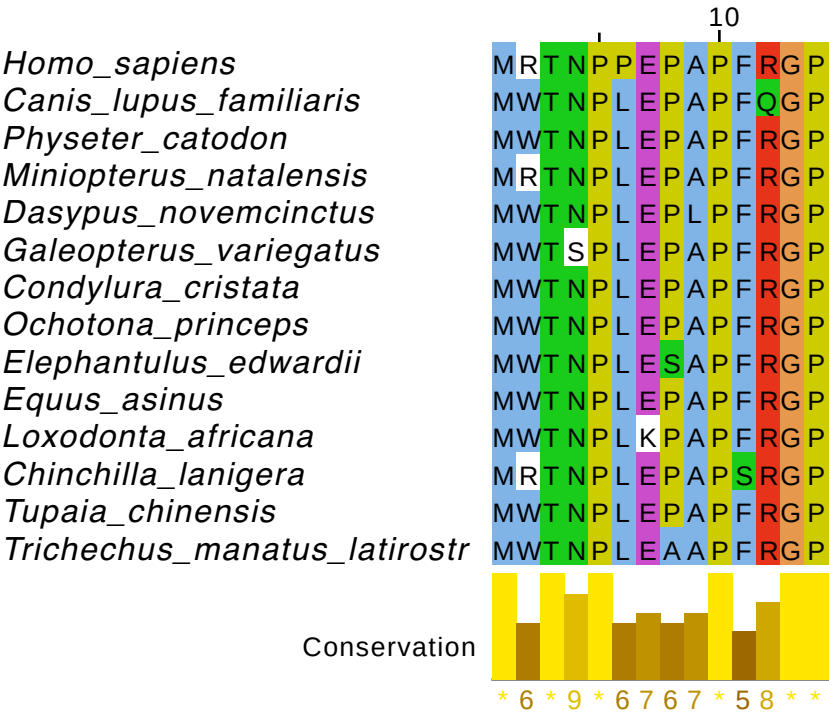
ENSG00000181751 (C5orf30)



HG0537

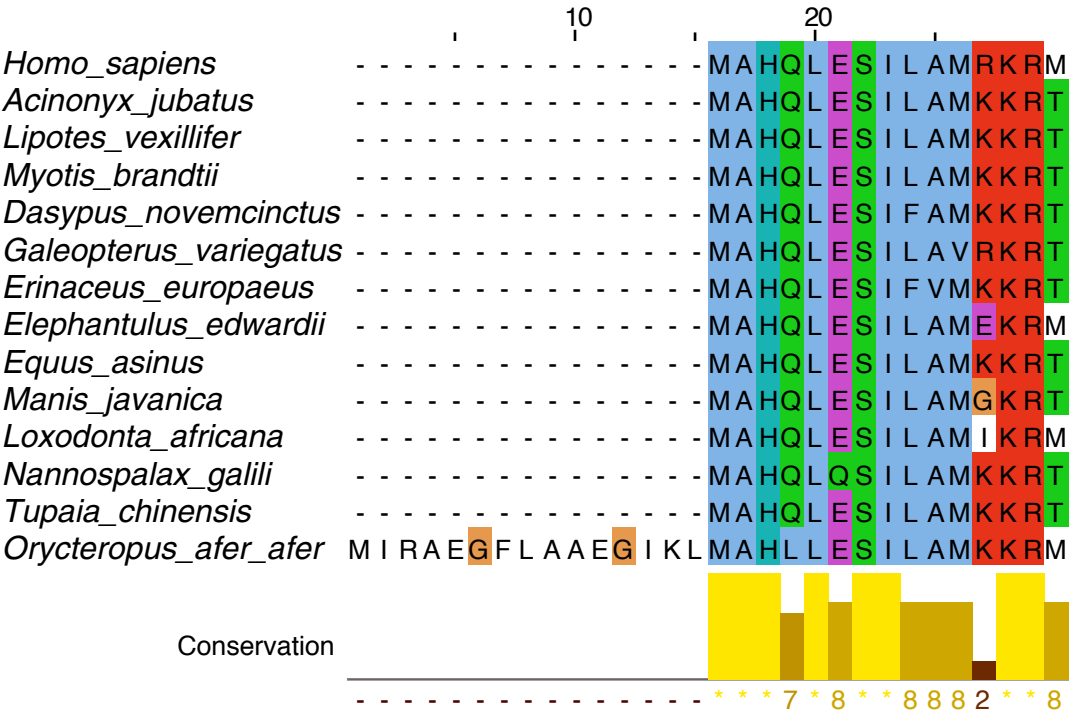
ENSG00000184481 (FOXO4)



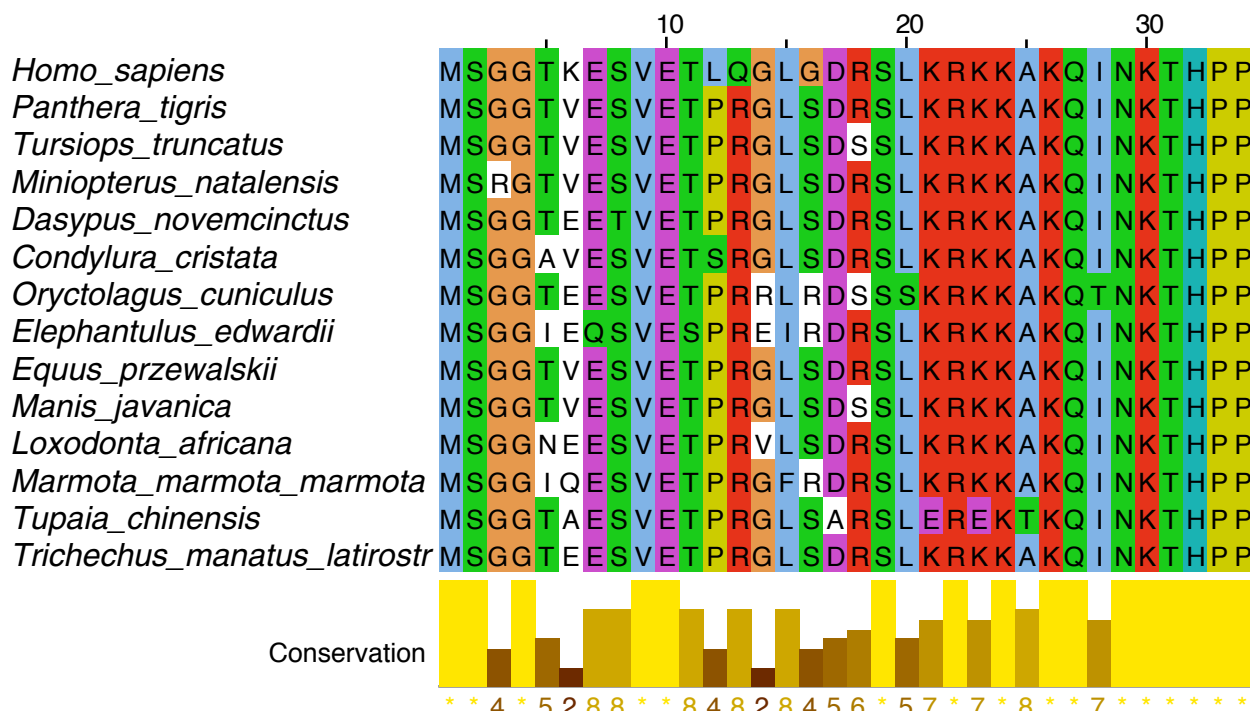


HG0539

ENSG00000115966 (ATF2)

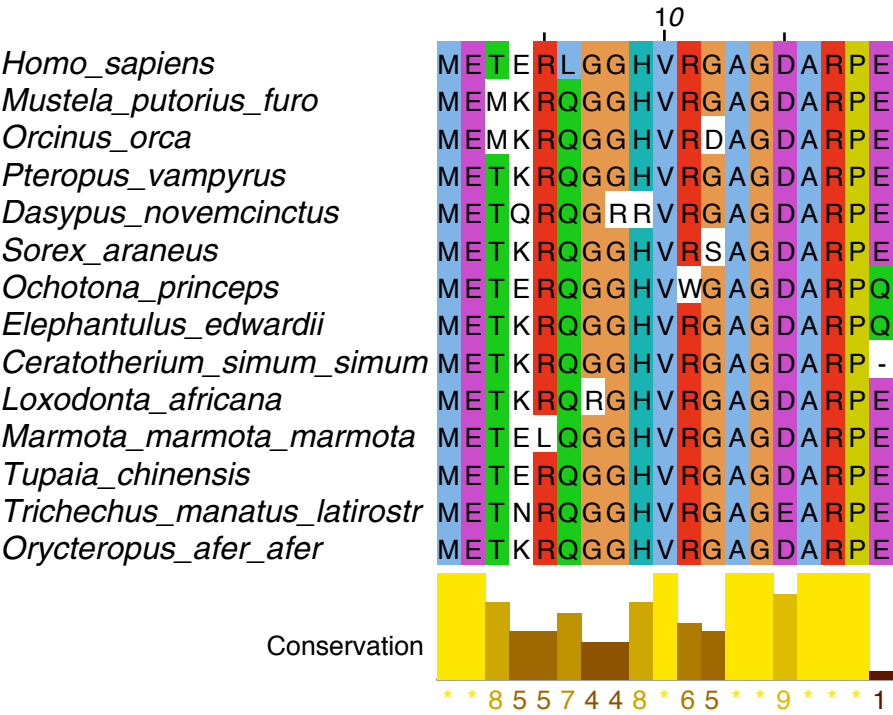


ENSG00000120519 (SLC10A7)



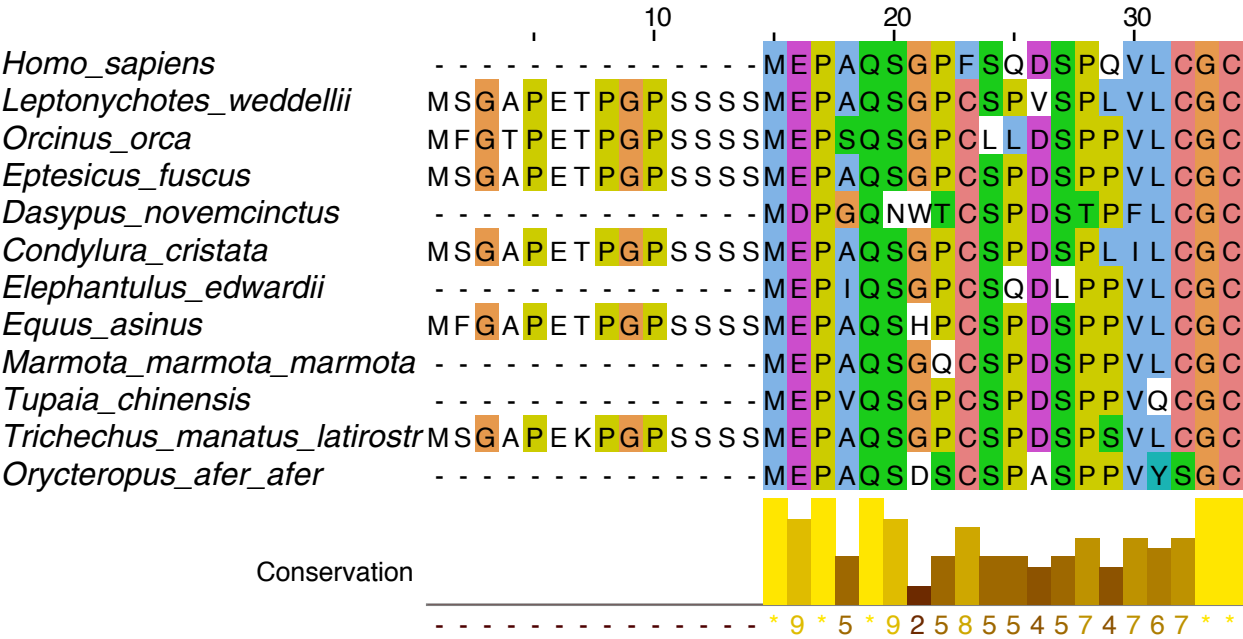
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ENSG00000122584 (NXPH1)



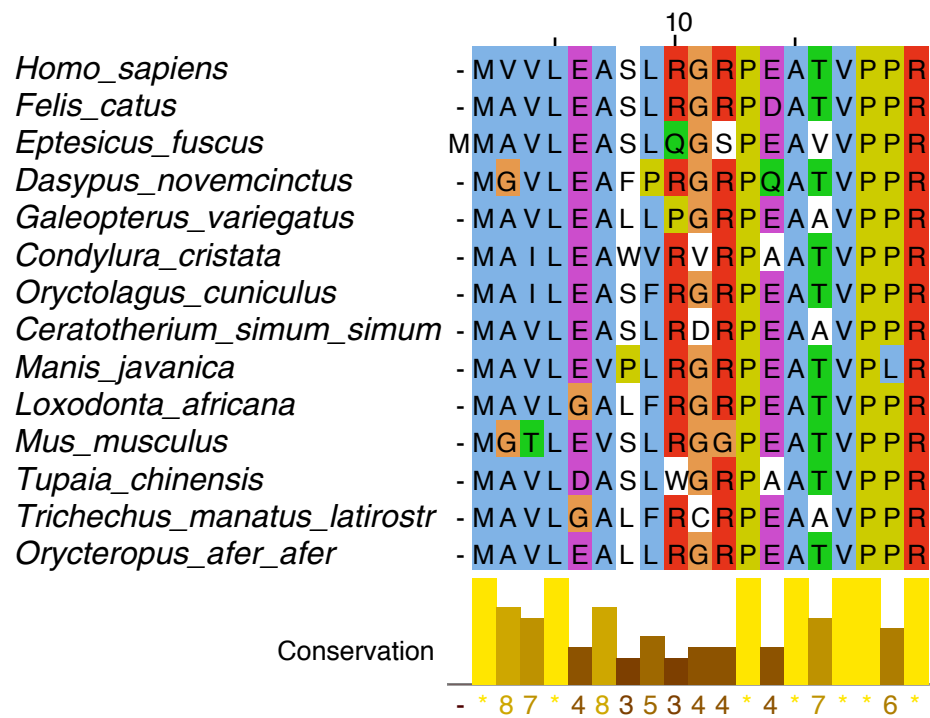
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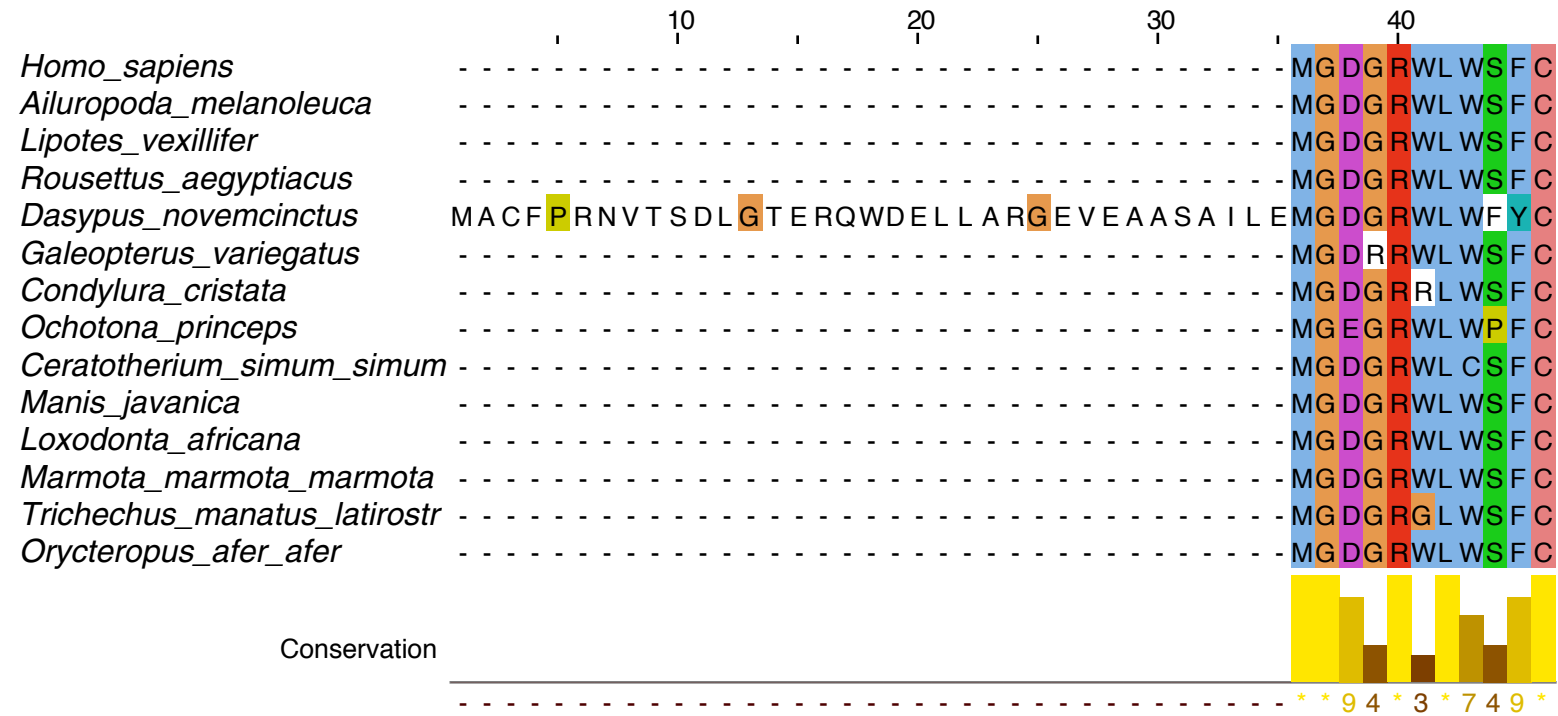


HG0542

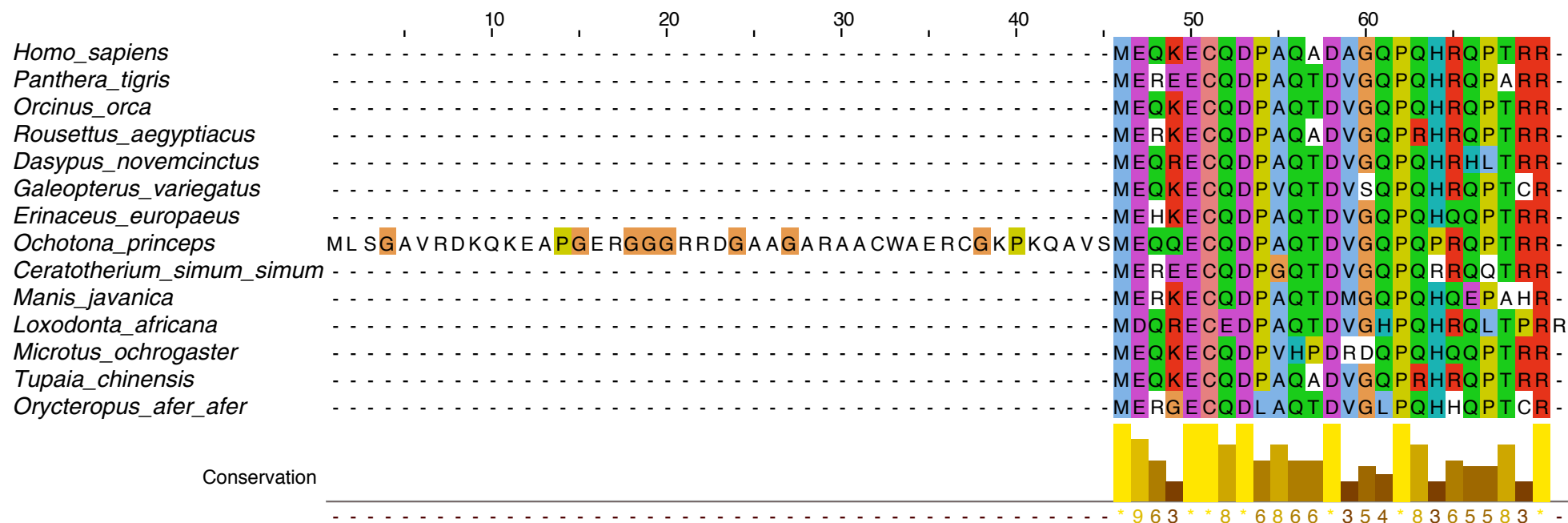
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HG0543
ENSG00000131931 (THAP1)

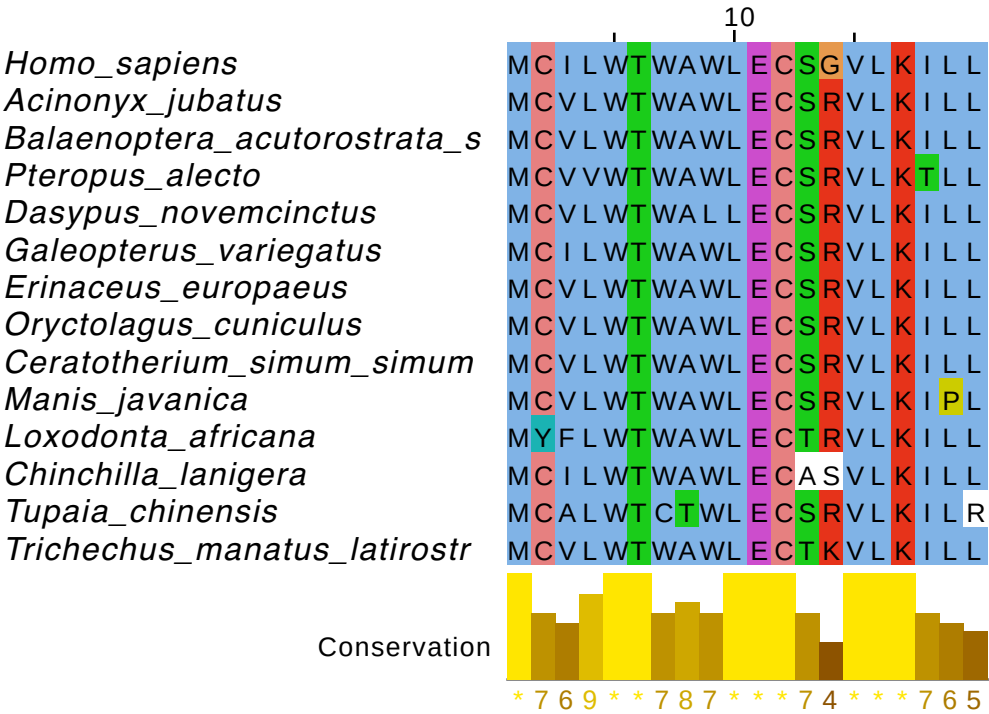


ENSG00000136802 (LRRC8A)

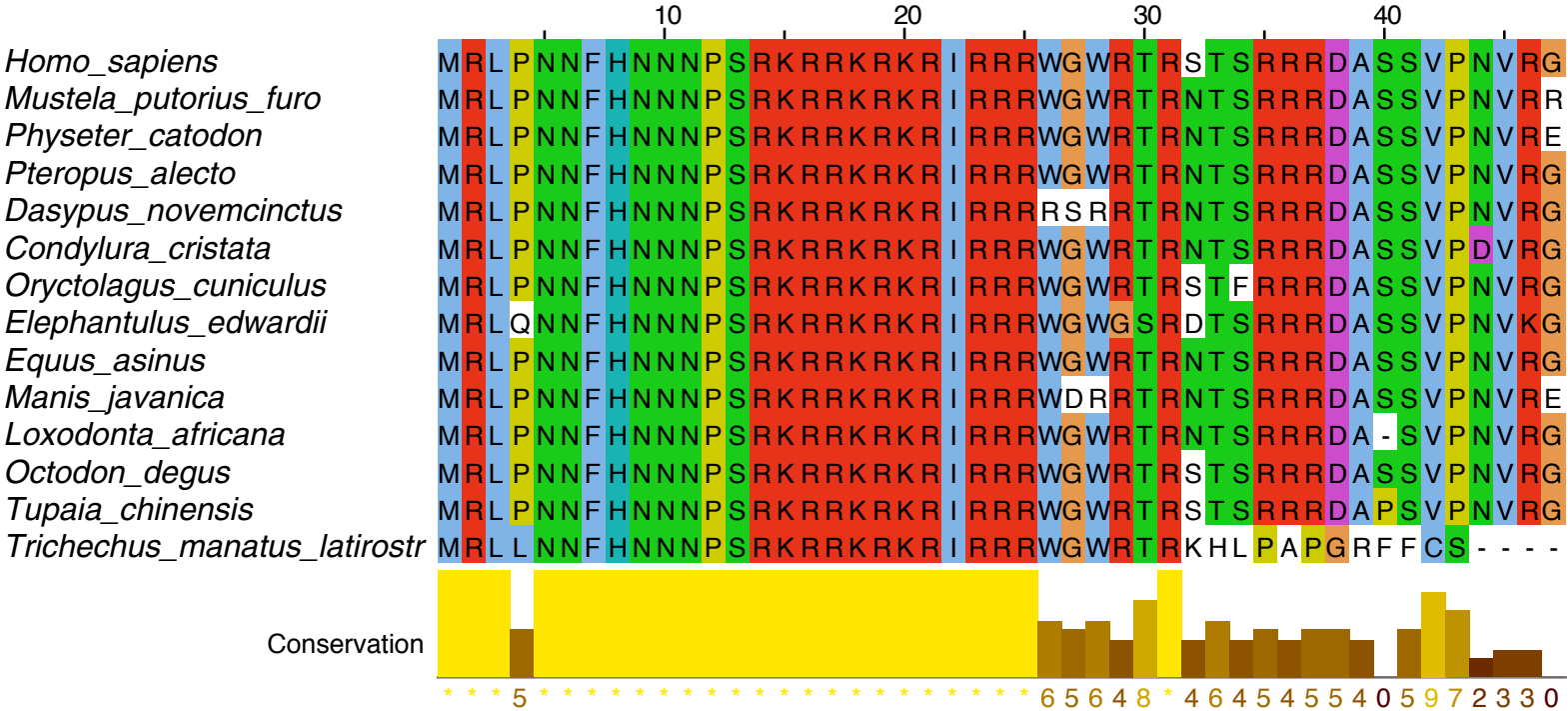


HG0545

ENSG00000142784 (WDTC1)

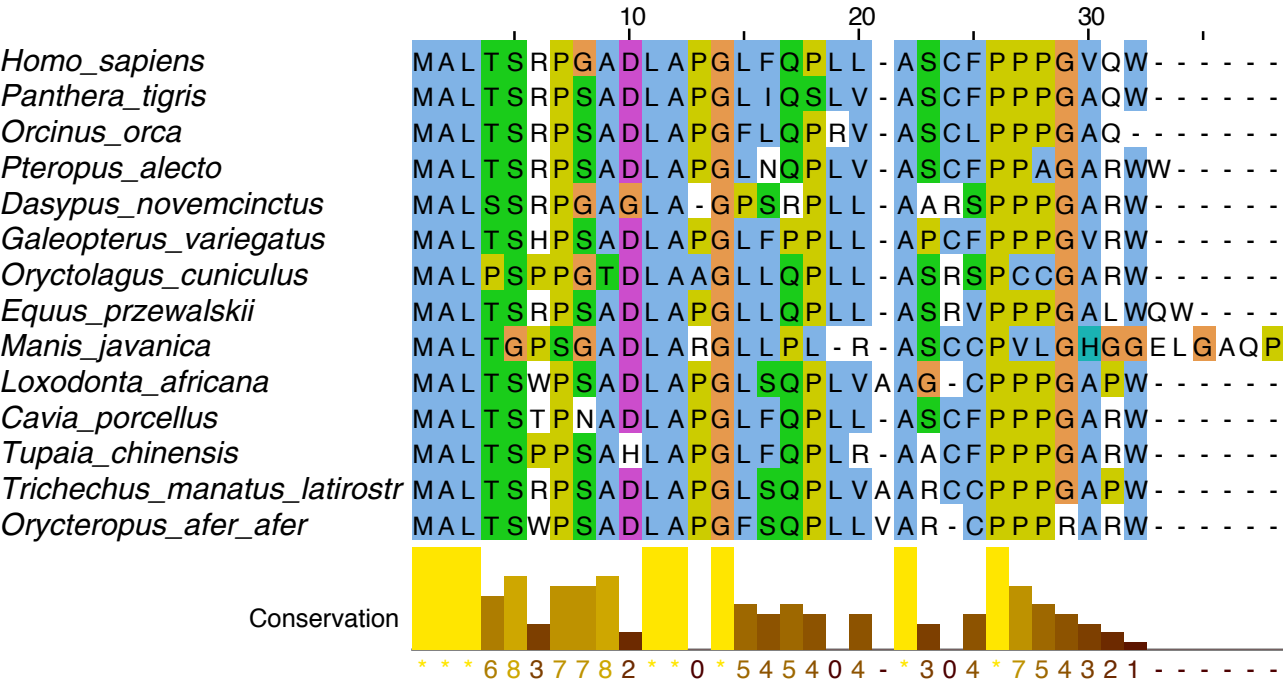


HG0546
ENSG00000148143 (ZNF462)

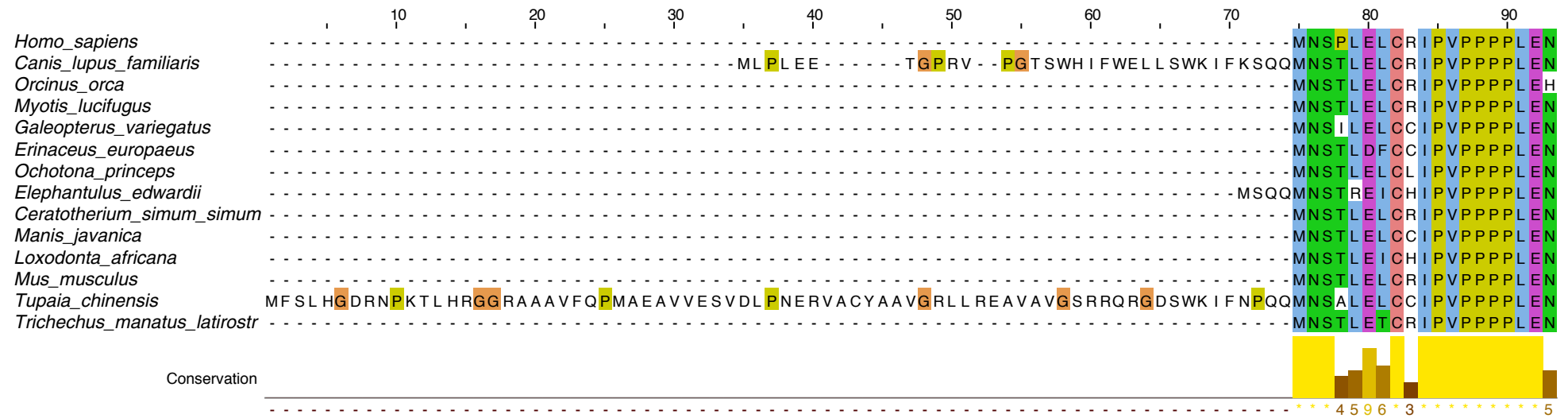


HG0547

ENSG00000149596 (JPH2)

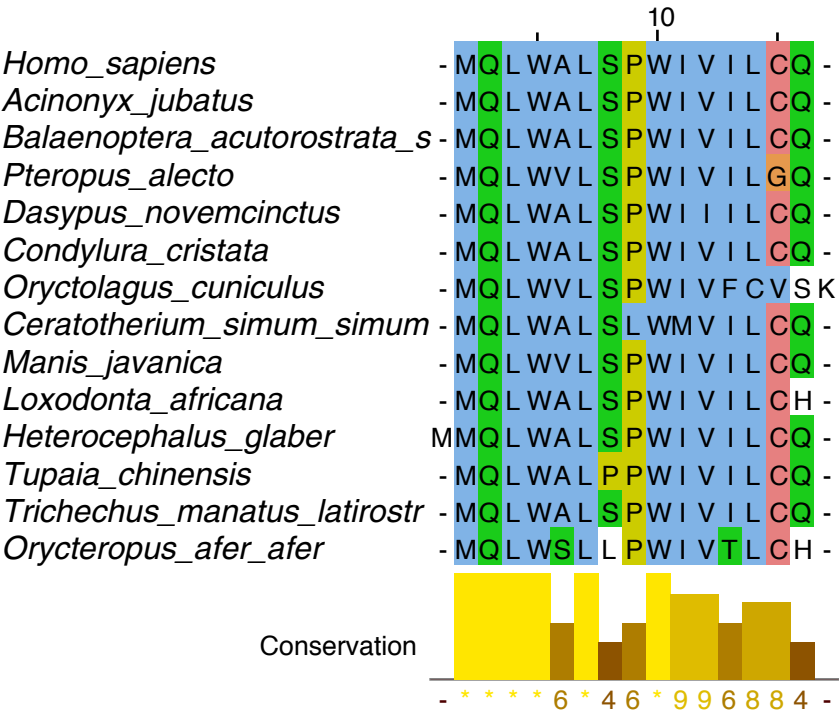


ENSG00000155744 (FAM126B)



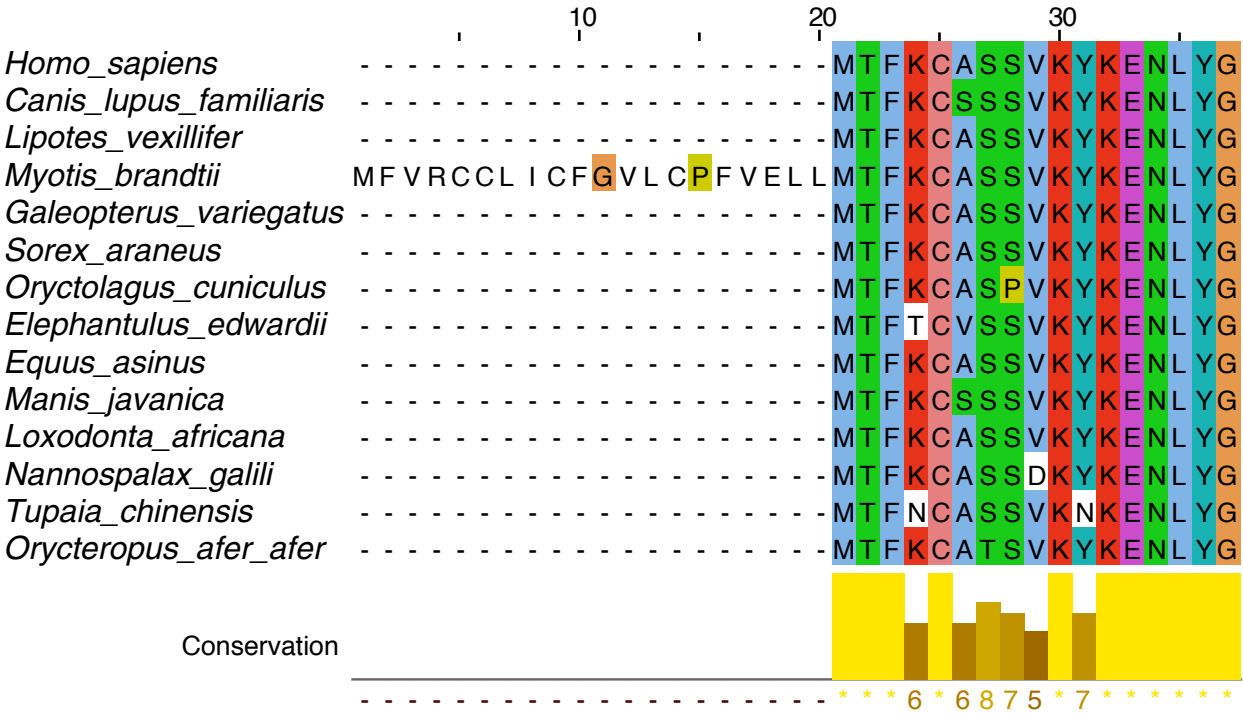
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ENSG00000156256 (USP16)



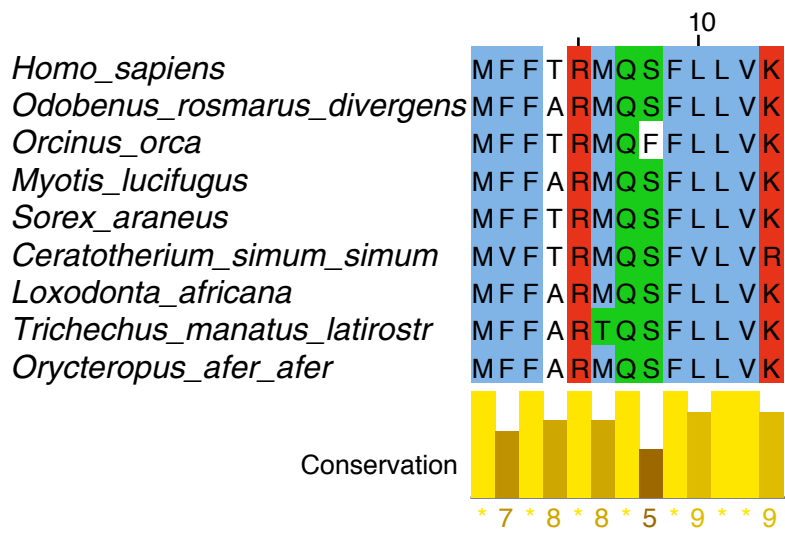
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ENSG00000156650 (KAT6B)



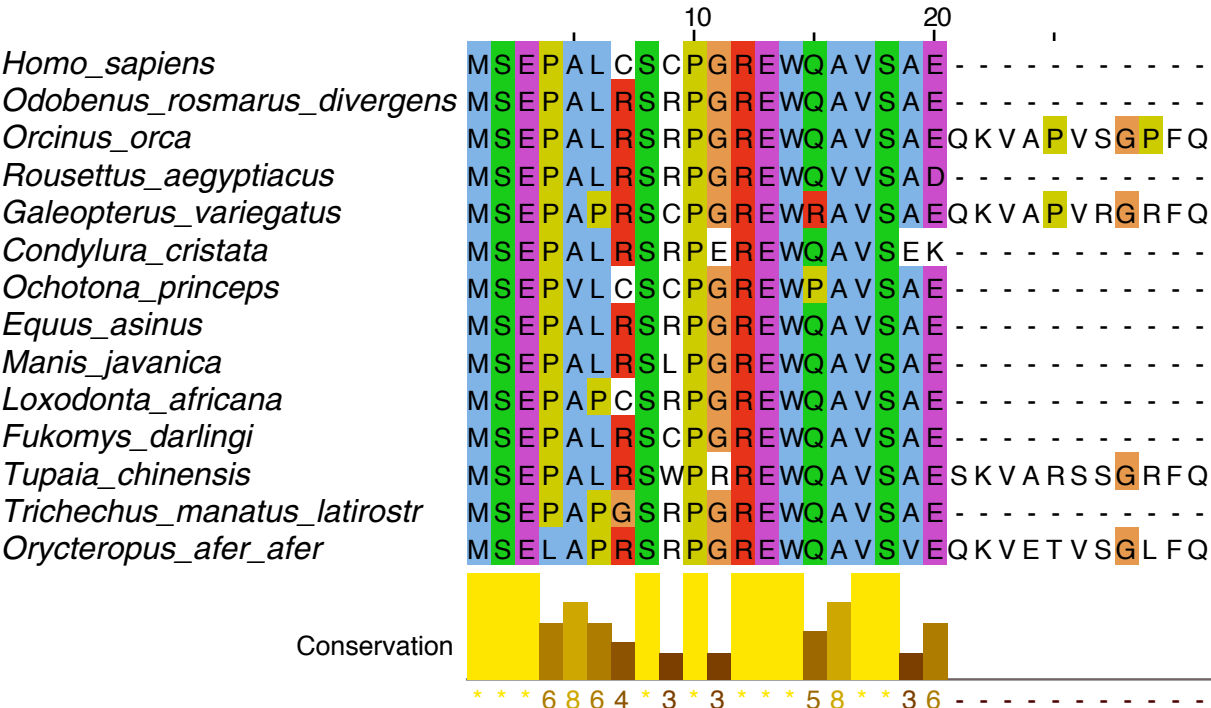
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ENSG00000156650 (KAT6B)



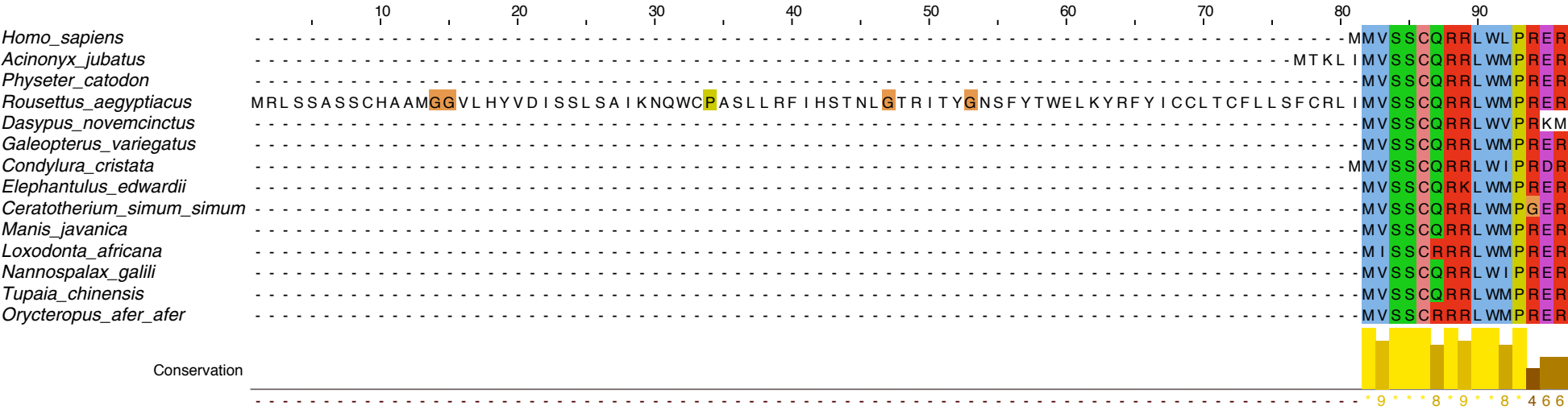
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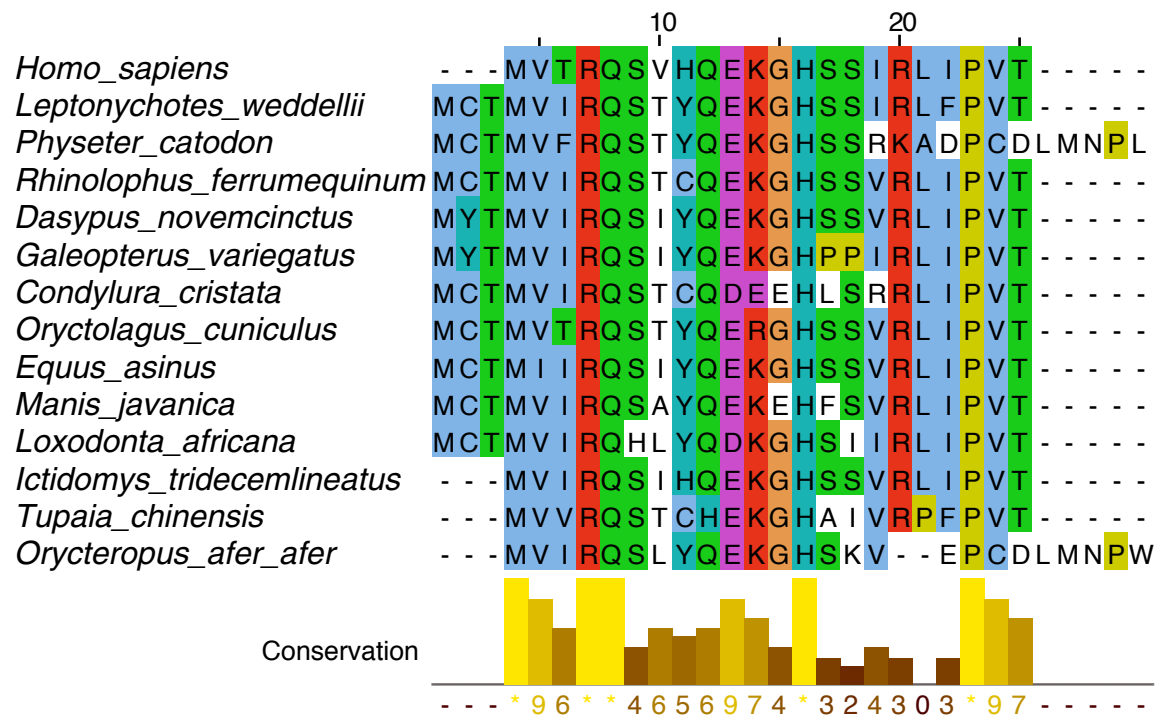
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ENSG00000169641 (LUZP1)



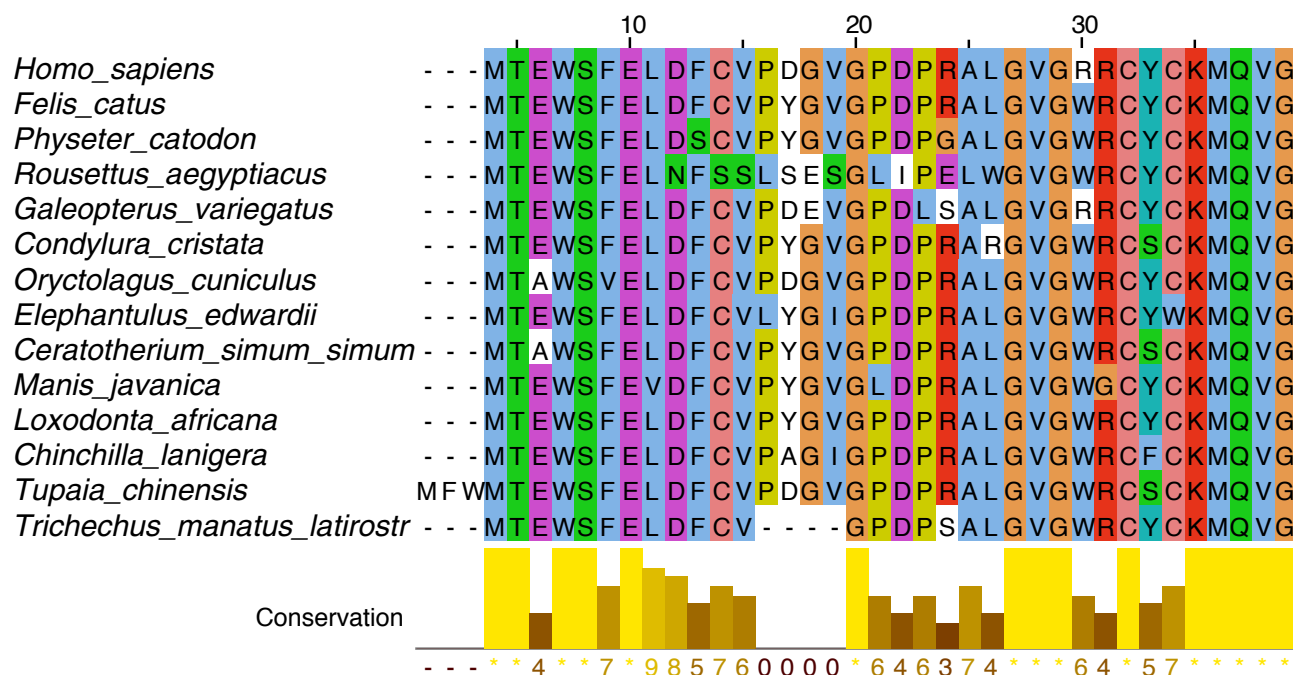
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ENSG00000183475 (ASB7)



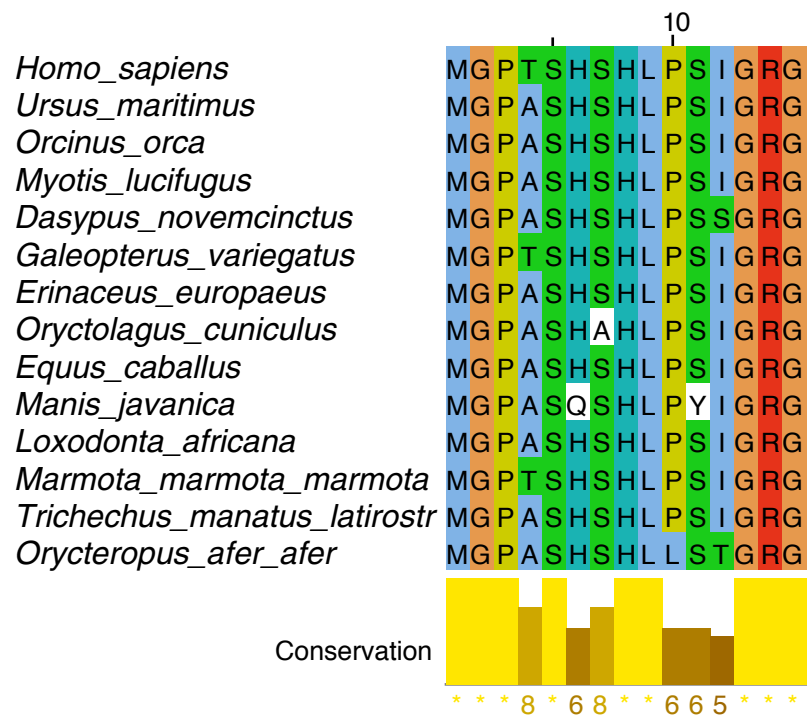
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ENSG00000196914 (ARHGEF12)

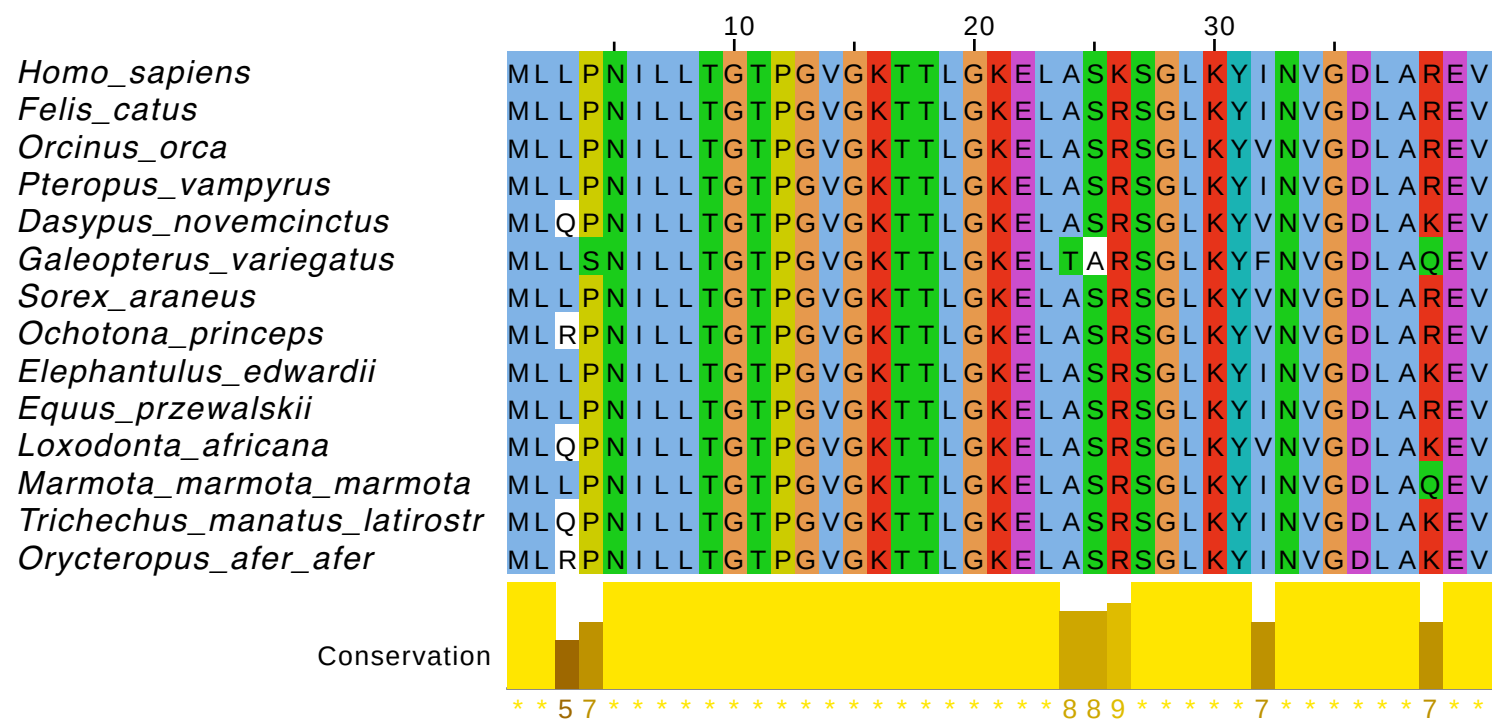


HG0555

ENSG00000204310 (AGPAT1)

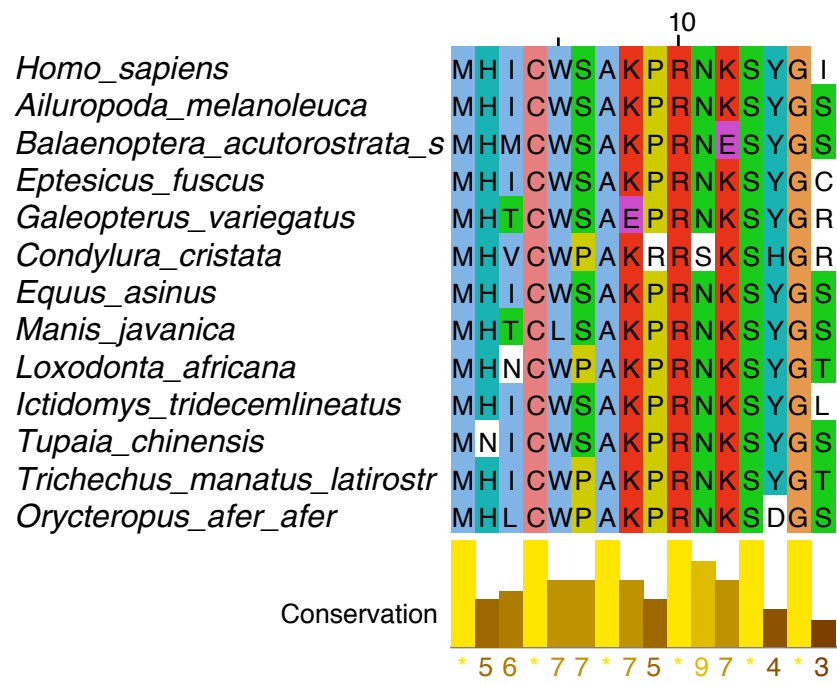


ENSG00000273841 (TAF9)



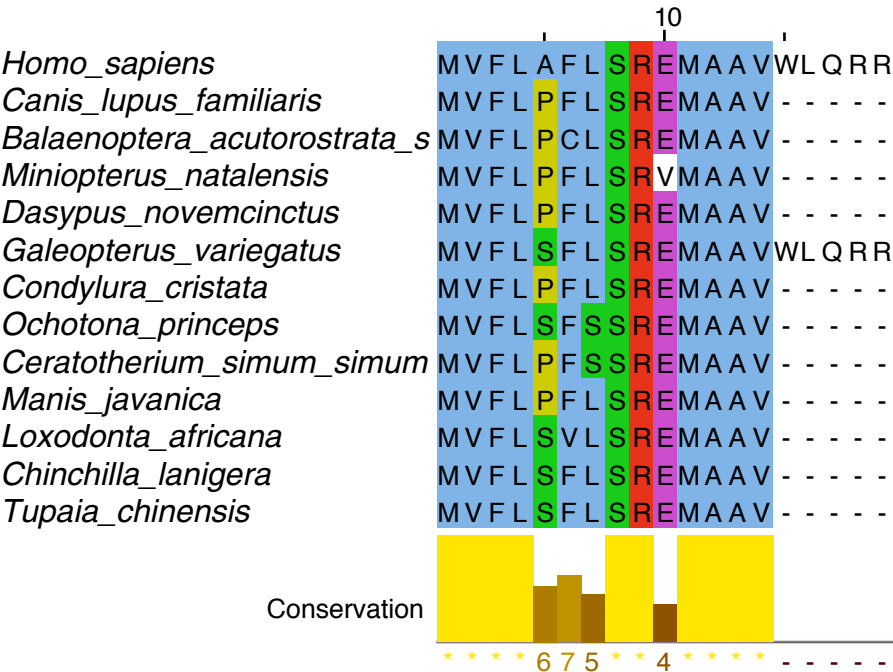
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ENSG00000012232 (EXTL3)



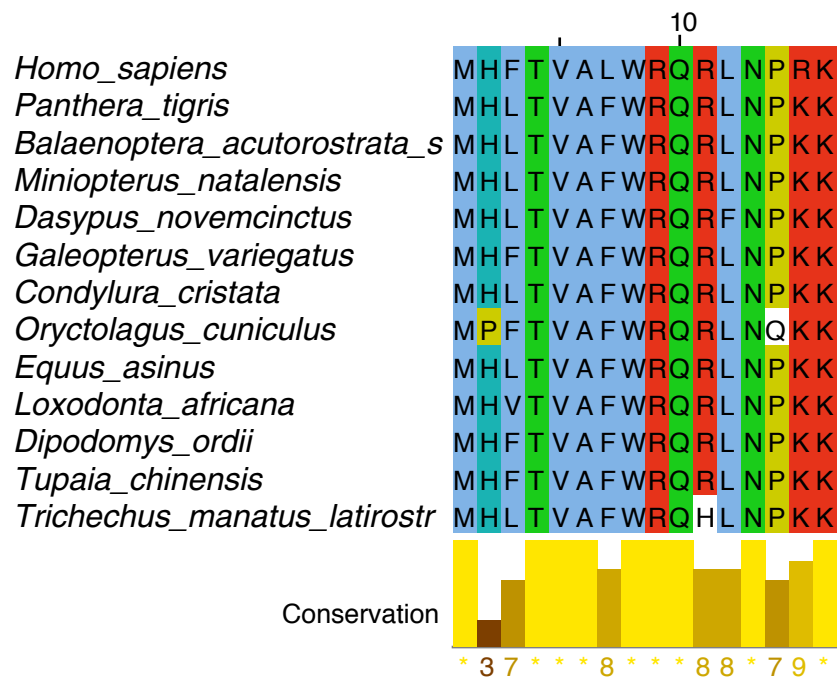
HG0558

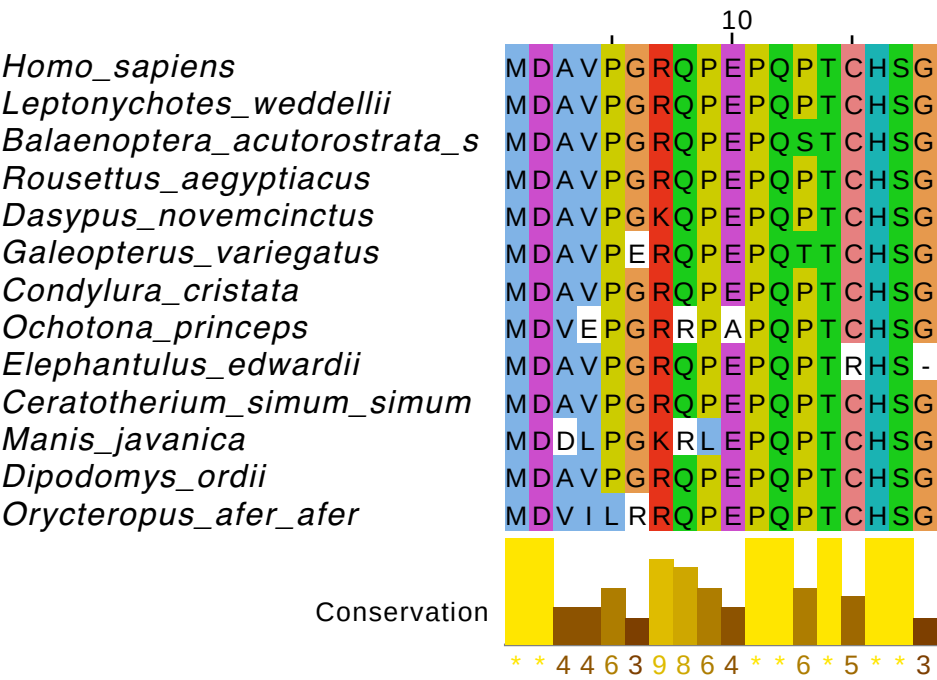
ENSG00000029363 (BCLAF1)



HG0559

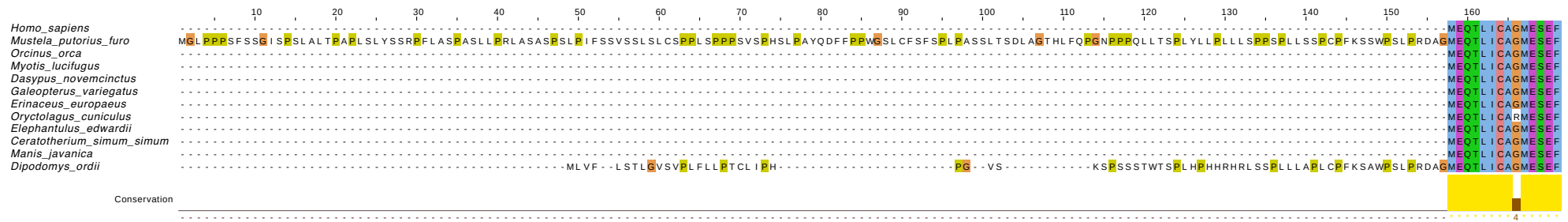
ENSG00000078747 (ITCH)





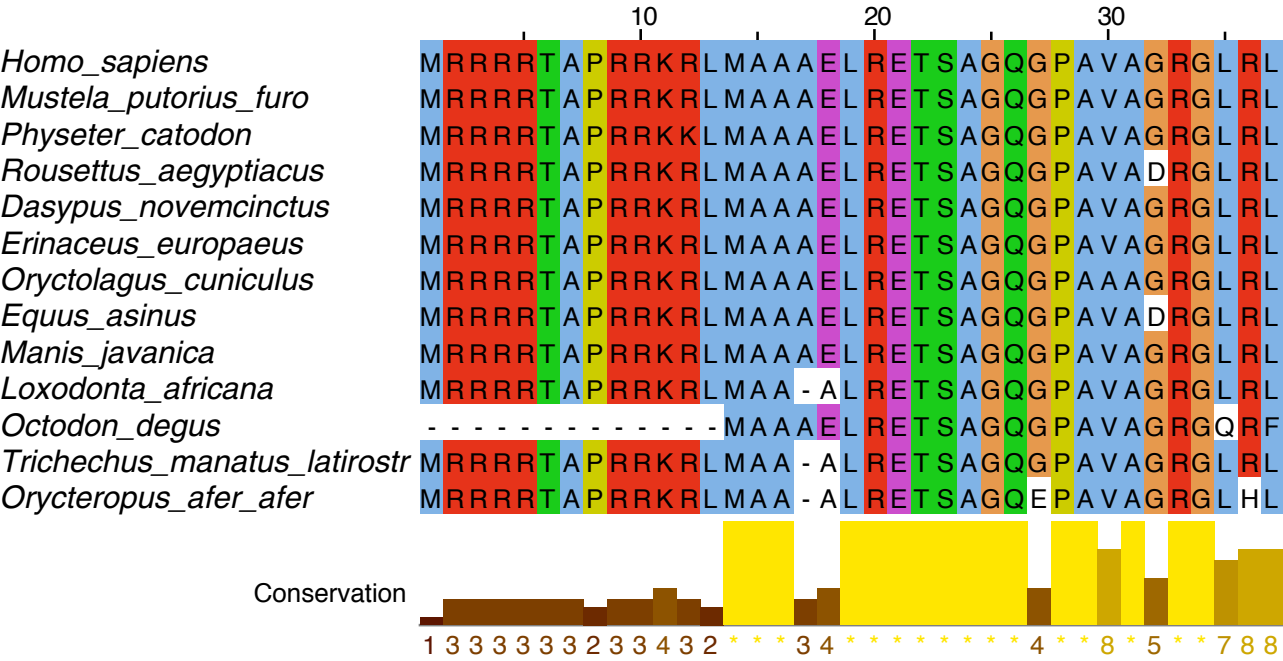
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ENSG00000092051 (JPH4)

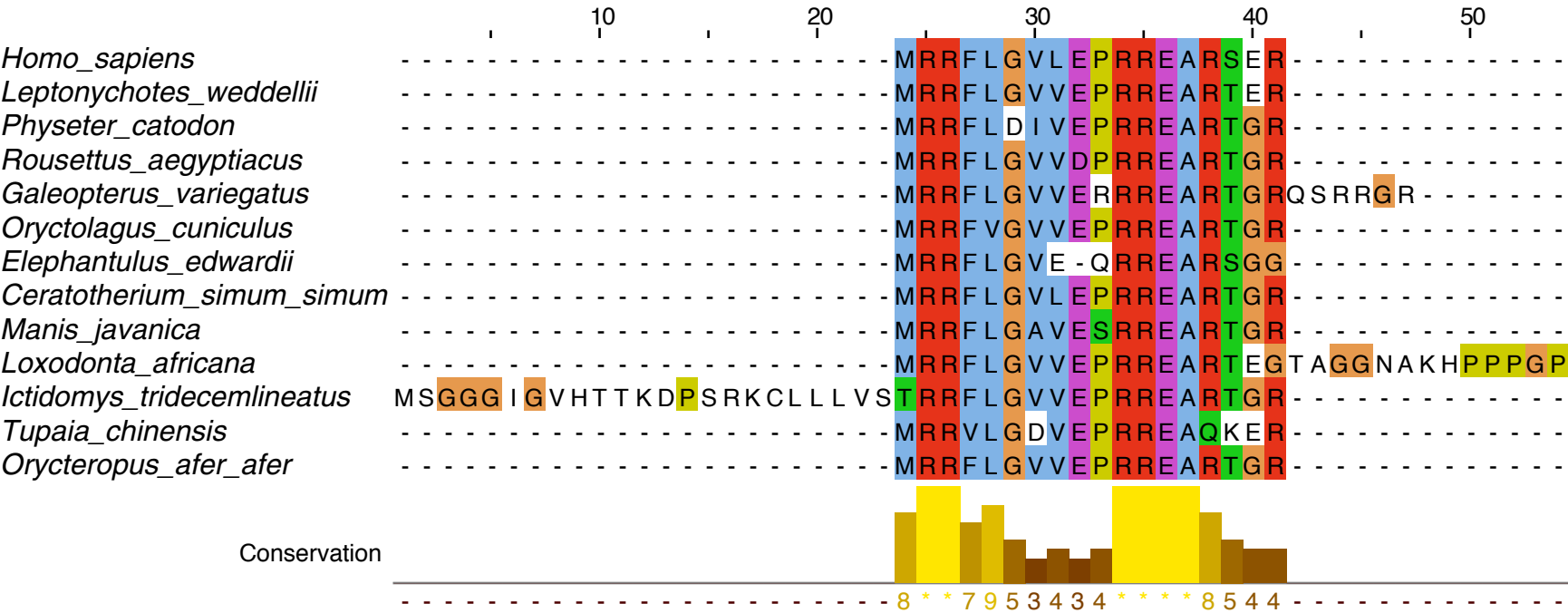


HG0561

ENSG00000100393 (EP300)

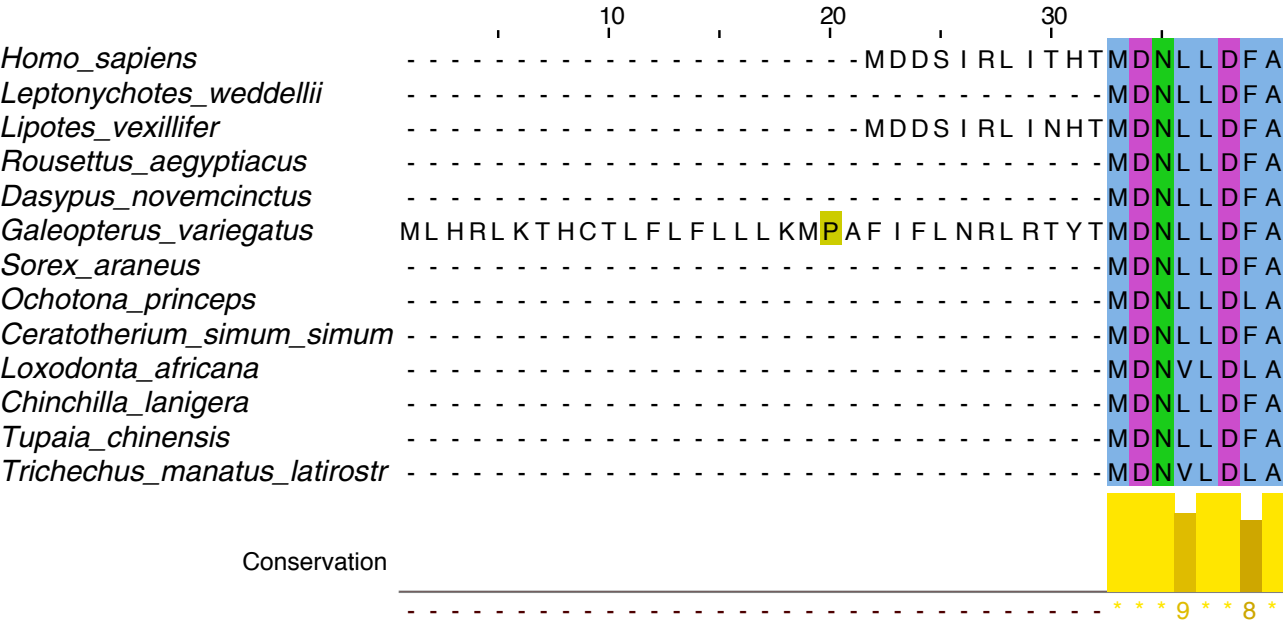


HG0562
ENSG00000105821 (DNAJC2)



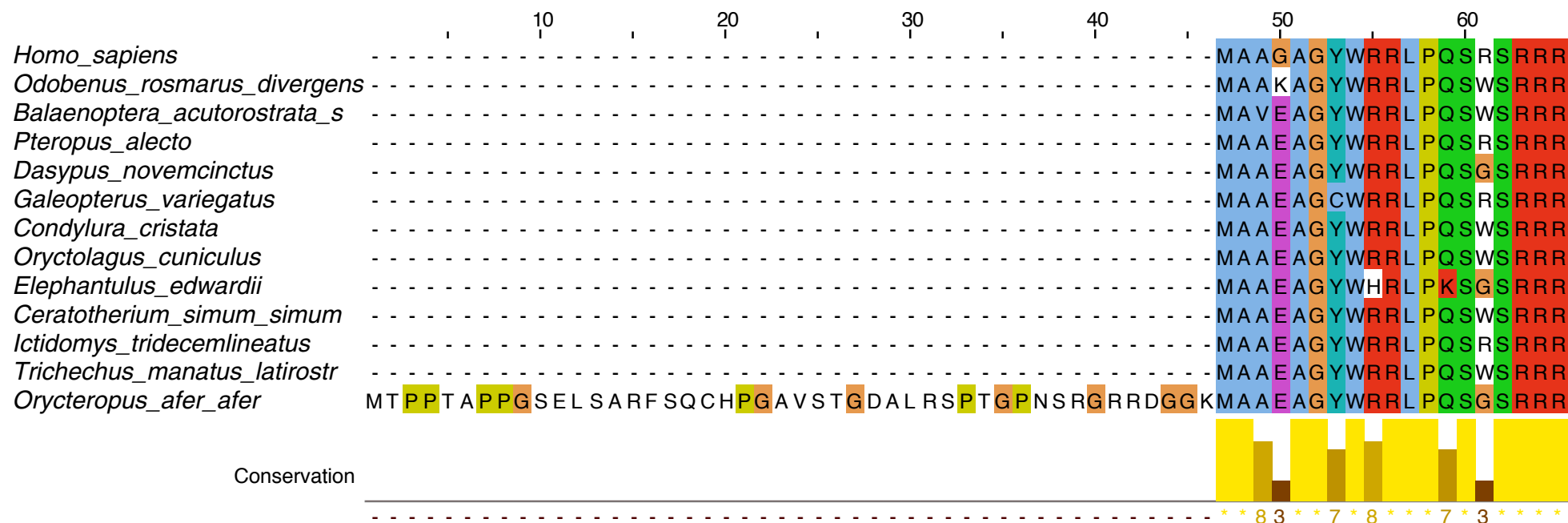
HG0563

ENSG00000107249 (GLIS3)



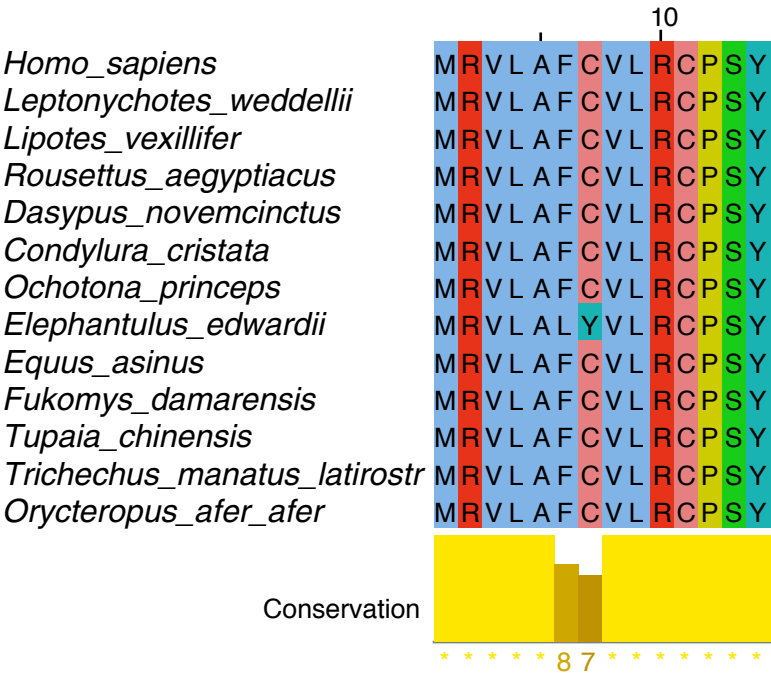
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ENSG00000109171 (SLAIN2)

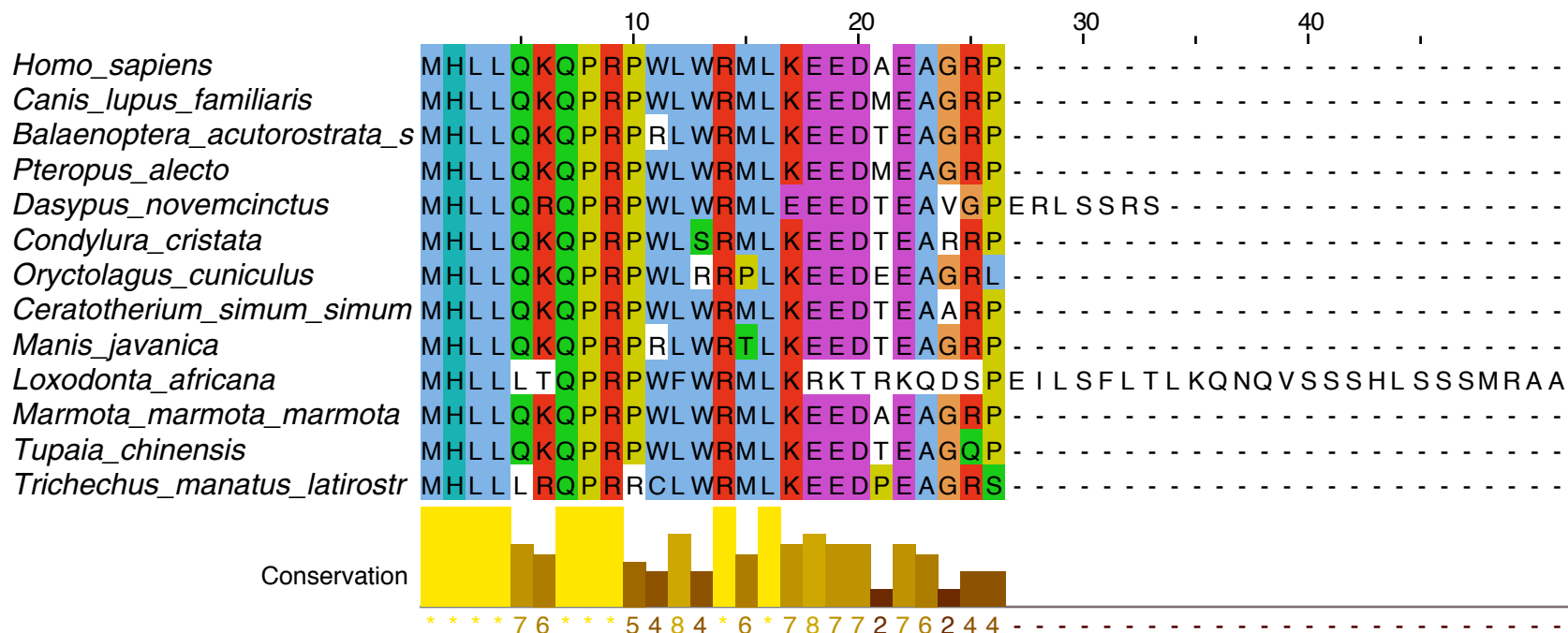


HG0565

ENSG00000120533 (ENY2)

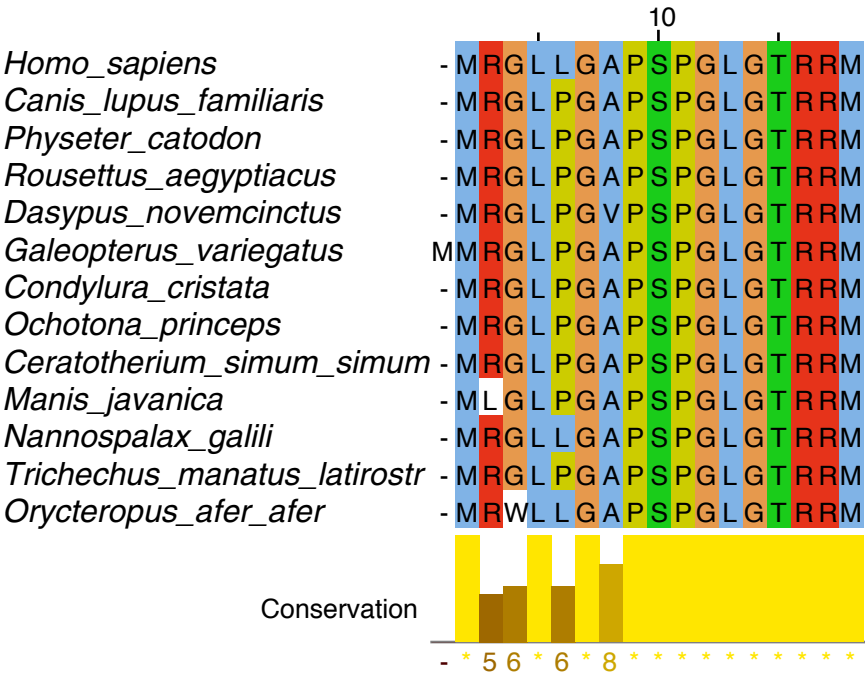


ENSG00000124496 (TRERF1)



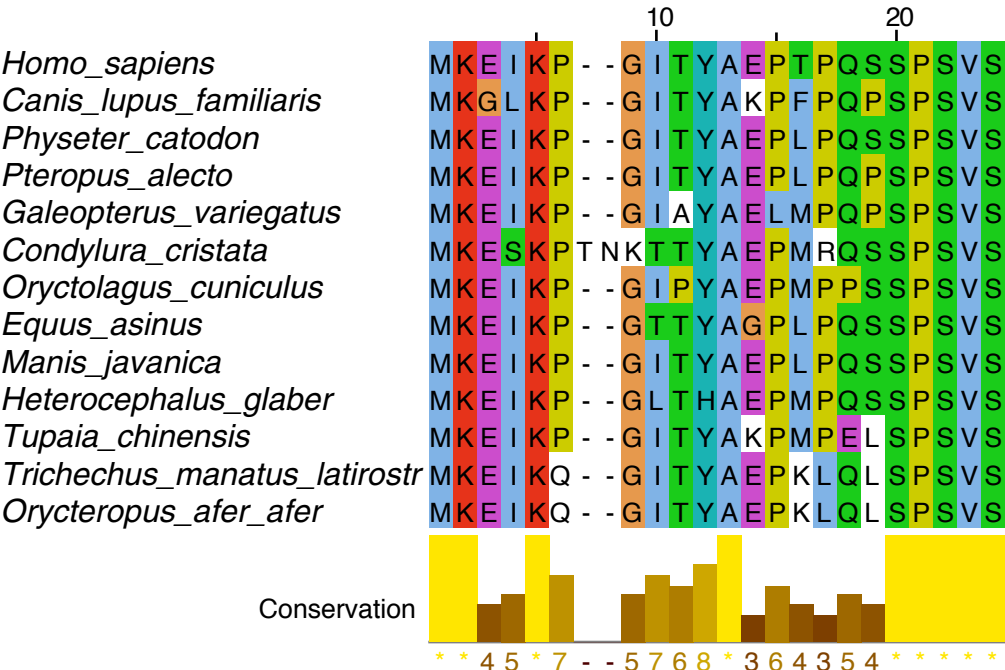
HG0567

ENSG00000132155 (RAF1)



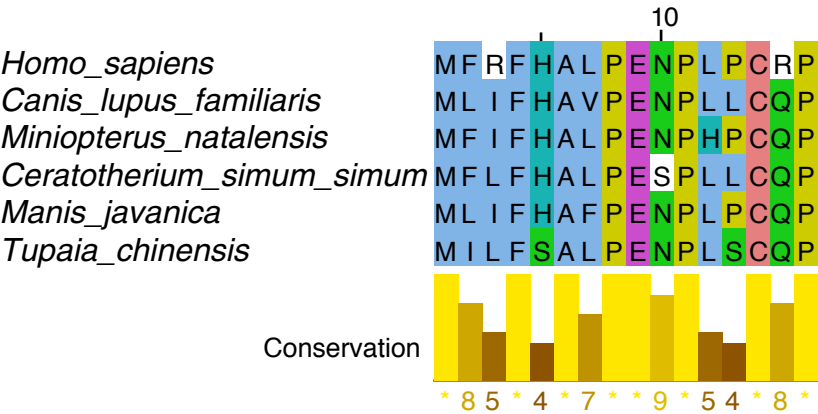
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ENSG00000138271 (GPR87)

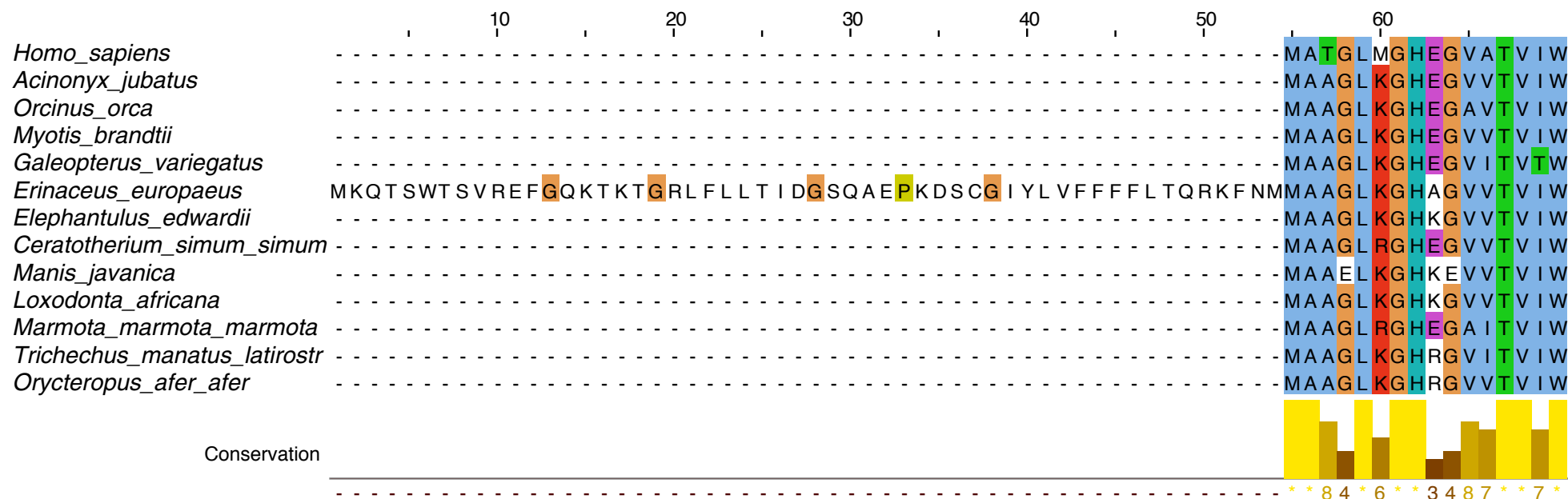


HG0568.2

ENSG00000138271 (GPR87)

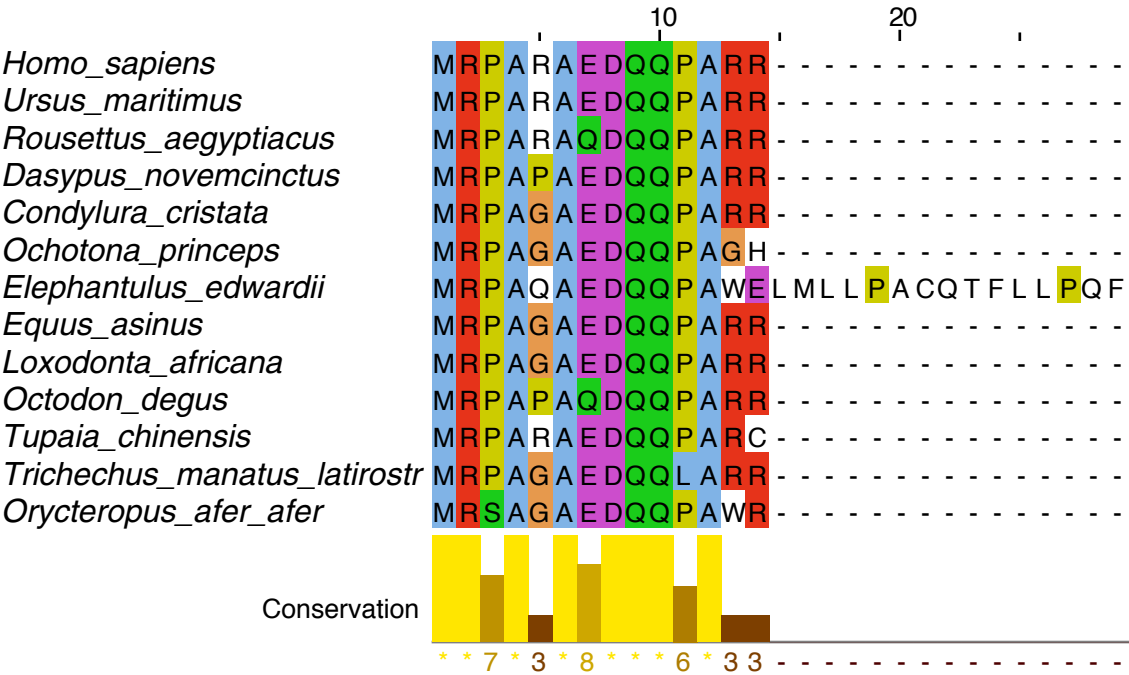


ENSG00000139651 (ZNF740)

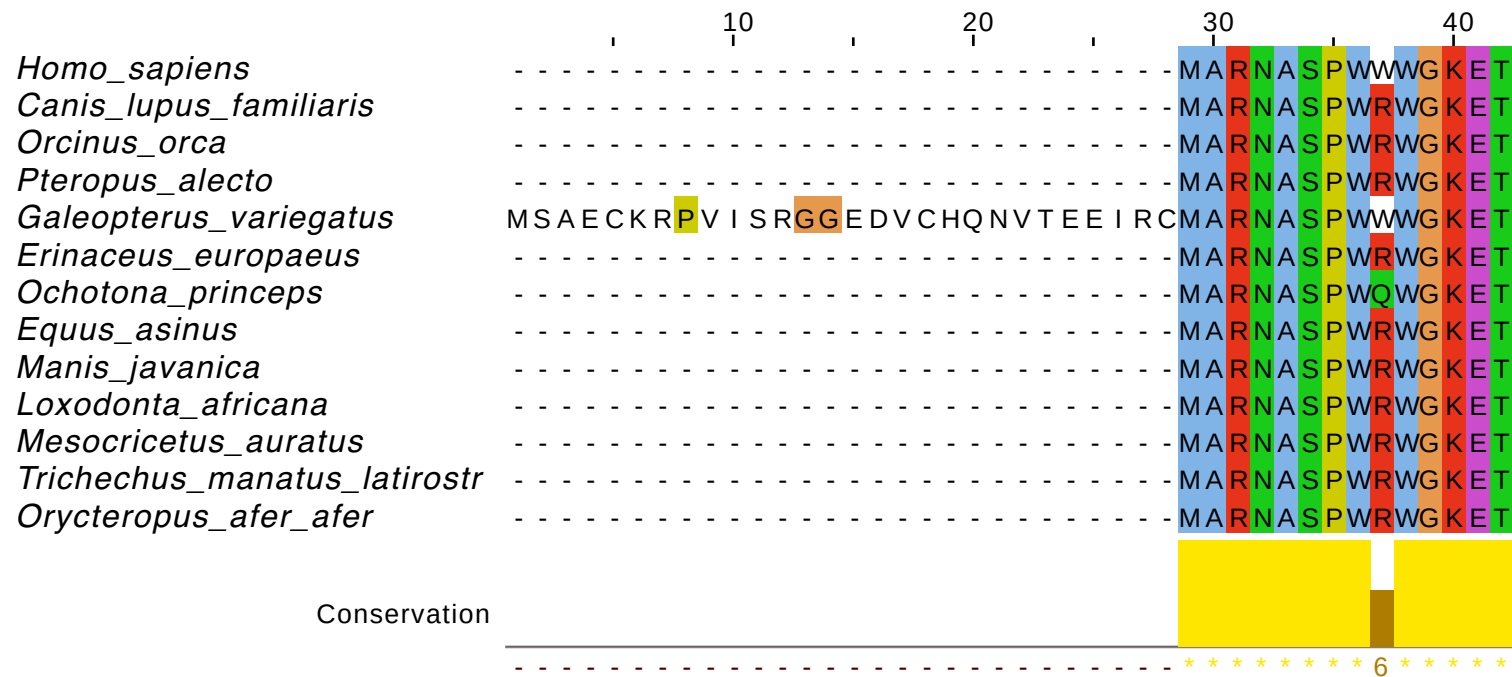


HG0570

ENSG00000152214 (RIT2)

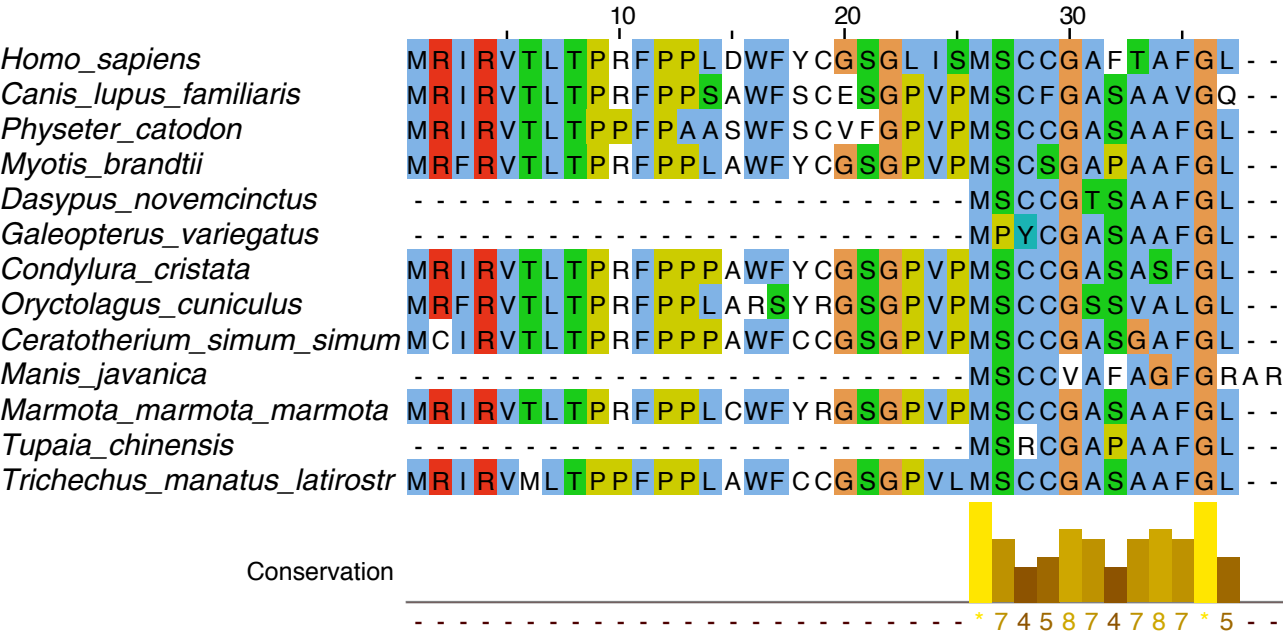


ENSG00000153266 (FEZF2)



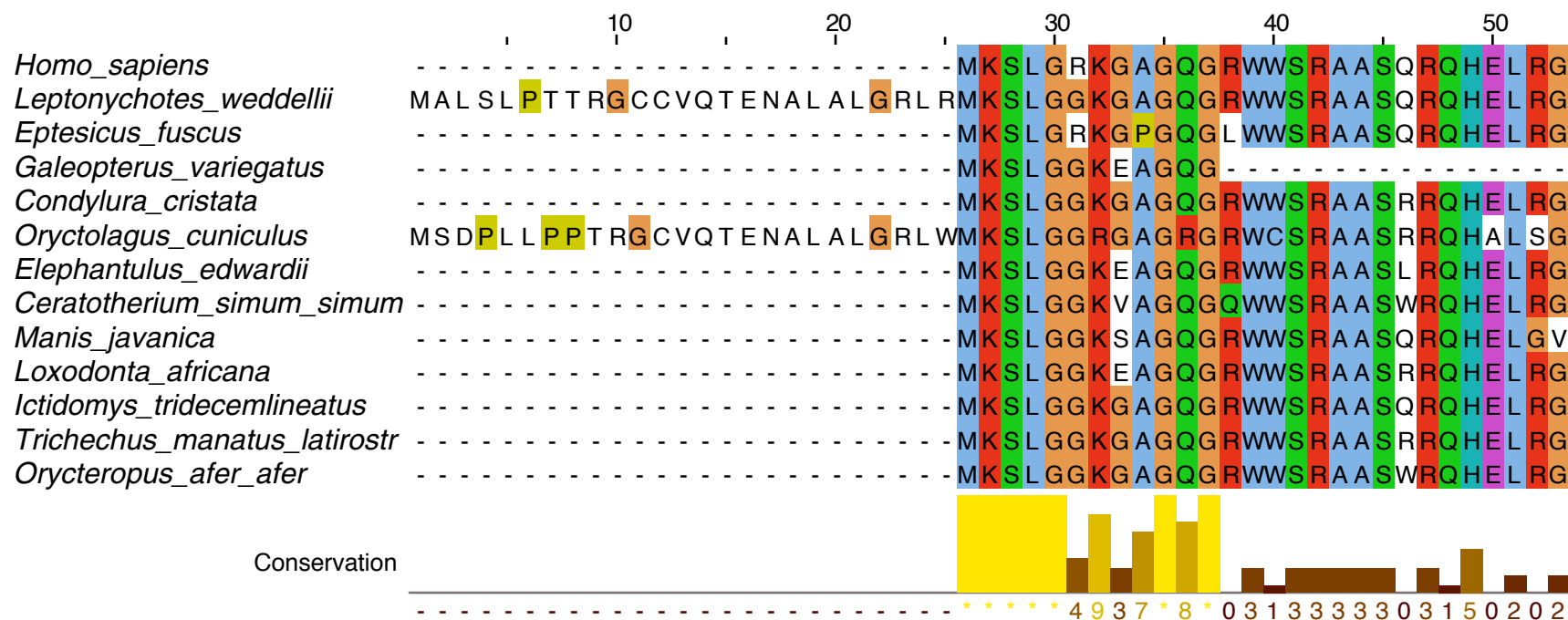
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ENSG00000158161 (EYA3)



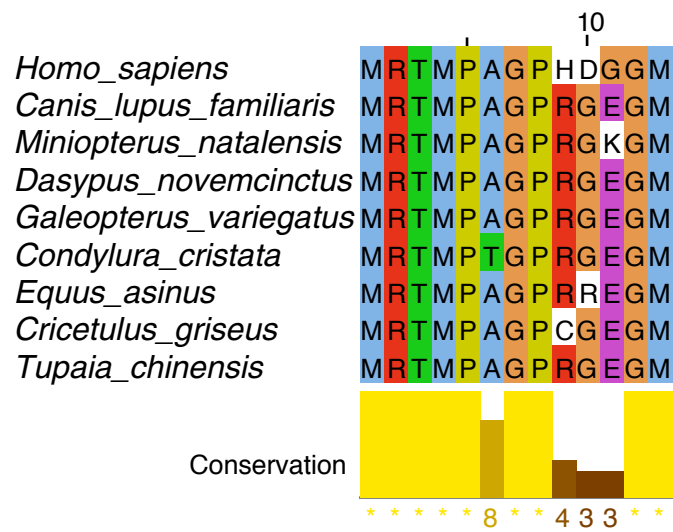
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ENSG00000162526 (TSSK3)



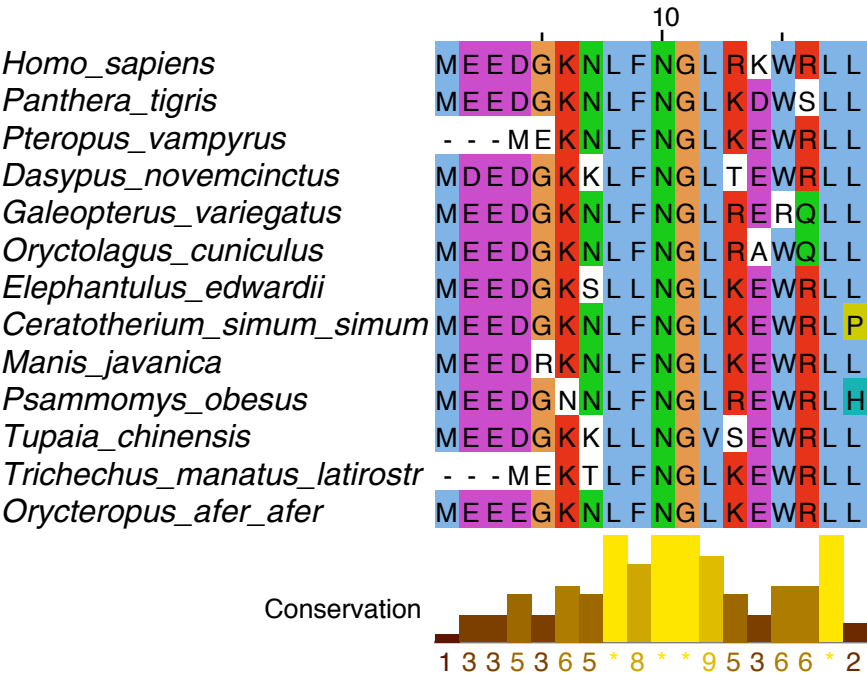
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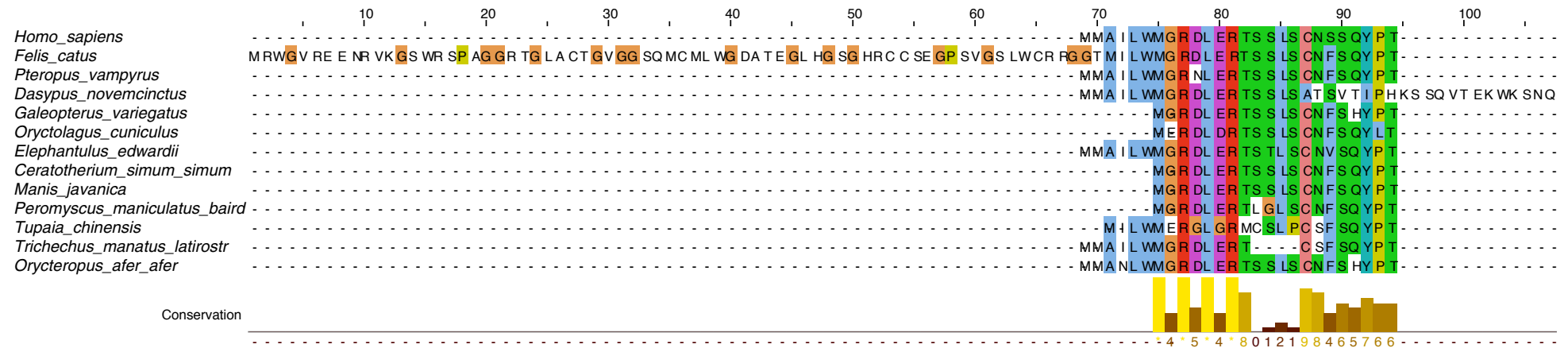


HG0574

ENSG00000164663 (USP49)

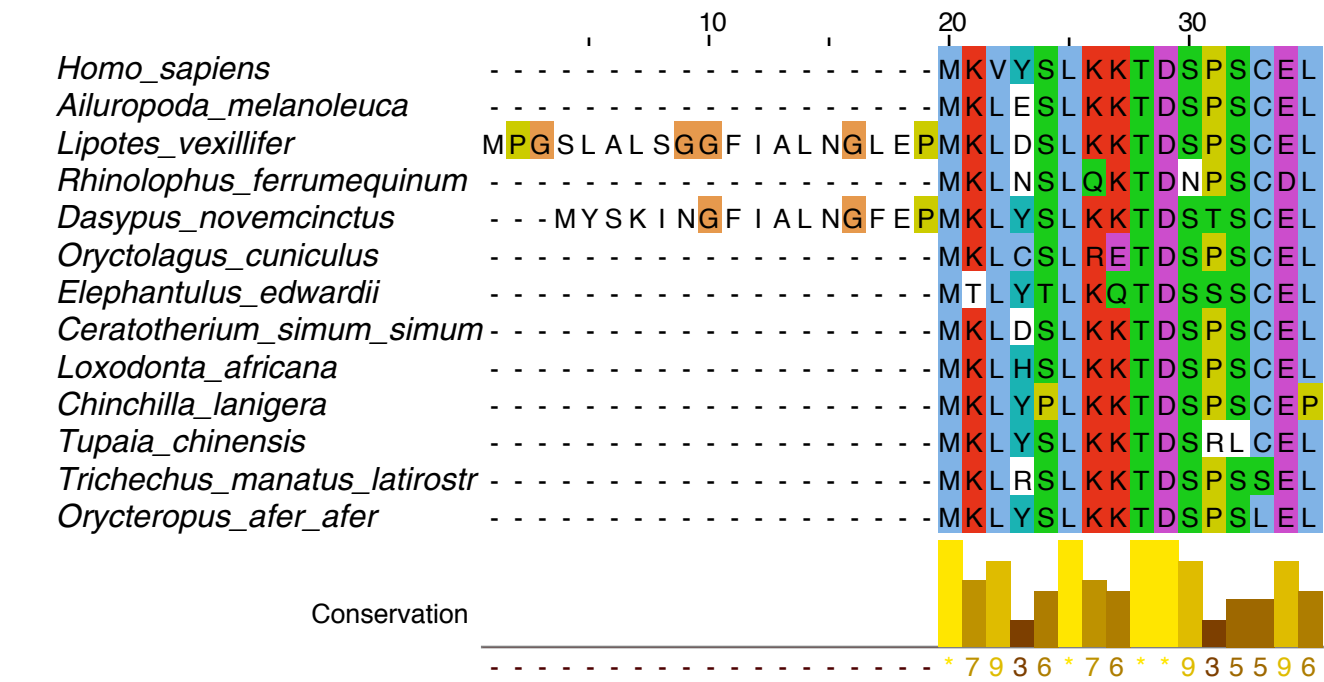


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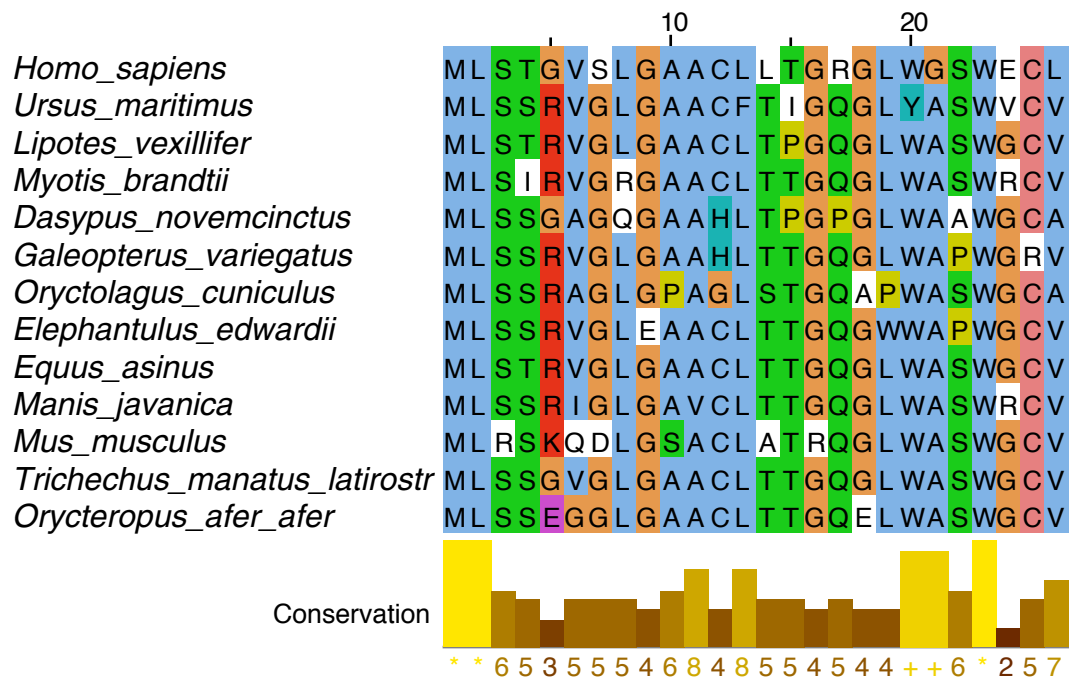
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ENSG00000175029 (CTBP2)



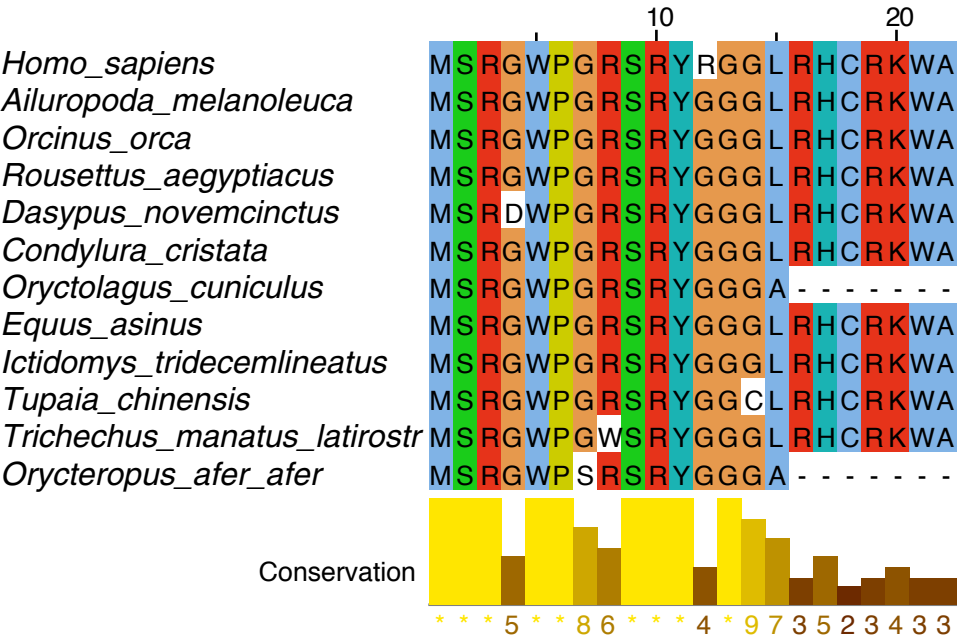
HG0577

ENSG00000250510 (GPR162)



HG0578

ENSG00000004897 (CDC27)

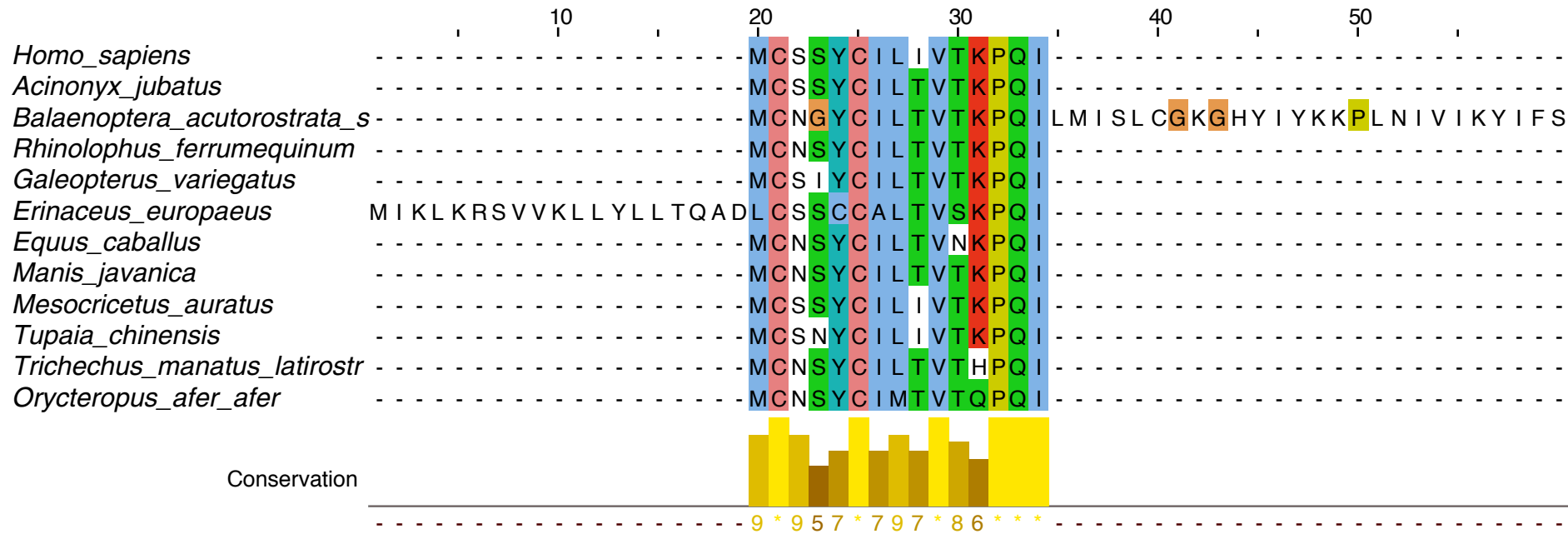


ENSG00000010818 (HIVEP2)

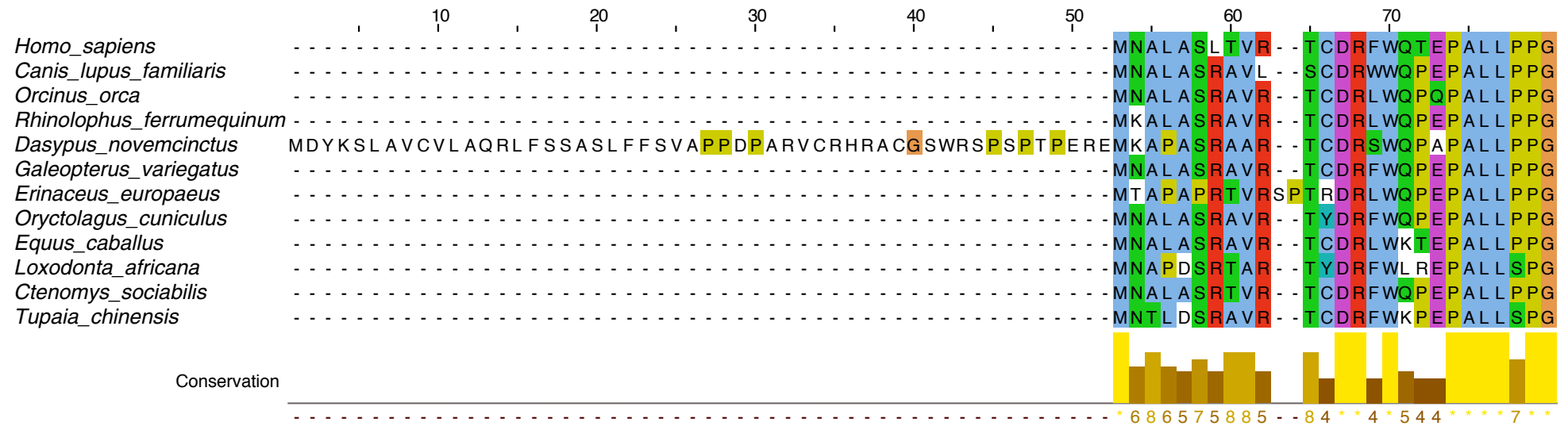


HG0580

ENSG00000073711 (PPP2R3A)

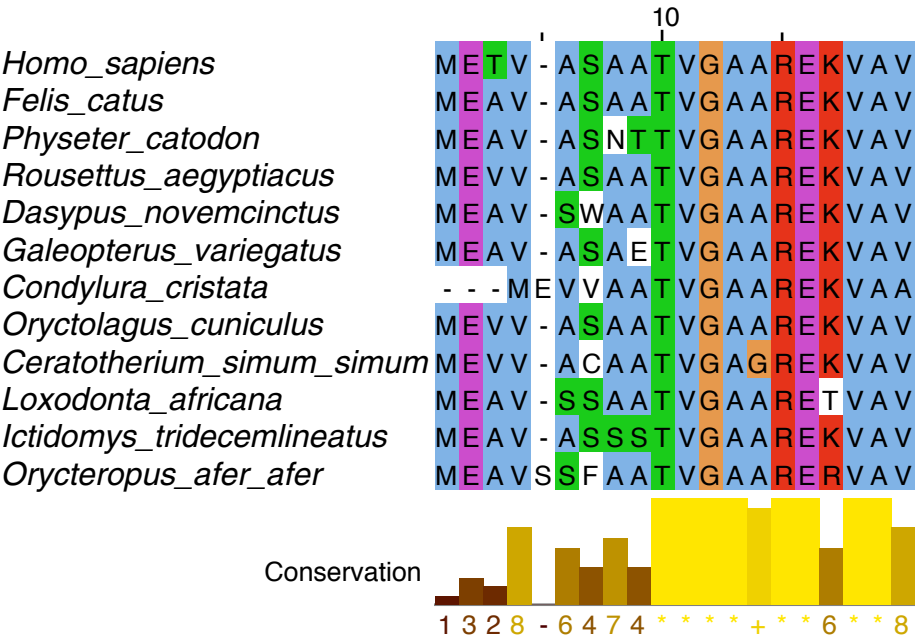


ENSG00000087074 (PPP1R15A)



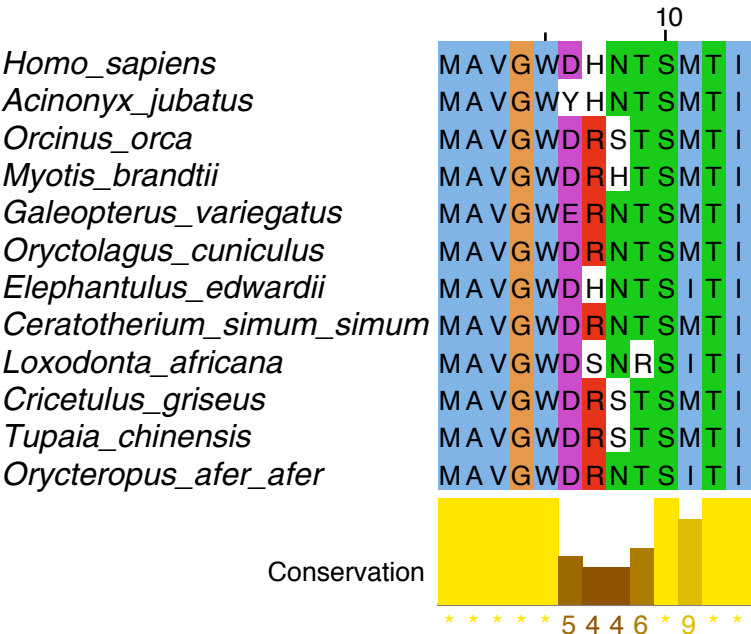
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ENSG00000087338 (GMCL1)



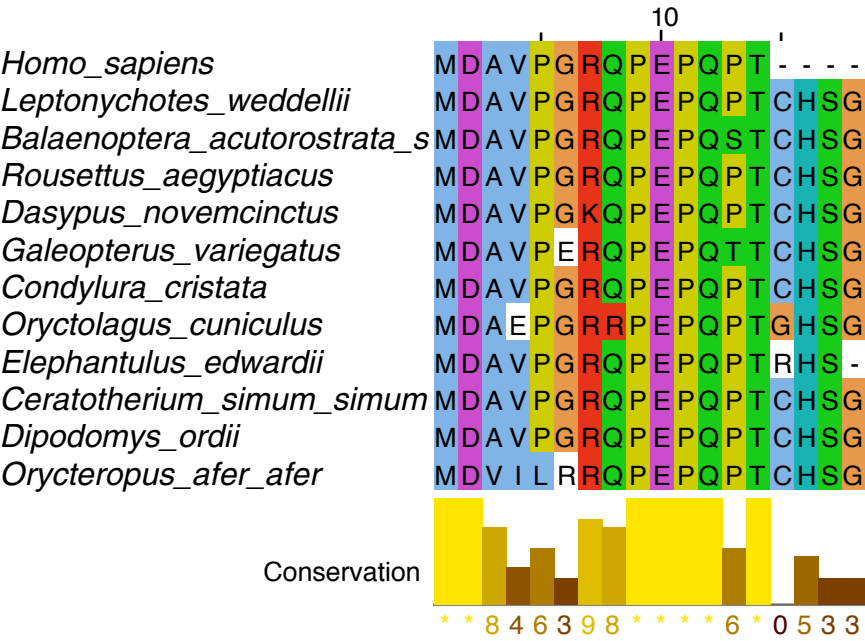
HG0583

ENSG00000087502 (ERGIC2)



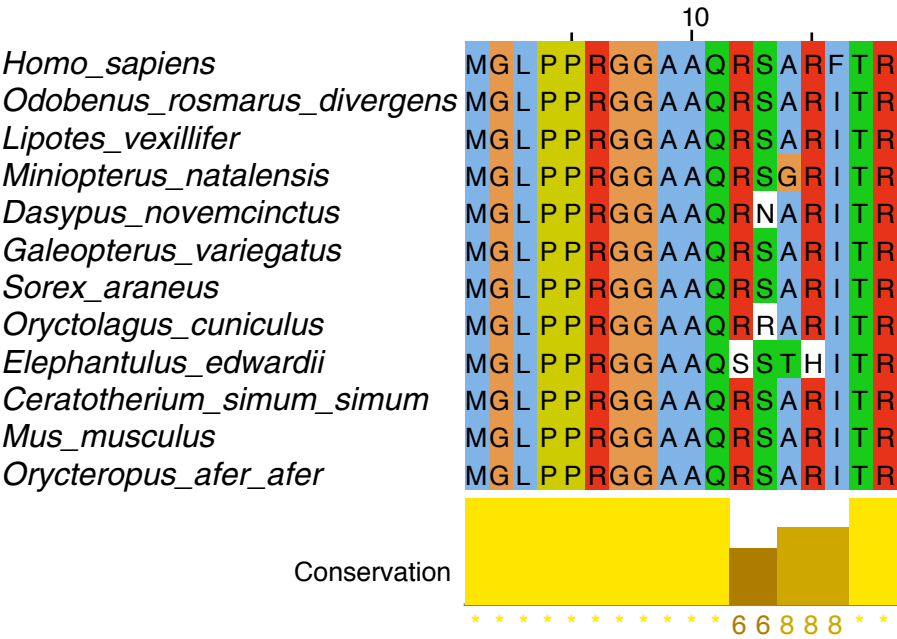
HG0584

ENSG00000092051 (JPH4)



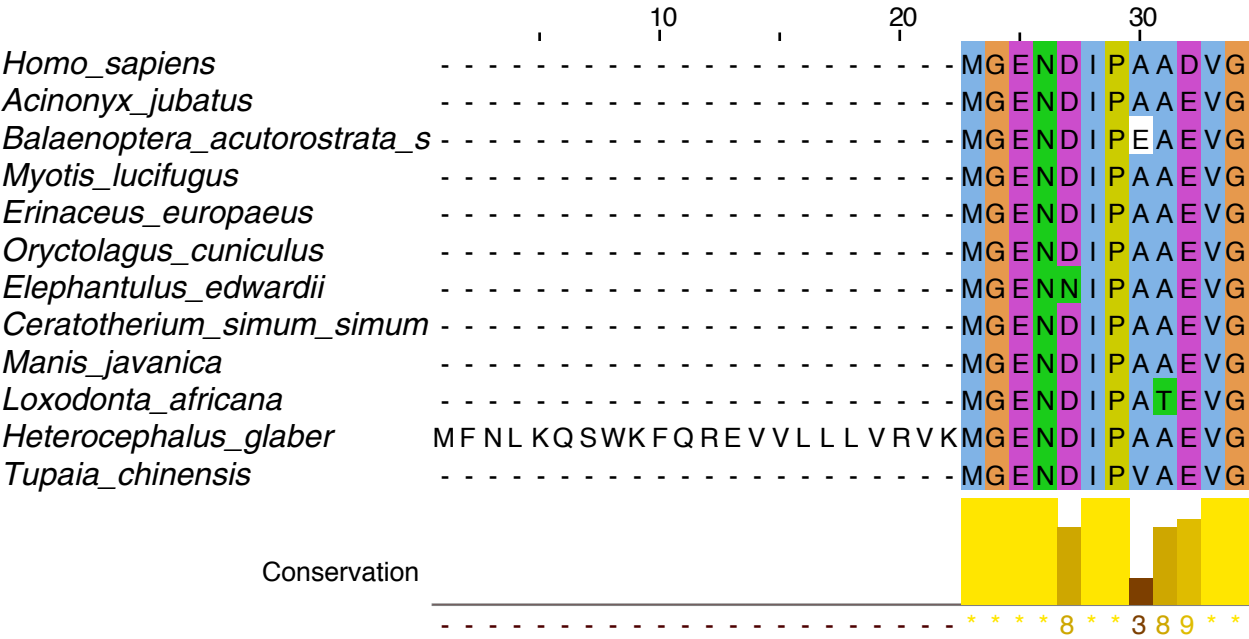
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ENSG00000106038 (EVX1)



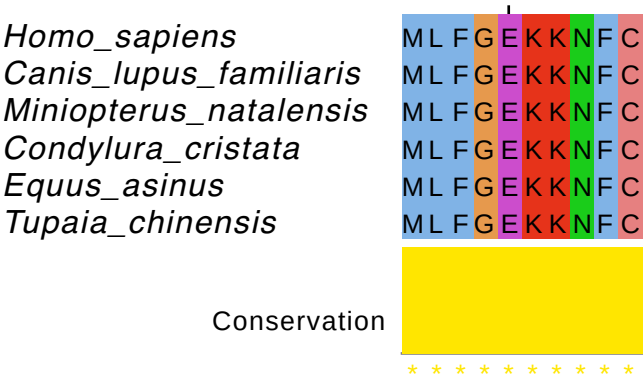
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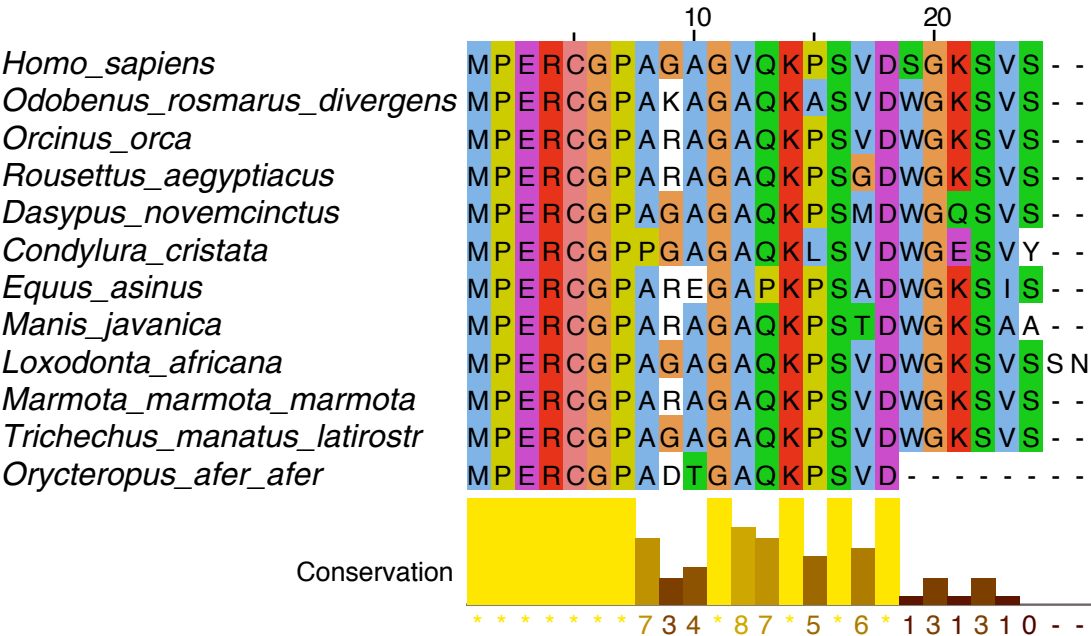
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ENSG00000108375 (RNF43)

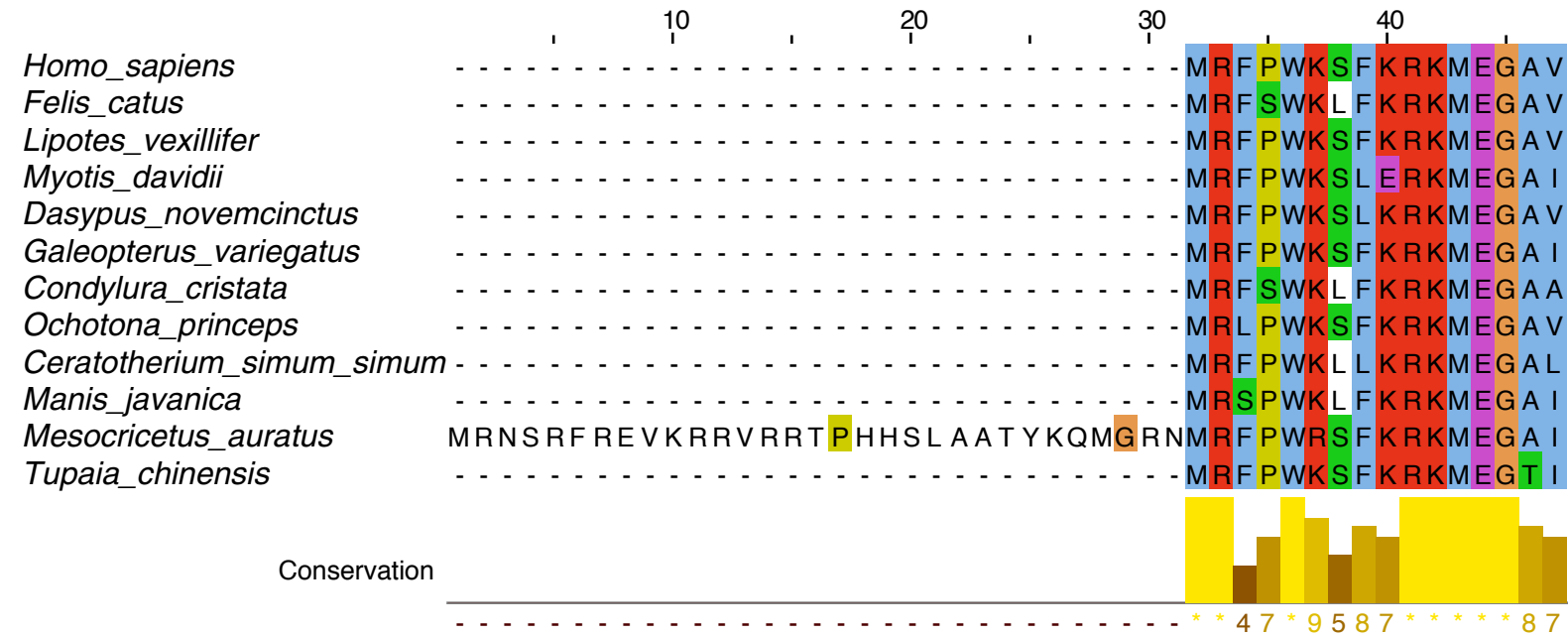


HG0587

ENSG00000119138 (KLF9)

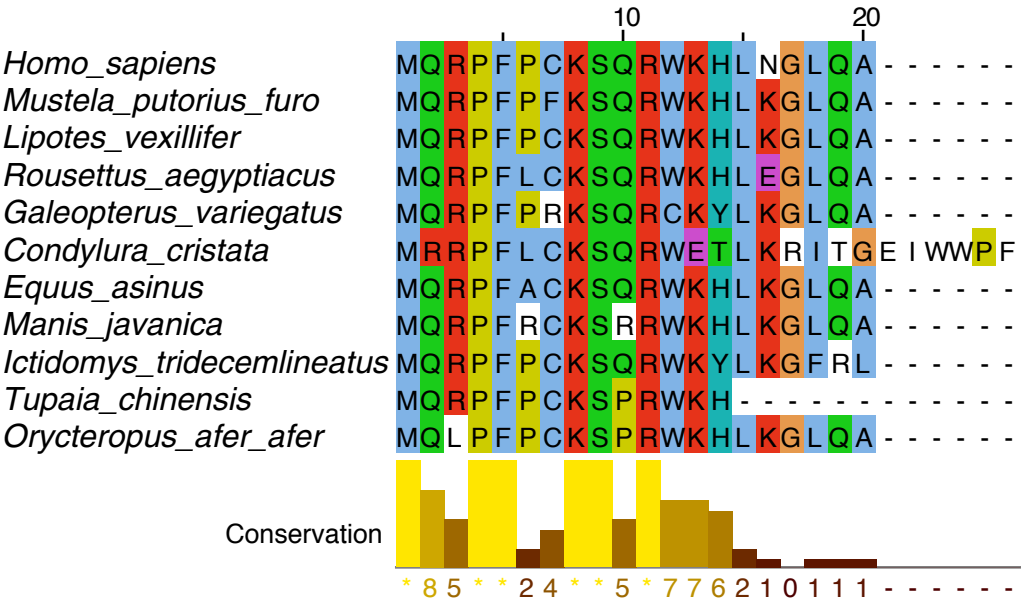


HG0588
ENSG00000120162 (MOB3B)



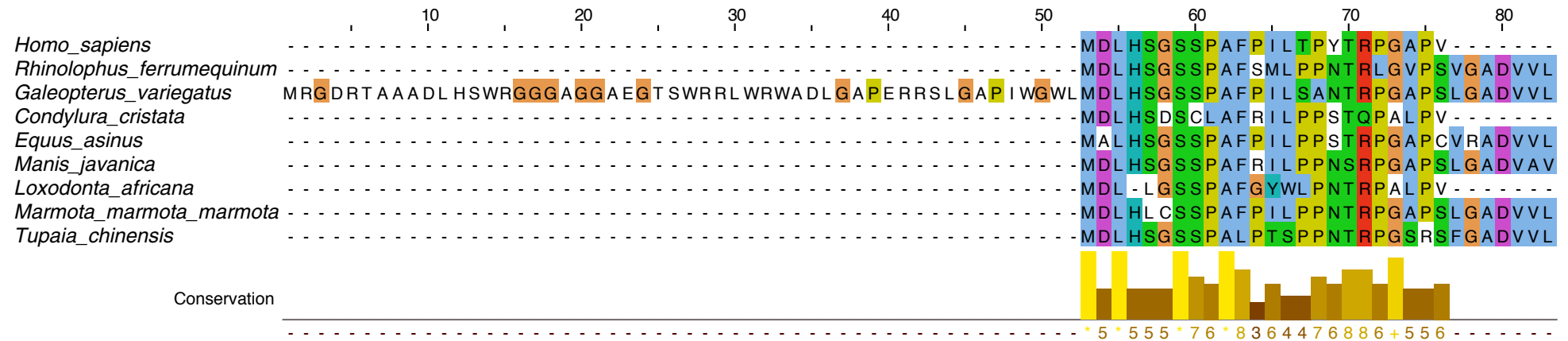
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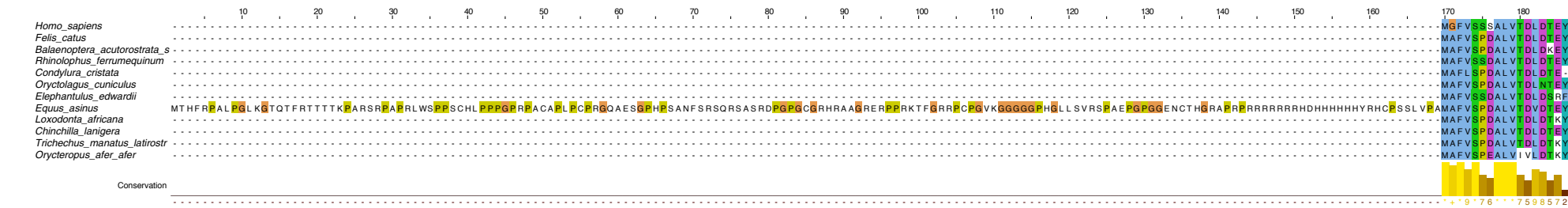
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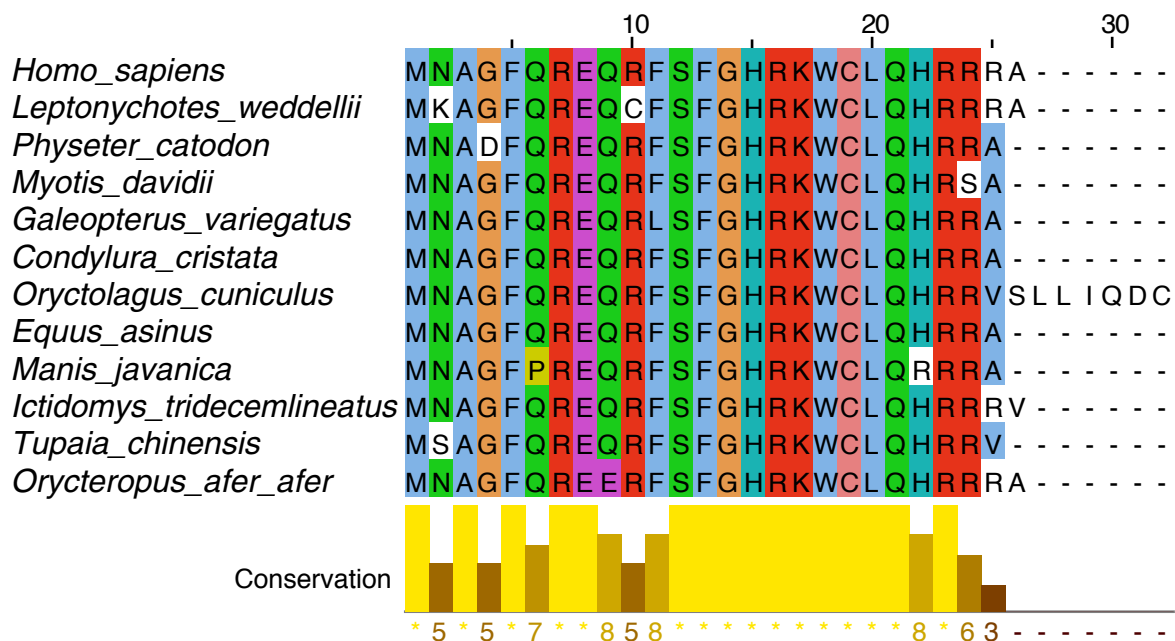


HG0590

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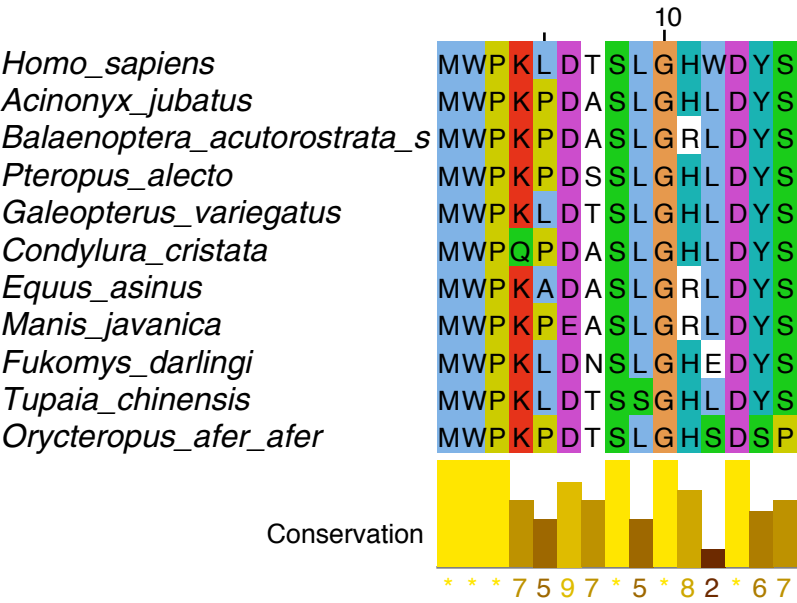


ENSG00000127124 (HIVEP3)



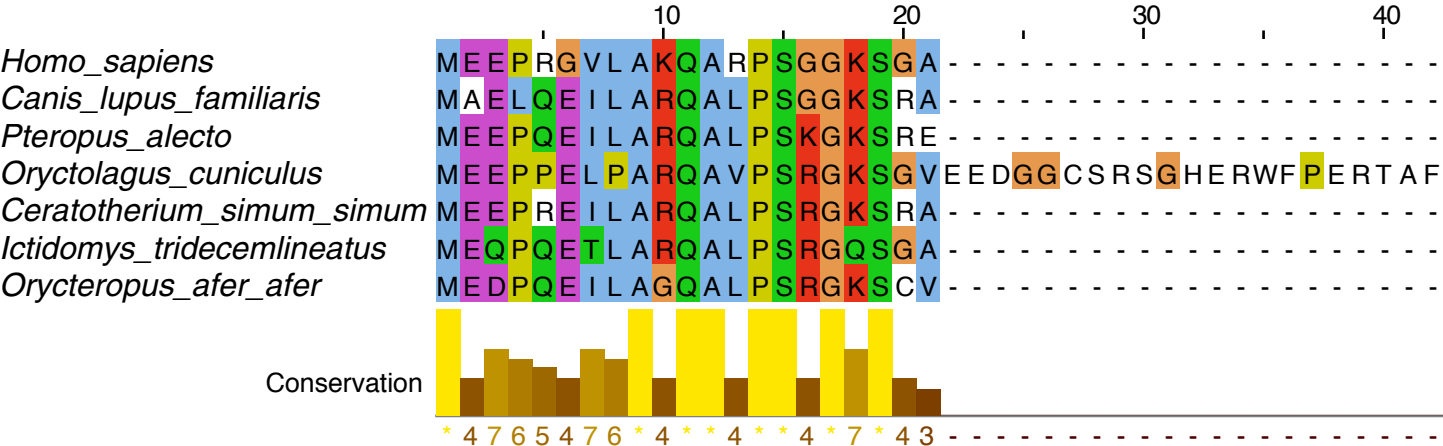
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ENSG00000127124 (HIVEP3)



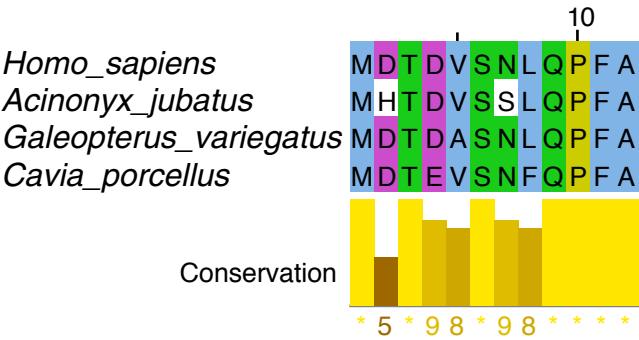
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ENSG00000127124 (HIVEP3)



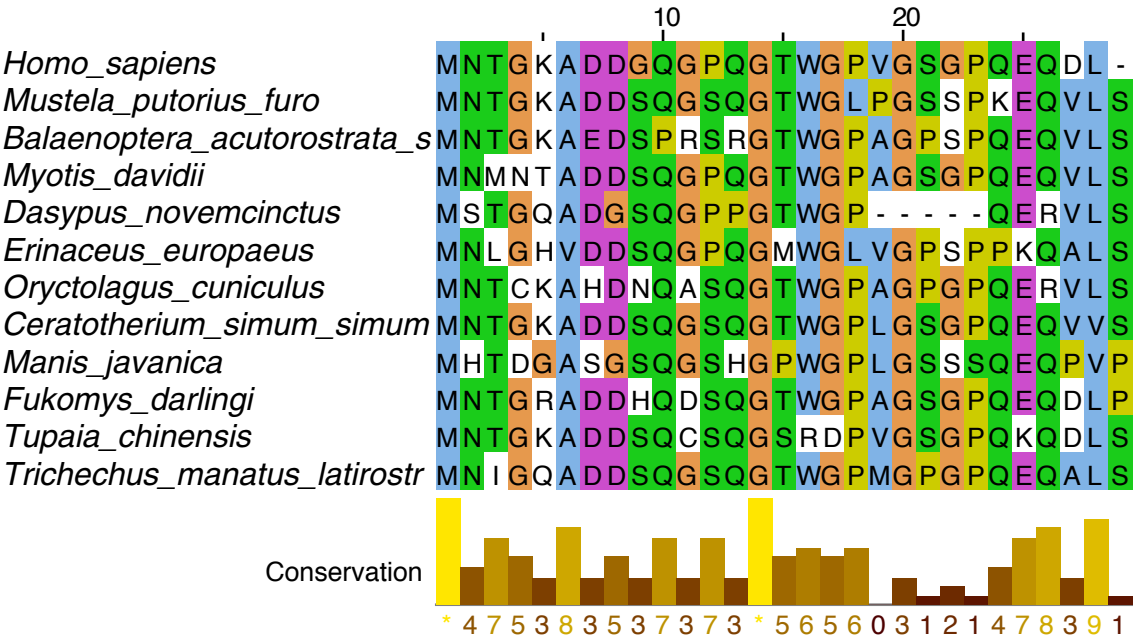
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ENSG00000127124 (HIVEP3)



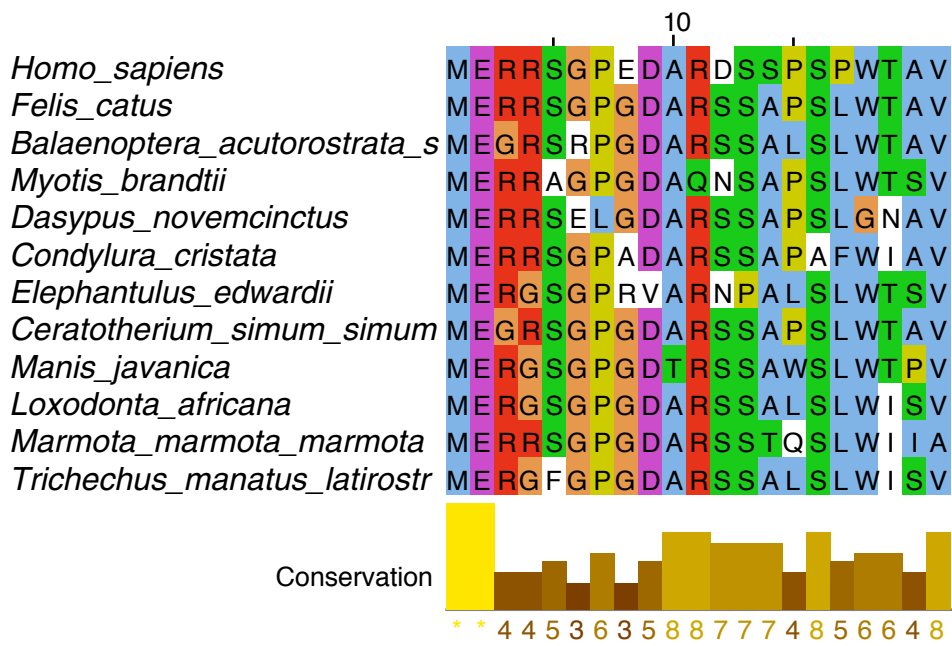
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ENSG00000133401 (PDZD2)



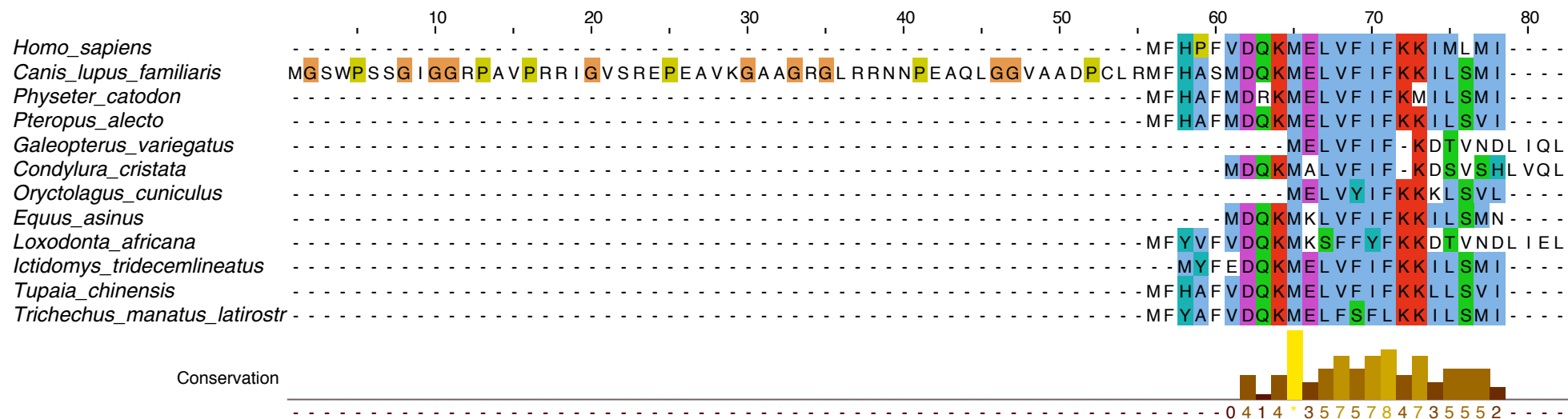
HG0593

ENSG00000135048 (TMEM2)



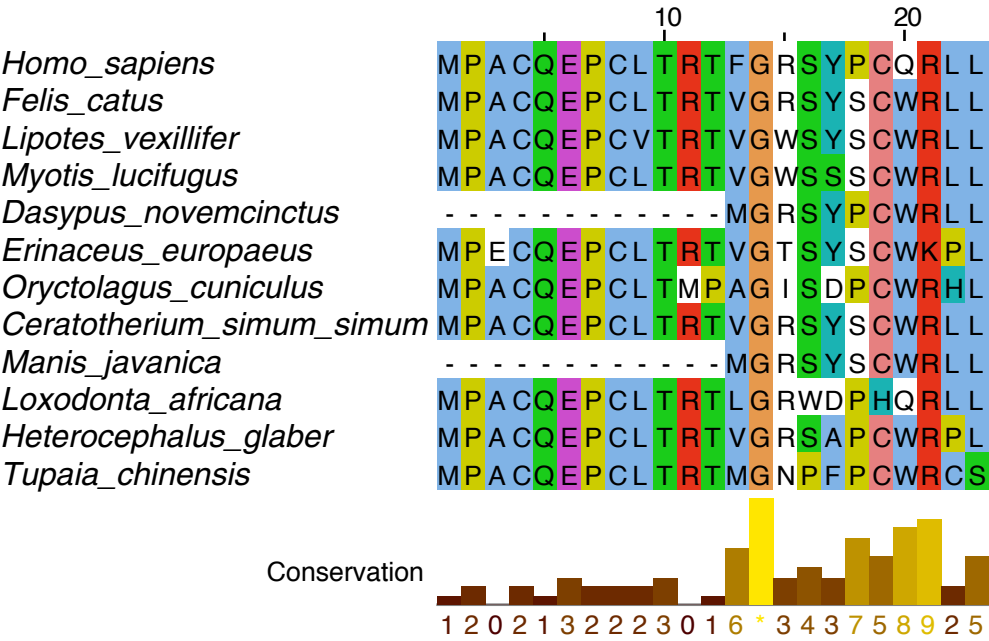
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ENSG00000136169 (SETDB2)



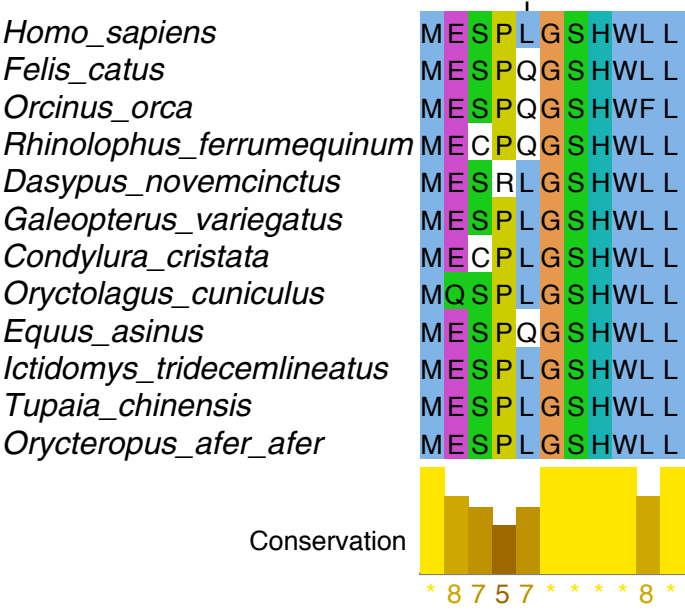
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ENSG00000141098 (GFOD2)



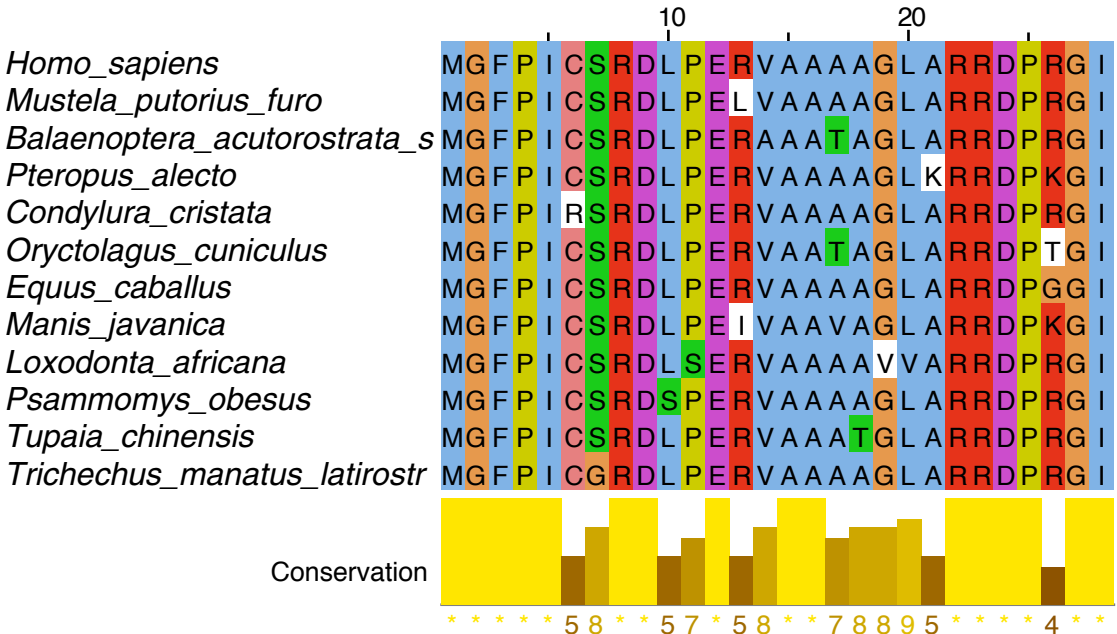
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ENSG00000157483 (MYO1E)

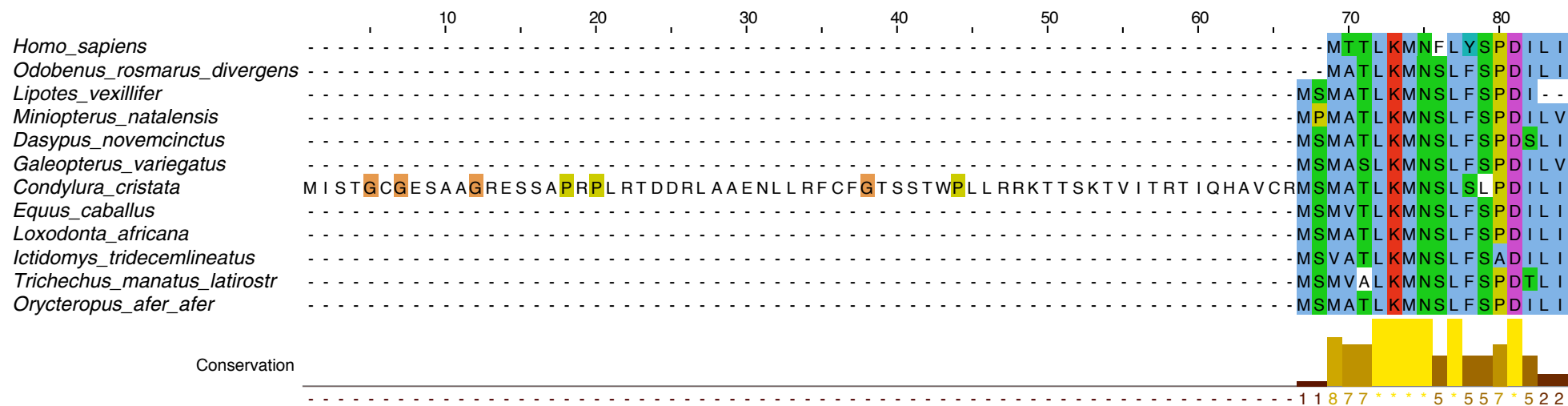


HG0597

ENSG00000163032 (VSNL1)

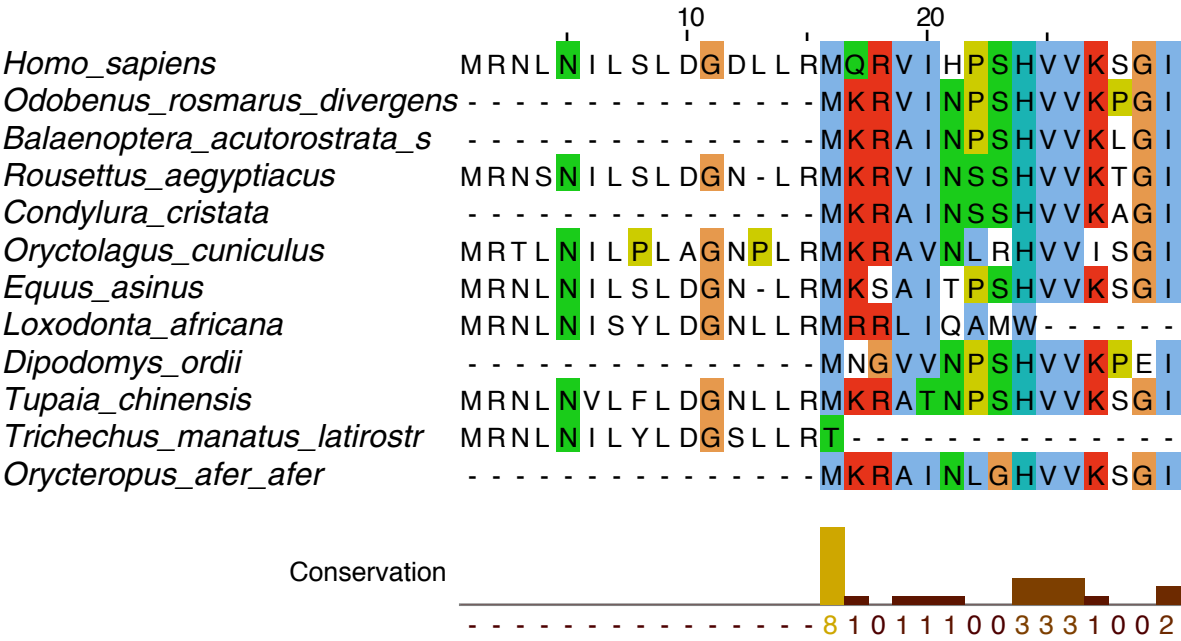


ENSG00000163788 (SNRK)

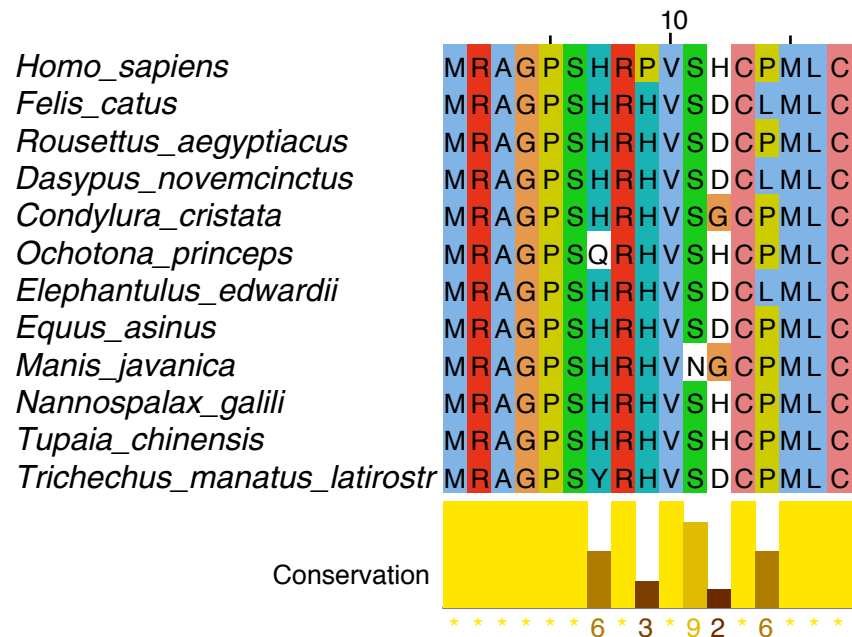


HG0599

ENSG00000164930 (FZD6)

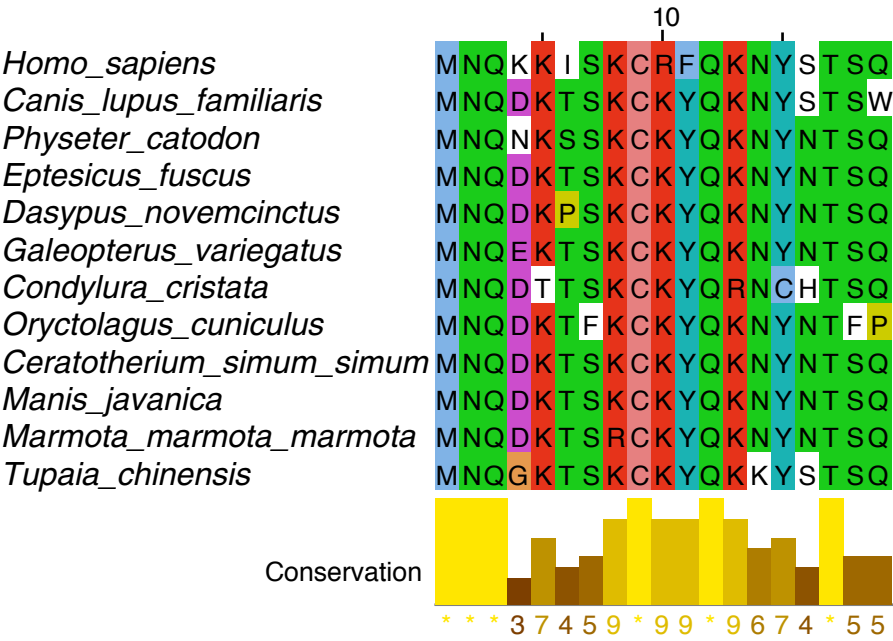


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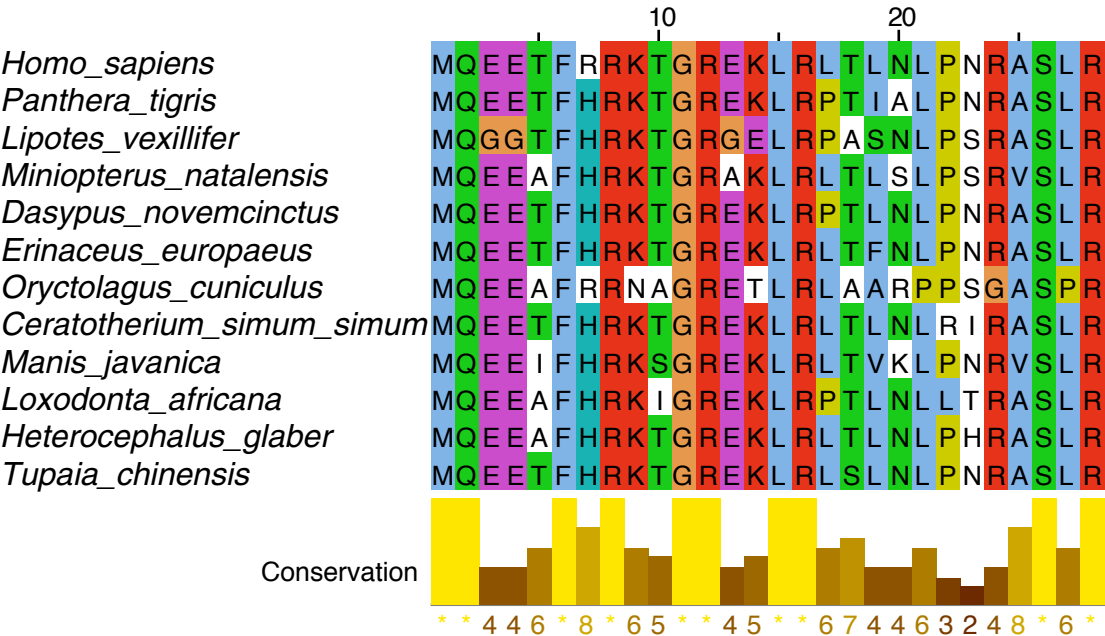
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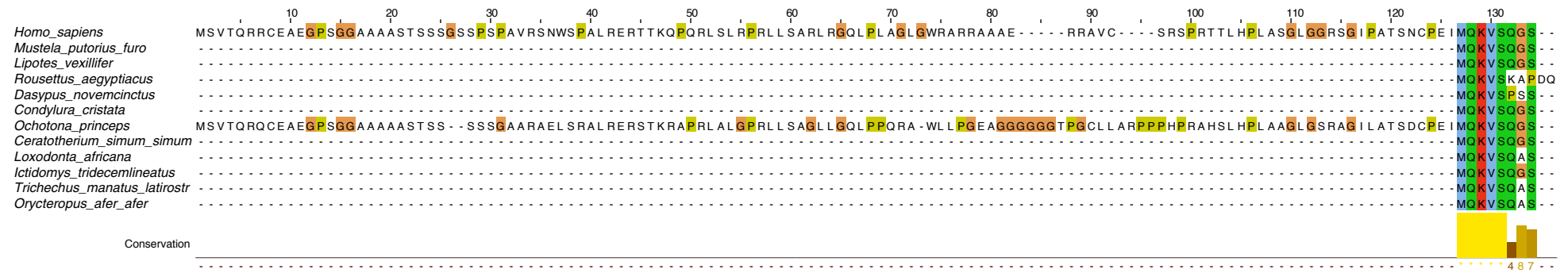


HG0602

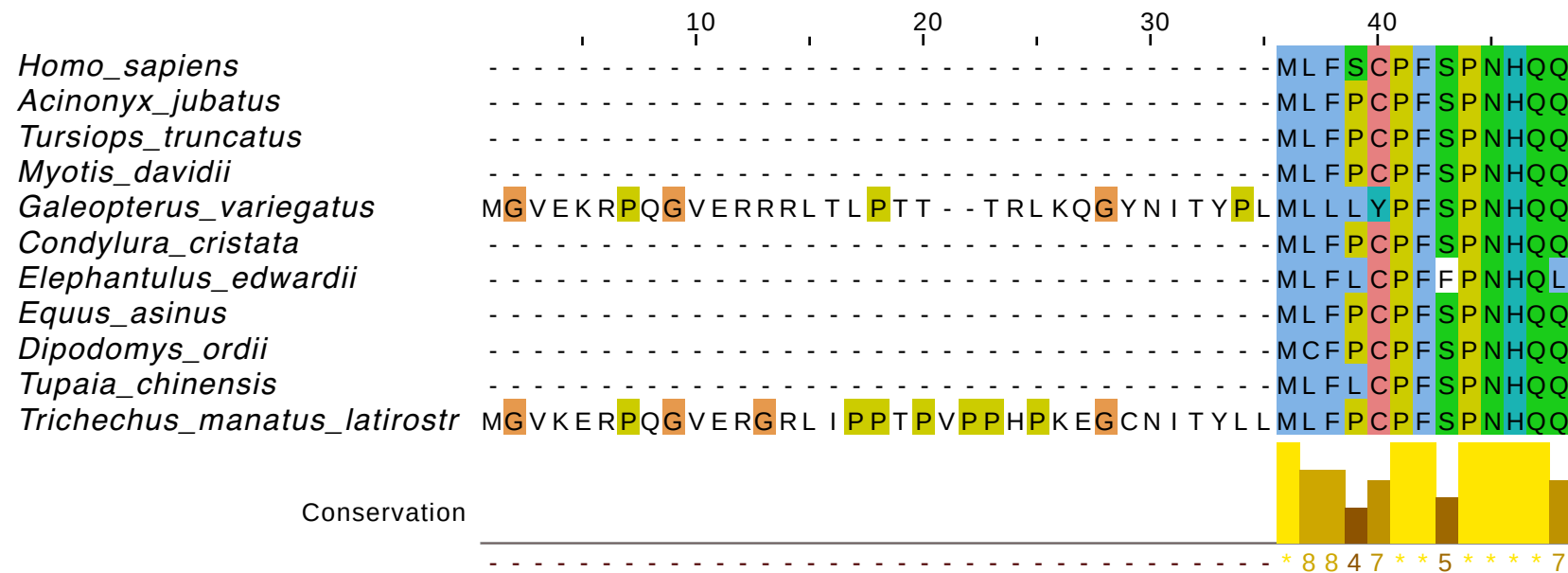
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ENSG00000197329 (PELI1)

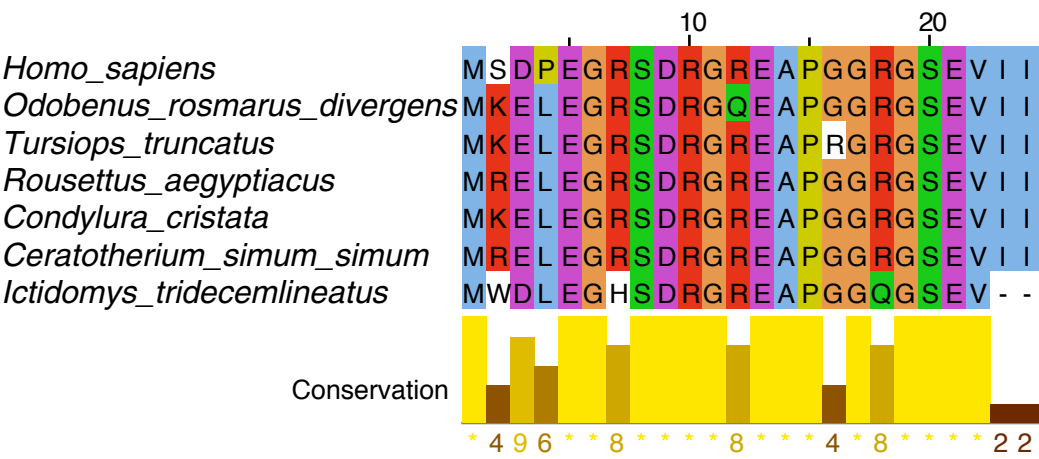


ENSG000000003147 (ICA1)



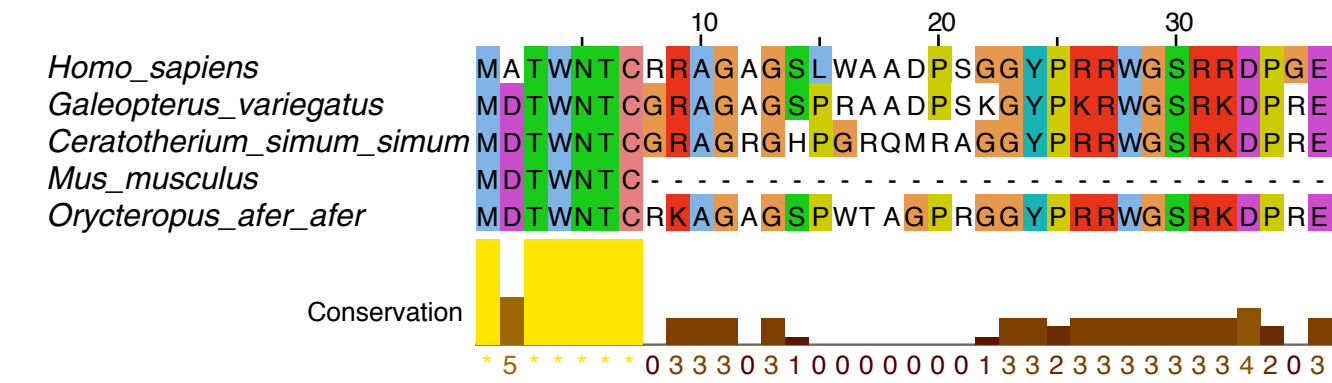
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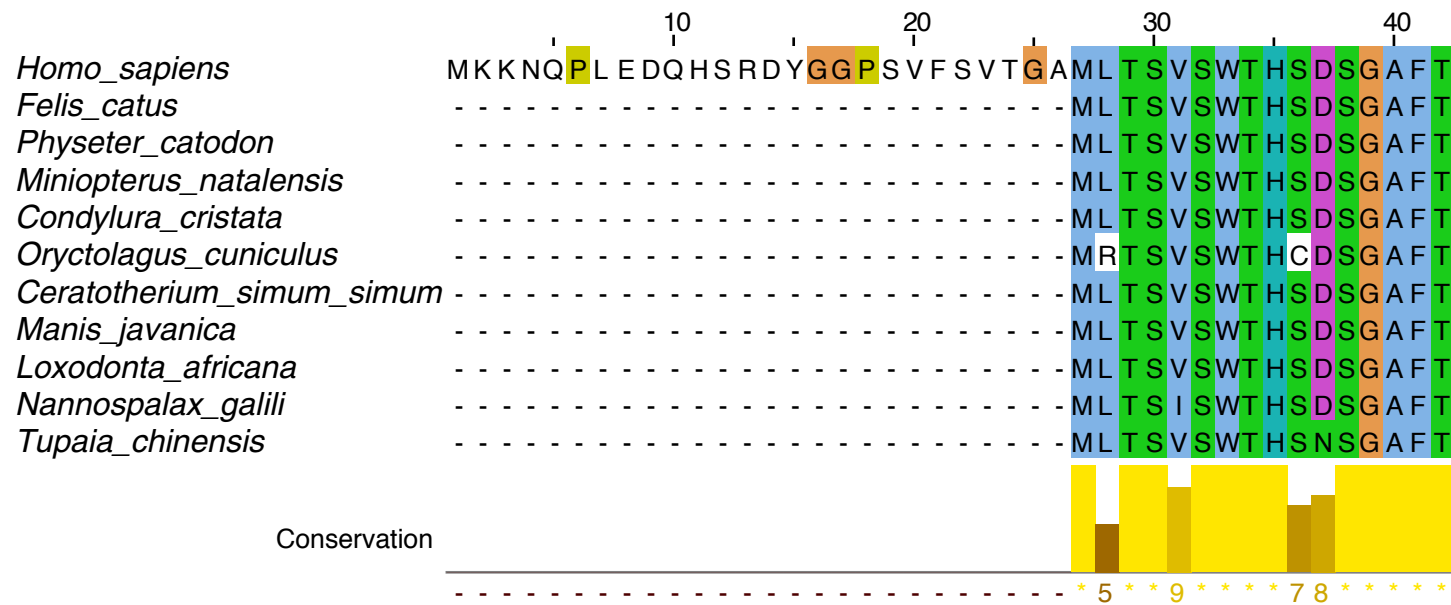


HG0604.3

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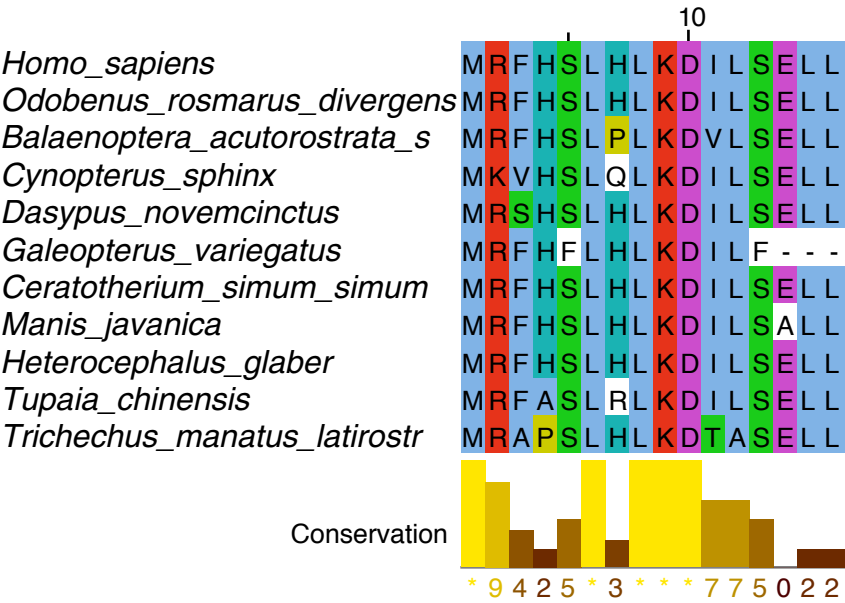


ENSG00000053254 (FOXN3)



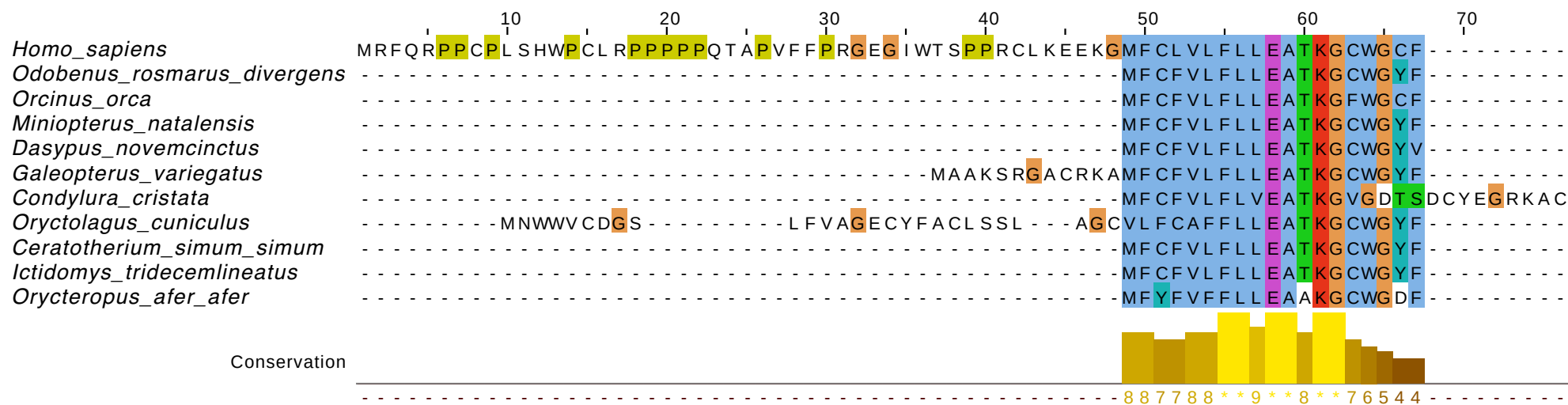
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ENSG00000055130 (CUL1)



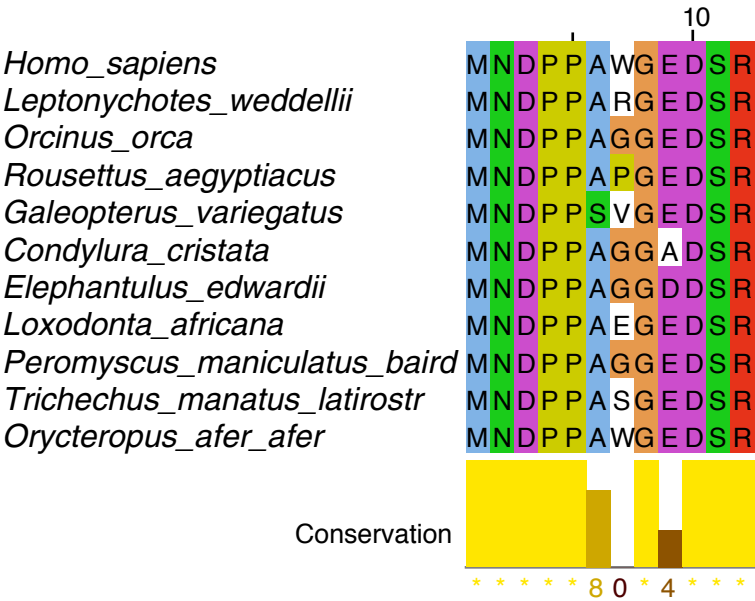
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ENSG00000074657 (ZNF532)



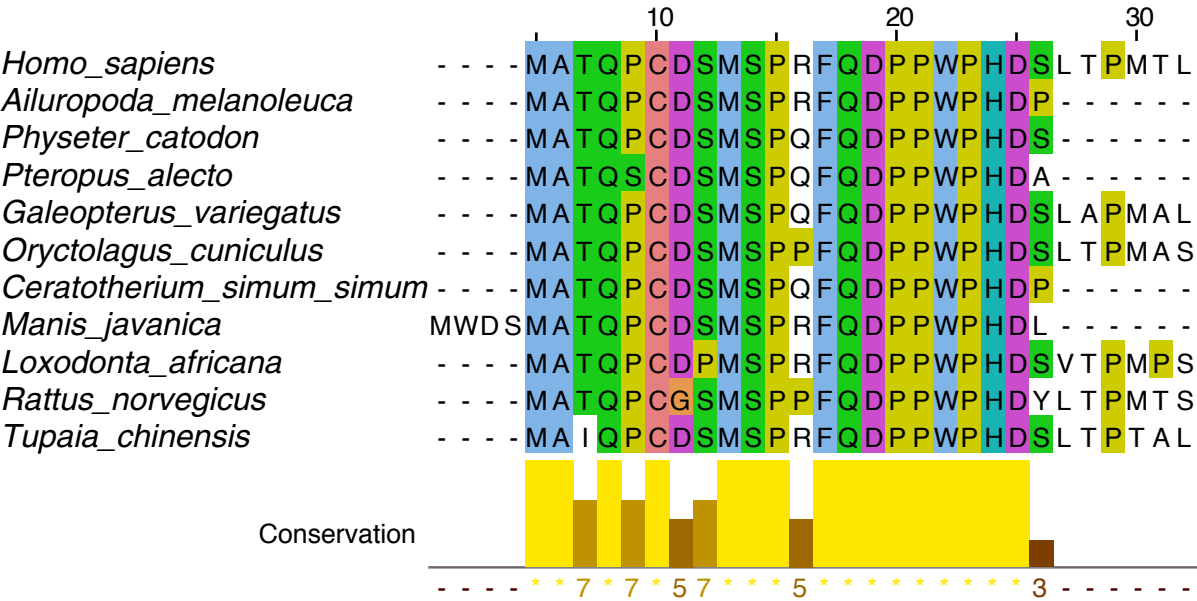
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ENSG00000084731 (KIF3C)



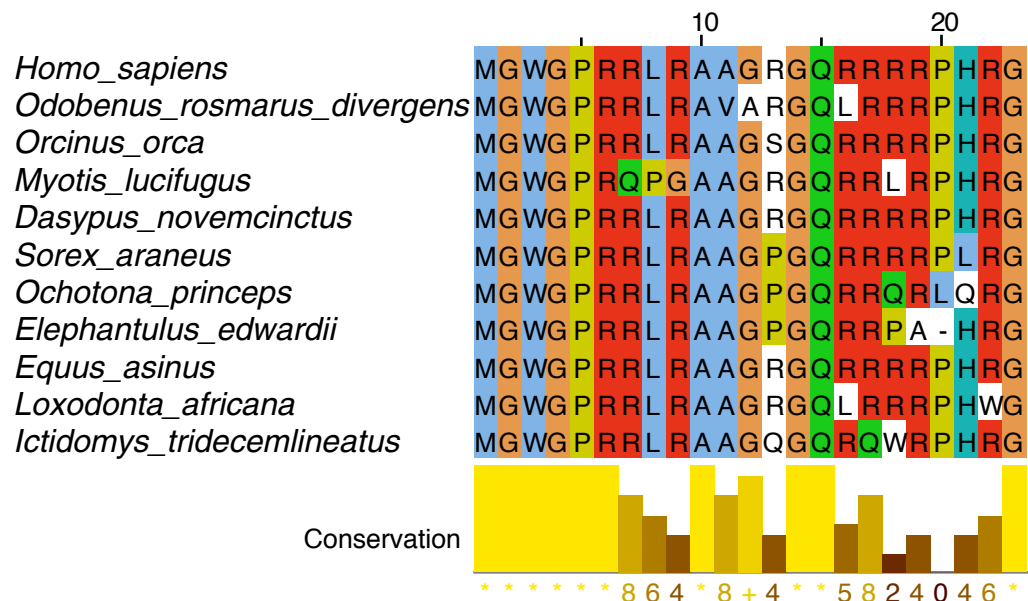
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ENSG00000095539 (SEMA4G)



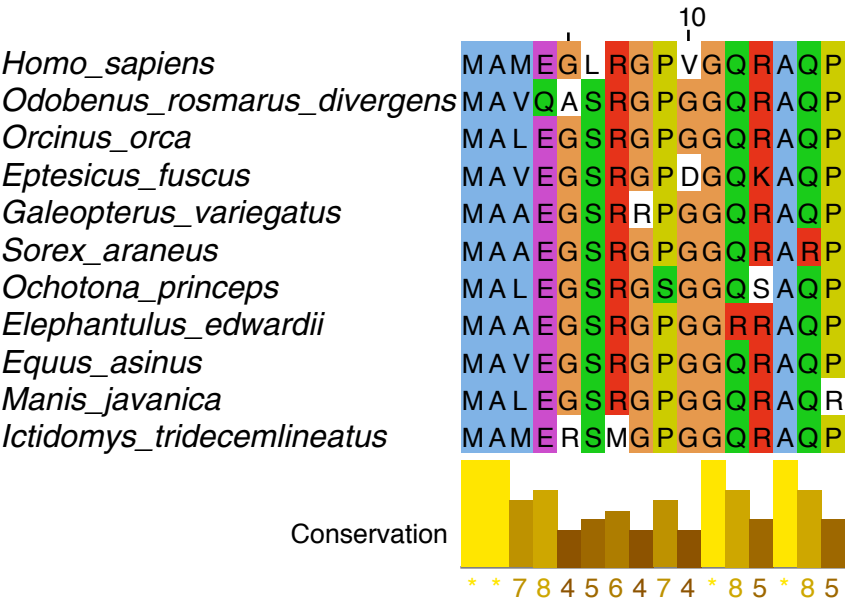
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ENSG00000106069 (CHN2)

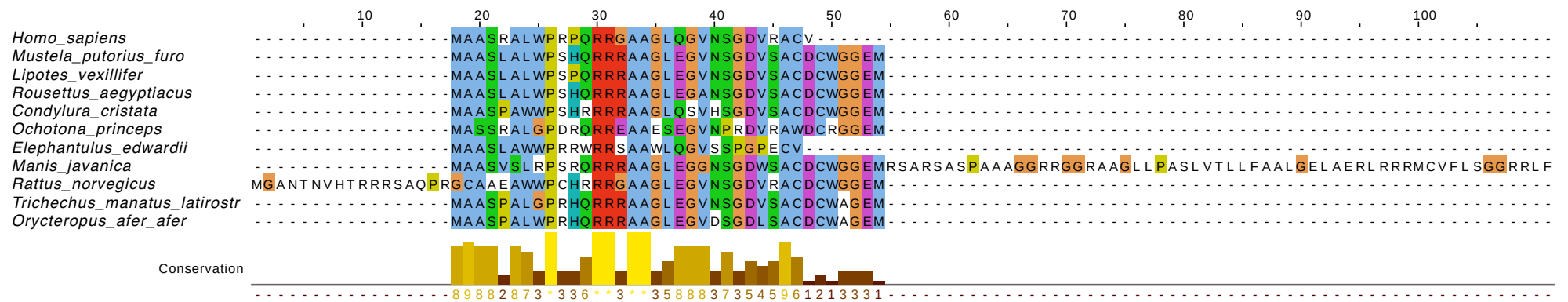


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ENSG00000108309 (RUNDC3A)

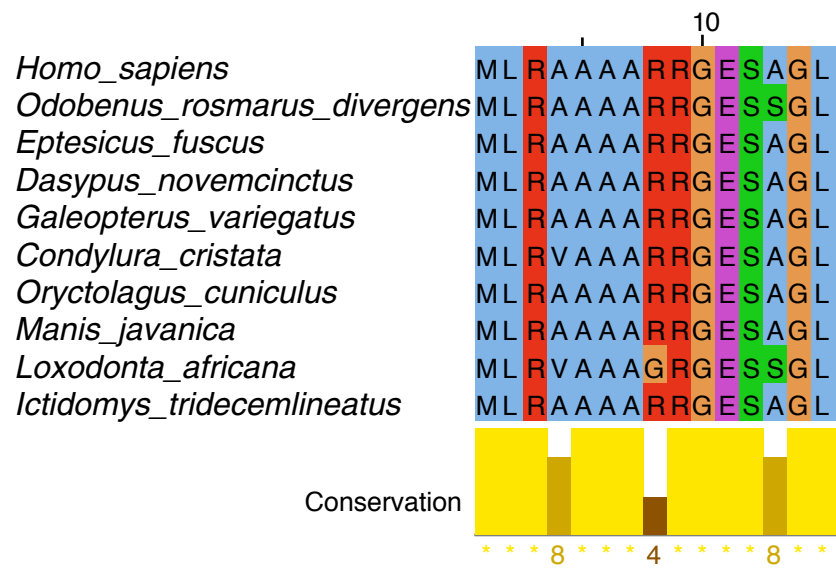


ENSG00000110422 (HIPK3)



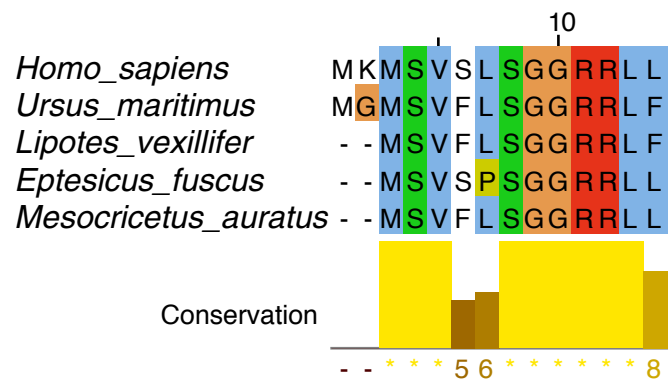
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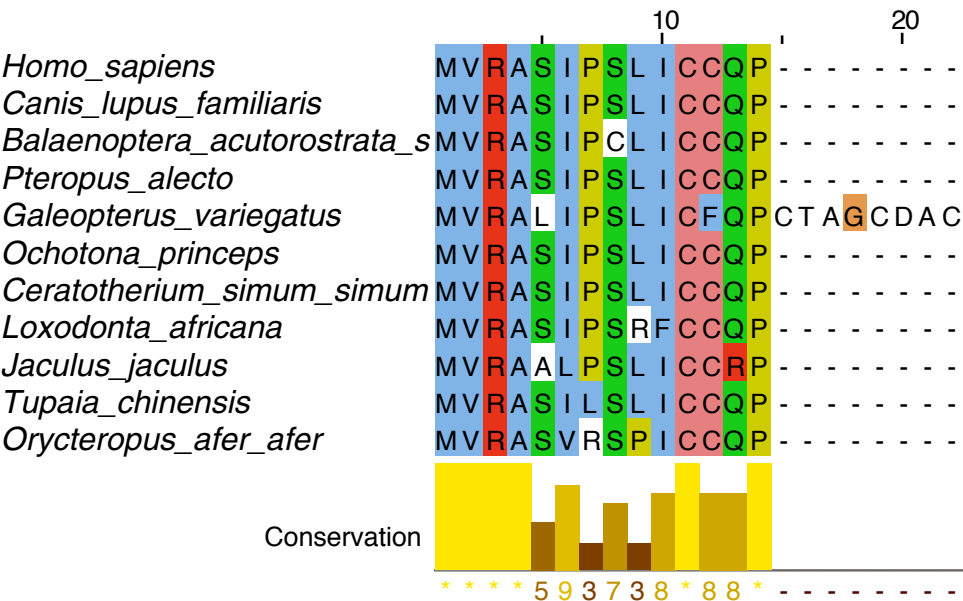
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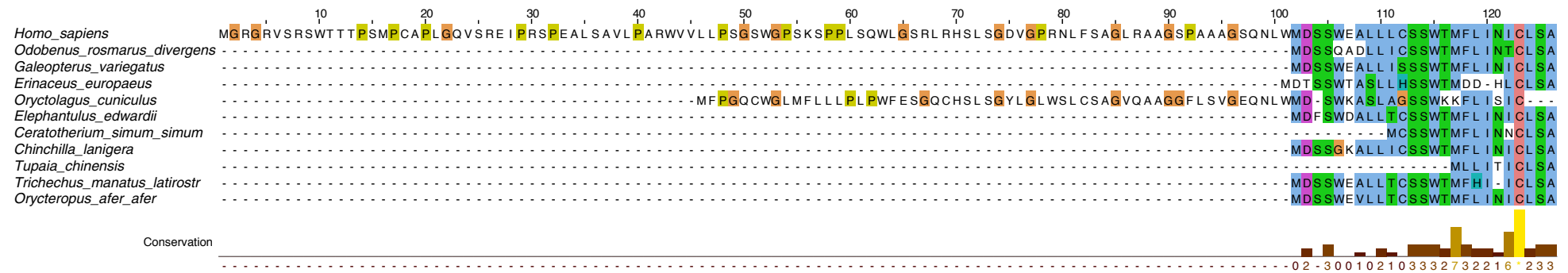


HG0613

ENSG00000114861 (FOXP1)

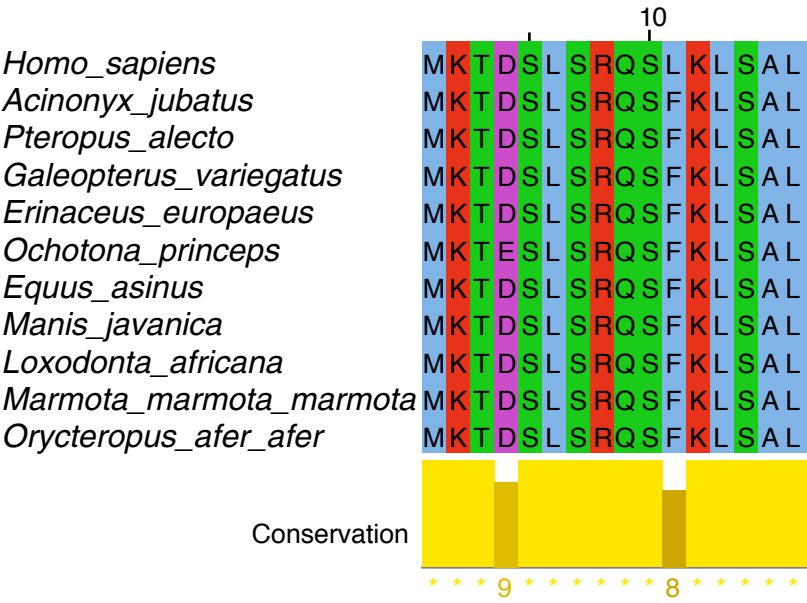


ENSG00000122203 (KIAA1191)



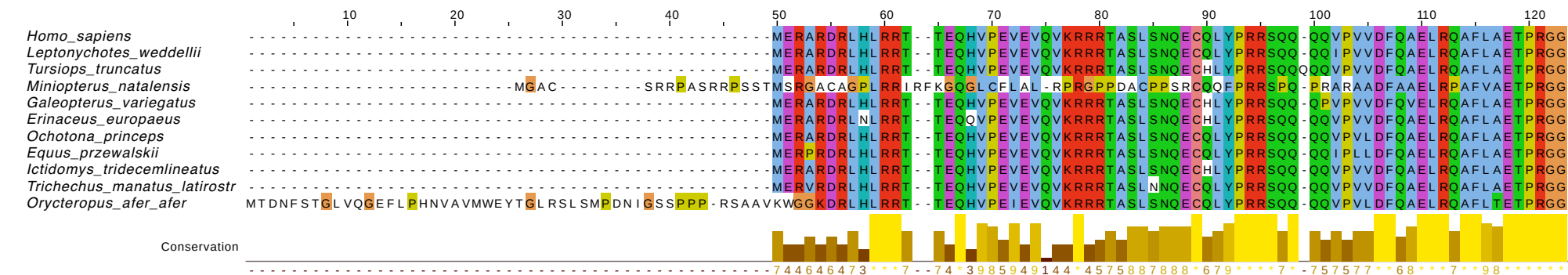
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ENSG00000128191 (DGCR8)



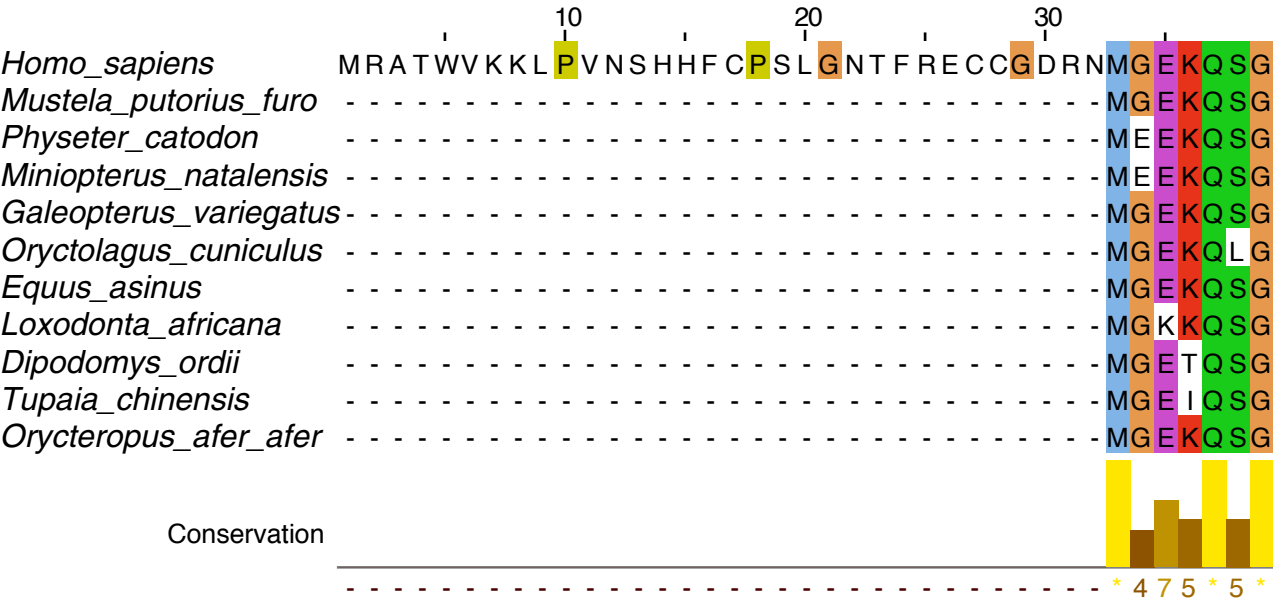
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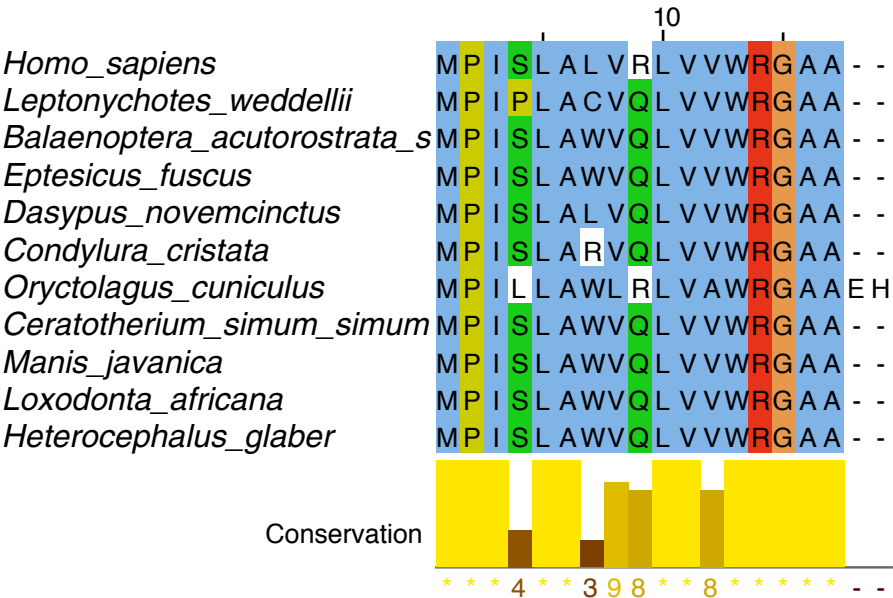
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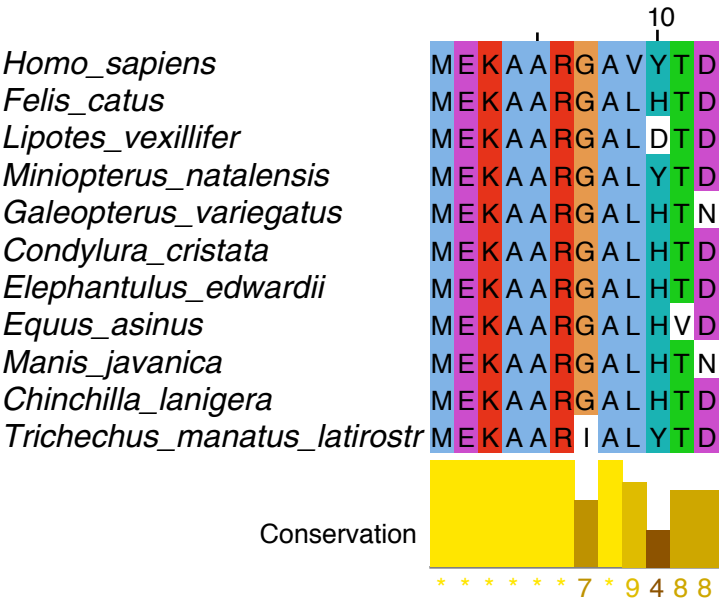
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ENSG00000137817 (PARP6)



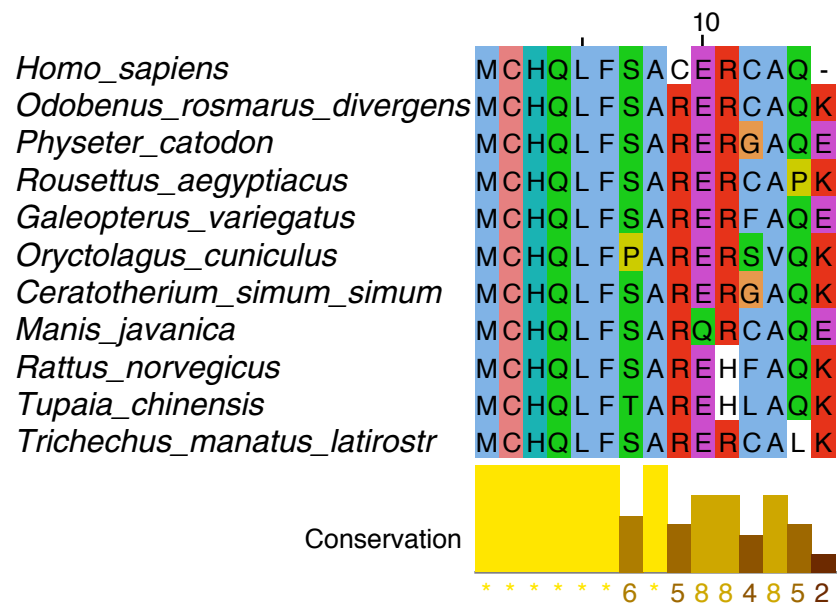
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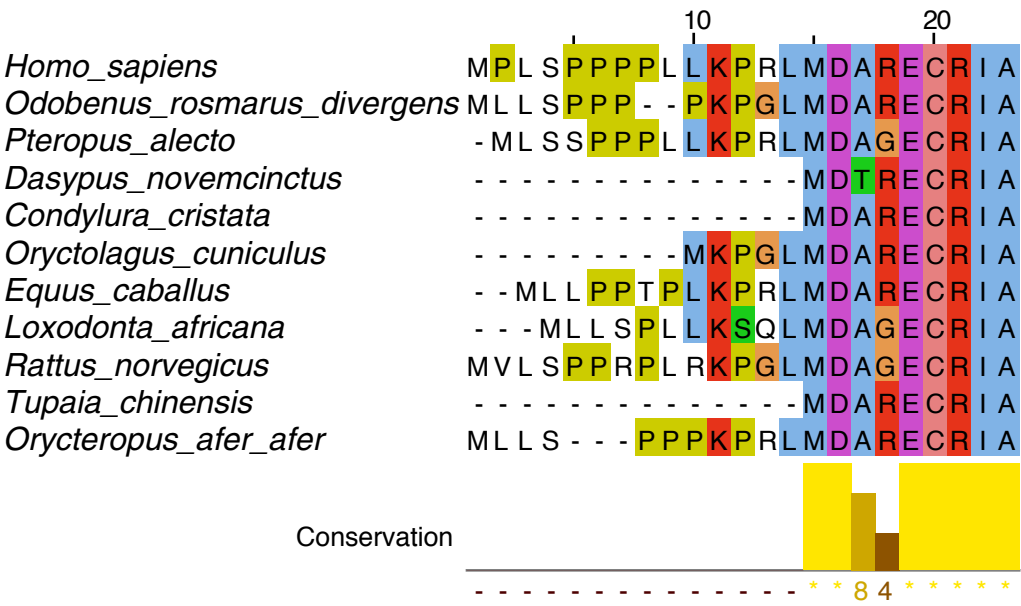
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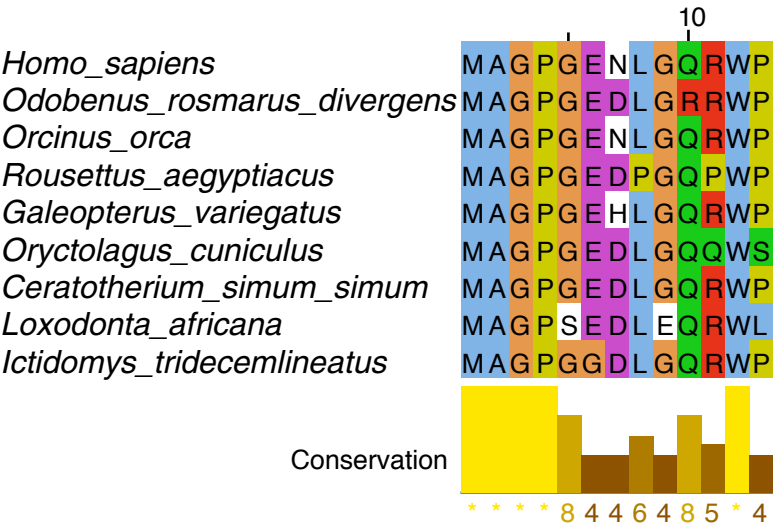
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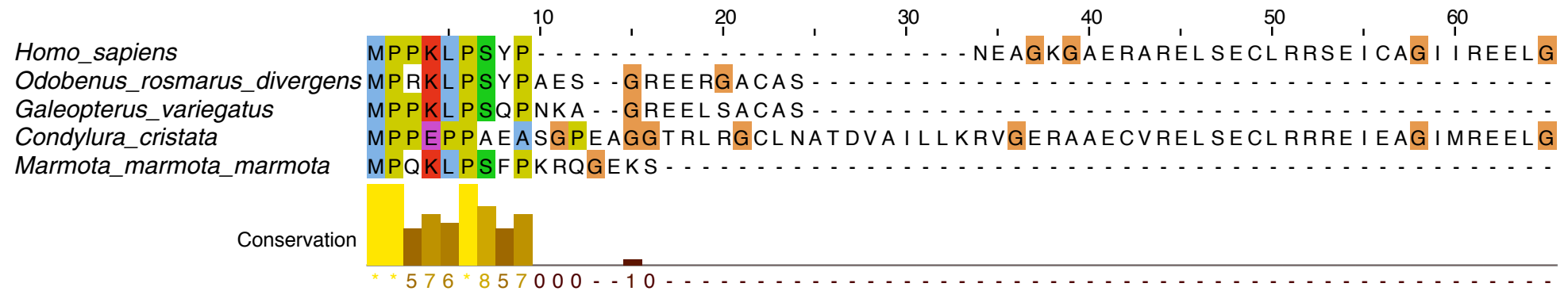


HG0621.2

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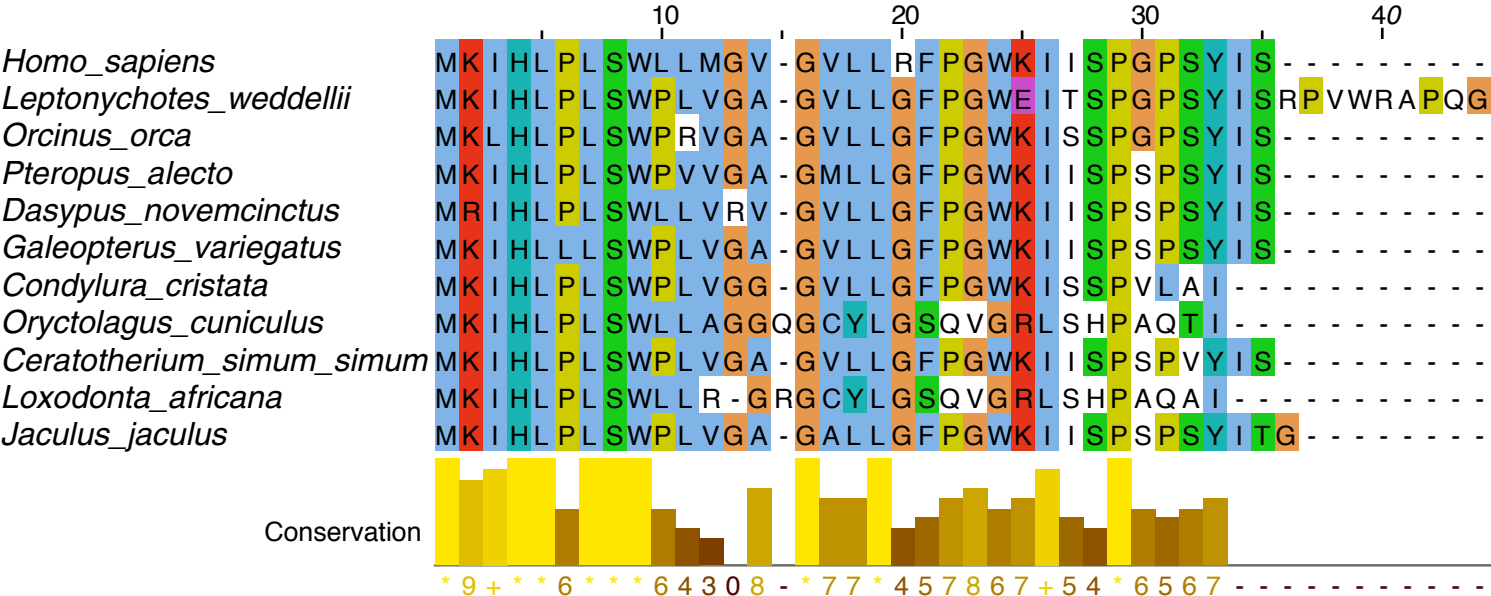


ENSG00000146352 (CLVS2)



HG0622

ENSG00000148677 (ANKRD1)



HG0623

ENSG00000151422 (FER)

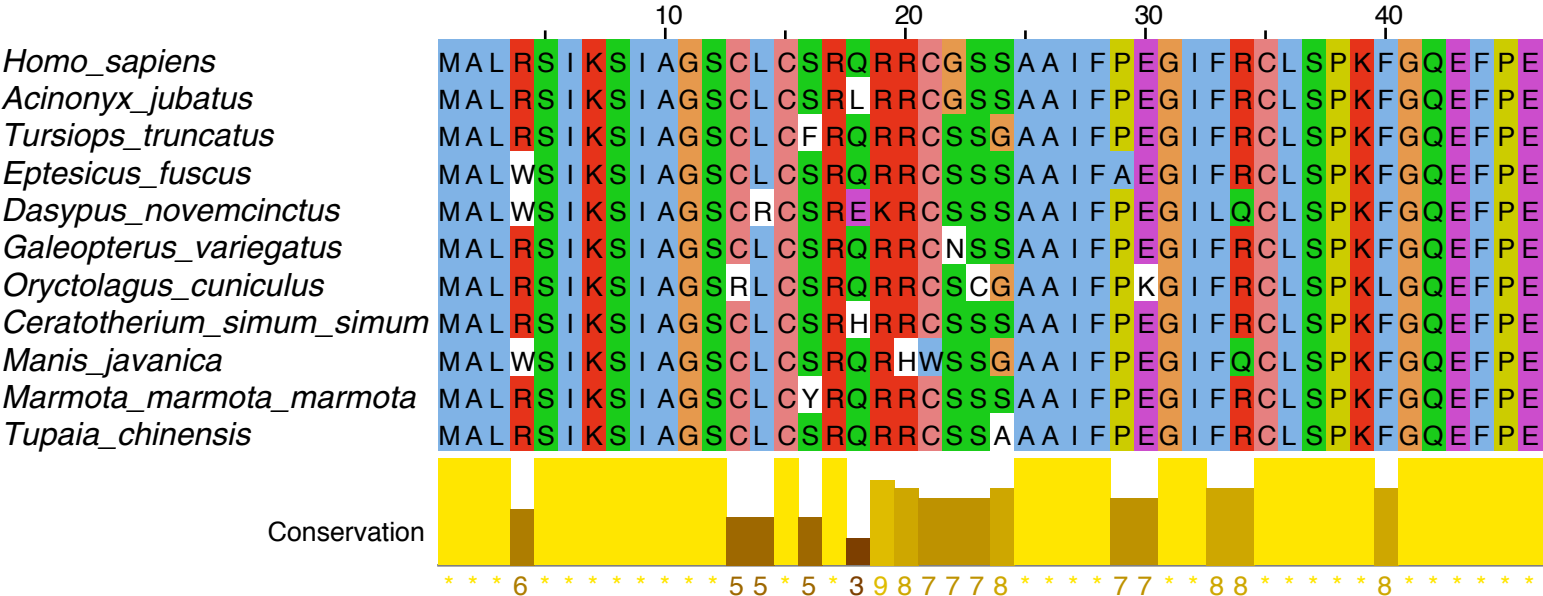
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Conservation



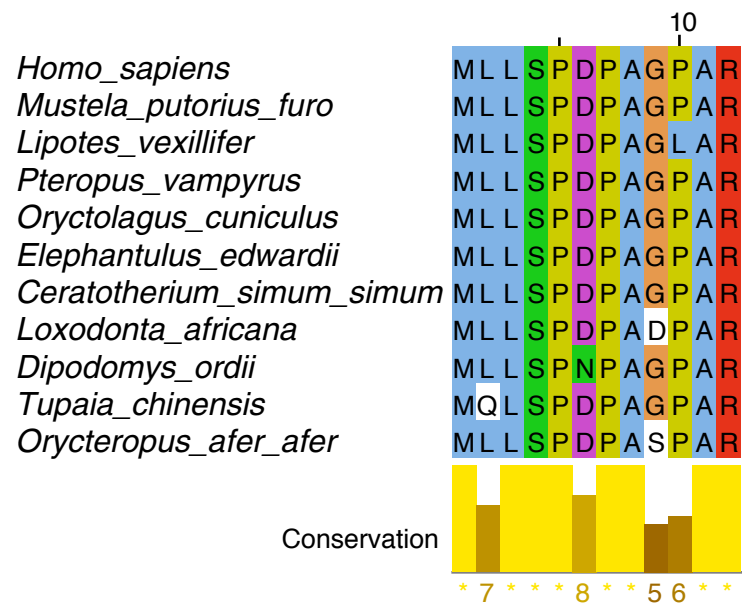
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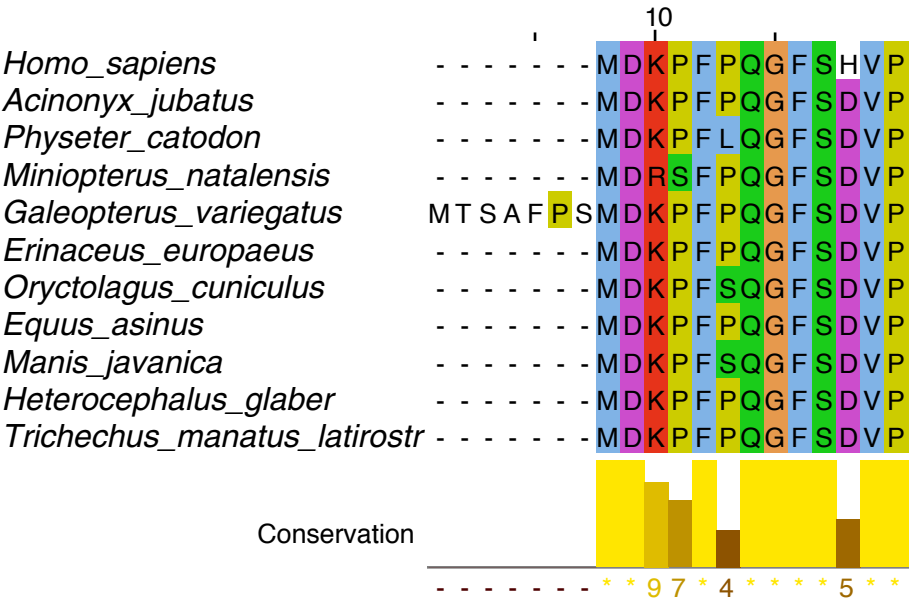
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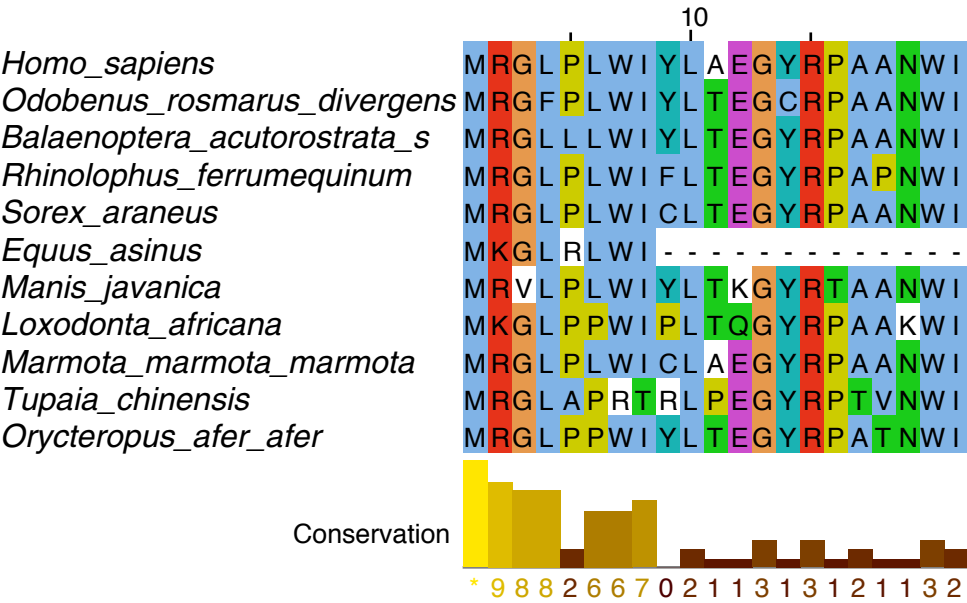
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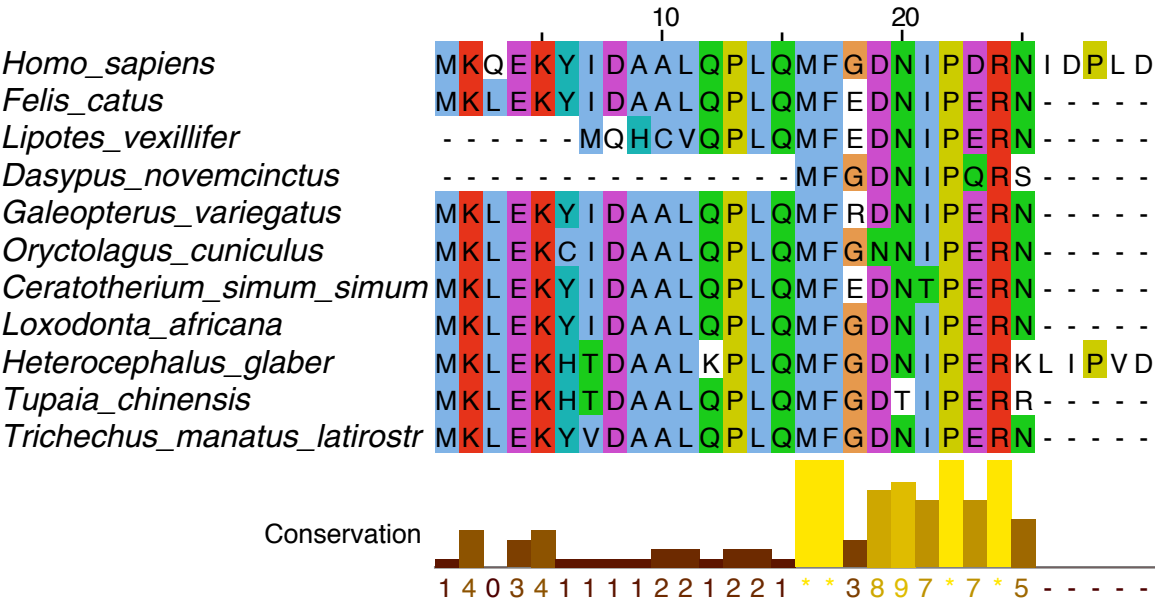
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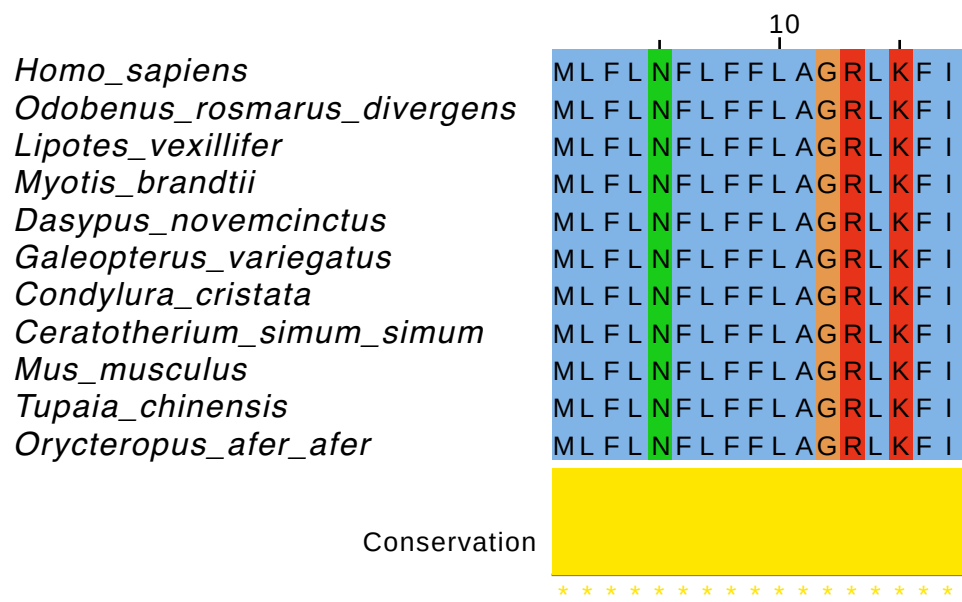
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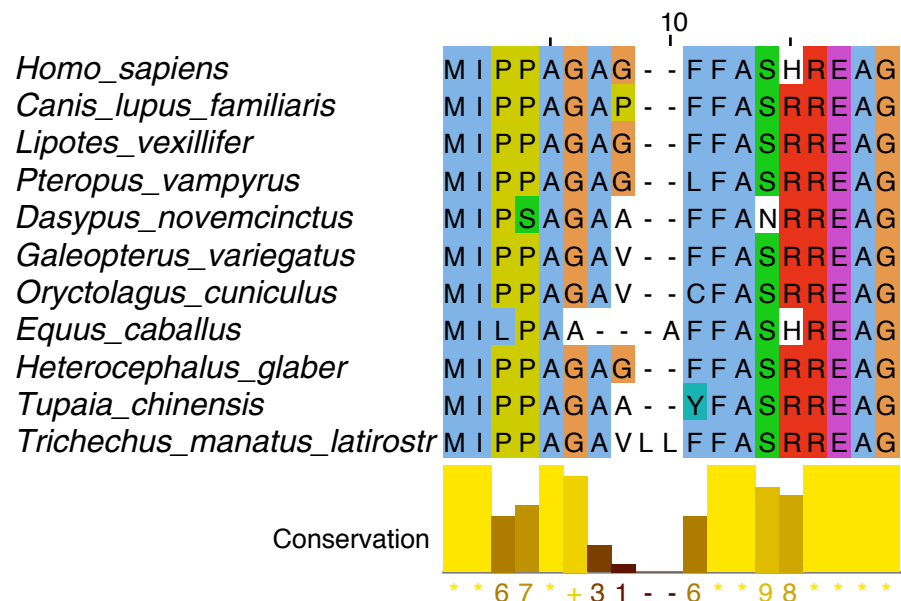
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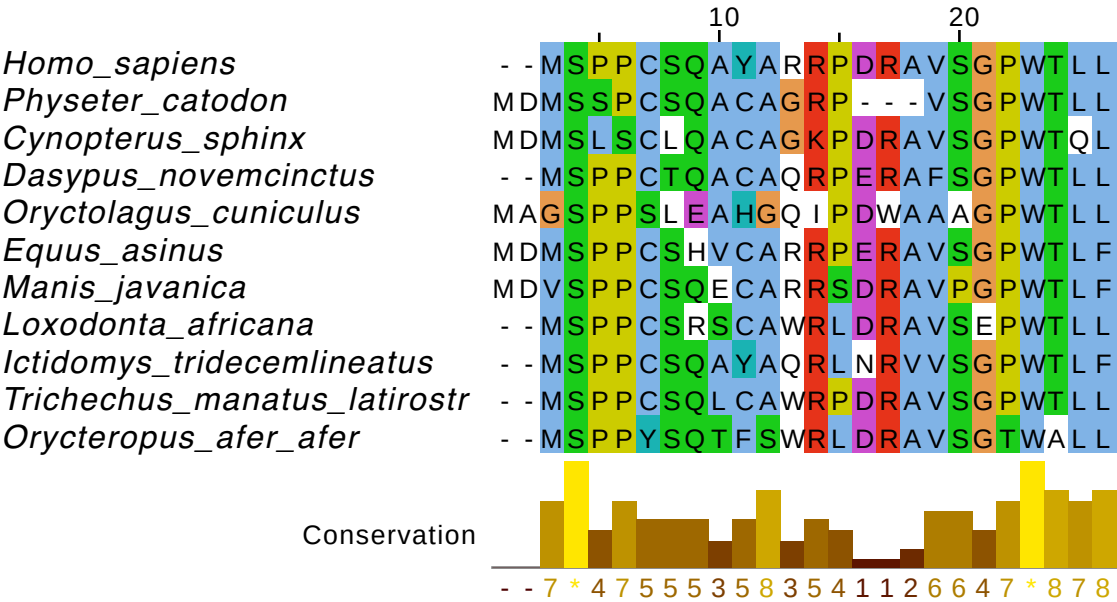
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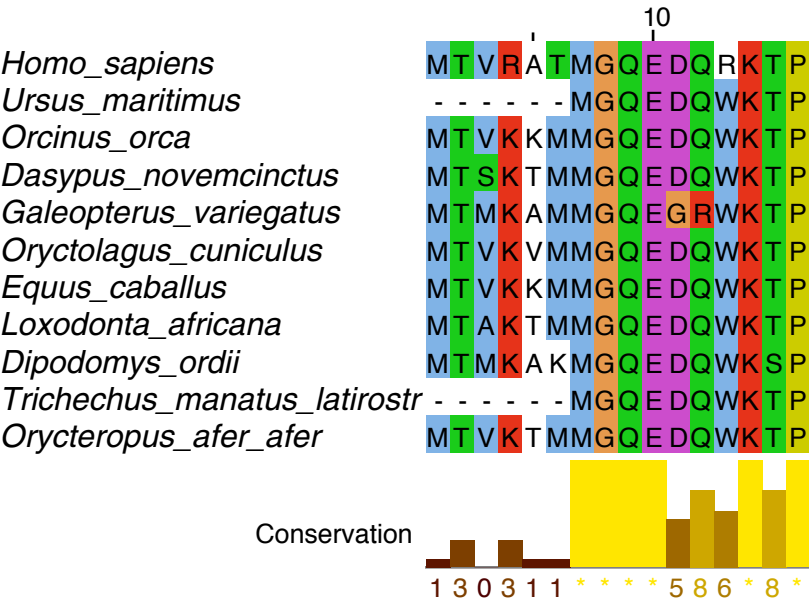
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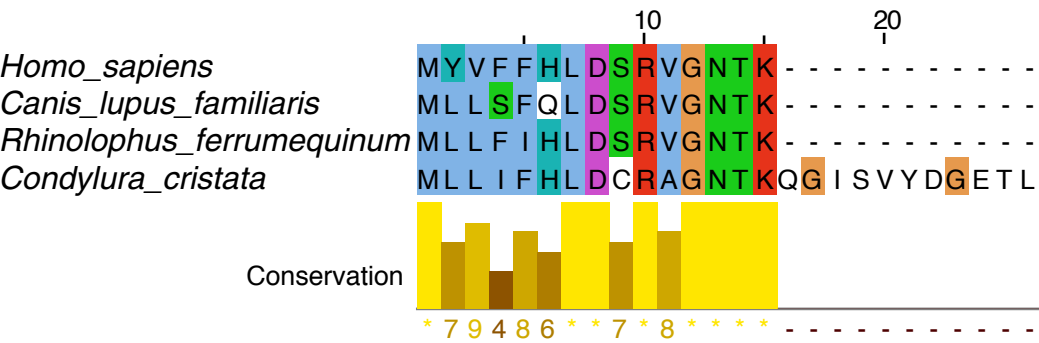
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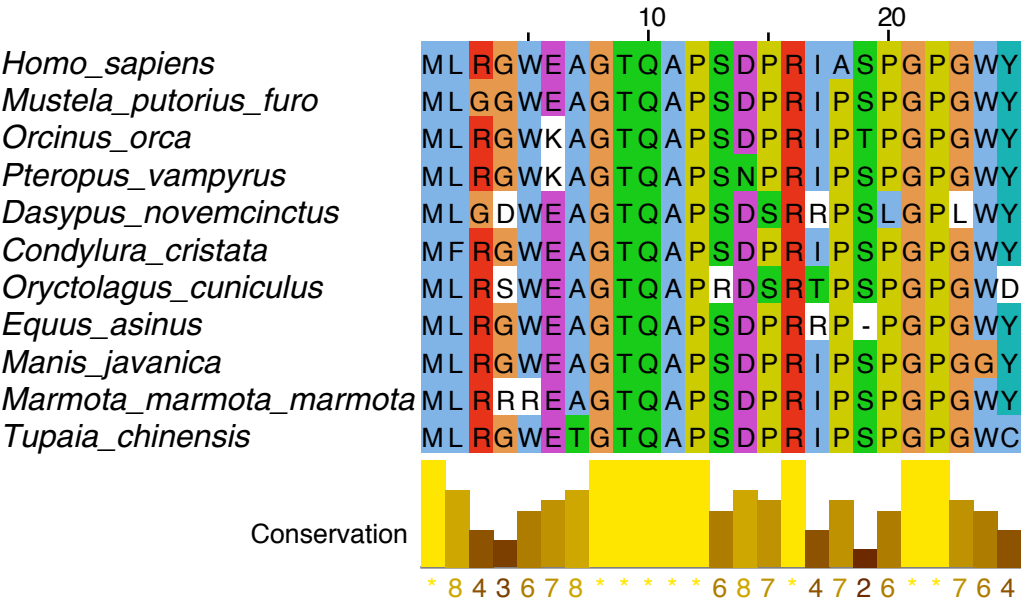
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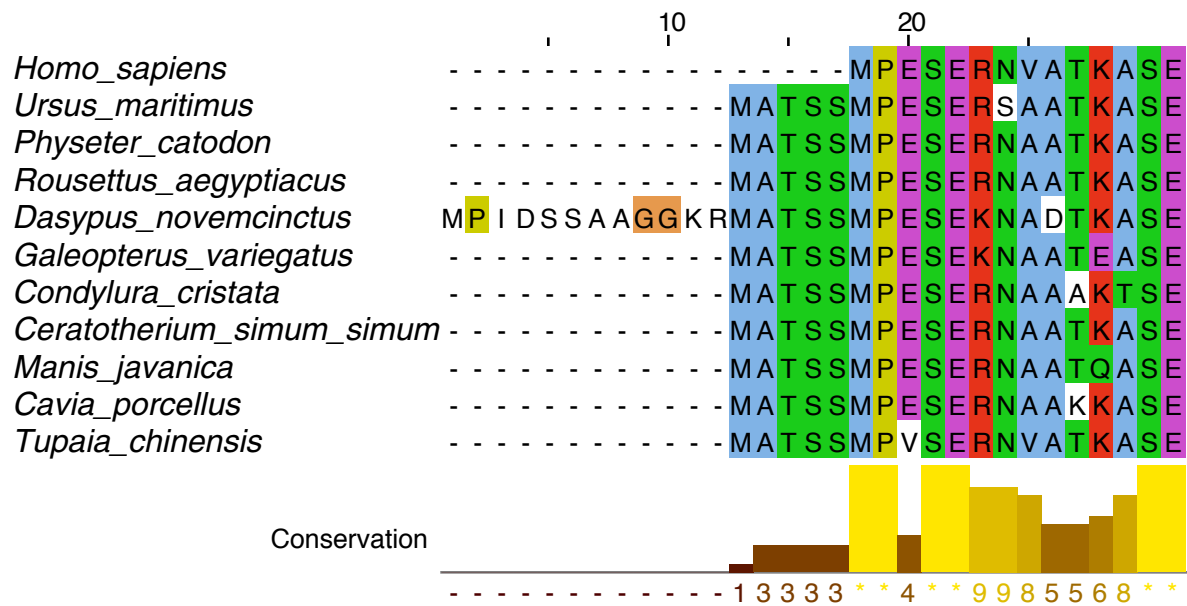
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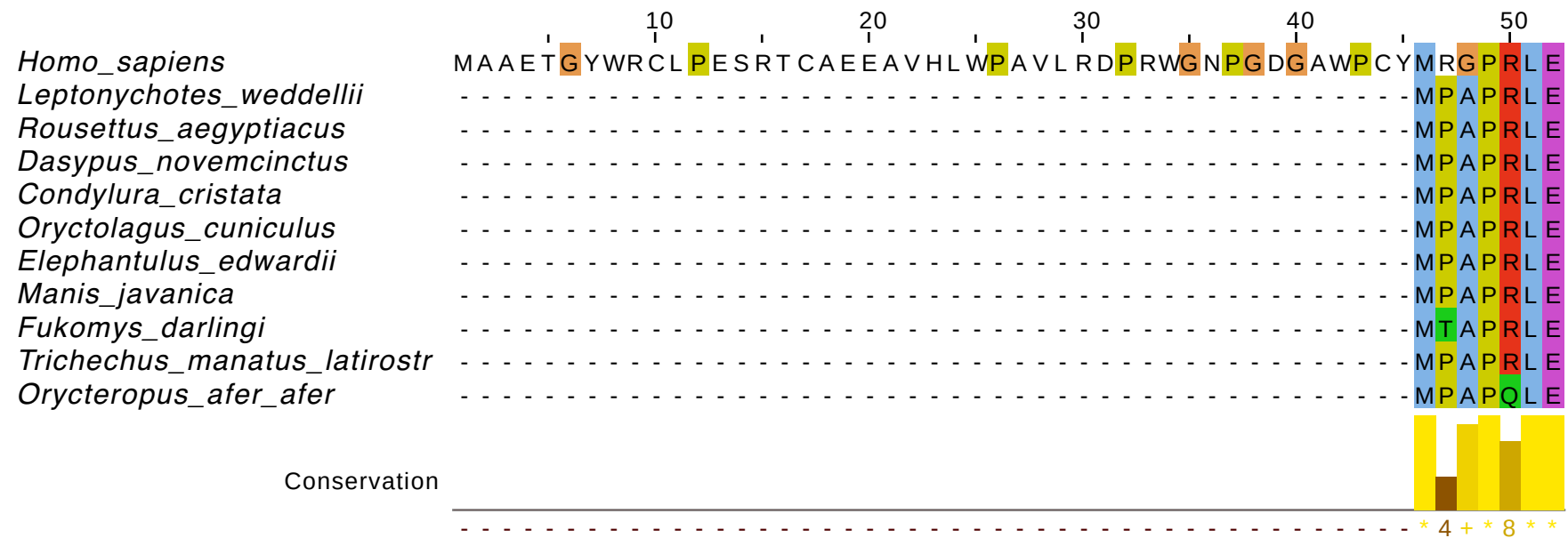
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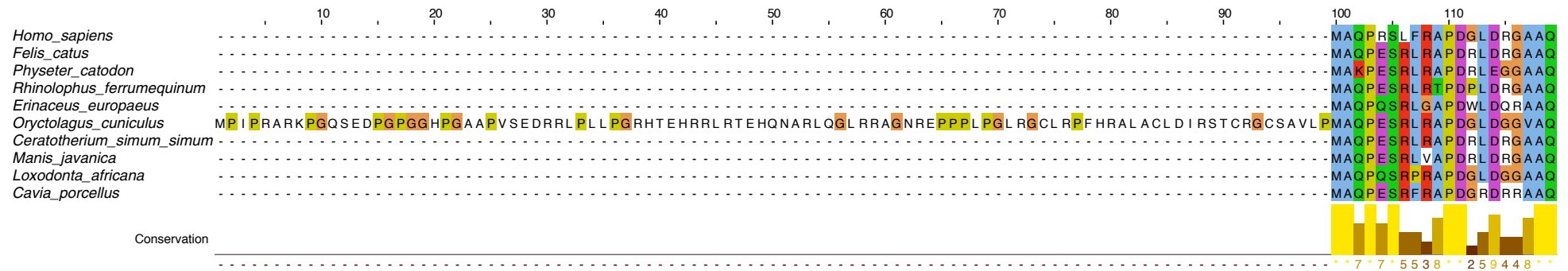
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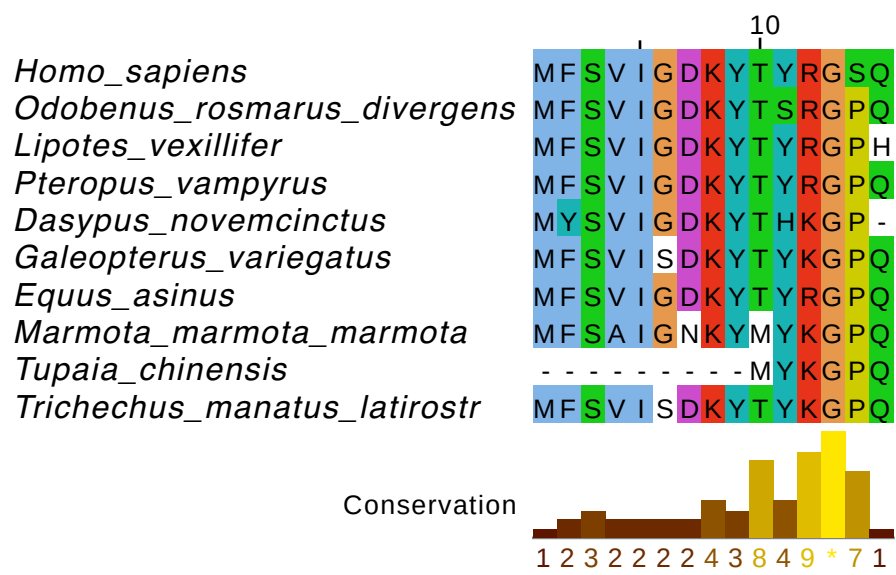
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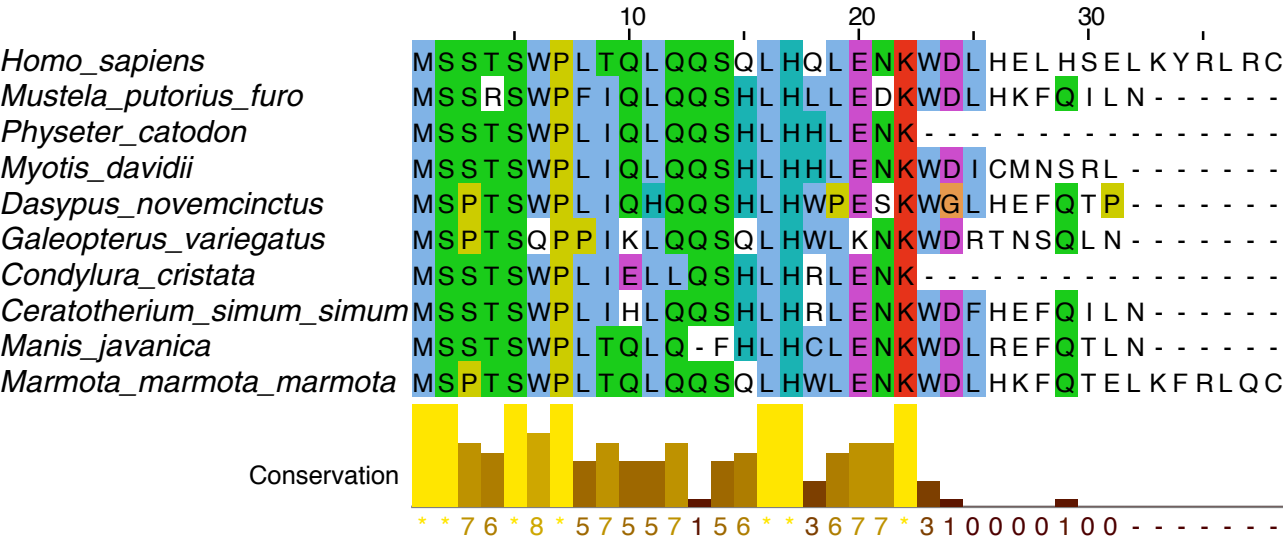
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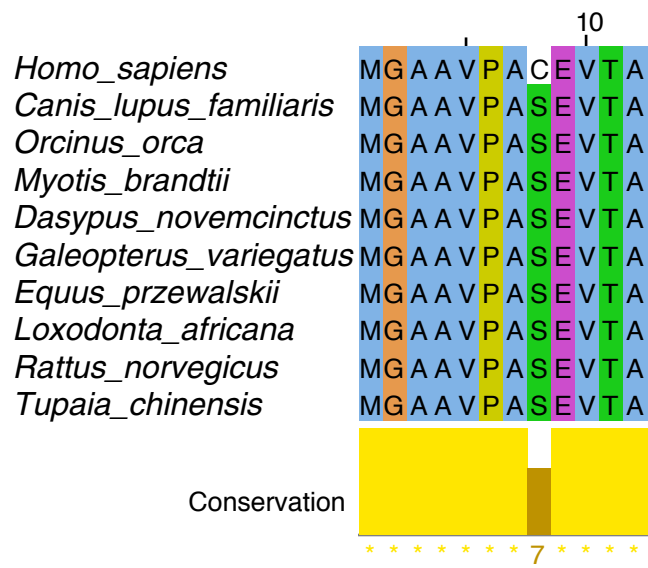
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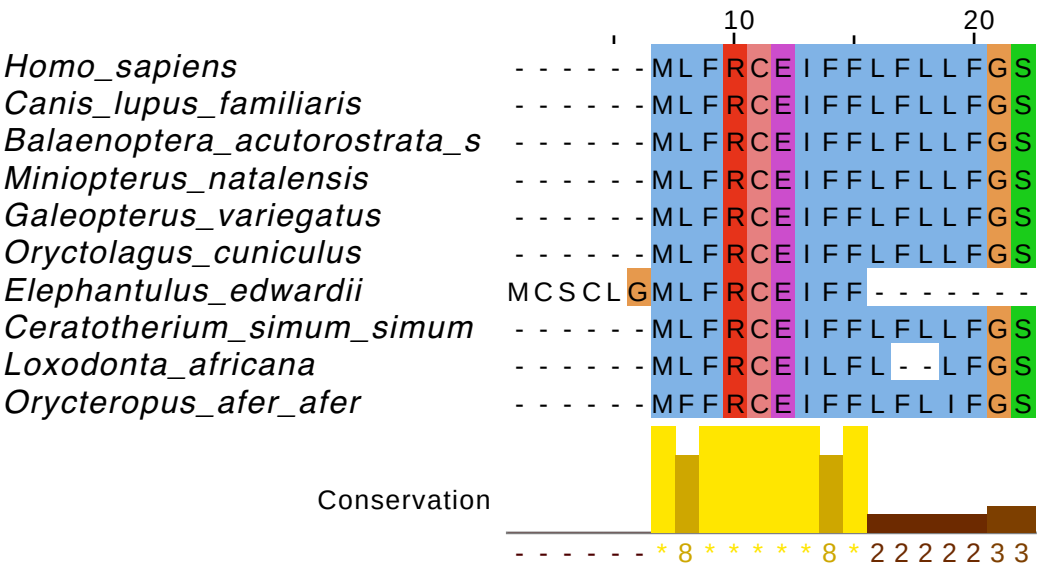
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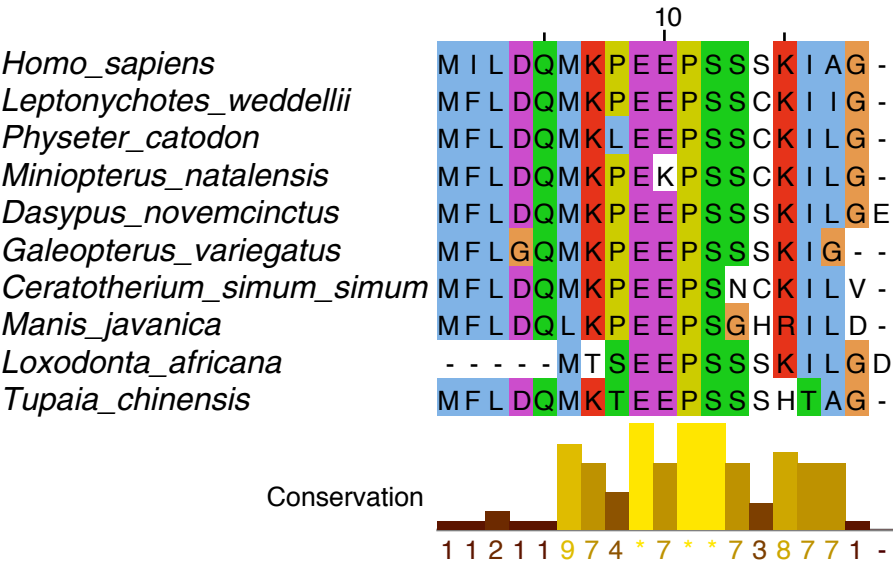
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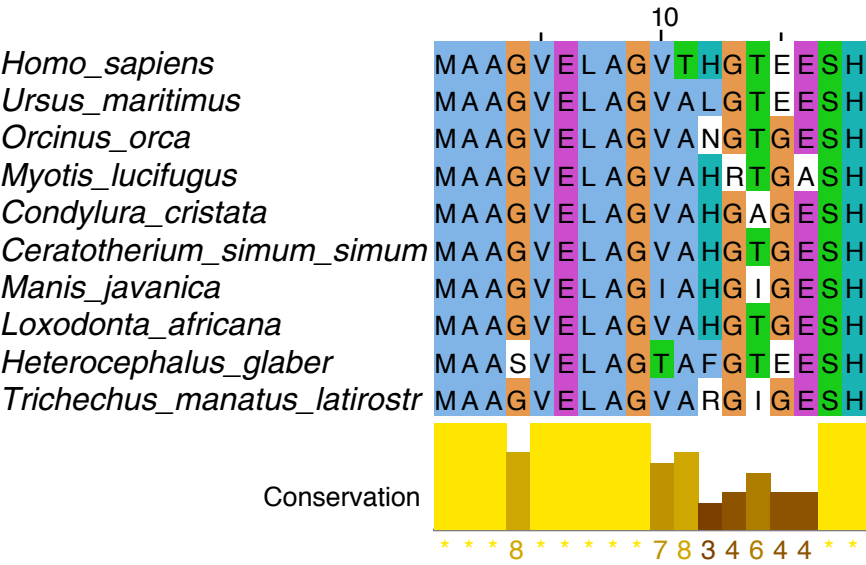
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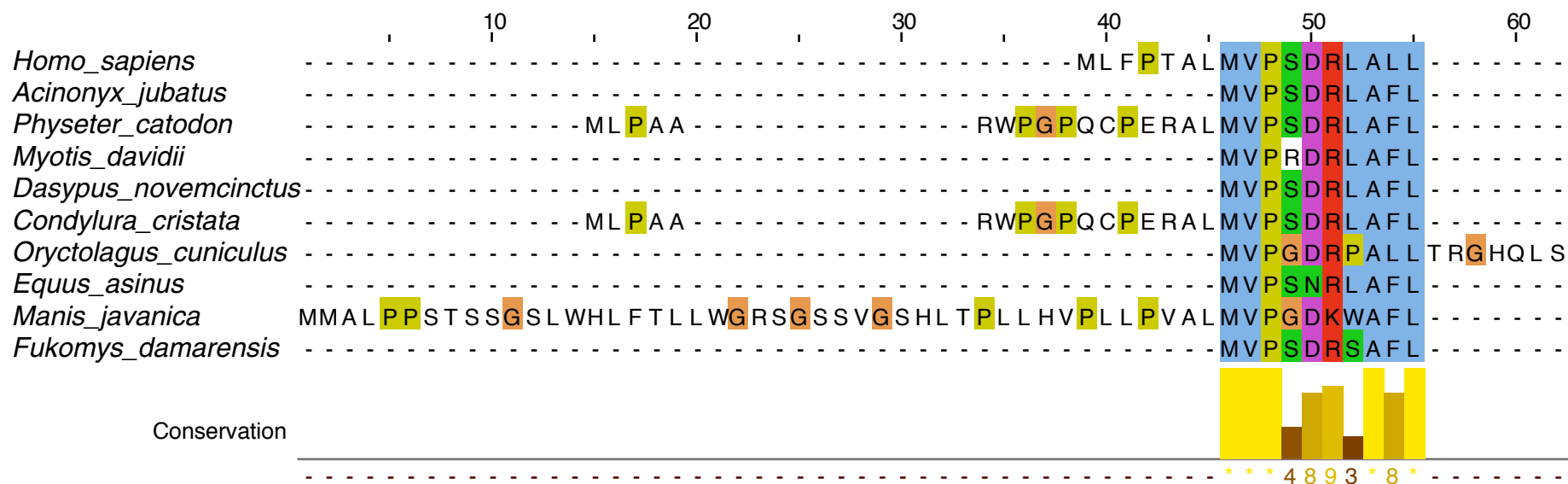


HG0642

ENSG00000100815 (TRIP11)

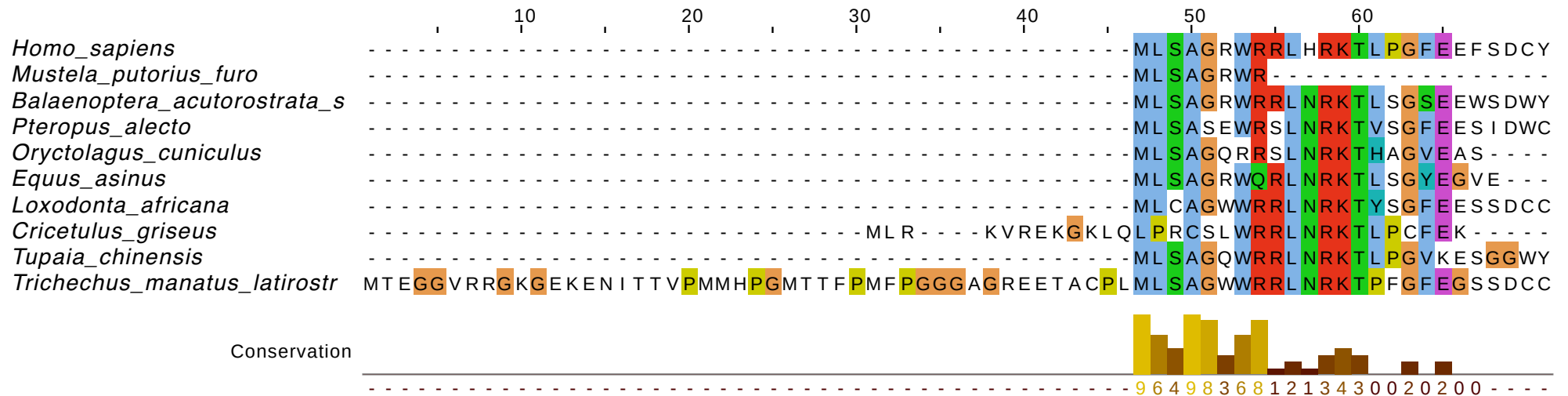


ENSG00000103653 (CSK)



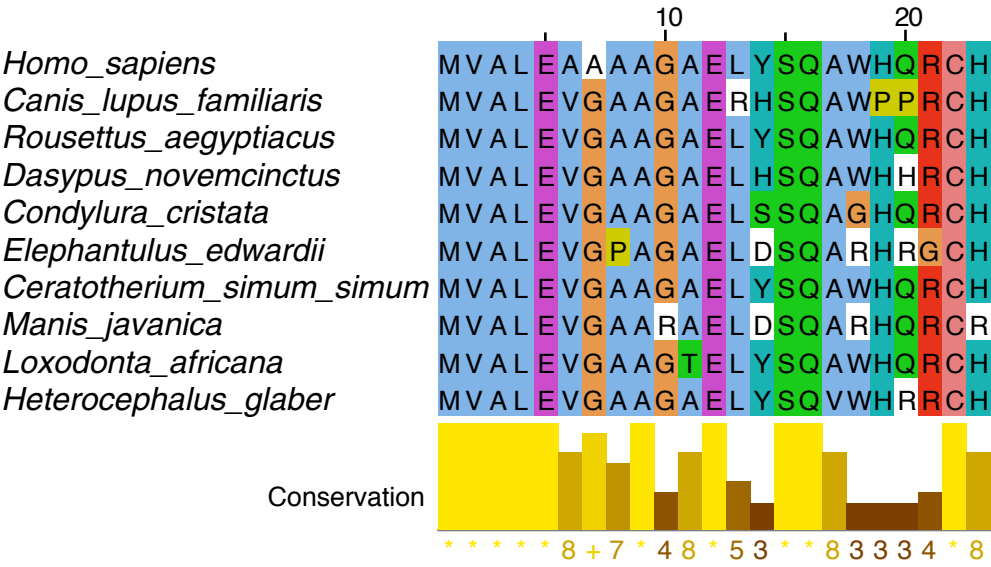
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ENSG00000104299 (INTS9)

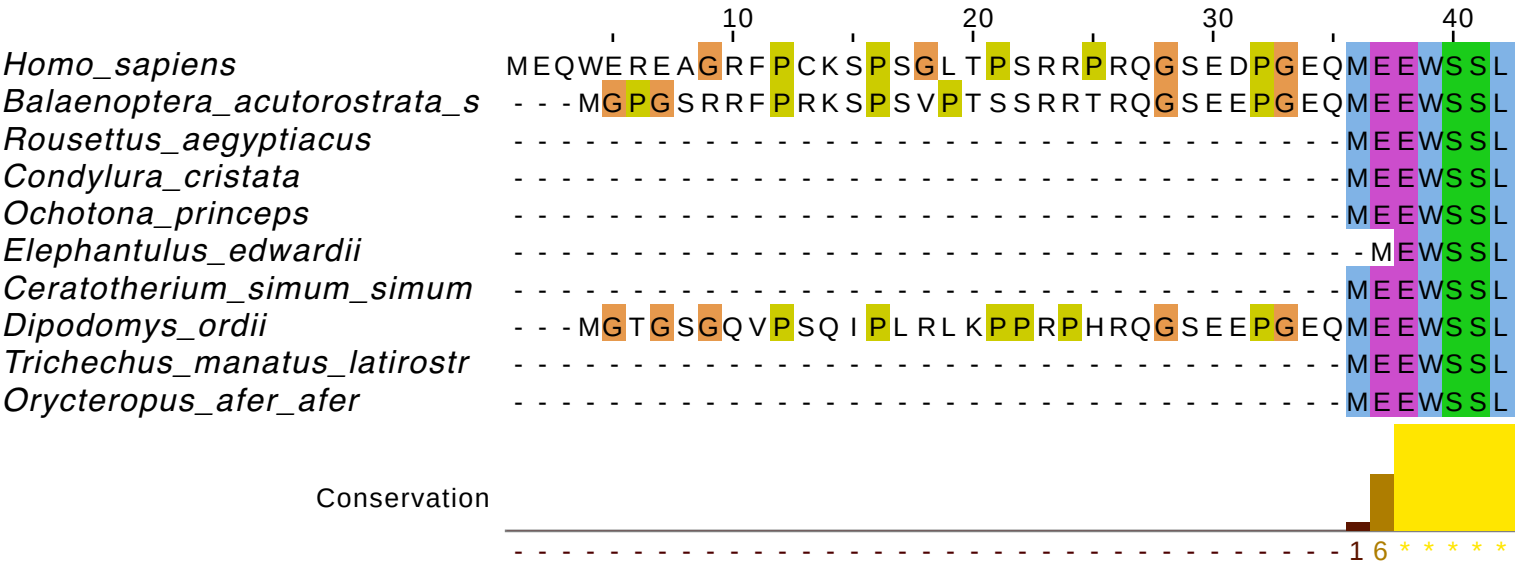


HG0645

ENSG00000107282 (APBA1)

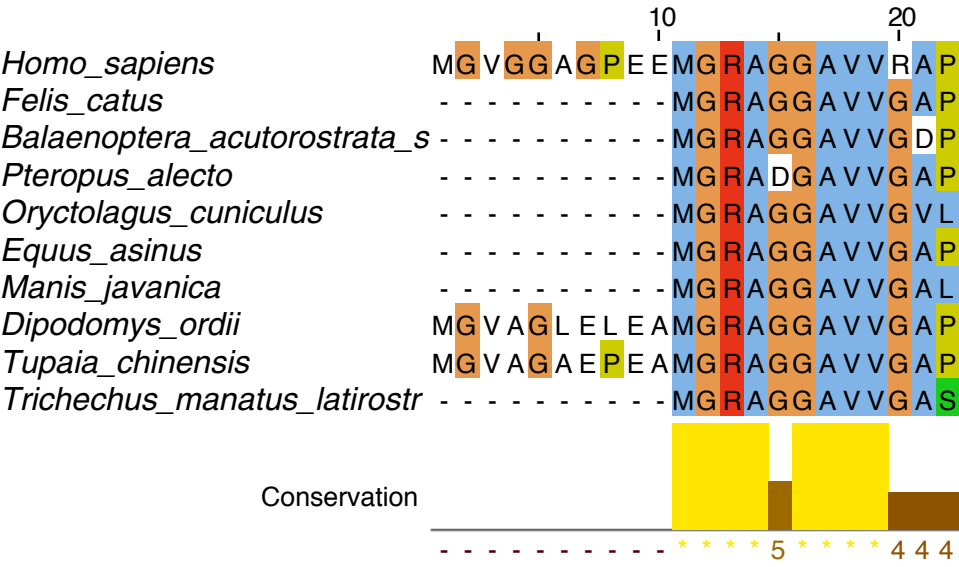


HG0646
ENSG00000108312 (UBTF)



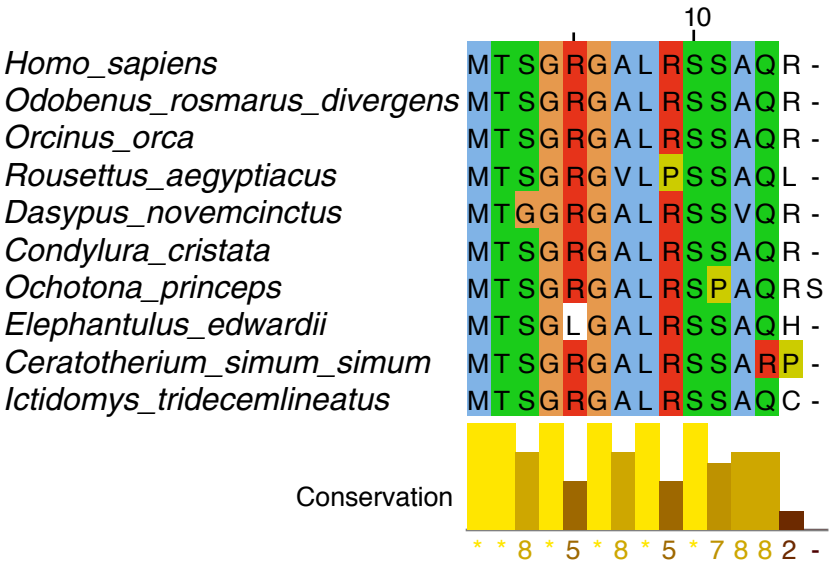
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ENSG00000108395 (TRIM37)



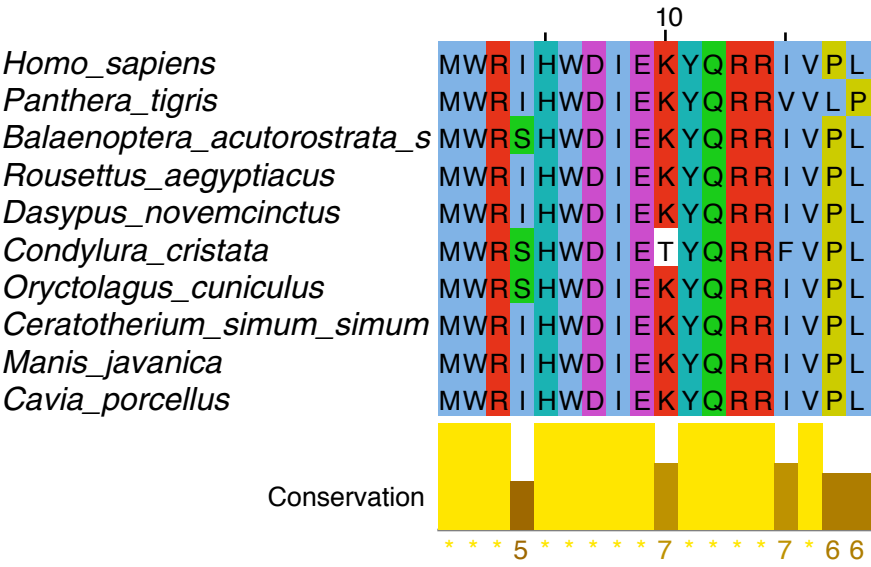
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ENSG00000114331 (ACAP2)



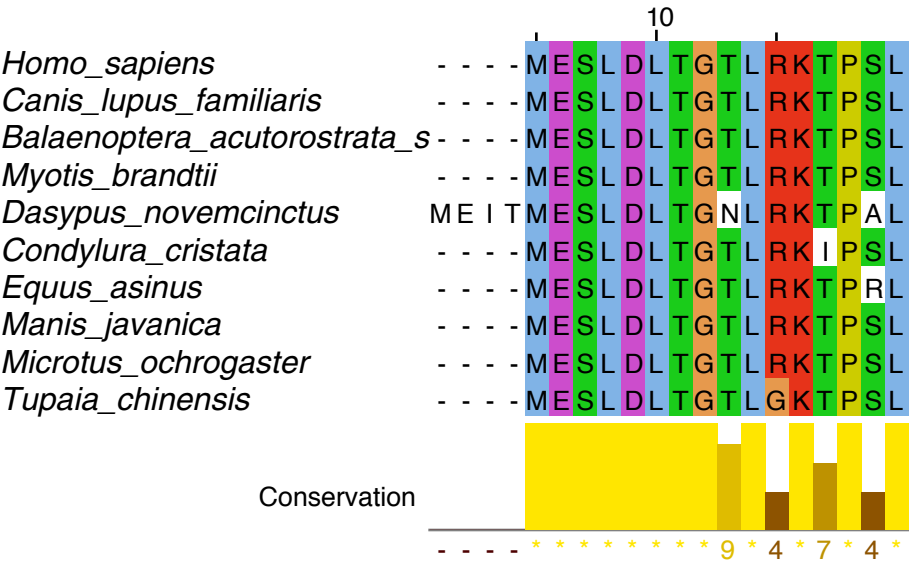
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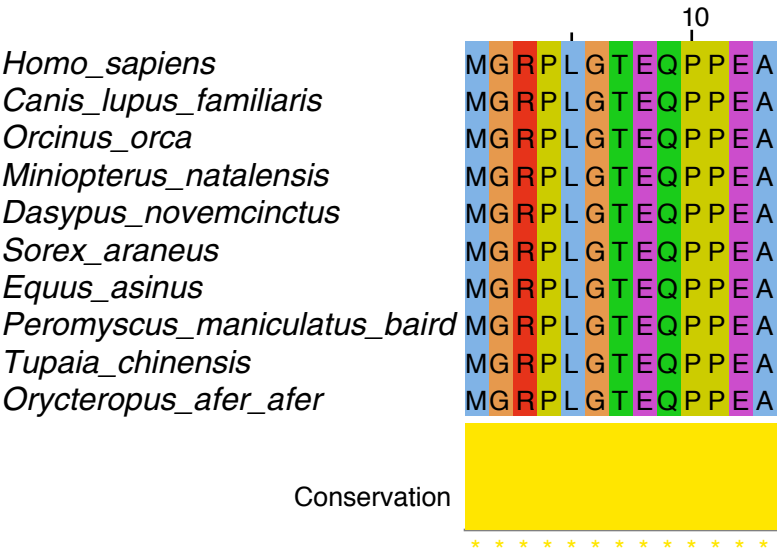
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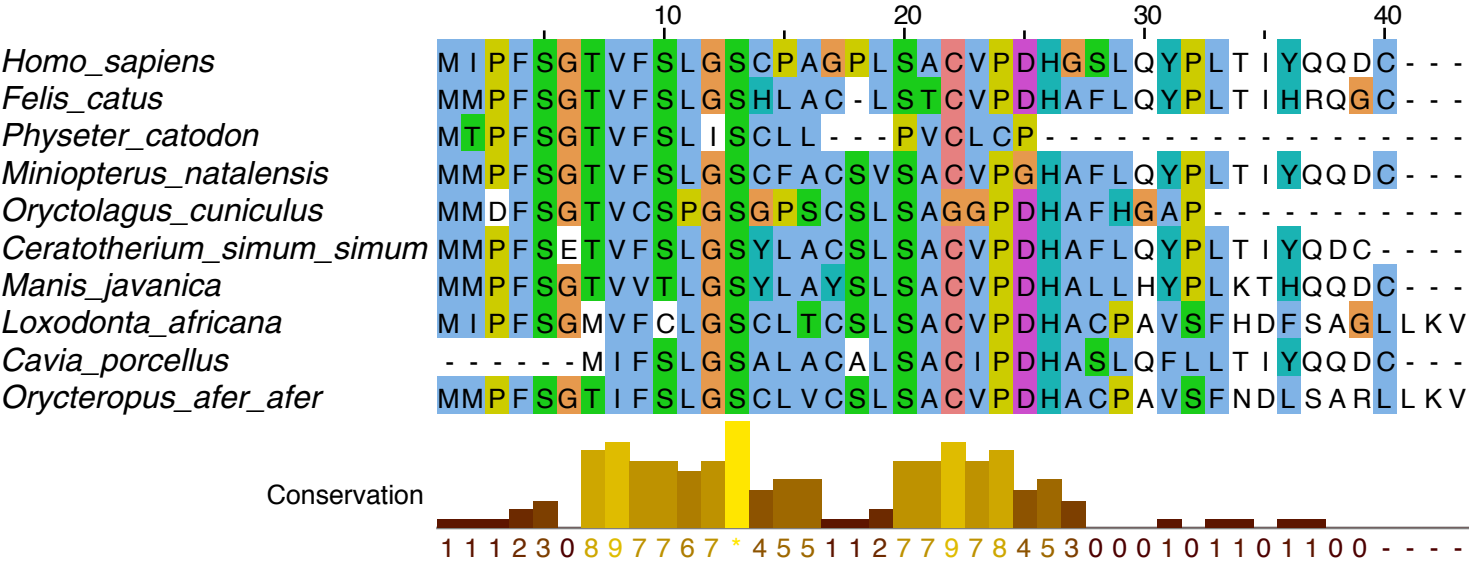
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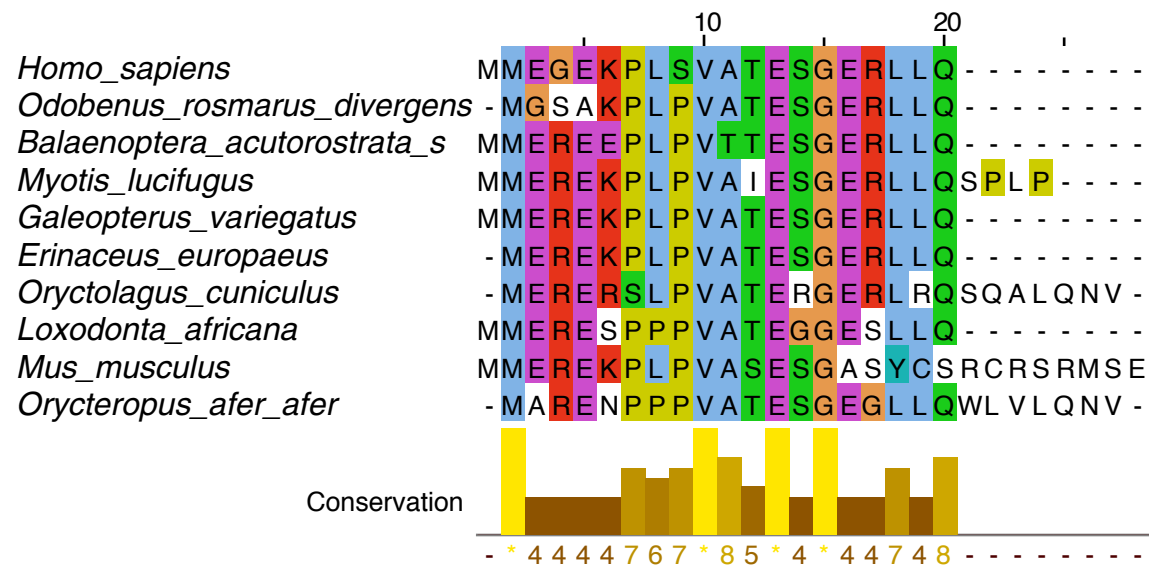
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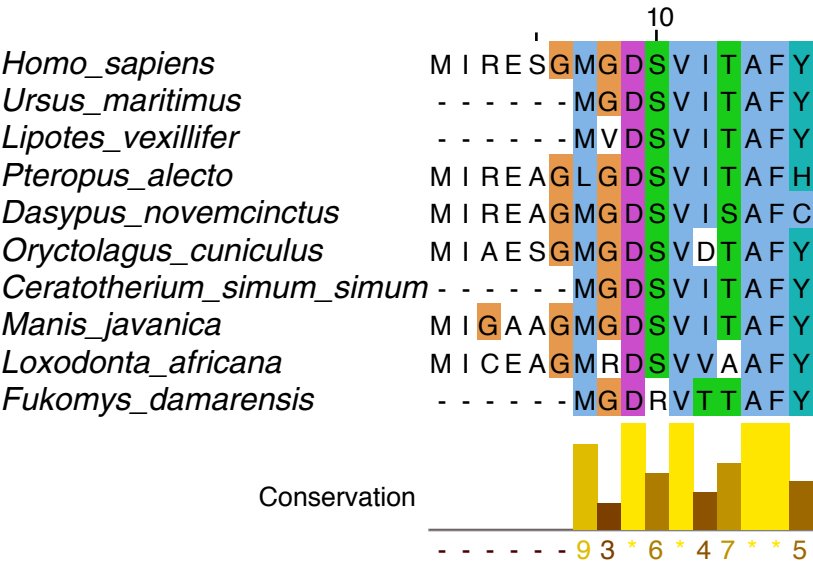
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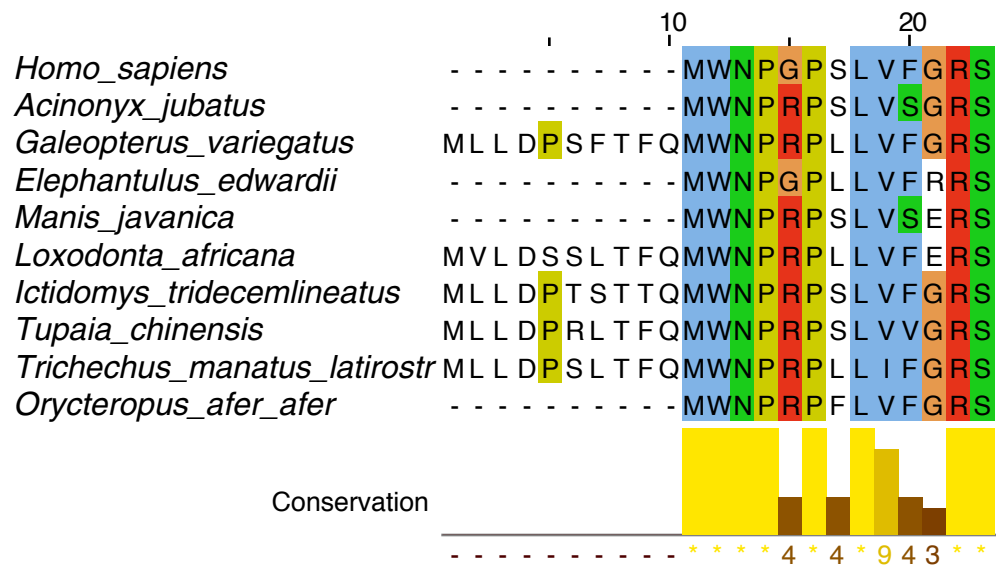
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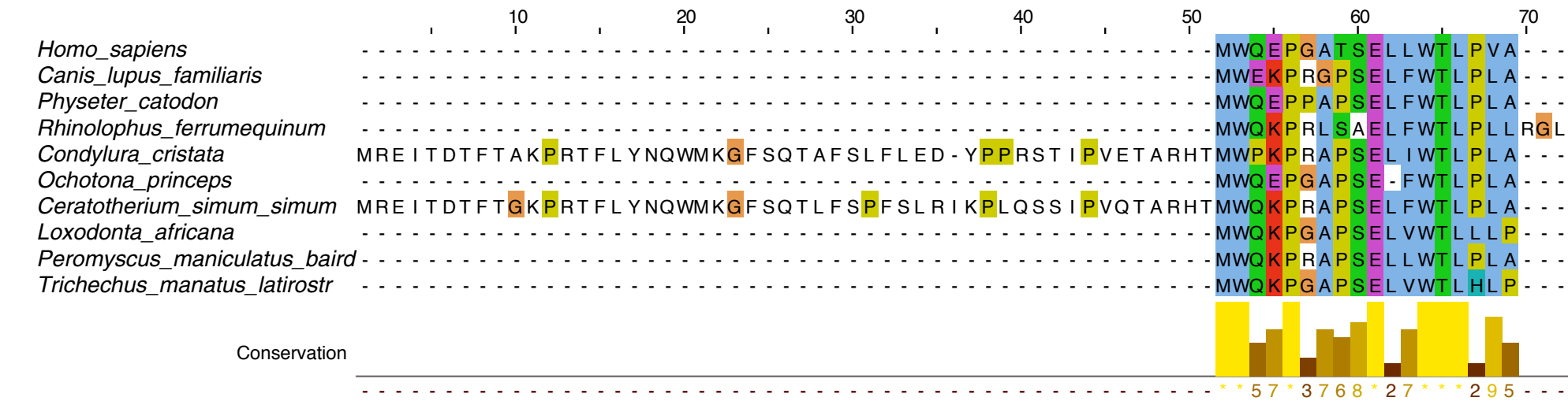
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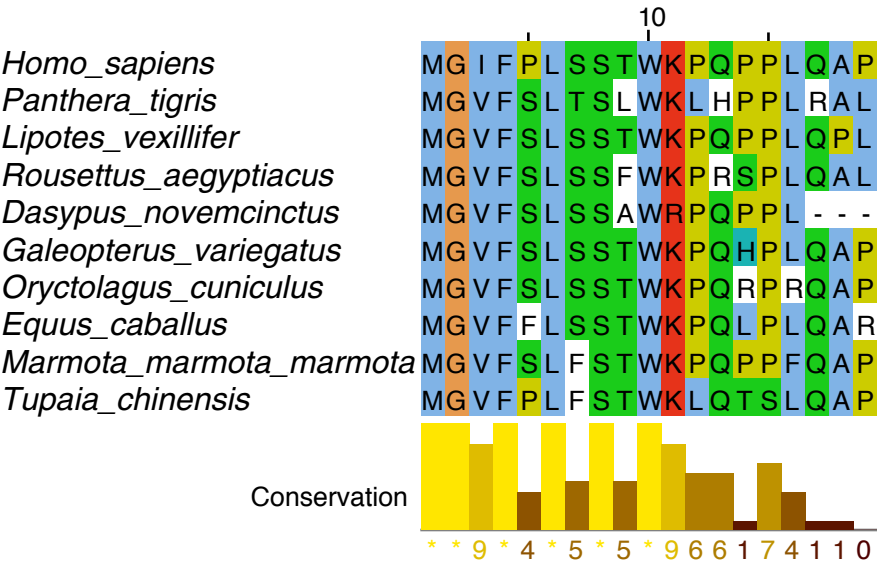
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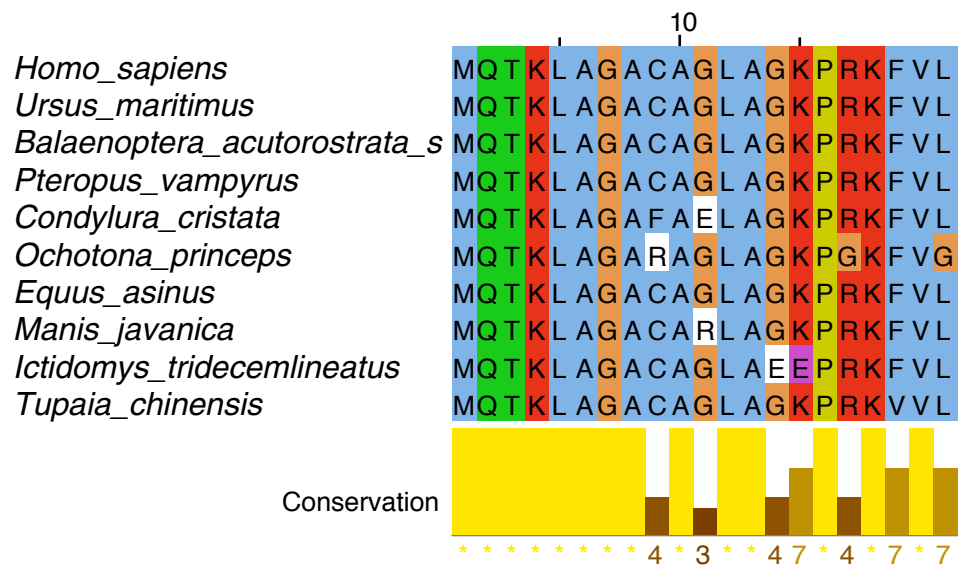
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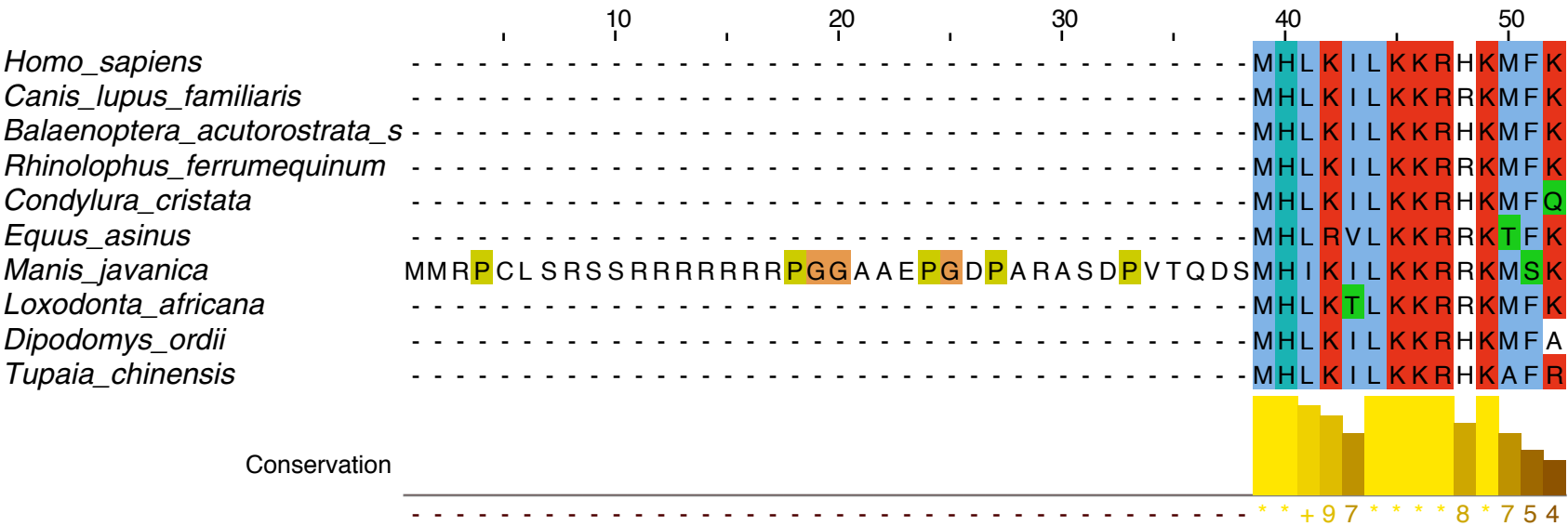
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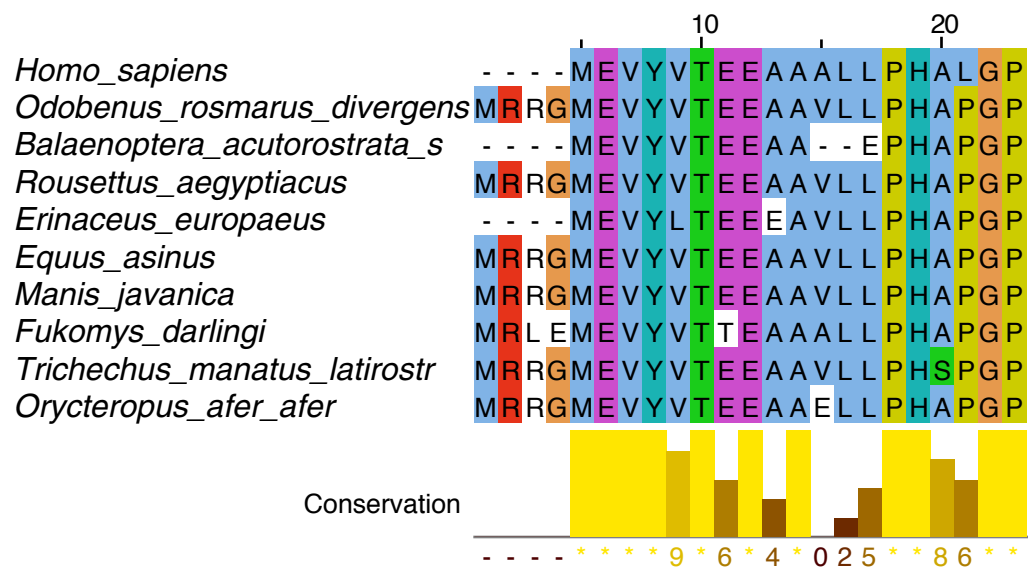
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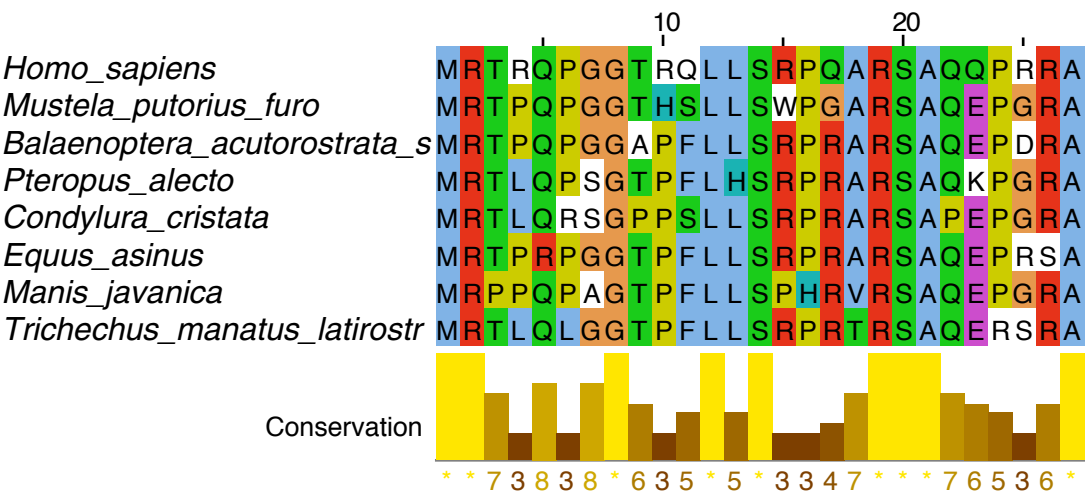
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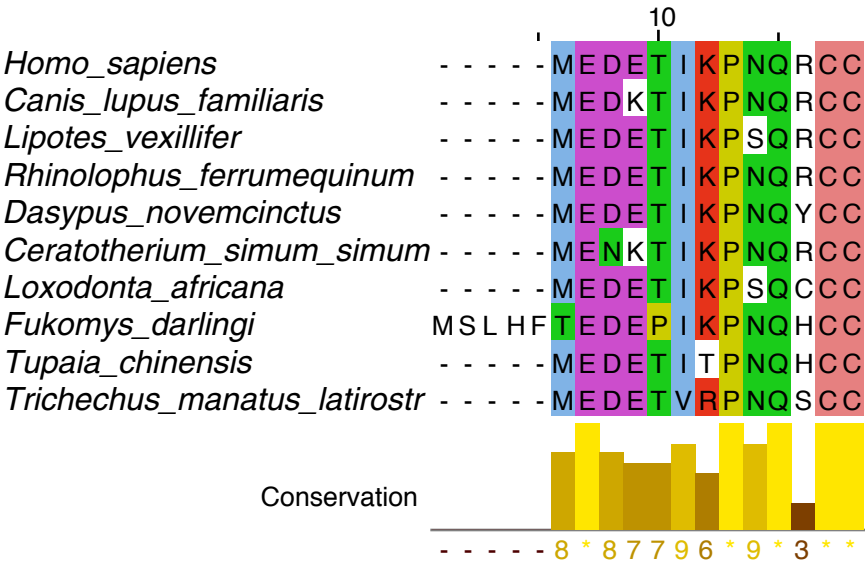
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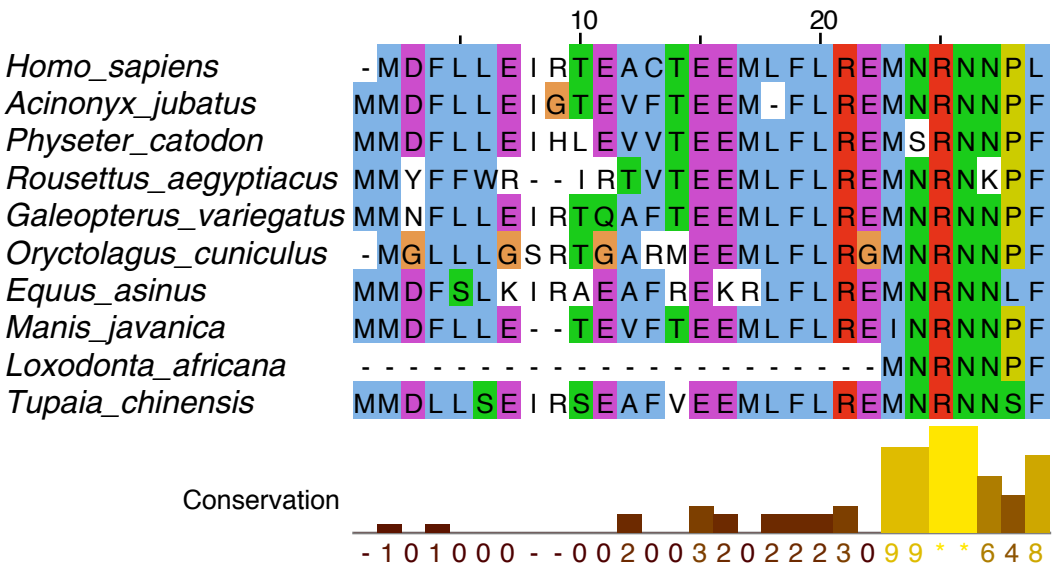
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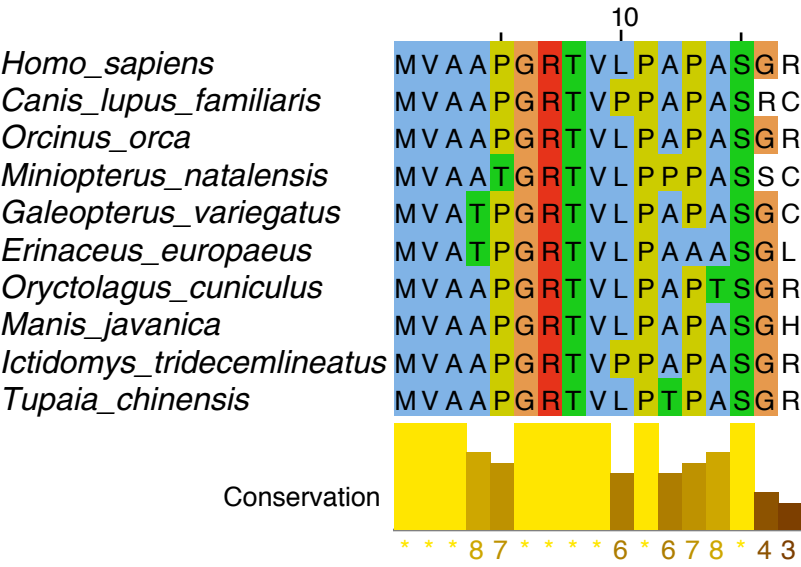
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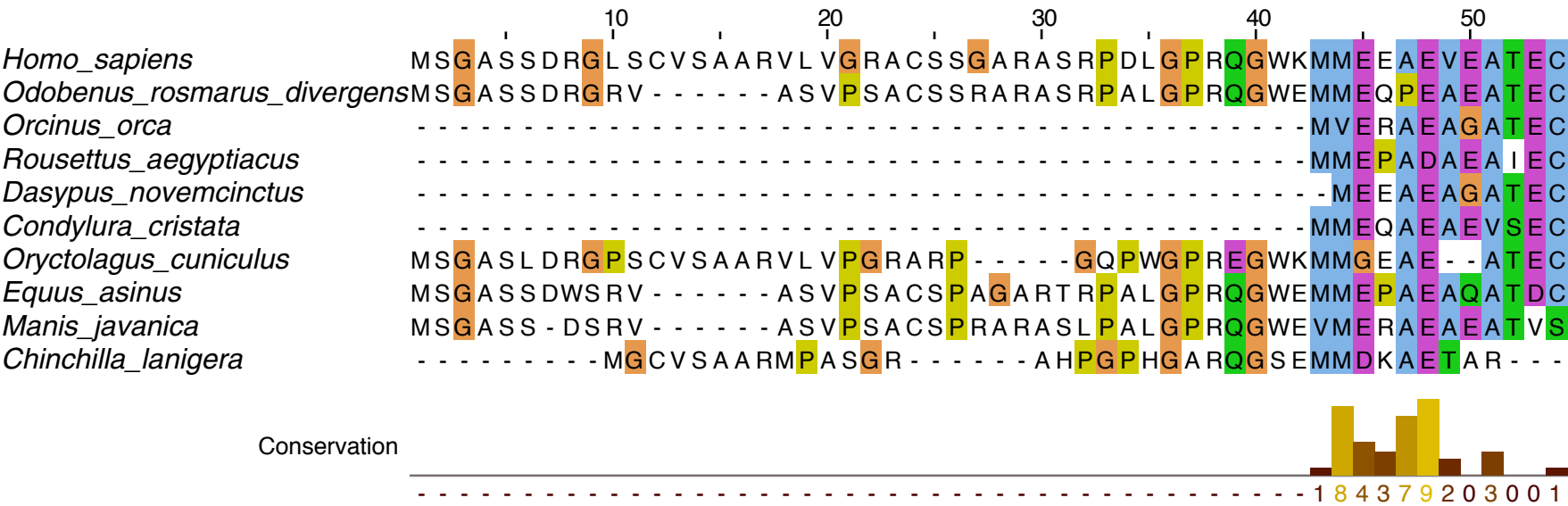


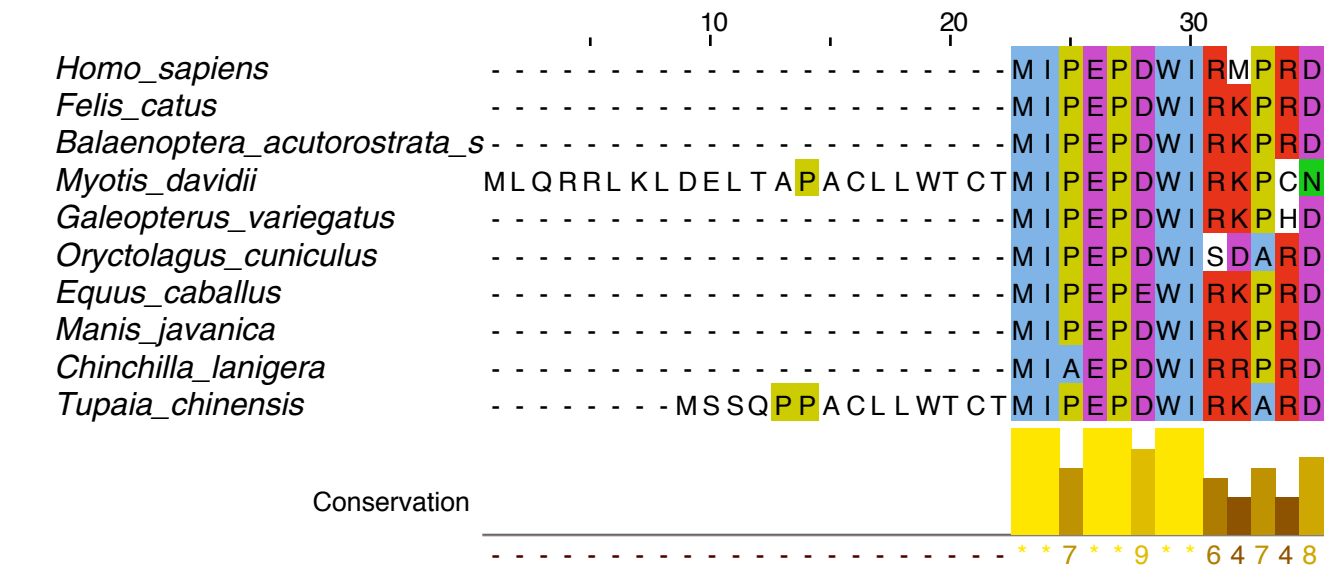
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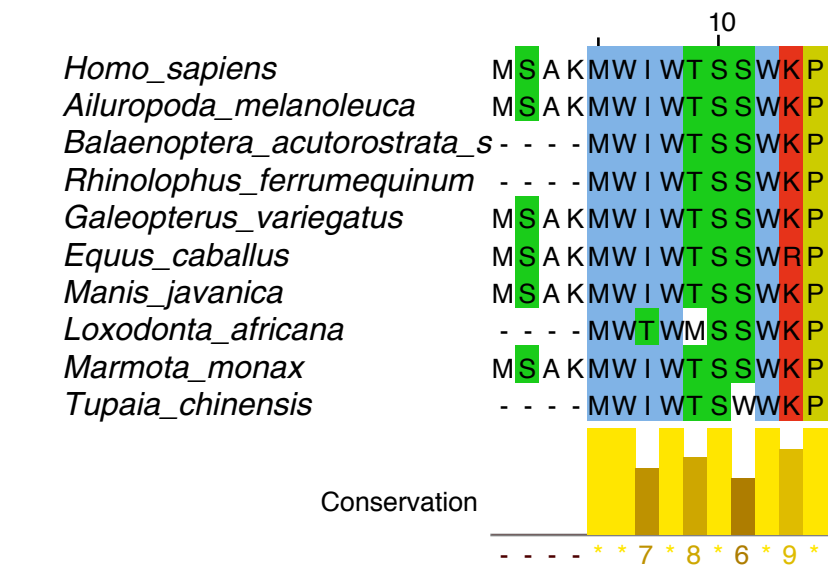
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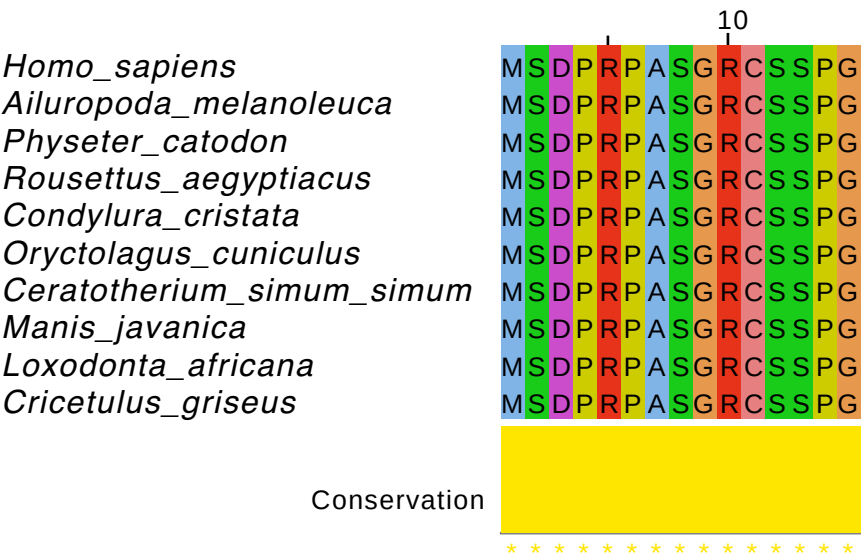
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HG0666

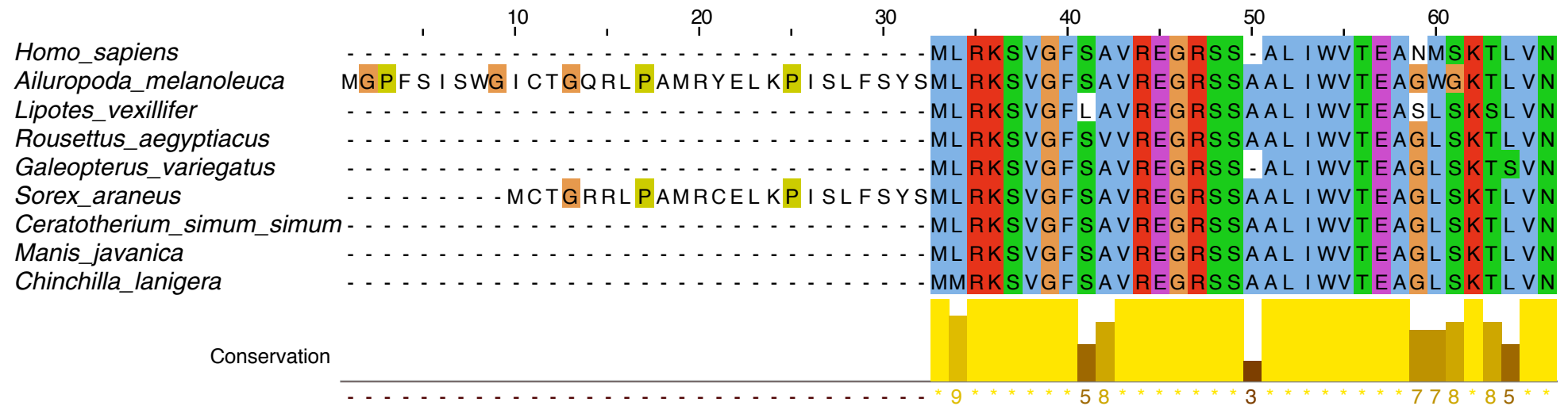
ENSG00000171943 (SRGAP2C)



										10								20	
<i>Homo_sapiens</i>	MC	QY	TV	RI	SL	ICT	VW	GP	HL	R	M	L	N	F	A	N			
<i>Acinonyx_jubatus</i>	MC	Q	L	Y	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Physeter_catodon</i>	MC	Q	L	Y	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Myotis_brandtii</i>	MC	Q	L	H	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Galeopterus_variegatus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	L
<i>Condylura_cristata</i>	MC	Q	L	Y	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Ceratotherium_simum_simum</i>	MC	Q	L	Y	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Manis_javanica</i>	MC	Q	L	Y	S	R	I	S	L	I	C	T	V	W	G	P	H	-	-
<i>Rattus_sp.</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	L
<i>Tupaia_chinensis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	L

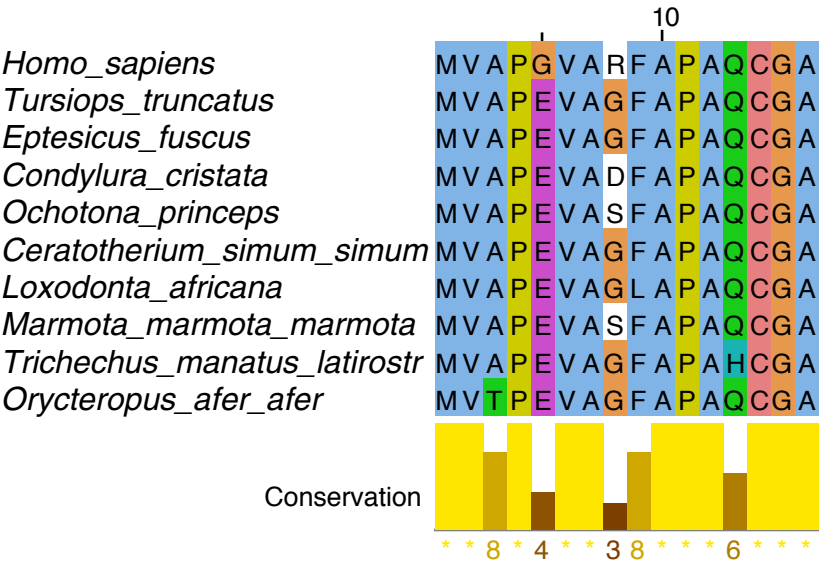


ENSG00000182700 (IGIP)



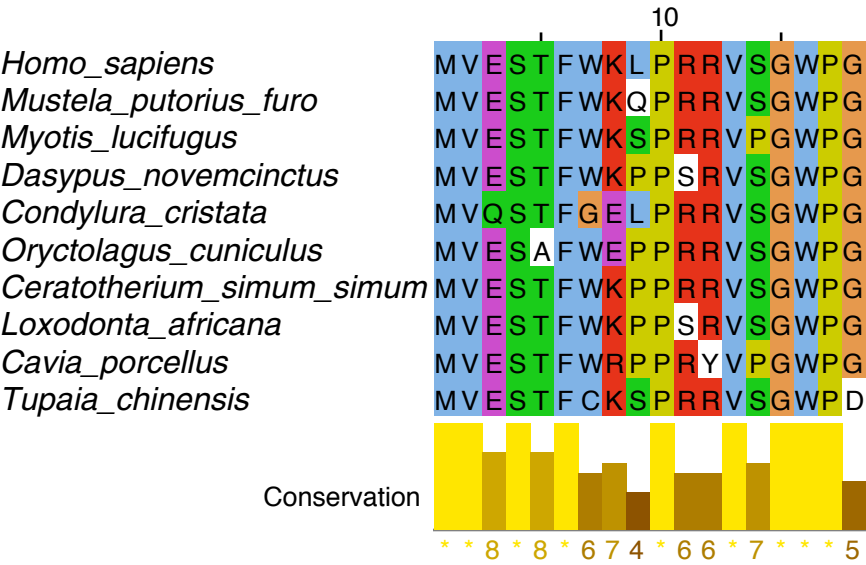
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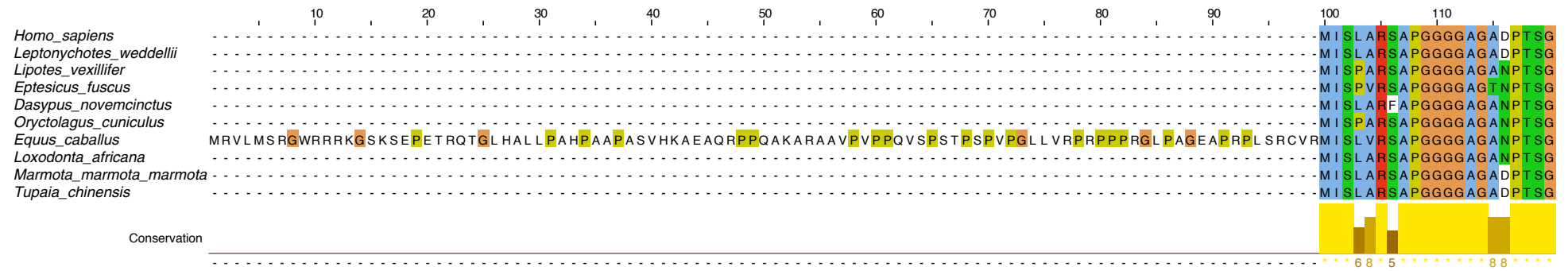


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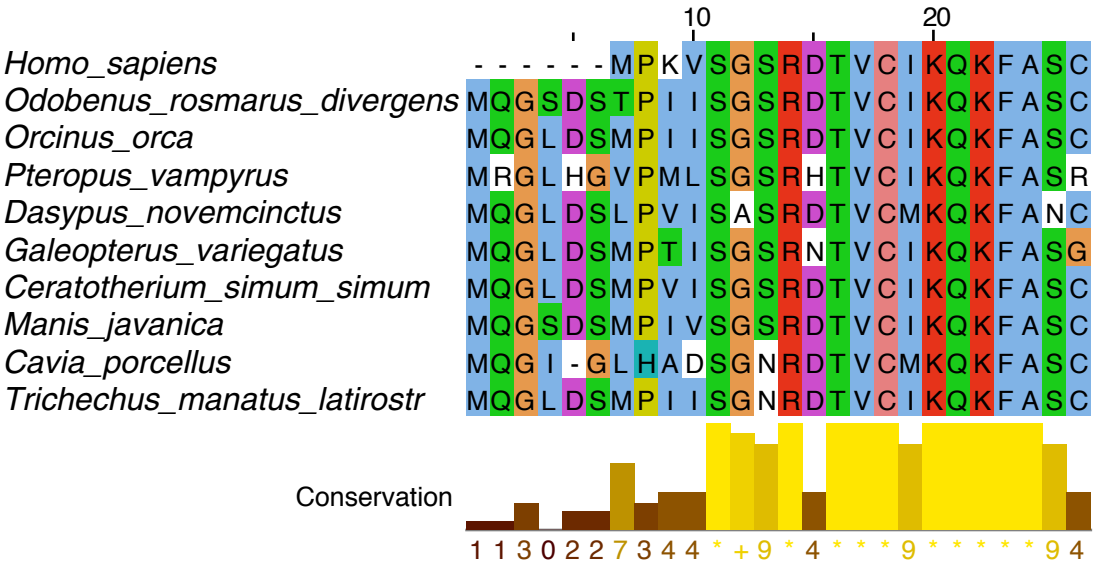


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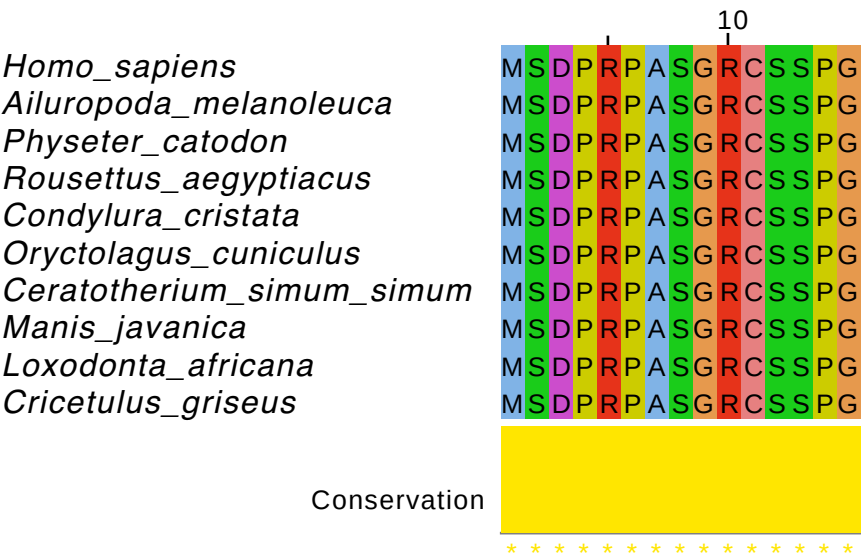
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ENSG00000189184 (PCDH18)



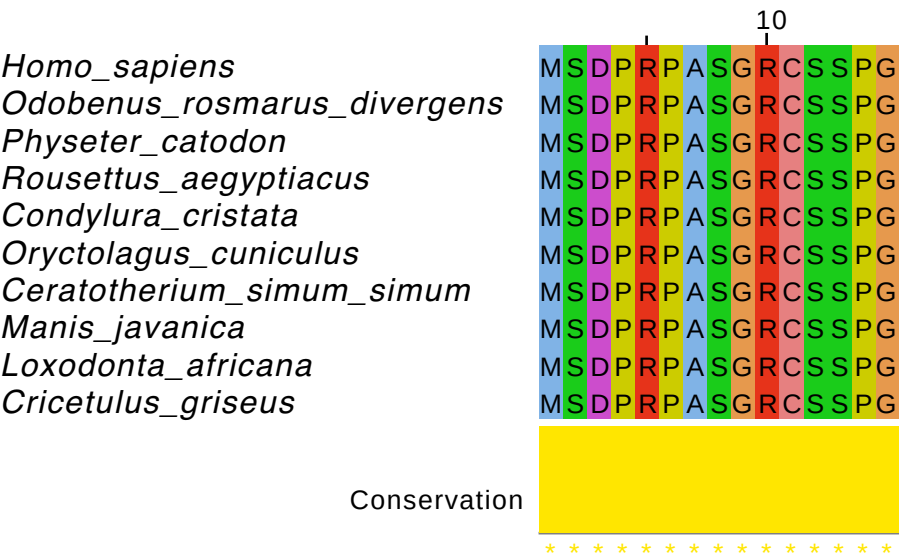
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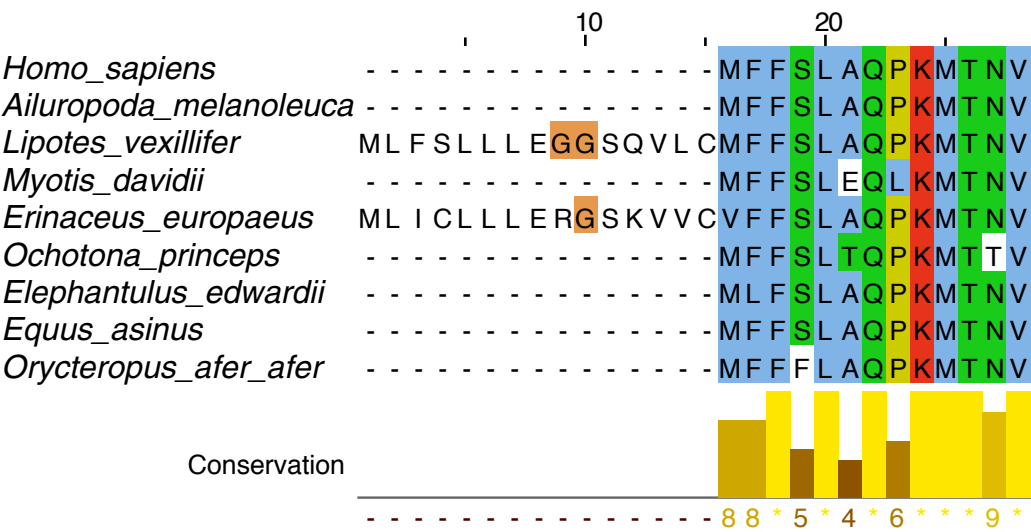
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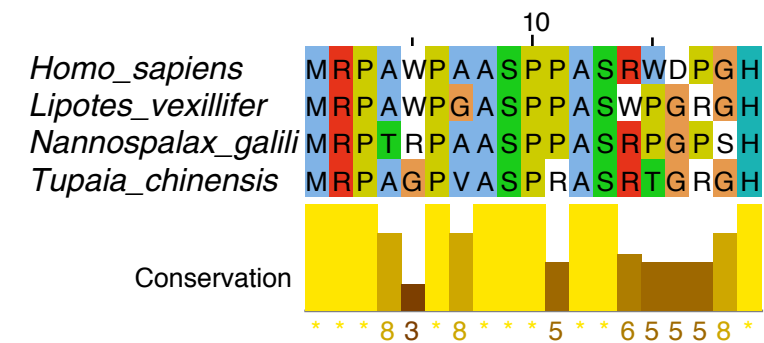
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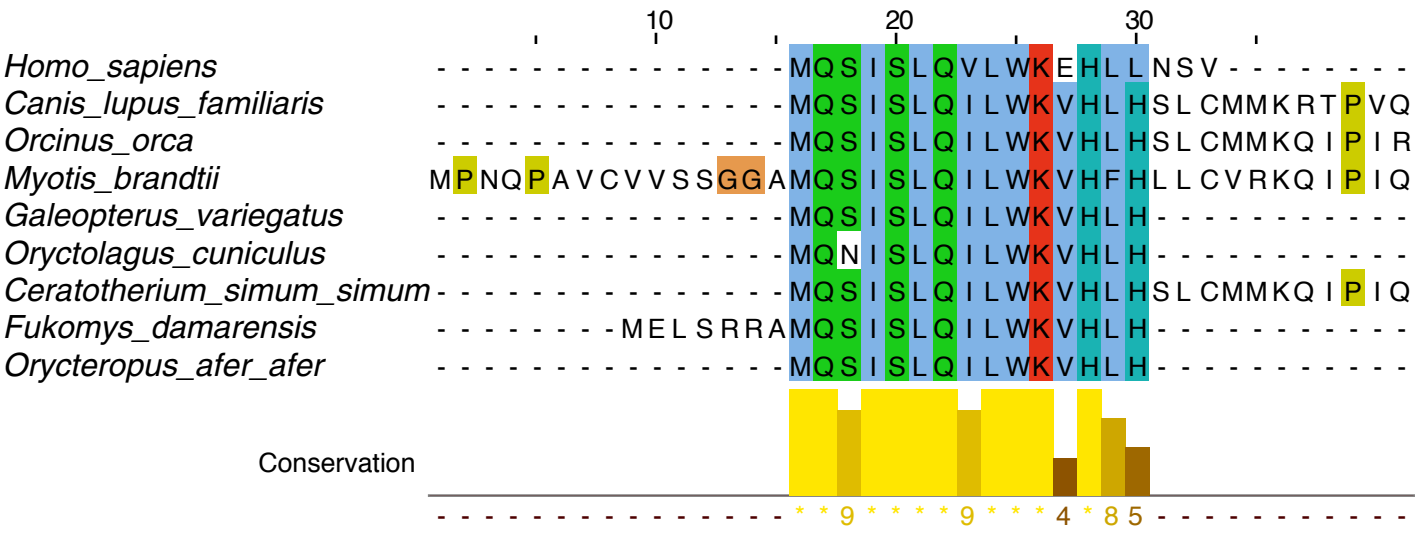
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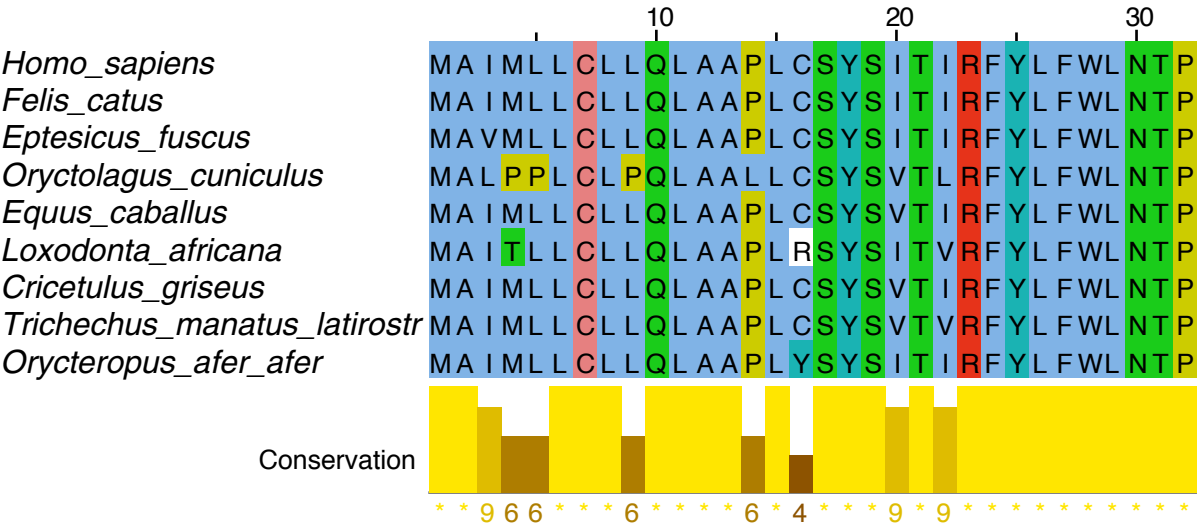
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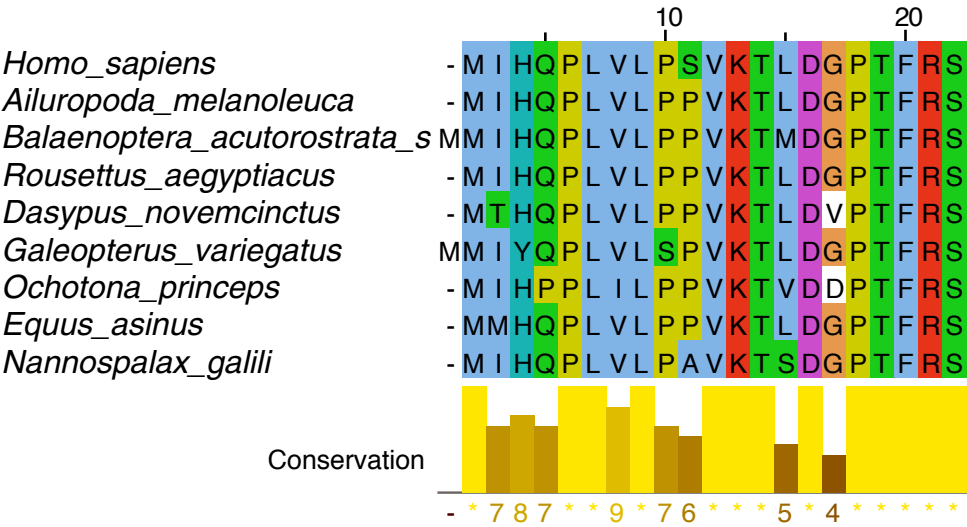
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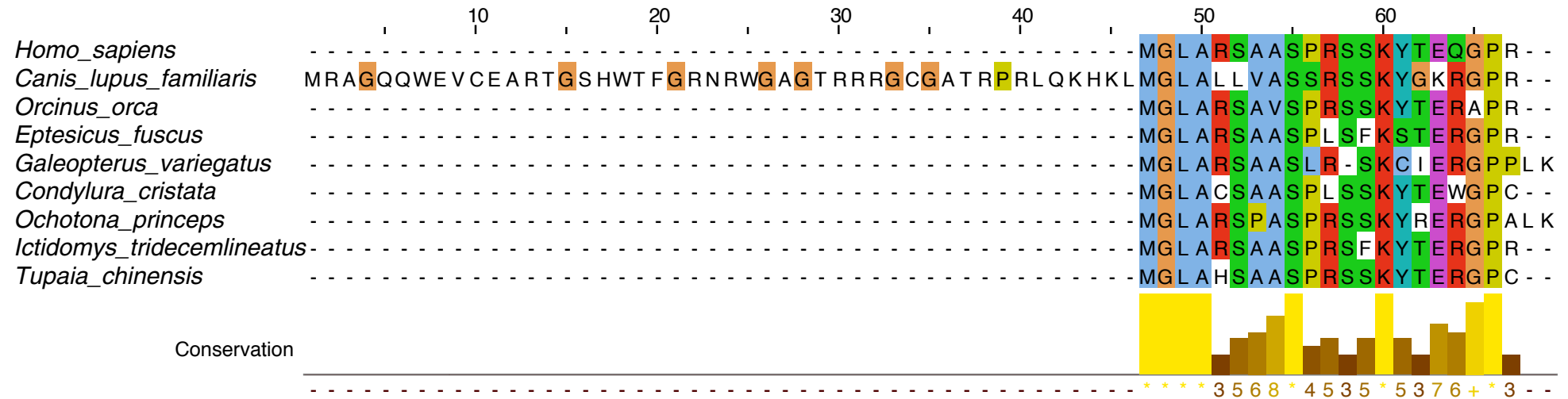
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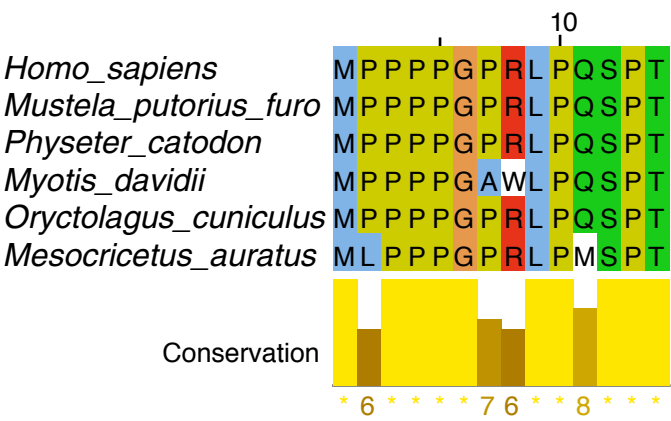
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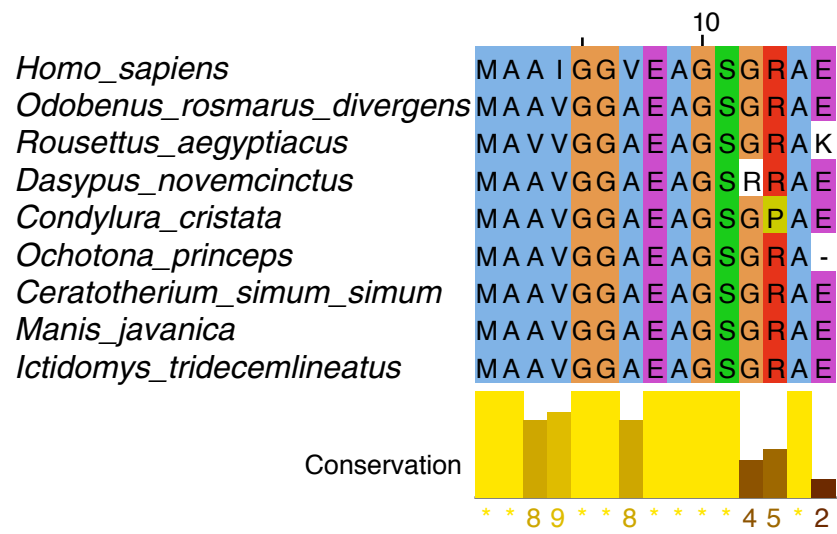
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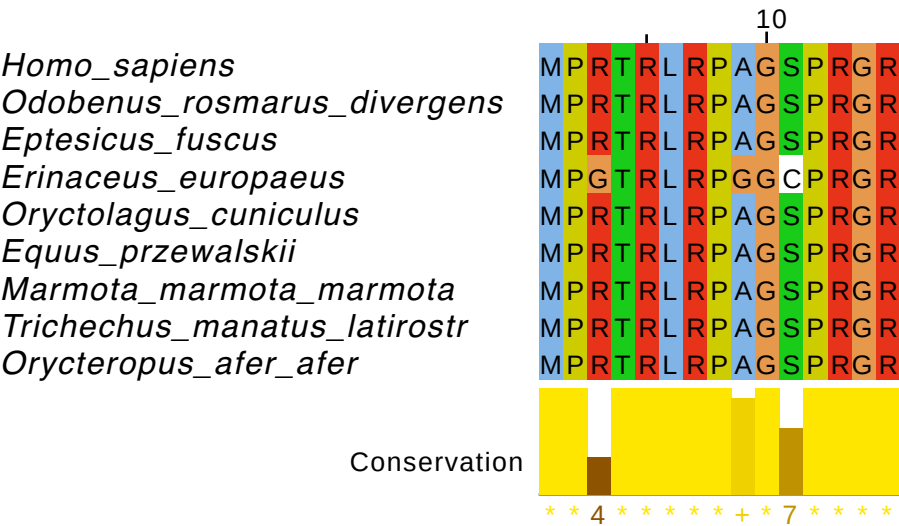
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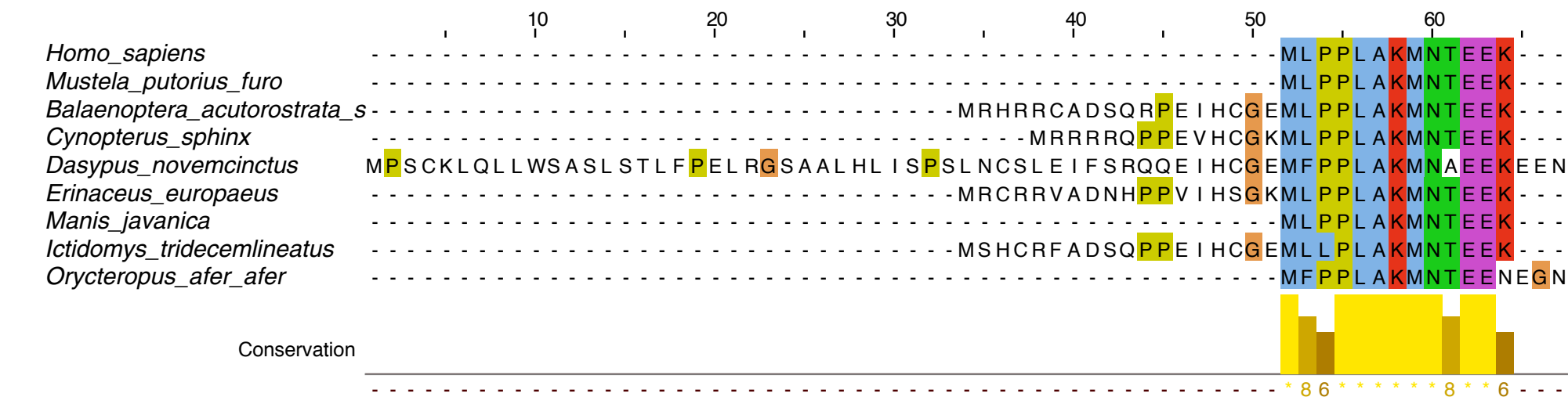


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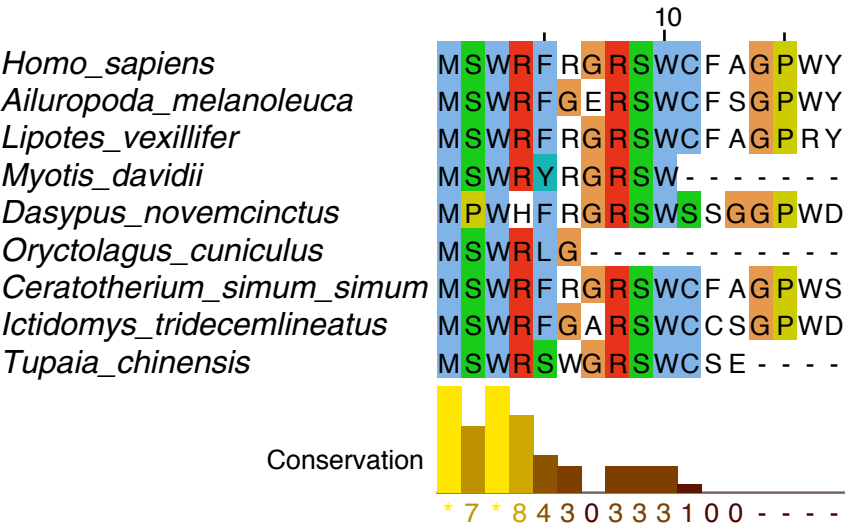


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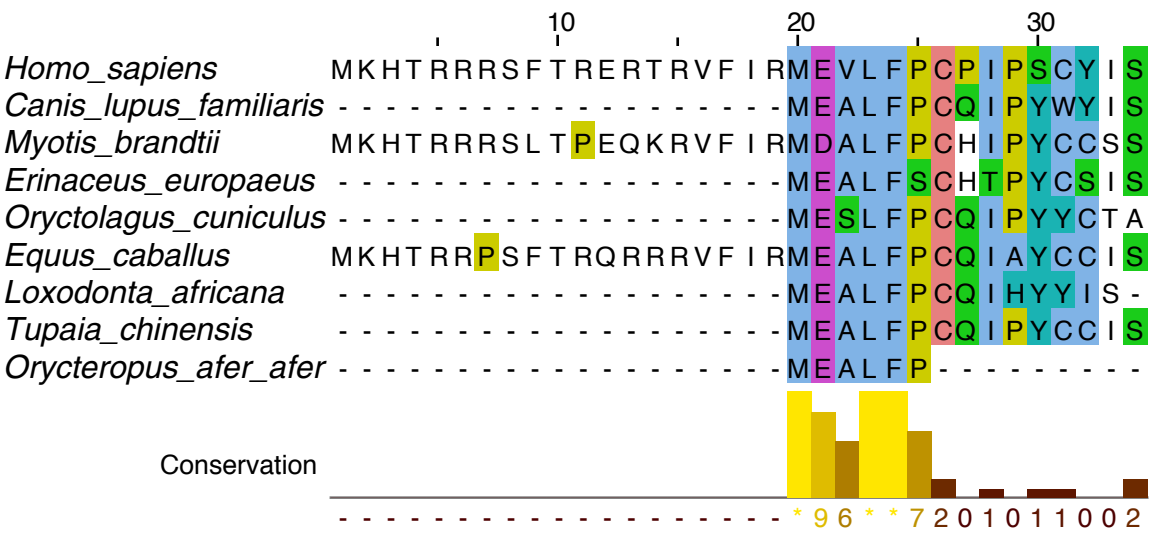
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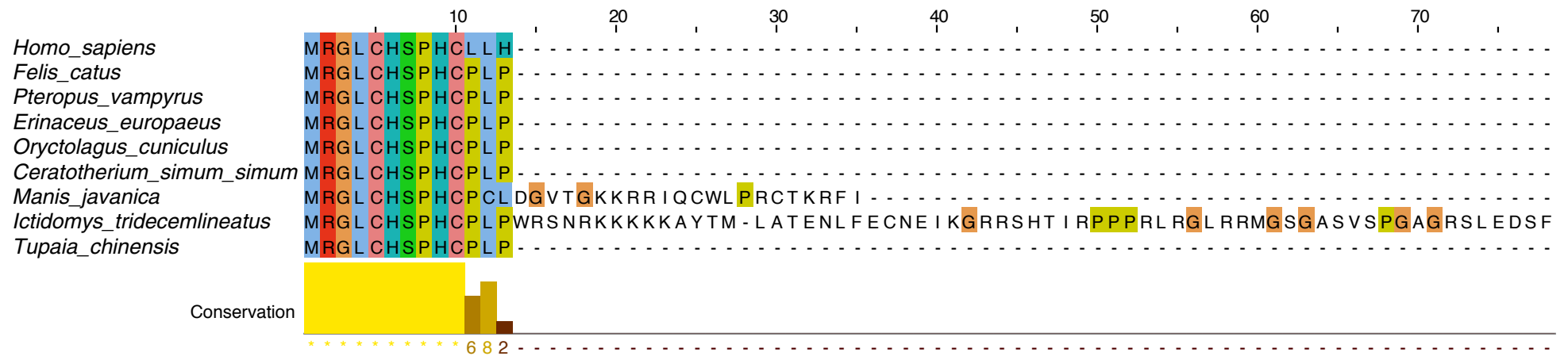


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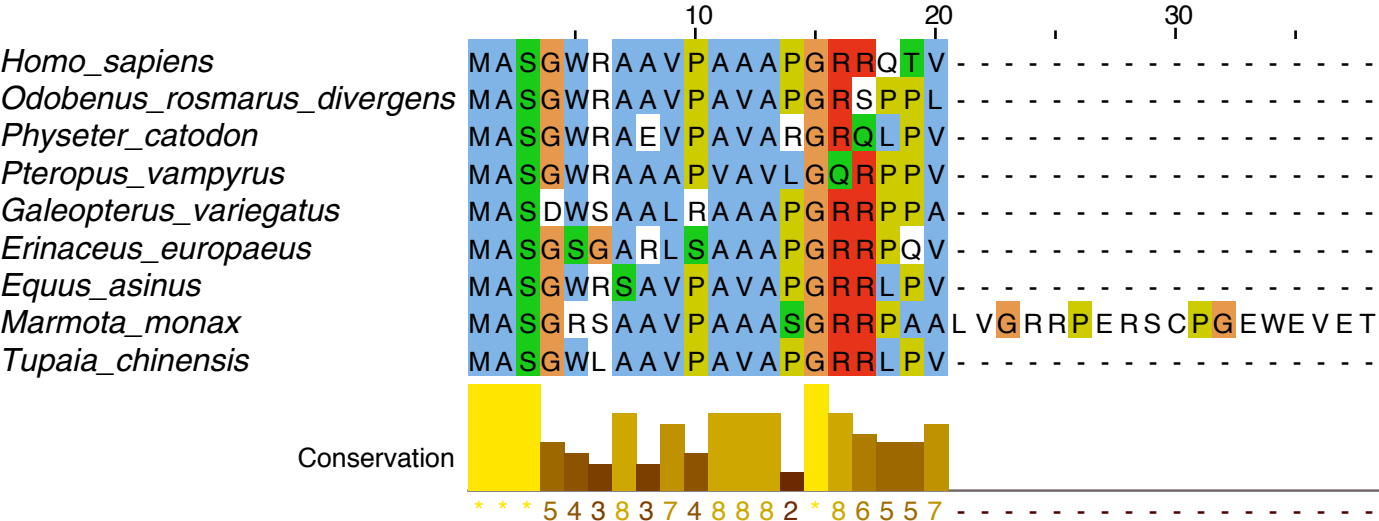


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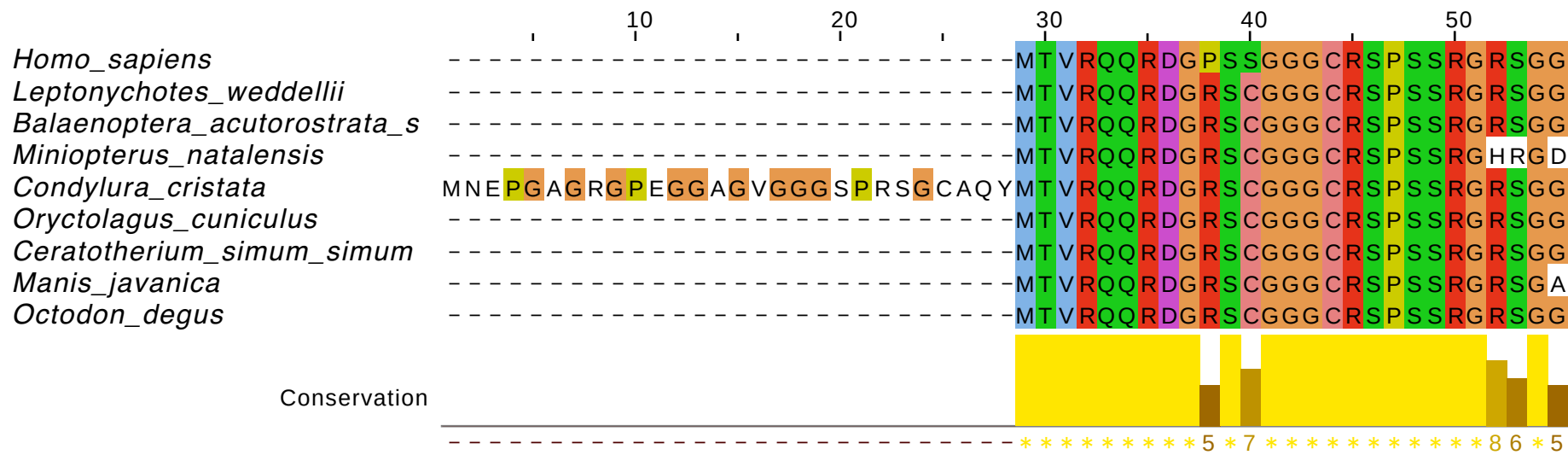


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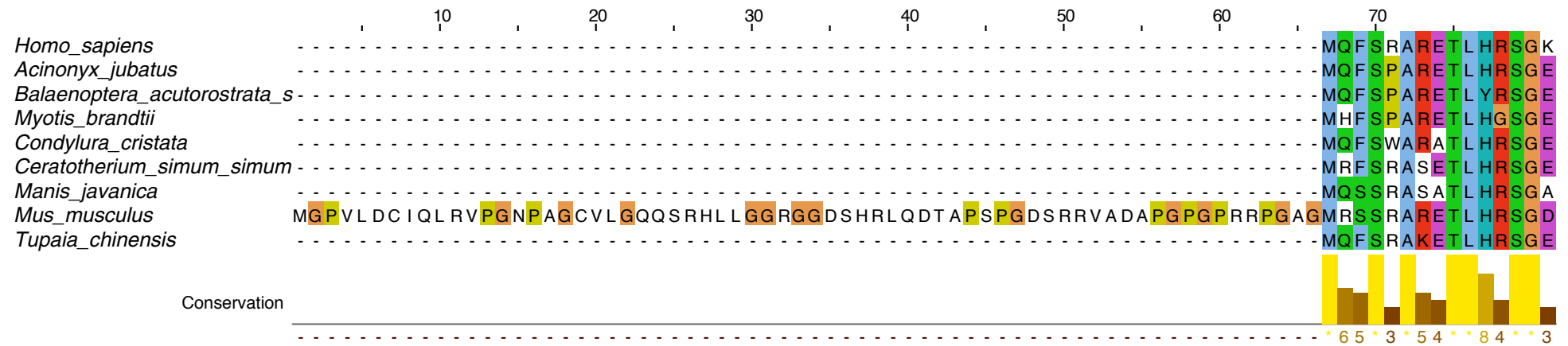


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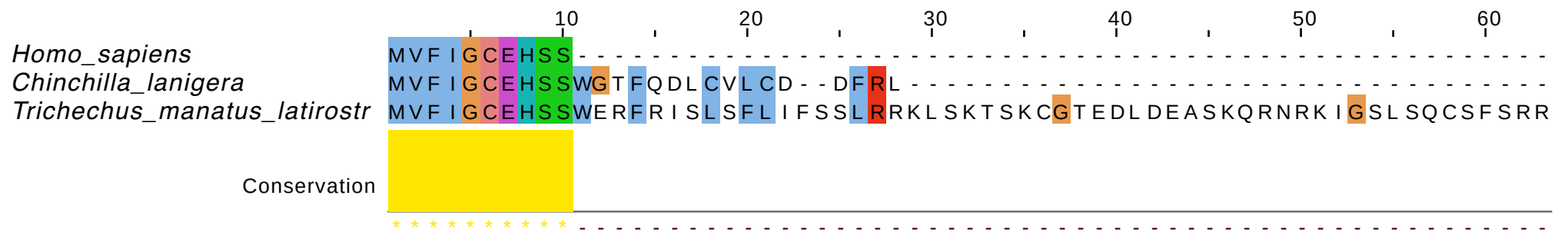
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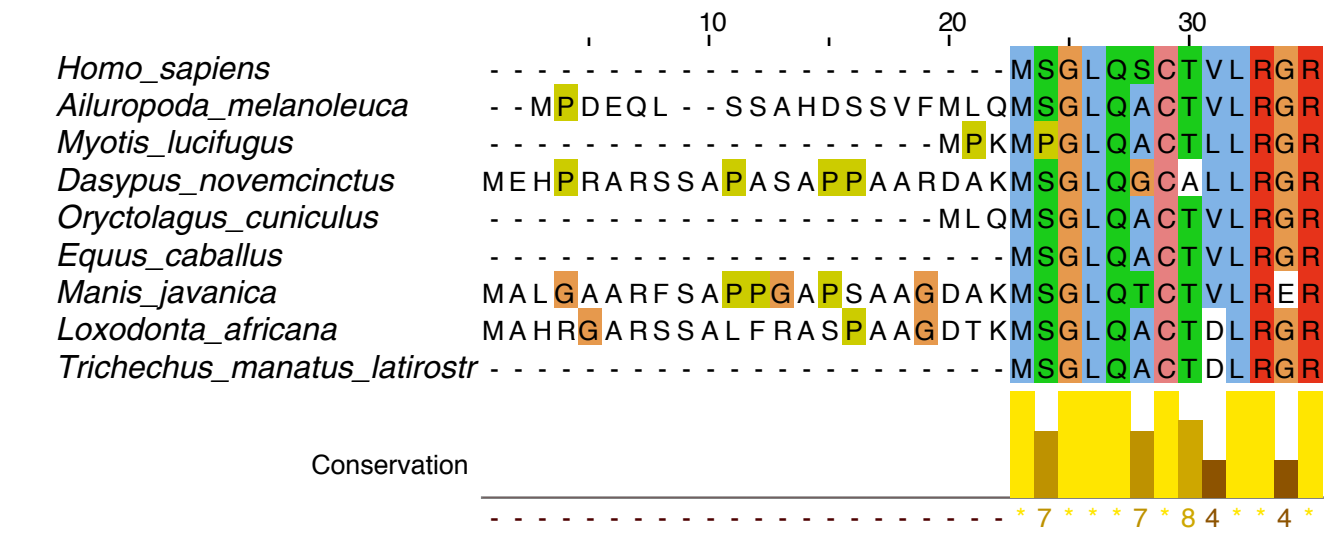
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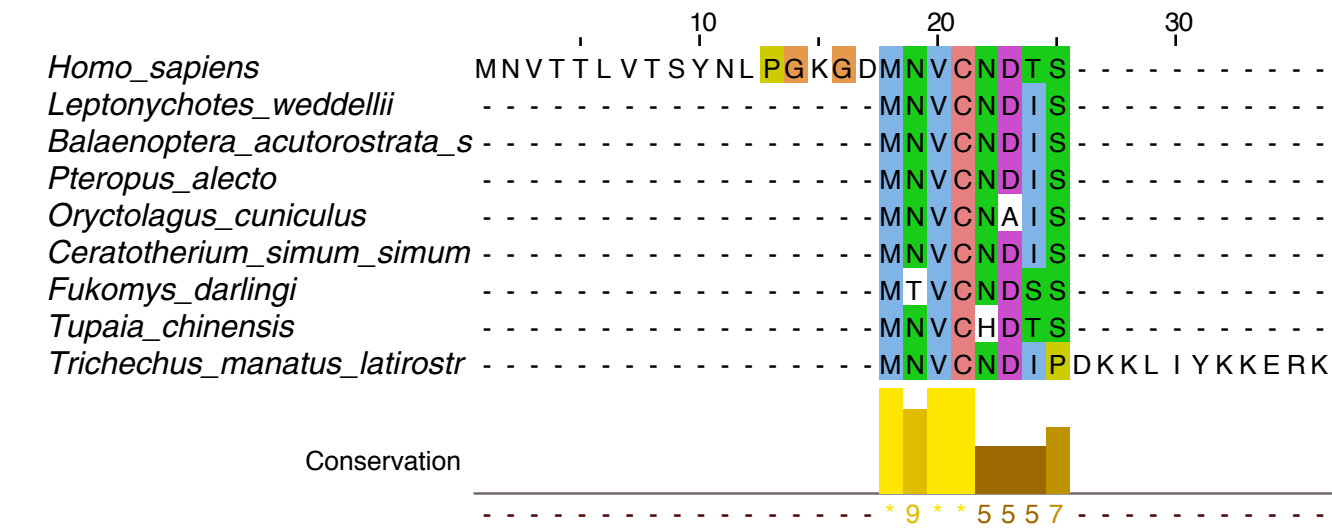
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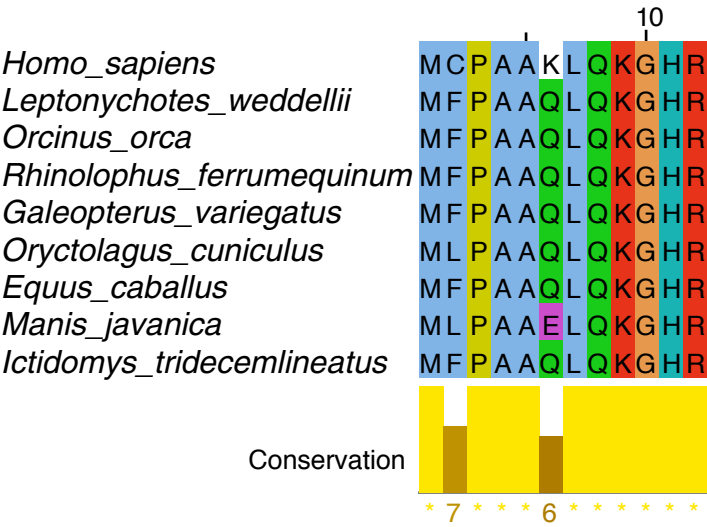
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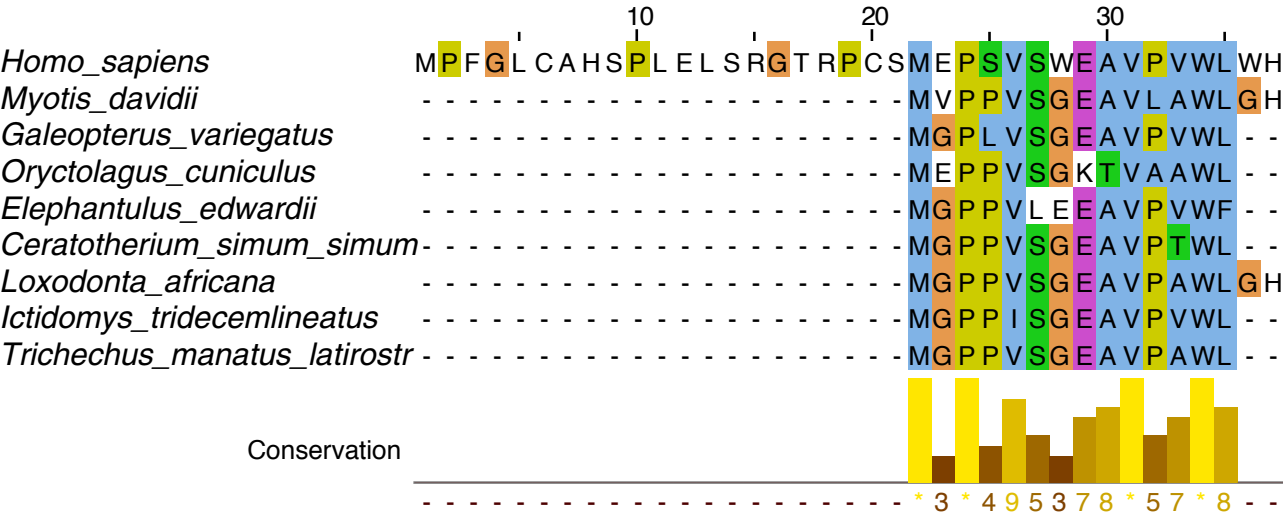
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HG0691

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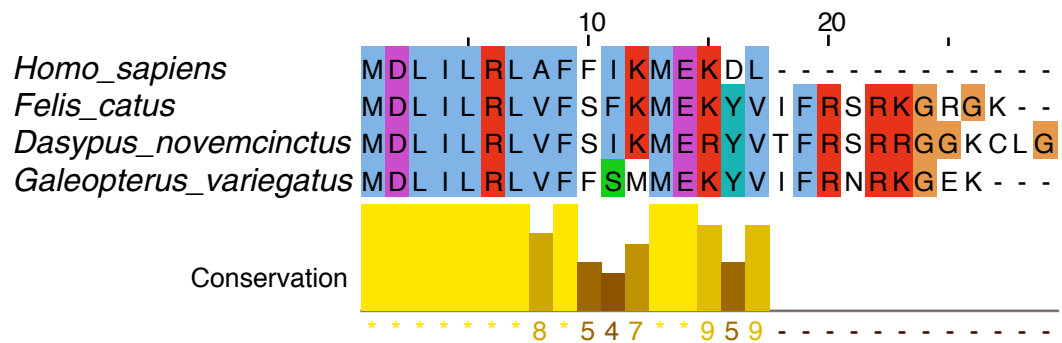
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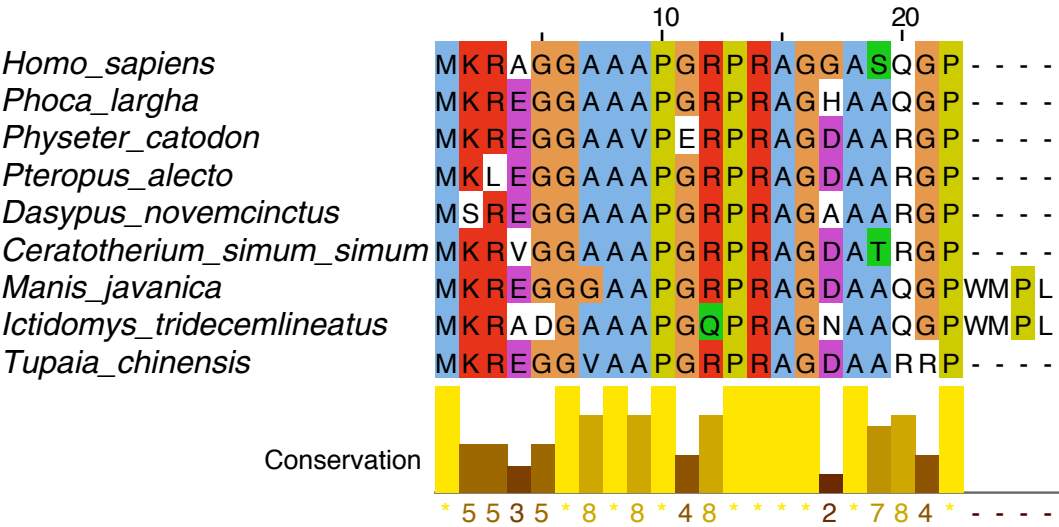
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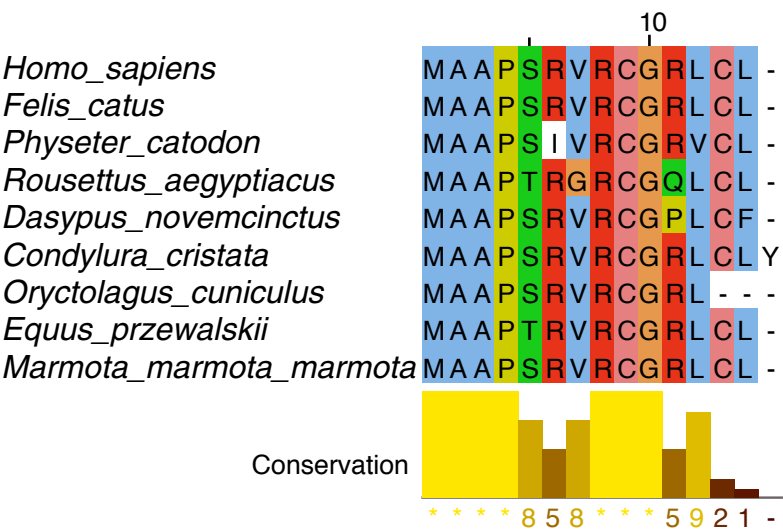
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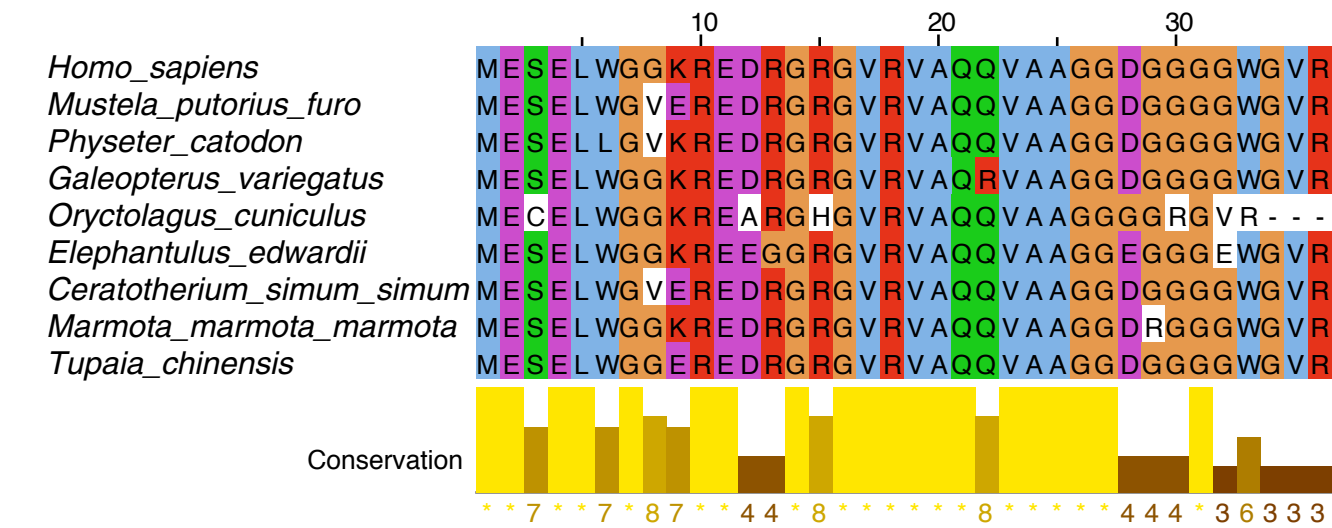
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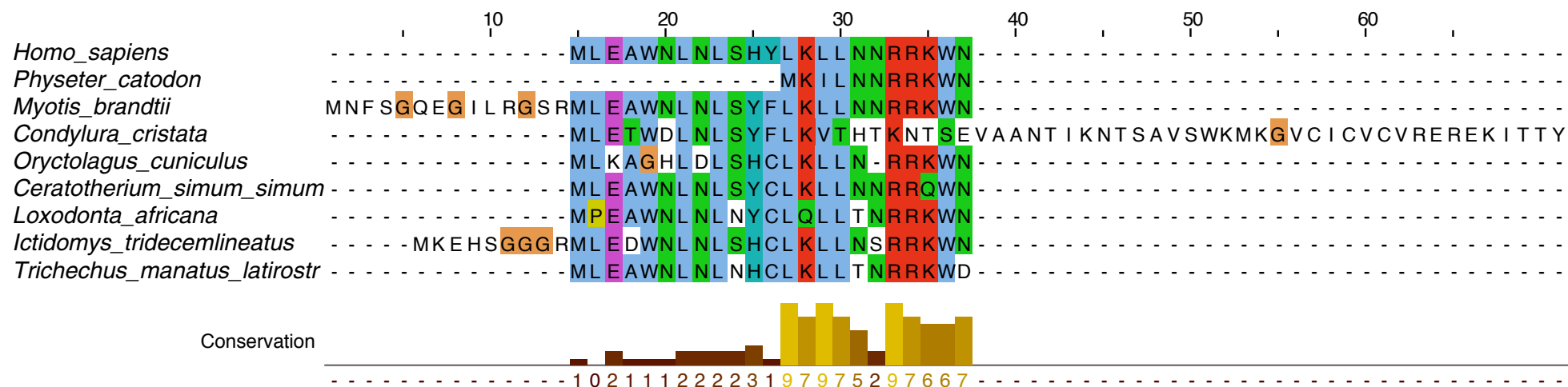


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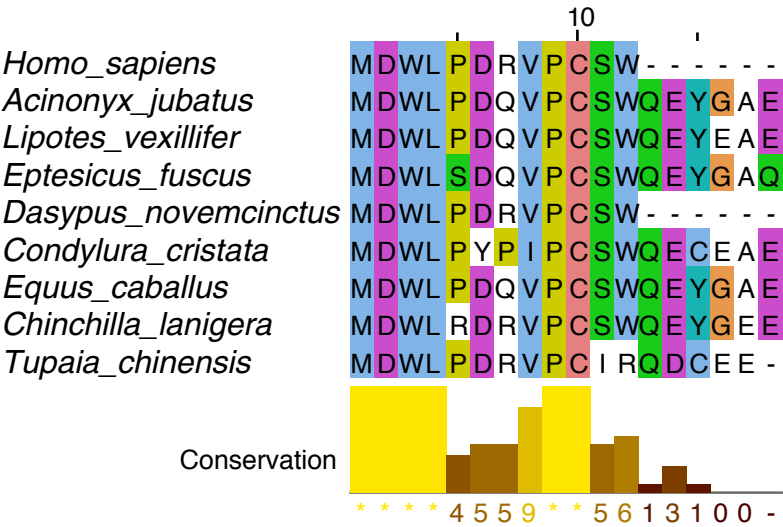


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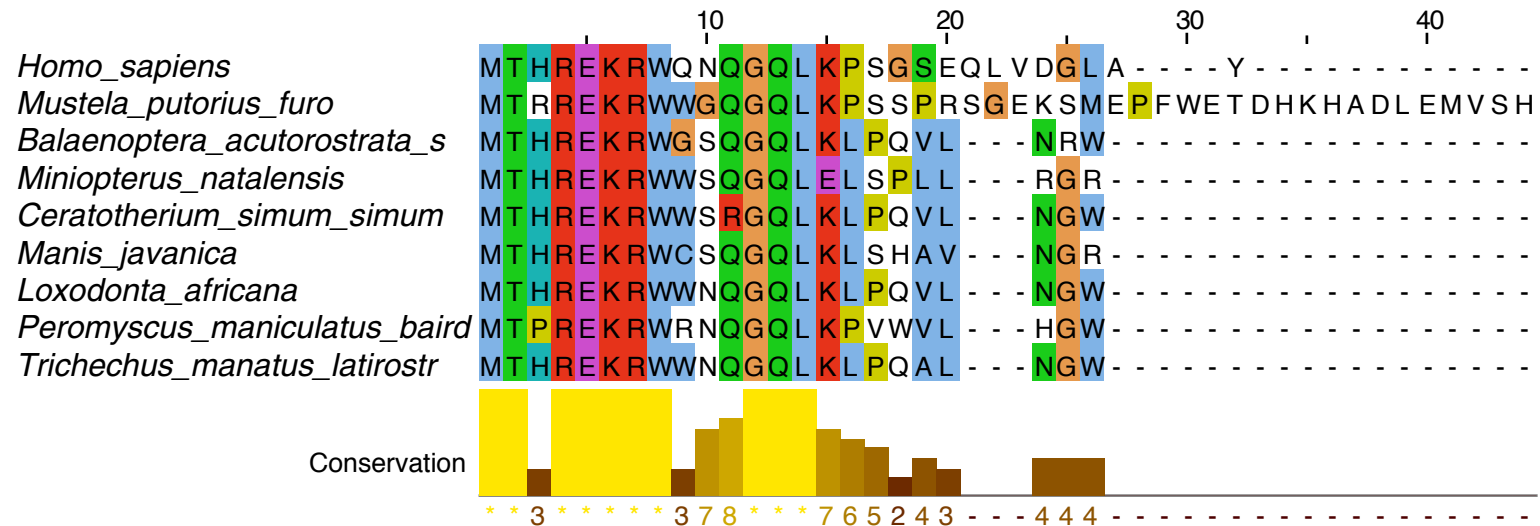


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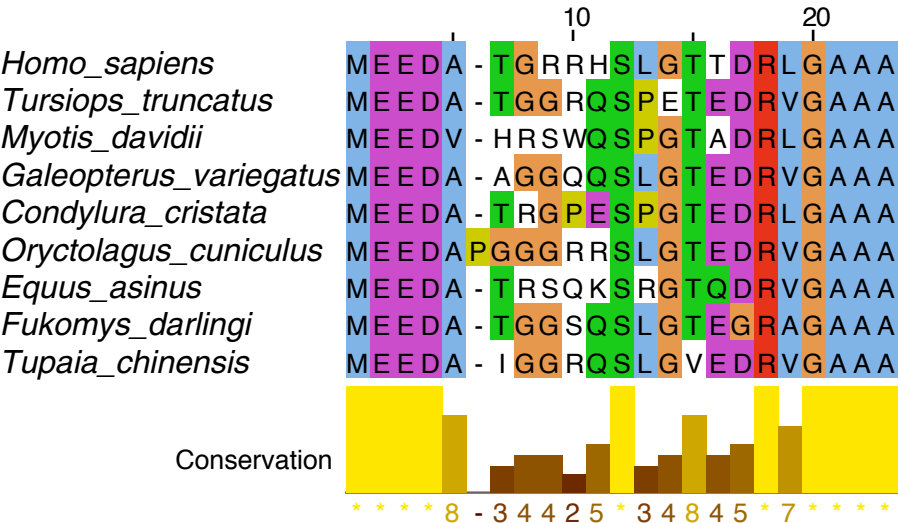


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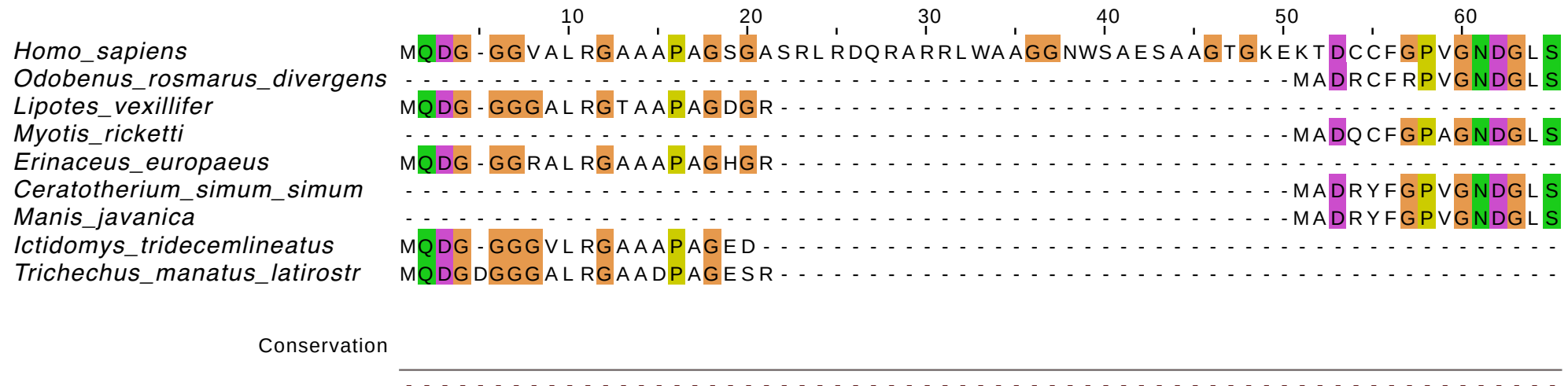
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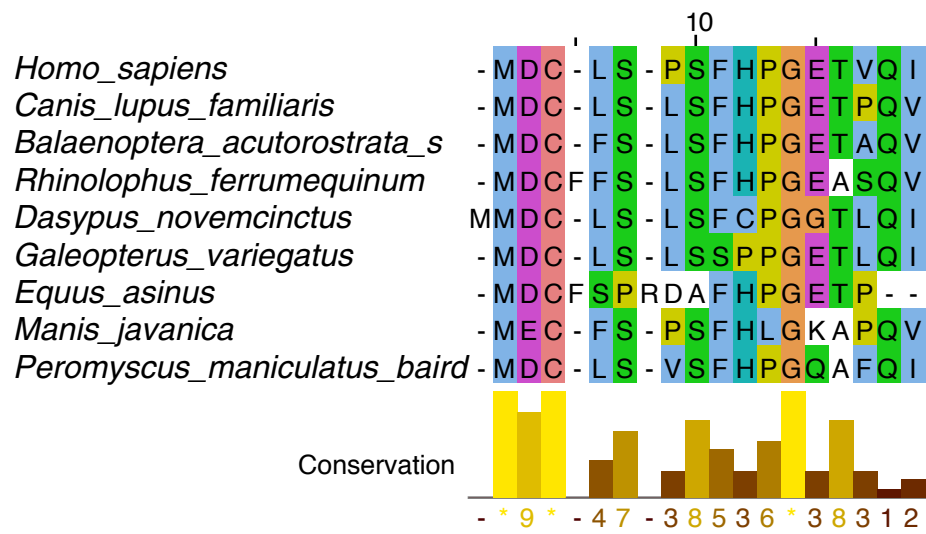
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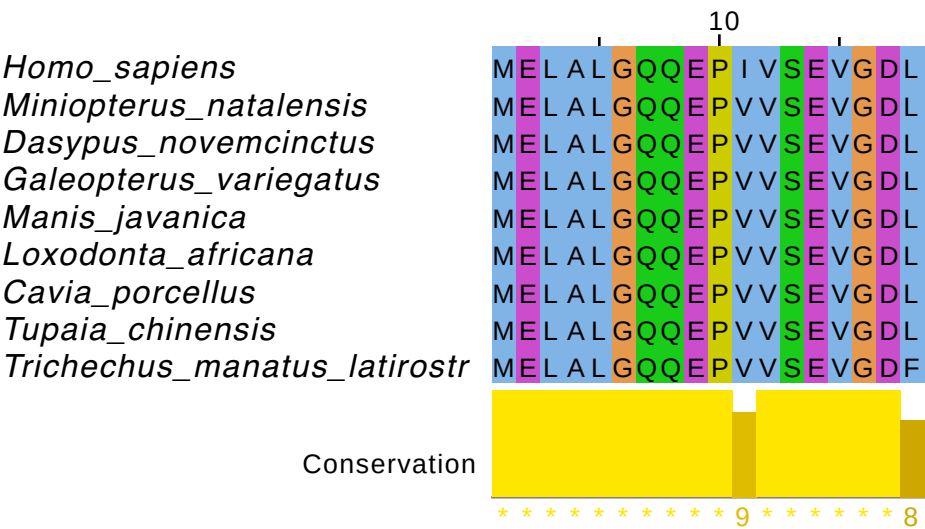
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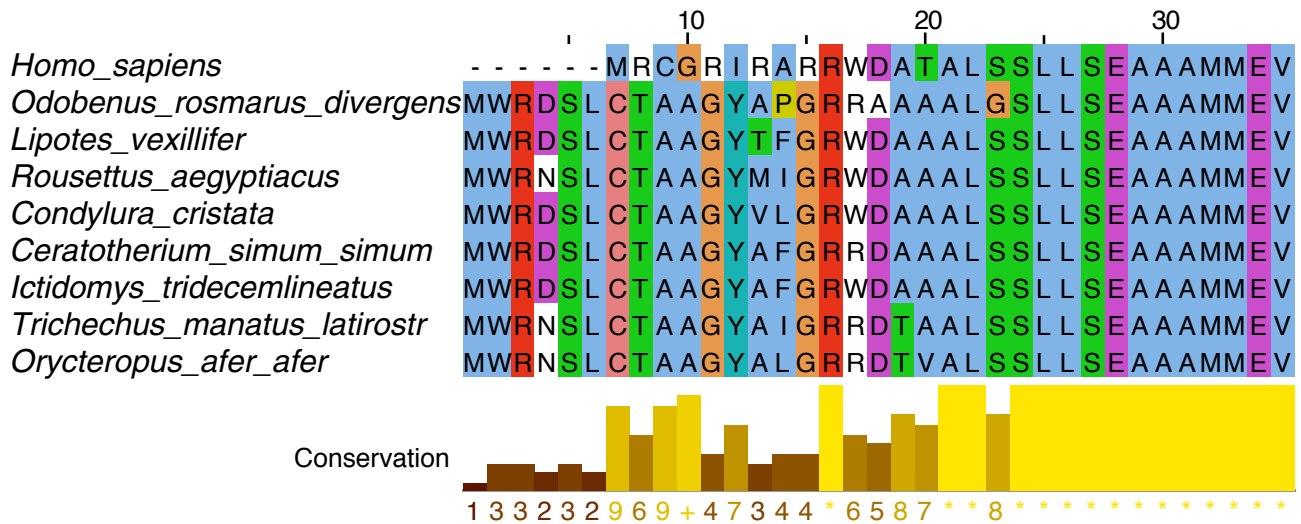
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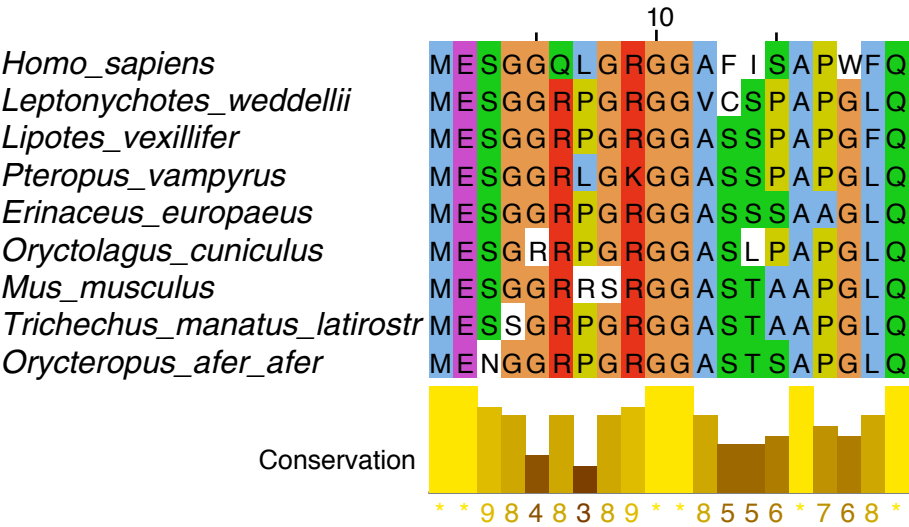
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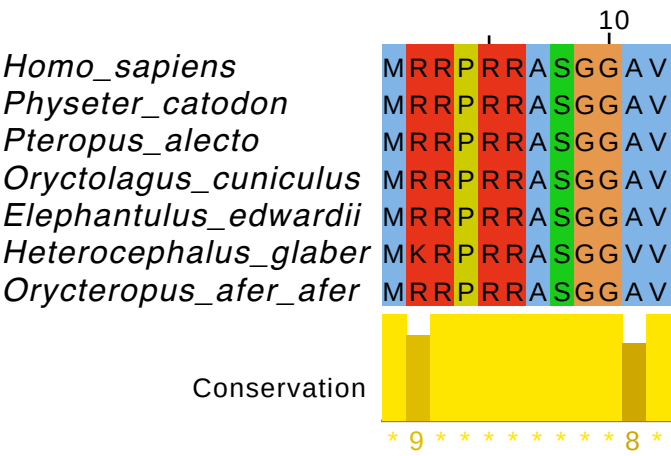
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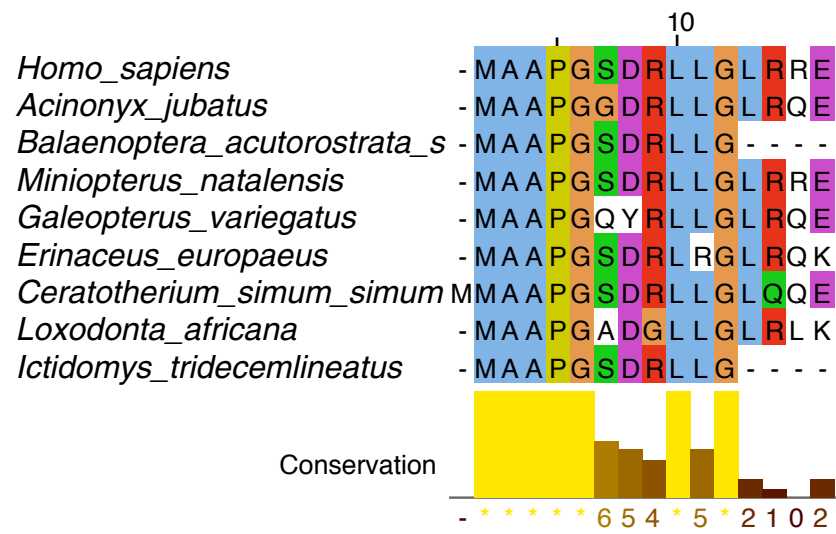
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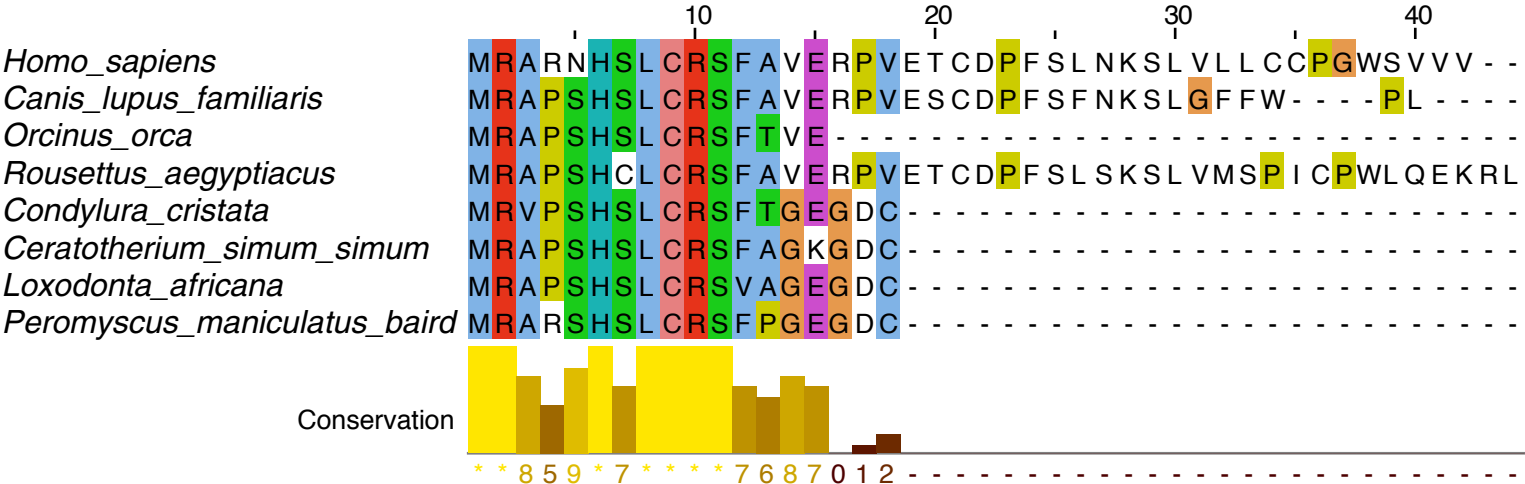
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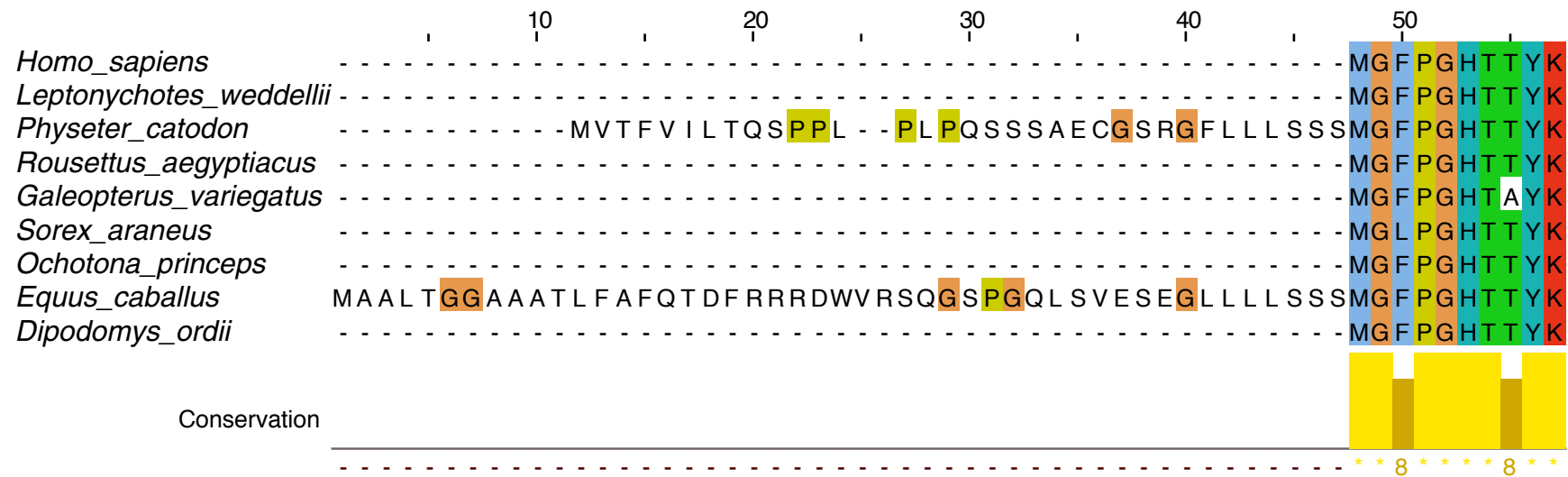


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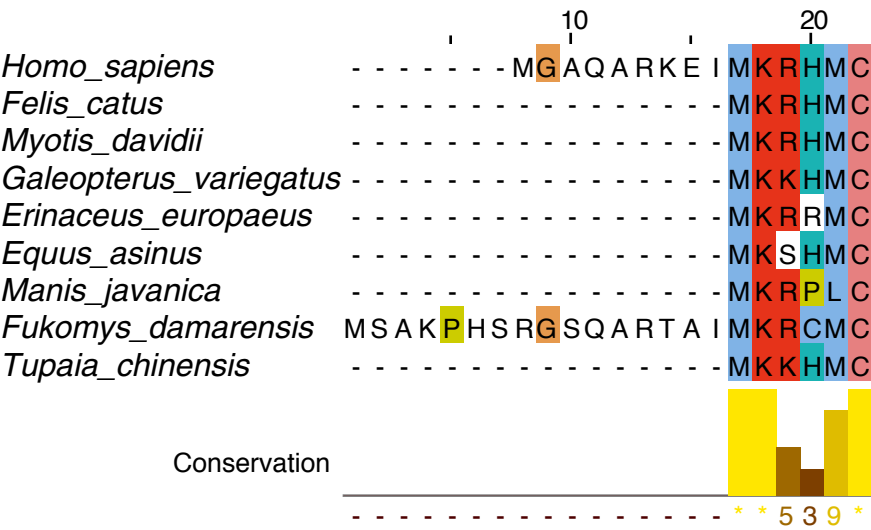


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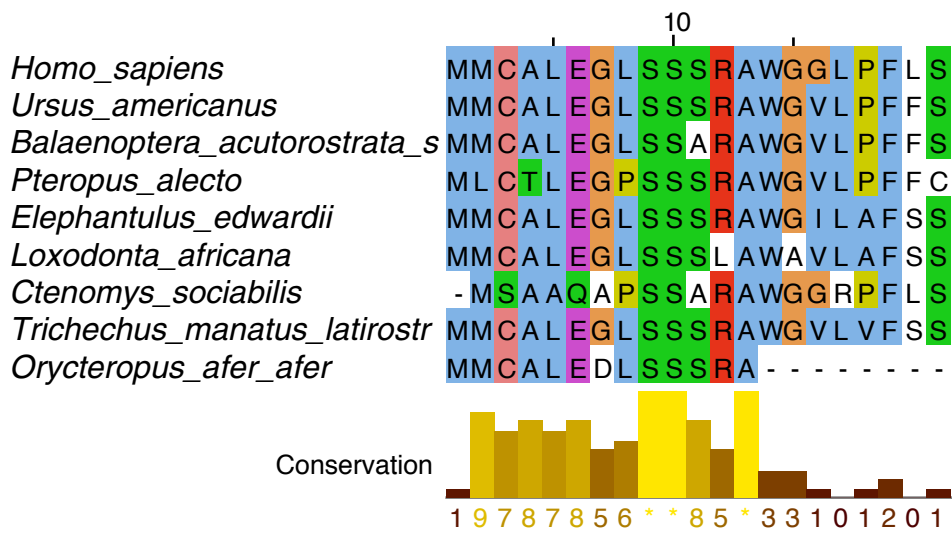
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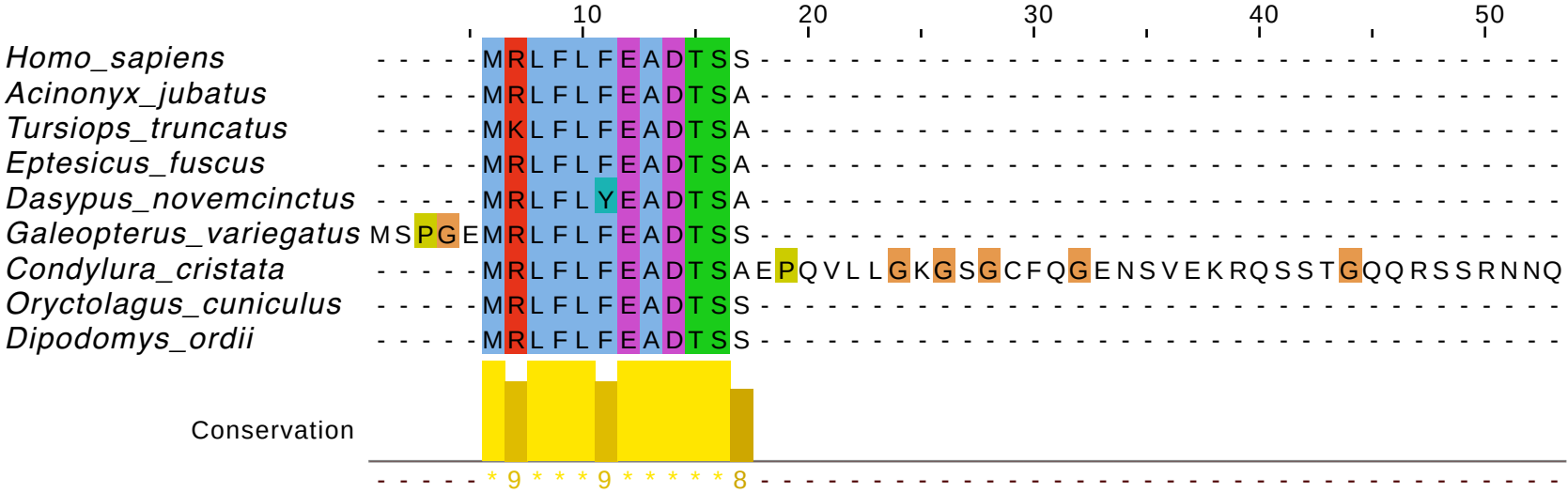


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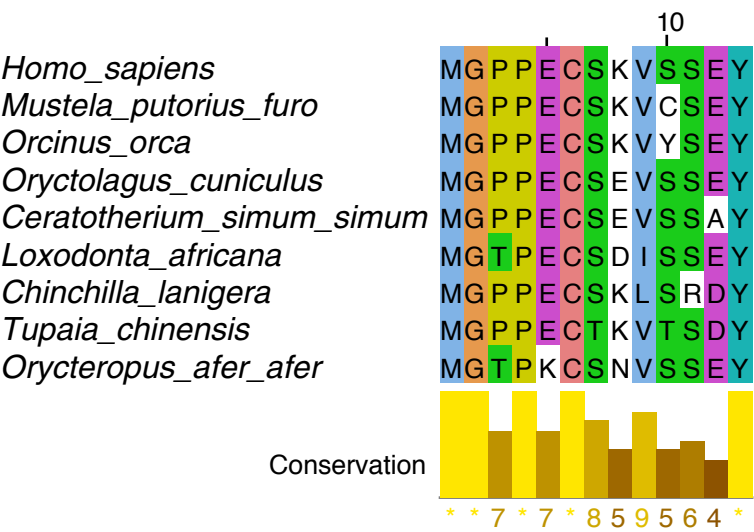


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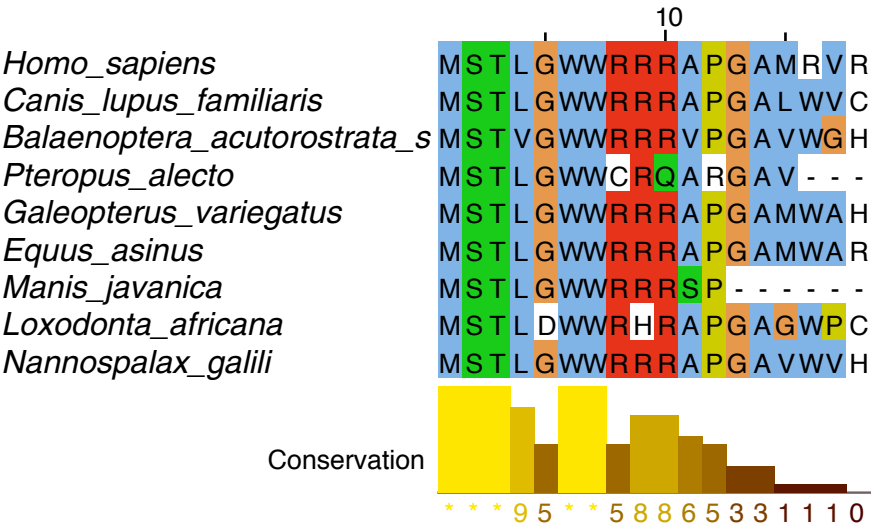
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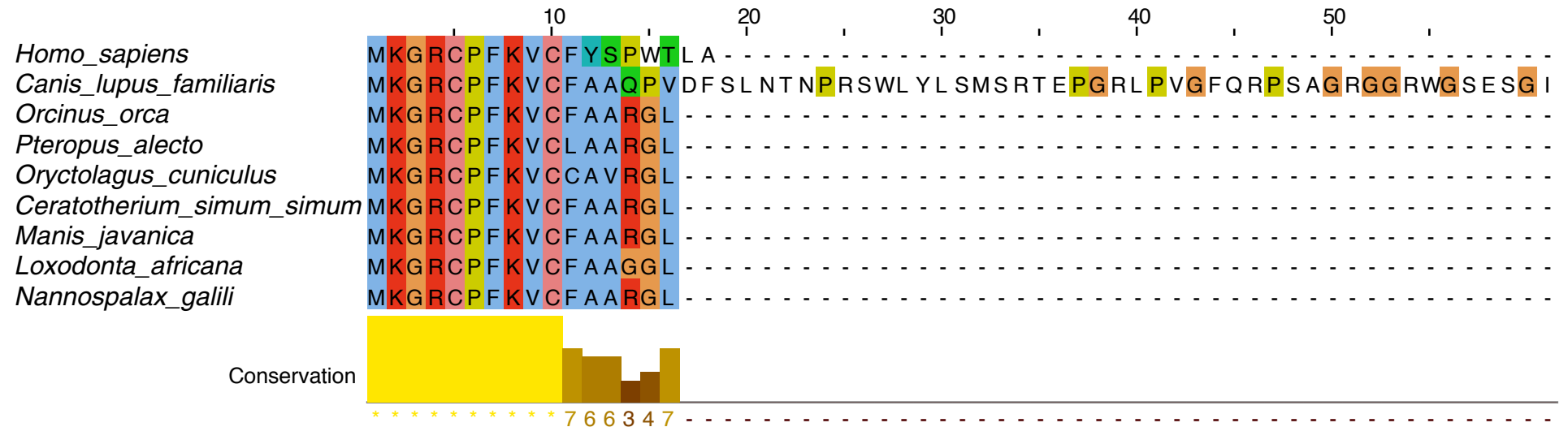


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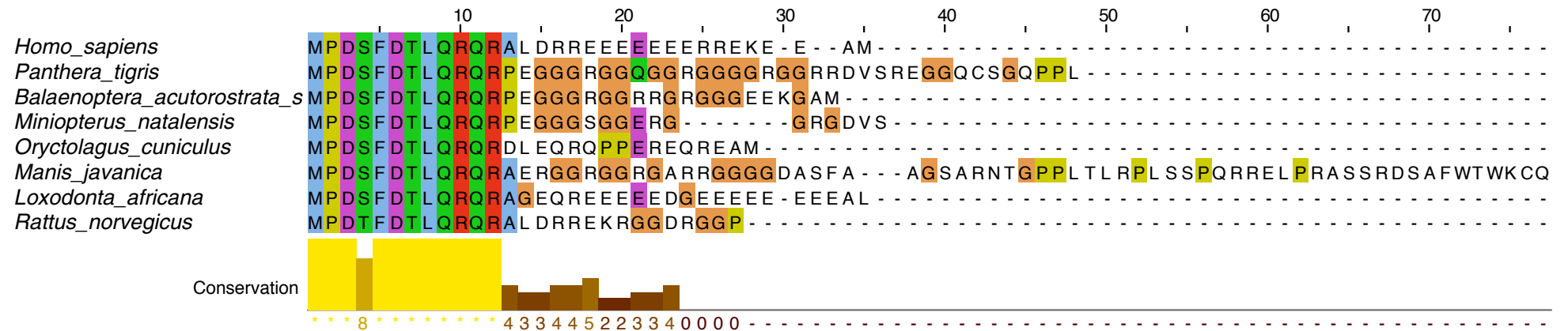


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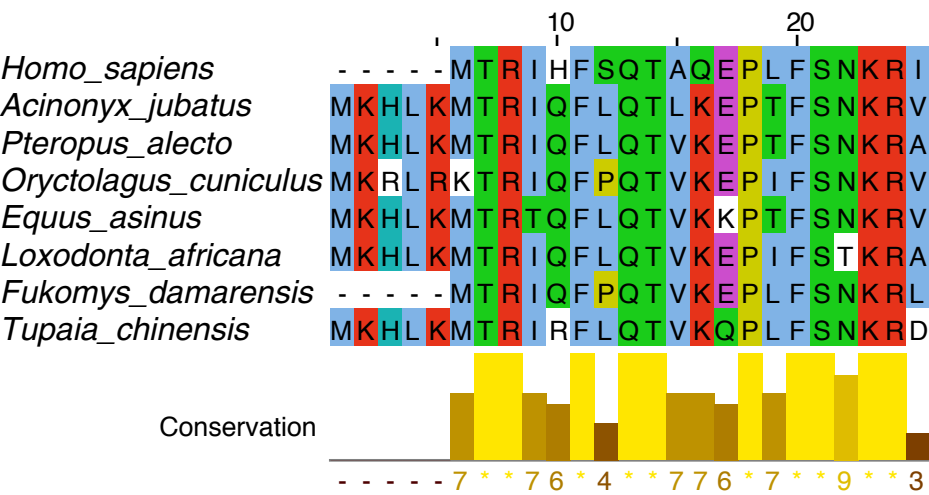
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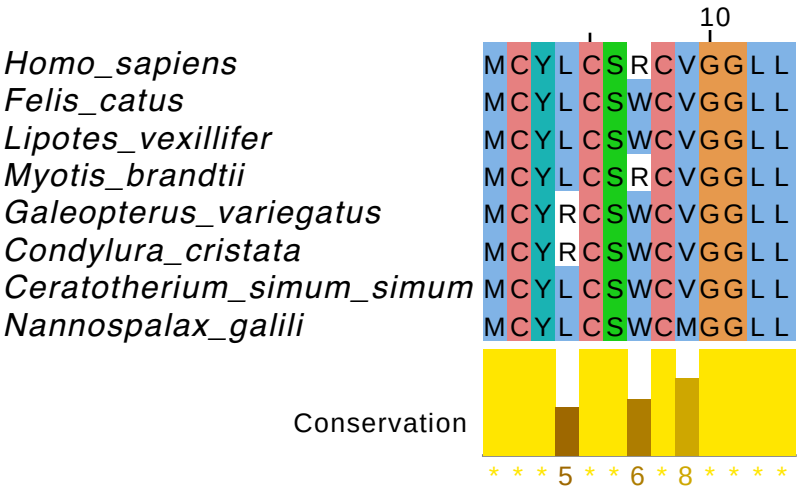
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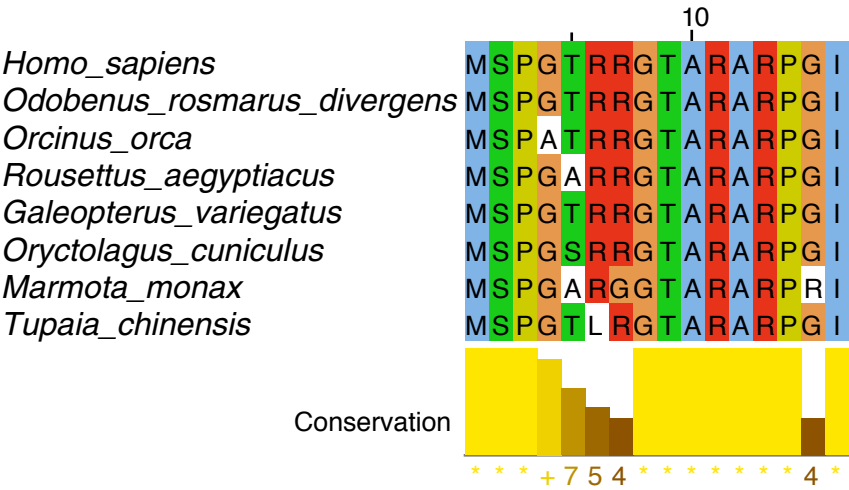
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ENSG00000071246 (VASH1)



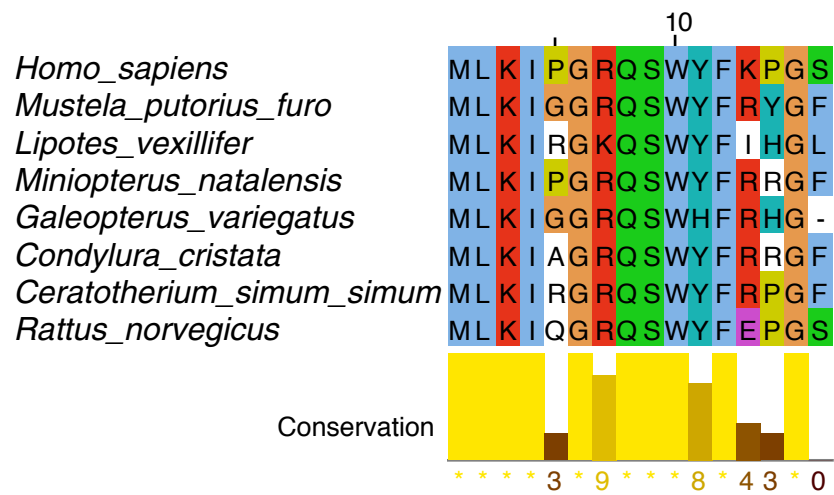
HG0716

ENSG00000075413 (MARK3)

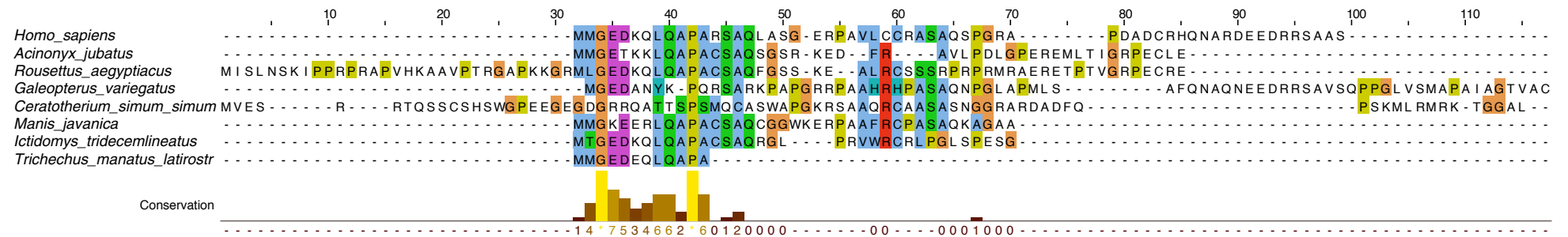


HG0717

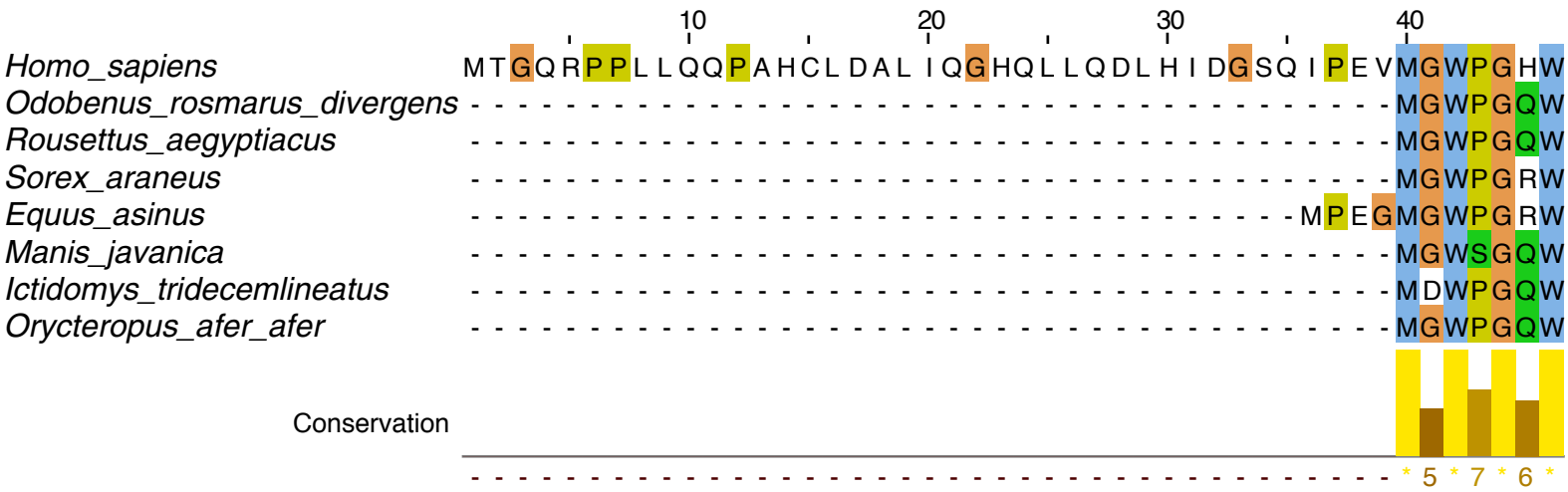
ENSG00000083857 (FAT1)



ENSG00000085274 (MYNN)

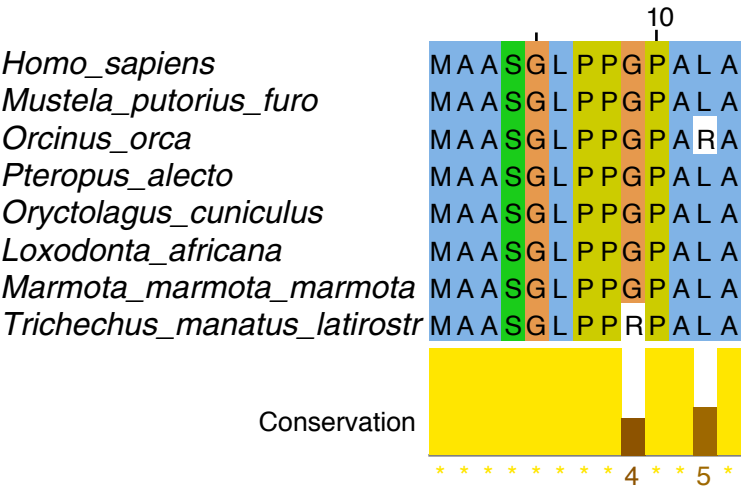


HG0719
ENSG00000085998 (POMGNT1)



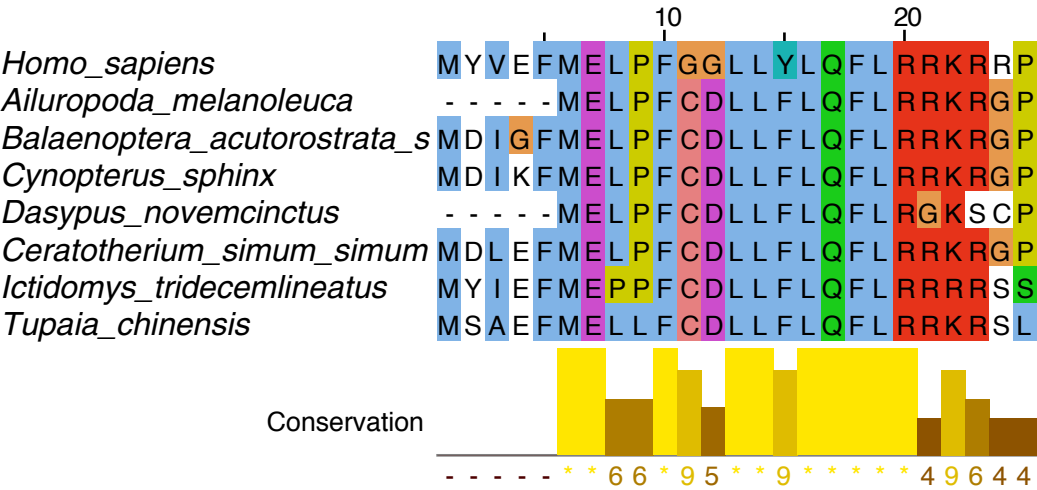
HG0720

ENSG00000087053 (MTMR2)



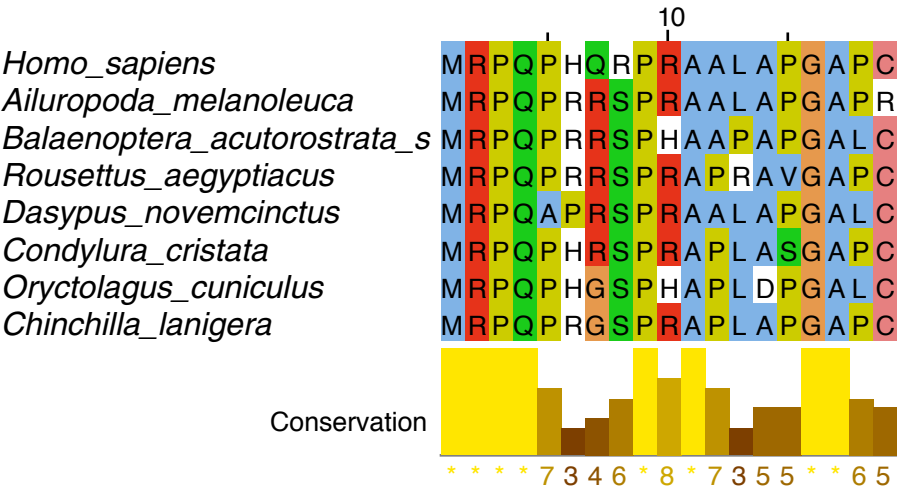
HG0721

ENSG00000095951 (HIVEP1)



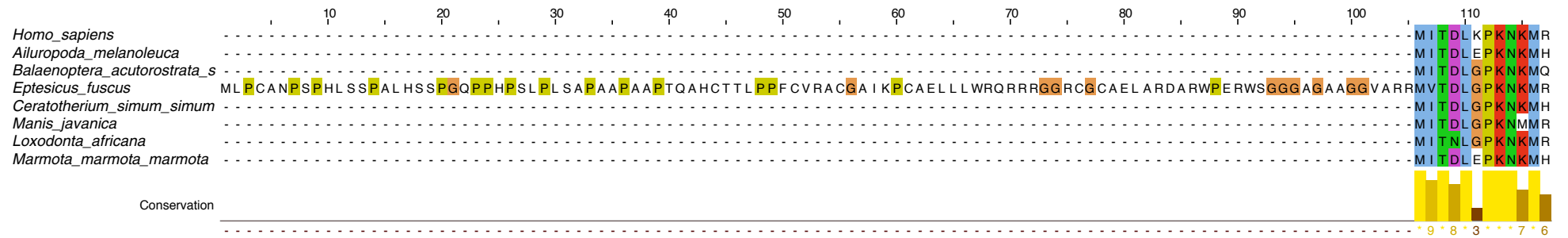
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ENSG00000101445 (PPP1R16B)



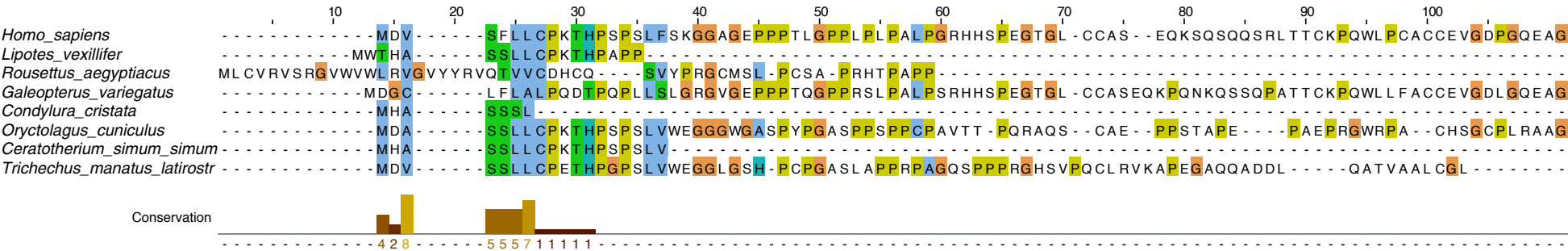
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ENSG00000102974 (CTCF)



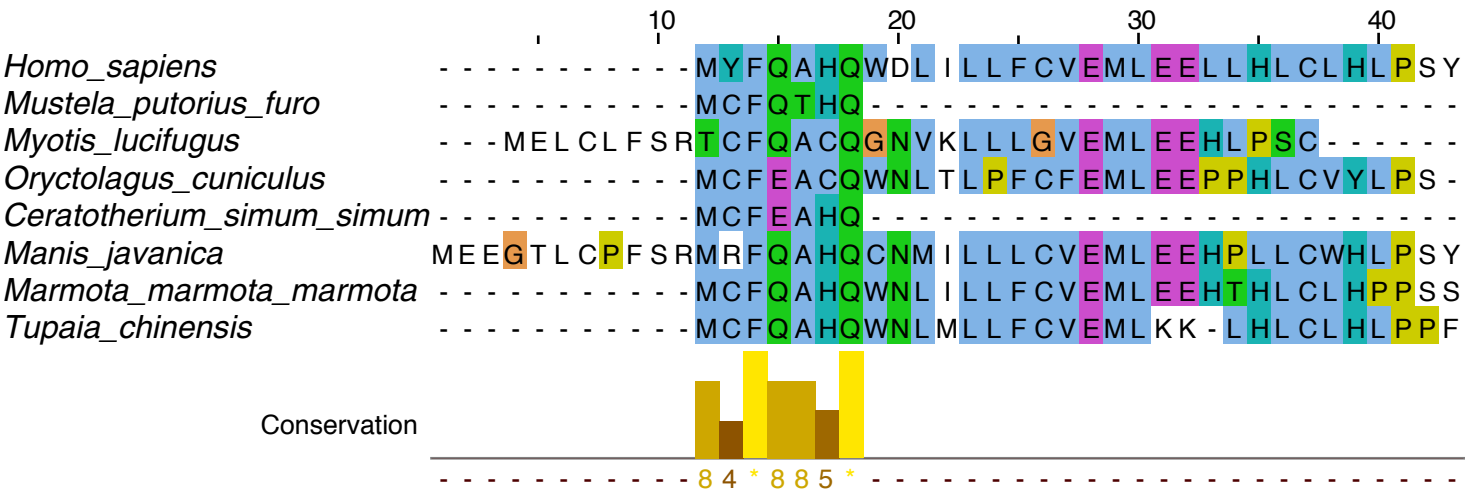
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ENSG00000104783 (KCNN4)



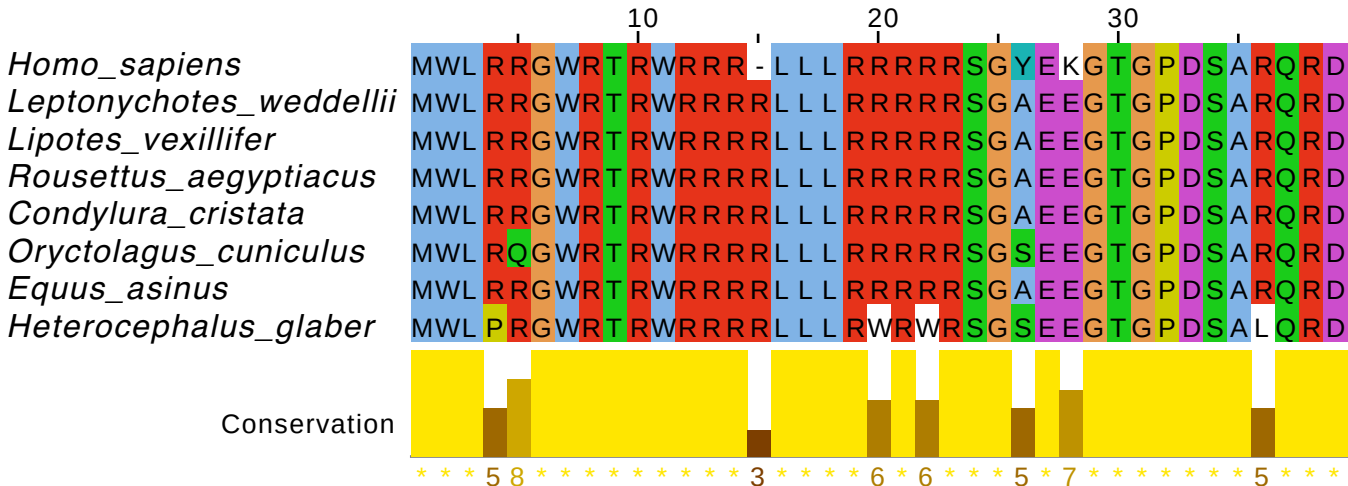
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ENSG00000112218 (GPR63)



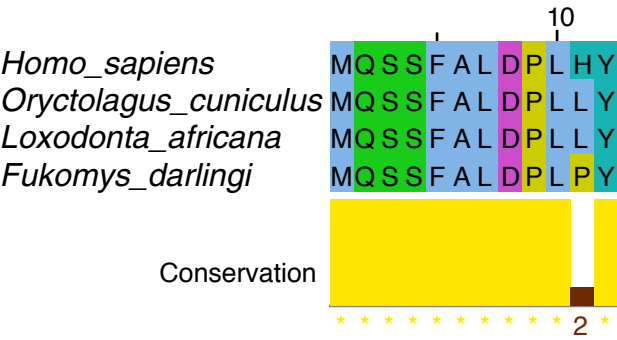
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ENSG00000115504 (EHBP1)



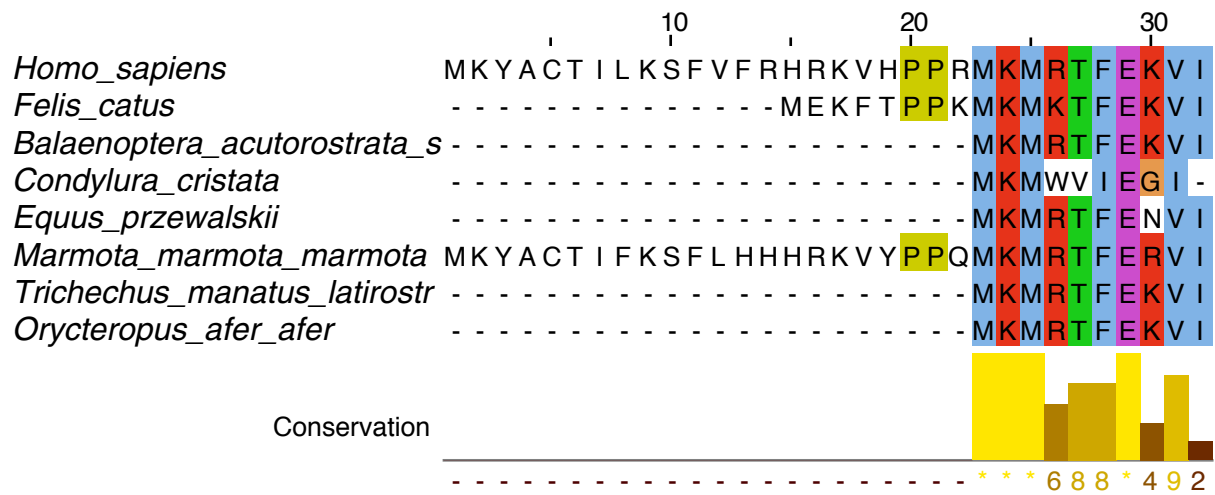
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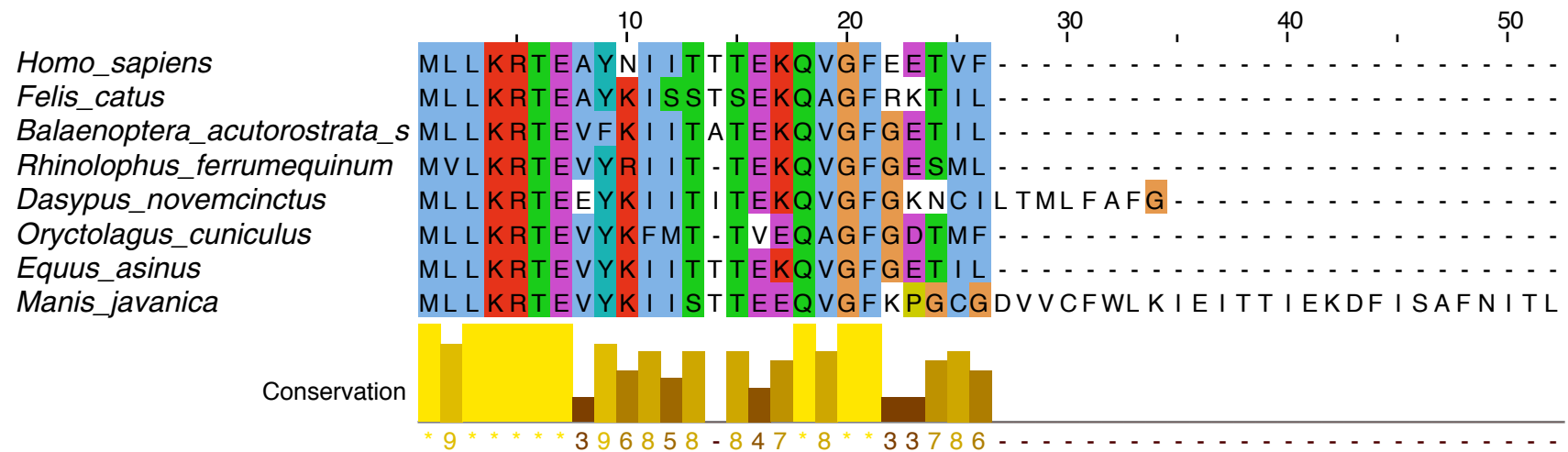


HG0727

ENSG00000115825 (PRKD3)

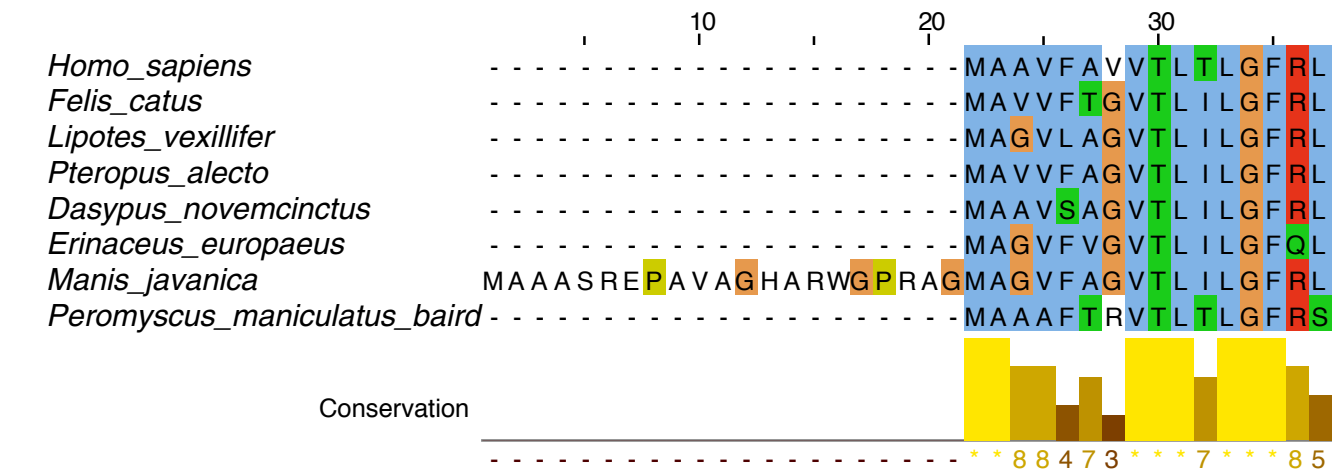


ENSG00000116991 (SIPA1L2)



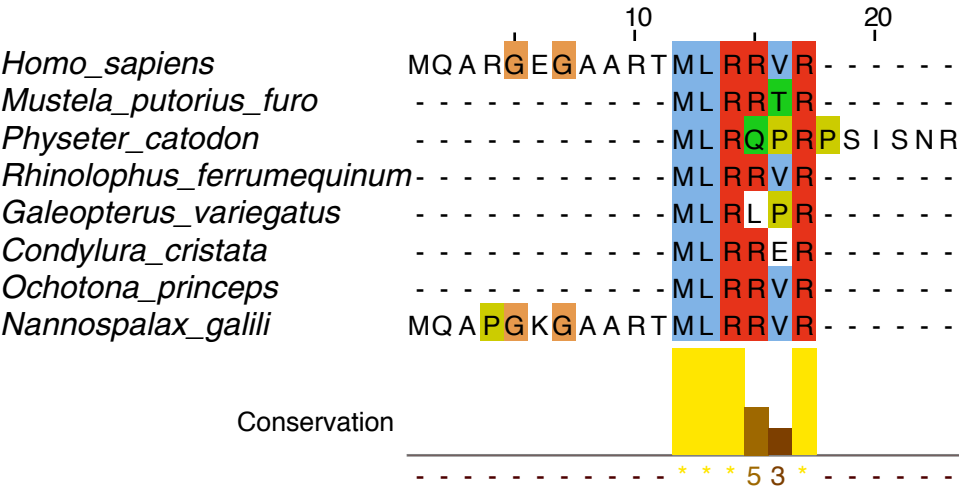
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ENSG00000119383 (PTPA)

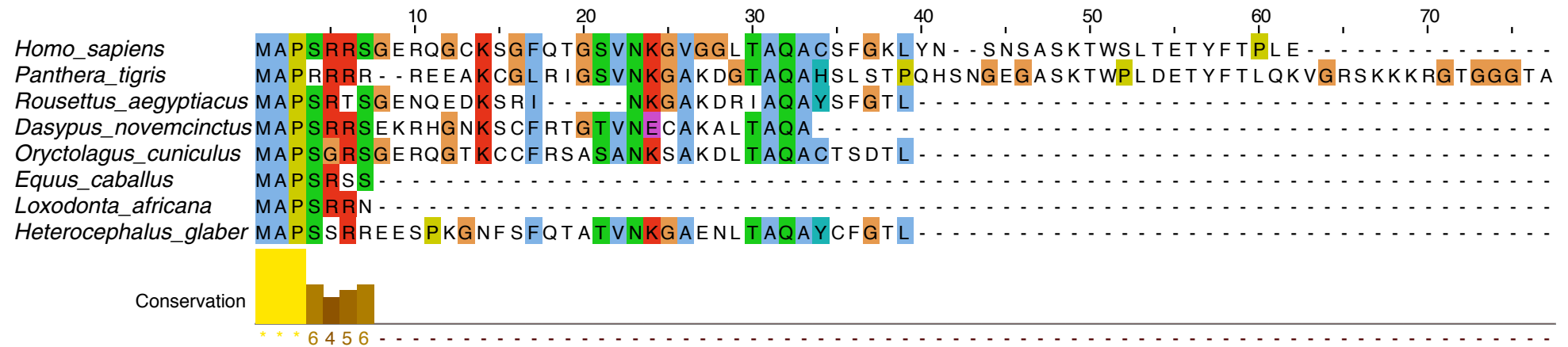


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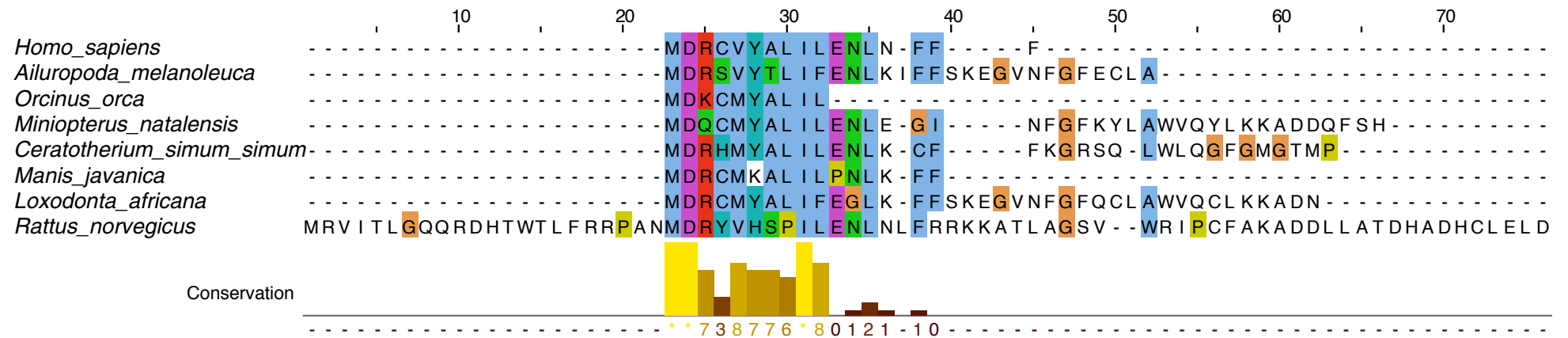
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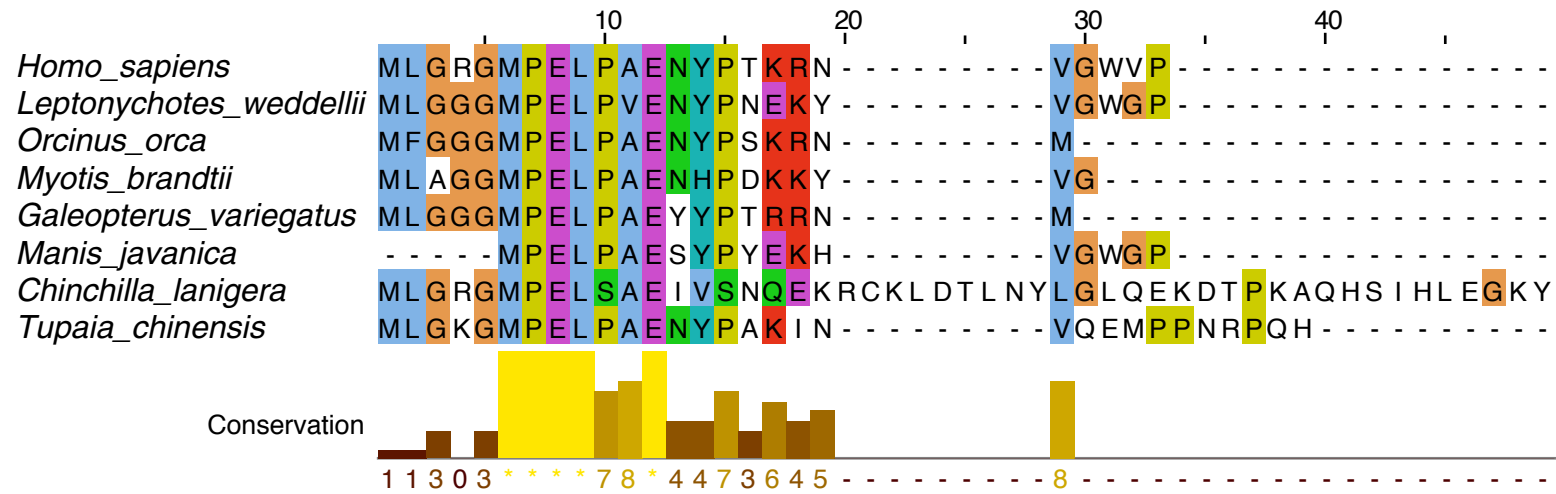
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ENSG00000135914 (HTR2B)

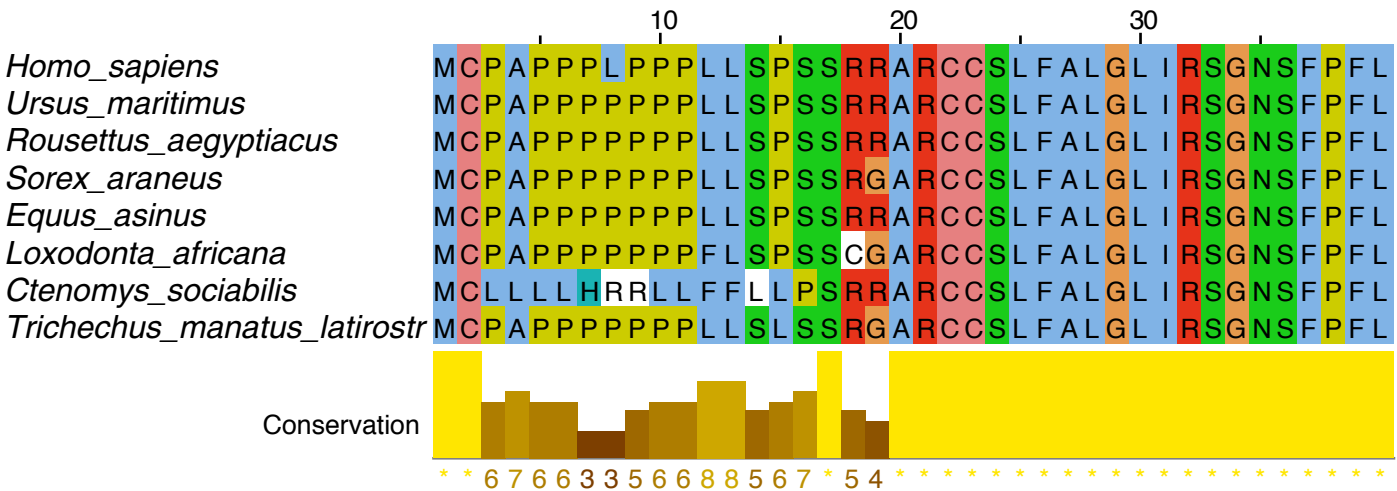


ENSG00000136247 (ZDHH4)



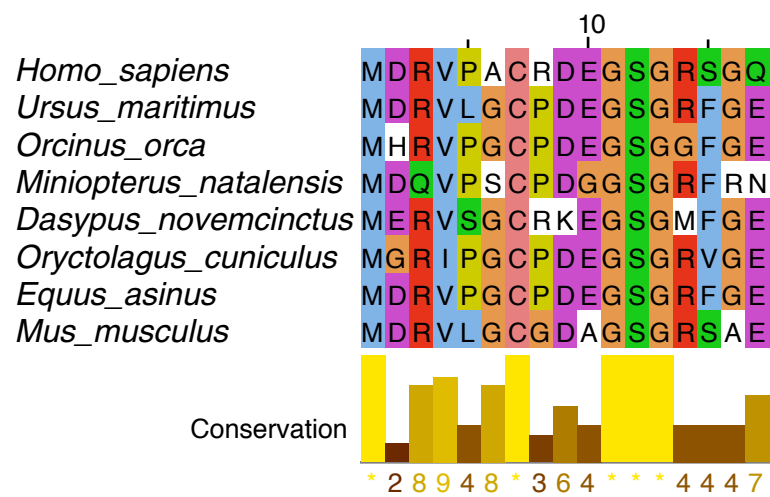
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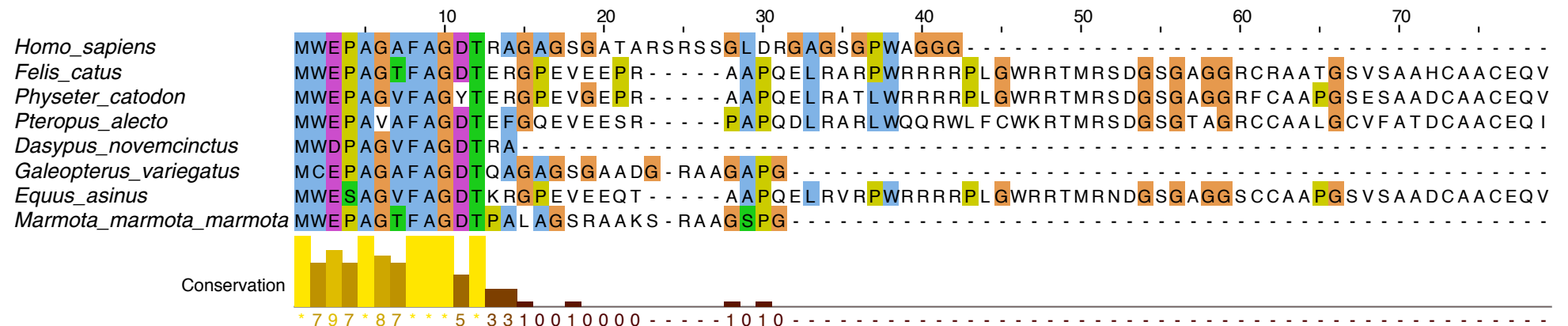


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ENSG00000139579 (NABP2)

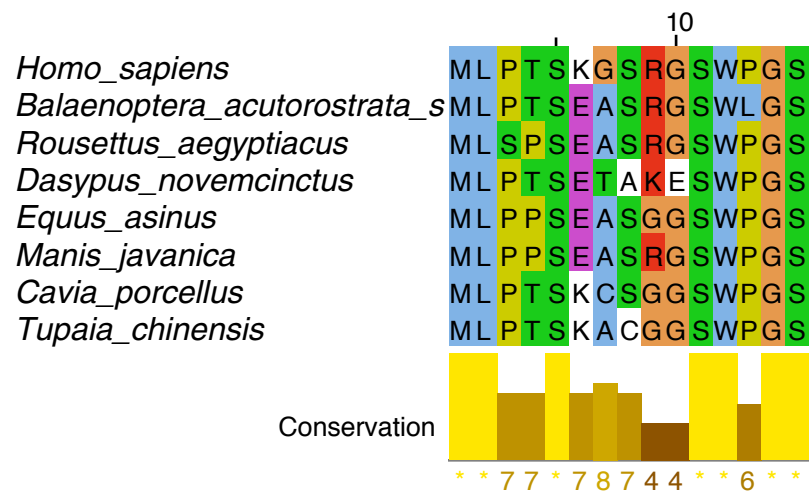


ENSG00000139826 (ABHD13)



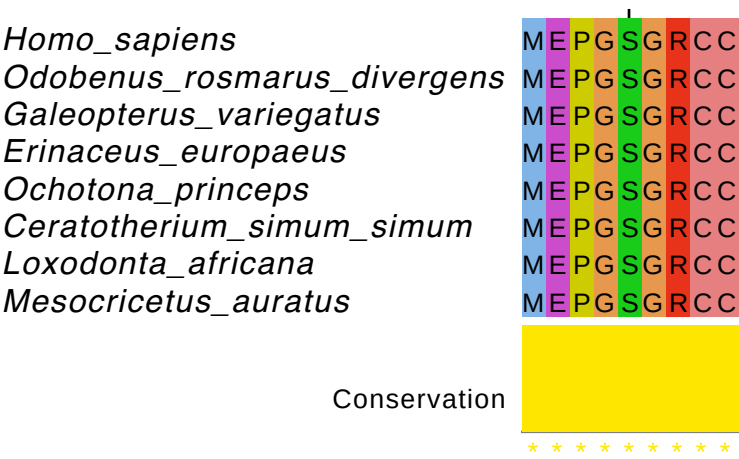
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ENSG00000141639 (MAPK4)



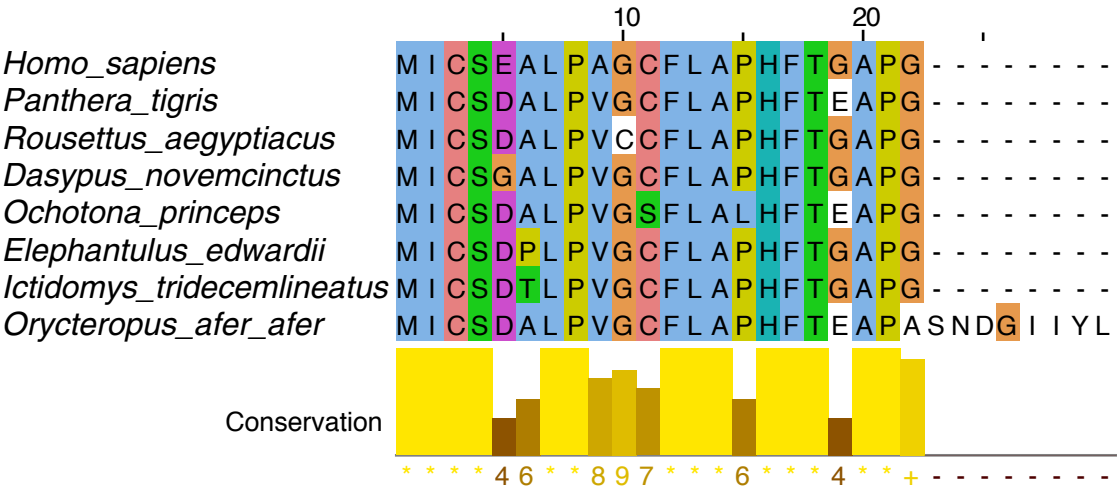
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ENSG00000143393 (PI4KB)



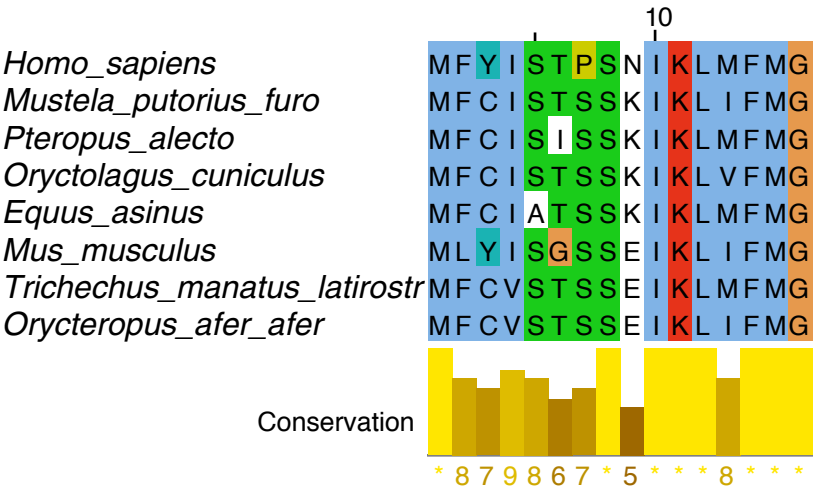
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ENSG00000144331 (ZNF385B)



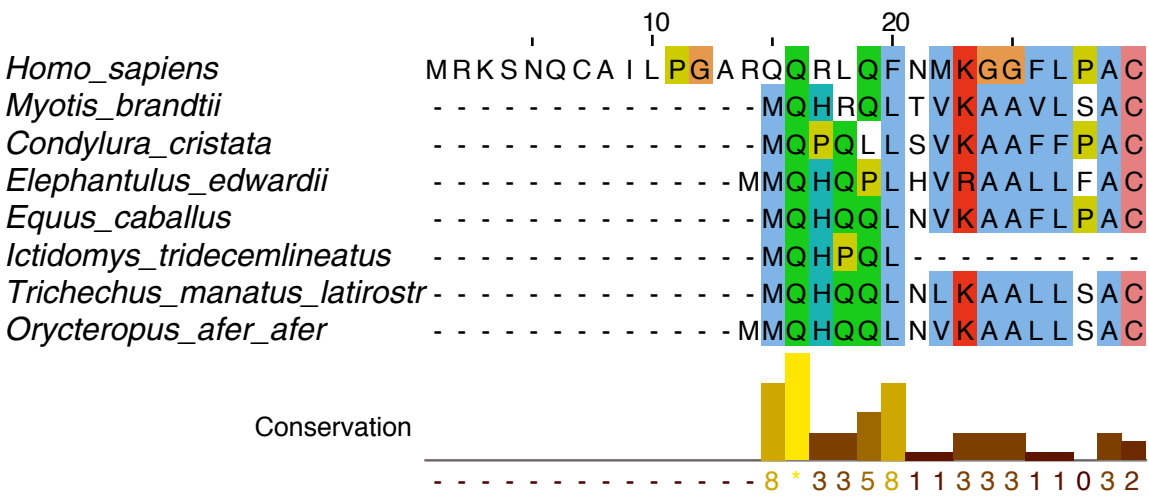
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ENSG00000144331 (ZNF385B)



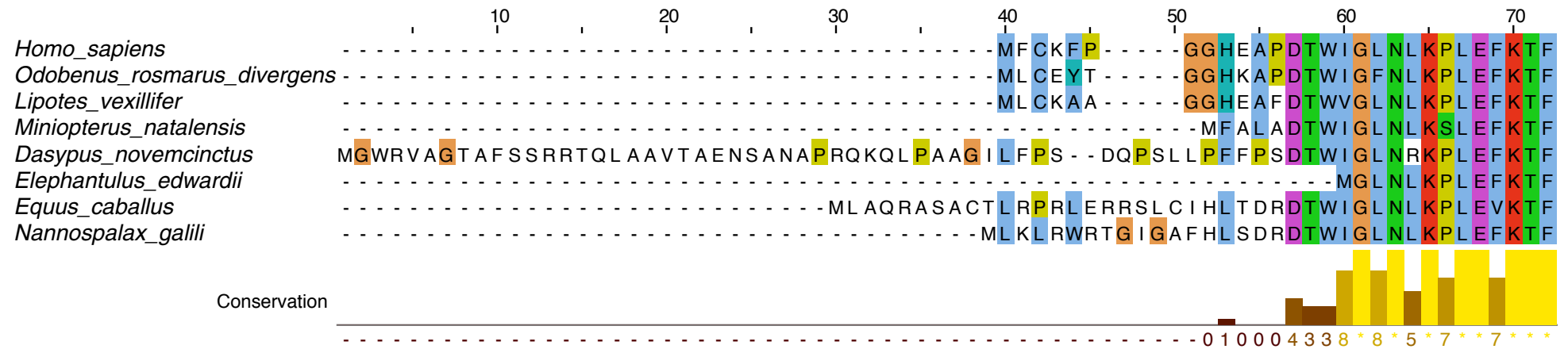
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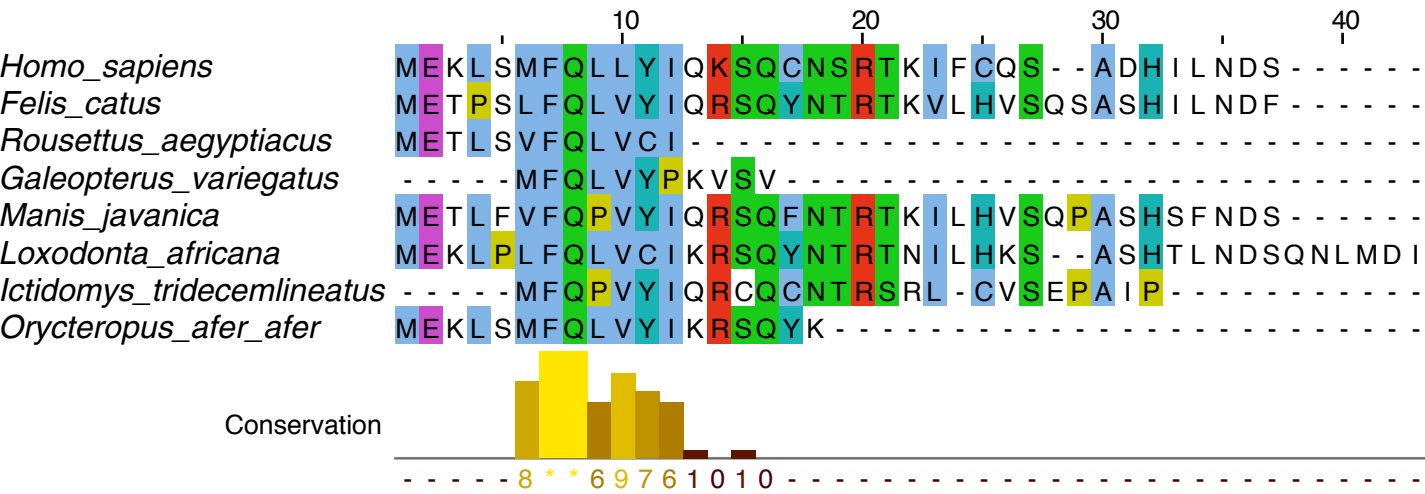


HG0742

ENSG00000154556 (SORBS2)

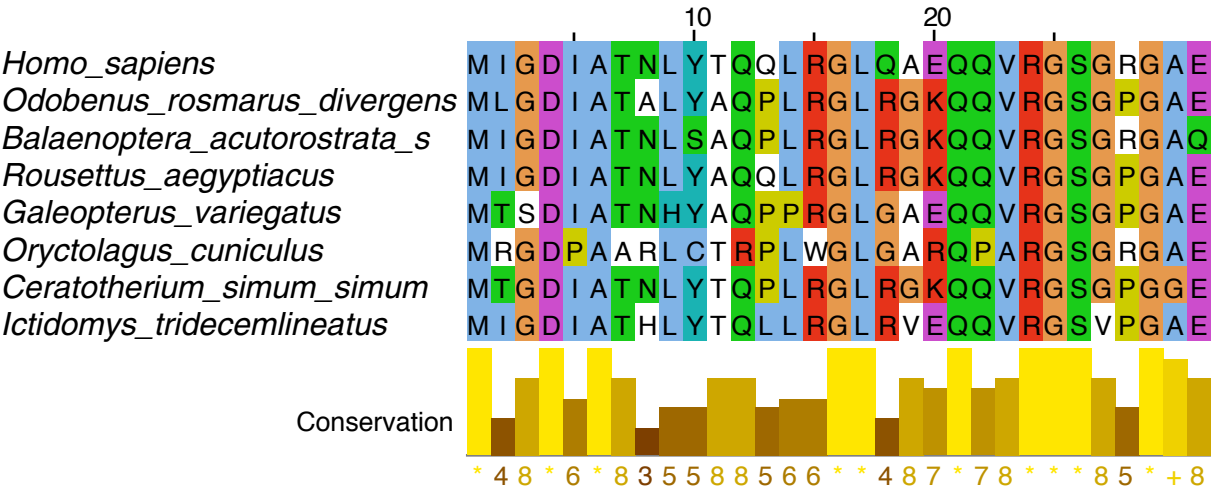


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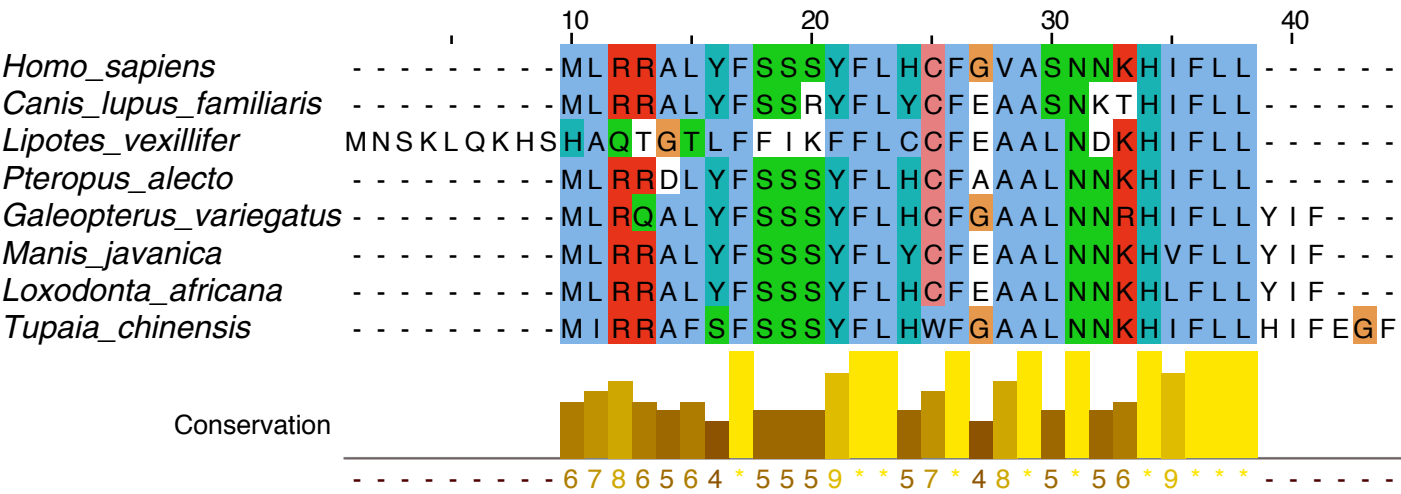
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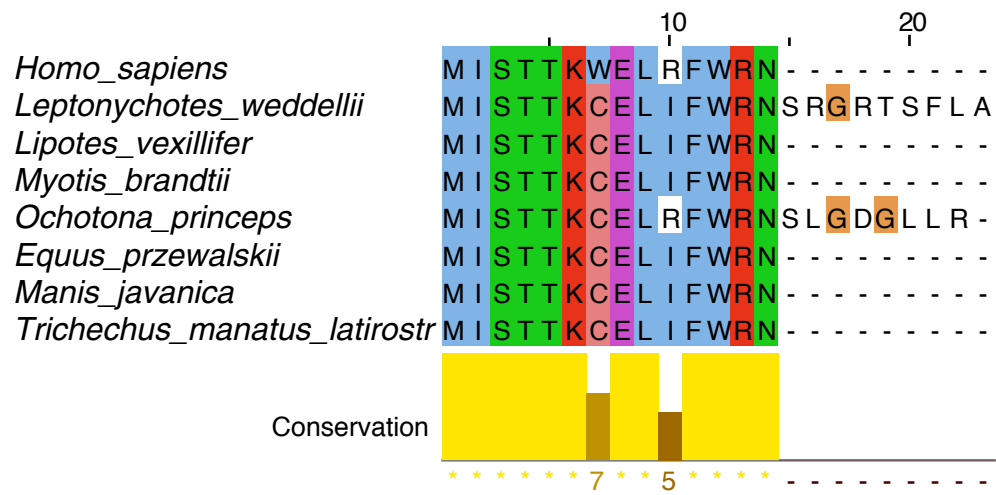
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ENSG00000163145 (C1QTNF7)



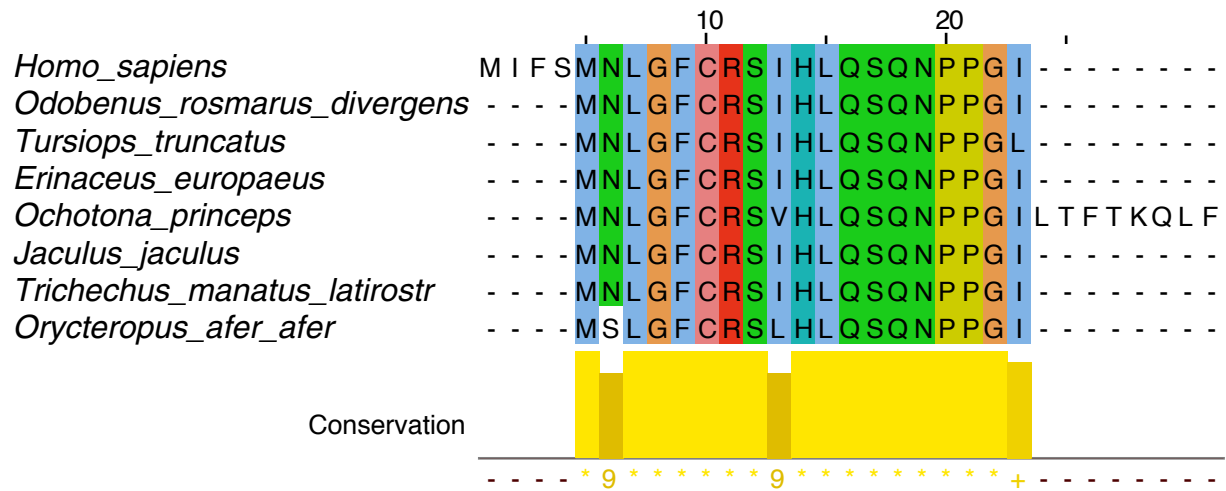
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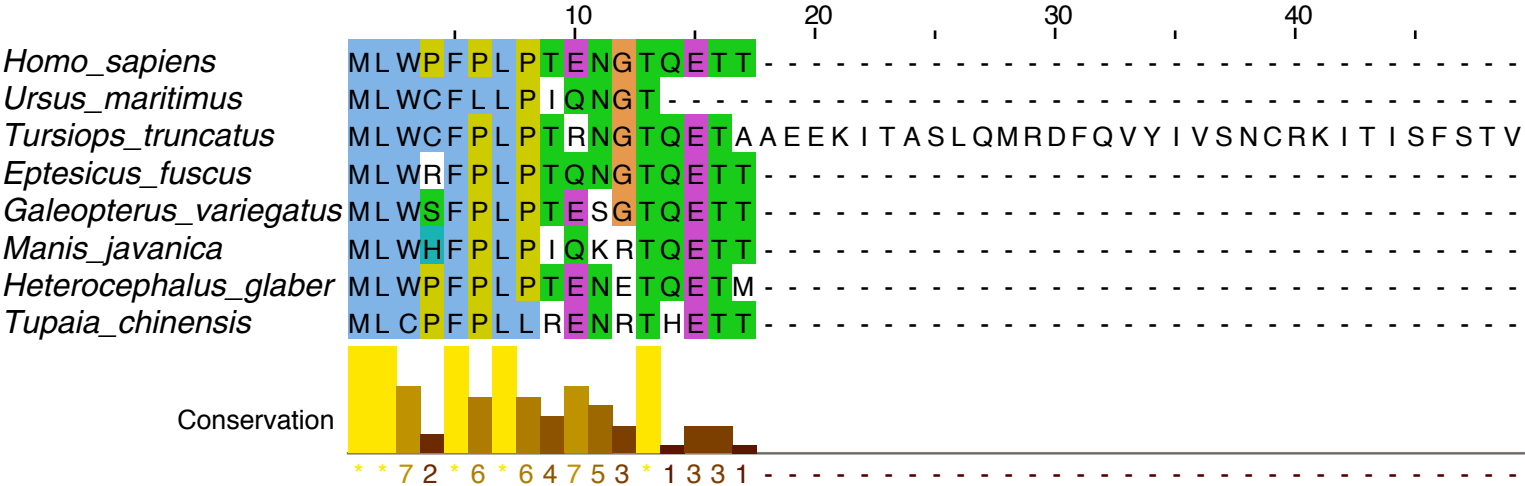


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ENSG00000168036 (CTNNB1)

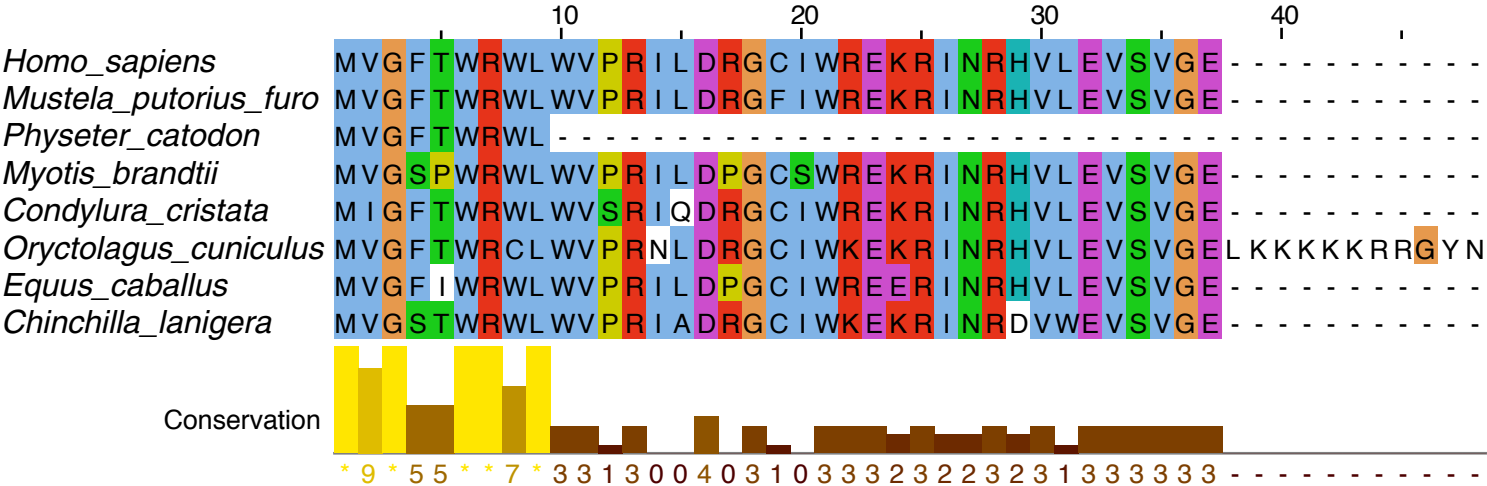


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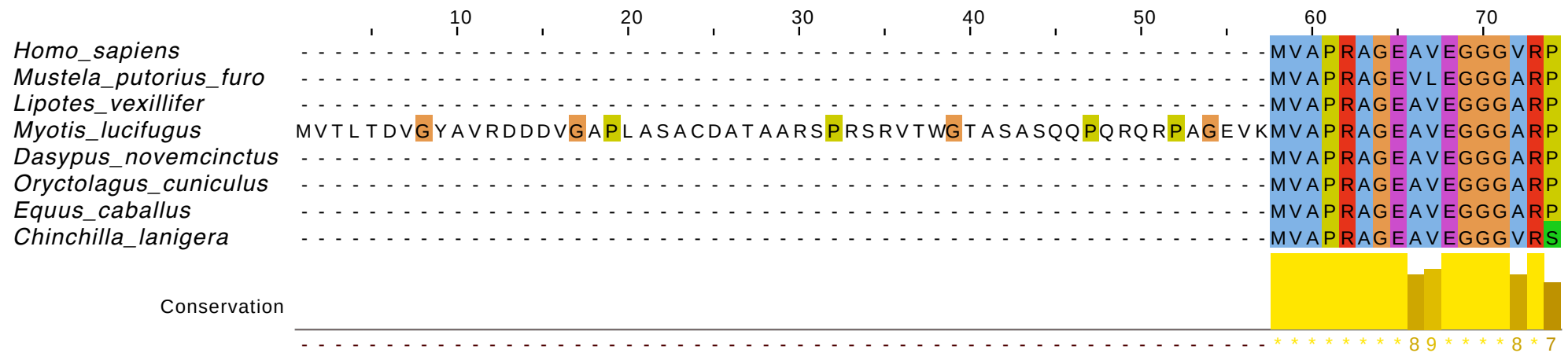


HG0749

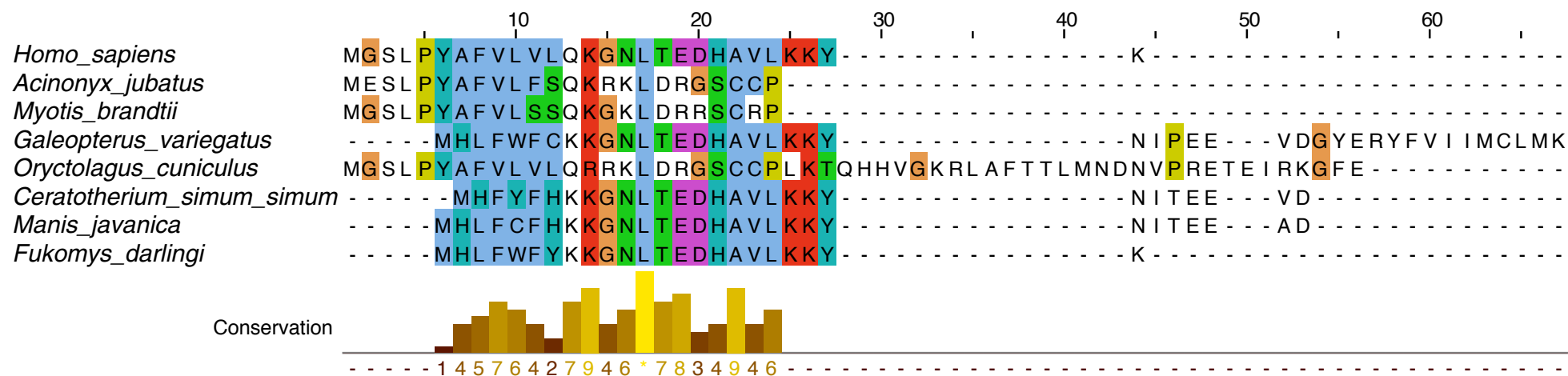
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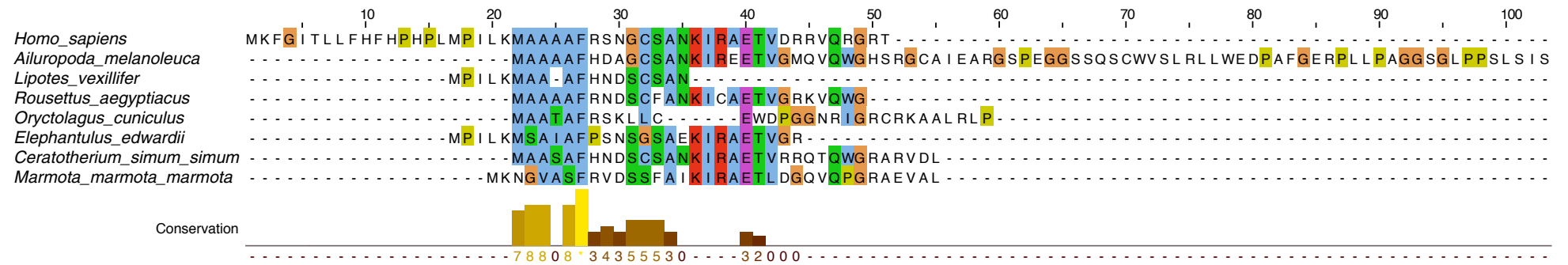
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ENSG00000171791 (BCL2)

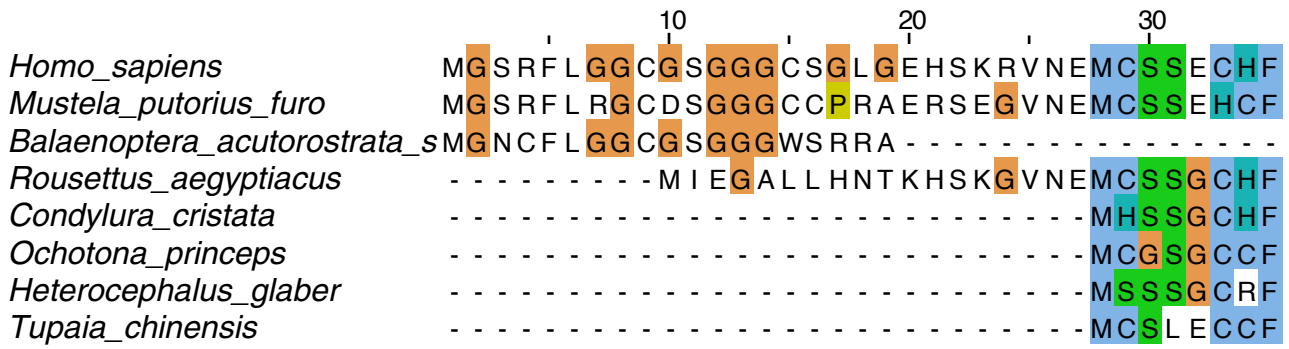


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HG0753

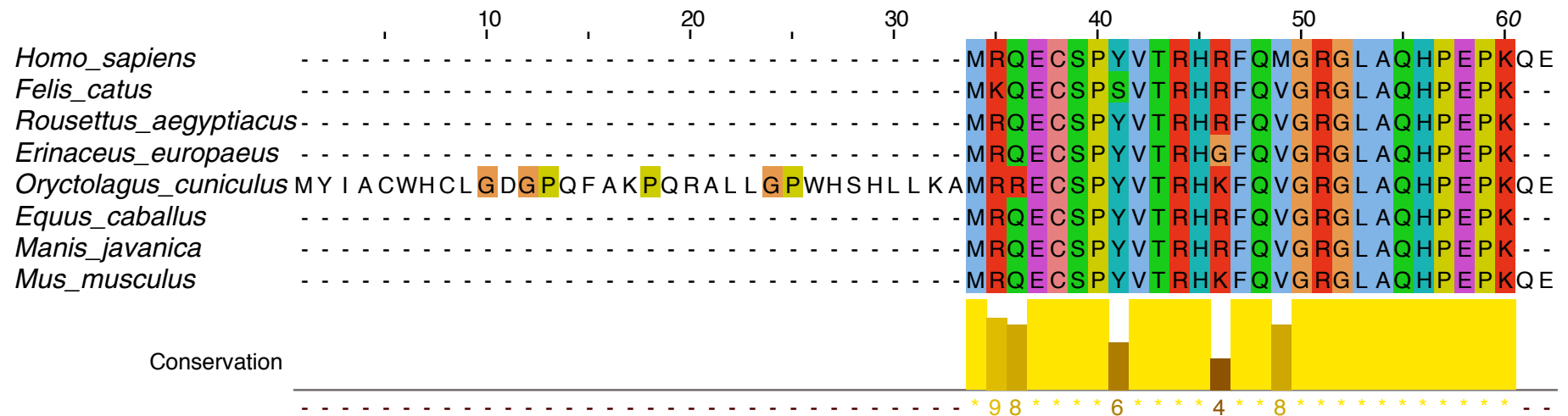
ENSG00000173406 (DAB1)



Conservation

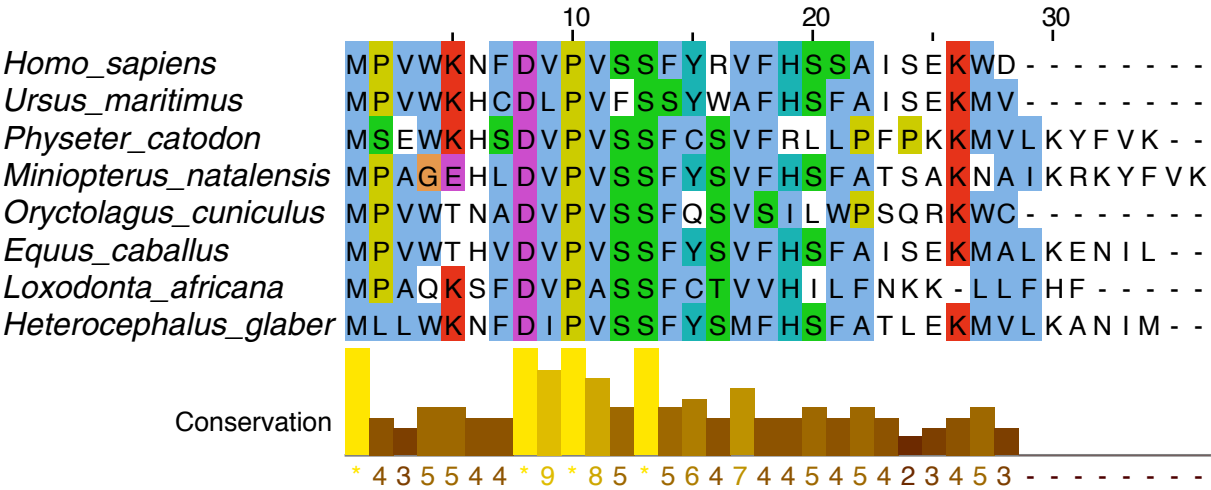


ENSG00000175182 (FAM131A)



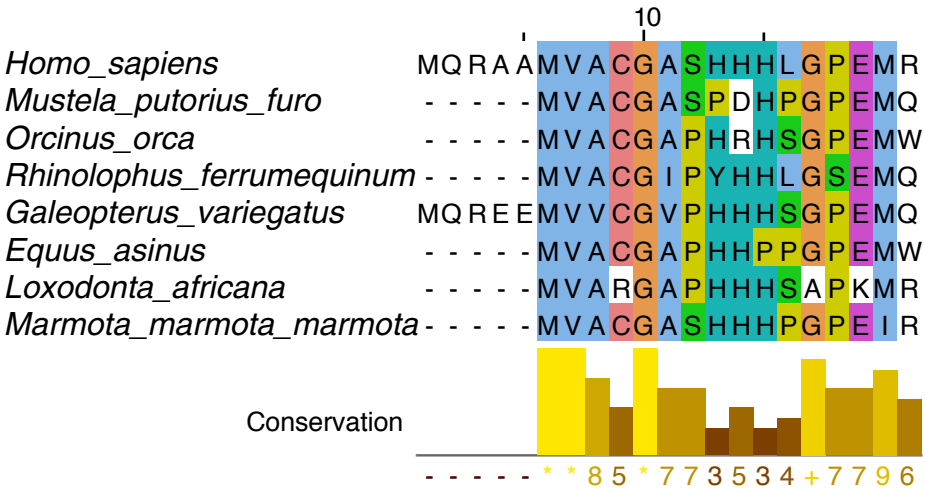
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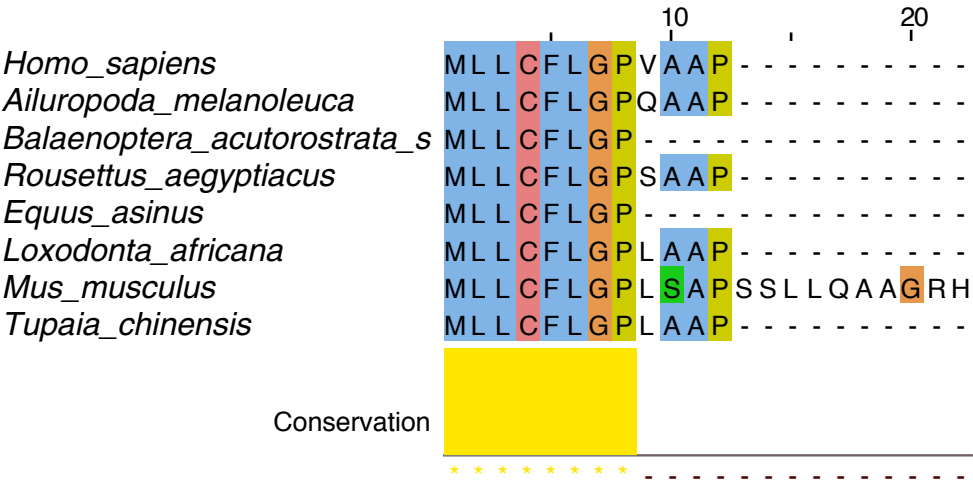
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ENSG00000177051 (FBXO46)



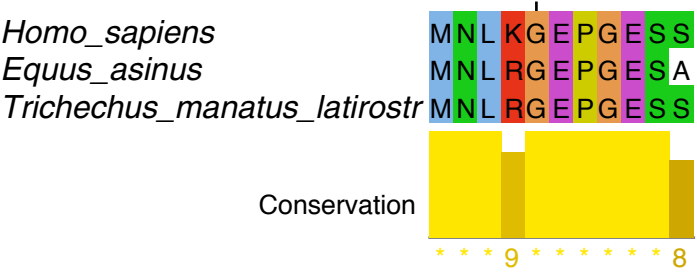
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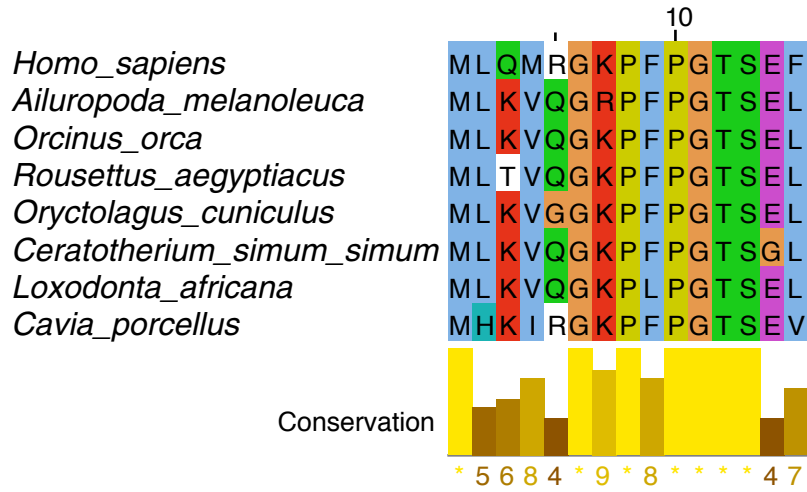
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ENSG00000182255 (KCNA4)



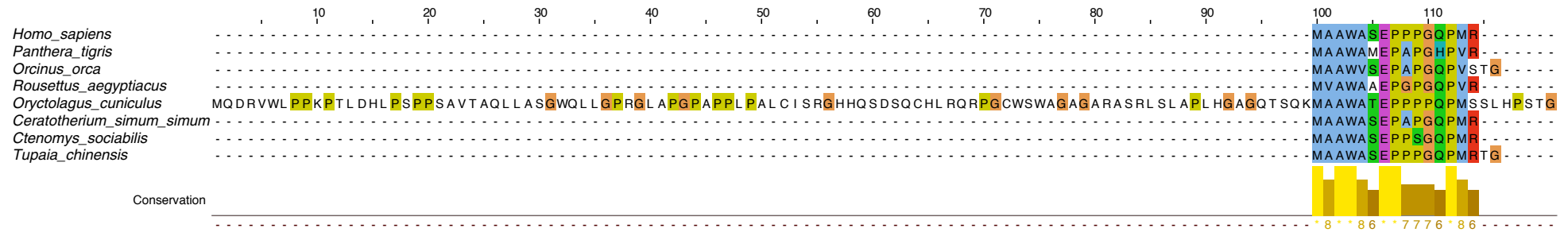
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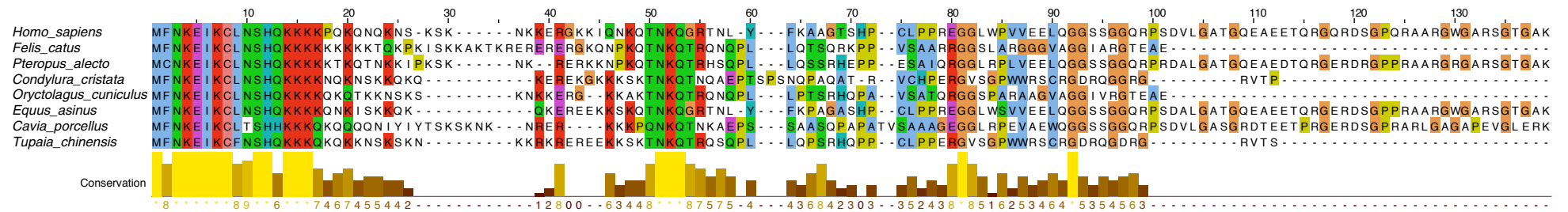


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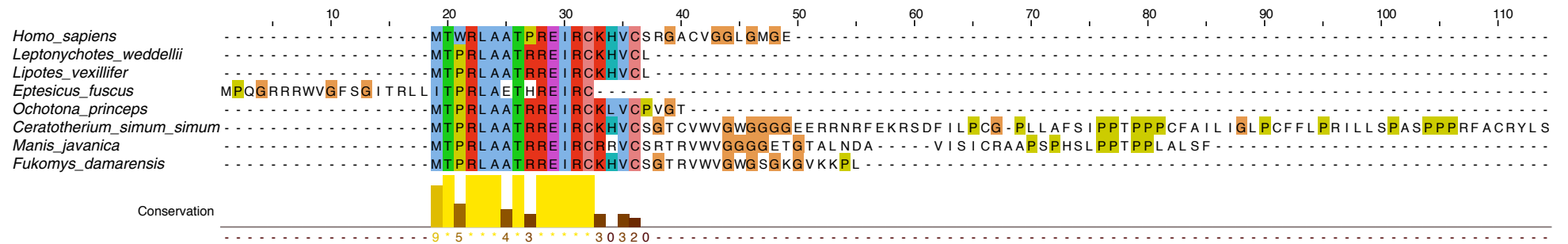
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ENSG00000182463 (TSHZ2)

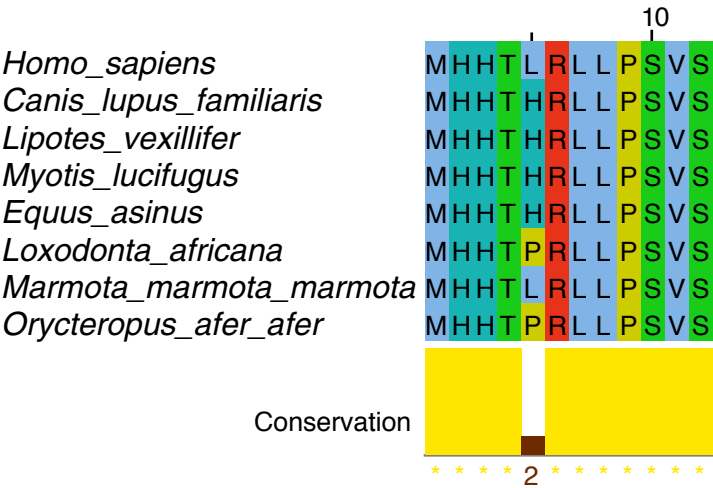


ENSG00000185985 (SLITRK2)



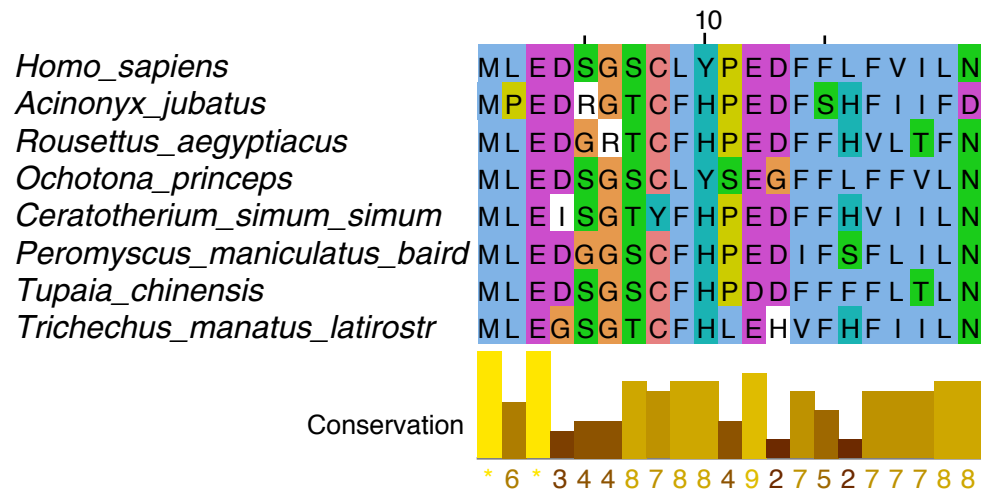
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ENSG00000187147 (RNF220)

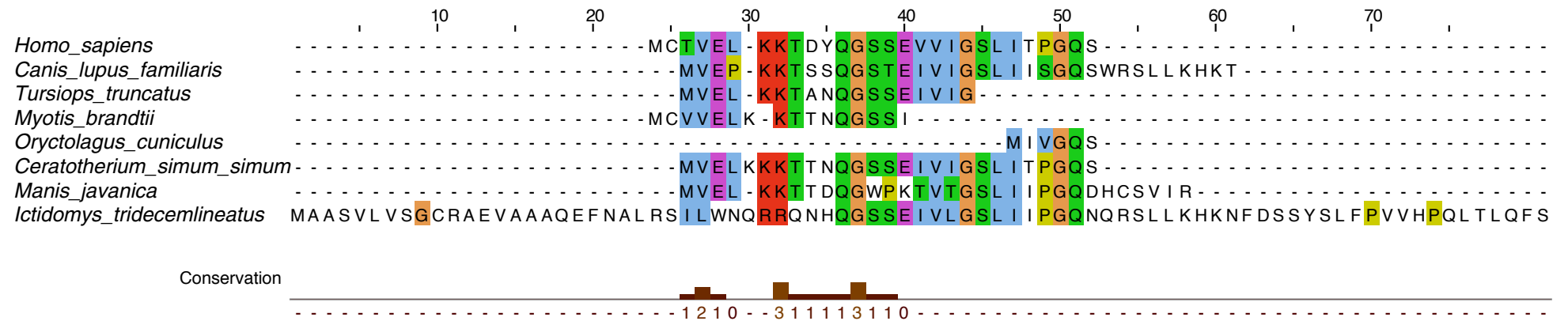


HG0763

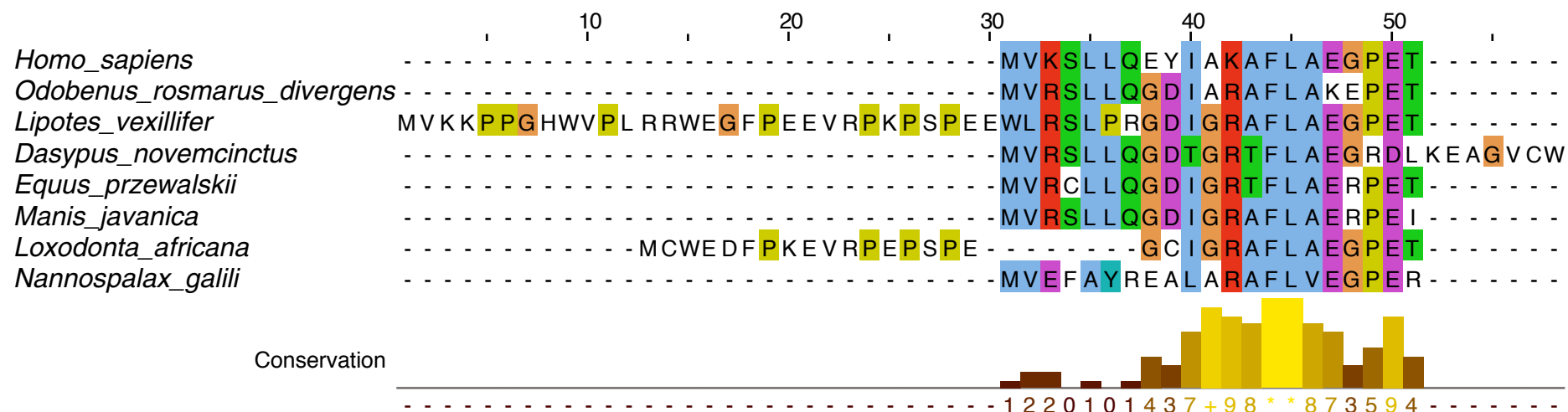
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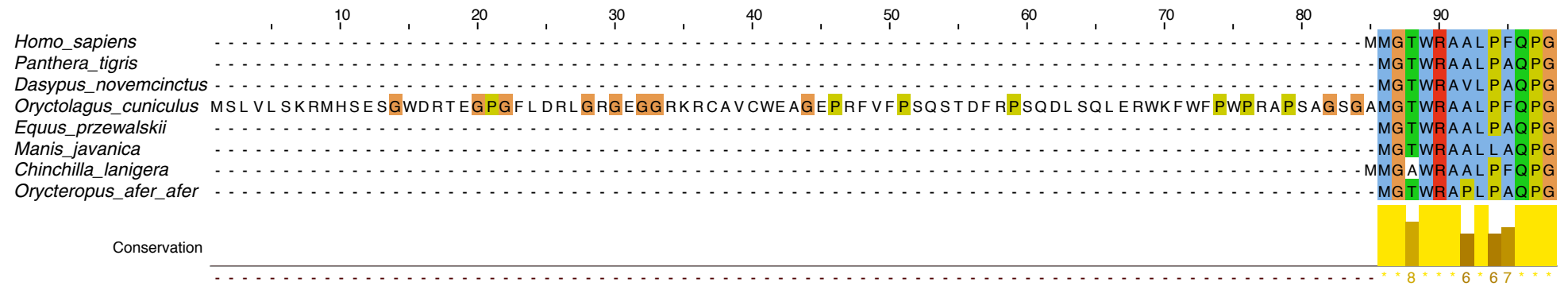
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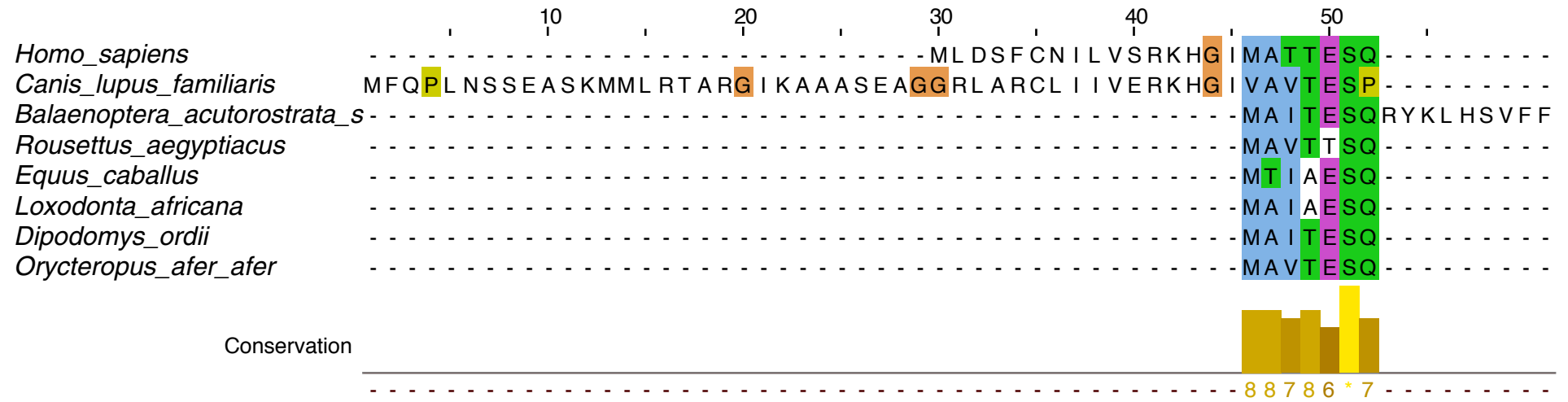
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ENSG00000196189 (SEMA4A)

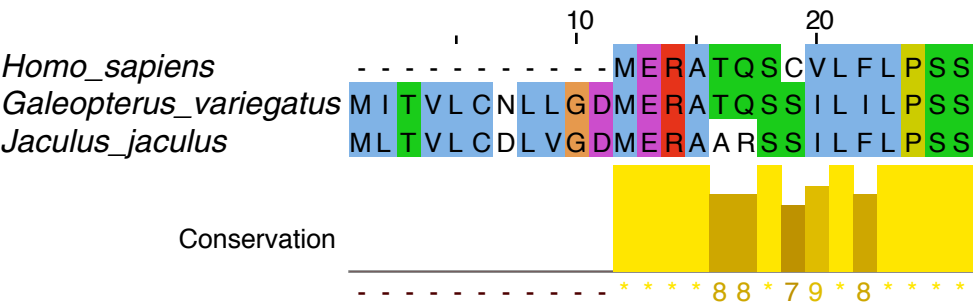


ENSG00000197555 (SIPA1L1)



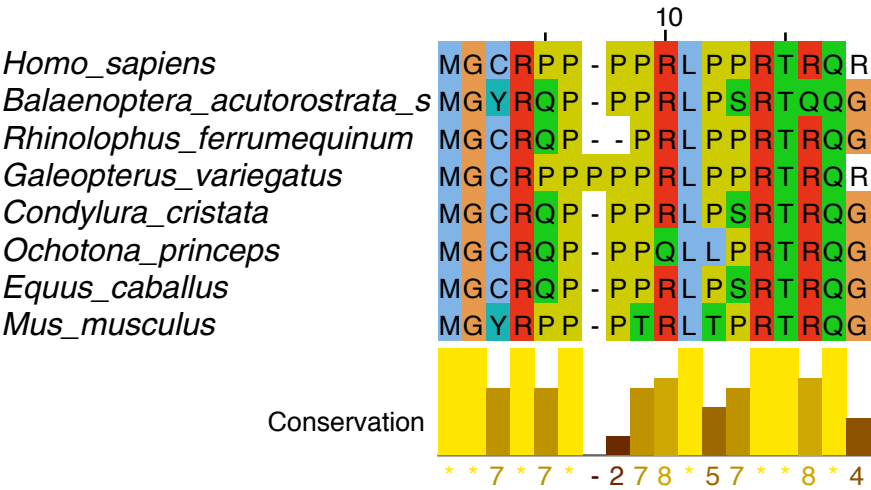
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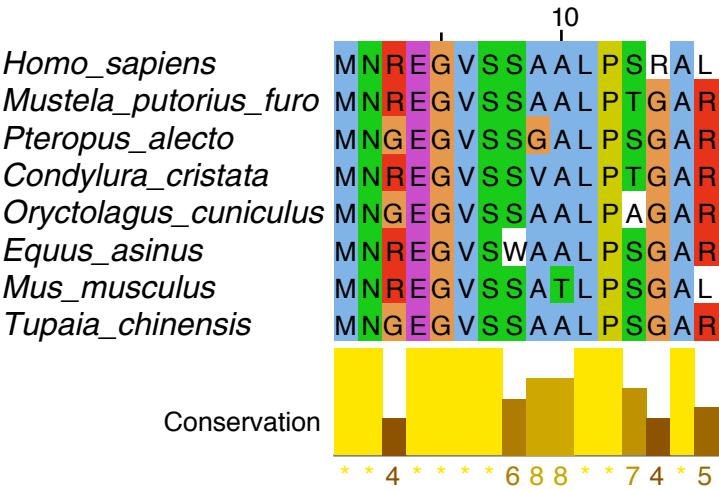
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ENSG00000213023 (SYT3)



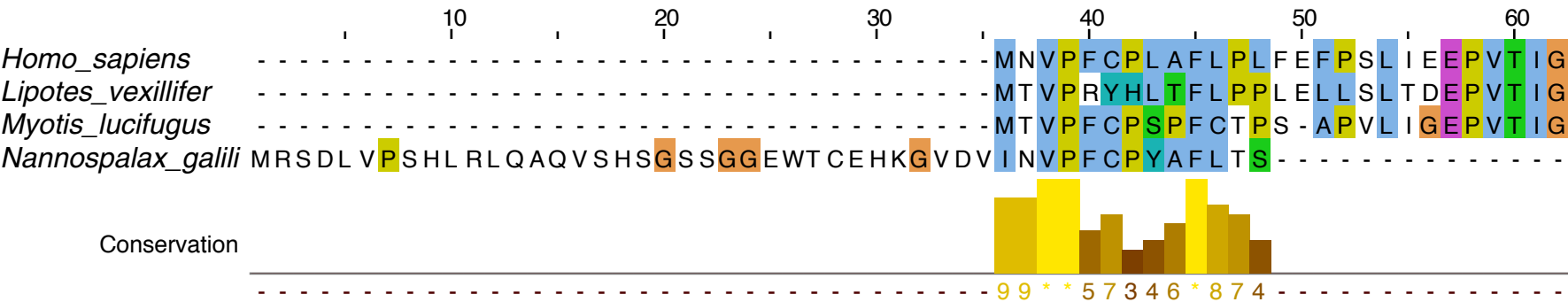
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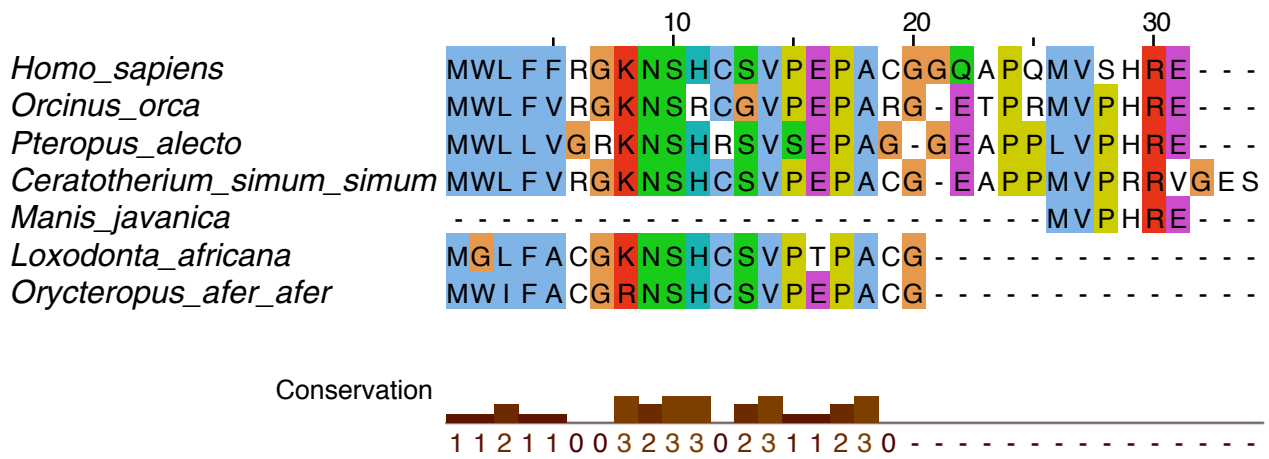
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ENSG00000197991



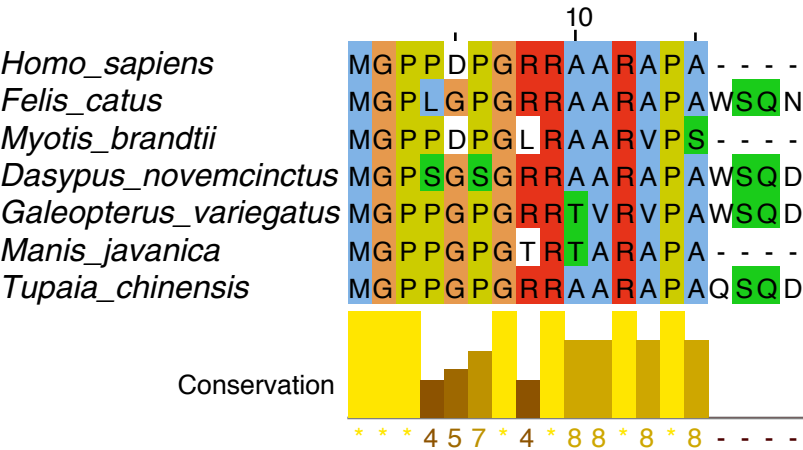
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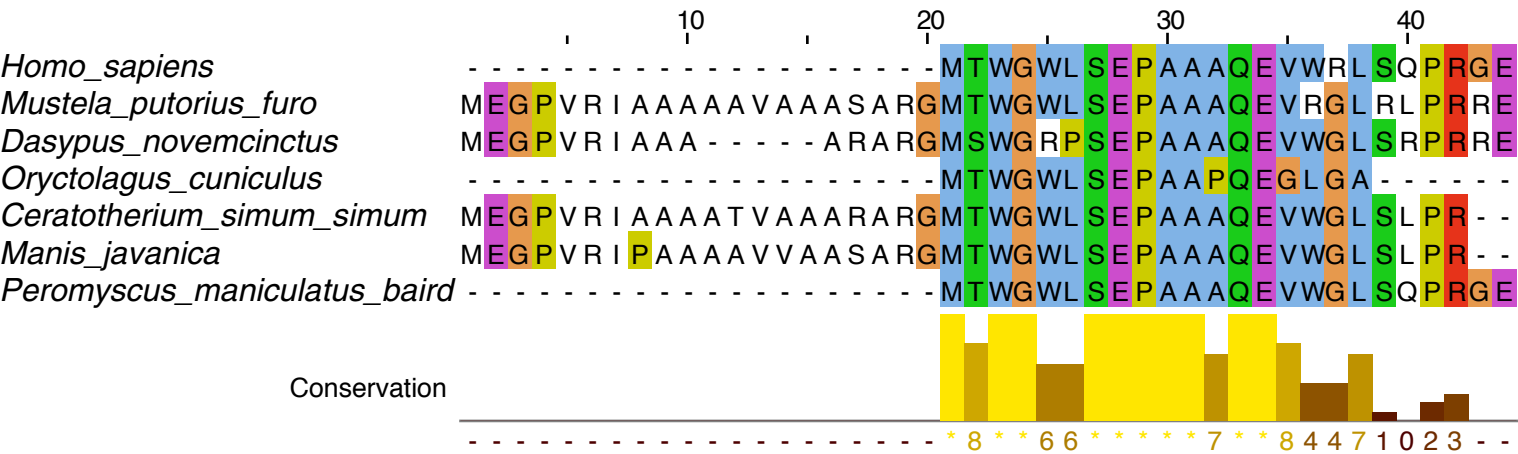


HG0771

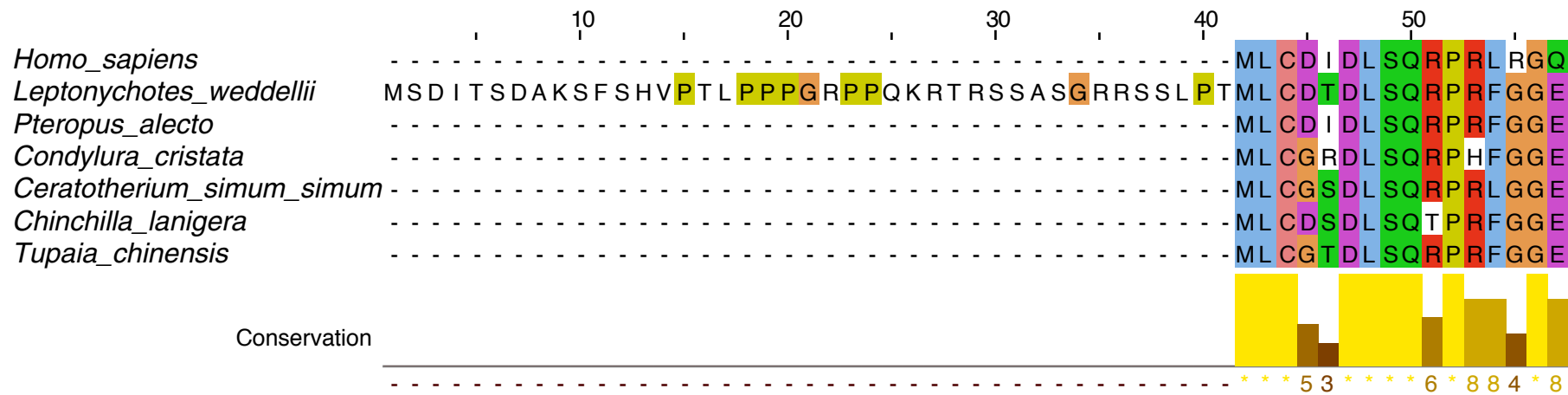
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HG0772
ENSG00000064309 (CDON)

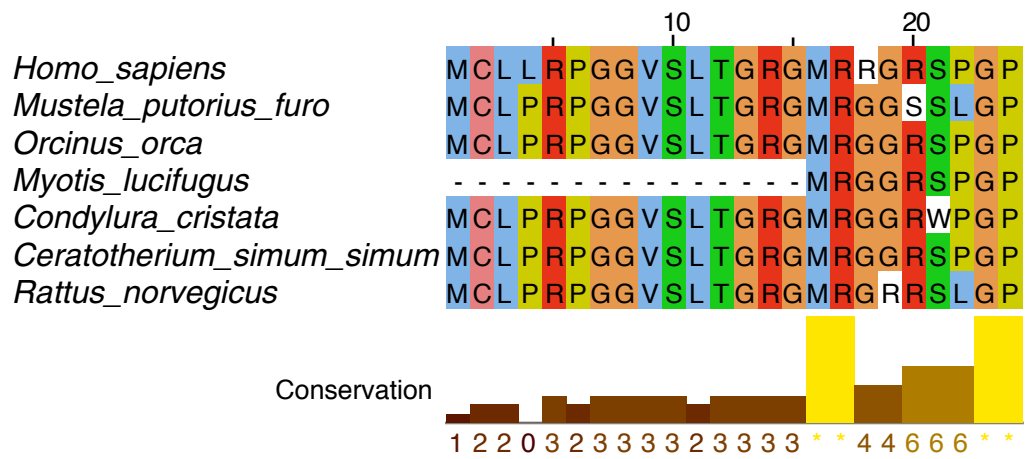


ENSG00000065548 (ZC3H15)



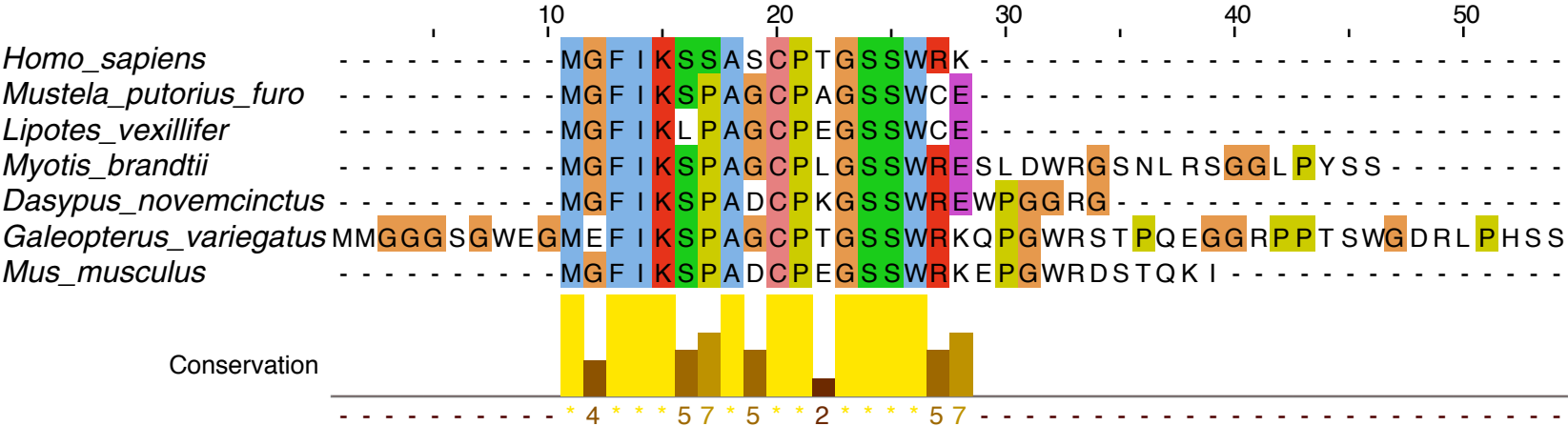
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ENSG00000066933 (MYO9A)



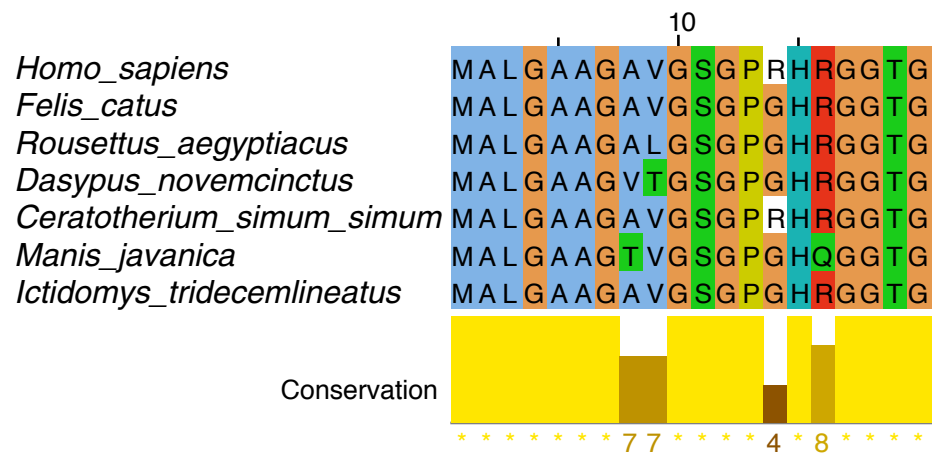
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ENSG00000068001 (HYAL2)



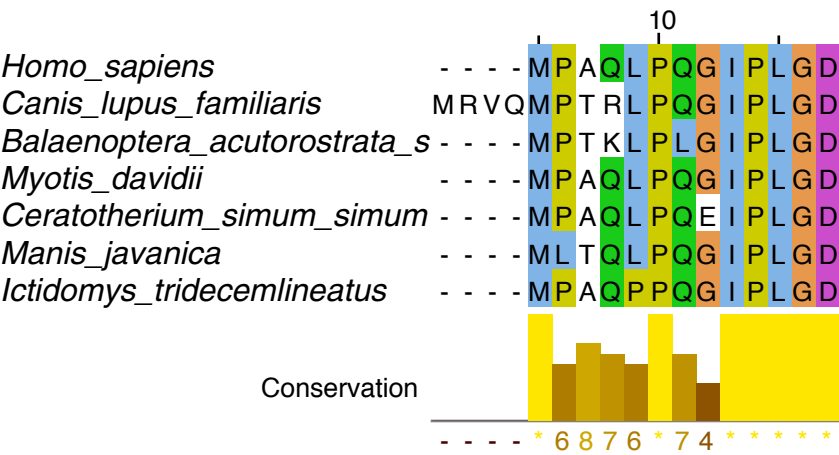
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ENSG00000082014 (SMARCD3)



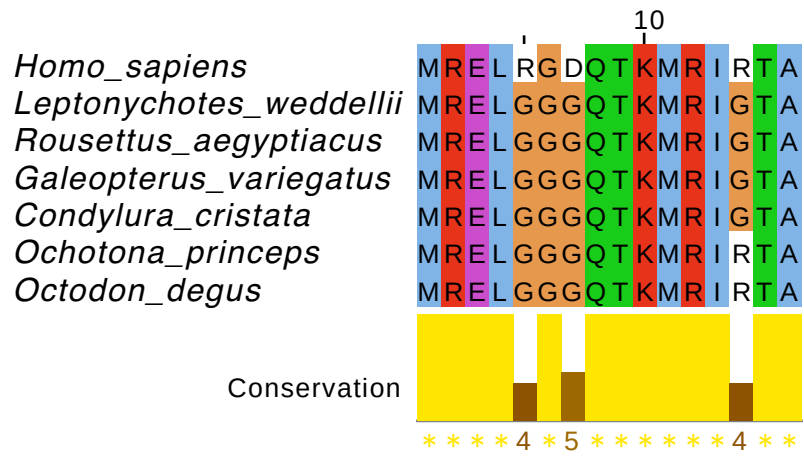
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ENSG00000085644 (ZNF213)



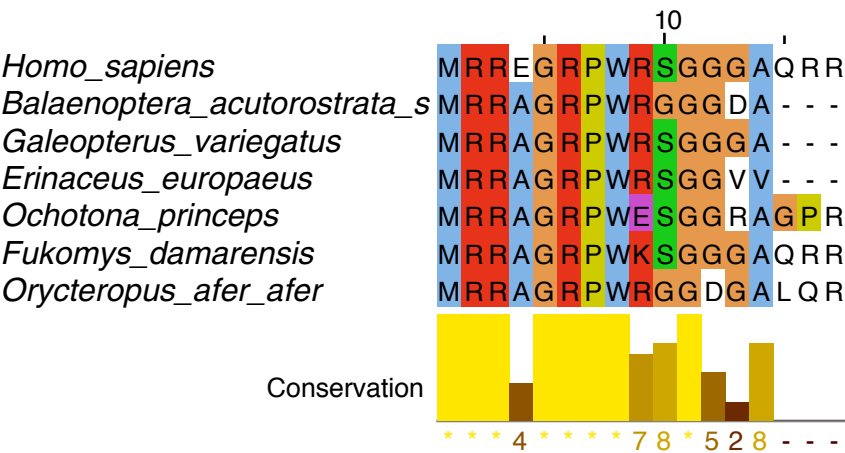
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ENSG00000089116 (LHX5)



HG0779

ENSG00000091140 (DLD)

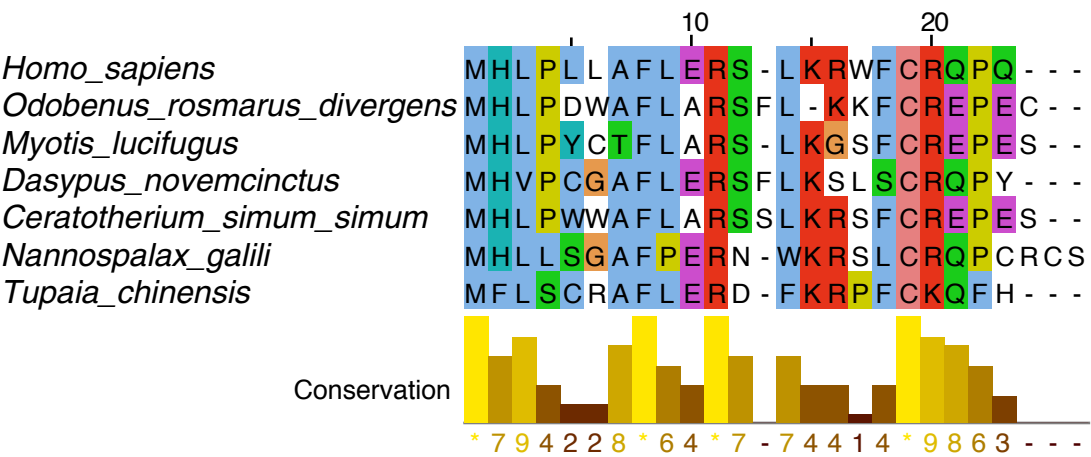


ENSG00000092199 (HNRNPC)



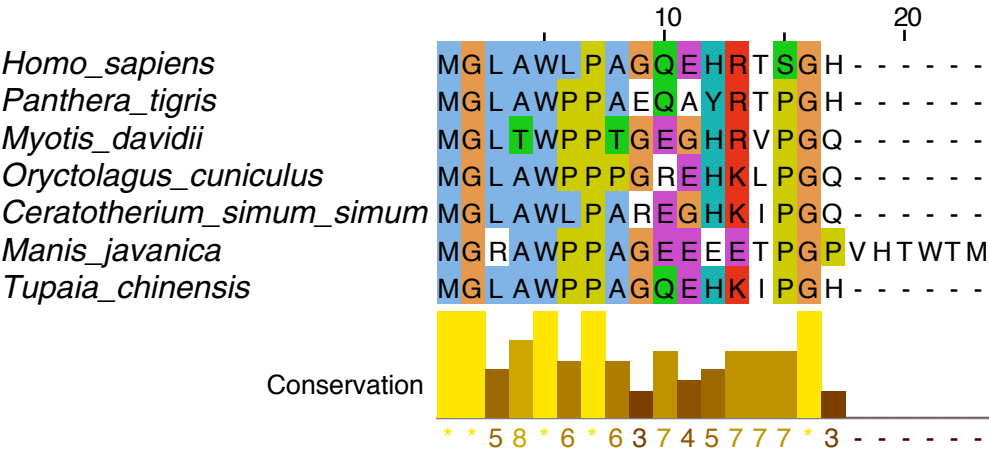
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ENSG00000100099 (HPS4)



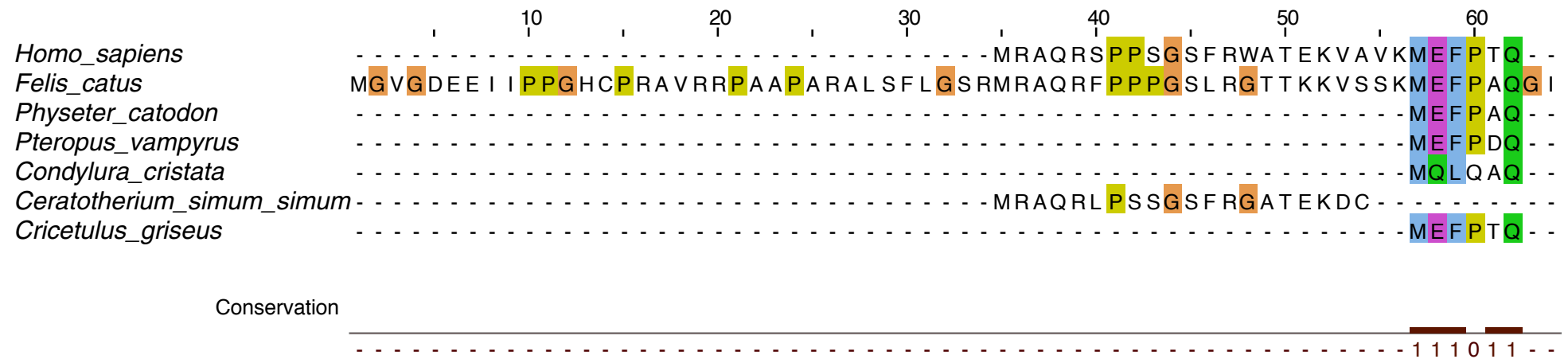
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ENSG00000100368 (CSF2RB)



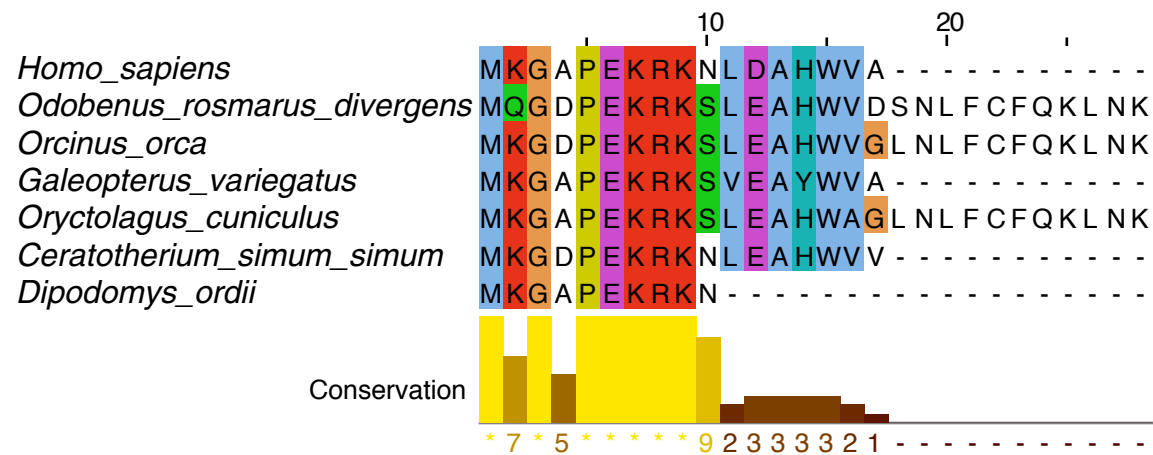
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ENSG00000105053 (VRK3)

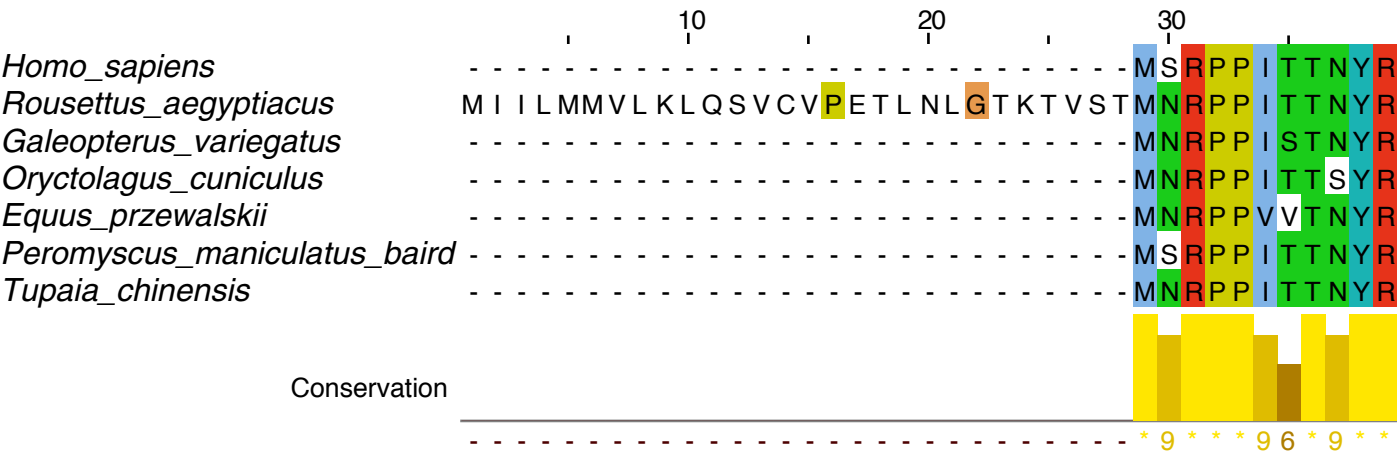


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ENSG00000105851 (PIK3CG)

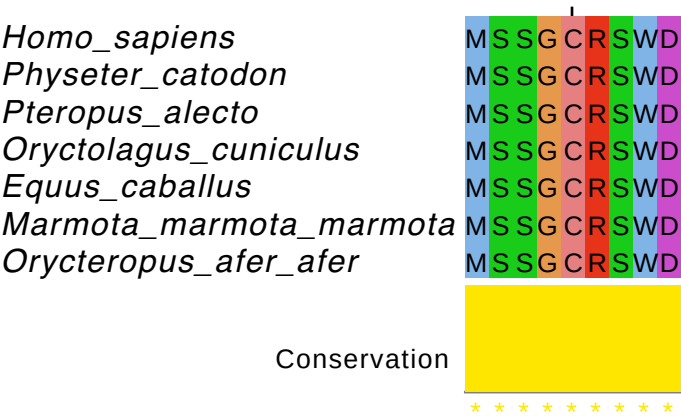


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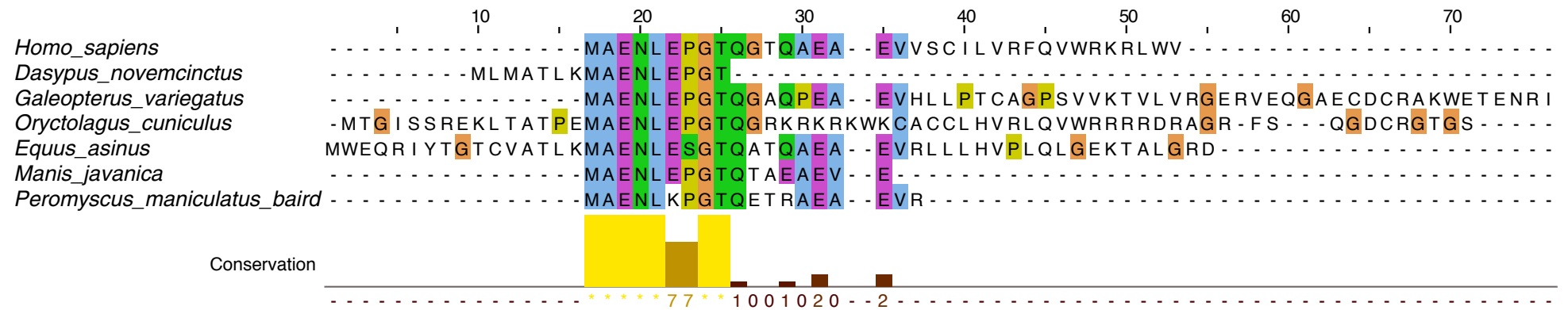


HG0786

ENSG00000107862 (GBF1)

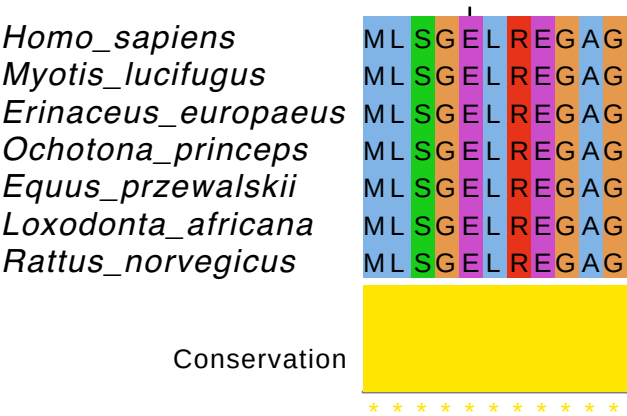


ENSG00000108592 (FTSJ3)



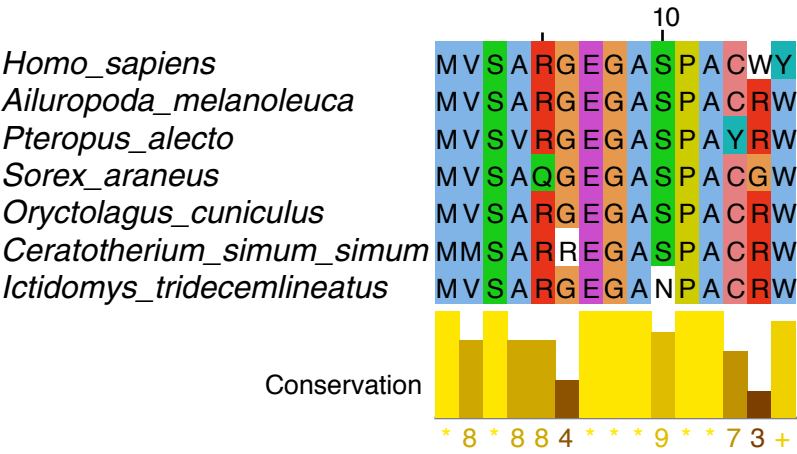
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ENSG00000113739 (STC2)

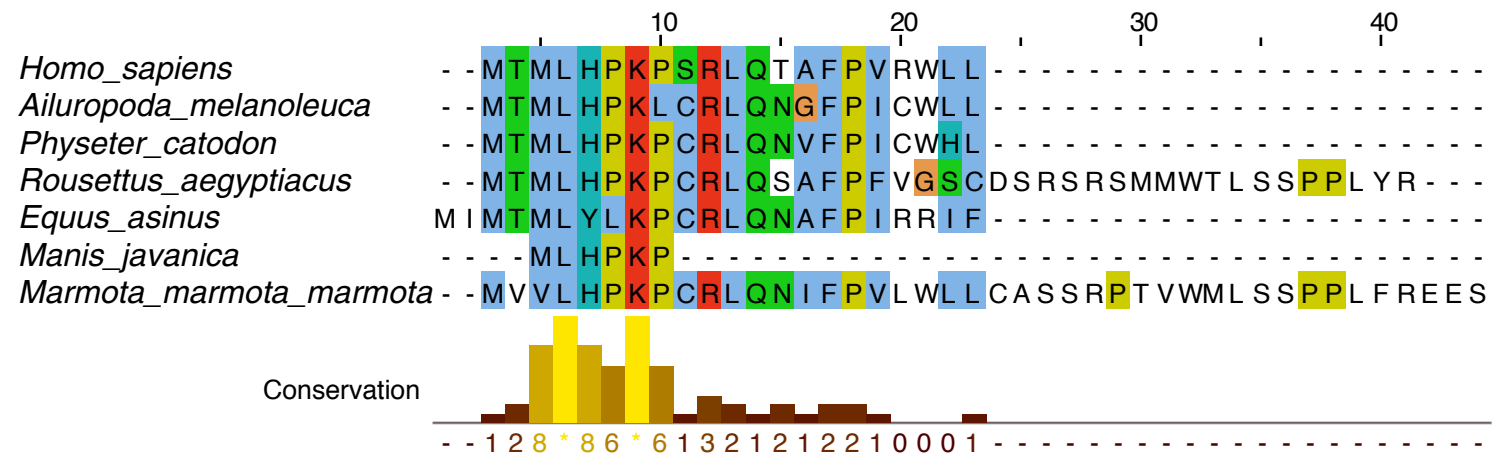


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ENSG00000115355 (CCDC88A)

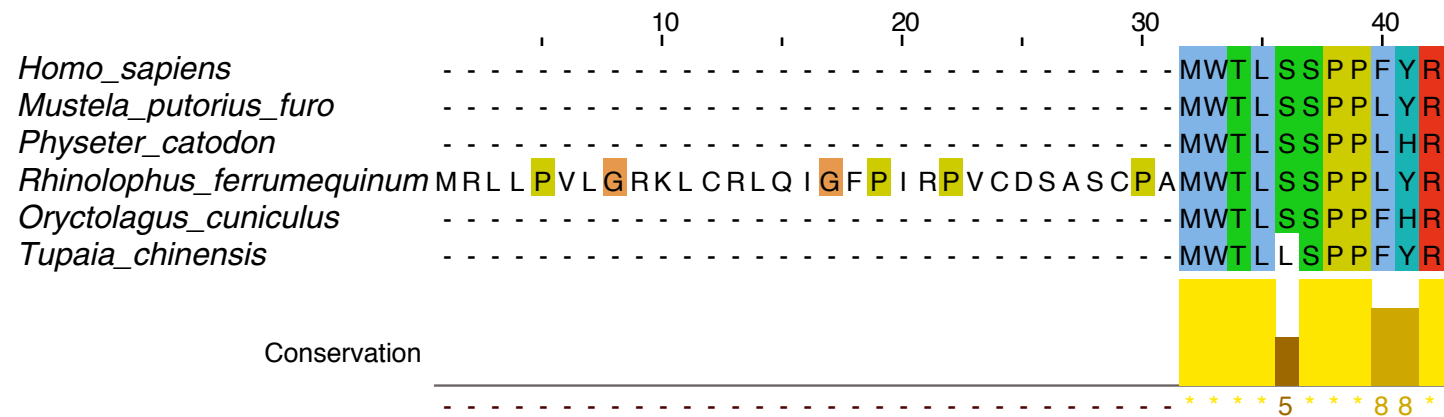


ENSG00000115568 (ZNF142)



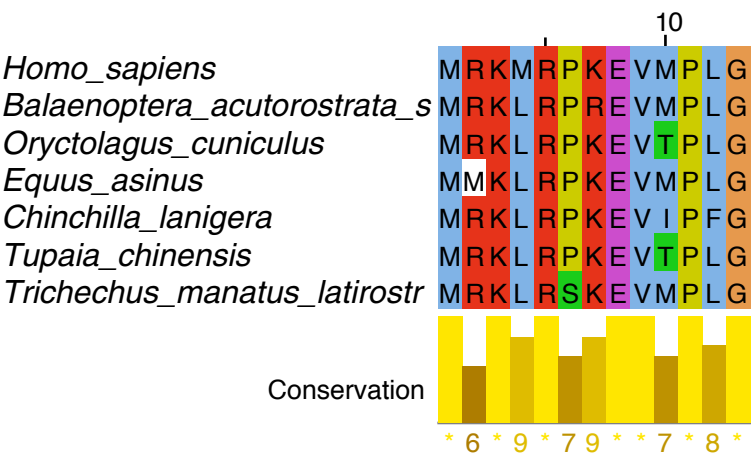
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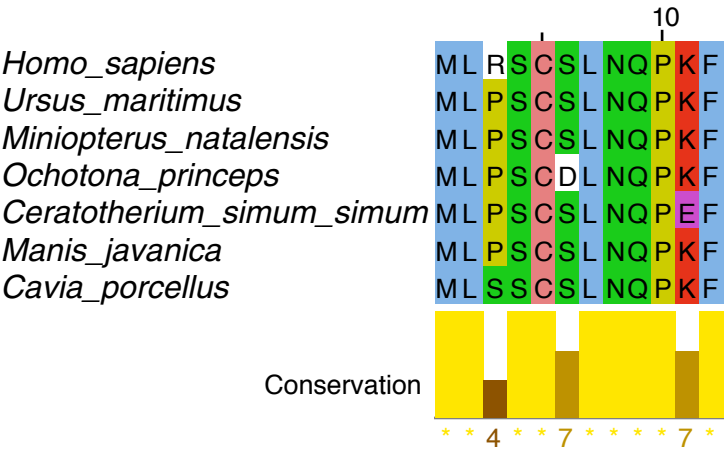
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ENSG00000131323 (TRAF3)



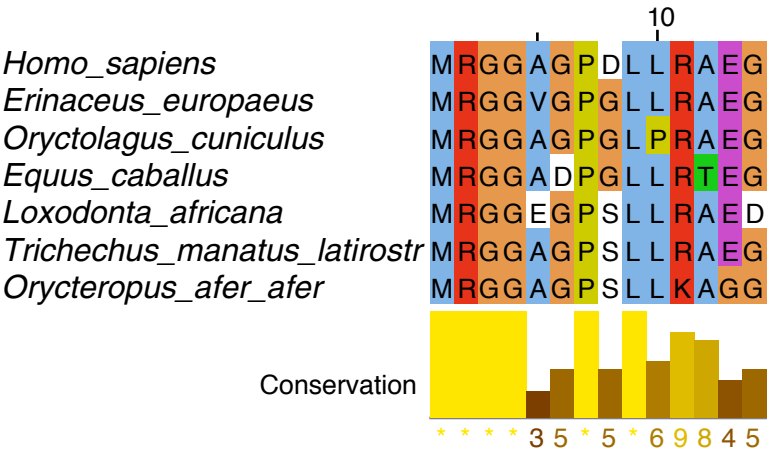
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ENSG00000132424 (PNISR)



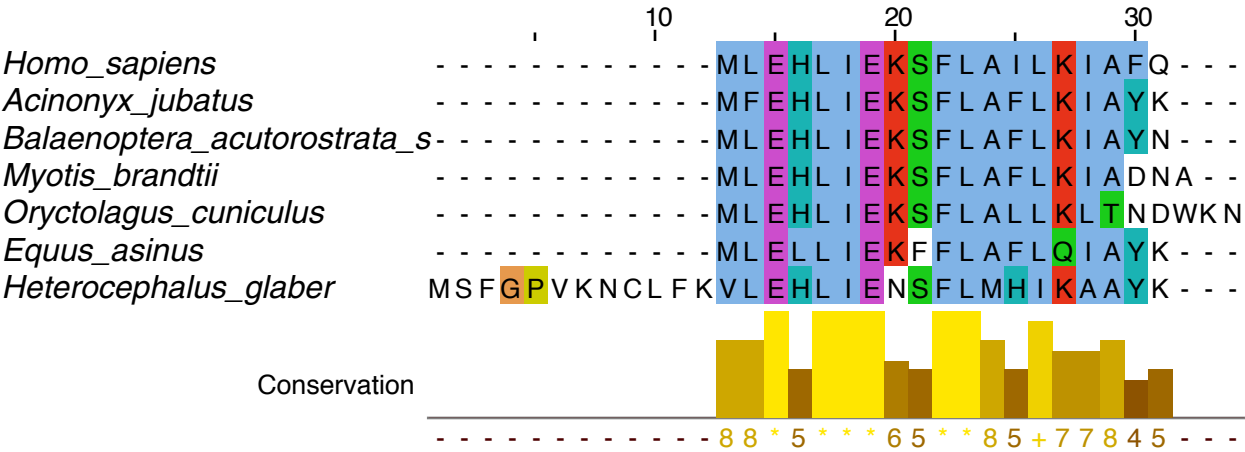
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ENSG00000132698 (RAB25)



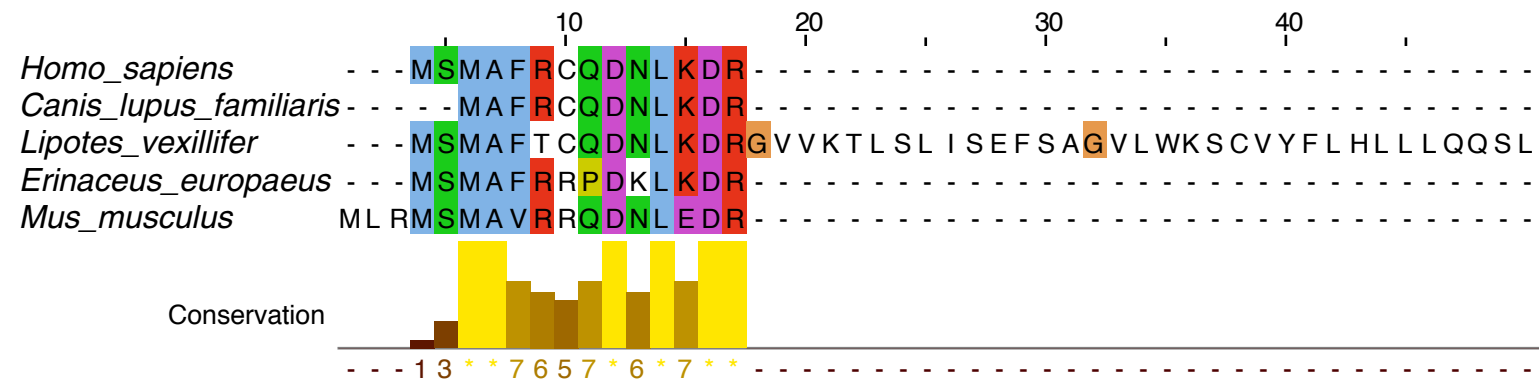
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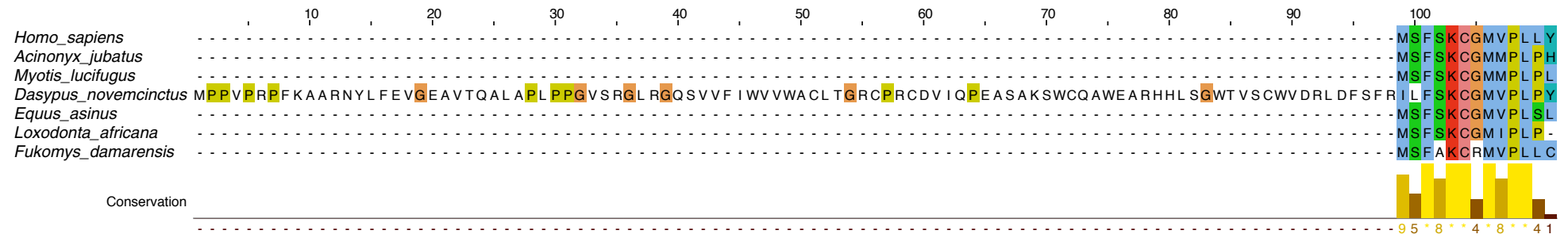
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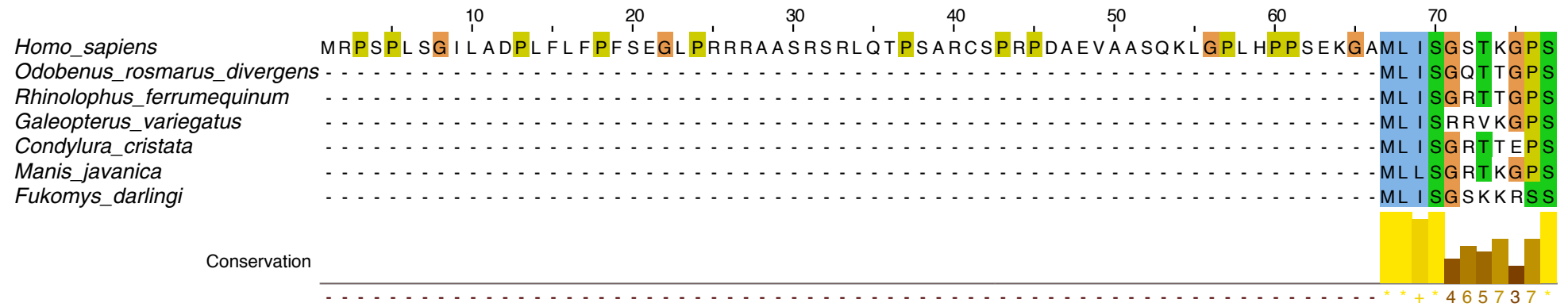
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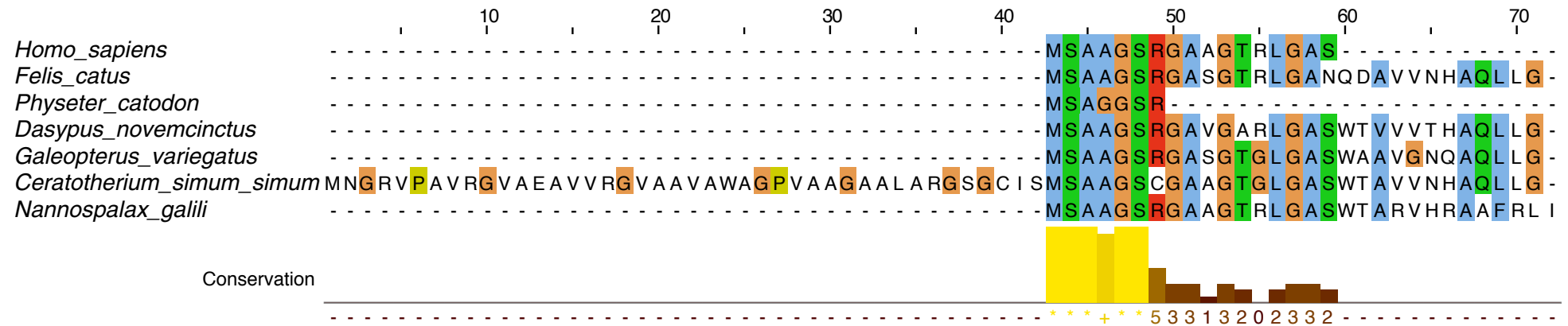


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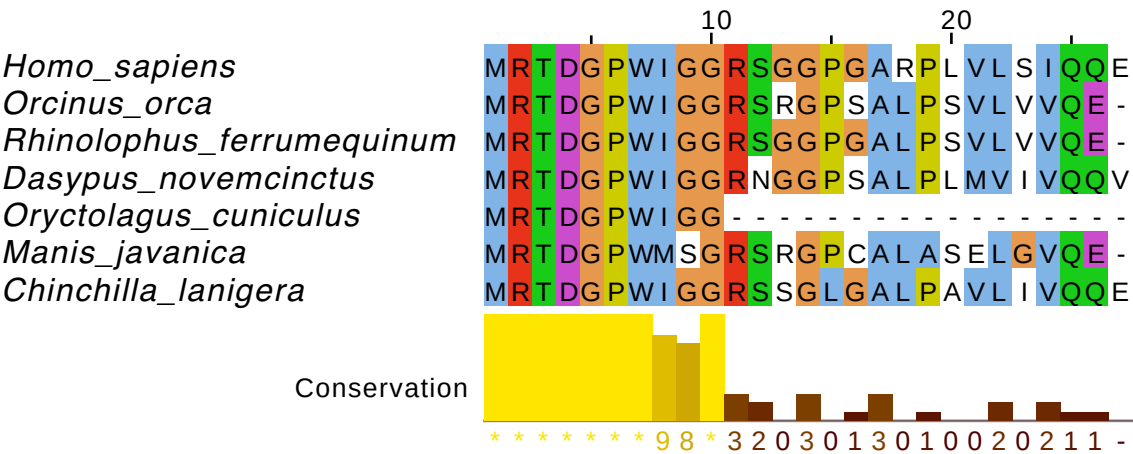
ENSG00000138074 (SLC5A6)



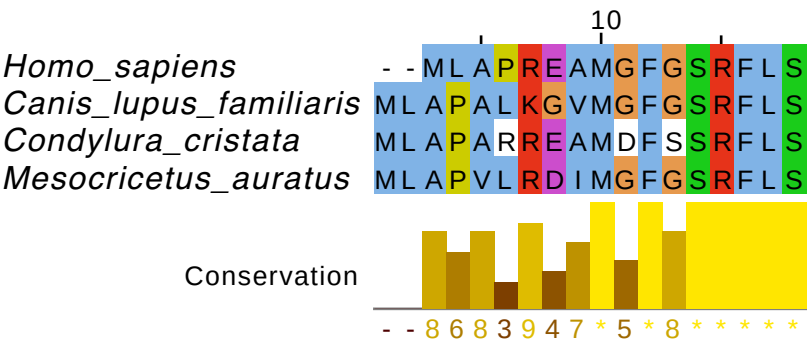
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ENSG00000142949 (PTPRF)

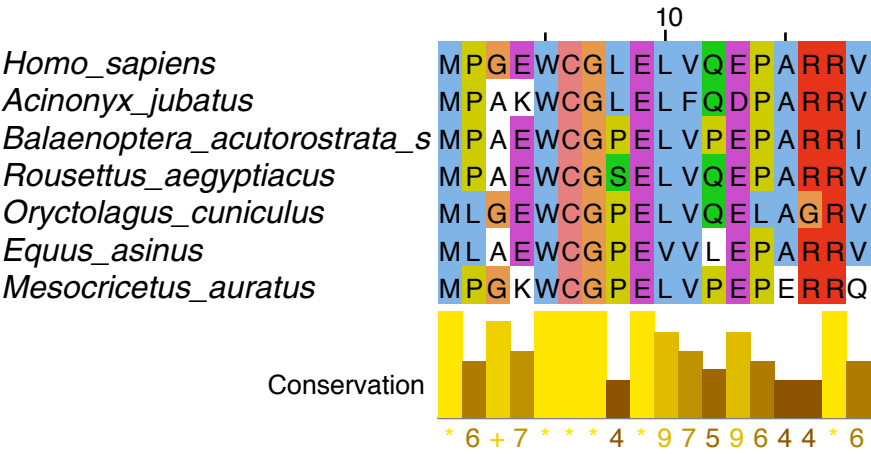


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ENSG00000153707 (PTPRD)

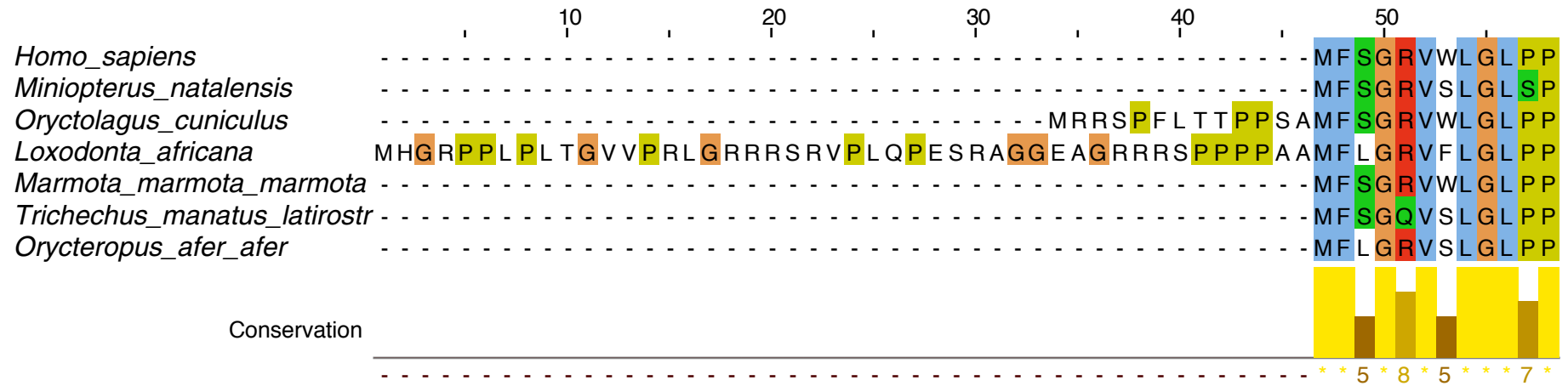


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ENSG00000143398 (PIP5K1A)

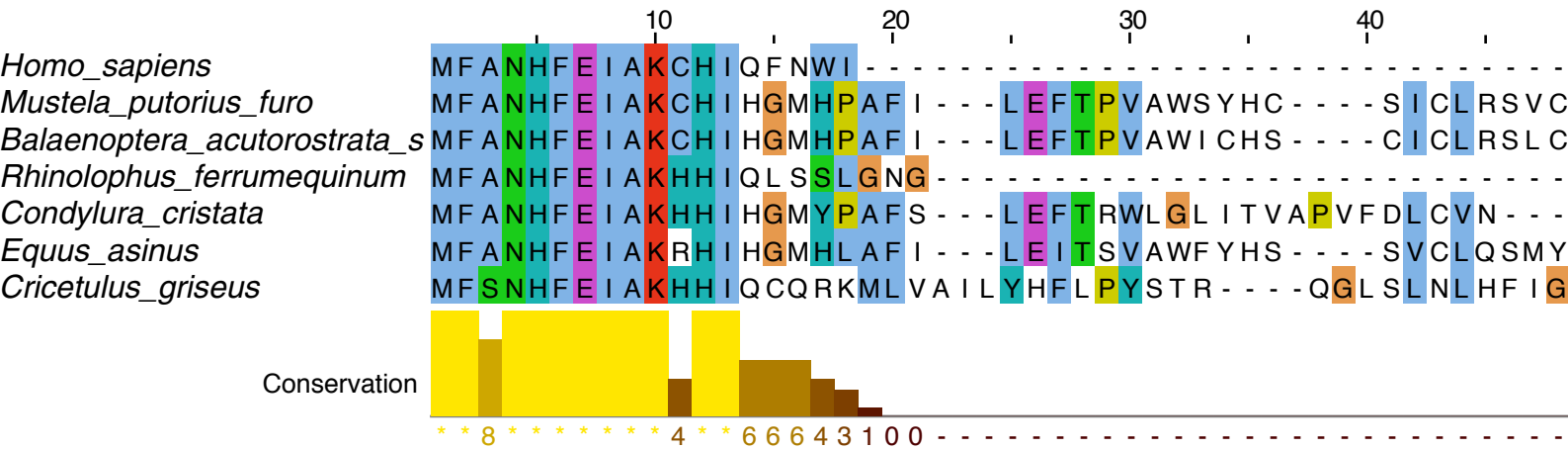


ENSG00000143612 (C1orf43)



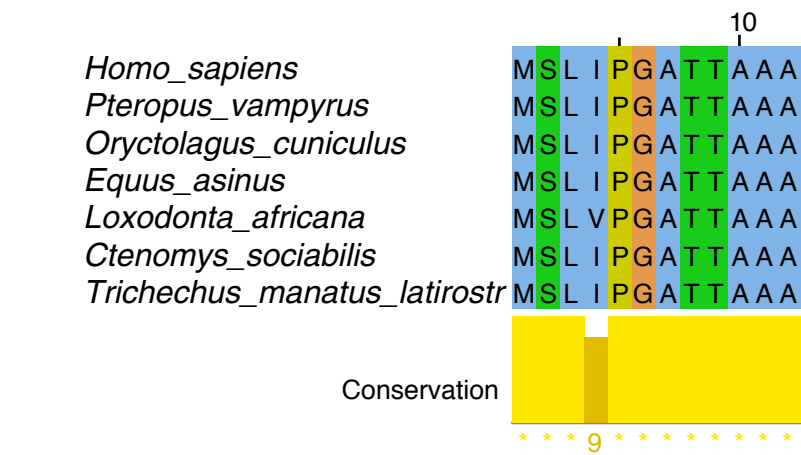
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ENSG00000144278 (GALNT13)



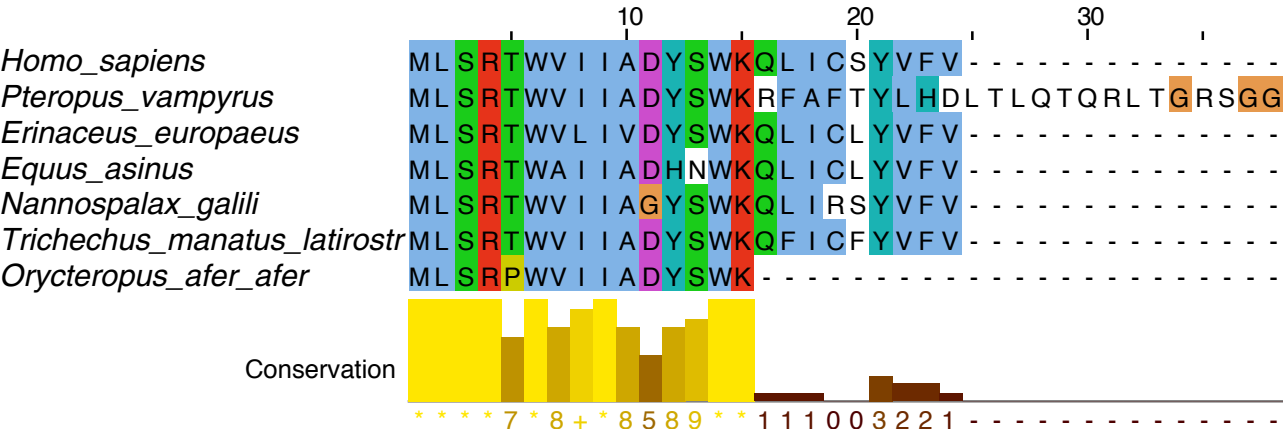
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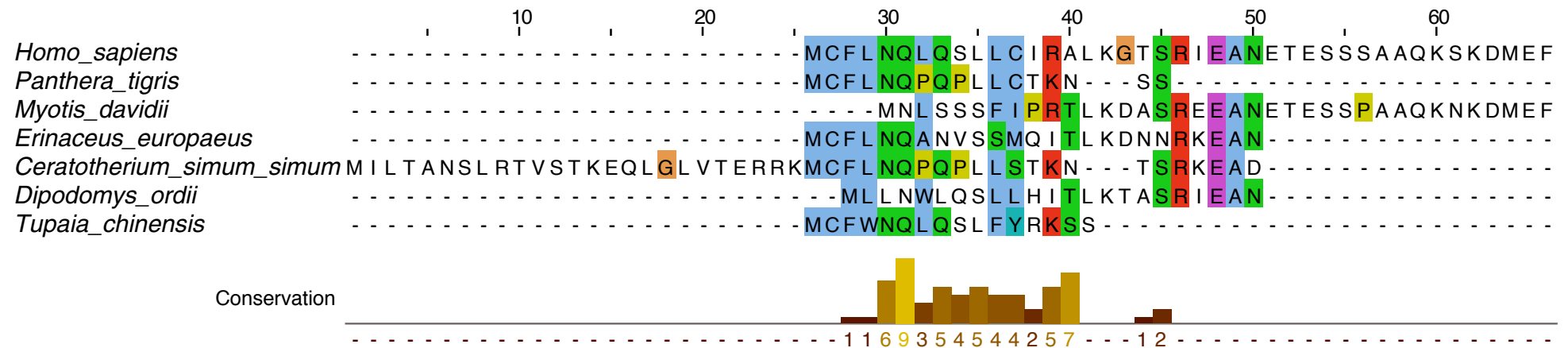
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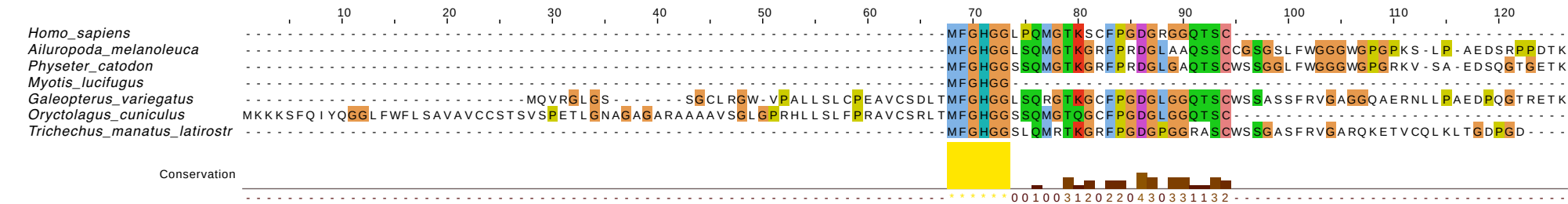
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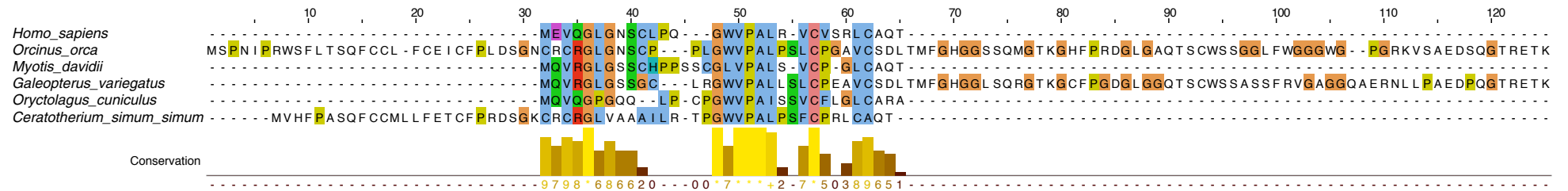
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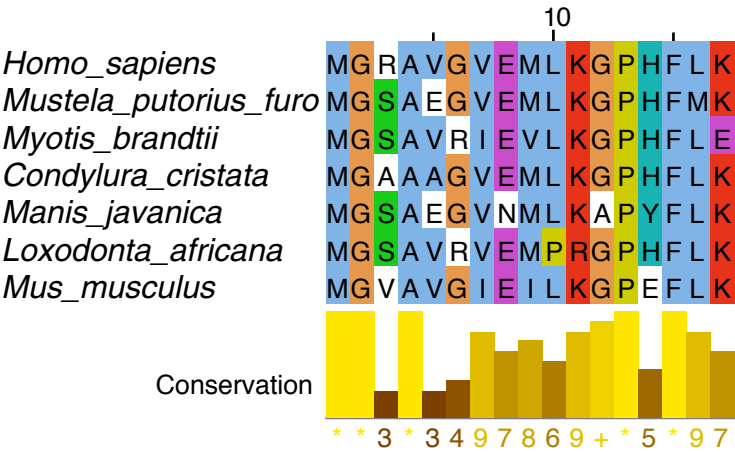
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ENSG00000145936 (KCNMB1)



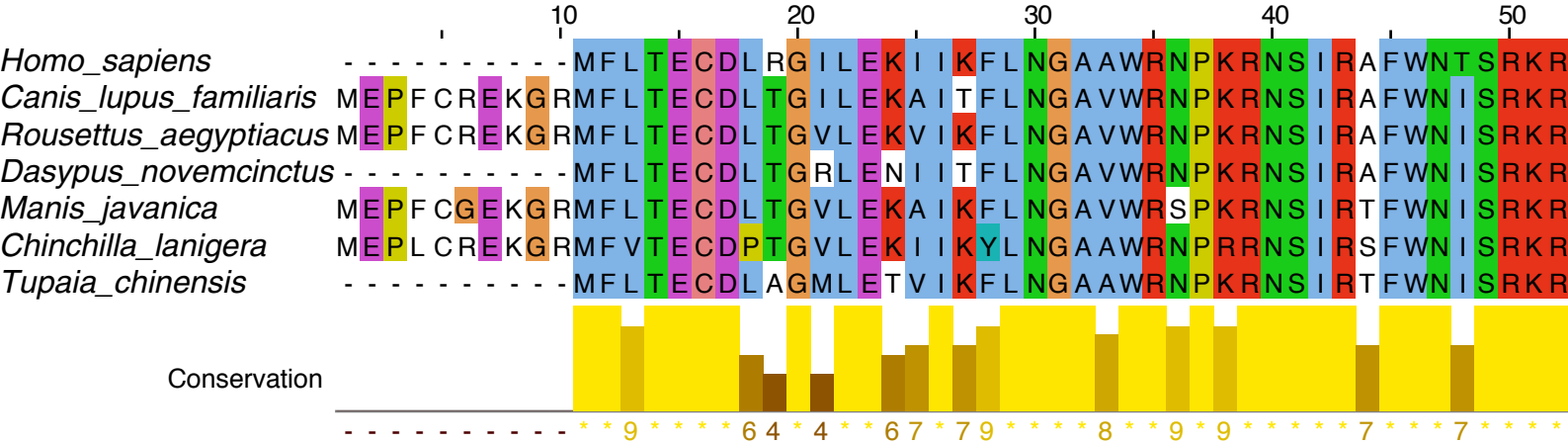
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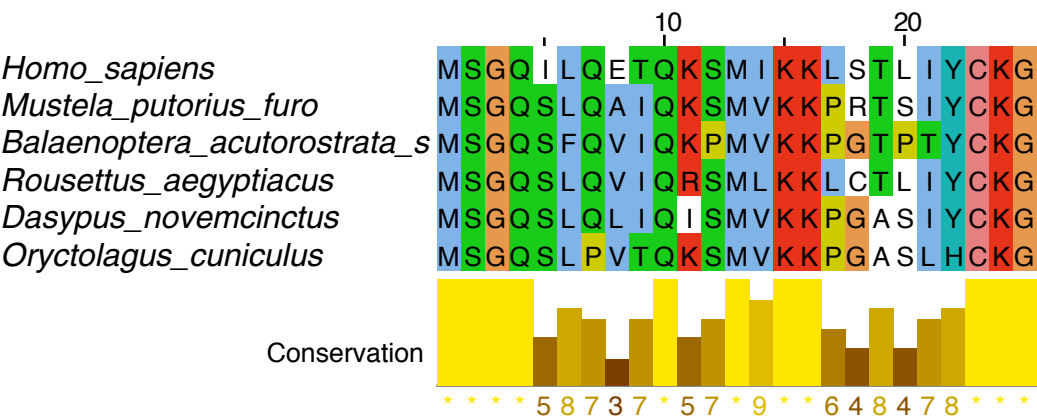
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ENSG00000147488 (ST18)



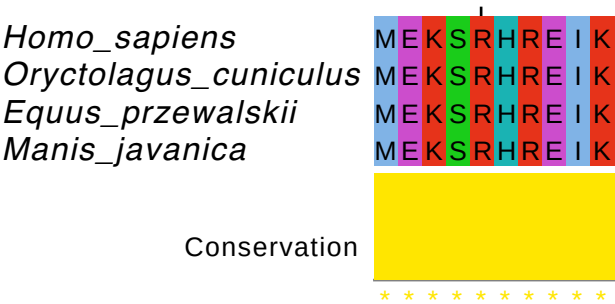
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ENSG00000147488 (ST18)



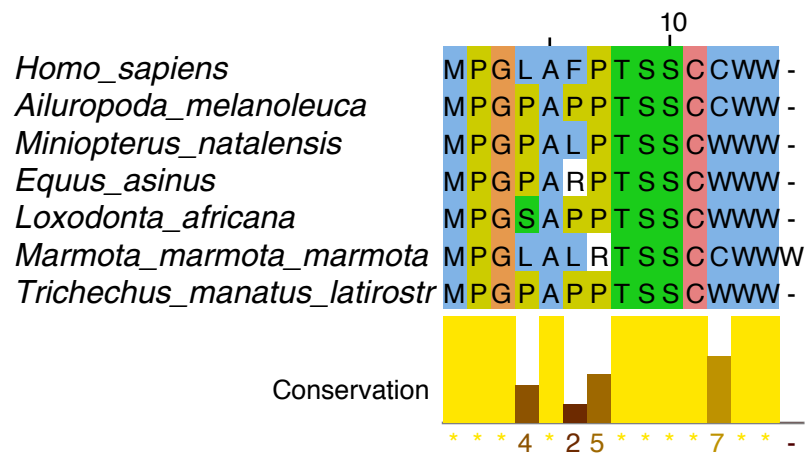
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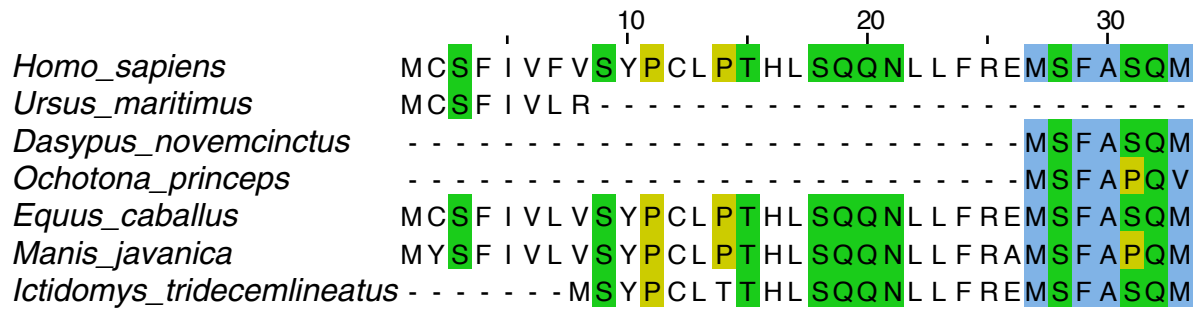
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HG0809

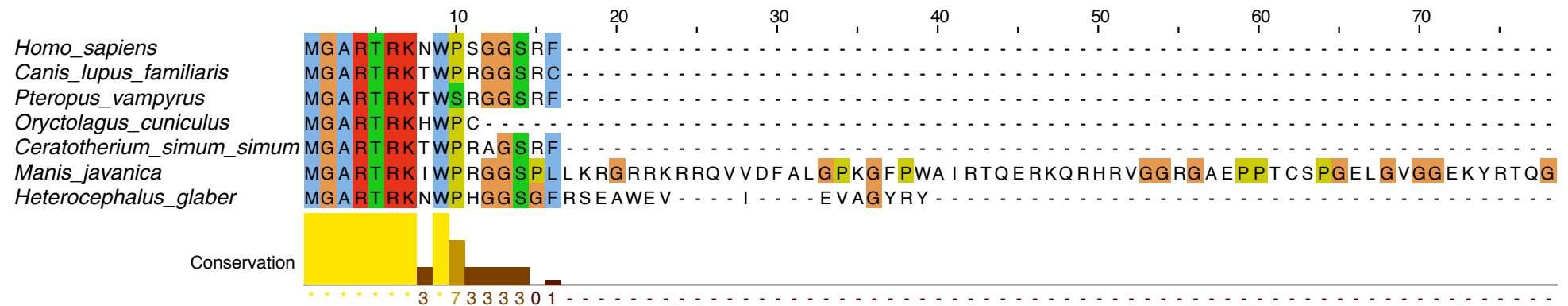
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Conservation

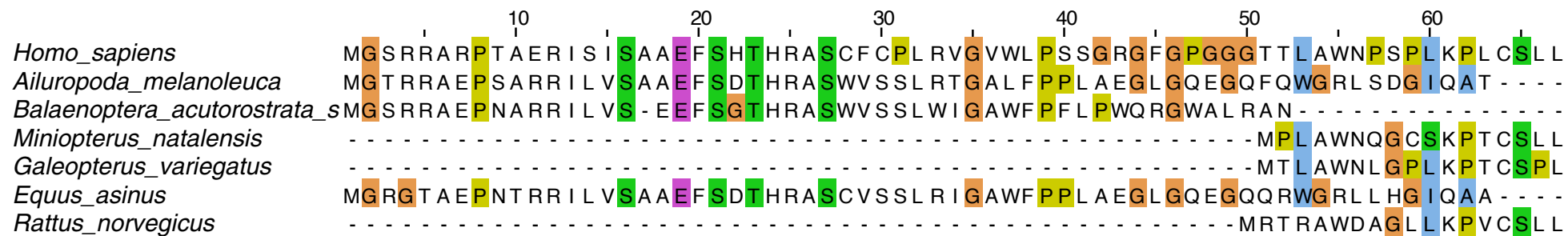


ENSG00000156504 (FAM122B)



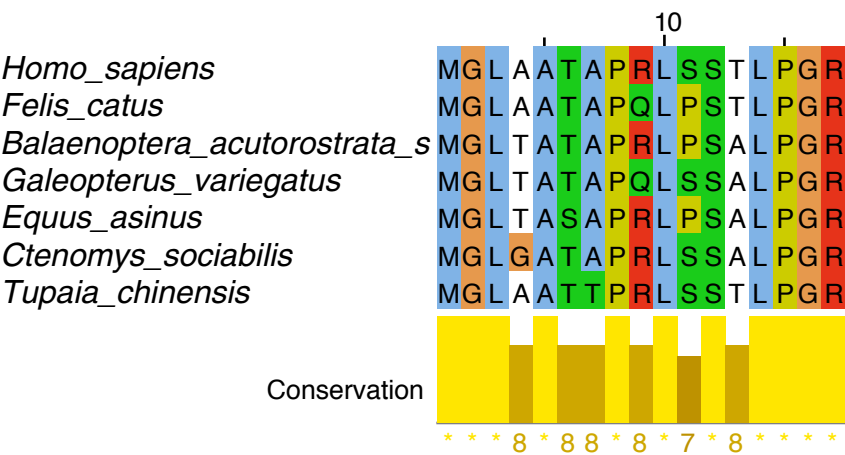
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ENSG00000157350 (ST3GAL2)



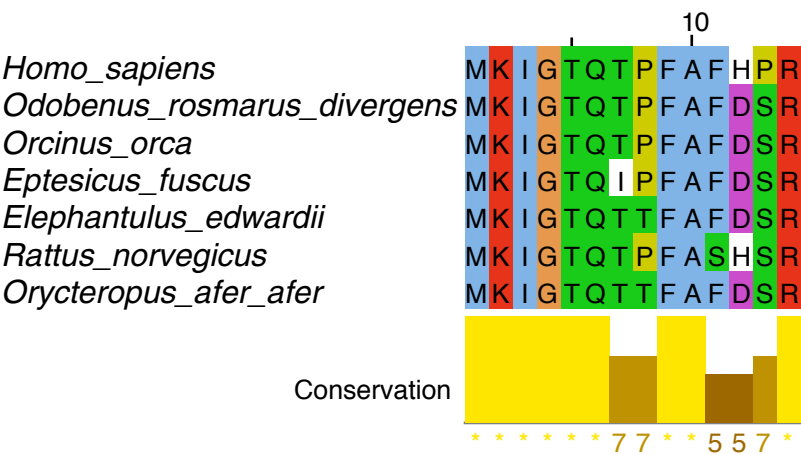
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ENSG00000157368 (IL34)



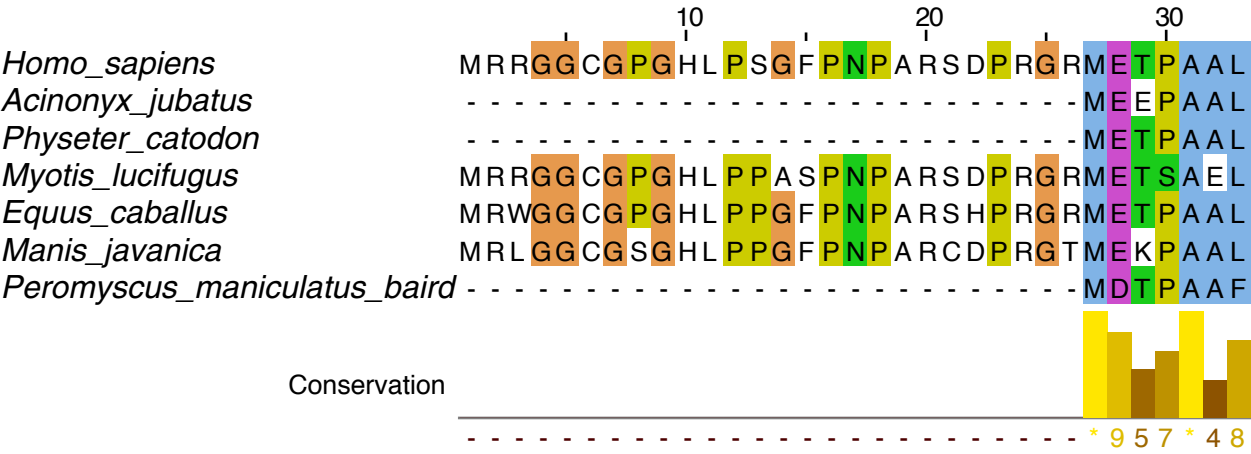
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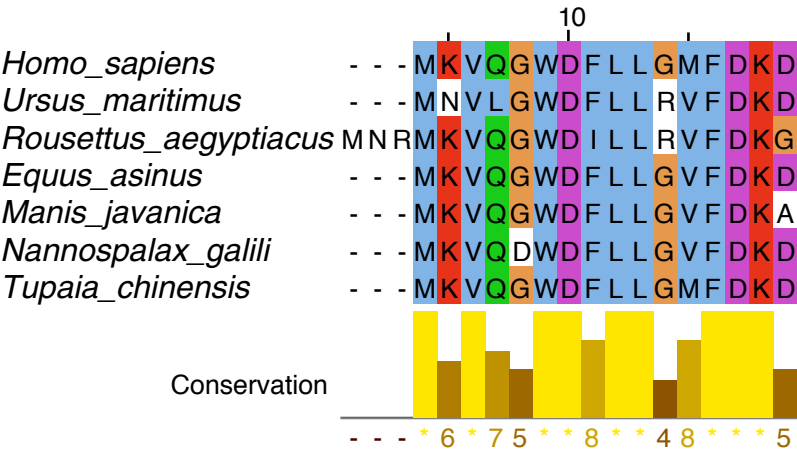
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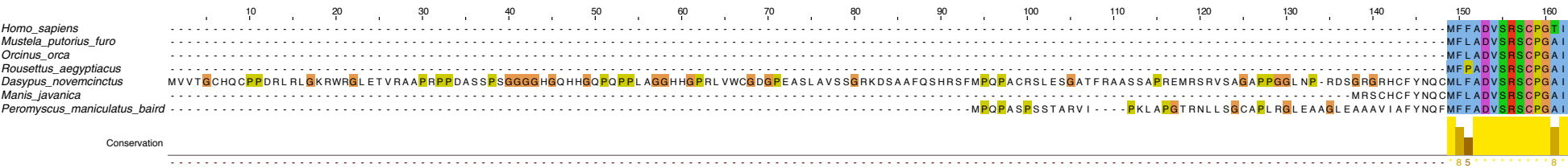
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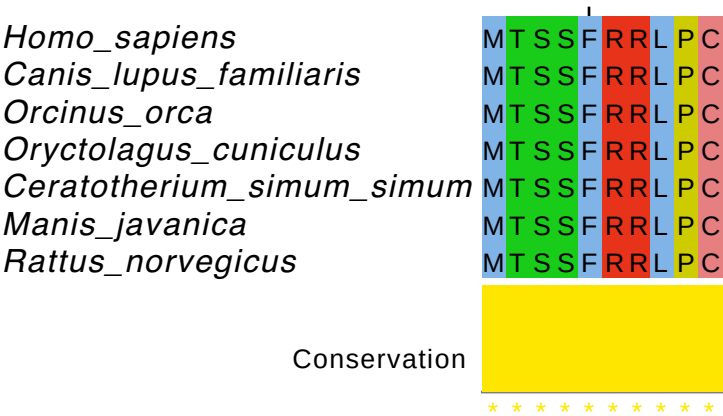
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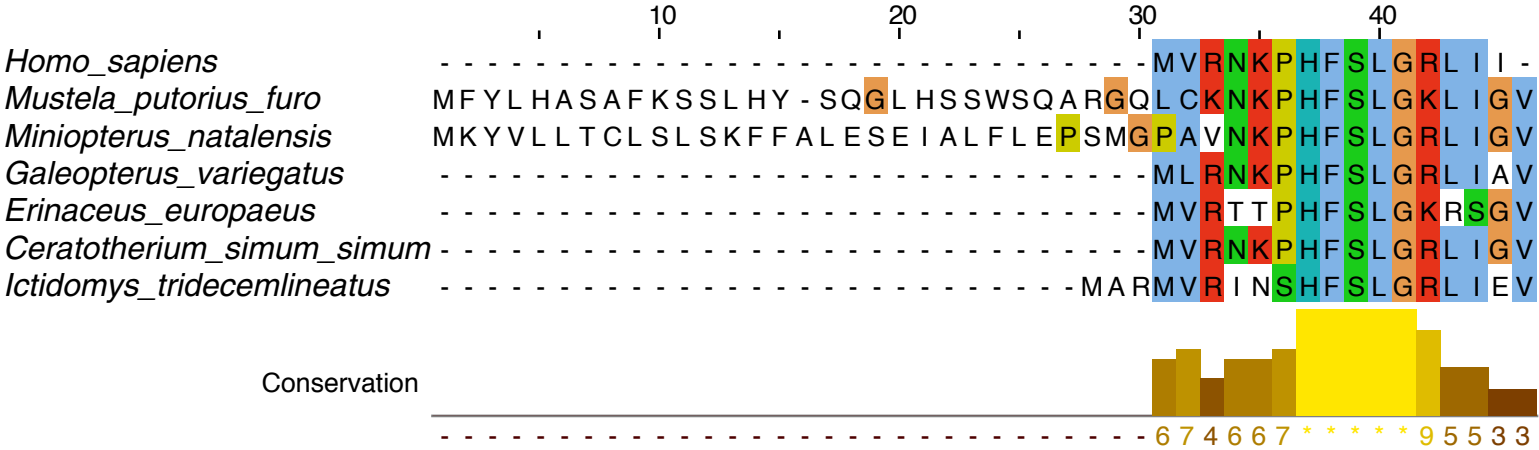


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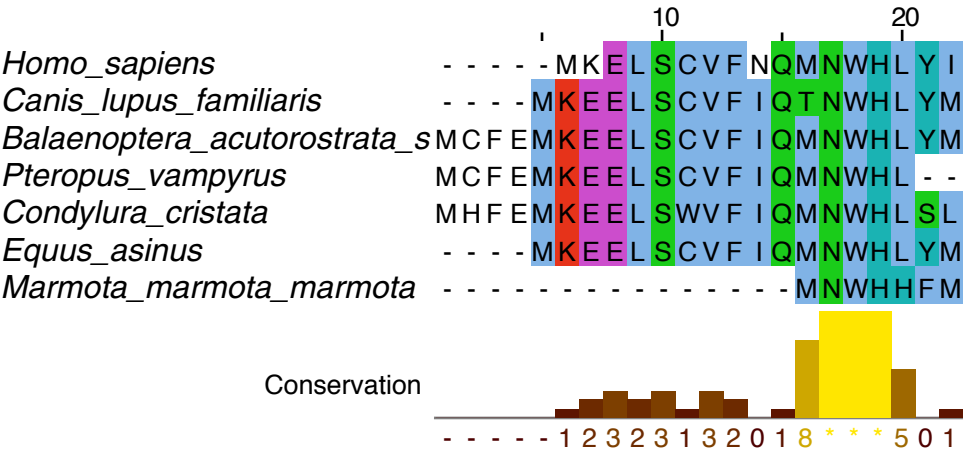


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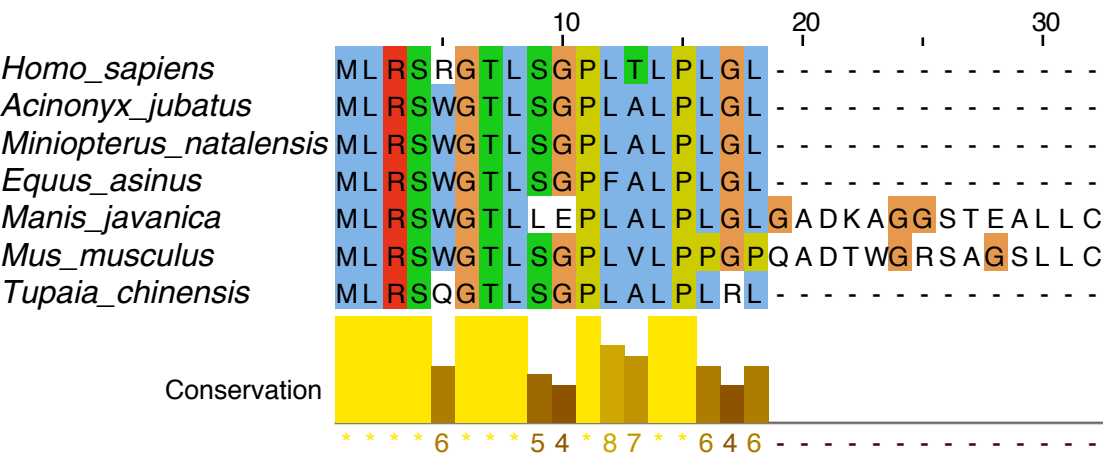
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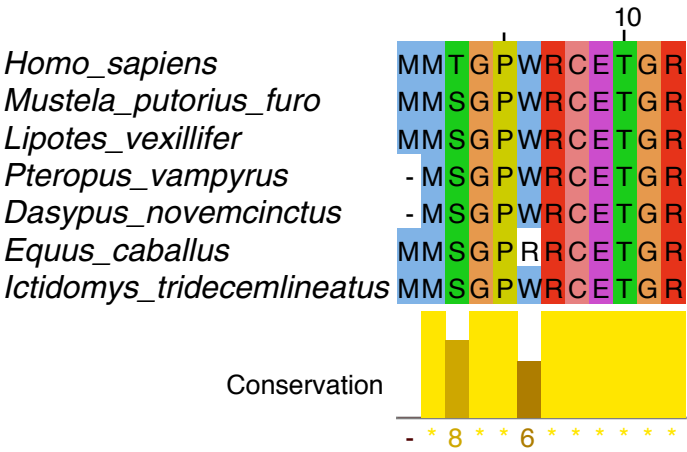
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ENSG00000164946 (FREM1)



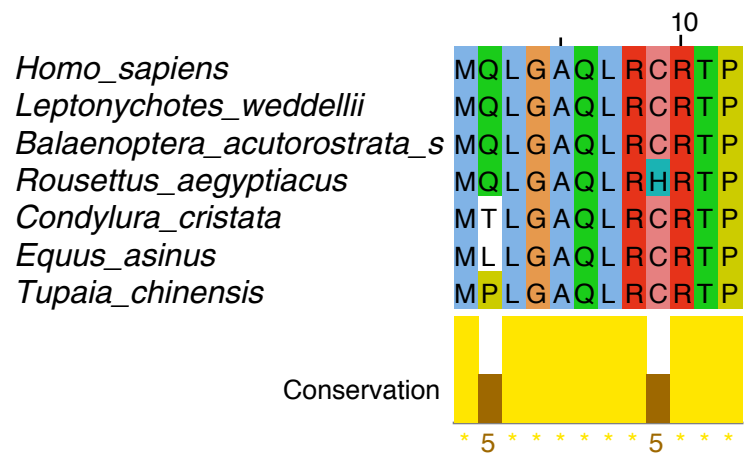
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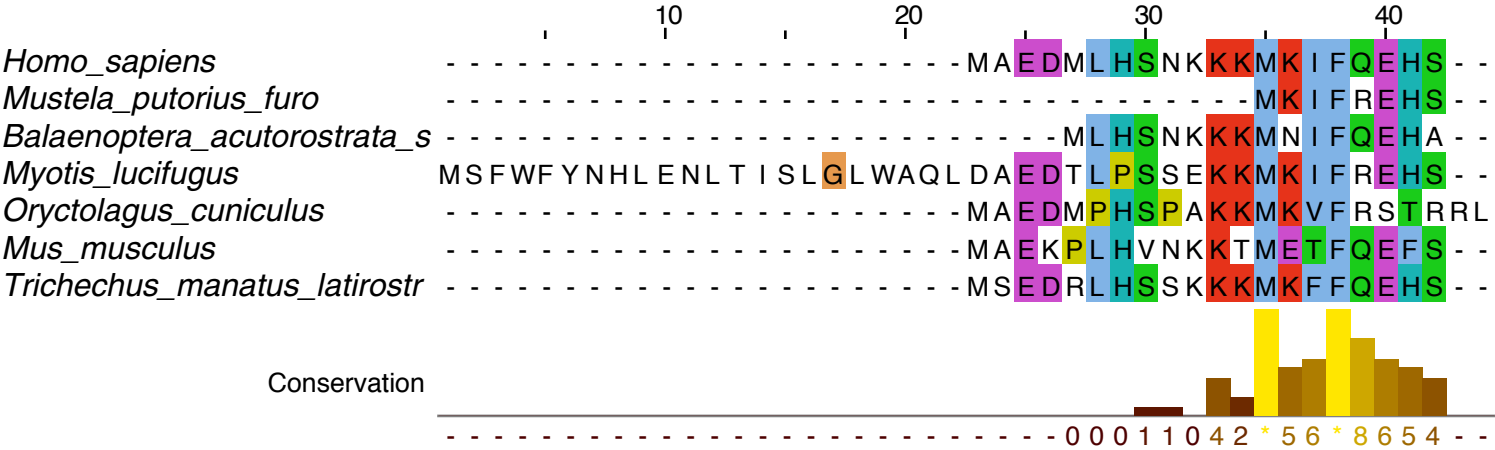


HG0822

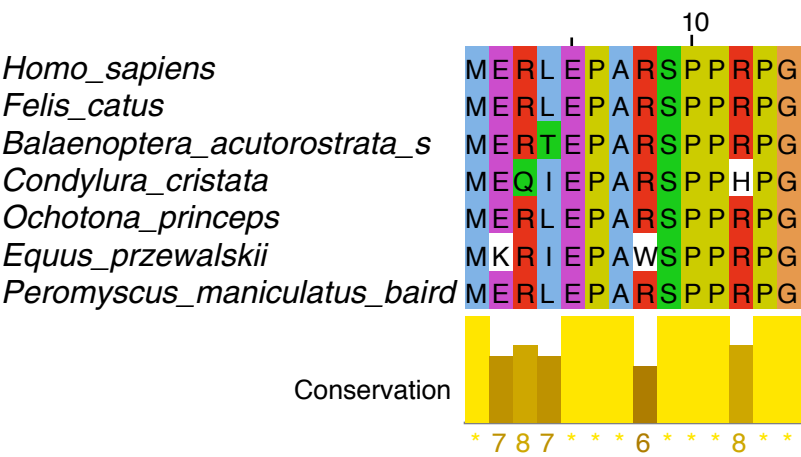
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HG0823
ENSG00000166268 (MYRFL)

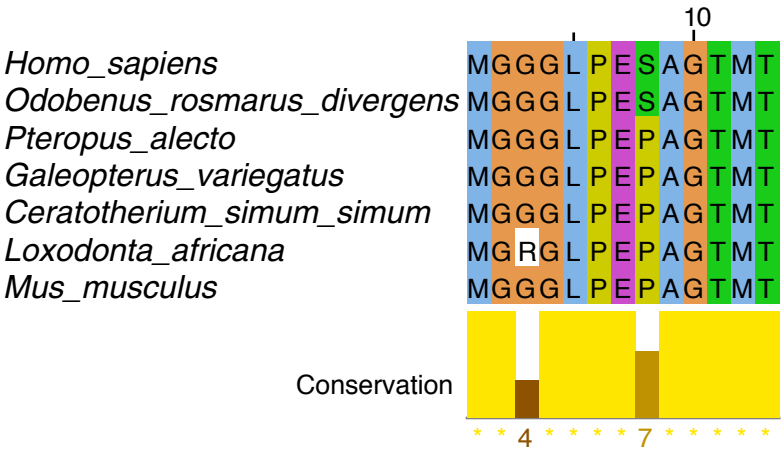


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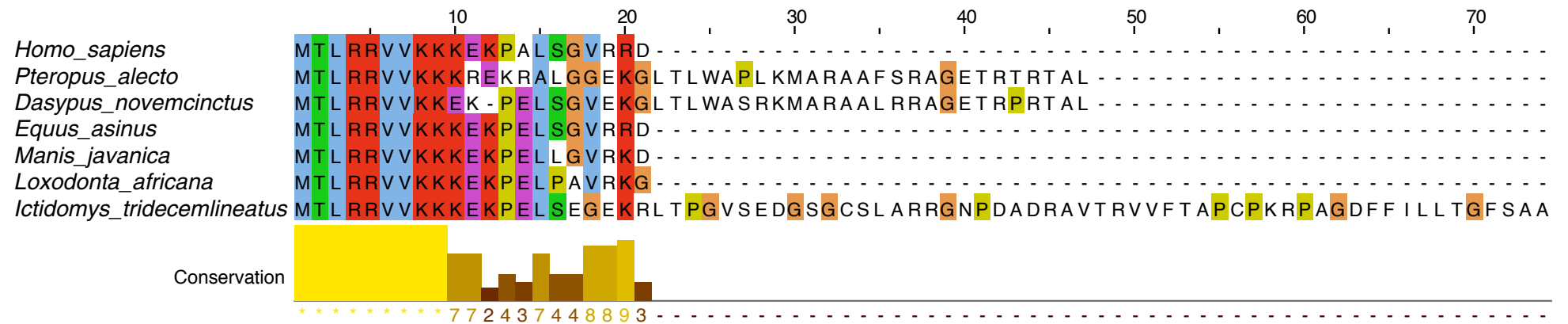


HG0825

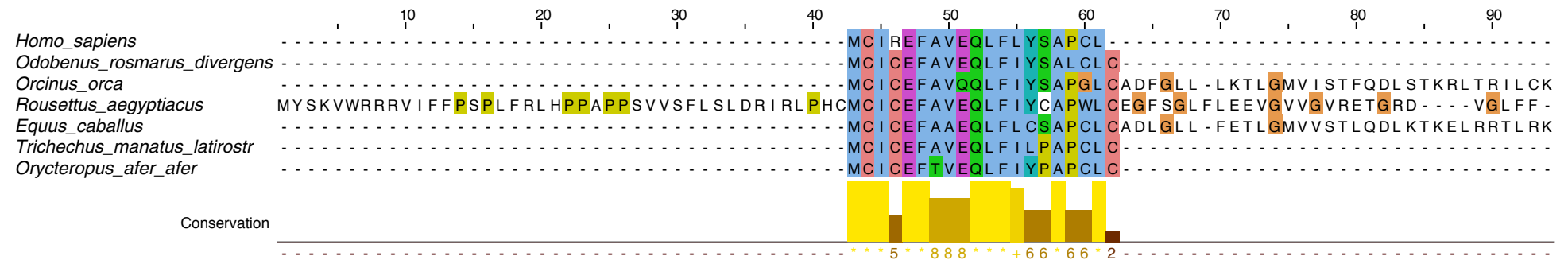
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ENSG00000169851 (PCDH7)

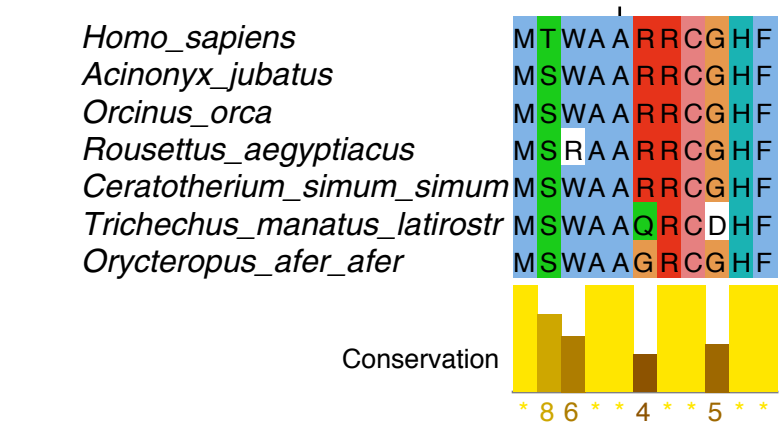


ENSG00000170365 (SMAD1)



HG0828

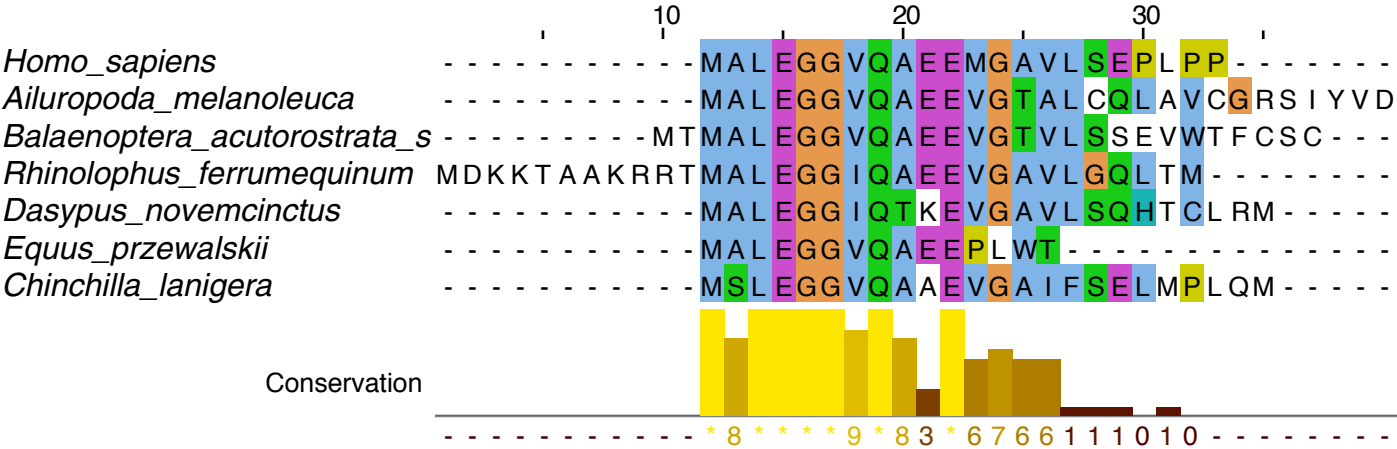
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ENSG00000171502 (COL24A1)

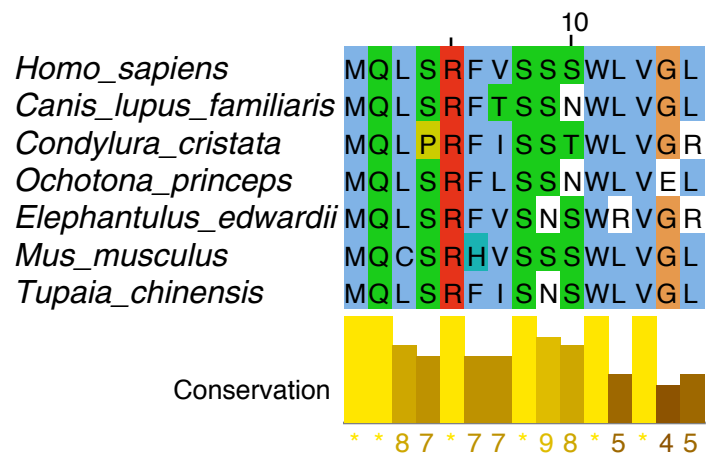


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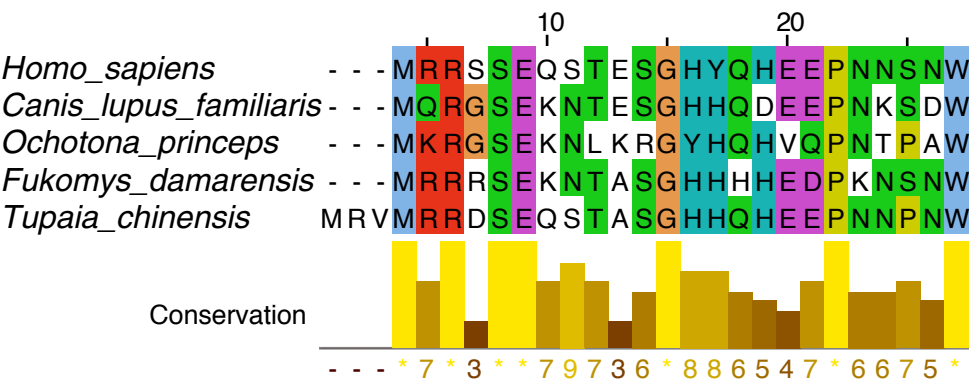
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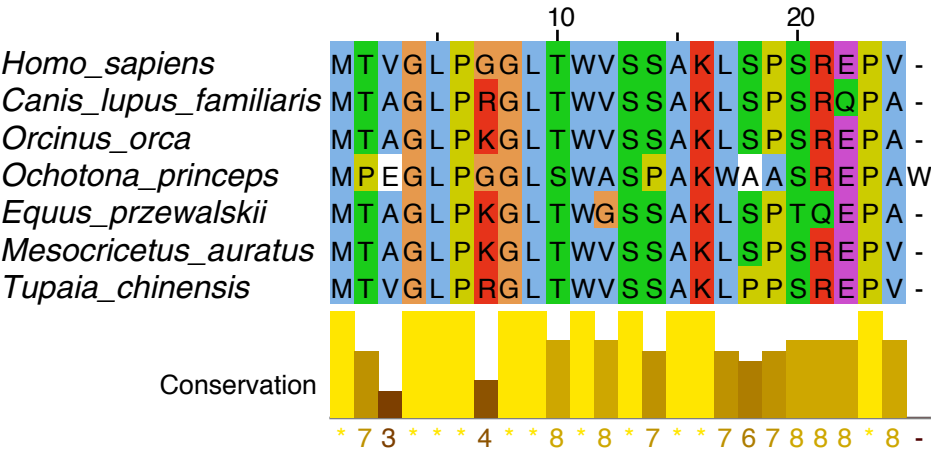
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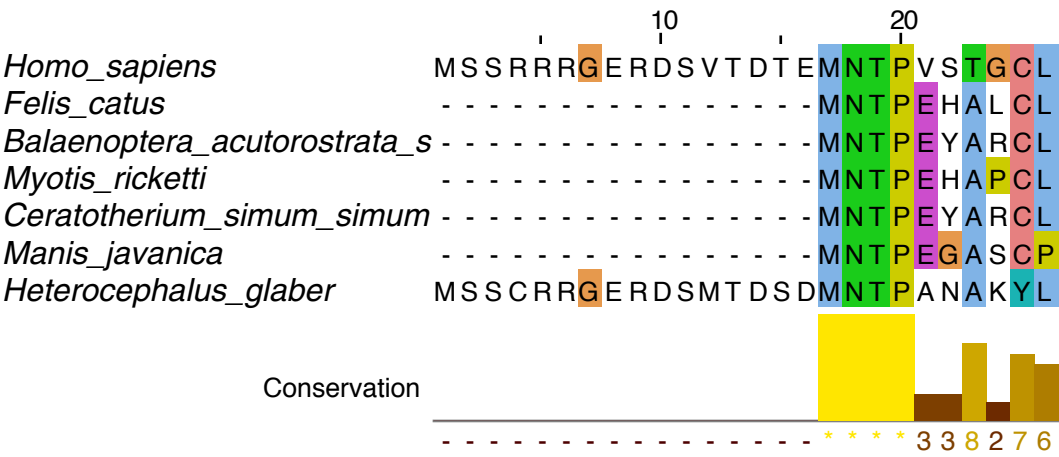
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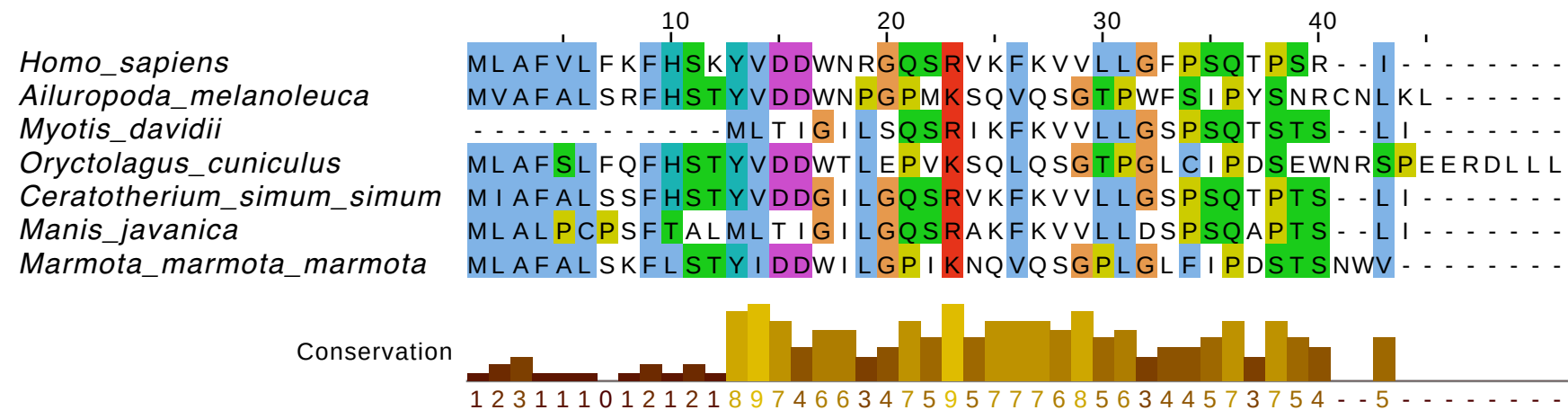


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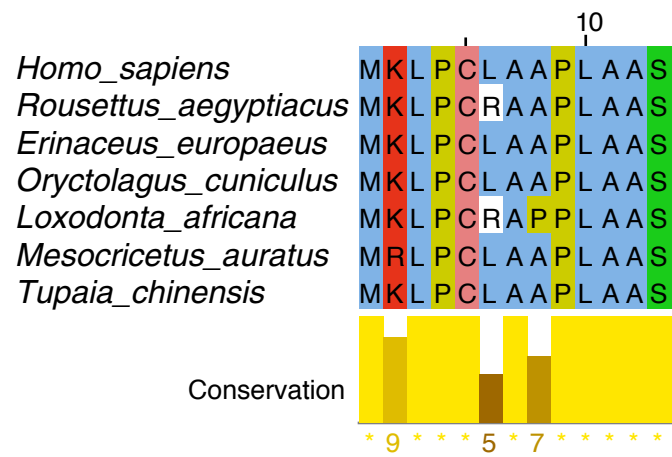


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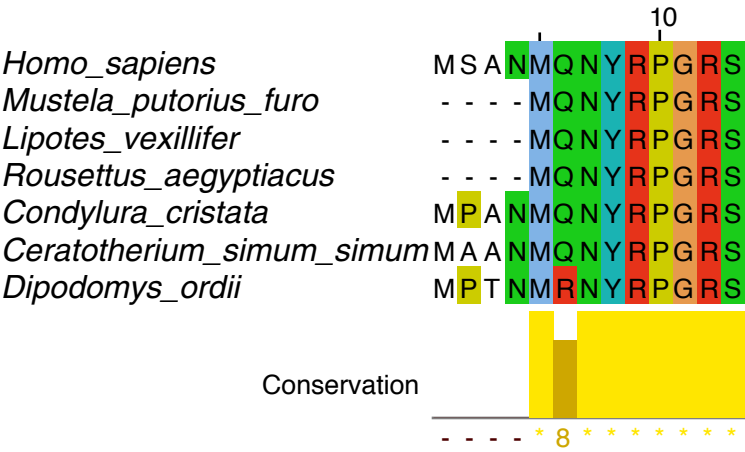
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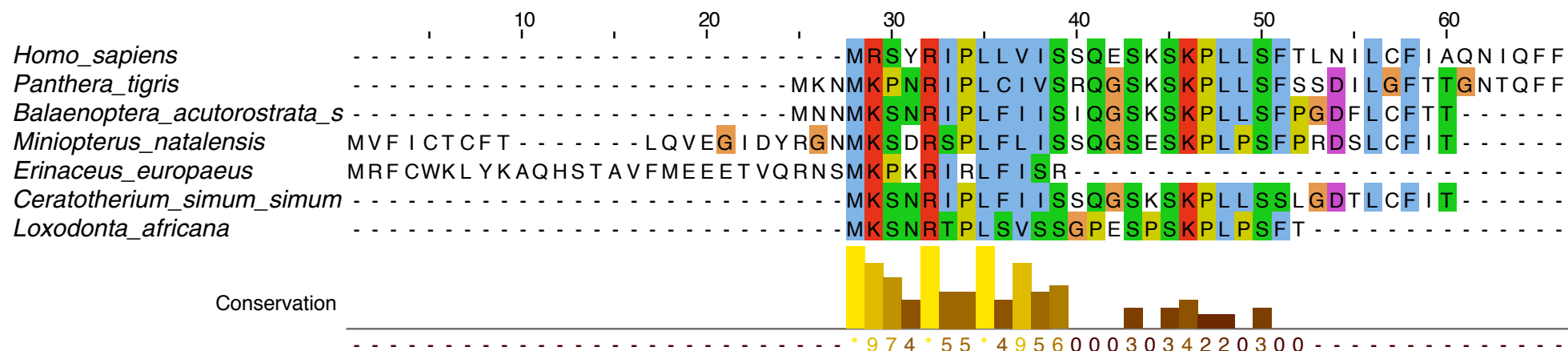


HG0836

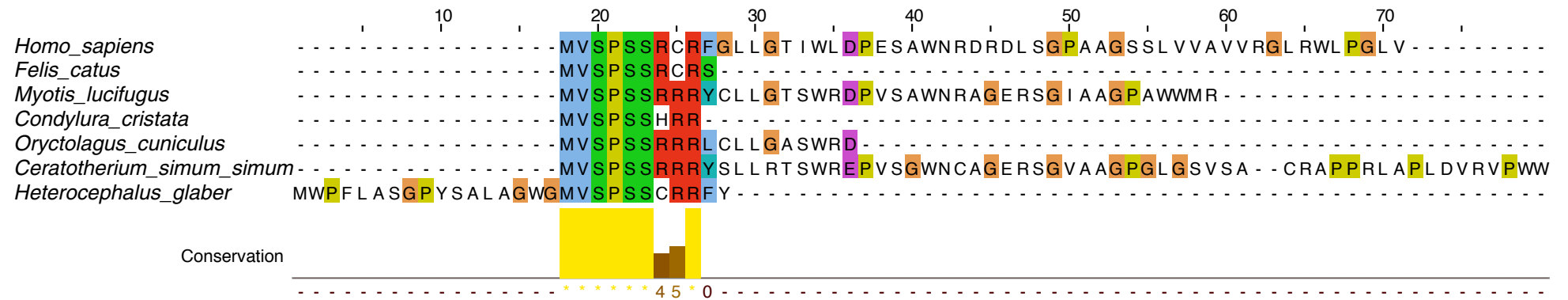
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ENSG00000198690 (FAN1)

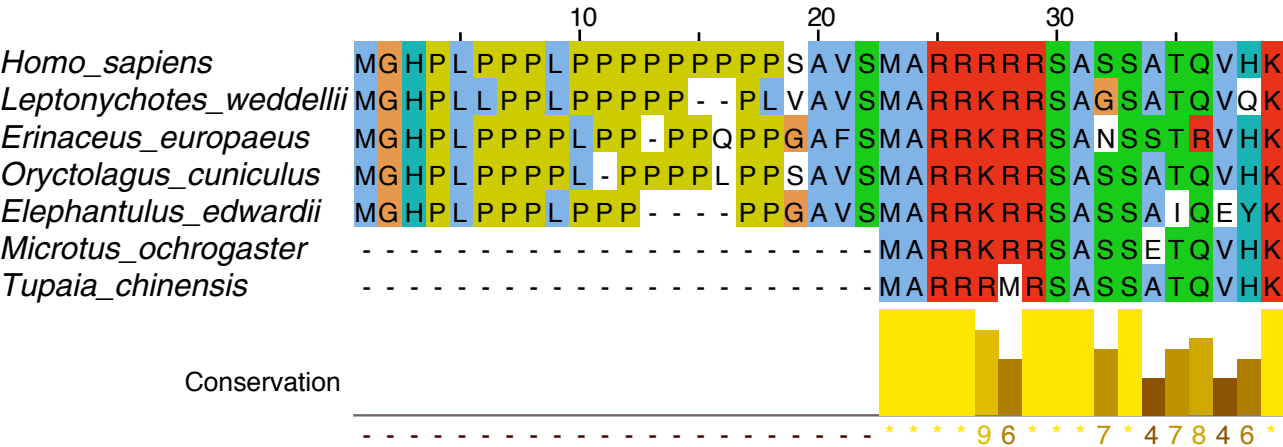


ENSG00000198707 (CEP290)



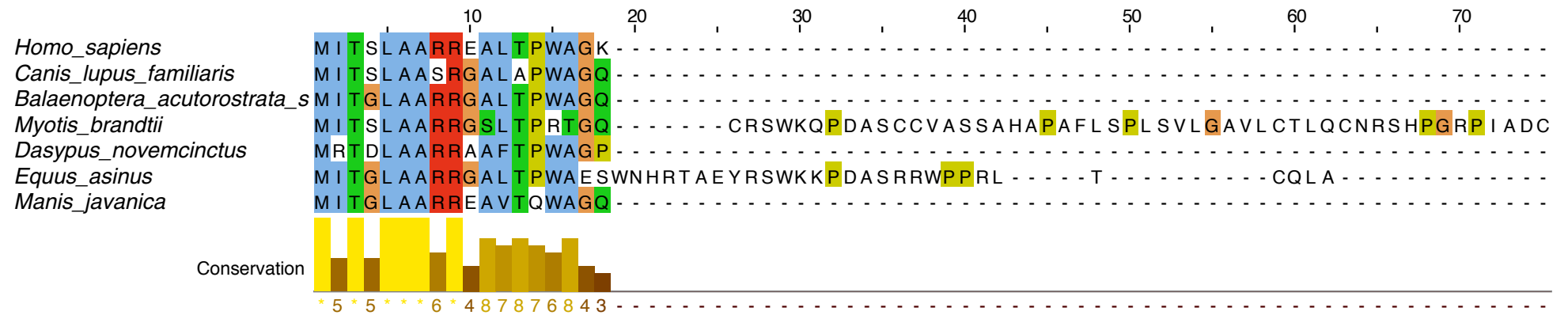
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ENSG00000198791 (CNOT7)



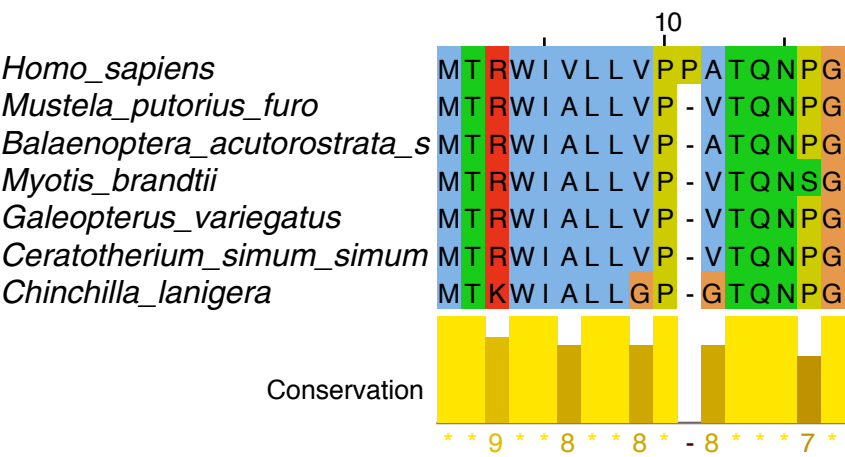
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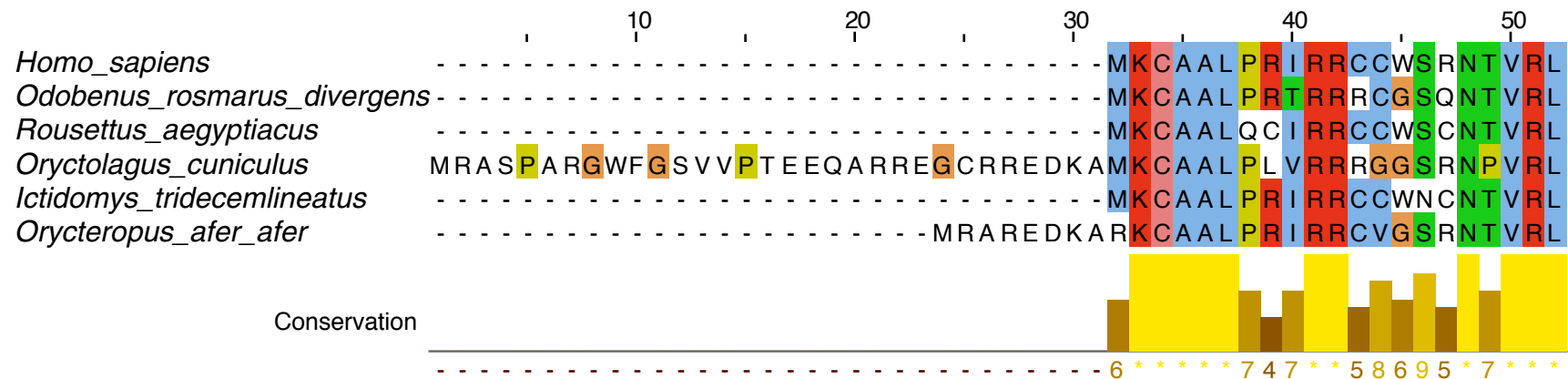


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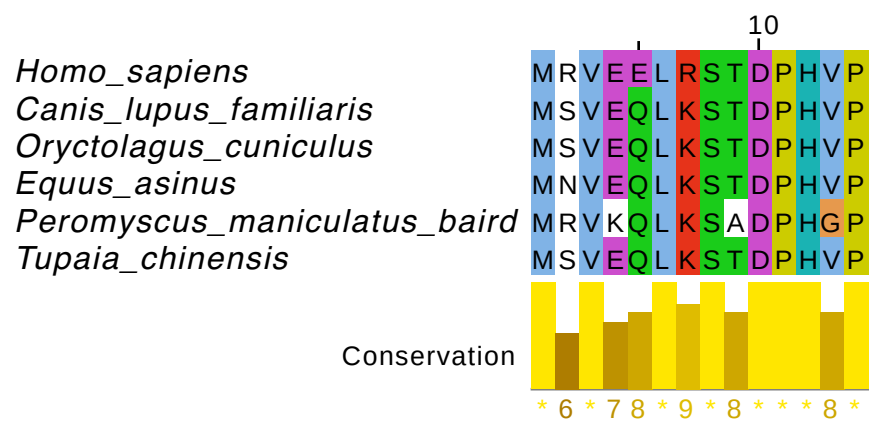


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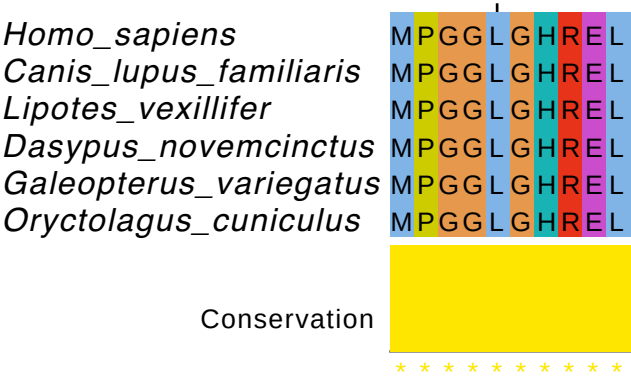
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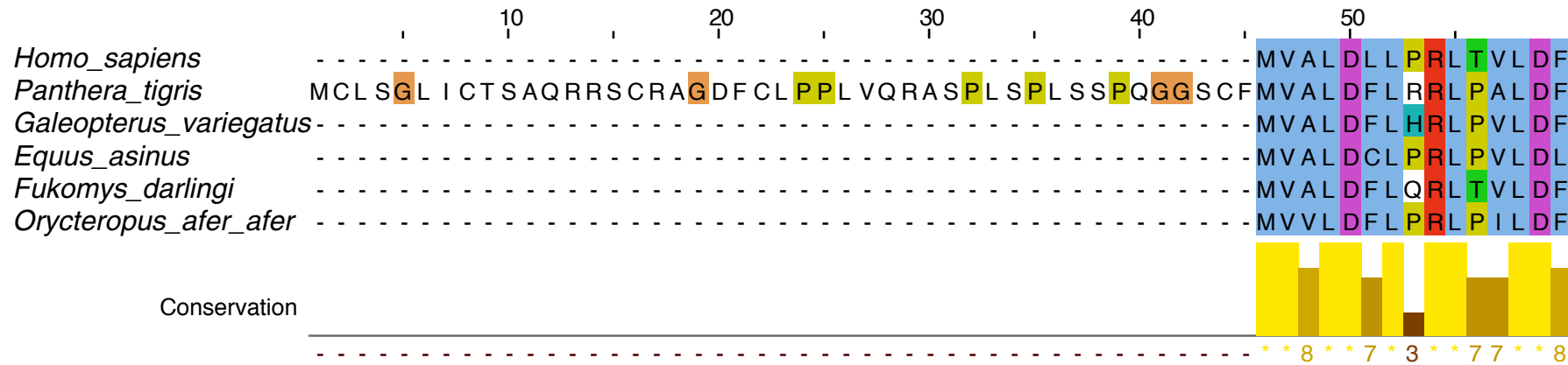
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ENSG00000091009 (RBM27)

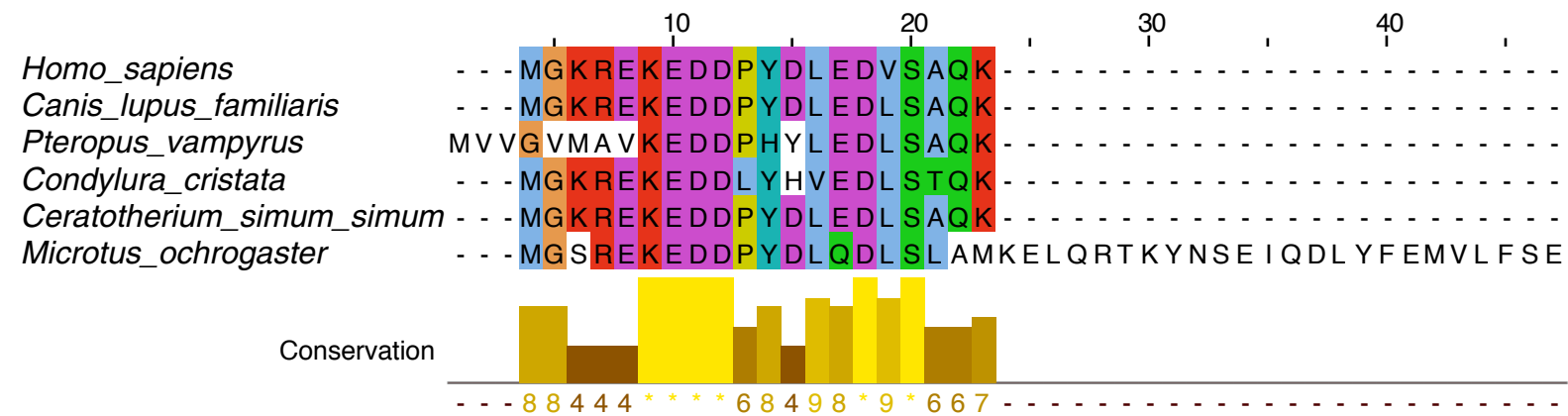


HG0845

ENSG00000099260 (PALMD)

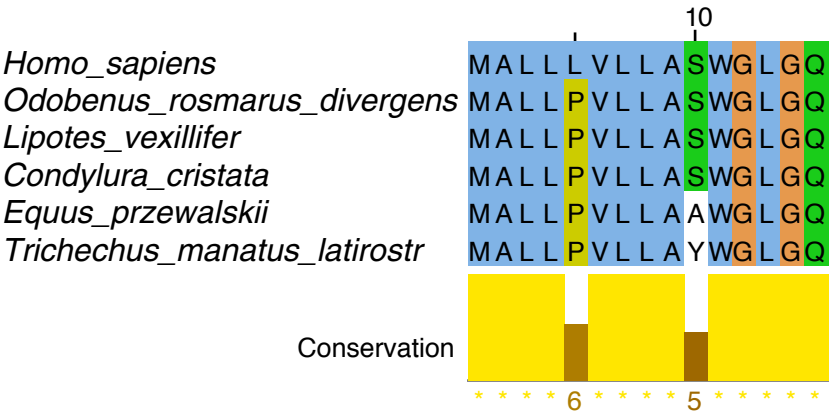


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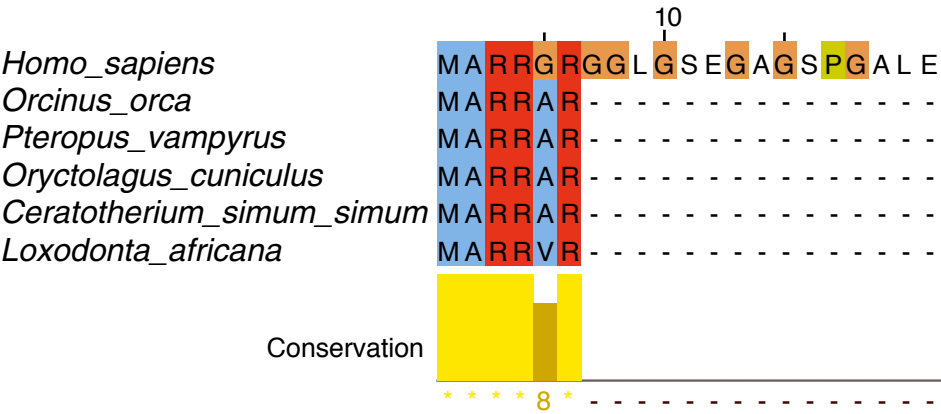
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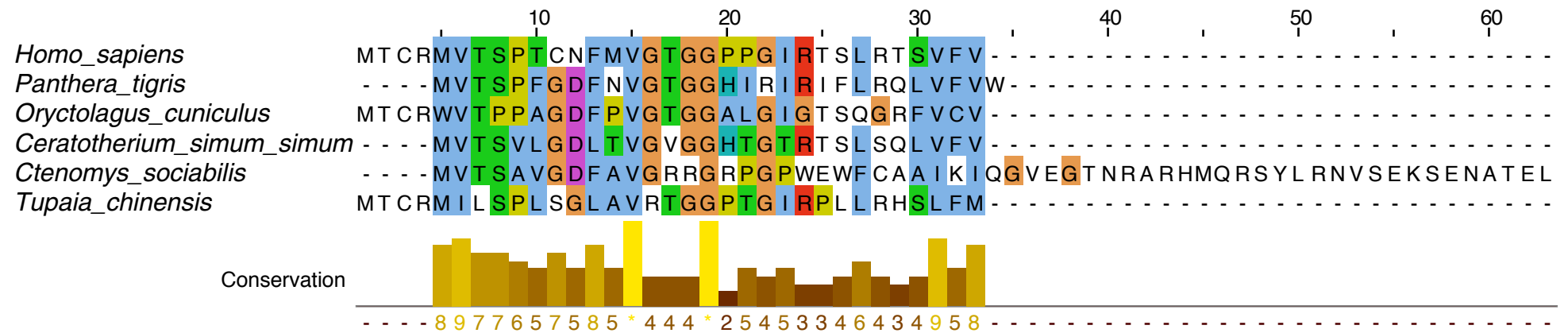


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ENSG00000111817 (DSE)

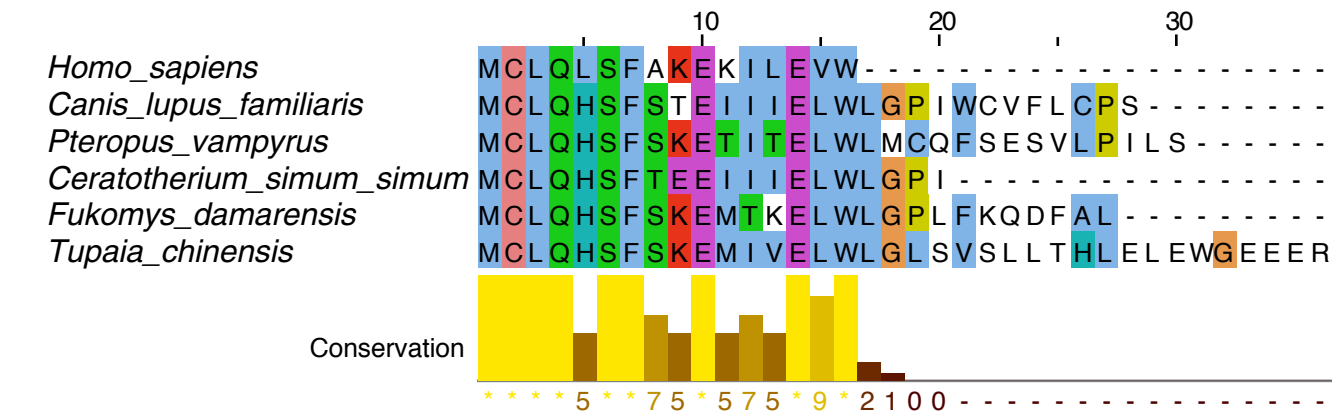


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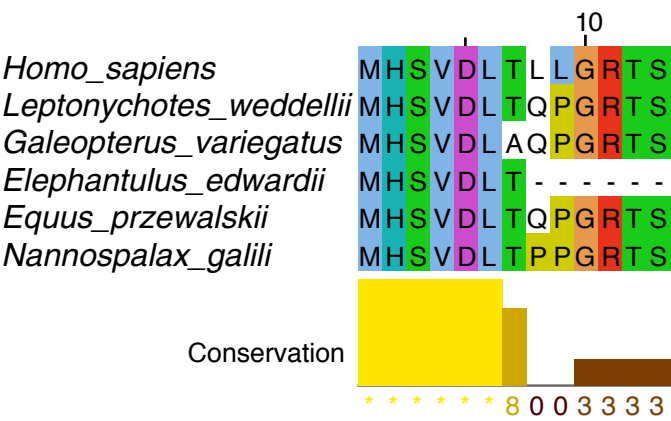
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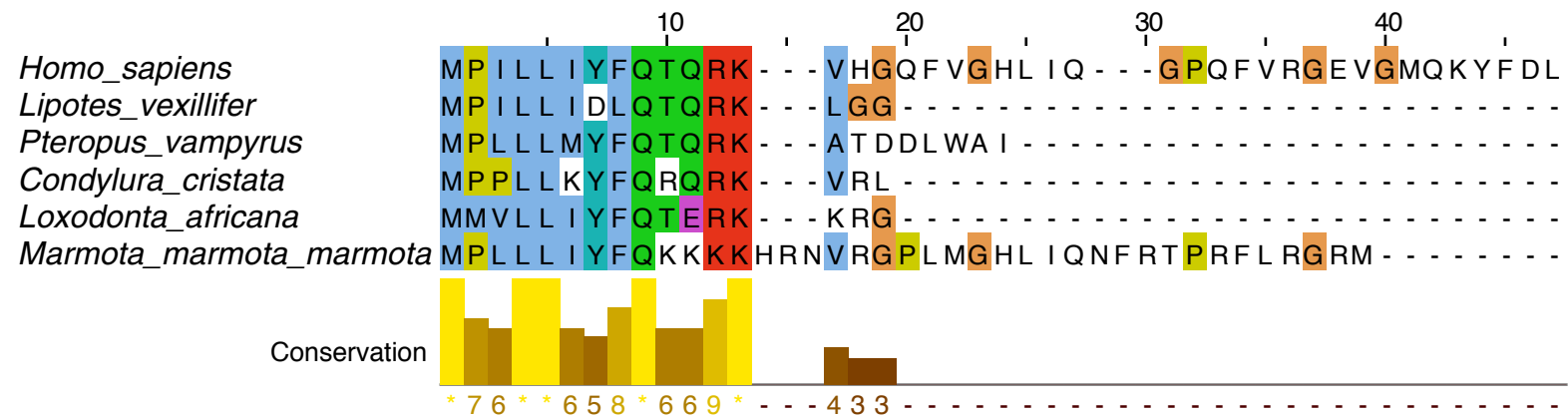
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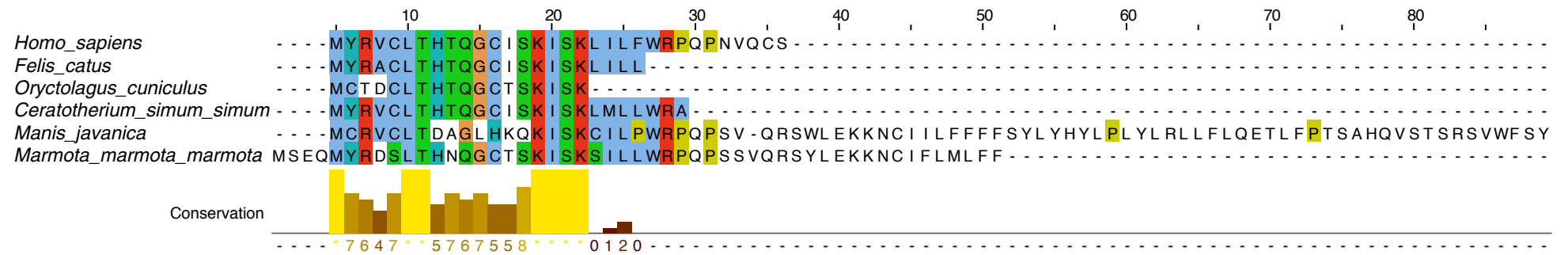


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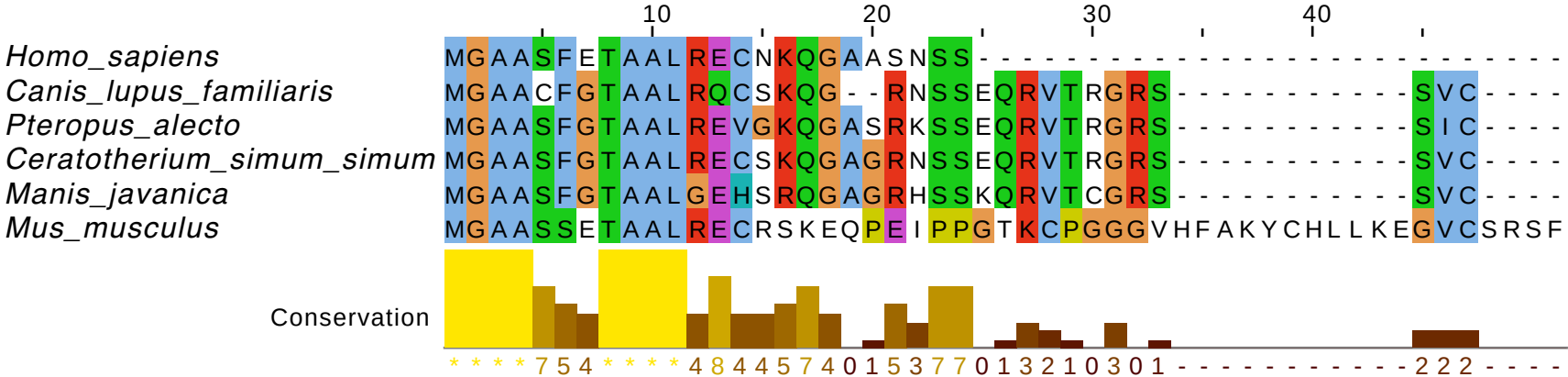
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ENSG00000121807 (CCR2)

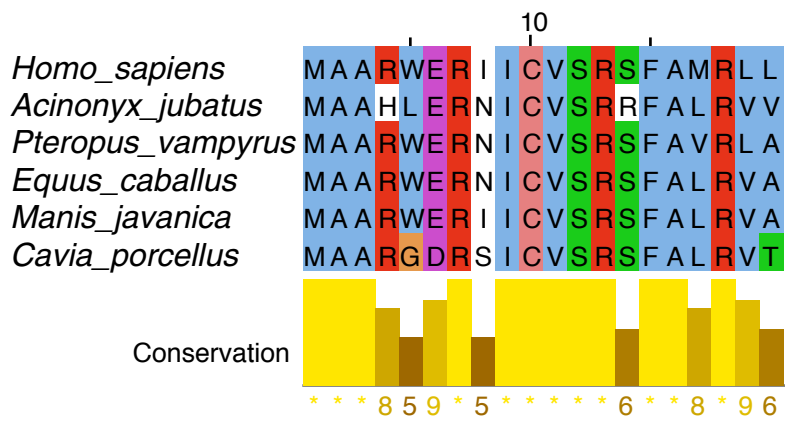


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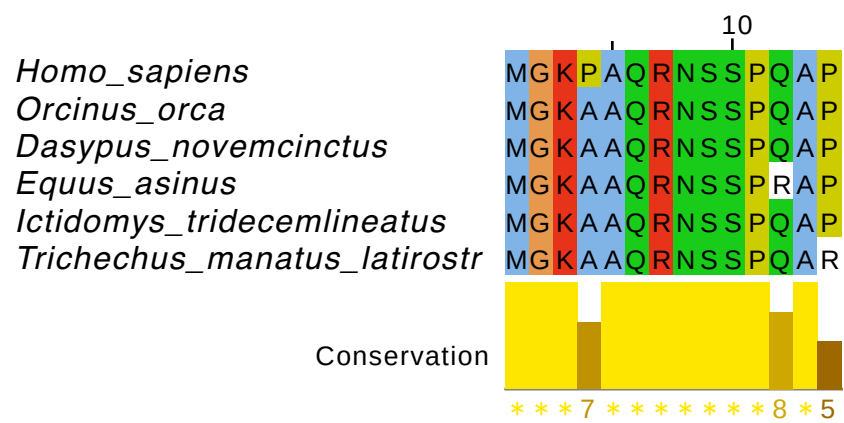
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ENSG00000127804 (METTL16)



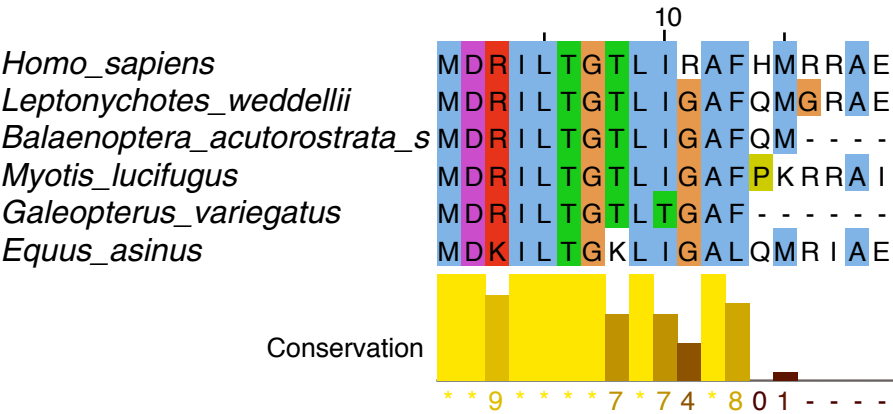
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ENSG00000130055 (GDPD2)



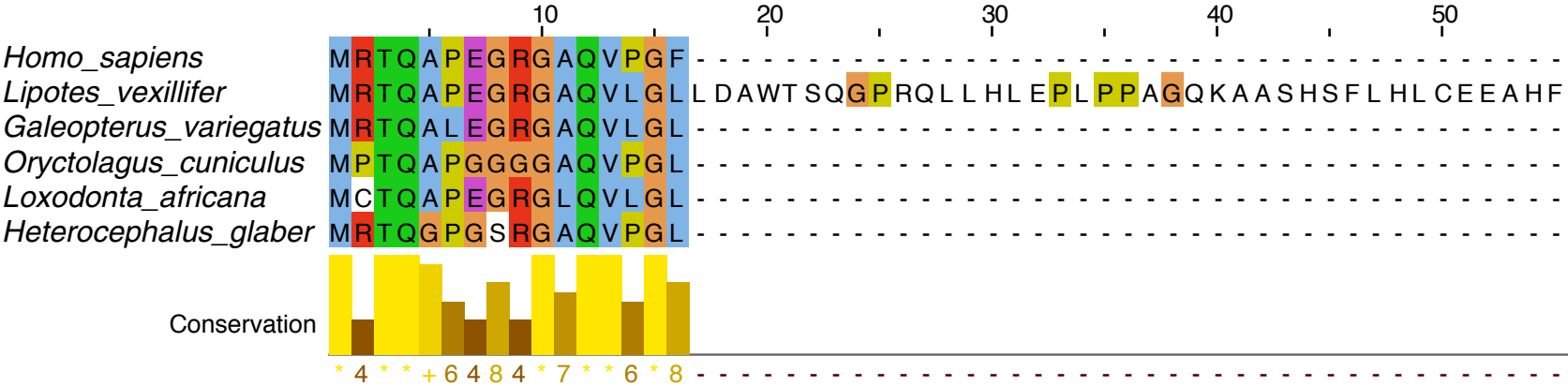
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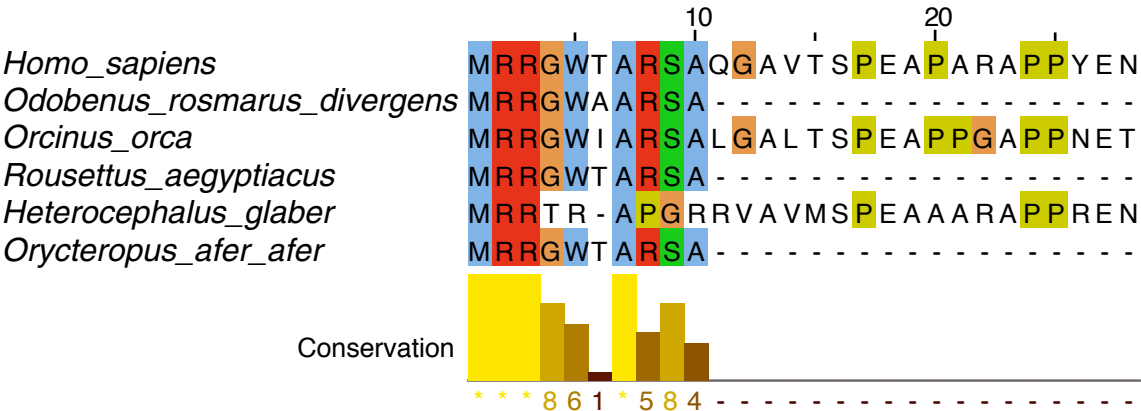
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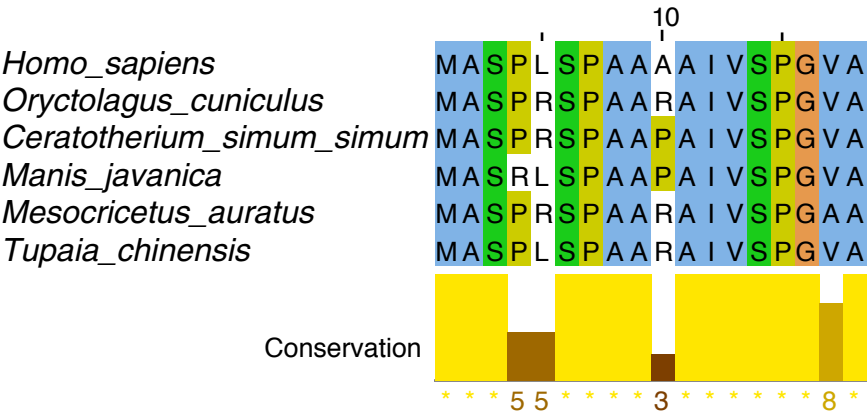
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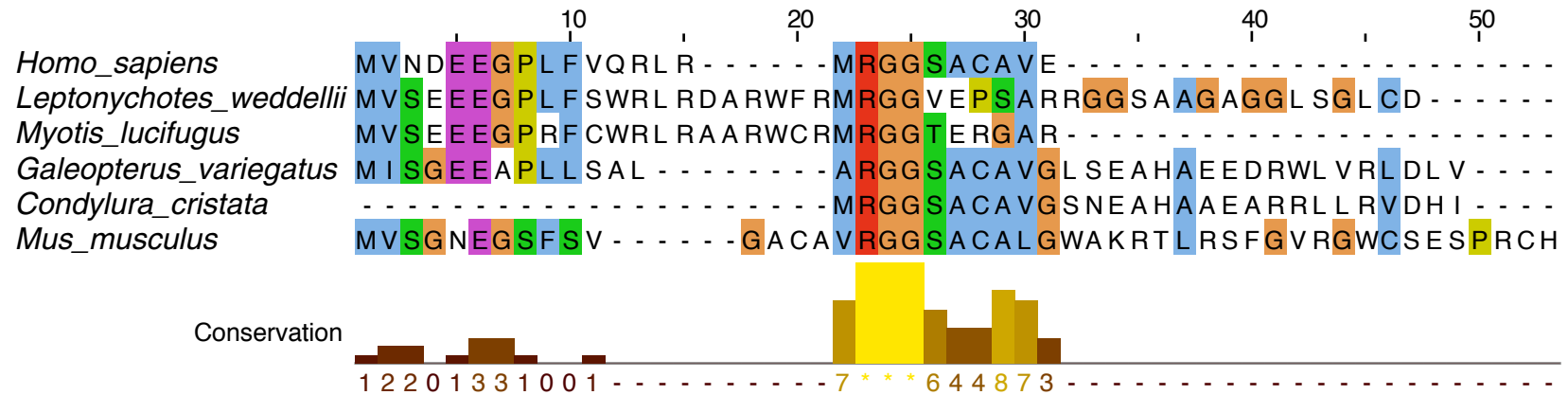


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ENSG00000133056 (PIK3C2B)

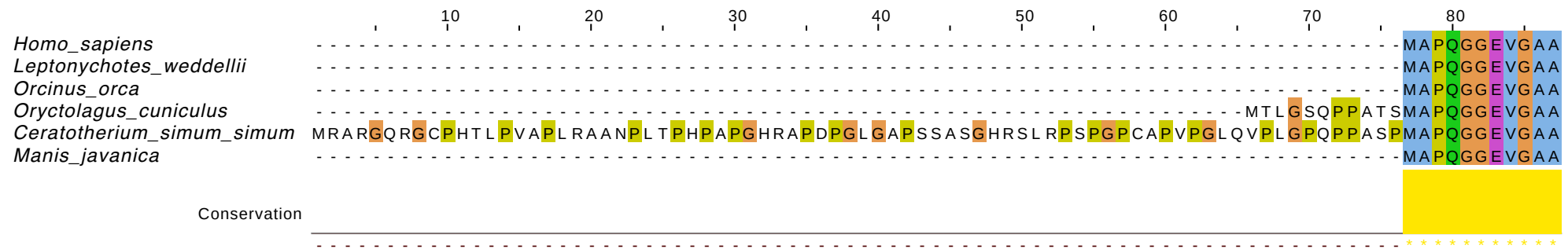


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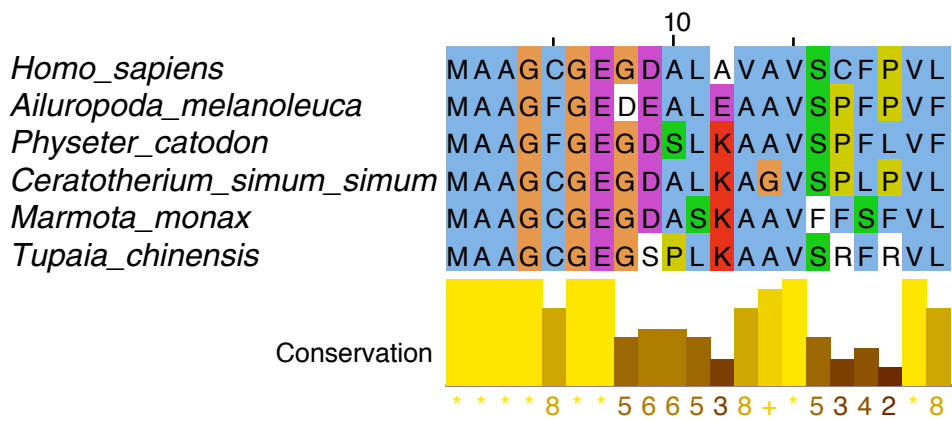
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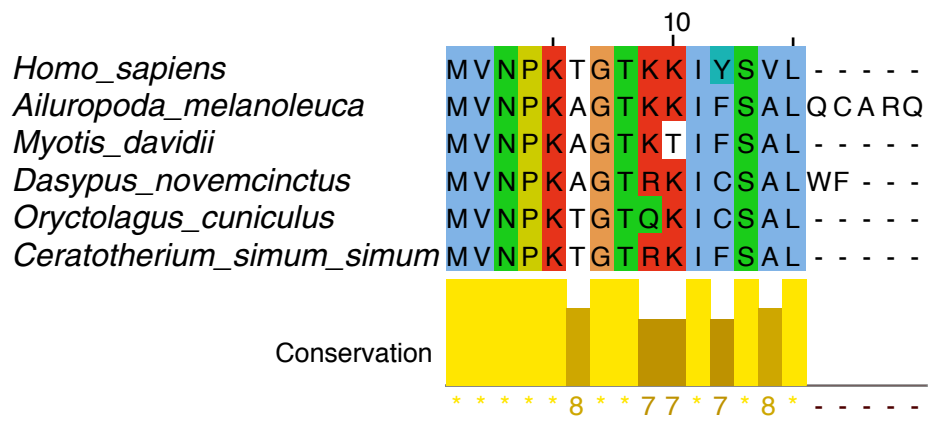
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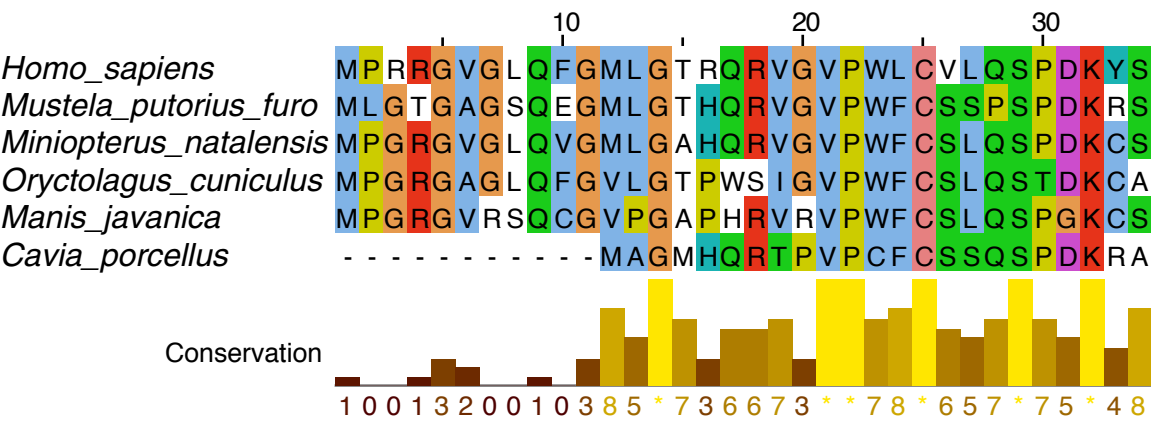
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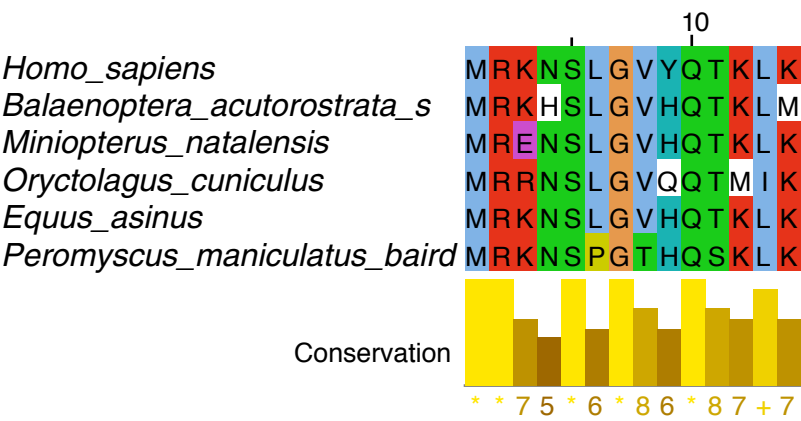
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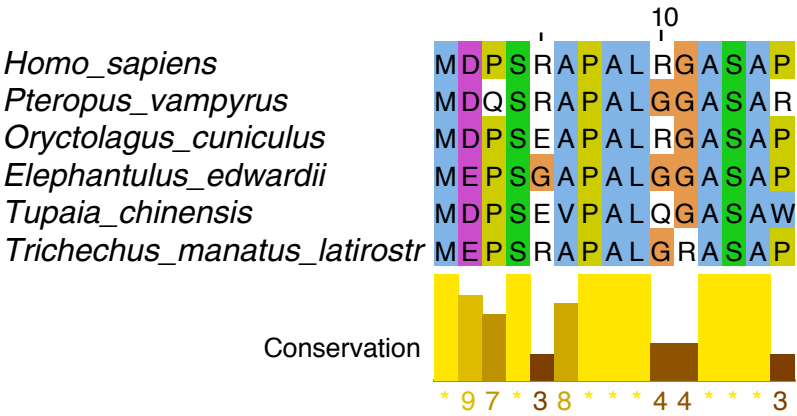
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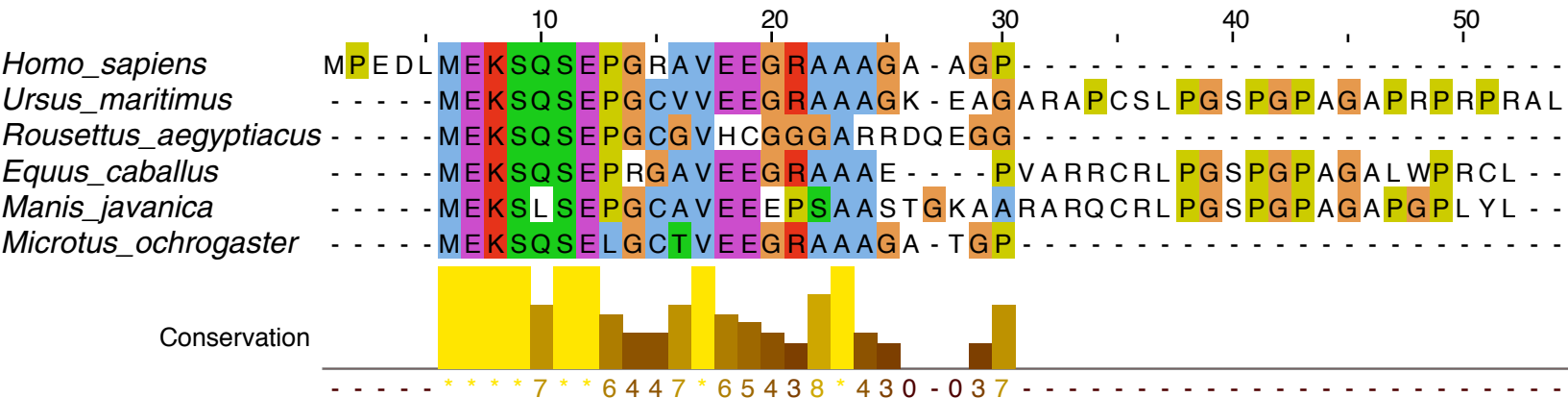


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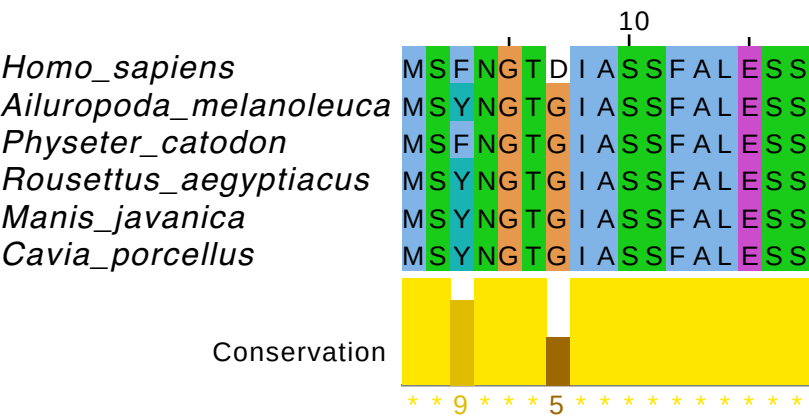


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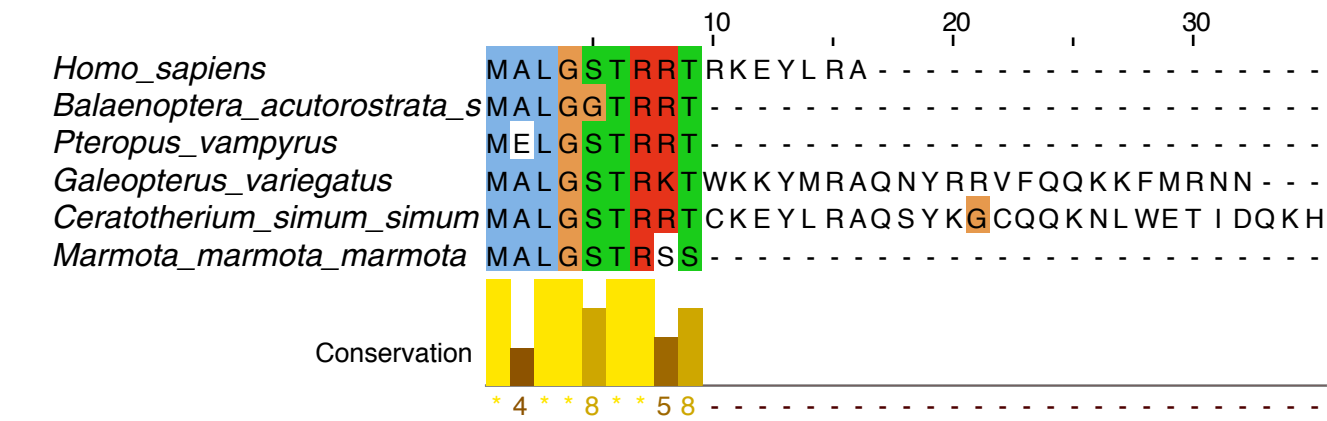
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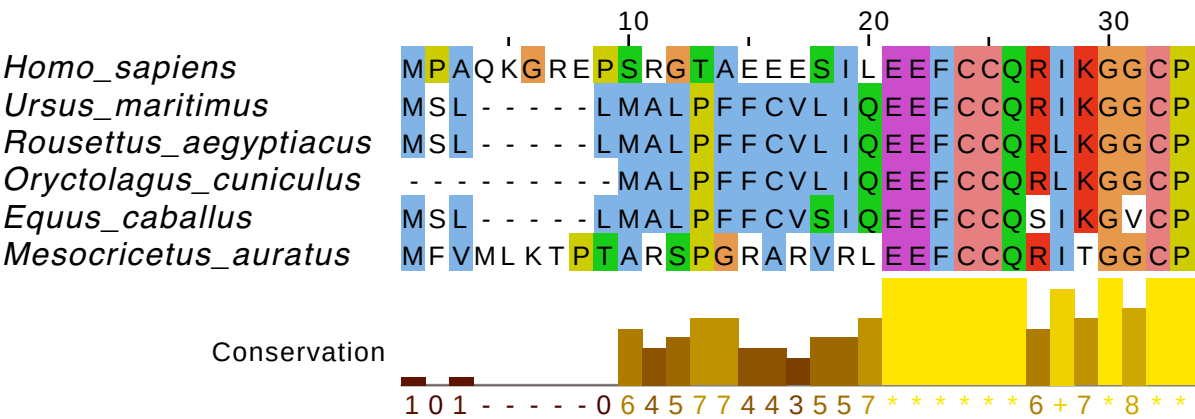
HG0870

ENSG00000140993 (TIGD7)



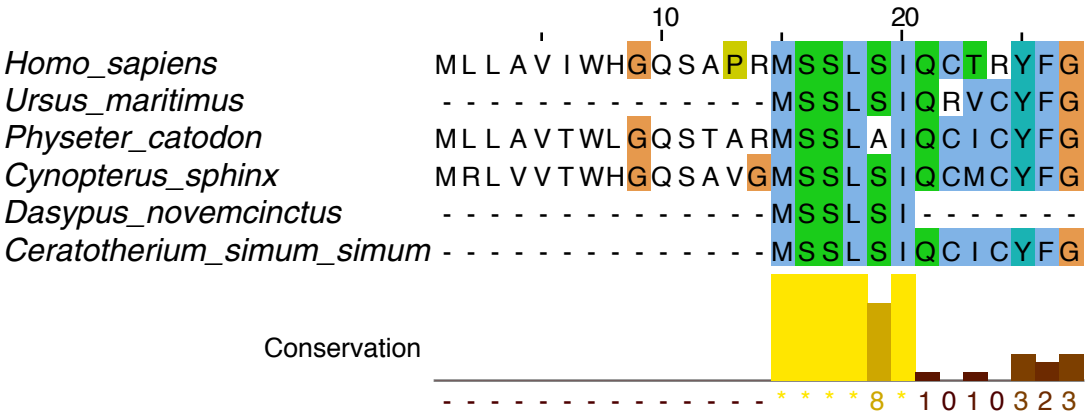
HG0871

ENSG00000141127 (PRPSAP2)

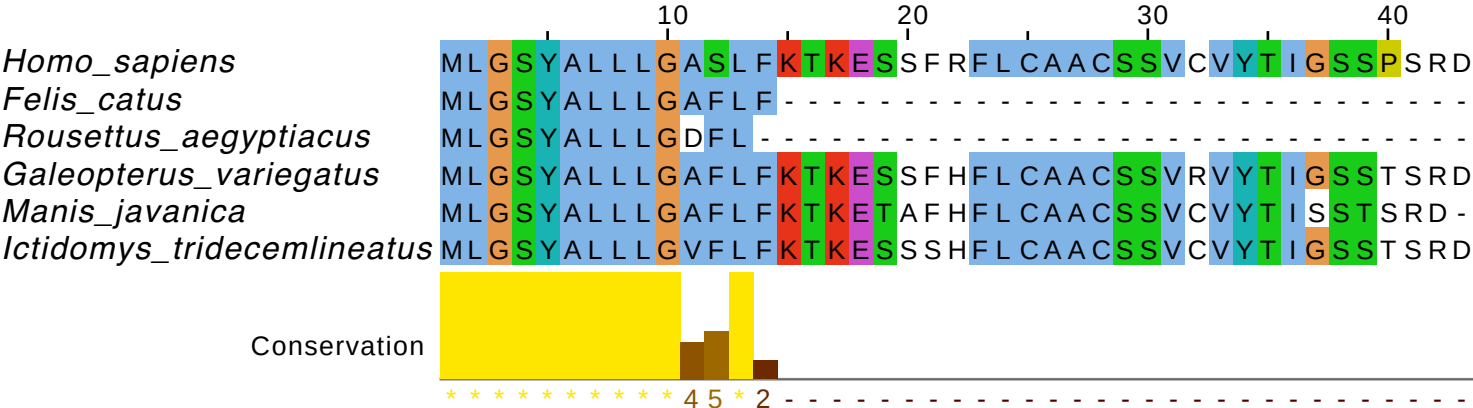


HG0872

ENSG00000142583 (SLC2A5)

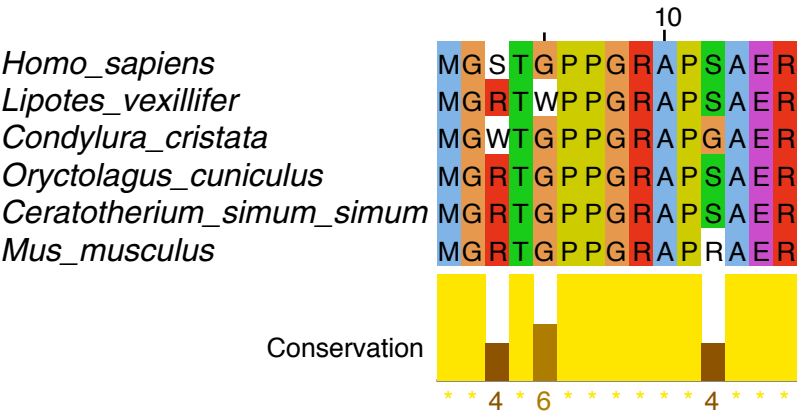


HG0873
ENSG00000142875 (PRKACB)



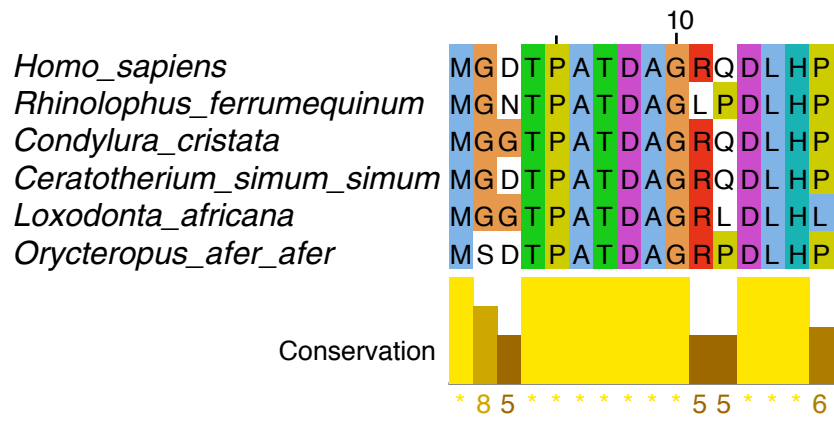
HG0874

ENSG00000143515 (ATP8B2)



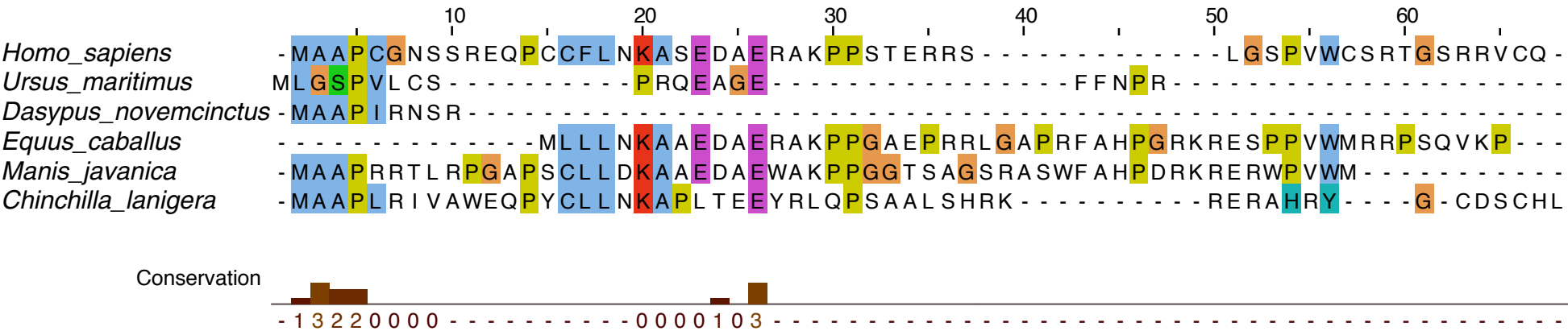
HG0875

ENSG00000145284 (SCD5)

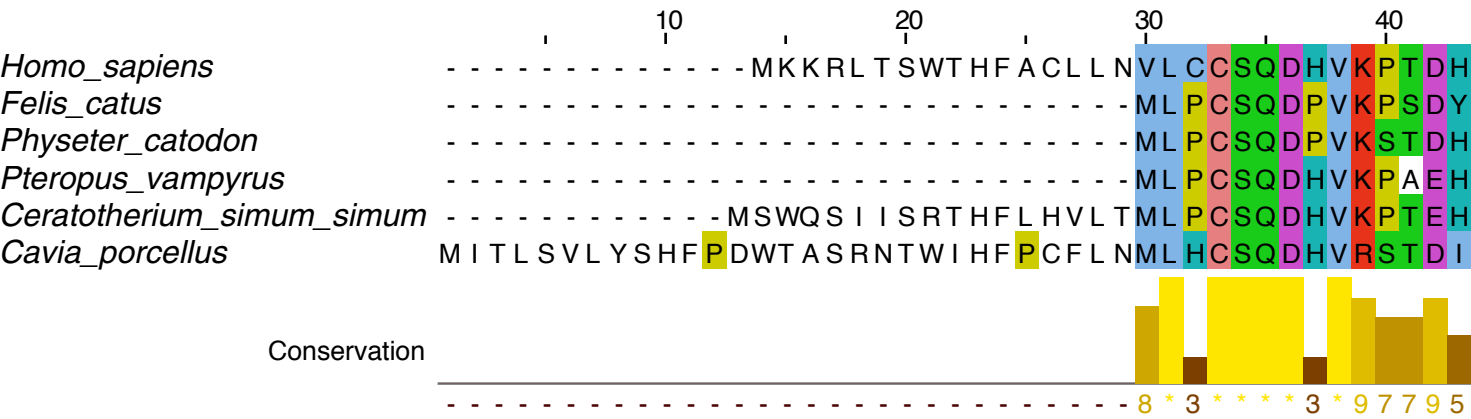


HG0876

ENSG00000145908 (ZNF300)

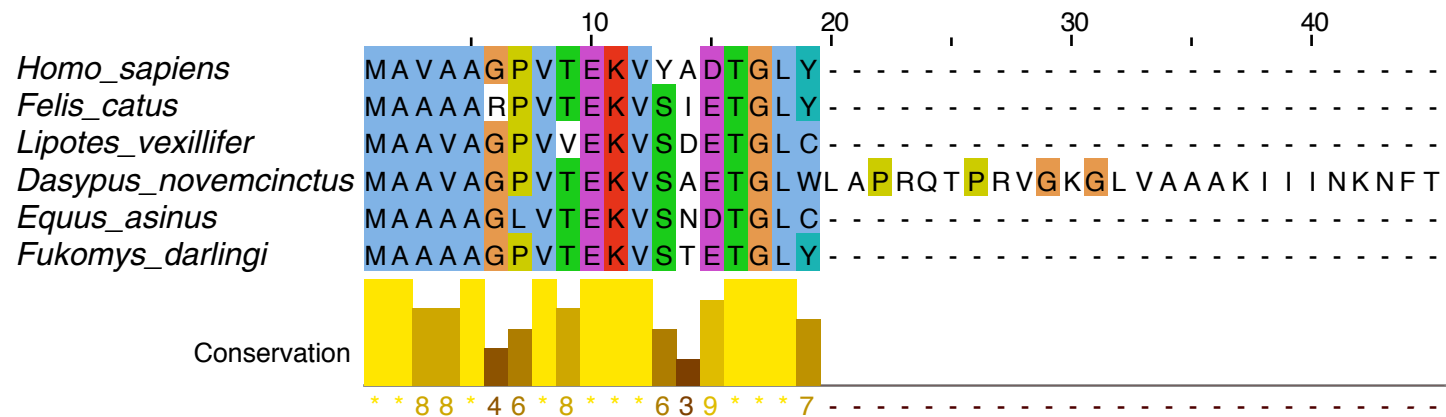


HG0877
ENSG00000146426 (TIAM2)



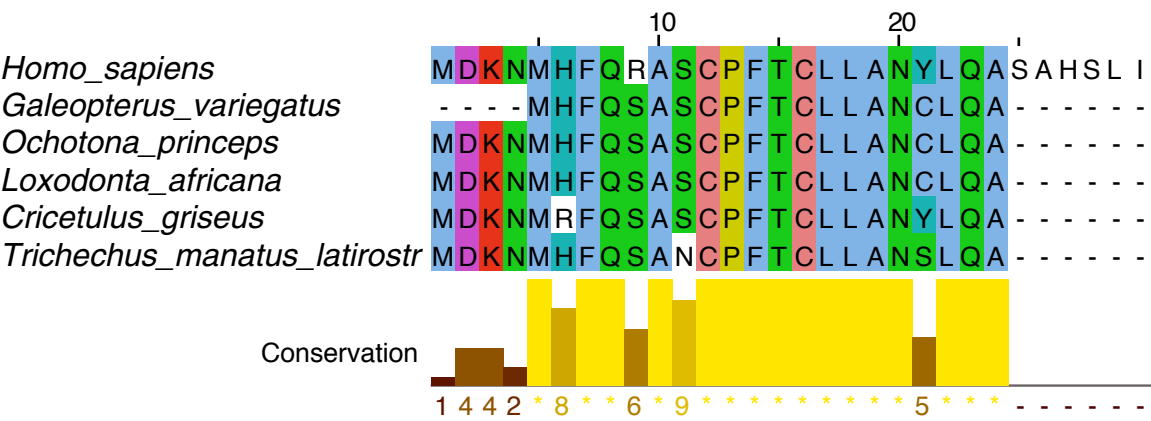
HG0878

ENSG00000146802 (TMEM168)



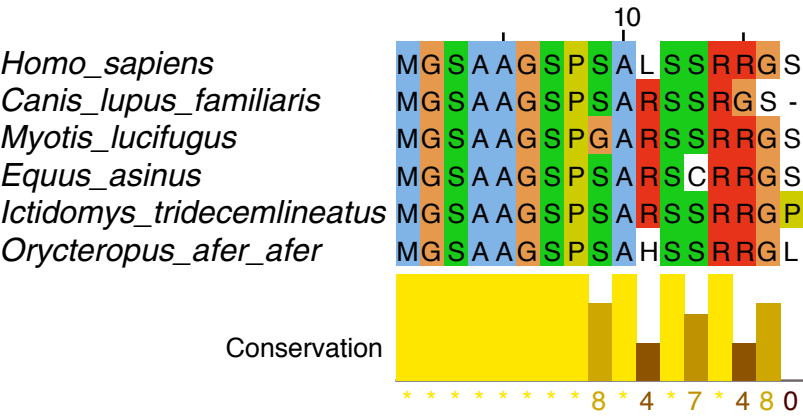
HG0879

ENSG00000147145 (LPAR4)



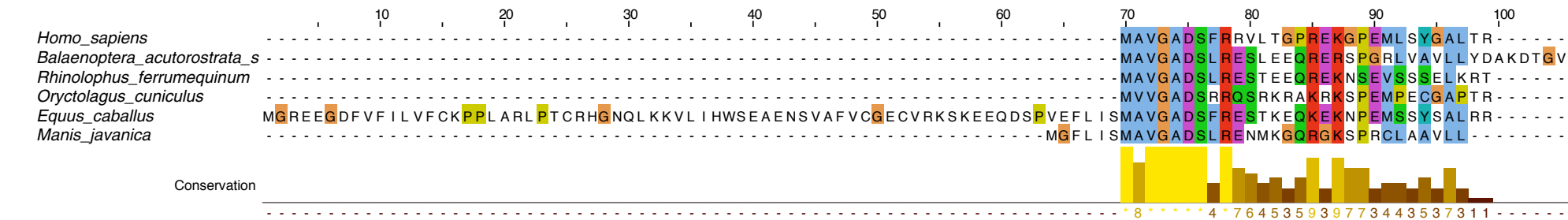
HG0880

ENSG00000151789 (ZNF385D)



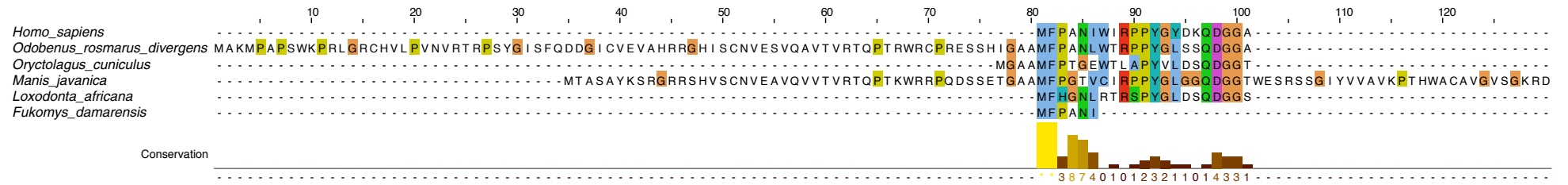
HG0881

ENSG00000153822 (KCNJ16)



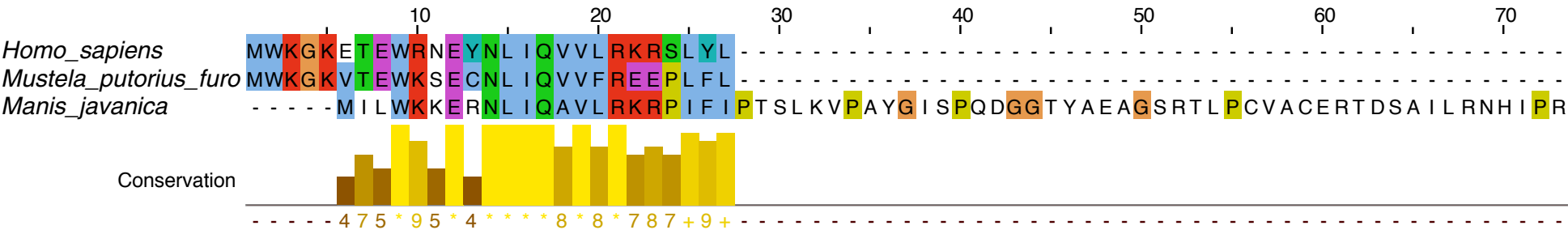
HG0882.1

ENSG00000154832 (CXXC1)



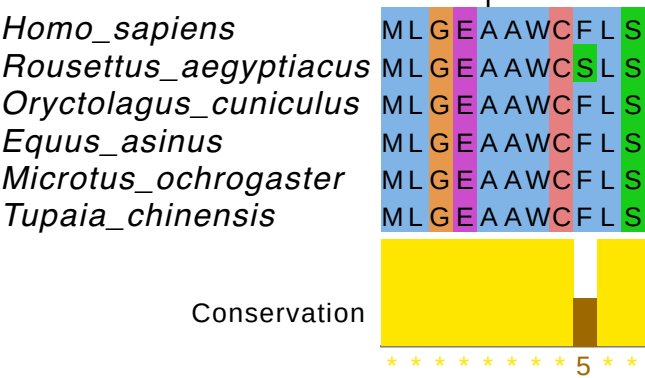
HG0882.2

ENSG00000154832 (CXXC1)



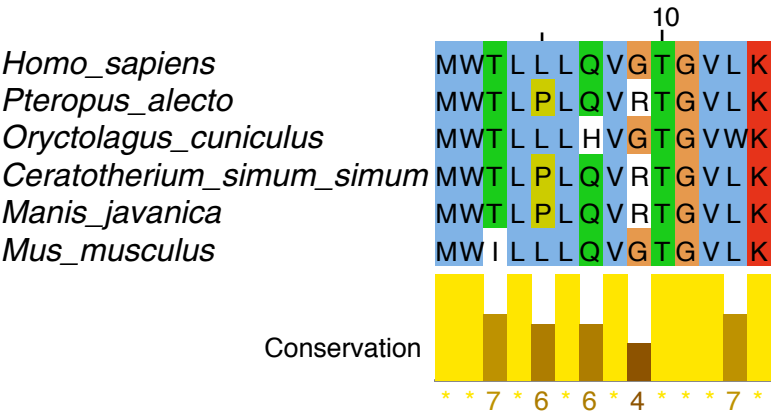
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ENSG00000156011 (PSD3)



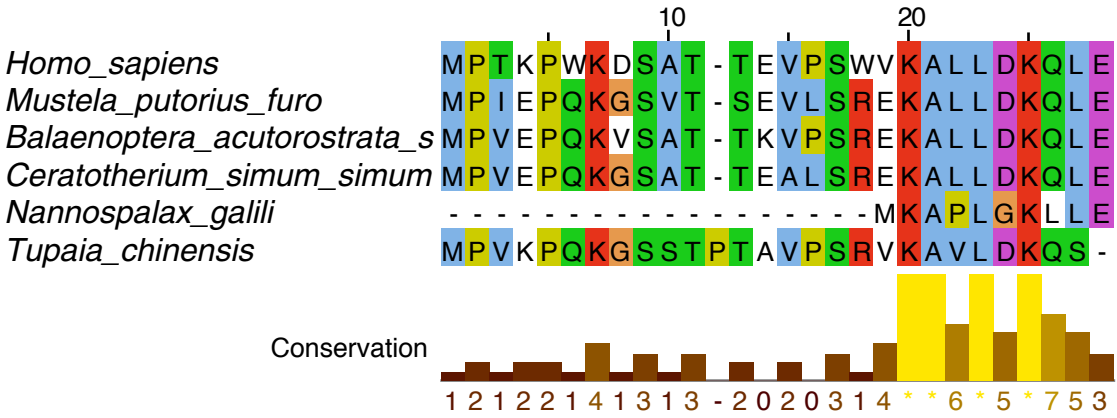
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ENSG00000156463 (SH3RF2)



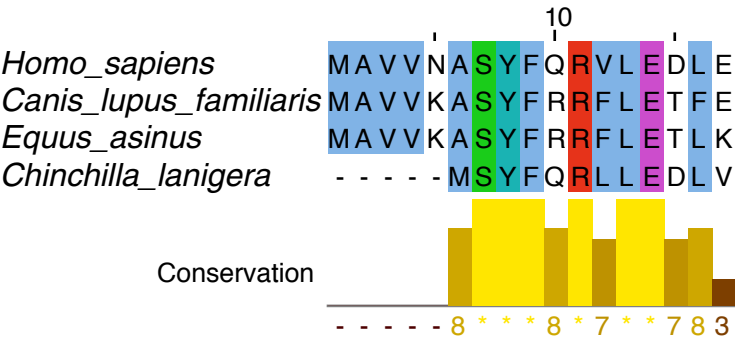
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ENSG00000157502 (MUM1L1)



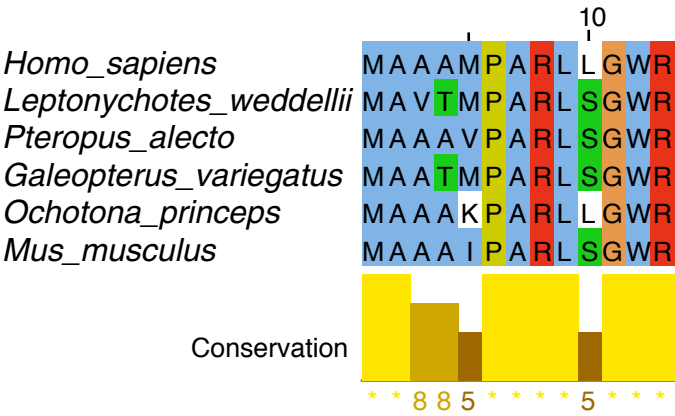
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ENSG00000157502 (MUM1L1)



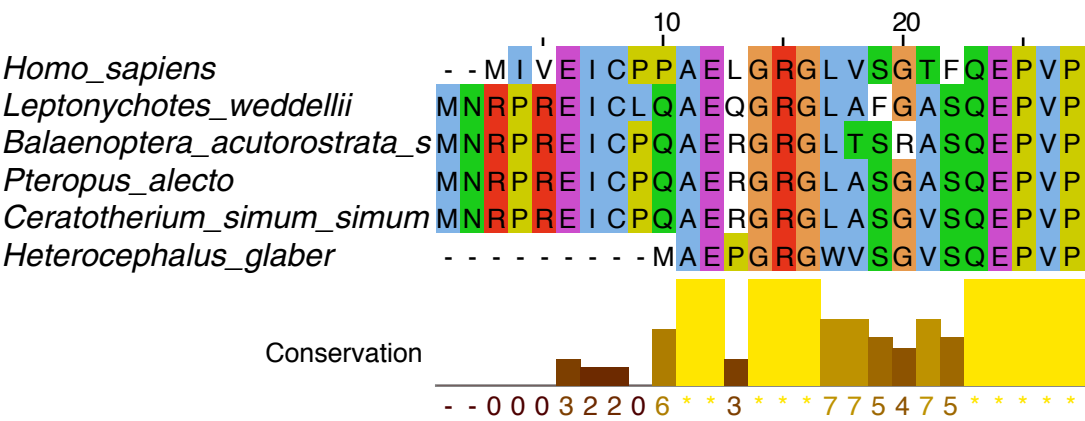
HG0886

ENSG00000158850 (B4GALT3)



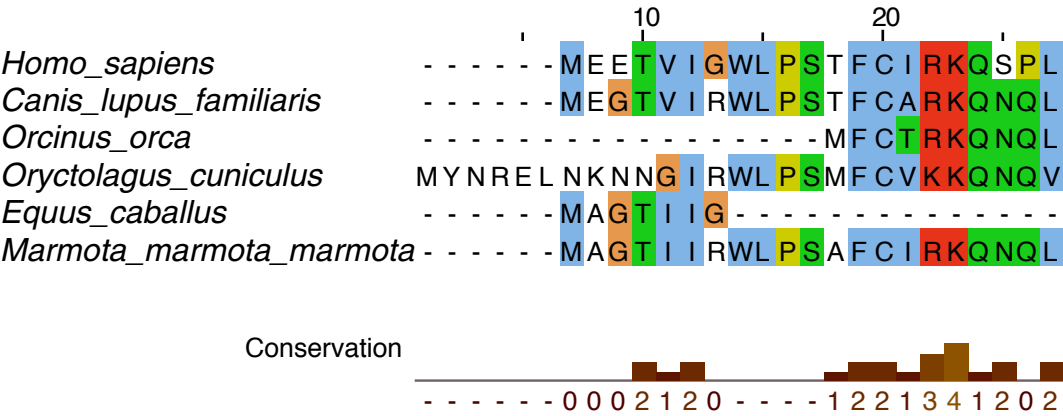
HG0887

ENSG00000160959



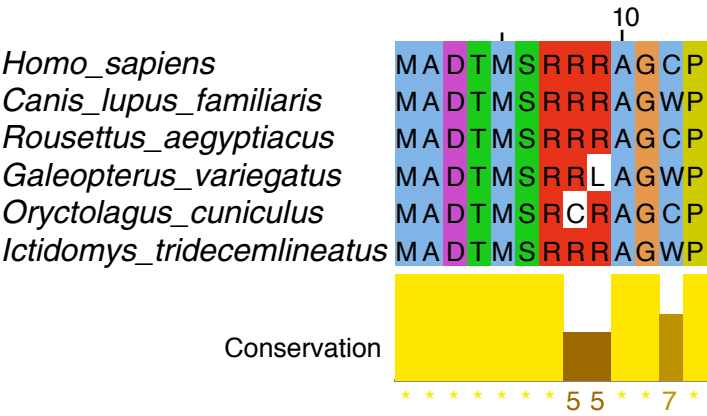
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ENSG00000164023 (SGMS2)

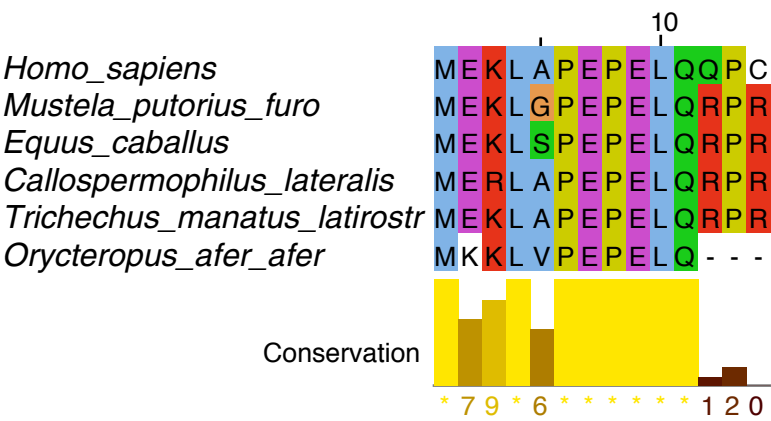


HG0889

ENSG00000164091 (WDR82)

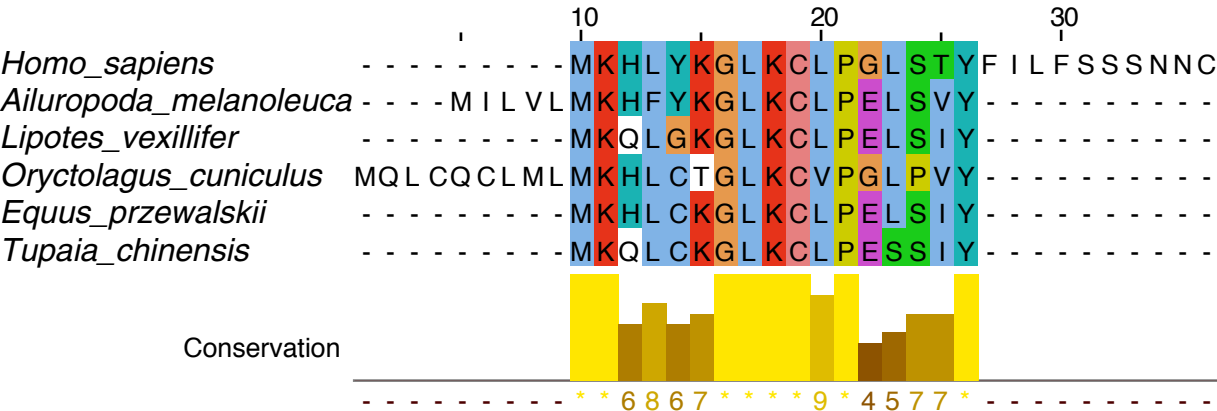


HG0890
ENSG00000165813

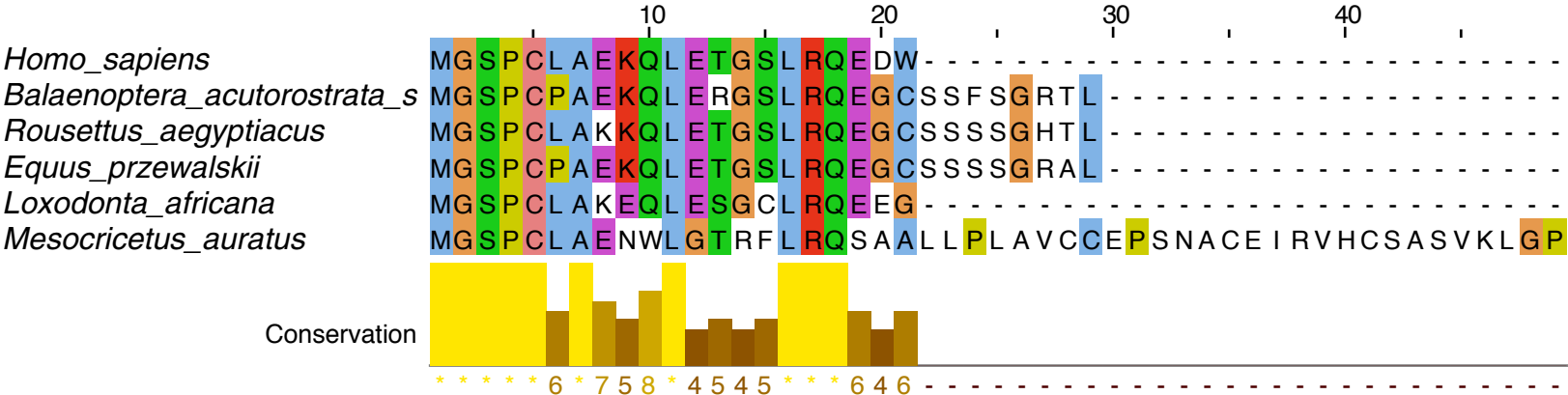


HG0891

ENSG00000166211 (SPIC)

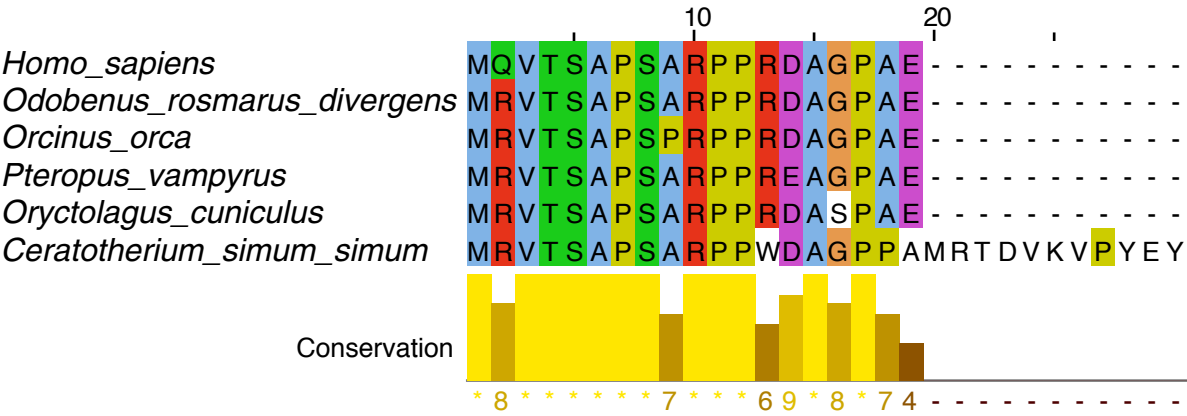


HG0892
ENSG00000168418 (KCNG4)



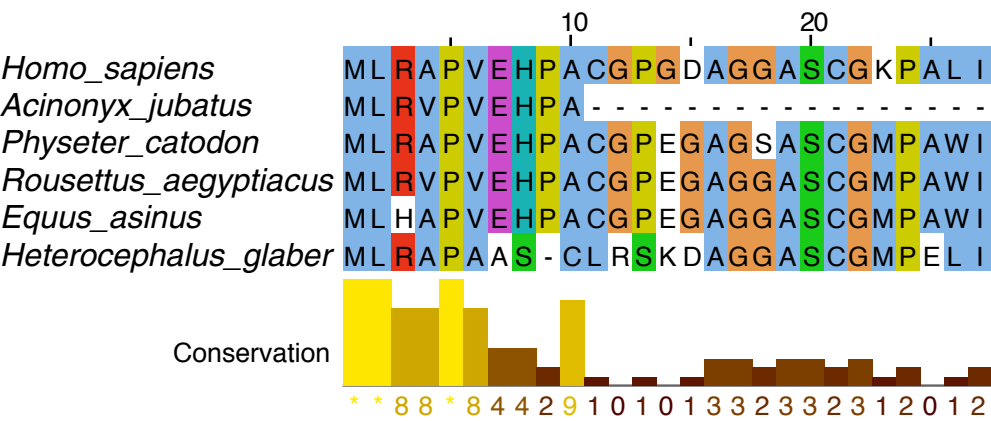
HG0893

ENSG00000168769 (TET2)



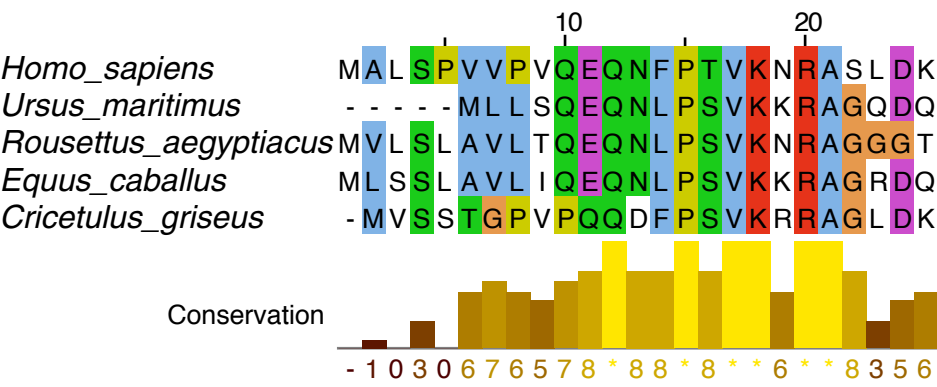
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ENSG00000169282 (KCNAB1)



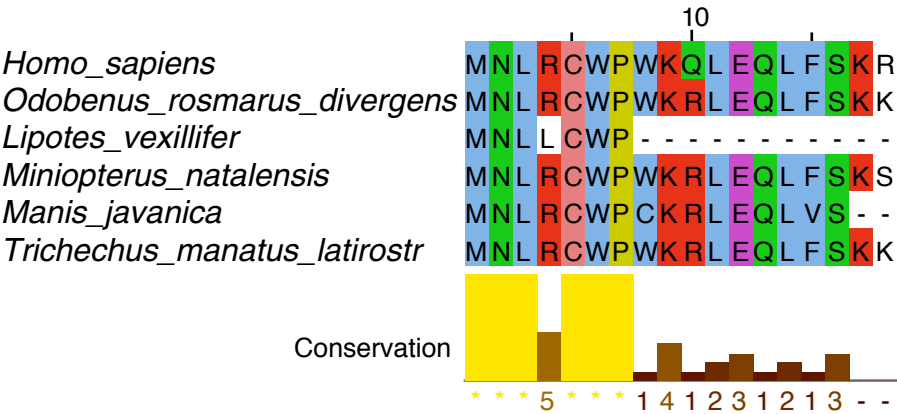
HG0894.2

ENSG00000069424 (KCNAB2)

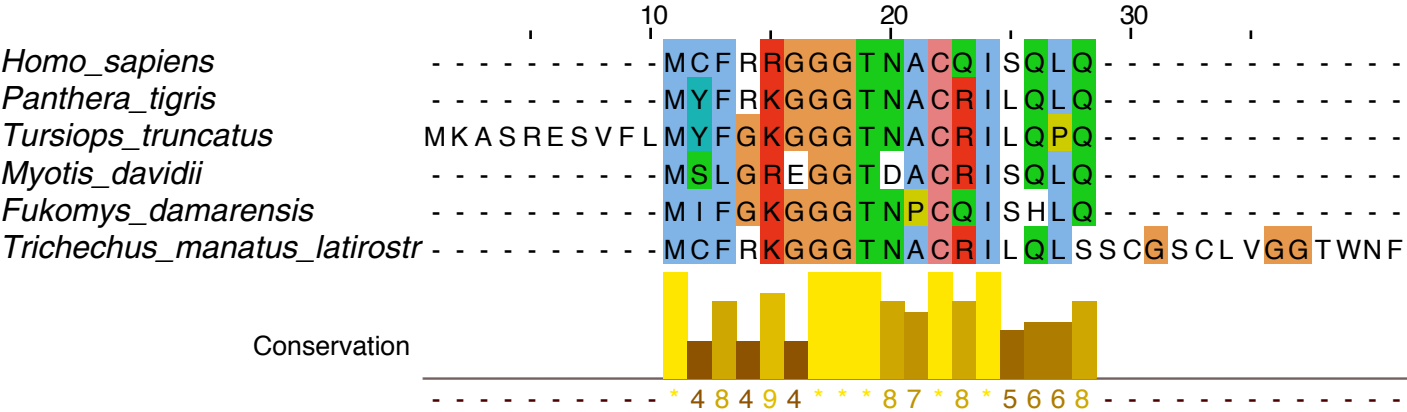


HG0895

ENSG00000170035 (UBE2E3)

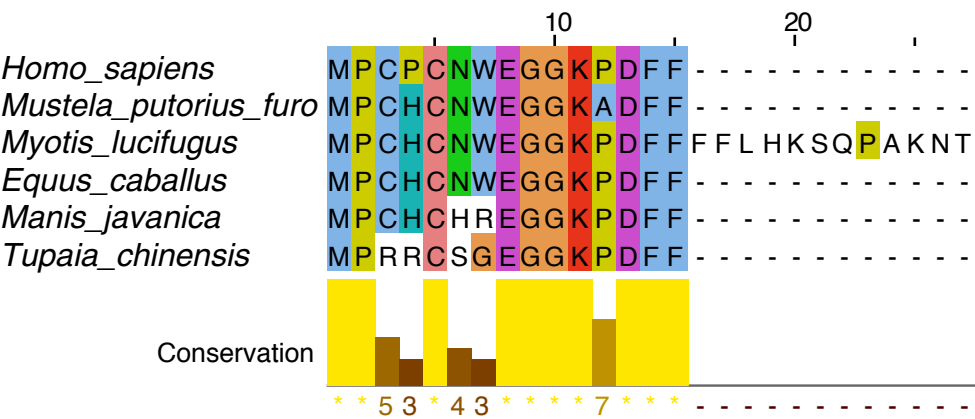


HG0896
ENSG00000170365 (SMAD1)

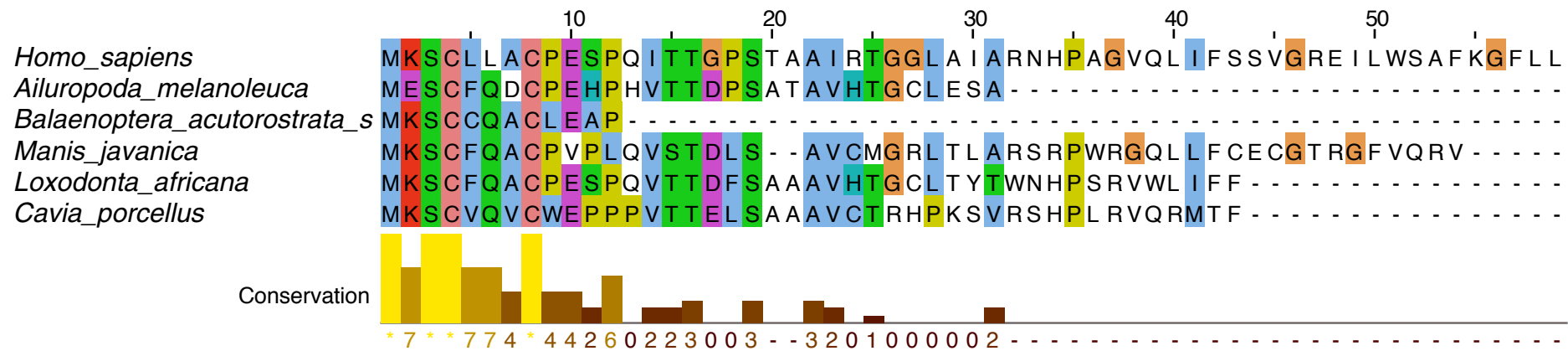


HG0897

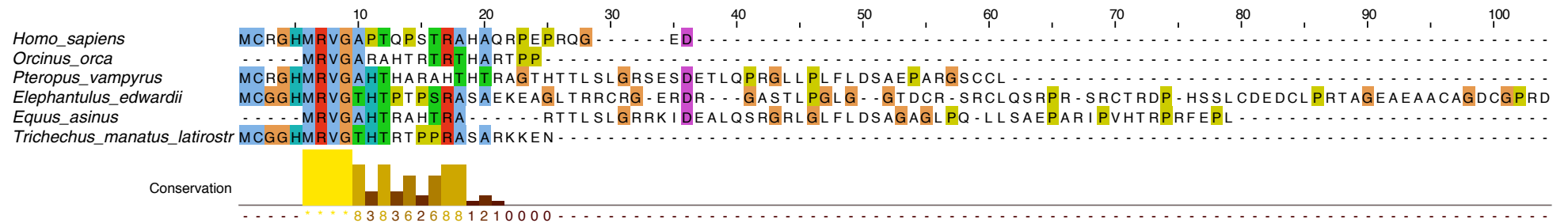
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ENSG00000171729 (TMEM51)

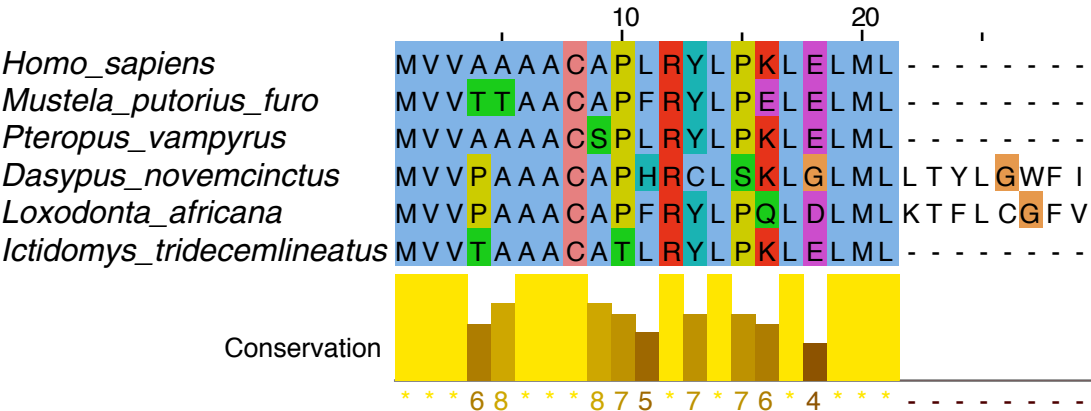


ENSG00000173320 (STOX2)



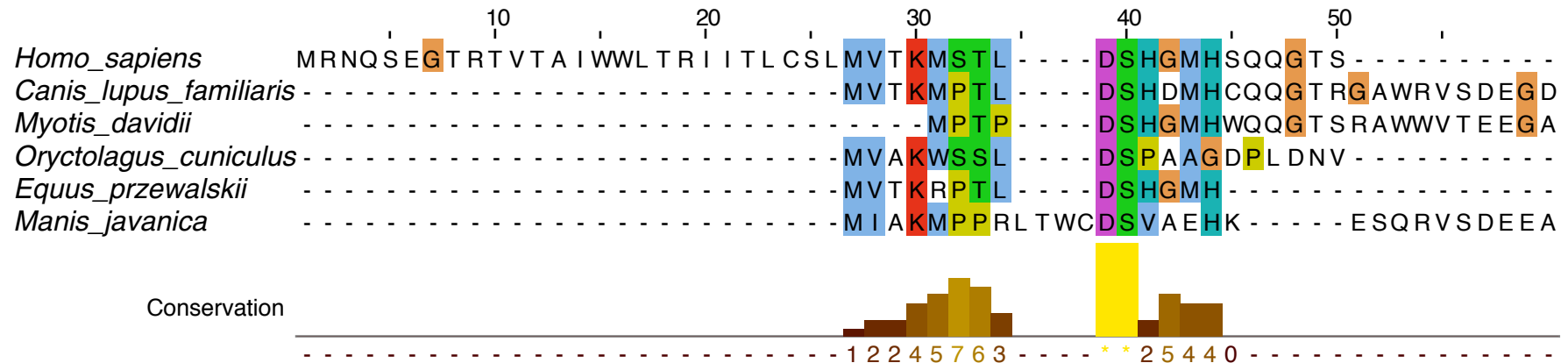
HG0900

ENSG00000173517 (PEAK1)



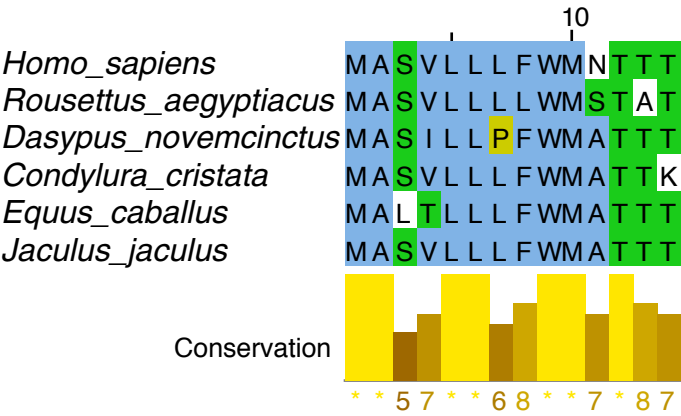
HG0901

ENSG00000175697 (GPR156)



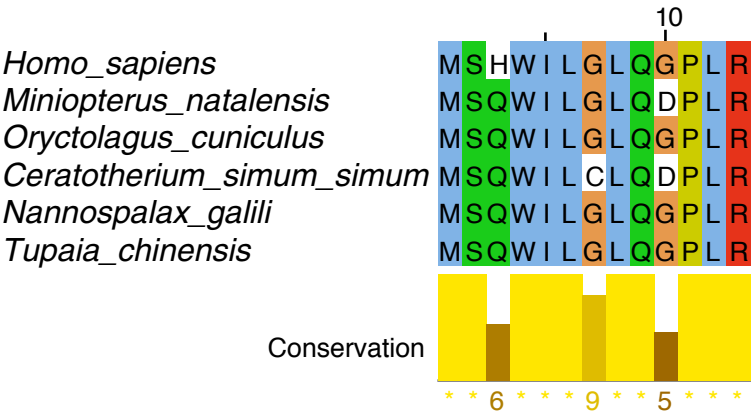
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ENSG00000177182 (CLVS1)



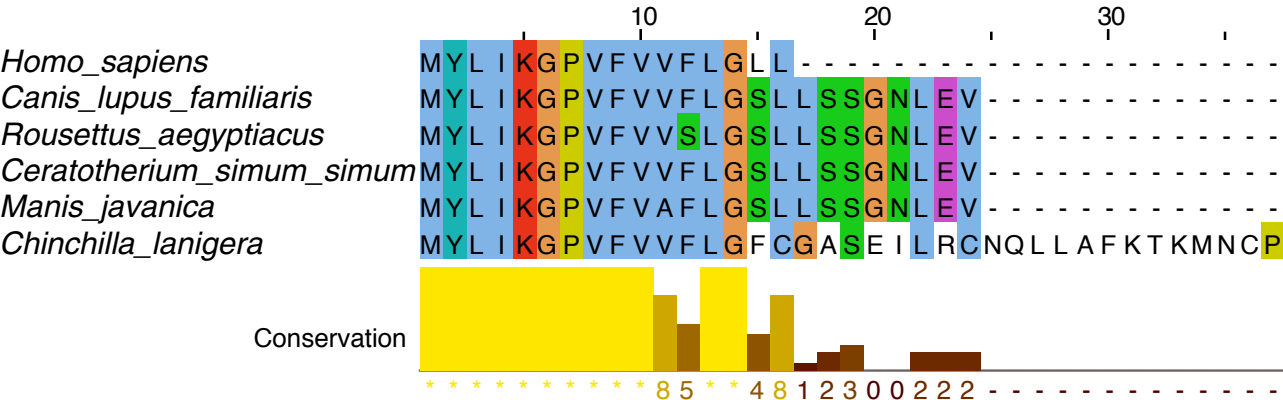
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ENSG00000180616 (SSTR2)



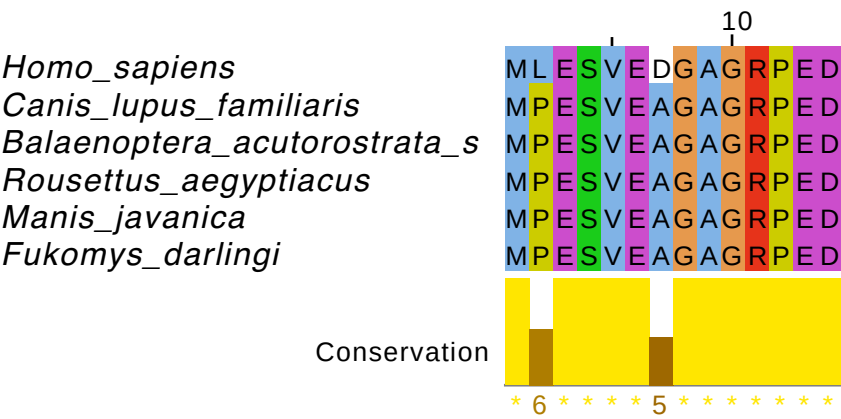
HG0904

ENSG00000182329



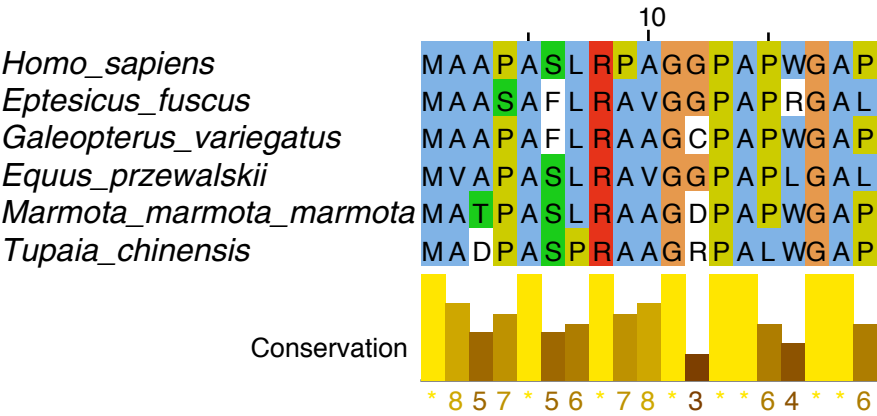
HG0905

ENSG00000183337 (BCOR)



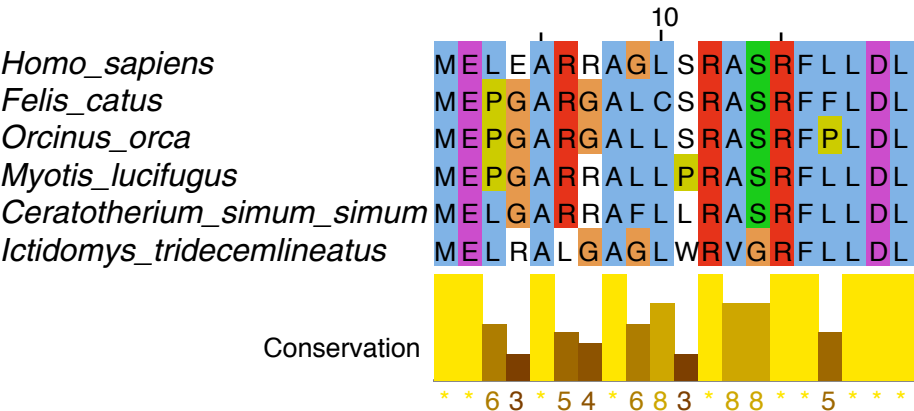
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ENSG00000183773 (AIFM3)



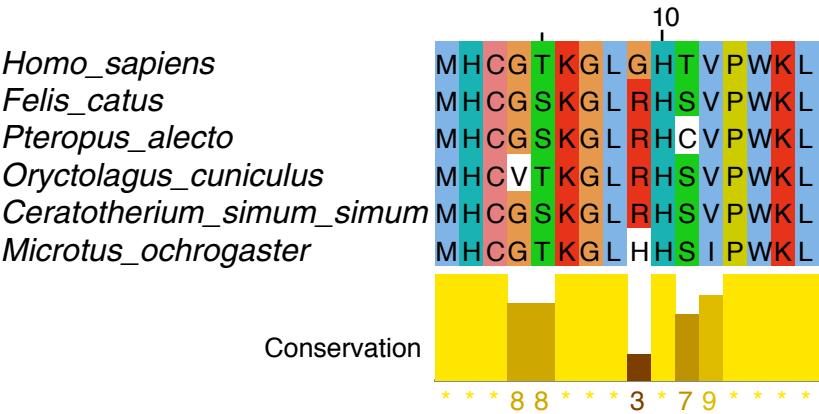
HG0907

ENSG00000186862 (PDZD7)



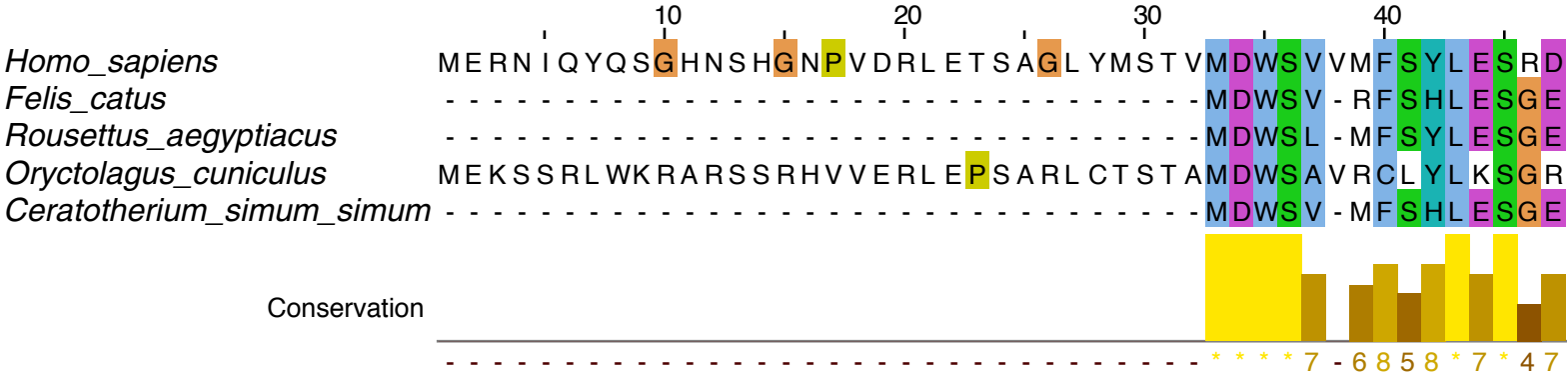
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ENSG00000188554 (NBR1)



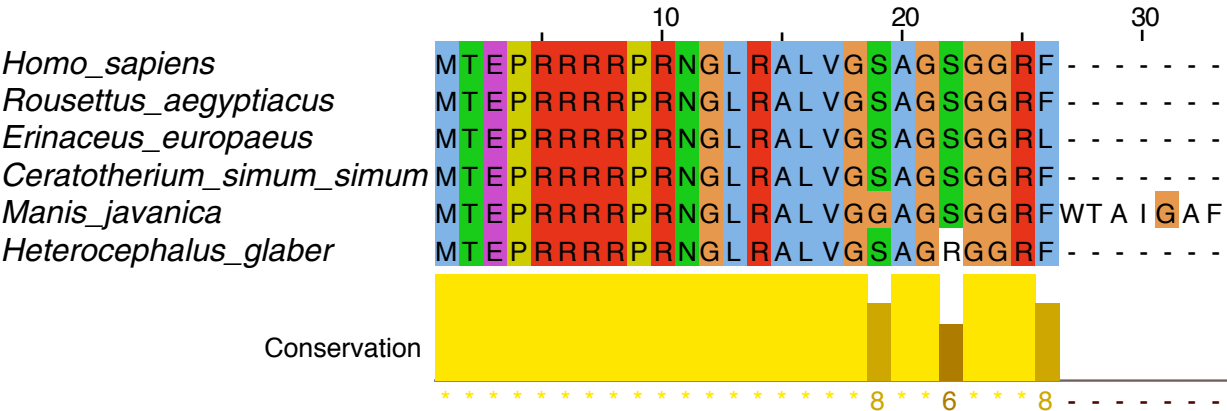
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ENSG00000188554 (NBR1)

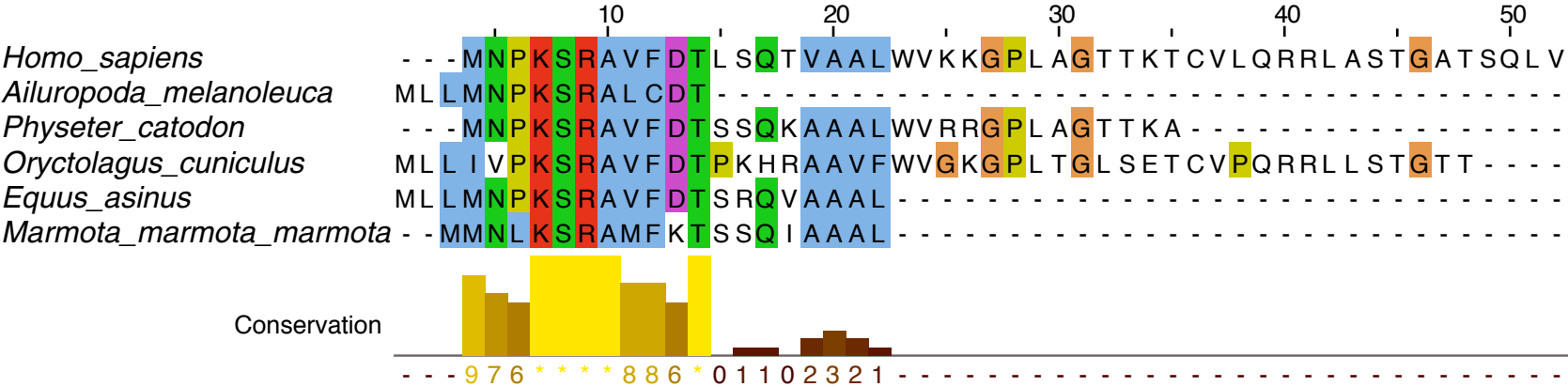


HG0909

ENSG00000189079 (ARID2)

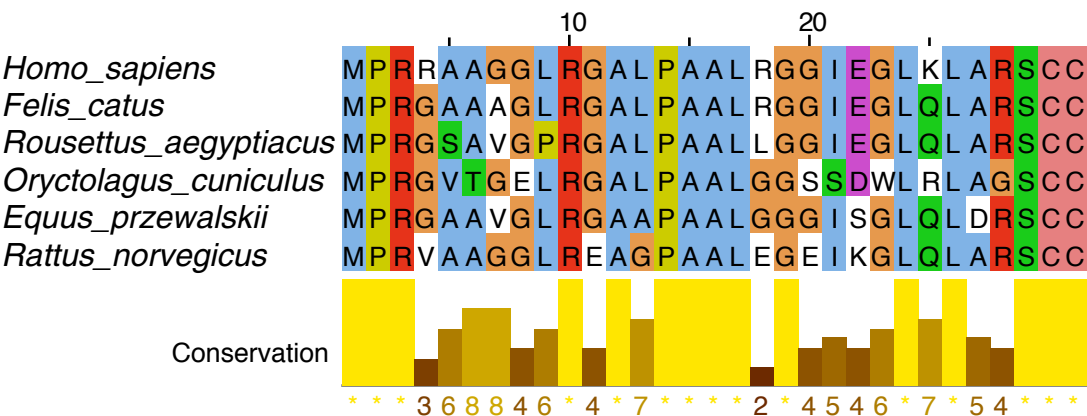


HG0910
ENSG00000197935 (ZNF311)

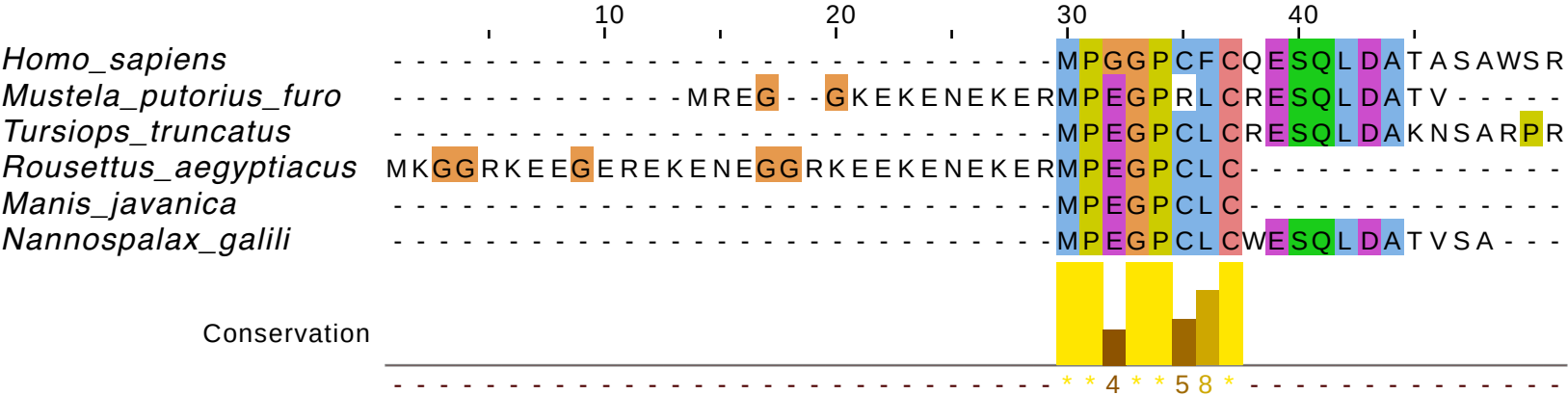


HG0911

ENSG00000198673 (FAM19A2)

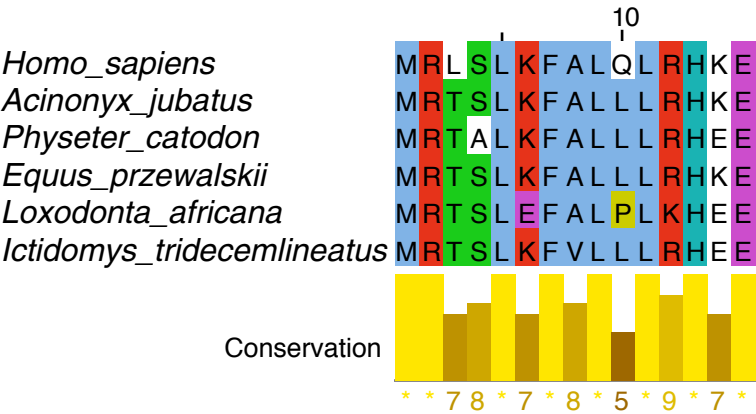


HG0912
ENSG00000198822 (GRM3)



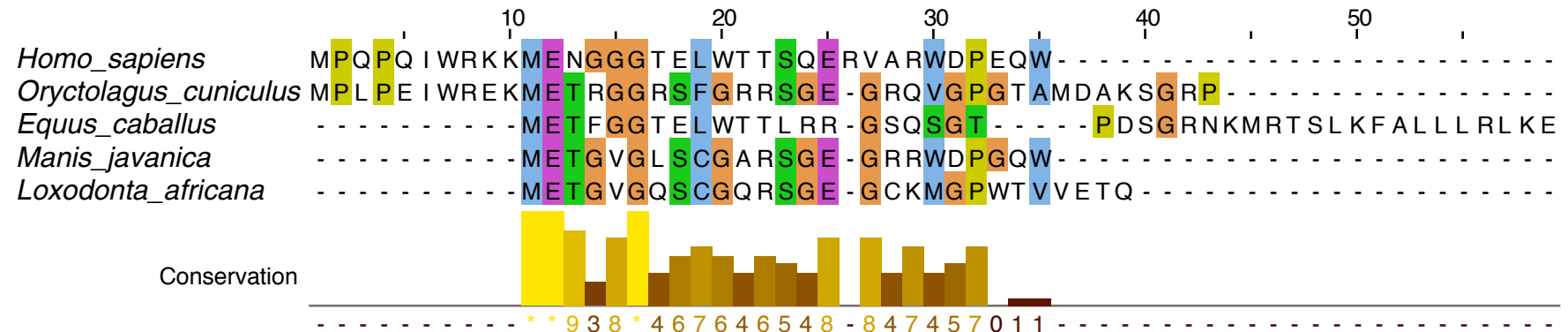
HG0913.1

ENSG00000204599 (TRIM39)



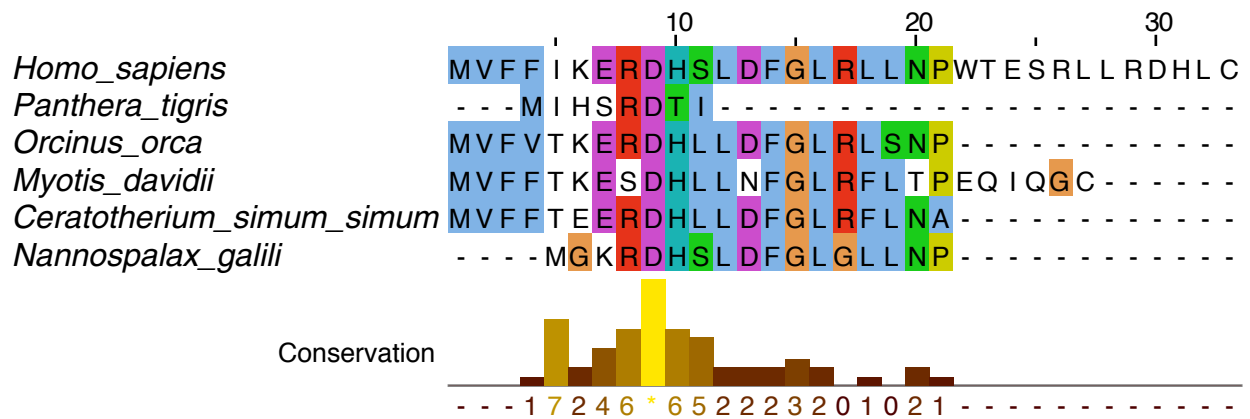
HG0913.2

ENSG00000204599 (TRIM39)



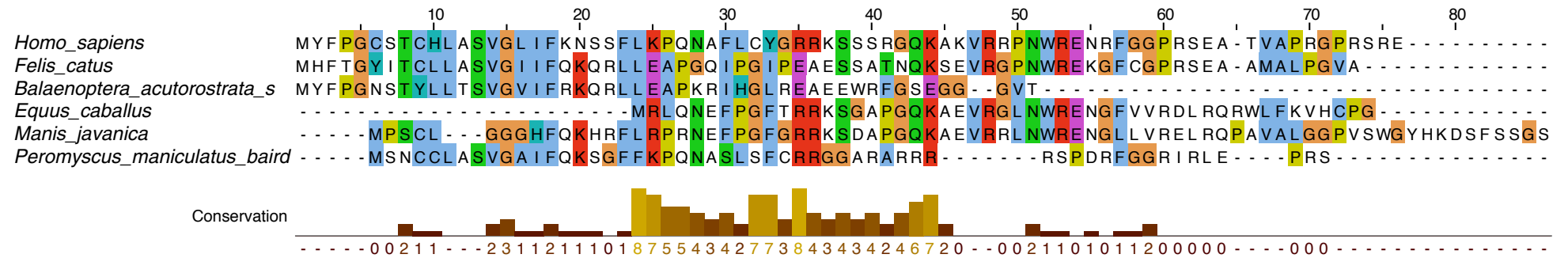
HG0914

ENSG00000227877 (MRLN)

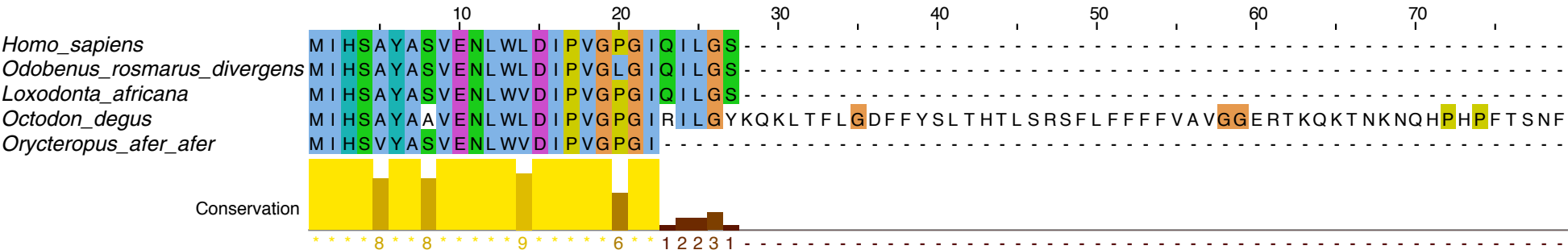


HG0915

ENSG00000254469 (AP002495.2)

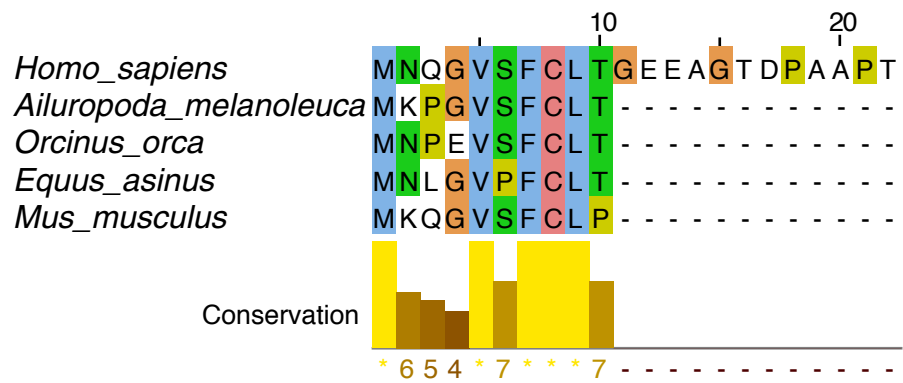


HG0916
ENSG00000020633 (RUNX3)



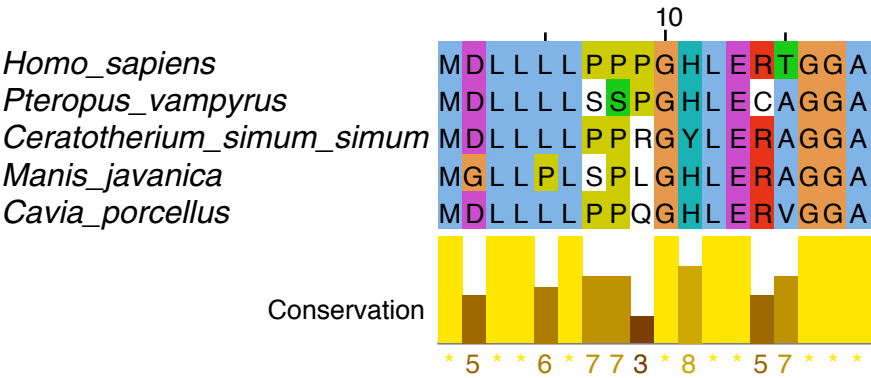
HG0917

ENSG00000042980 (ADAM28)



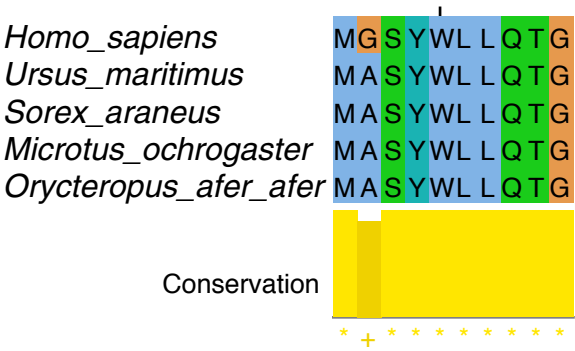
HG0918

ENSG00000047648 (ARHGAP6)



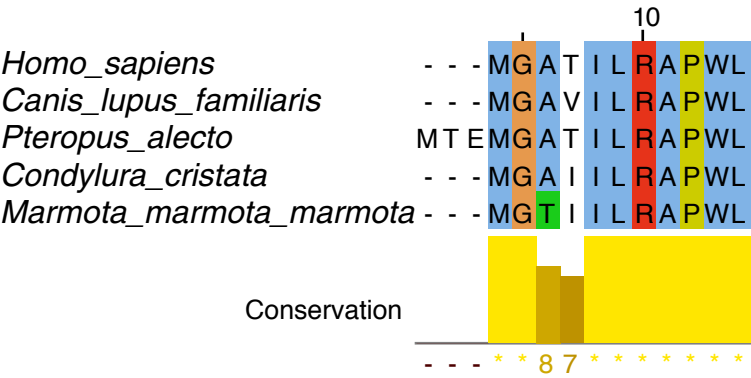
HG0919

ENSG00000051009 (FAM160A2)



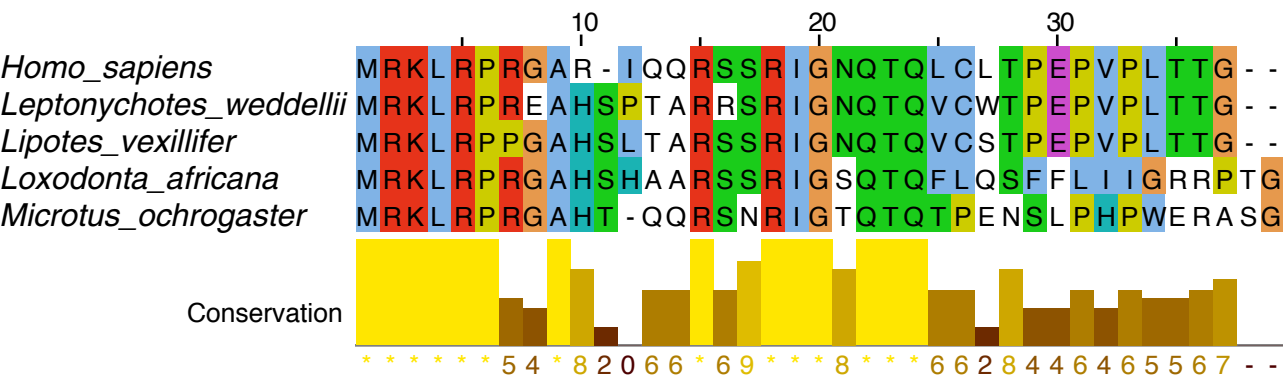
HG0920

ENSG00000051382 (PIK3CB)



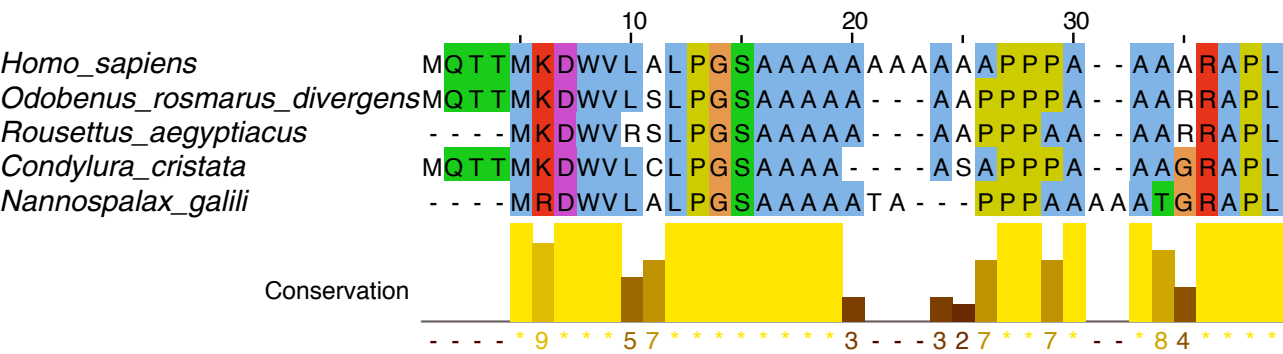
HG0921

ENSG00000058799 (YIPF1)



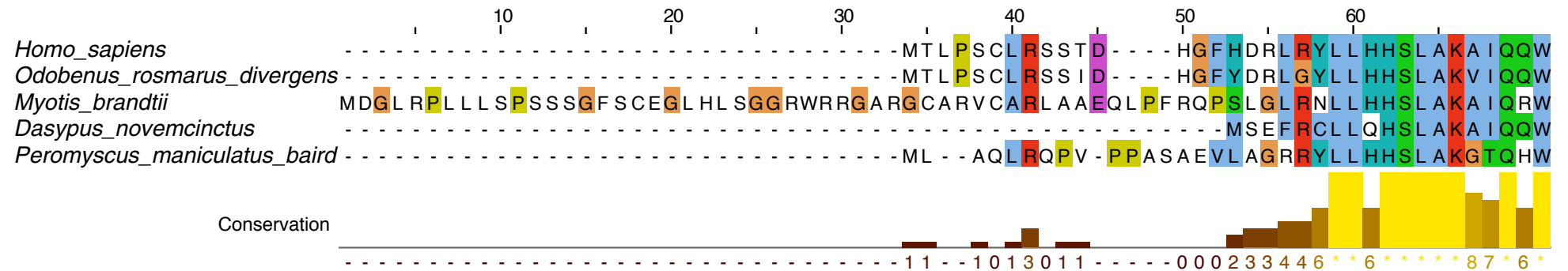
HG0922

ENSG00000079841 (RIMS1)



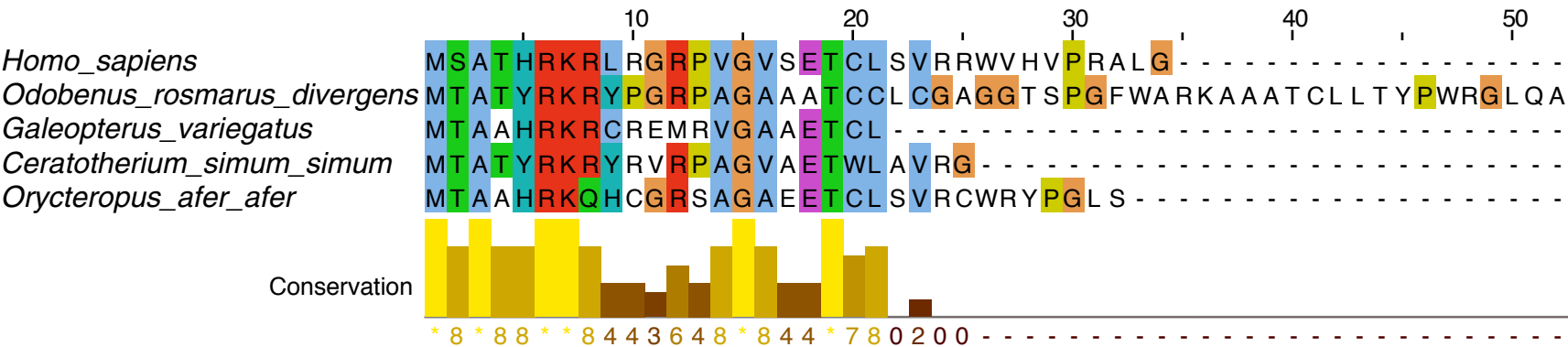
HG0923

ENSG00000081138 (CDH7)



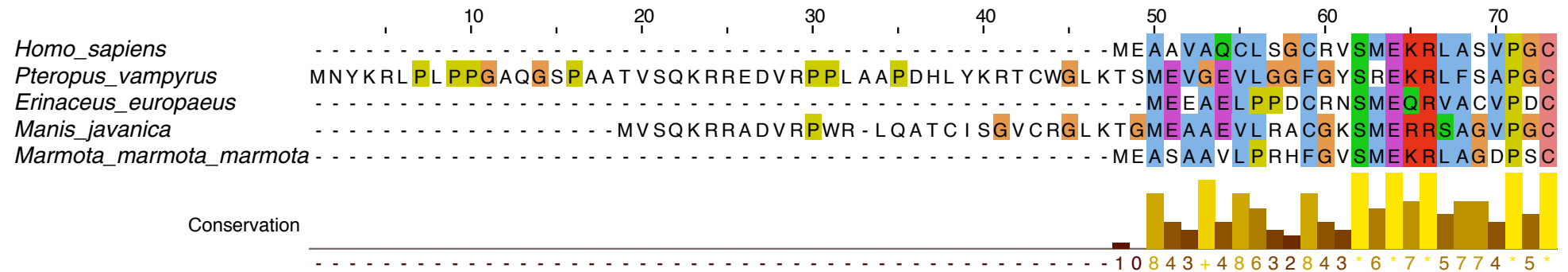
HG0924

ENSG00000081307 (UBA5)



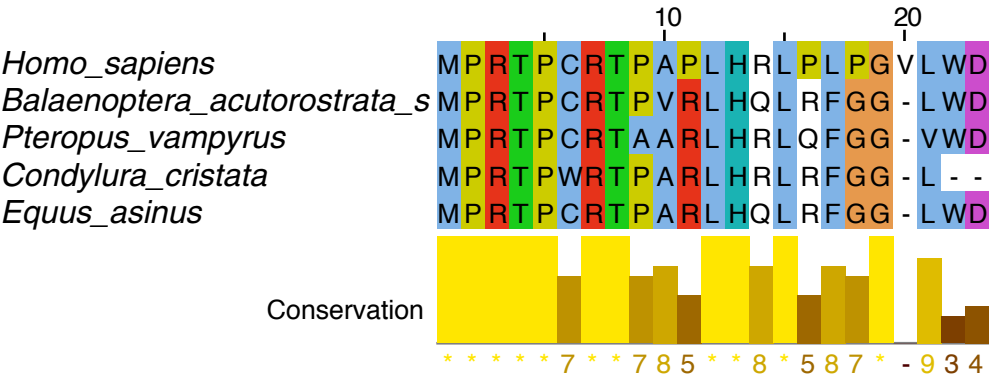
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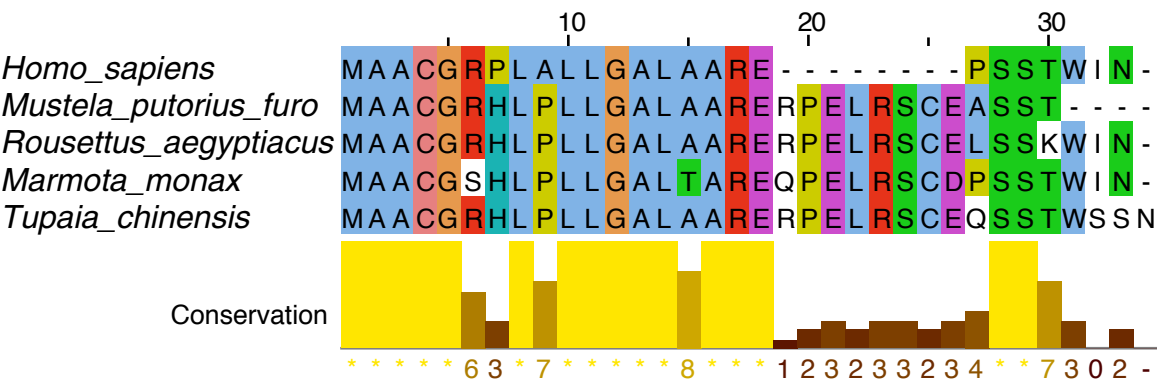
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ENSG00000095397 (WHRN)



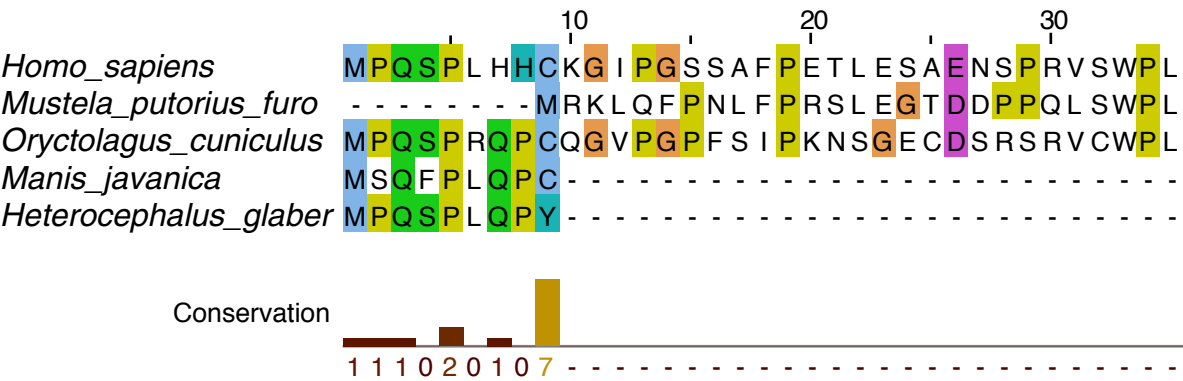
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ENSG00000095951 (HIVEP1)



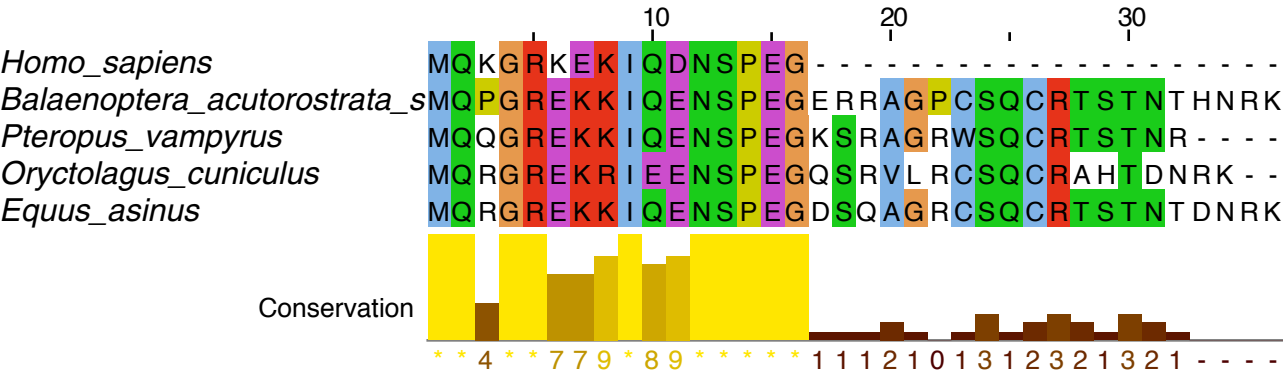
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ENSG00000102057 (KCND1)



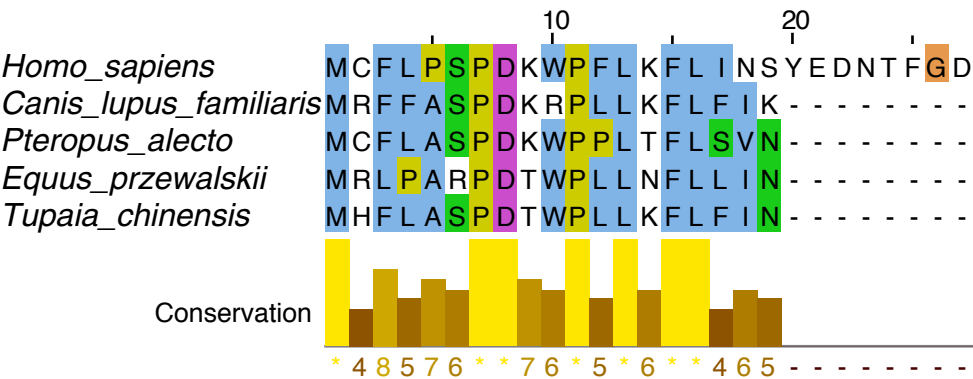
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ENSG00000102524 (TNFSF13B)



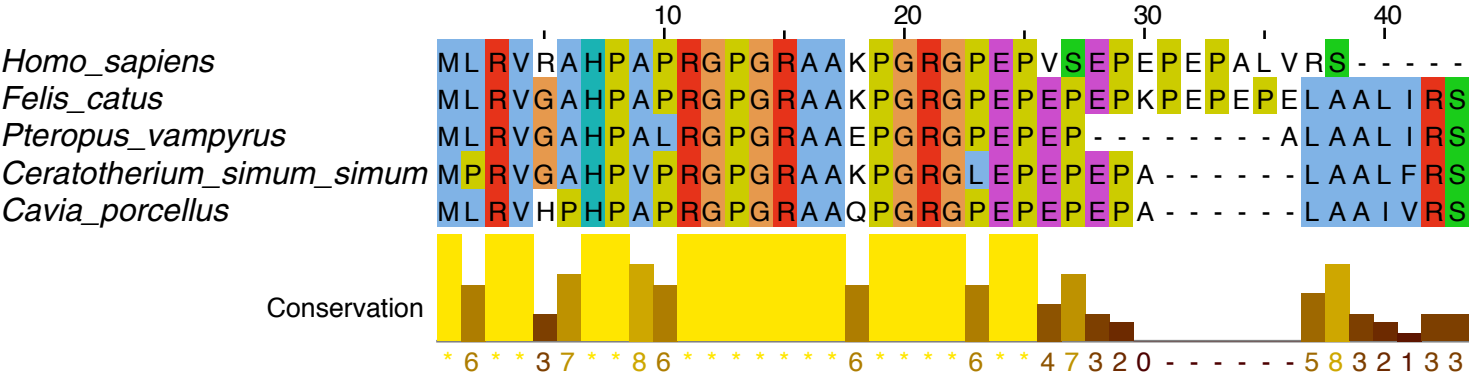
HG0931

ENSG00000104951 (IL4I1)



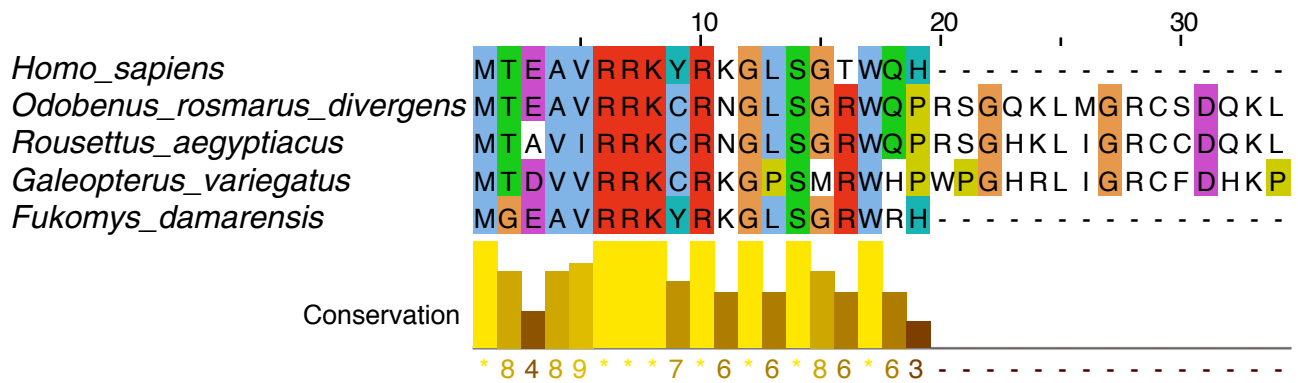
HG0932

ENSG00000105997 (HOXA3)



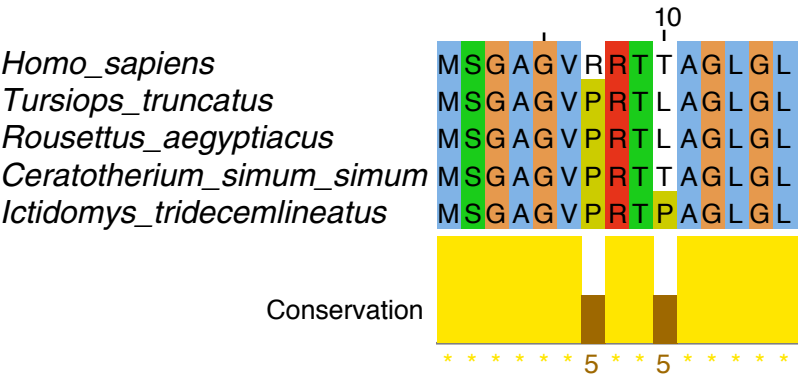
HG0933

ENSG00000106330 (MOSPD3)

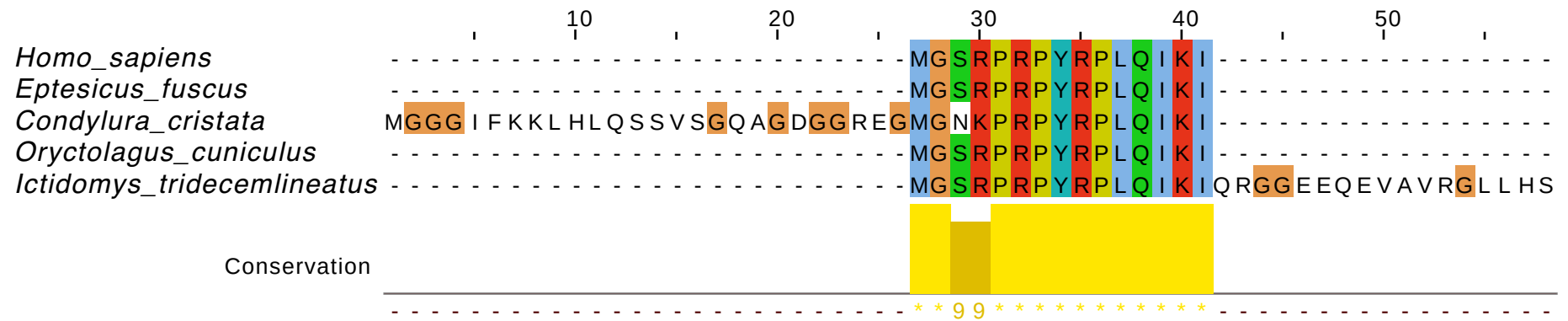


HG0934

ENSG00000107443 (CCNJ)

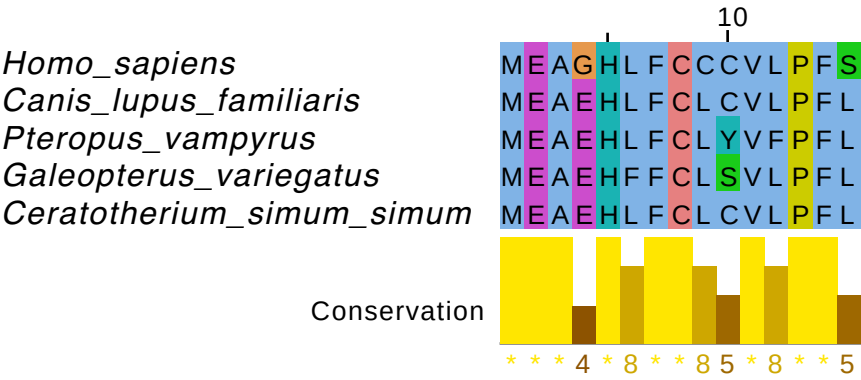


ENSG00000108518 (PFN1)



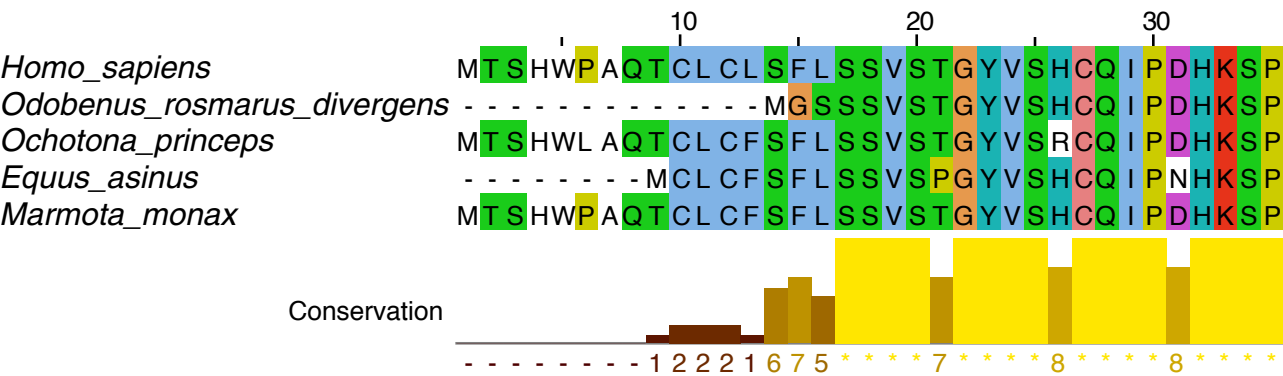
HG0936

ENSG00000108799 (EZH1)



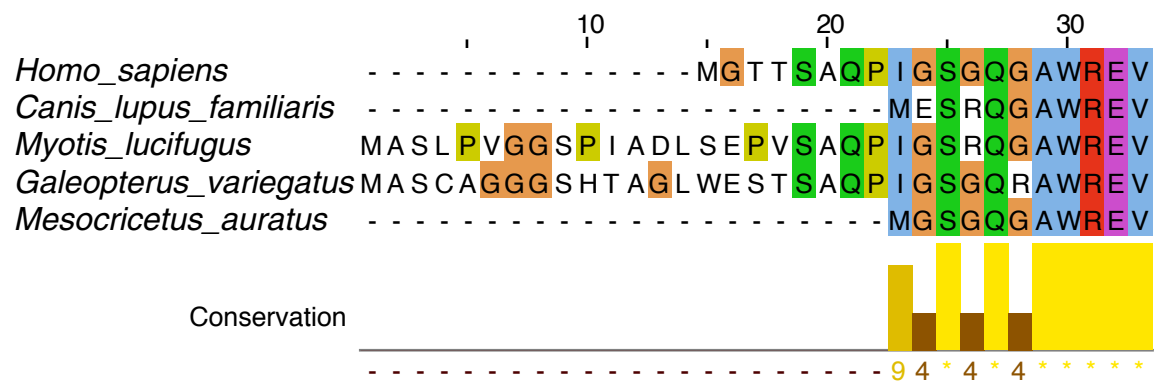
HG0937

ENSG00000109846 (CRYAB)

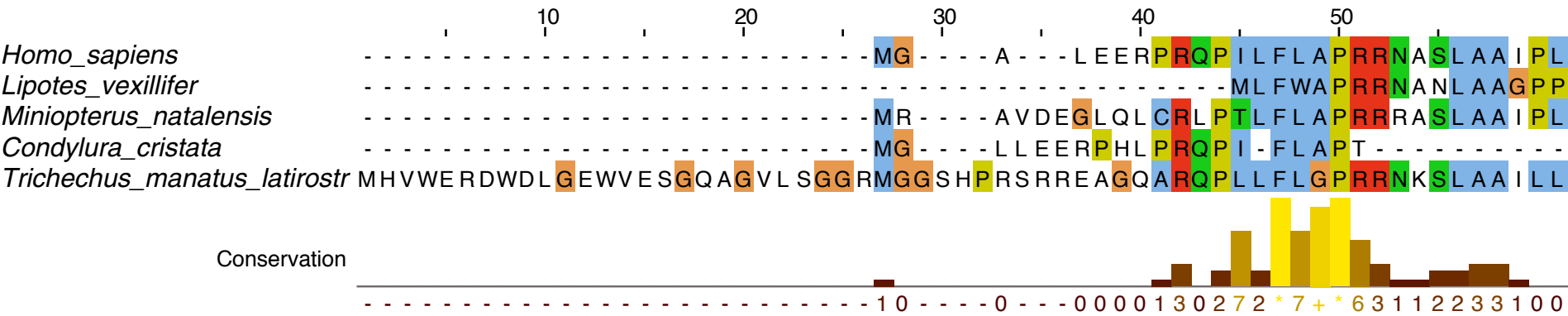


HG0938

ENSG00000111665 (CDCA3)

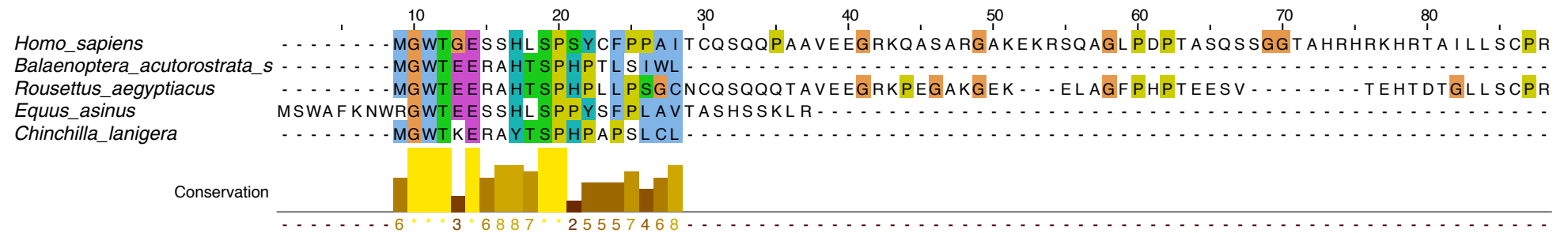


HG0939
ENSG00000111674 (ENO2)



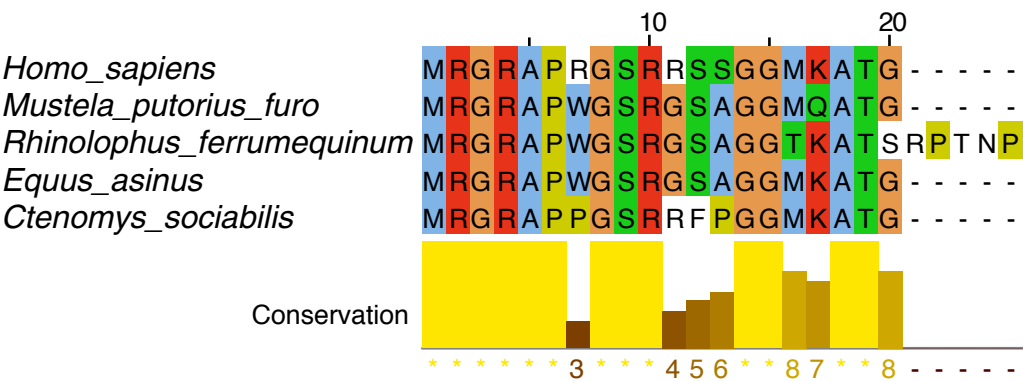
HG0940

ENSG00000115556 (PLCD4)



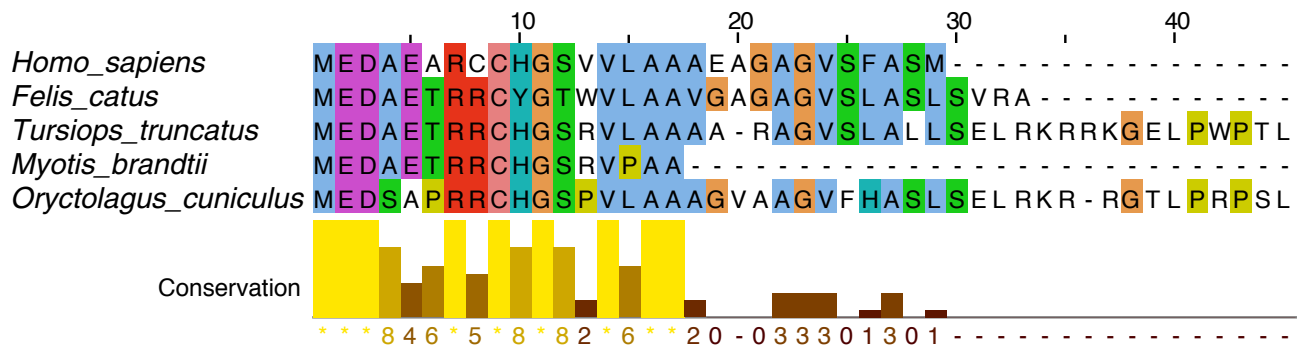
HG0941

ENSG00000116285 (ERRFI1)

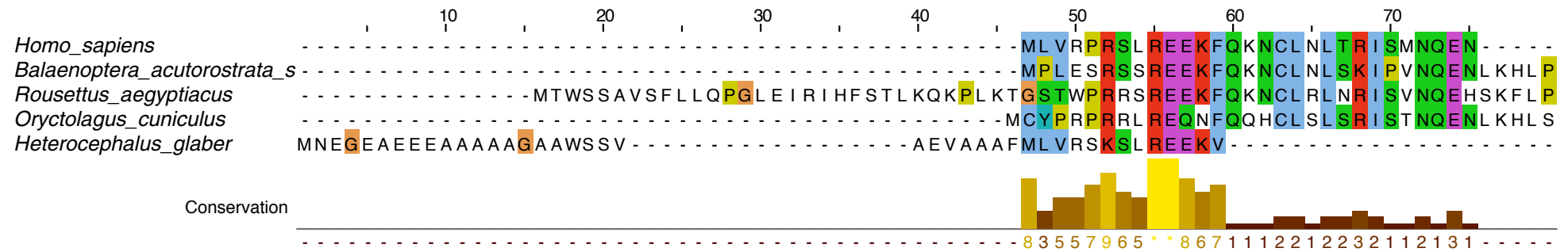


HG0942

ENSG00000117477

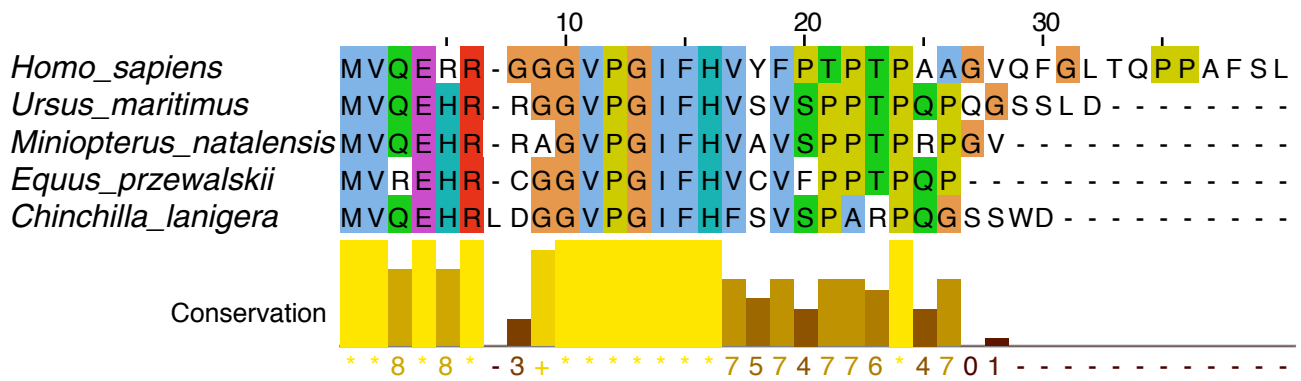


ENSG00000120690 (ELF1)



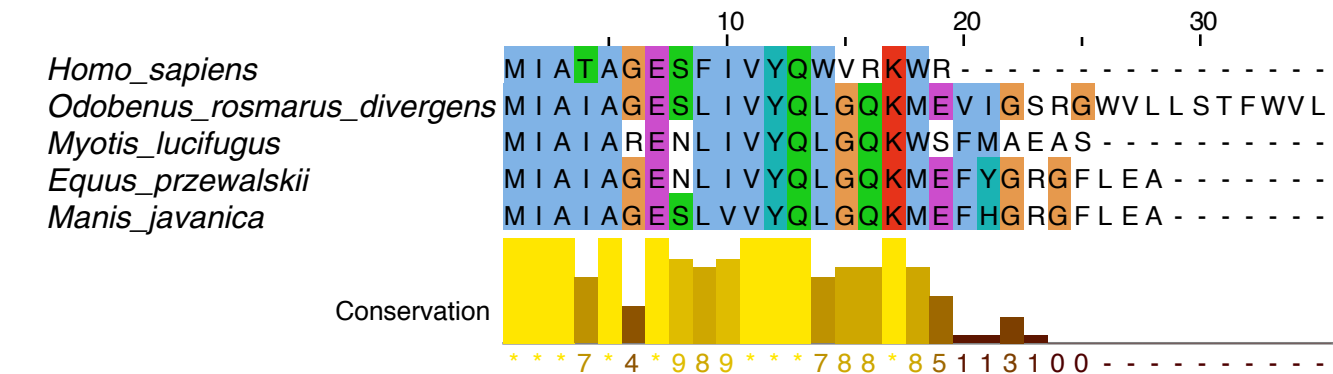
HG0944

ENSG00000120833 (SOCS2)



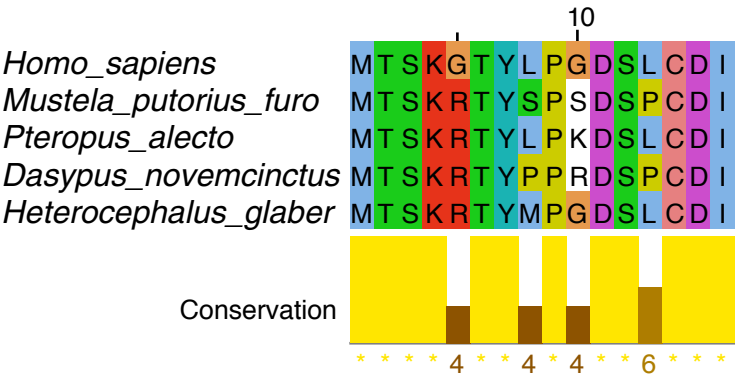
HG0945

ENSG00000124782 (RREB1)



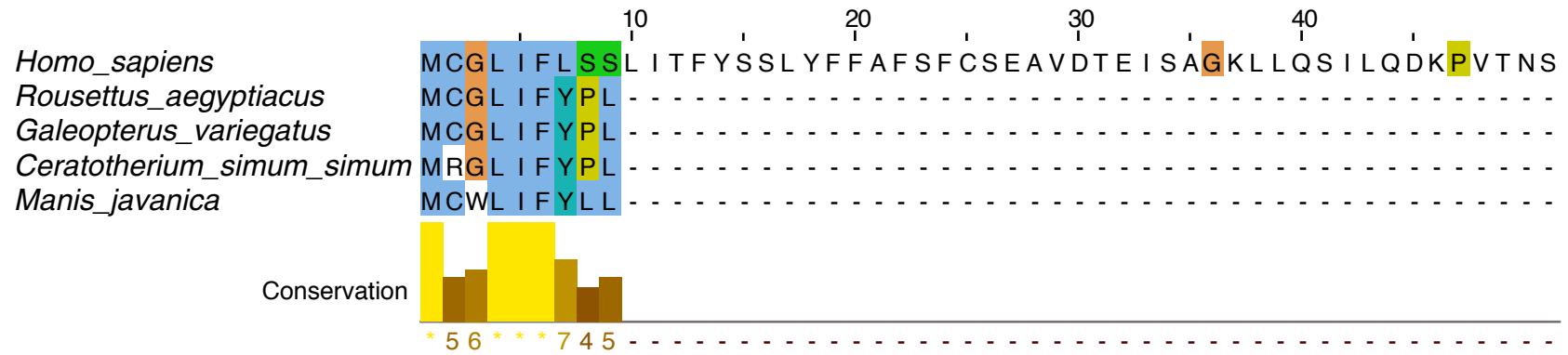
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ENSG00000127324 (TSPAN8)

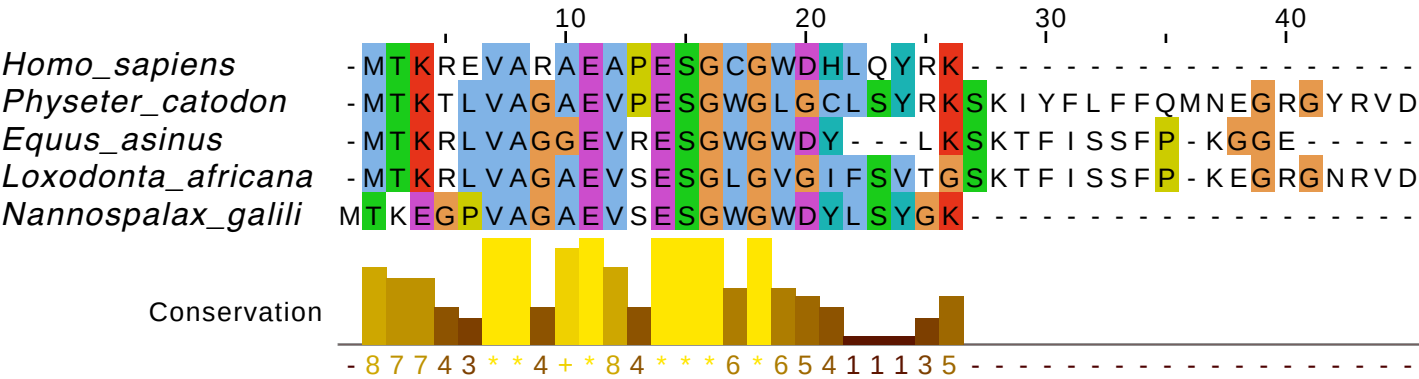


HG0946.2

ENSG00000127324 (TSPAN8)

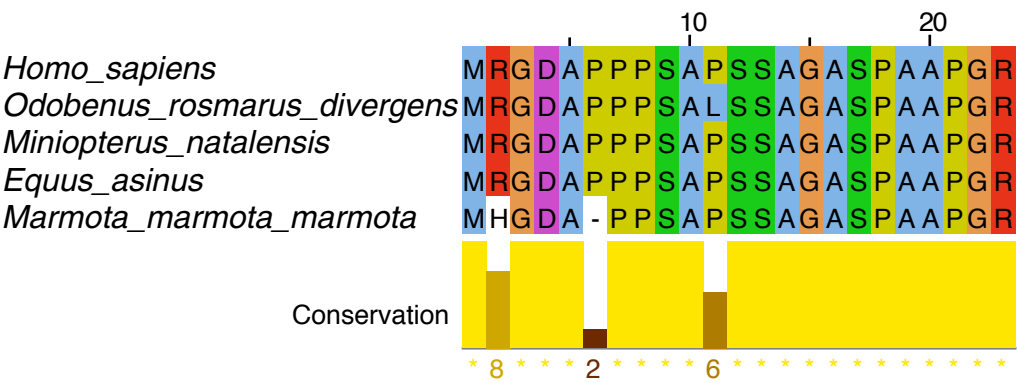


HG0947
ENSG00000129226 (CD68)



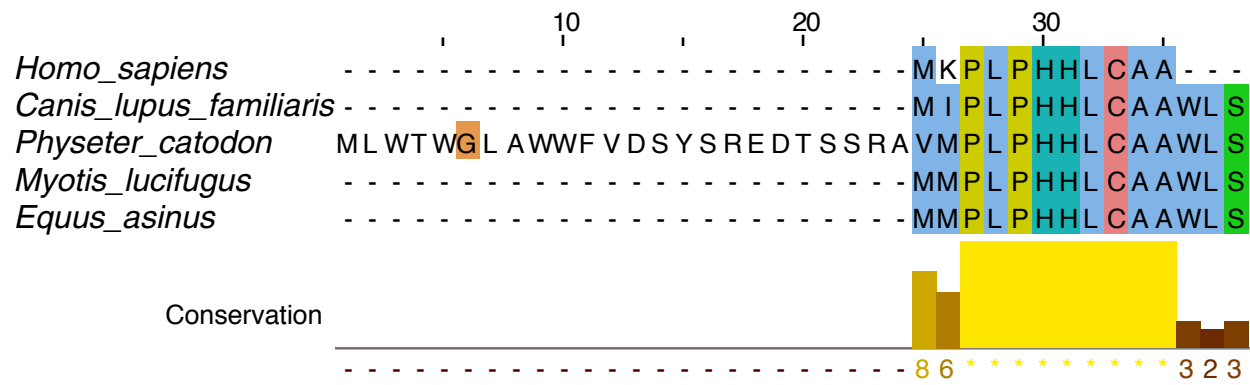
HG0948

ENSG00000129595 (EPB41L4A)



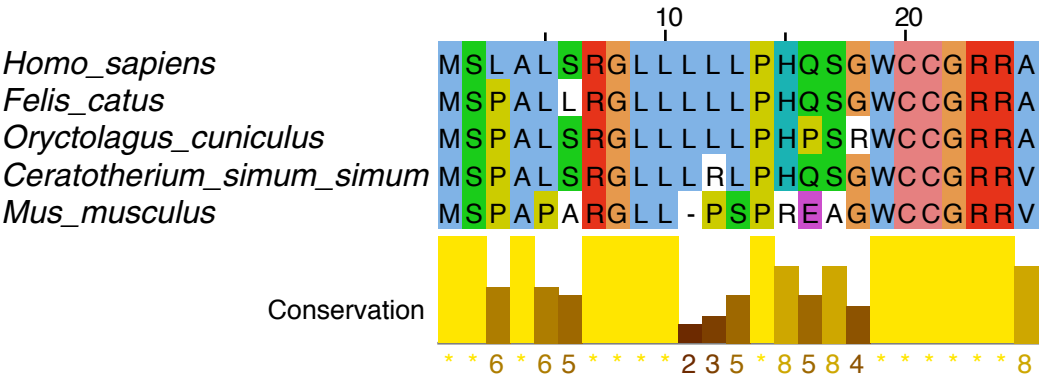
HG0949

ENSG00000131381 (RBSN)



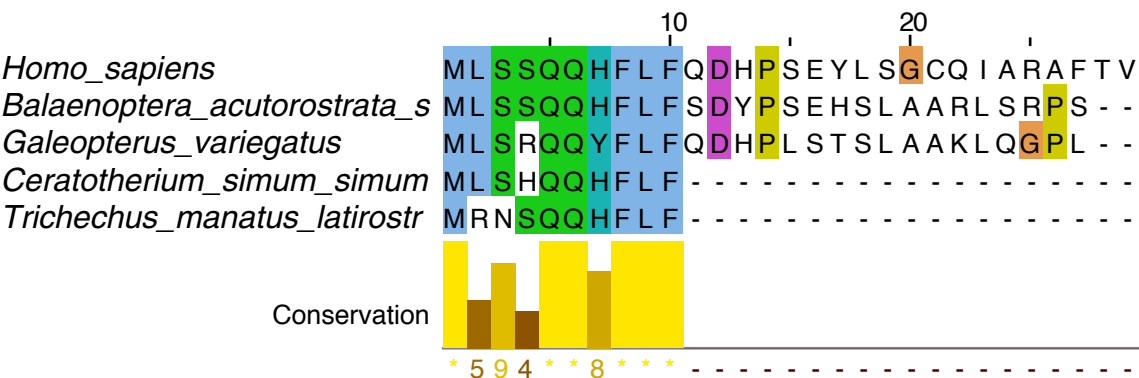
HG0950

ENSG00000132964 (CDK8)



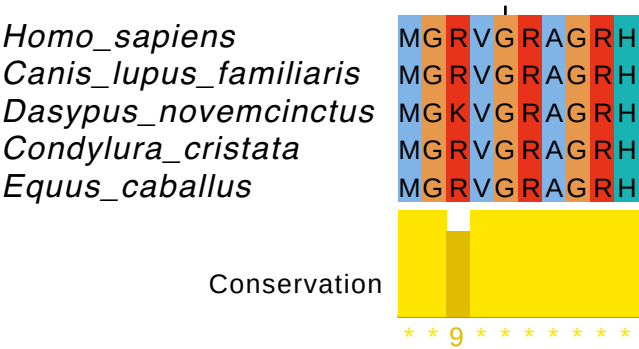
HG0951

ENSG00000134061 (CD180)



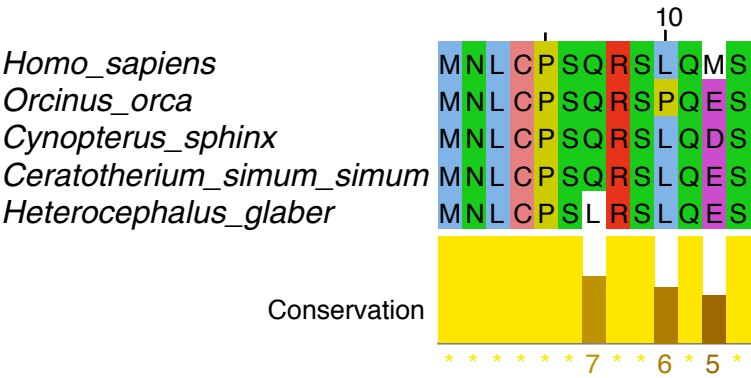
HG0952

ENSG00000134453 (RBM17)



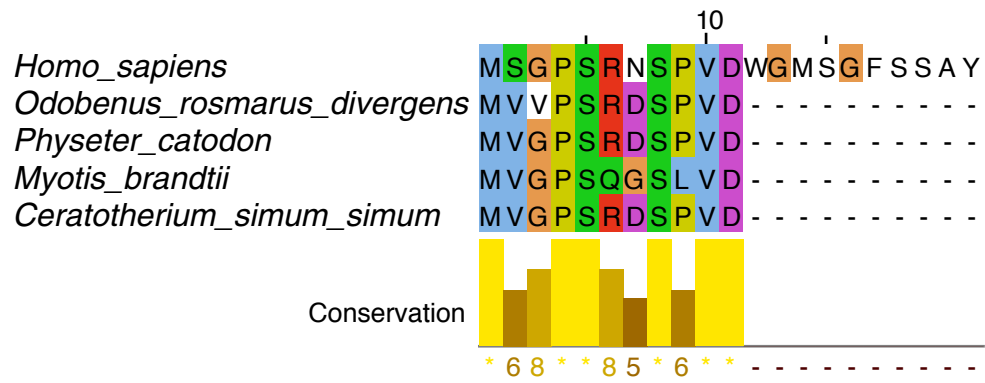
HG0953

ENSG00000134815 (DHX34)



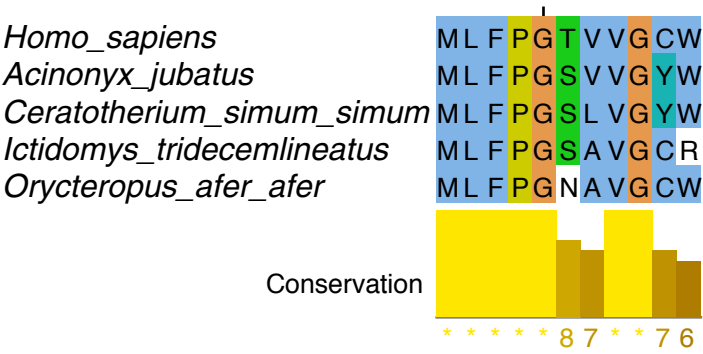
HG0954

ENSG00000134874 (DZIP1)



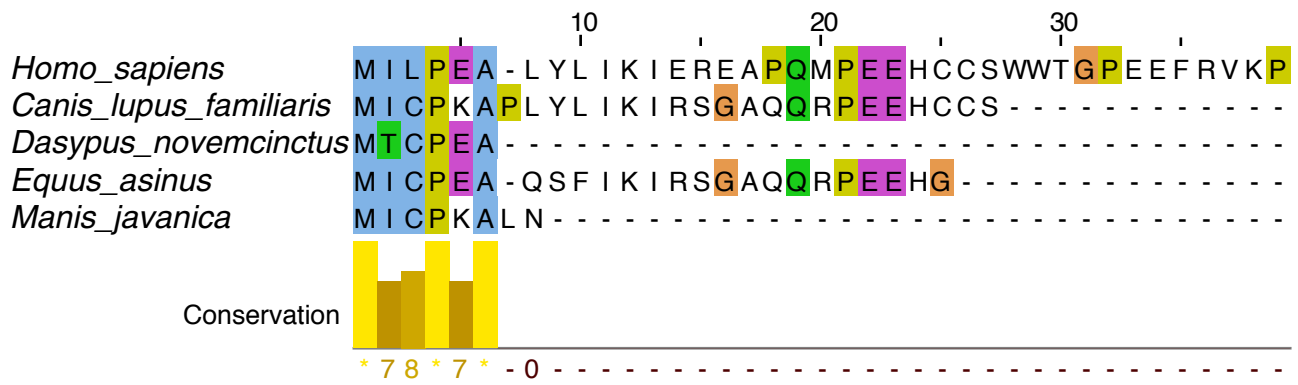
HG0955

ENSG00000134982 (APC)

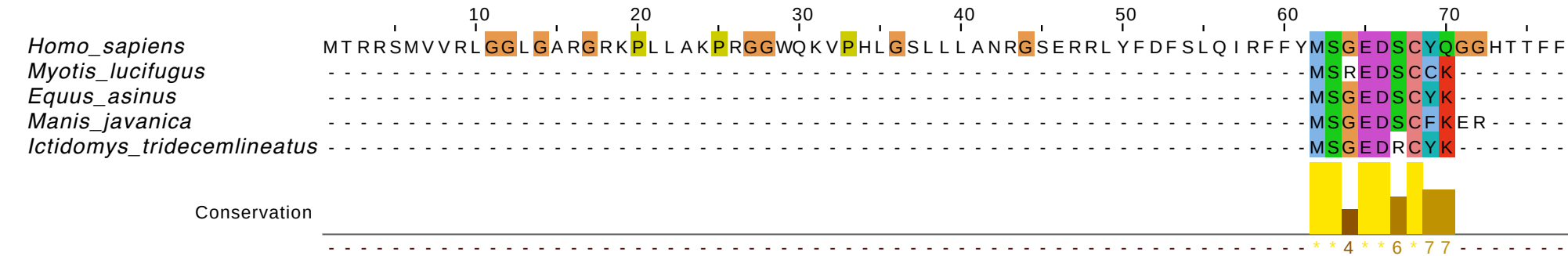


HG0956

ENSG00000136235 (GPNMB)

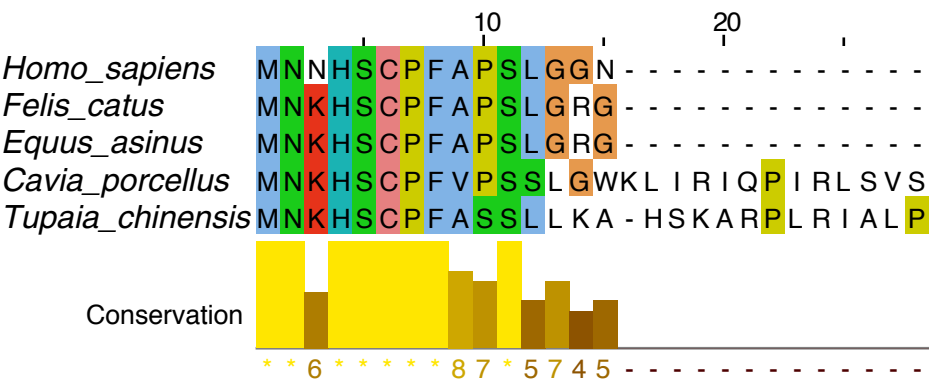


HG0957
ENSG00000136874 (STX17)

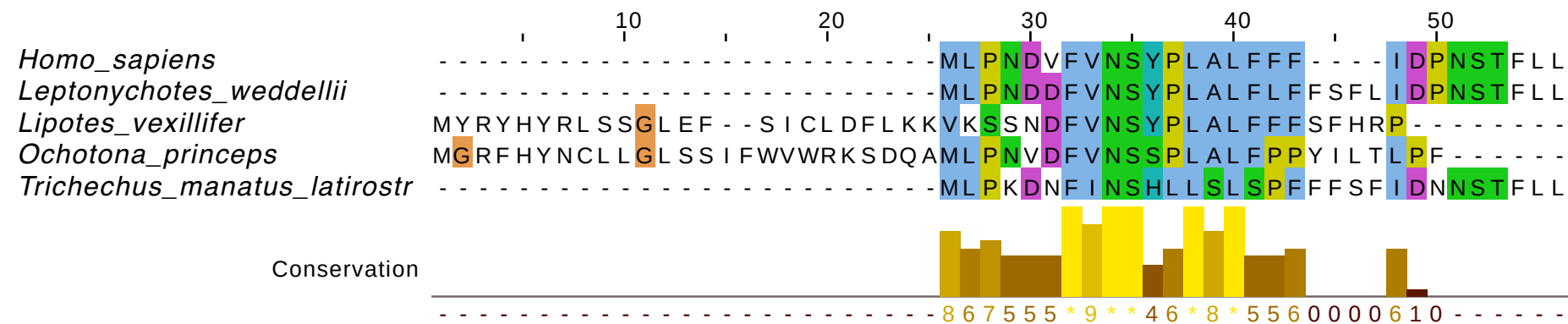


HG0958

ENSG00000137497 (NUMA1)

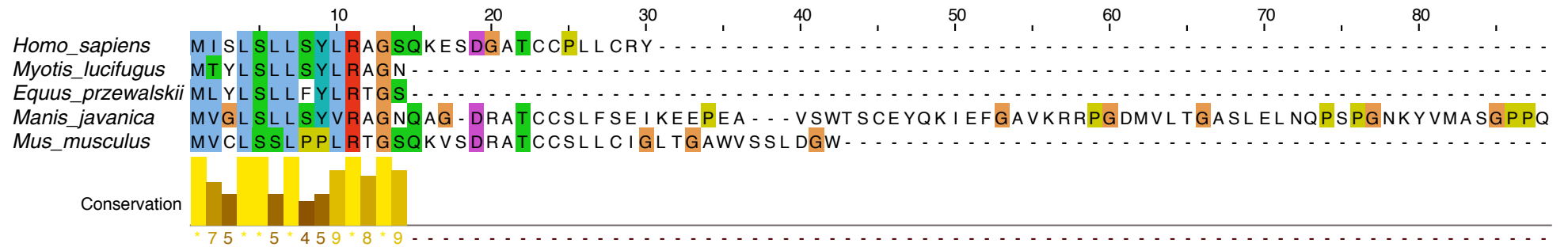


HG0959
ENSG00000137558 (PI15)



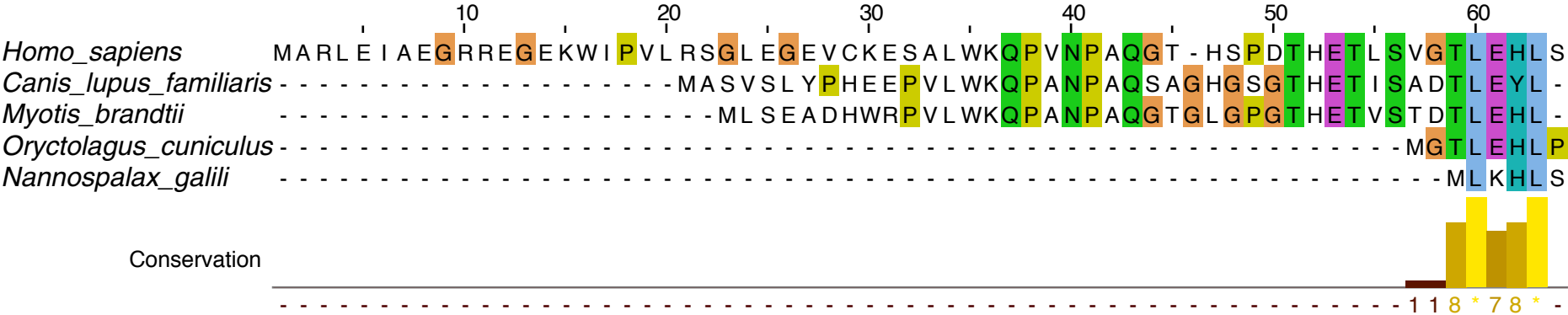
HG0960

ENSG00000140297 (GCNT3)



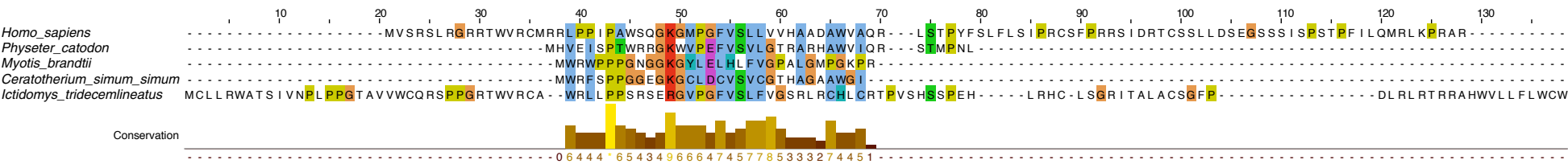
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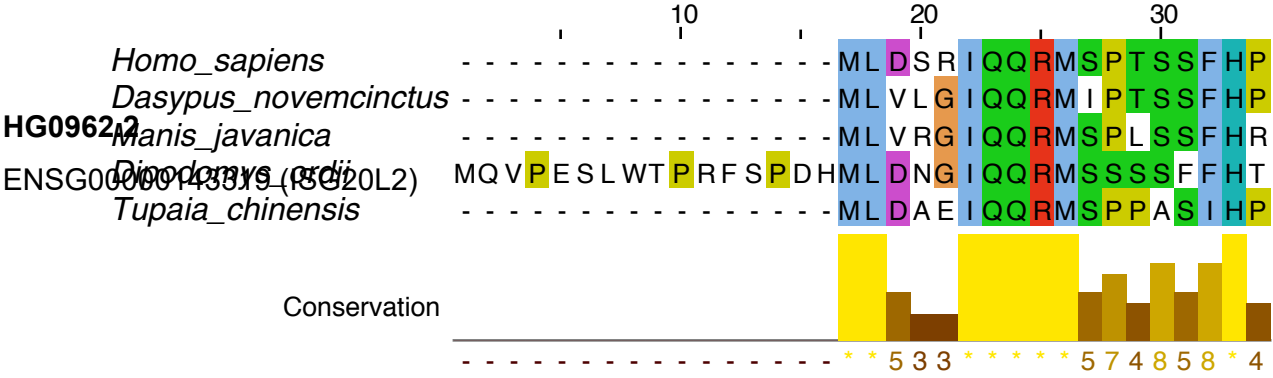
ENSG00000140853 (NLRC5)



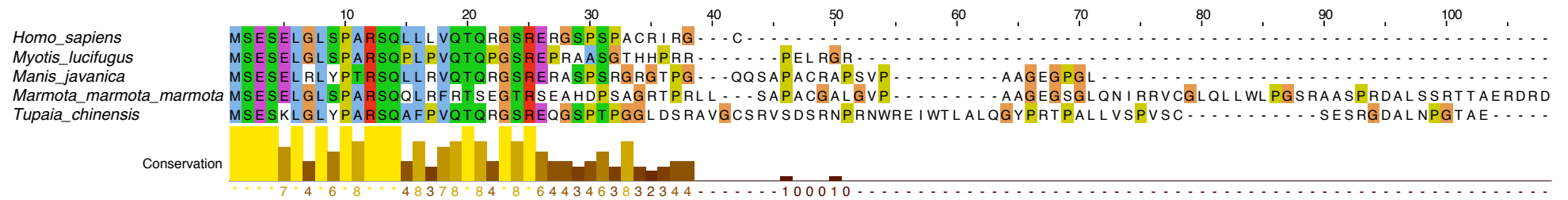
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ENSG00000143319 (ISG20L2)



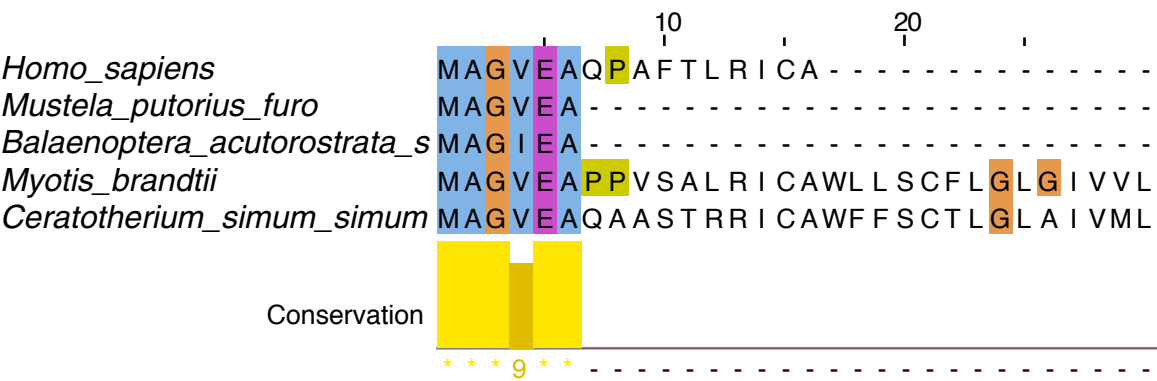


ENSG00000143867 (OSR1)



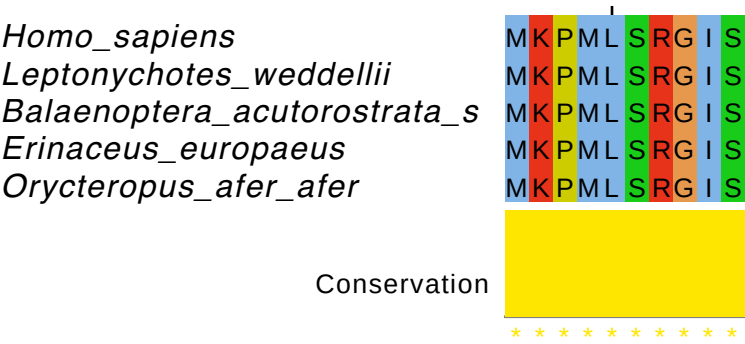
HG0964

ENSG00000145246 (ATP10D)



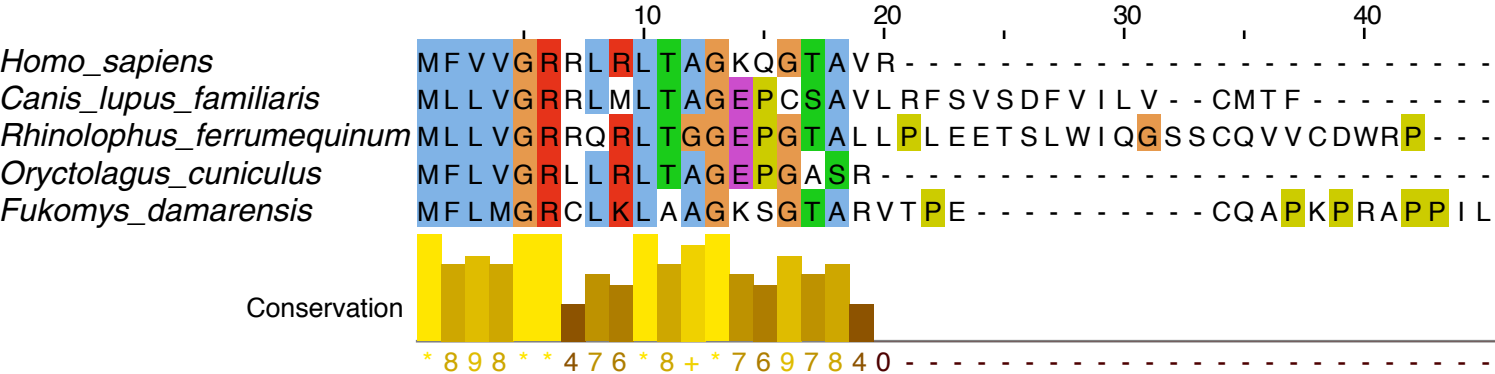
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ENSG00000146006 (LRRTM2)



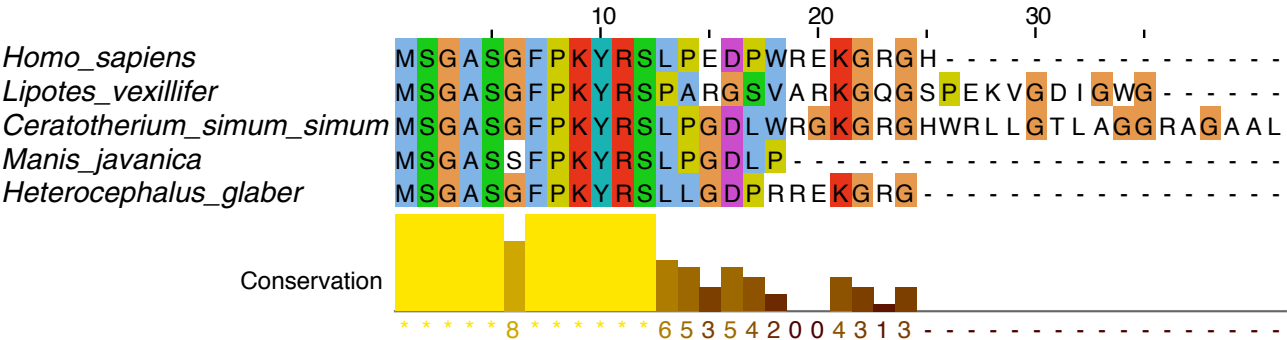
HG0966

ENSG00000148356 (LRSAM1)



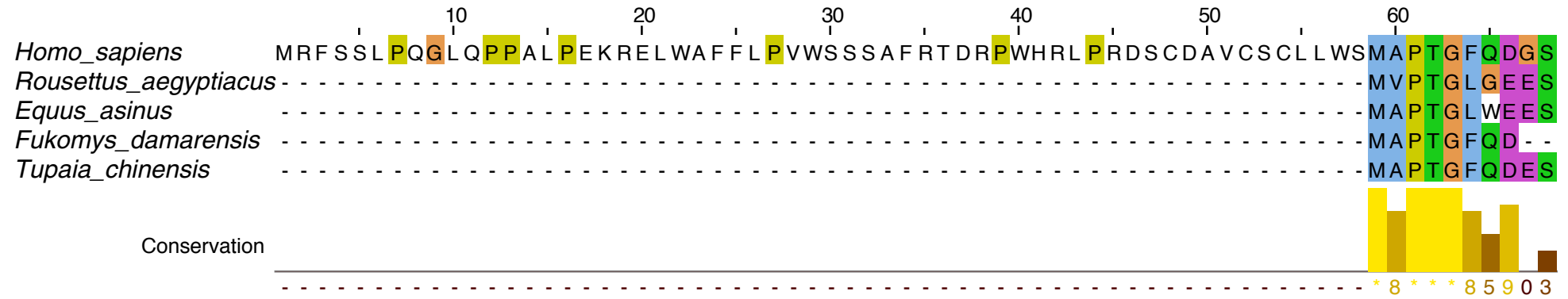
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ENSG00000149925 (ALDOA)



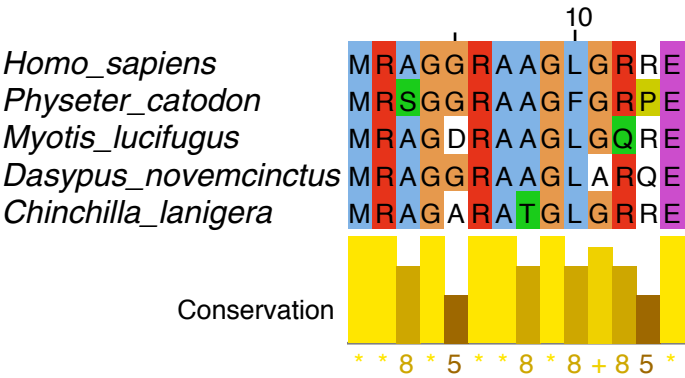
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ENSG00000154319 (FAM167A)



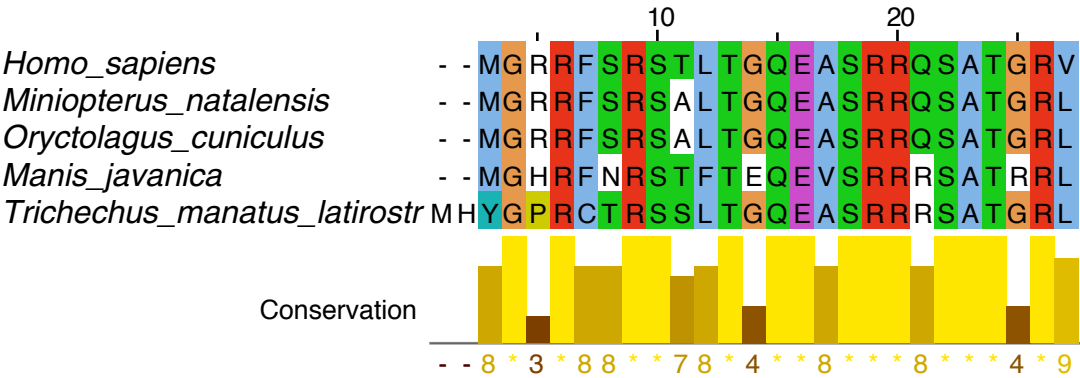
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ENSG00000154645 (CHODL)



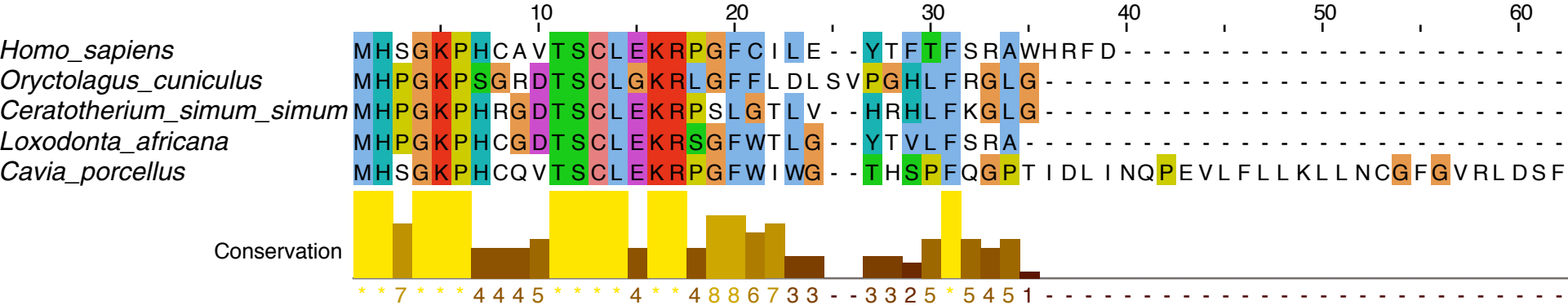
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ENSG00000154727 (GABPA)

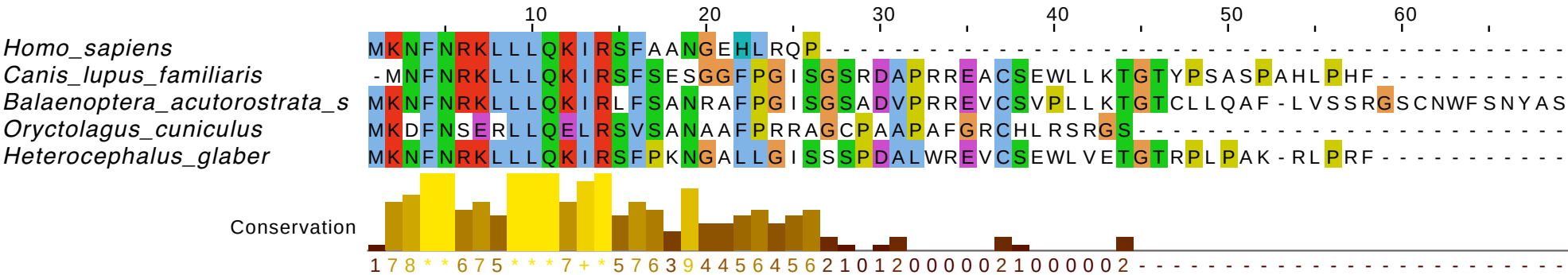


HG0971

ENSG00000155592 (ZKSCAN2)

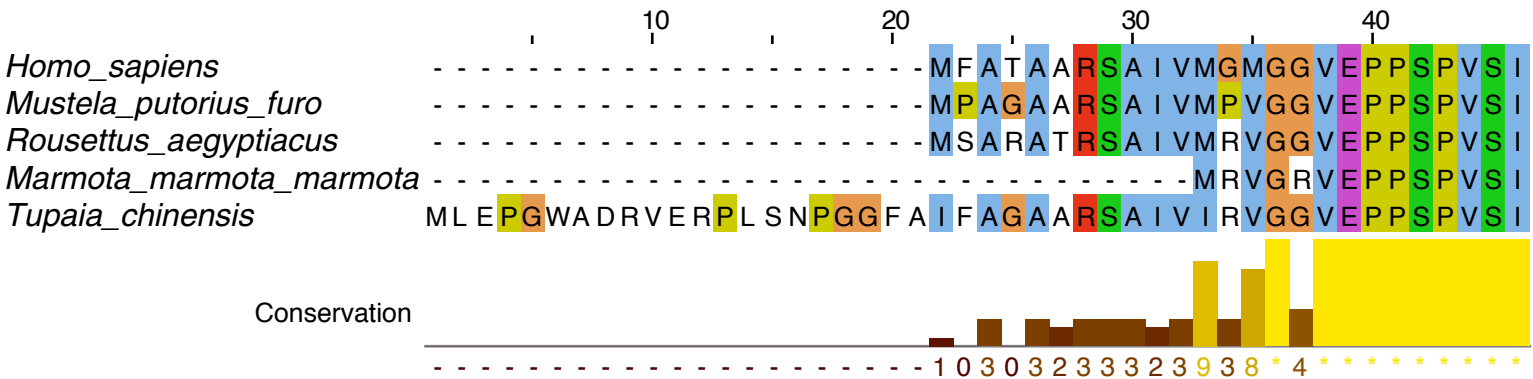


HG0972
ENSG00000155926 (SLA)



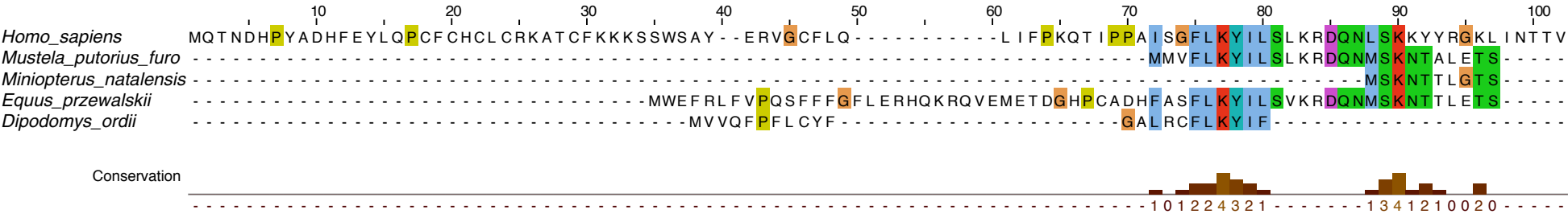
HG0973

ENSG00000156535 (CD109)



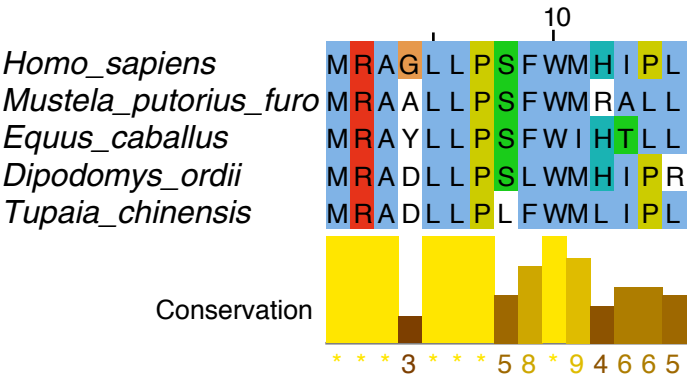
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ENSG00000157578 (LCA5L)



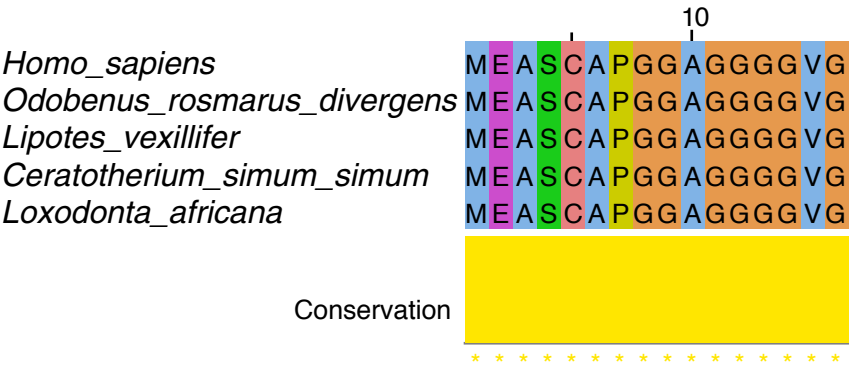
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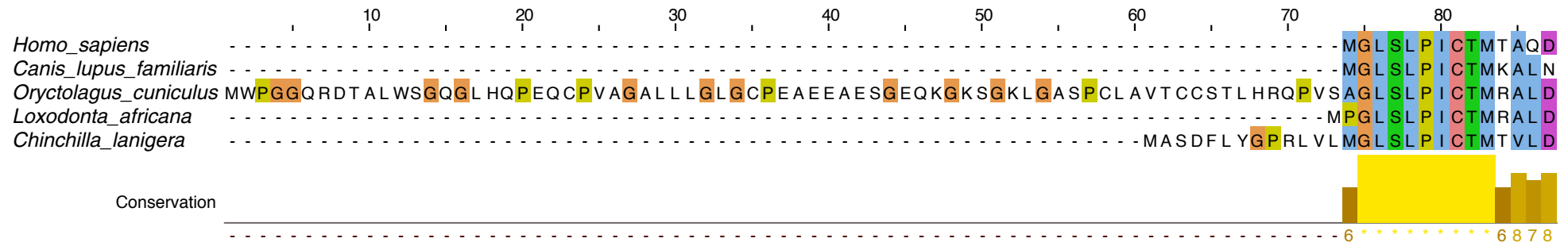
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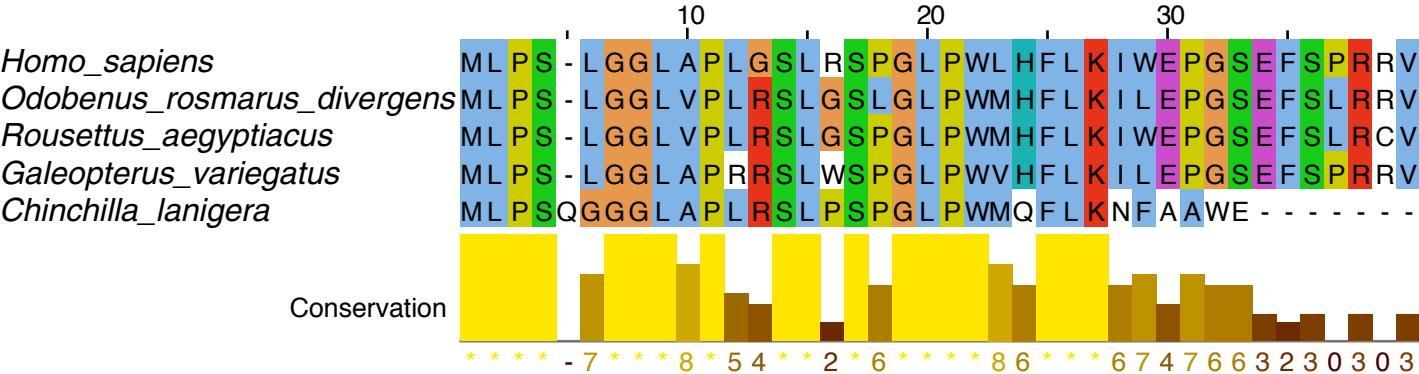


HG0976

ENSG00000158008 (EXTL1)

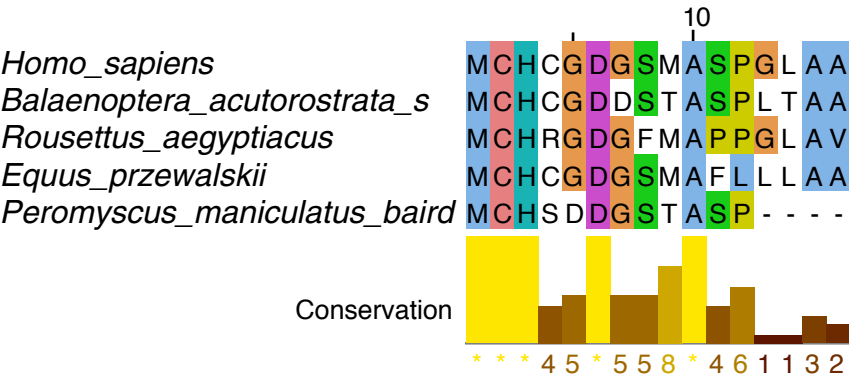


HG0977
ENSG00000158321 (AUTS2)



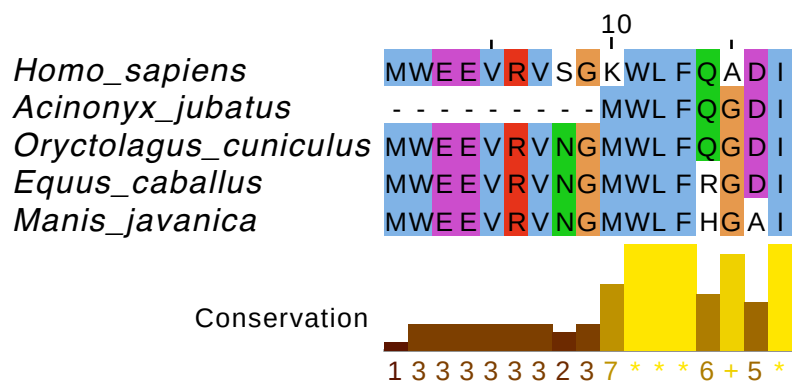
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ENSG00000159023 (EPB41)



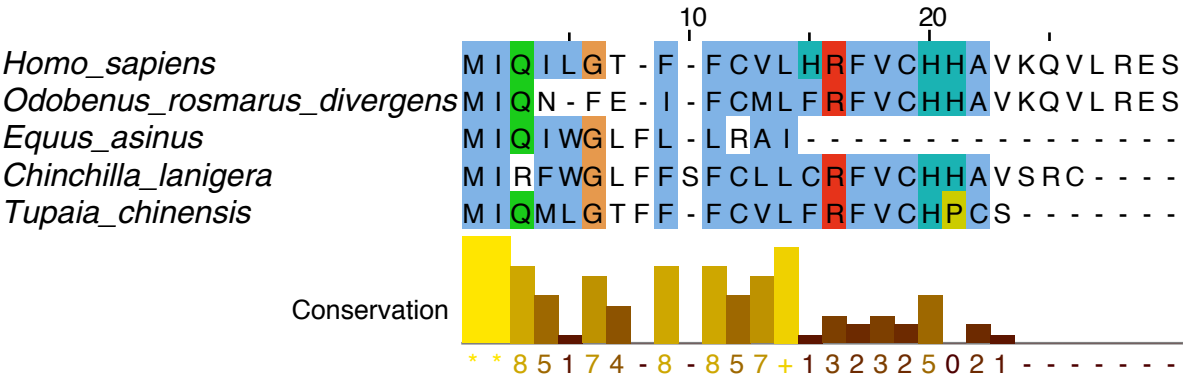
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ENSG00000159202 (UBE2Z)



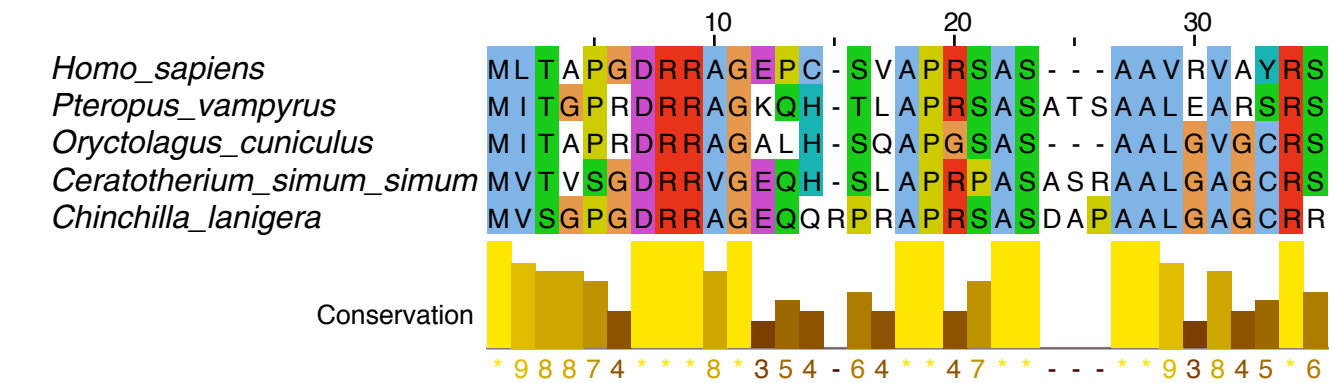
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ENSG00000162670 (BRINP3)



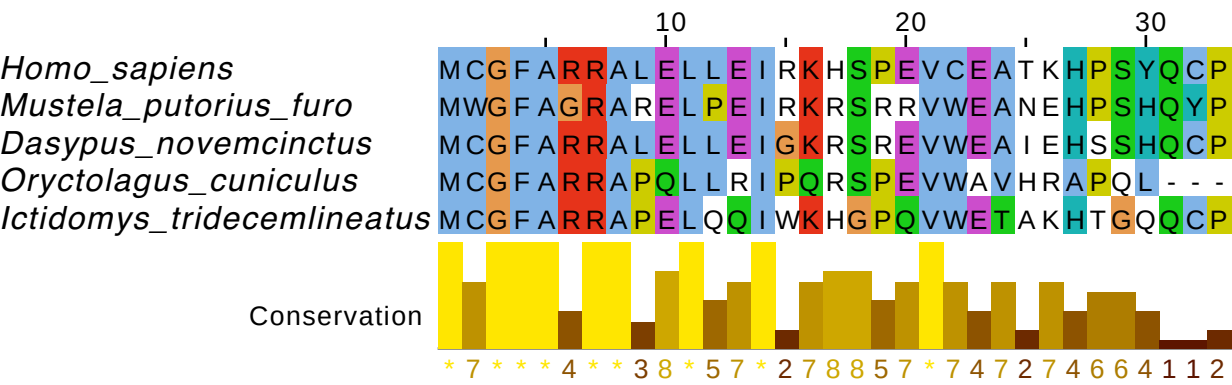
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ENSG00000163629 (PTPN13)



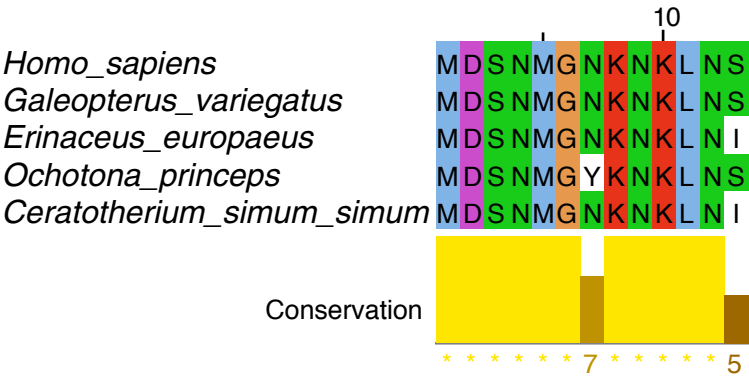
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ENSG00000164116 (GUCY1A3)



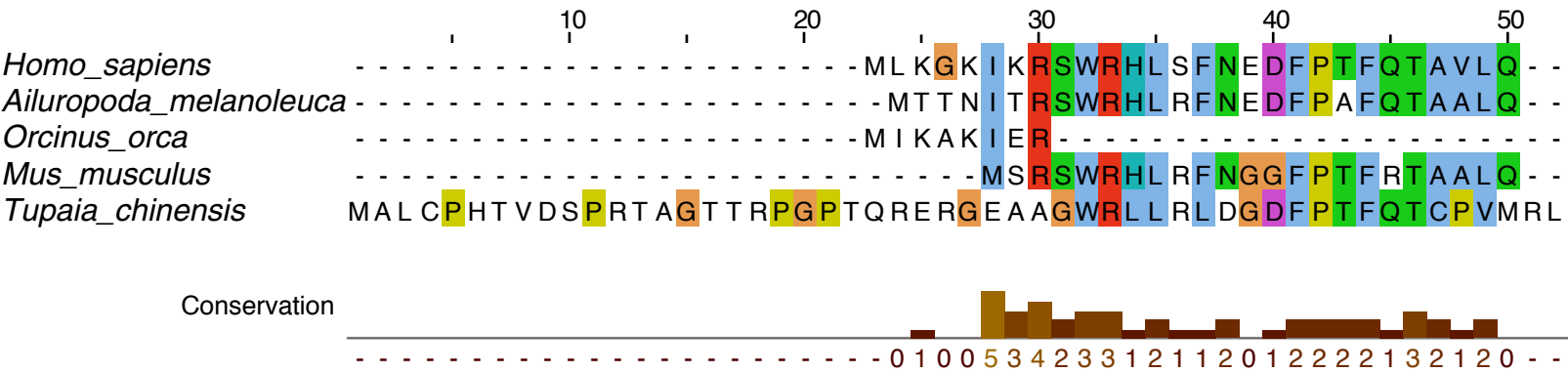
HG0983

ENSG00000164128 (NPY1R)



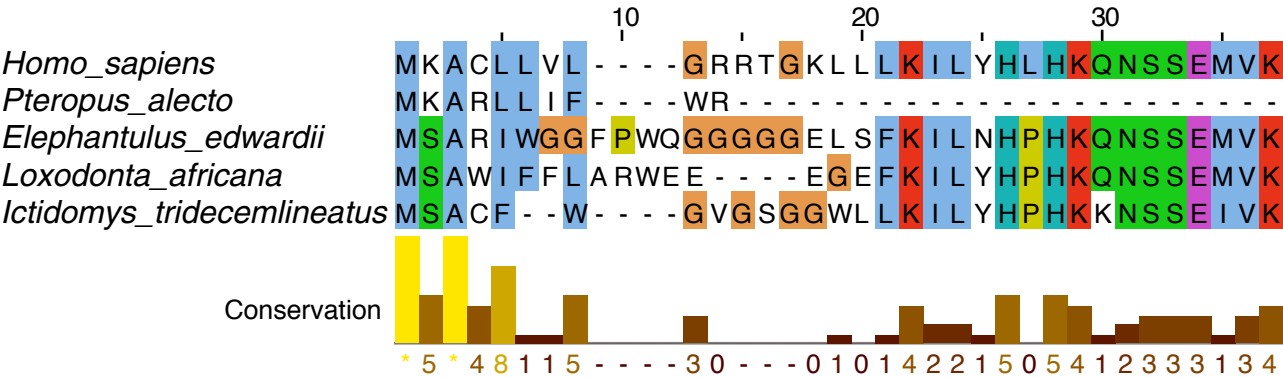
HG0984

ENSG00000164185 (ZNF474)



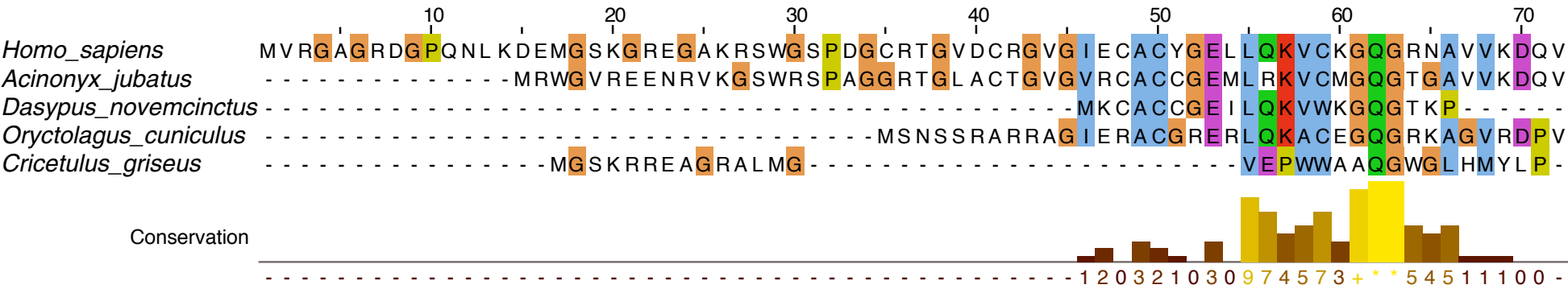
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ENSG00000164604 (GPR85)



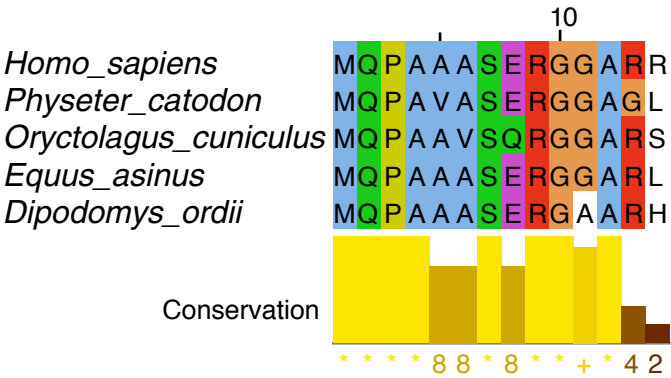
HG0986

ENSG00000164663 (USP49)

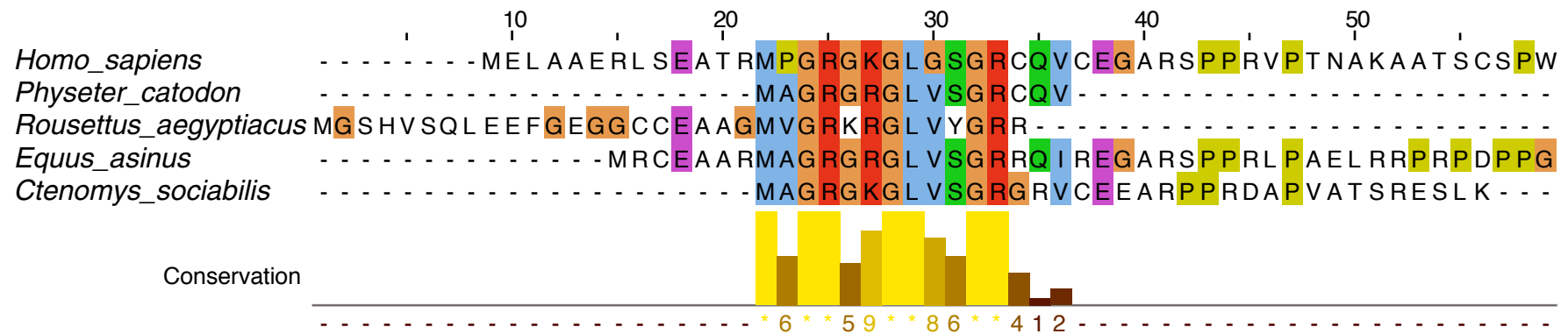


HG0987

ENSG00000164932 (CTHRC1)

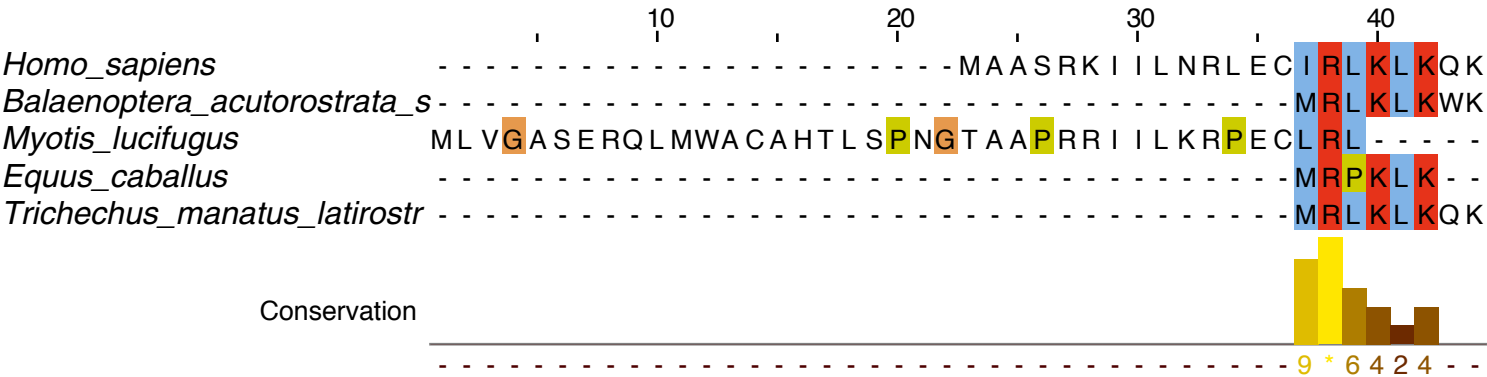


ENSG00000166130 (IKBIP)



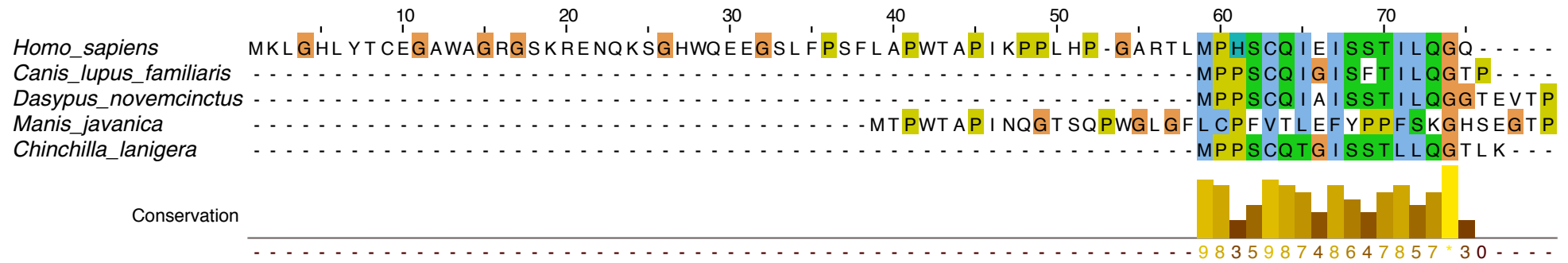
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ENSG00000166603 (MC4R)



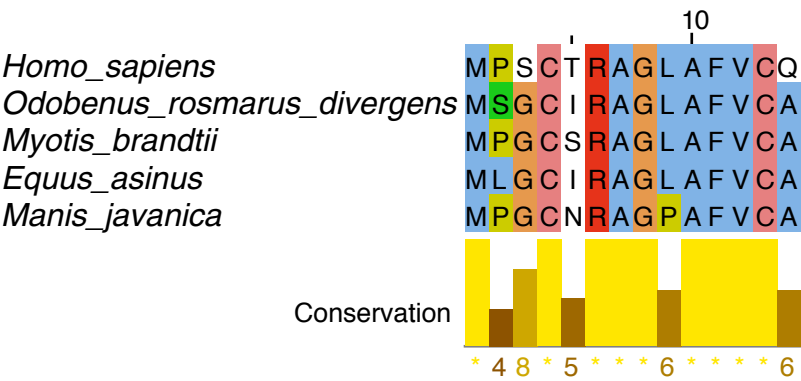
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ENSG00000166866 (MYO1A)



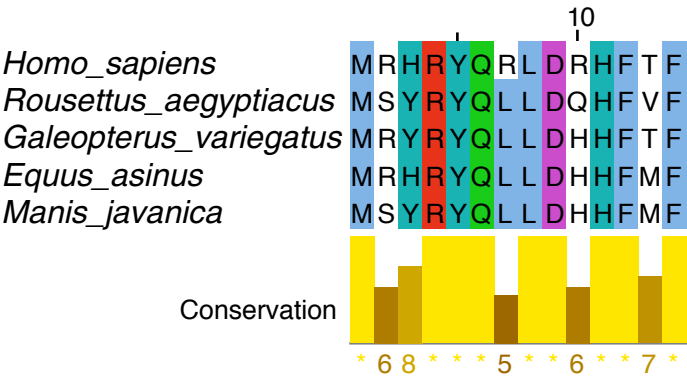
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ENSG00000167654 (ATCAY)



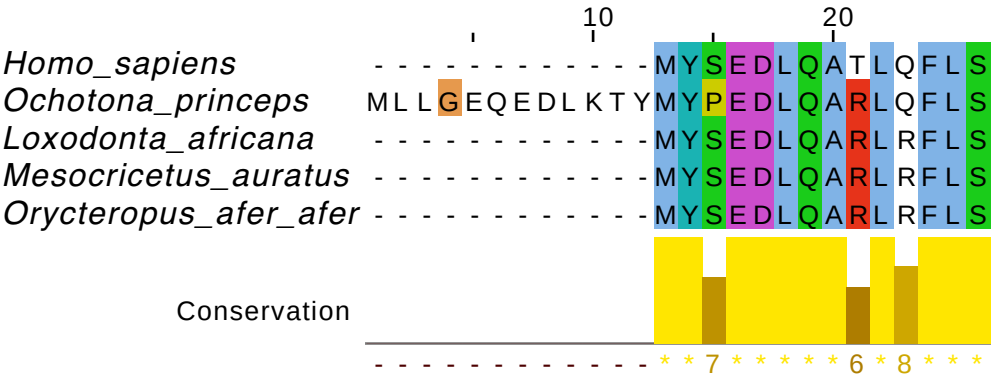
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ENSG00000168000 (BSCL2)



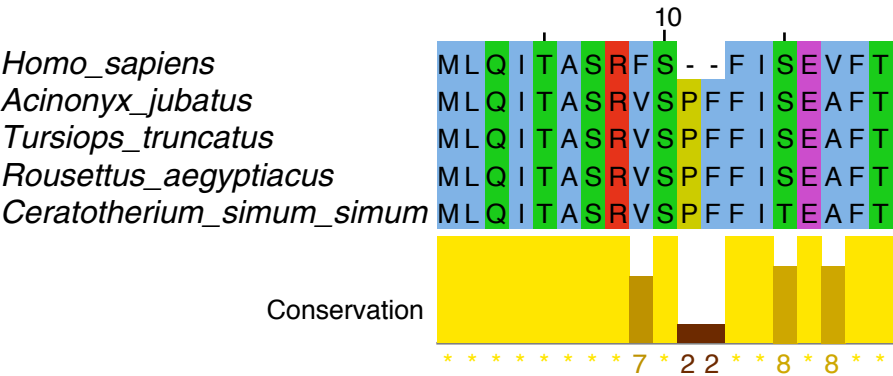
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ENSG00000169306 (IL1RAPL1)



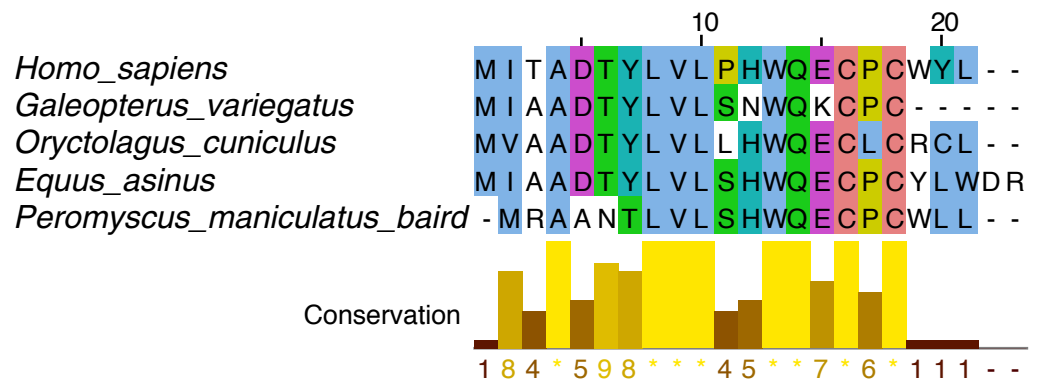
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ENSG00000170852 (KBTBD2)



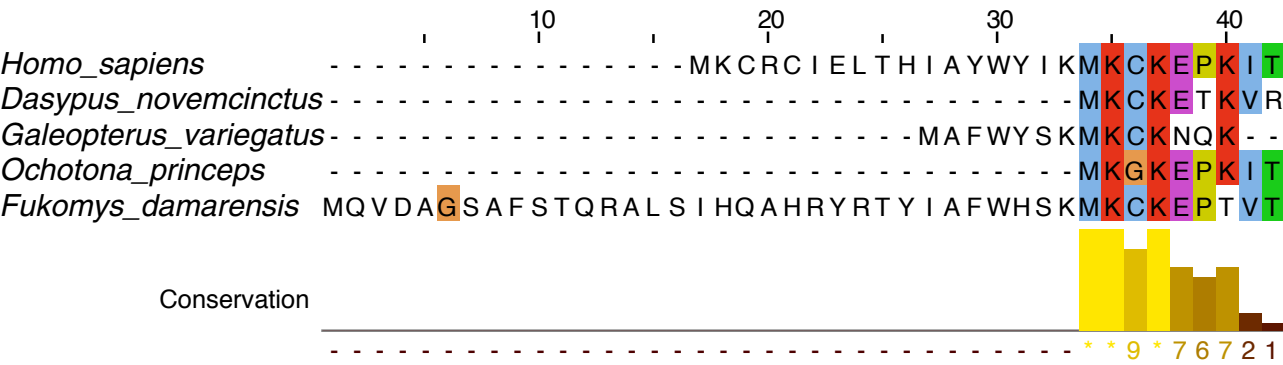
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ENSG00000171307 (ZDHHC16)



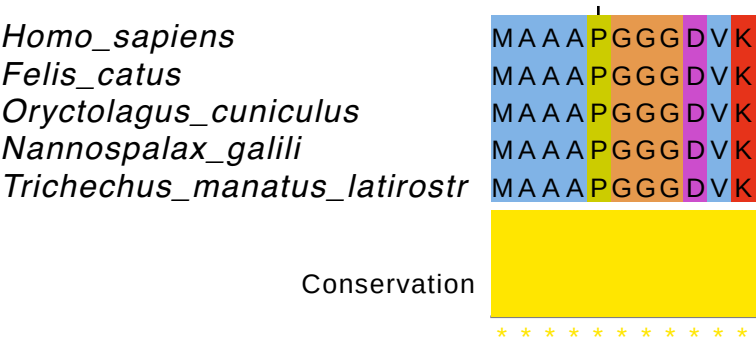
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ENSG00000173890 (GPR160)



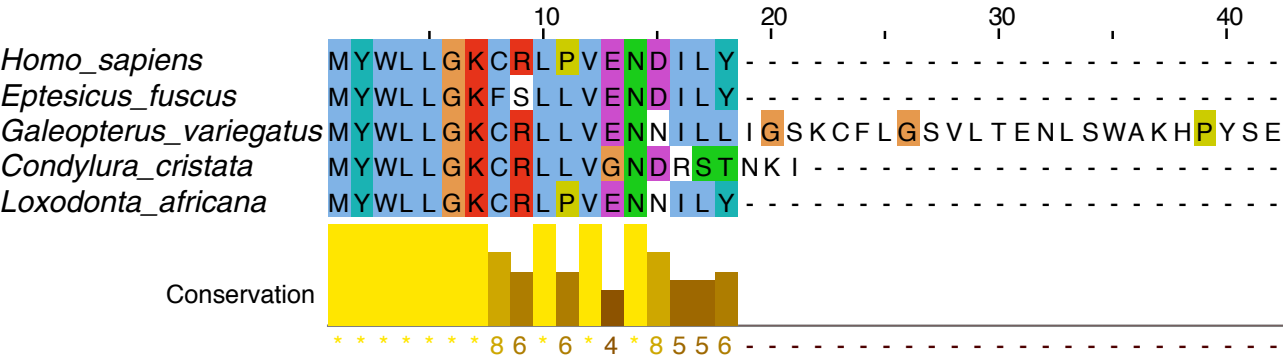
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ENSG00000177728 (TMEM94)



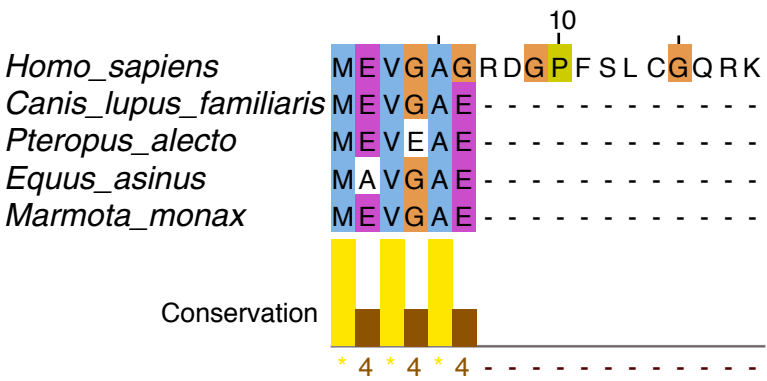
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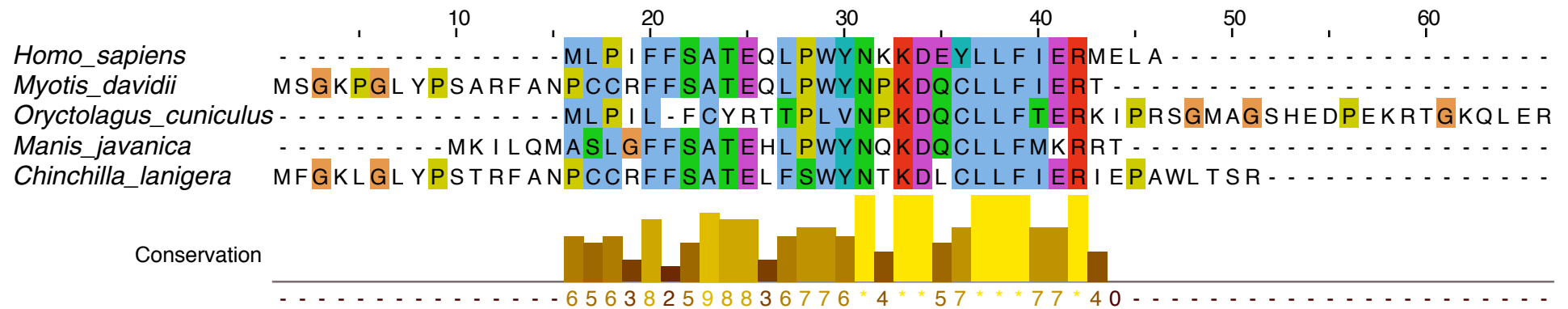


HG0999

ENSG00000178401 (DNAJC22)

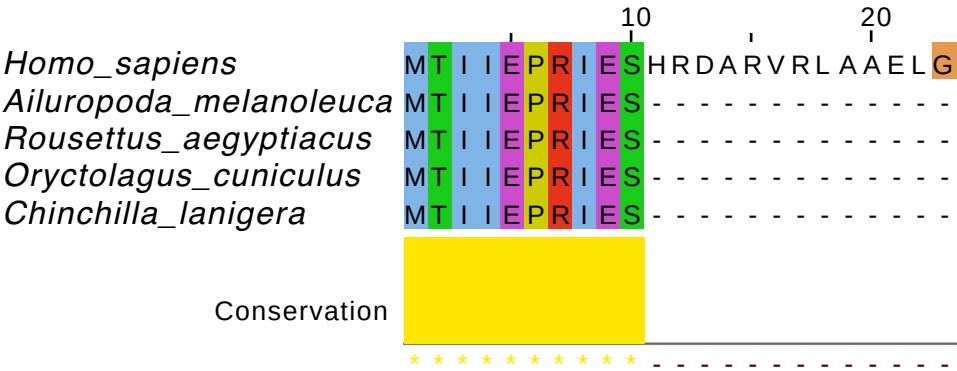


ENSG00000179083 (FAM133A)

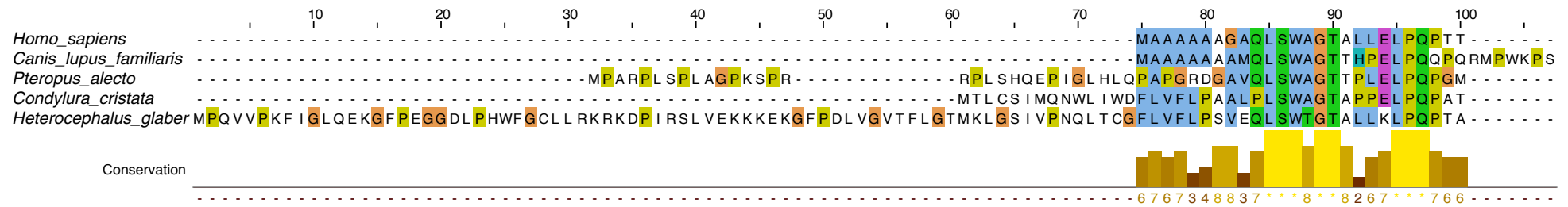


HG1001

ENSG00000179761 (PIPOX)

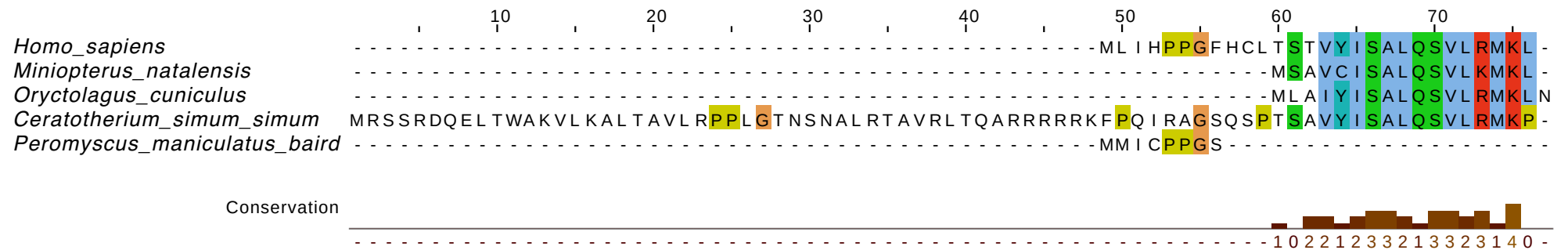


ENSG00000181027 (FKRP)



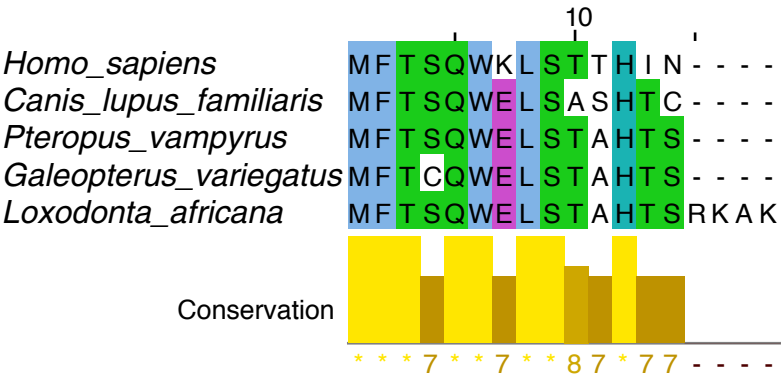
HG1003

ENSG00000184867 (ARMCX2)



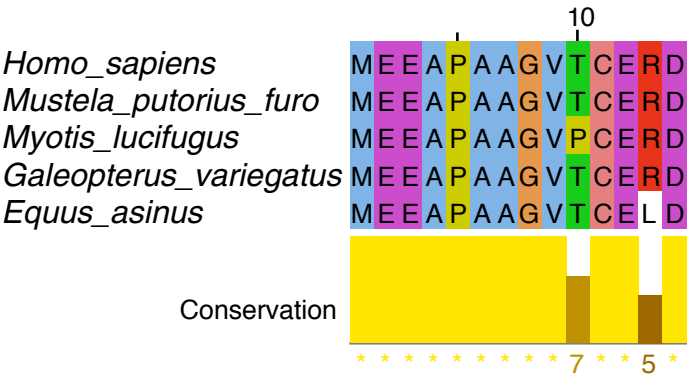
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ENSG00000185875 (THNSL1)



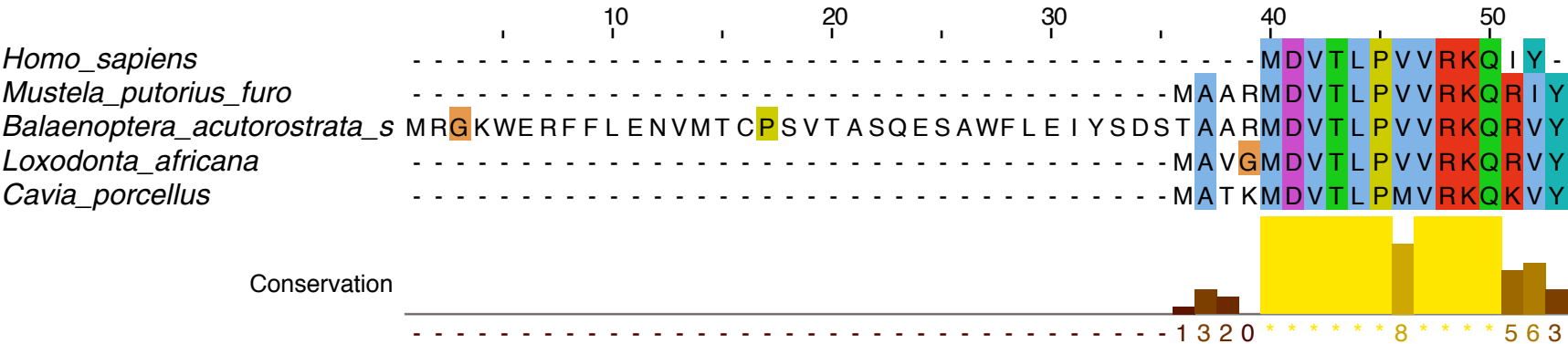
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ENSG00000186472 (PCLO)



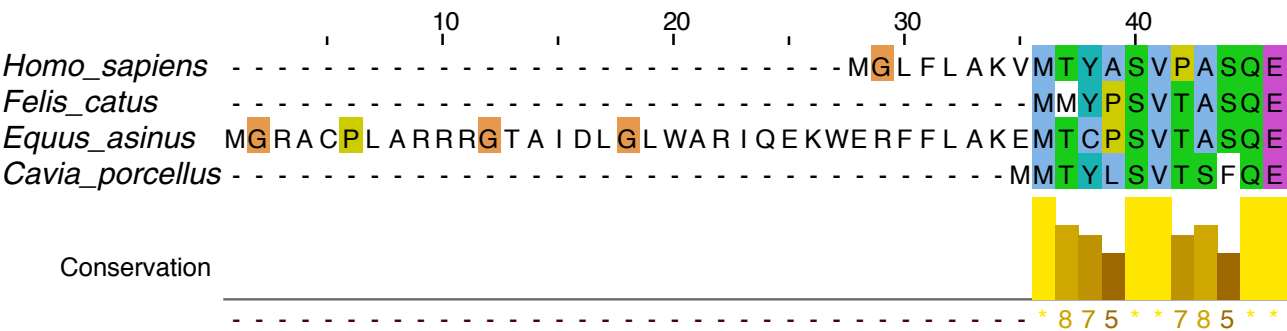
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ENSG00000188227 (ZNF793)



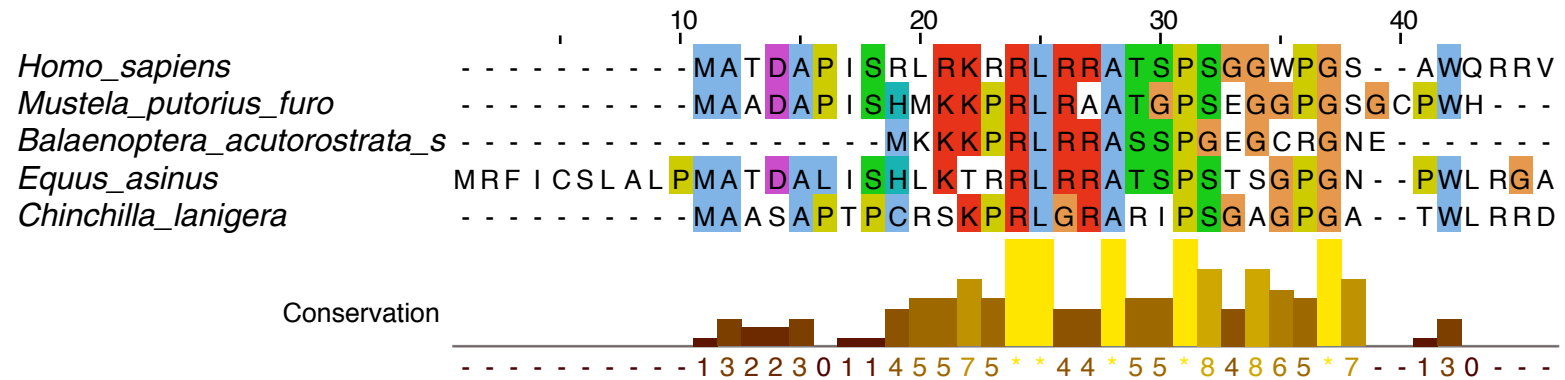
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ENSG00000188227 (ZNF793)



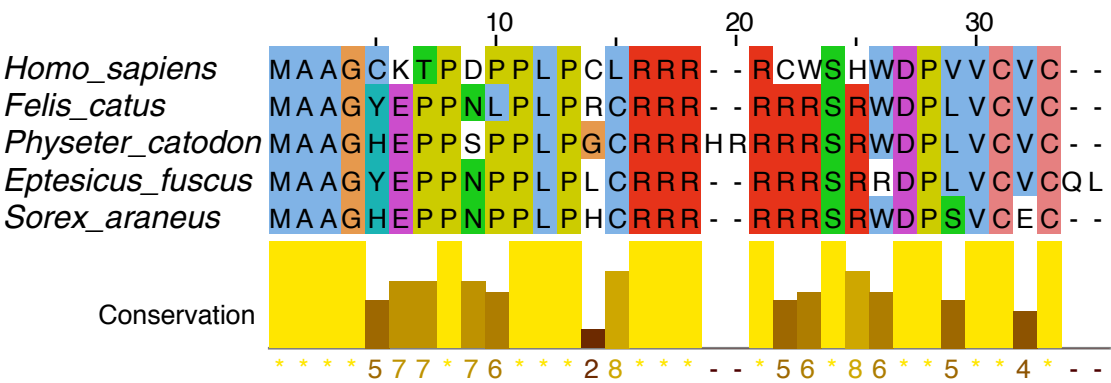
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ENSG00000188910 (GJB3)



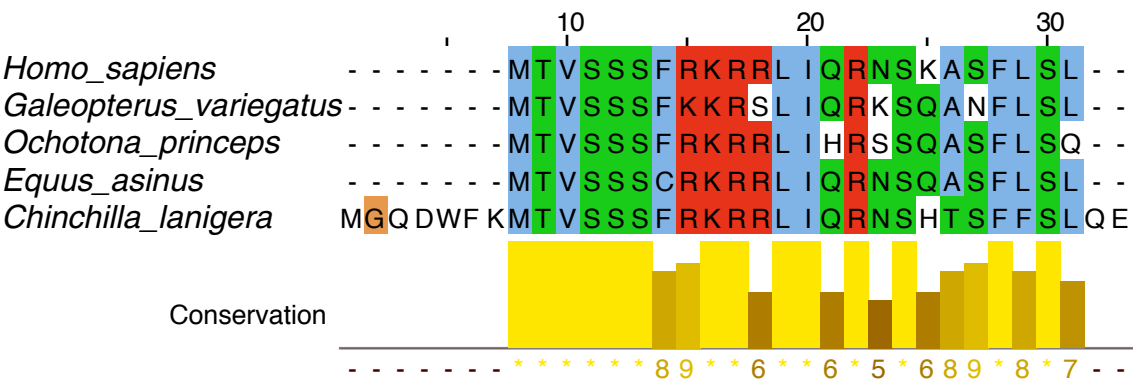
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ENSG00000198252 (STYX)



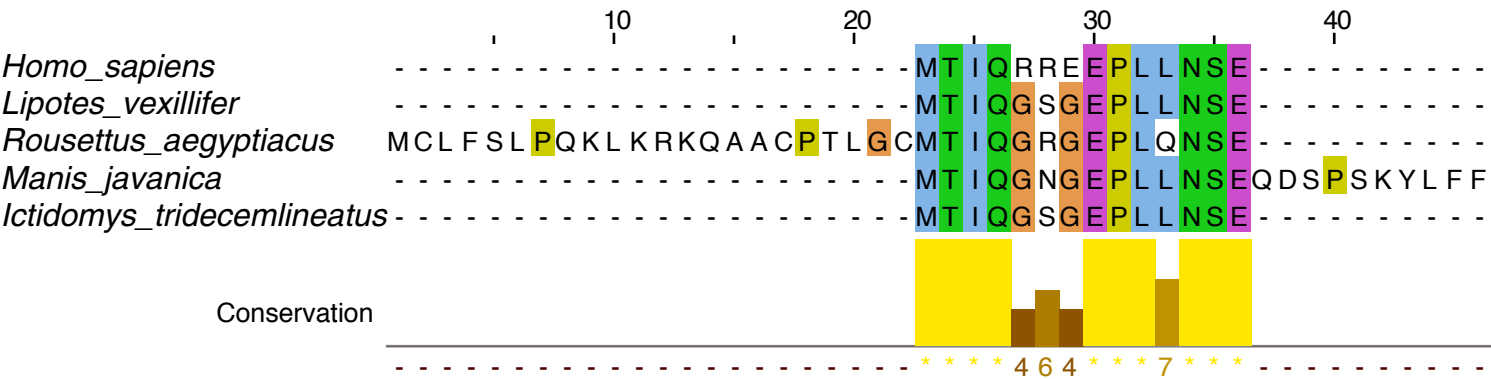
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ENSG00000203740 (METTL11B)



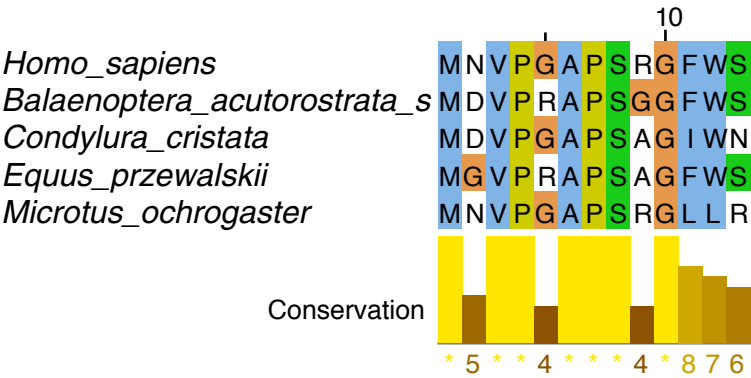
HG1011

ENSG00000204439 (C6orf47)



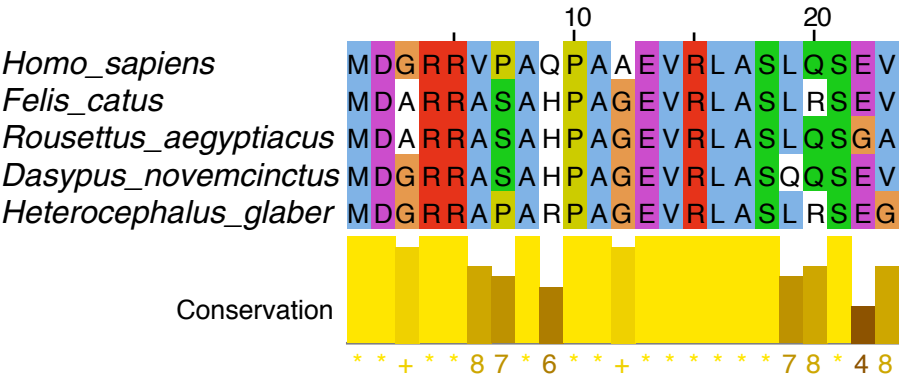
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ENSG00000213694 (S1PR3)



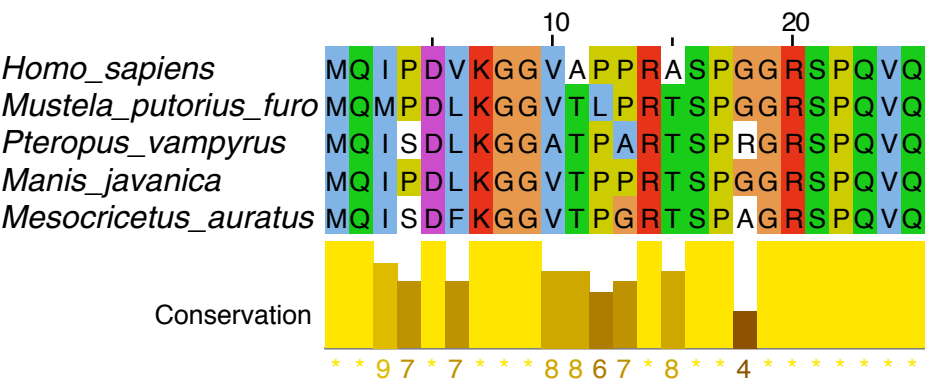
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ENSG00000214022 (REPIN1)



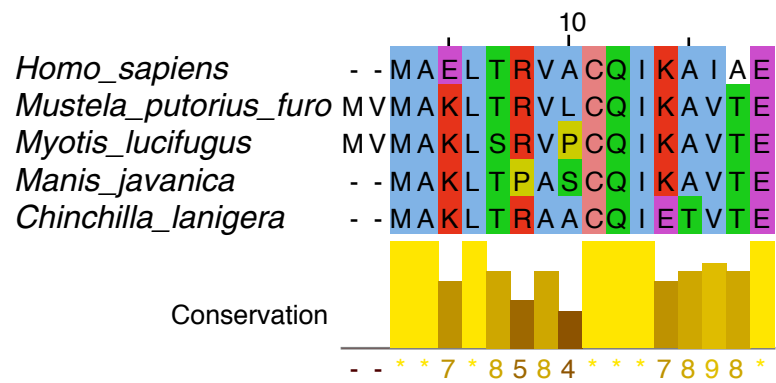
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ENSG00000214595 (EML6)



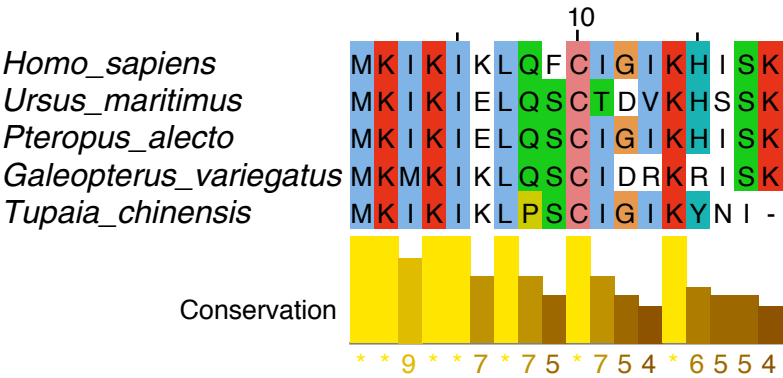
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ENSG00000214595 (EML6)



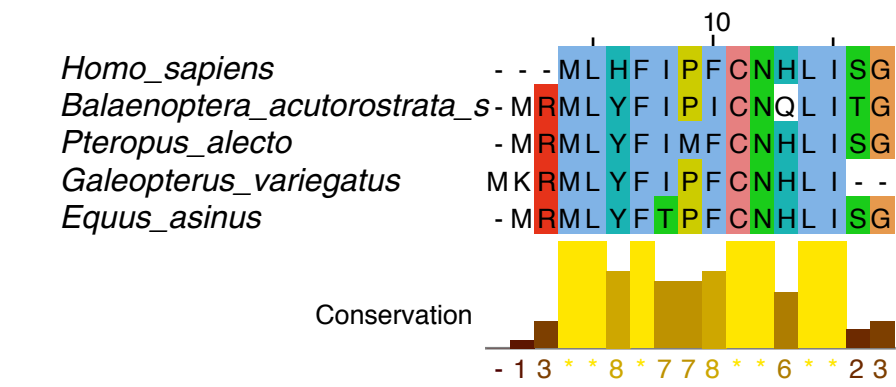
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ENSG00000240720 (LRRD1)



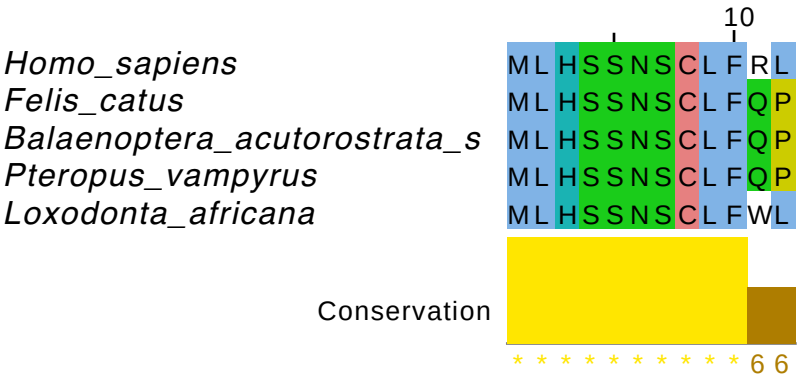
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ENSG00000254004 (ZNF260)



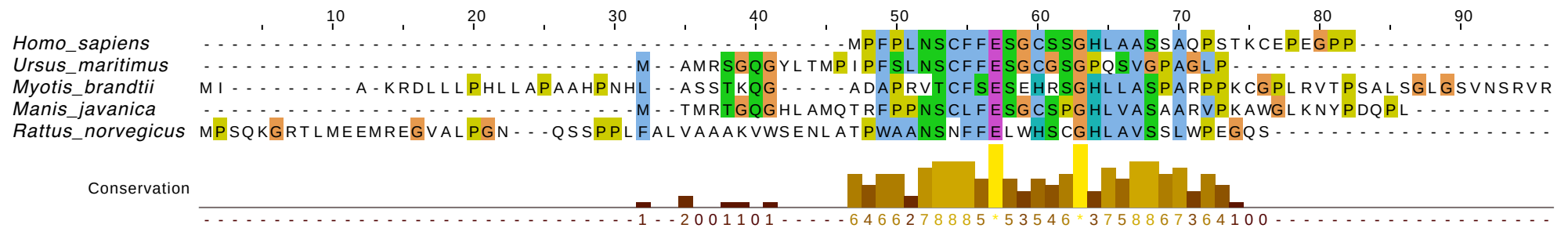
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ENSG00000255154 (HTD2)



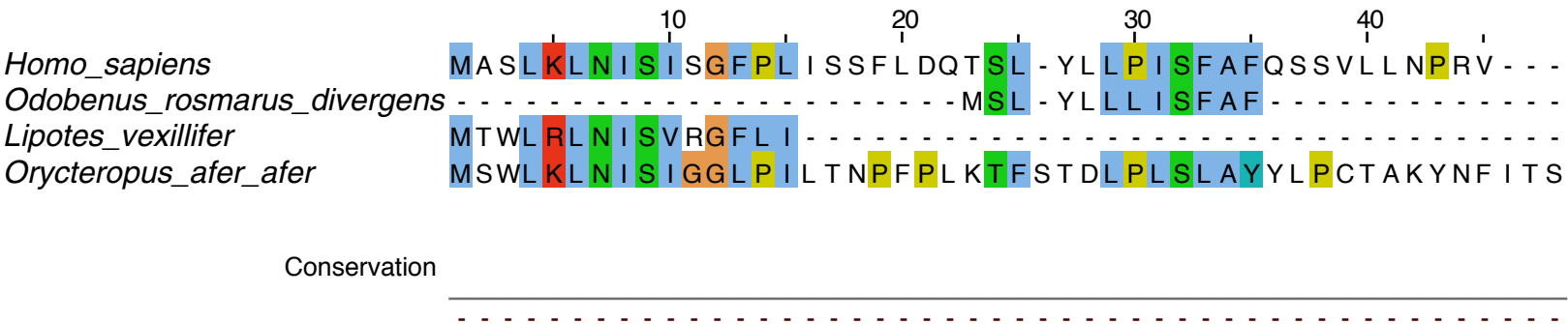
HG1018

ENSG00000259120 (SMIM6)



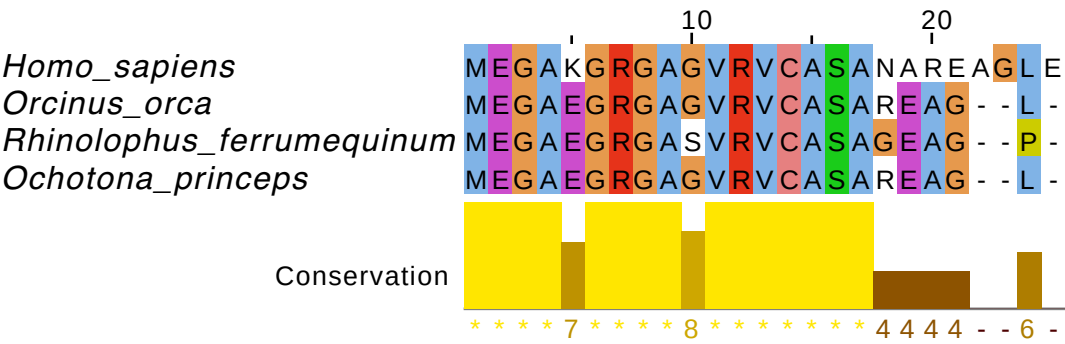
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ENSG00000019995 (ZRANB1)



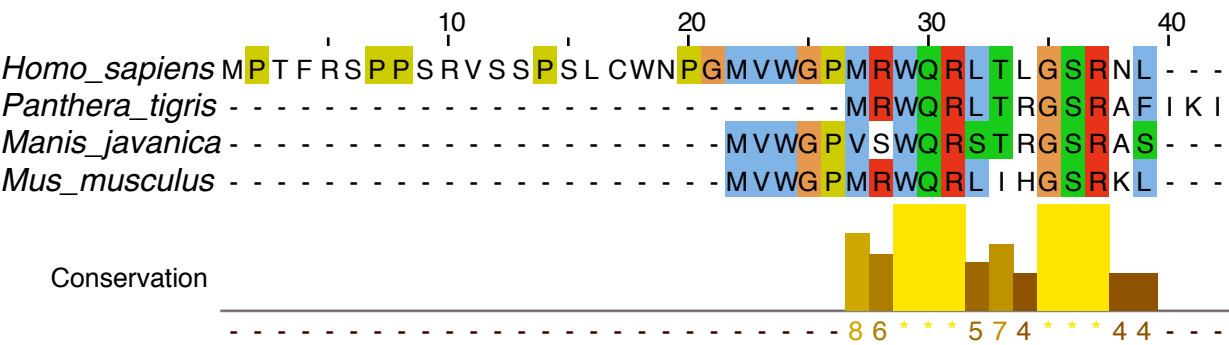
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ENSG00000023902 (PLEKHO1)



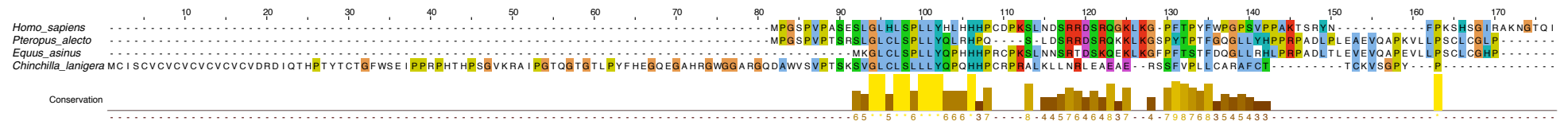
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ENSG00000064692 (SNCAIP)



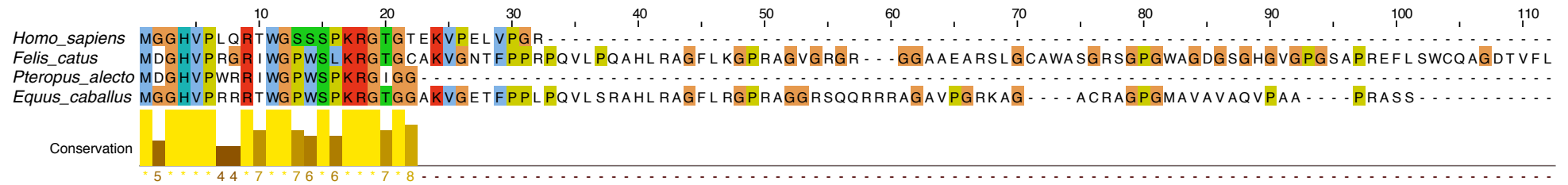
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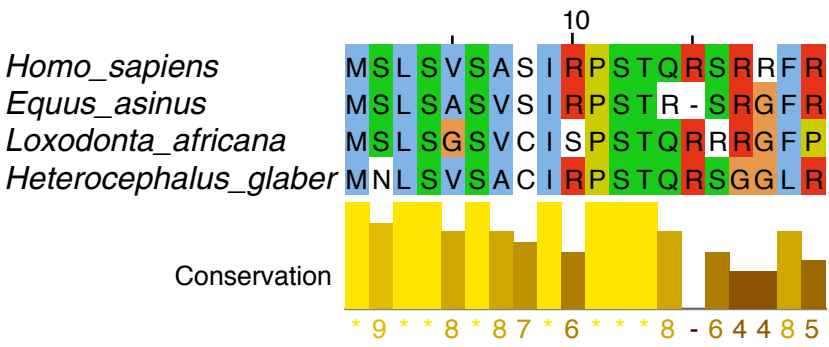
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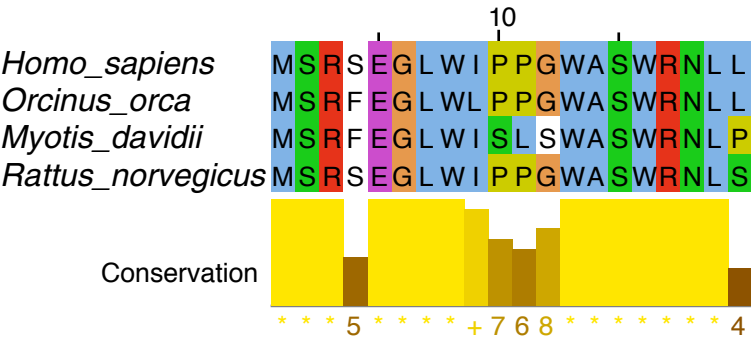
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ENSG00000073464 (CLCN4)



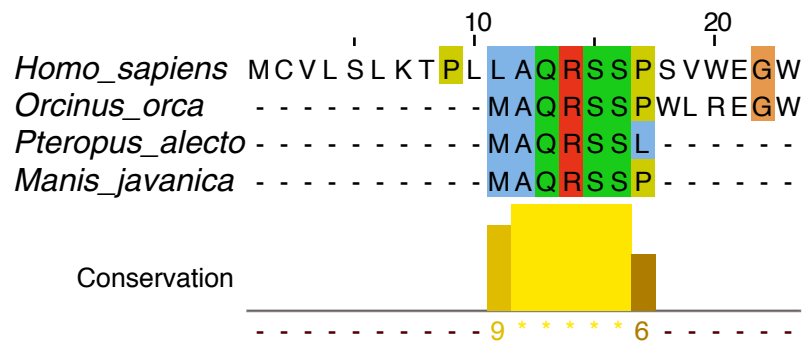
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ENSG00000074621 (SLC24A1)



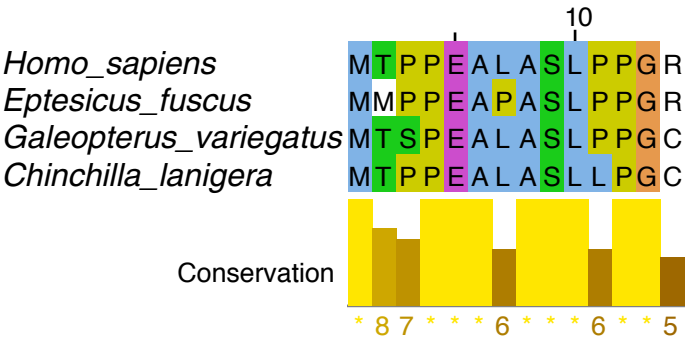
HG1026.1

ENSG00000075035 (WSCD2)



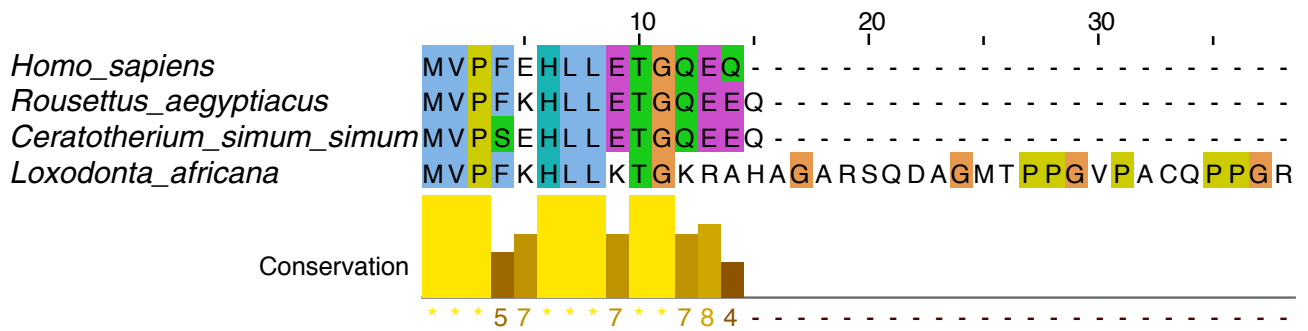
HG1026.2

ENSG00000179314 (WSCD1)



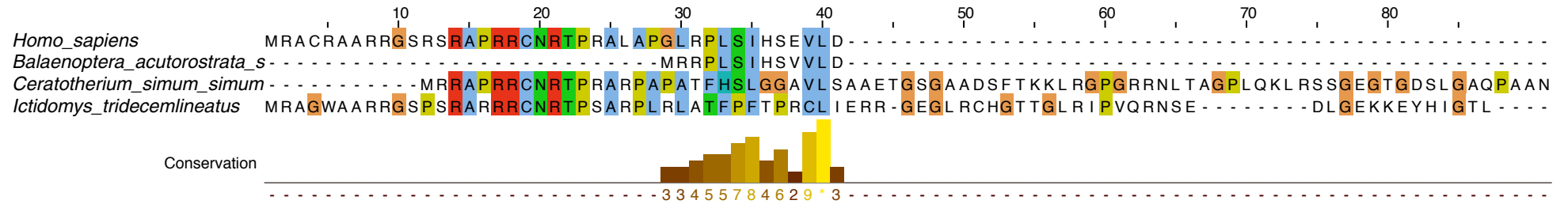
HG1026.3

ENSG00000179314 (WSCD1)



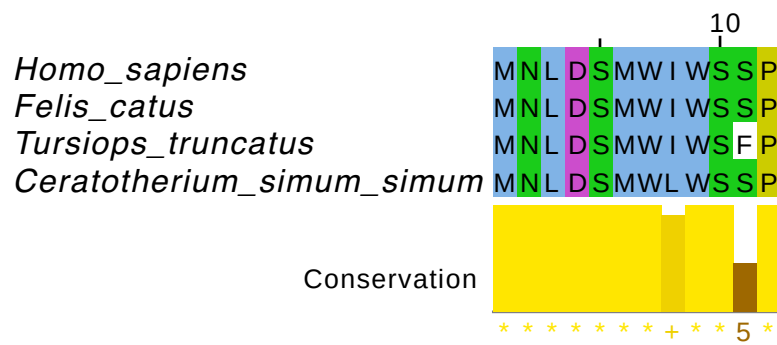
HG1027

ENSG00000075223 (SEMA3C)



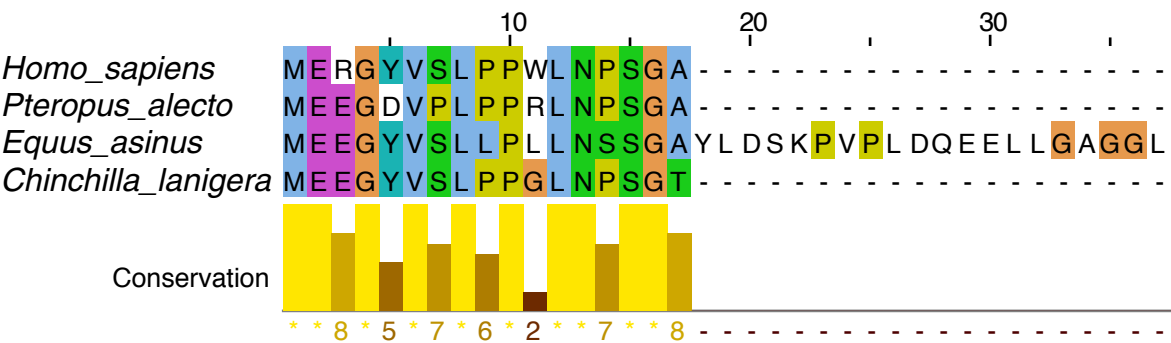
HG1028

ENSG00000076356 (PLXNA2)



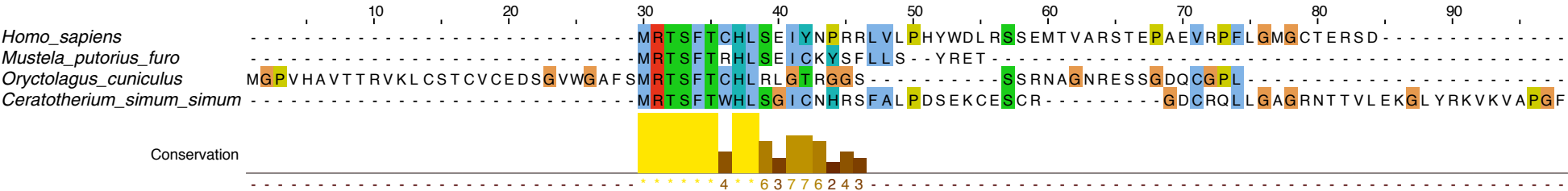
HG1029

ENSG00000079482 (OPHN1)



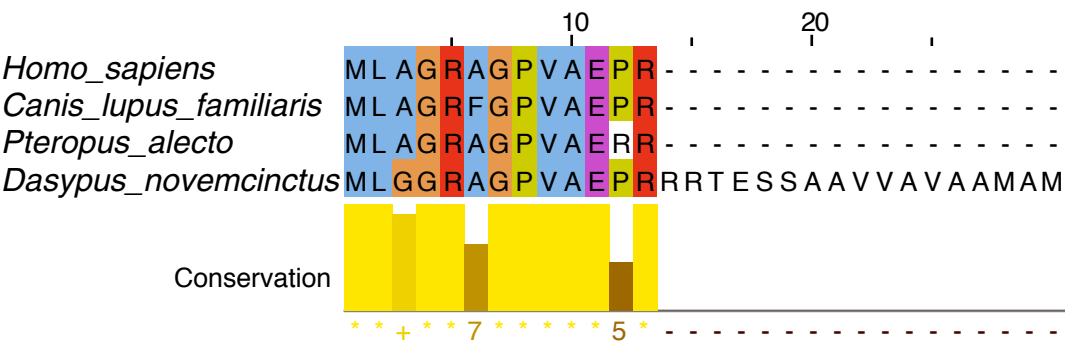
HG1030

ENSG00000082175 (PGR)



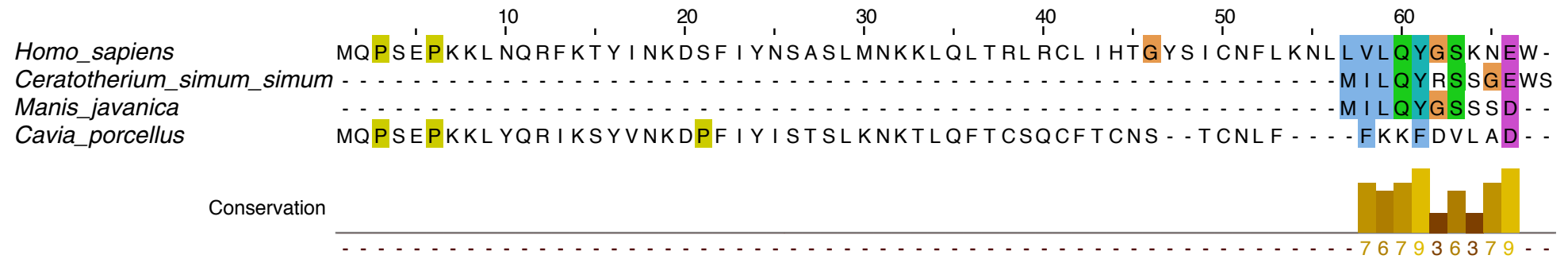
HG1031

ENSG00000082269 (FAM135A)



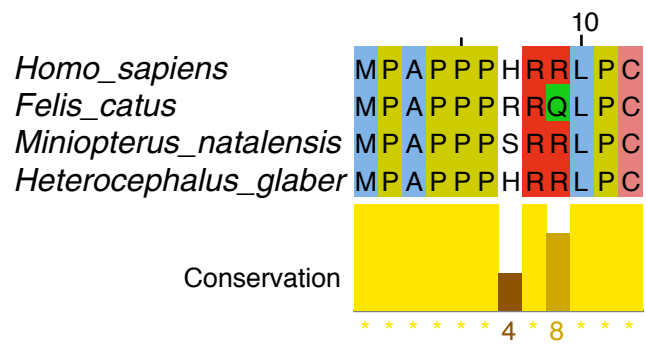
HG1032

ENSG00000084453 (SLCO1A2)



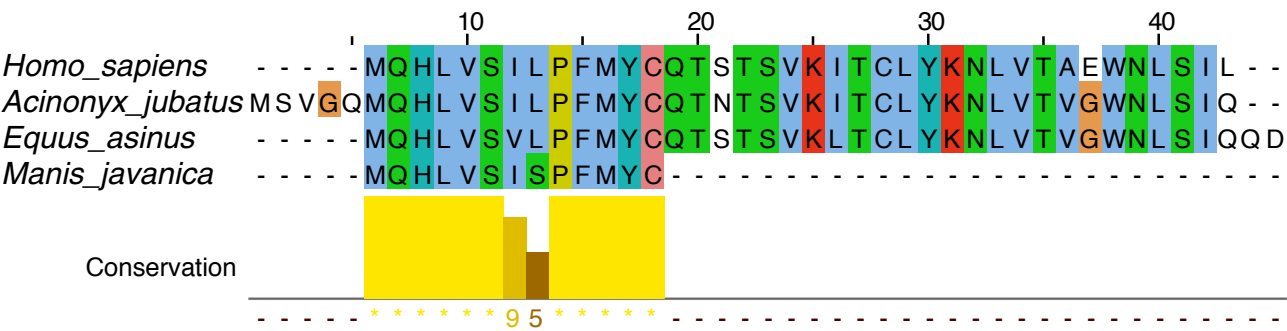
HG1033

ENSG00000089225 (TBX5)



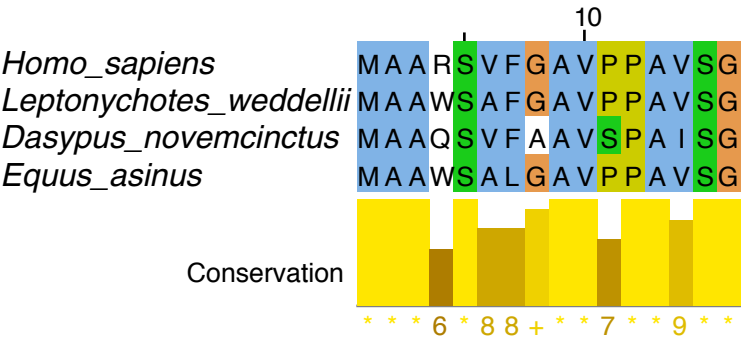
HG1034

ENSG00000090487 (SPG21)



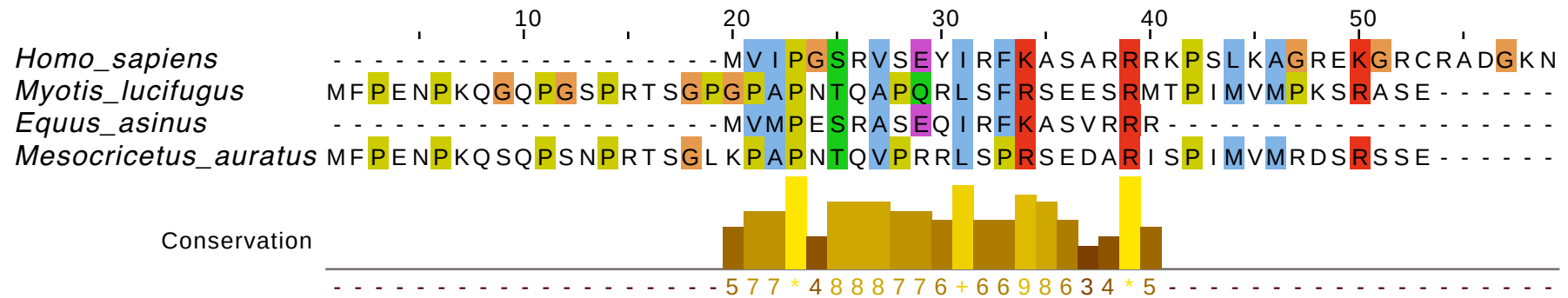
HG1035

ENSG00000093000 (NUP50)



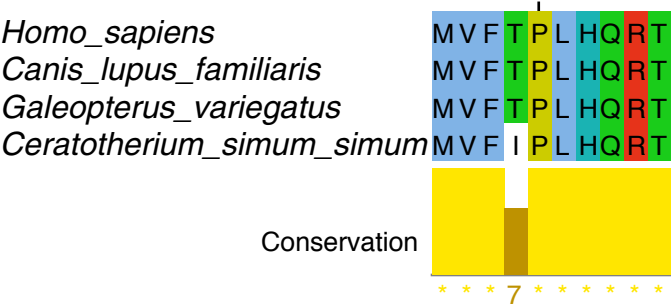
HG1036

ENSG00000100813 (ACIN1)



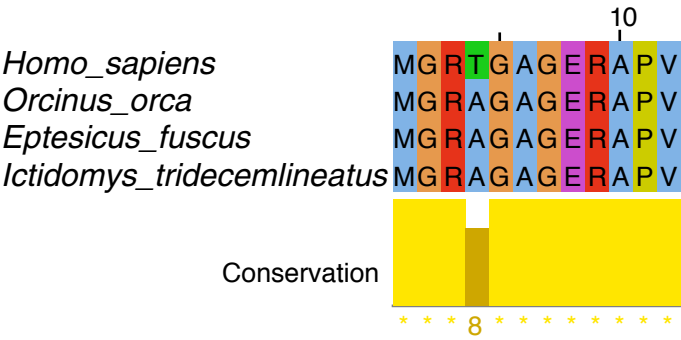
HG1037

ENSG00000102710 (SUPT20H)



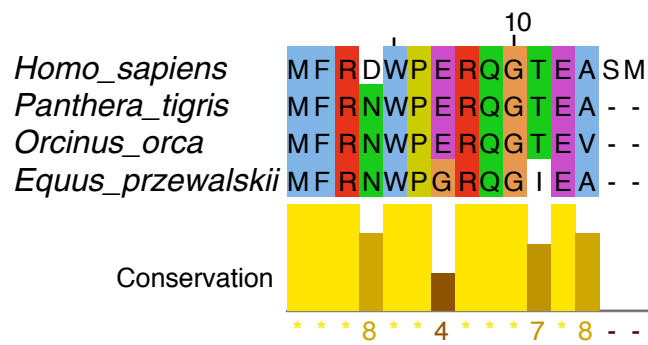
HG1038

ENSG00000104331 (IMPAD1)

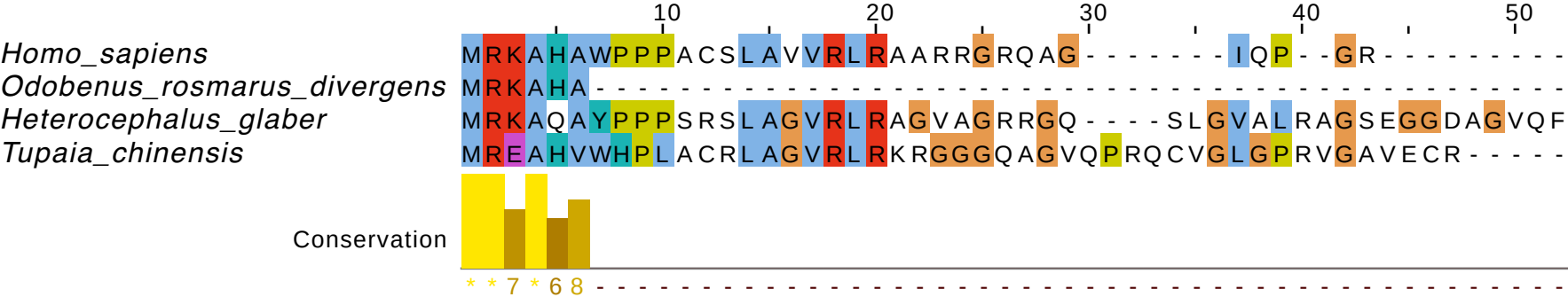


HG1039

ENSG00000104804 (TULP2)

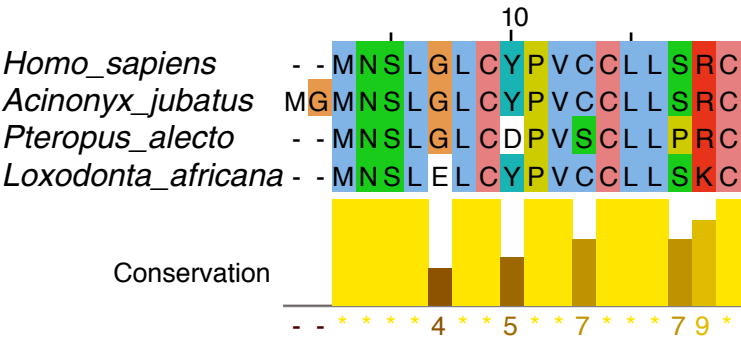


HG1040
 ENSG00000105223 (PLD3)



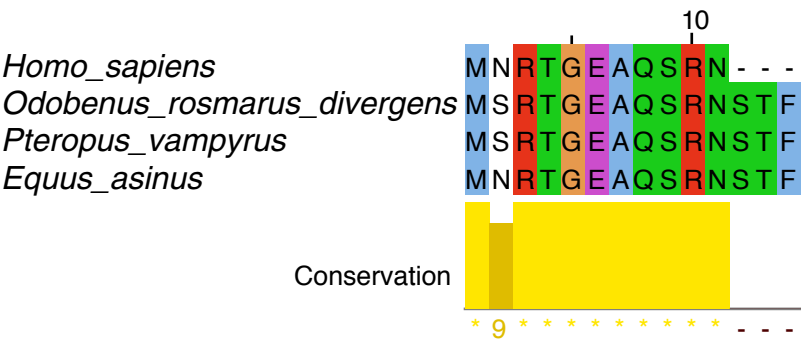
HG1041

ENSG00000106536 (POU6F2)



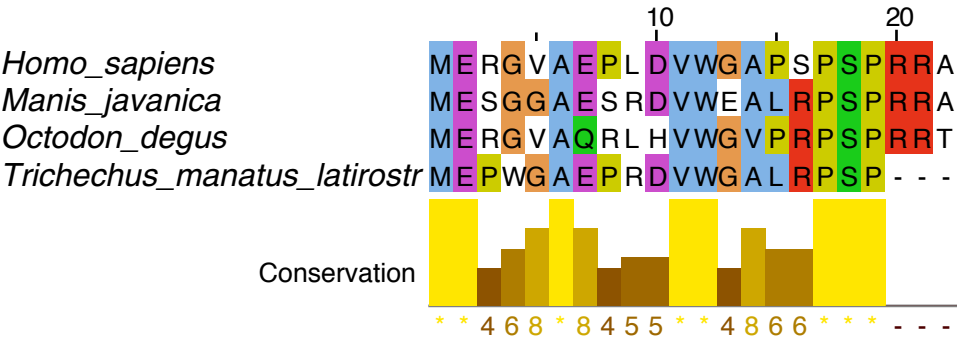
HG1042

ENSG00000107249 (GLIS3)



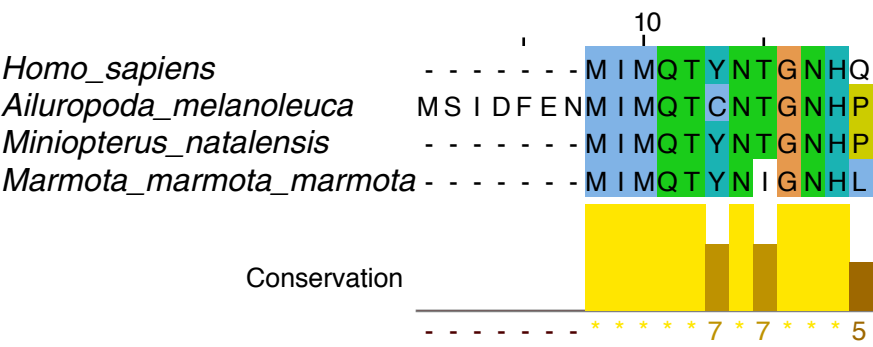
HG1043

ENSG00000107736 (CDH23)

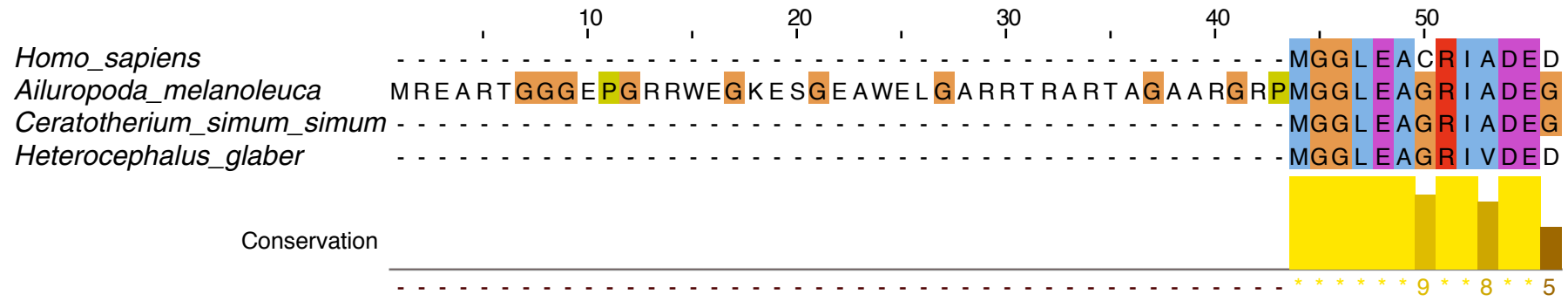


HG1044

ENSG00000109381 (ELF2)

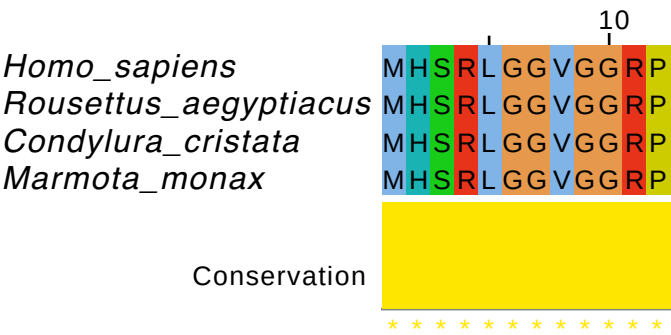


ENSG00000110925 (CSRNP2)



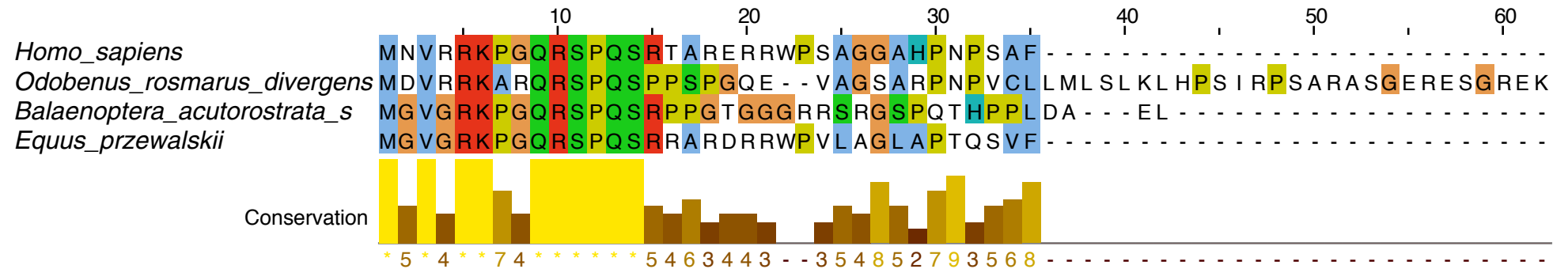
HG1046

ENSG00000112701 (SENP6)



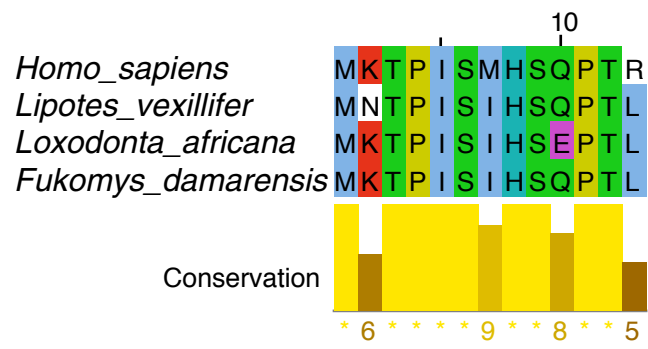
ENSG00000112769 (LAMA4)

ENSG00000112769 (LAMA4)



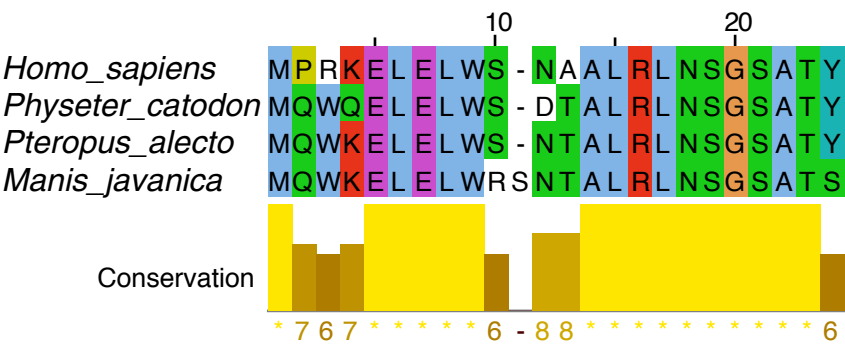
HG1048

ENSG00000115295 (CLIP4)

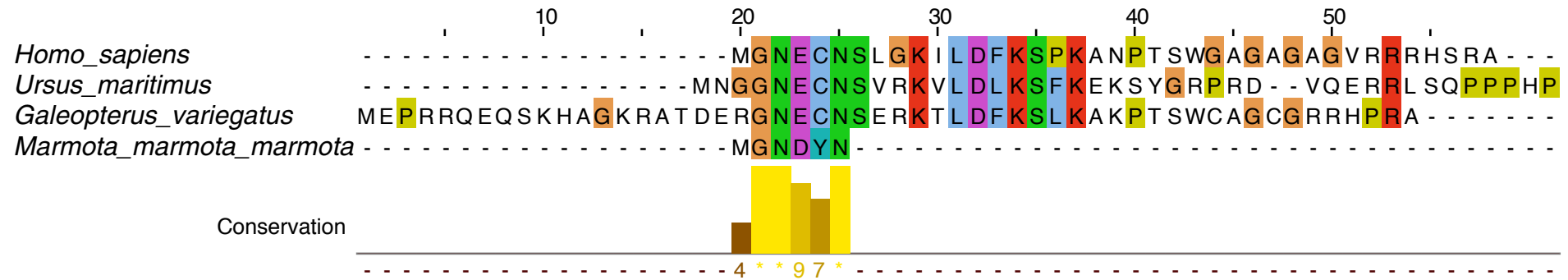


HG1049

ENSG00000116212

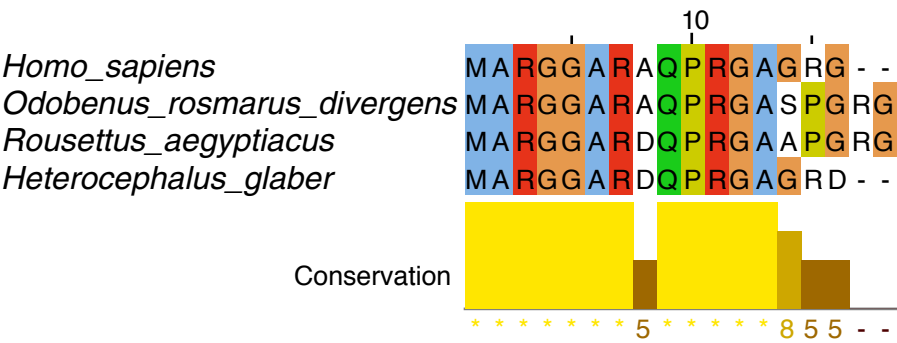


ENSG00000116489 (CAPZA1)



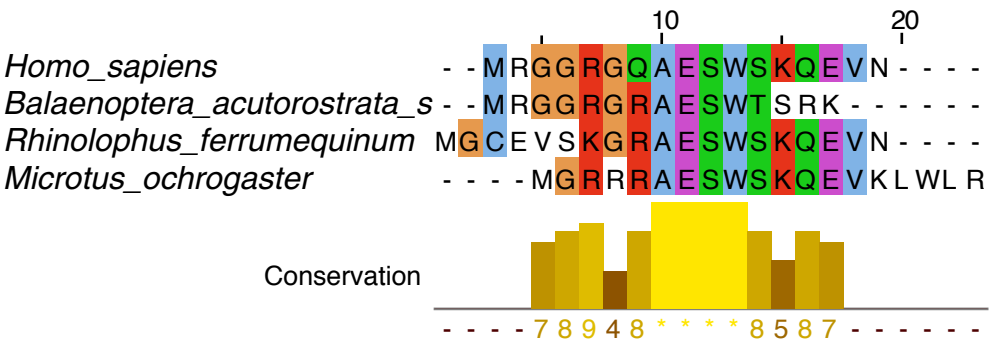
HG1051

ENSG00000116852 (KIF21B)



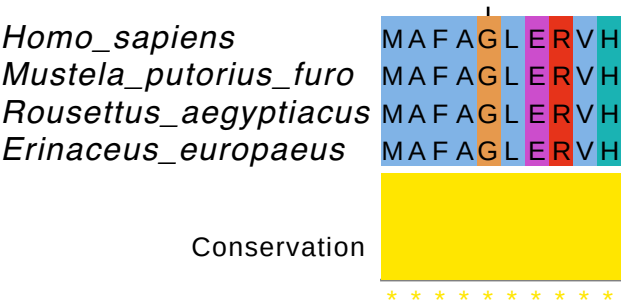
HG1052

ENSG00000118640 (VAMP8)



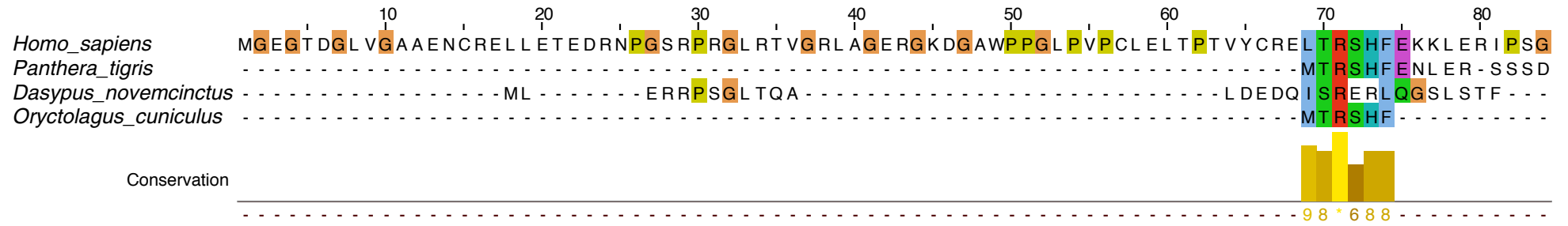
HG1053

ENSG00000119522 (DENND1A)



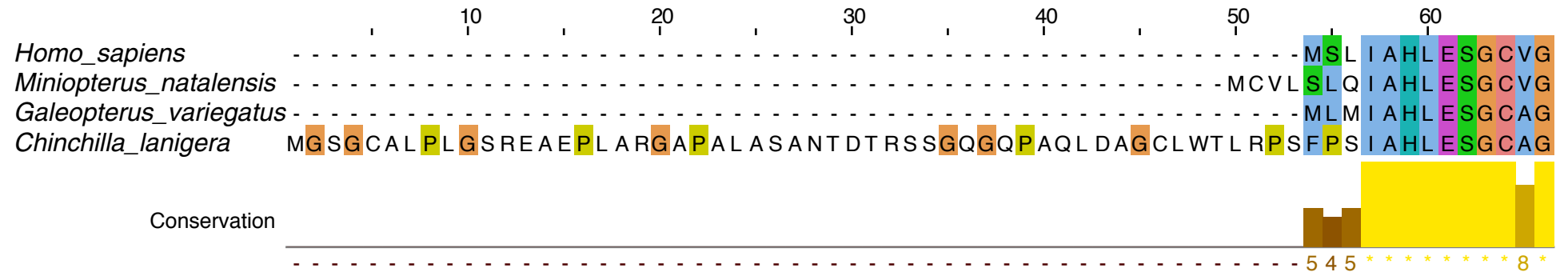
HG1054

ENSG00000120832 (MTERF2)



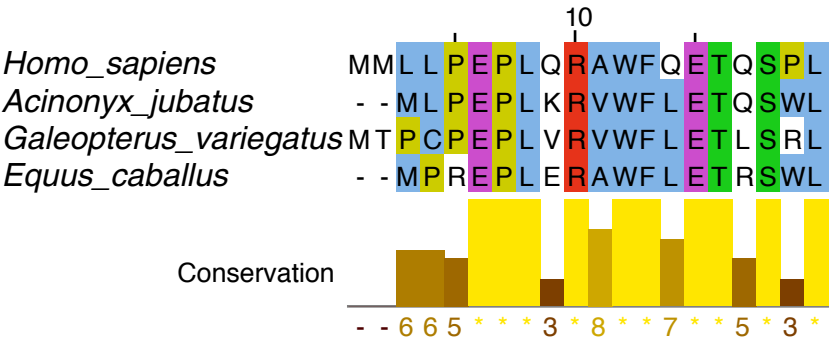
HG1055

ENSG00000122299 (ZC3H7A)



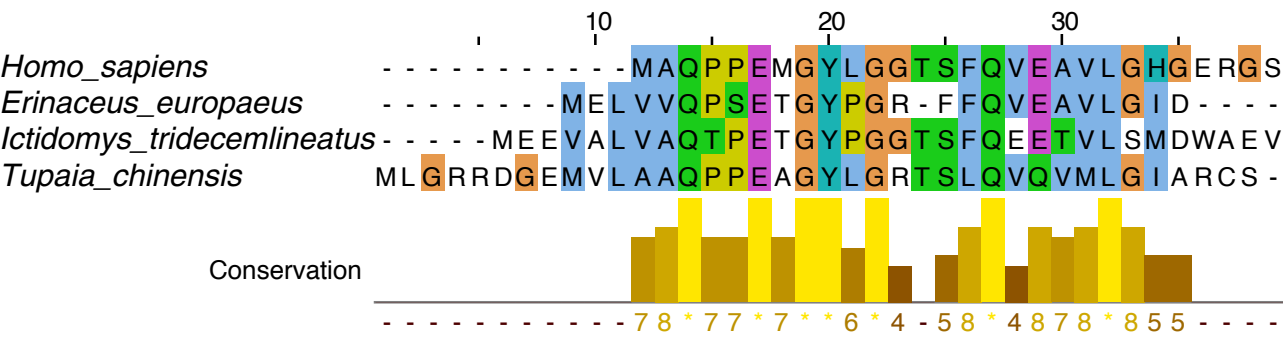
HG1056

ENSG00000128271 (ADORA2A)

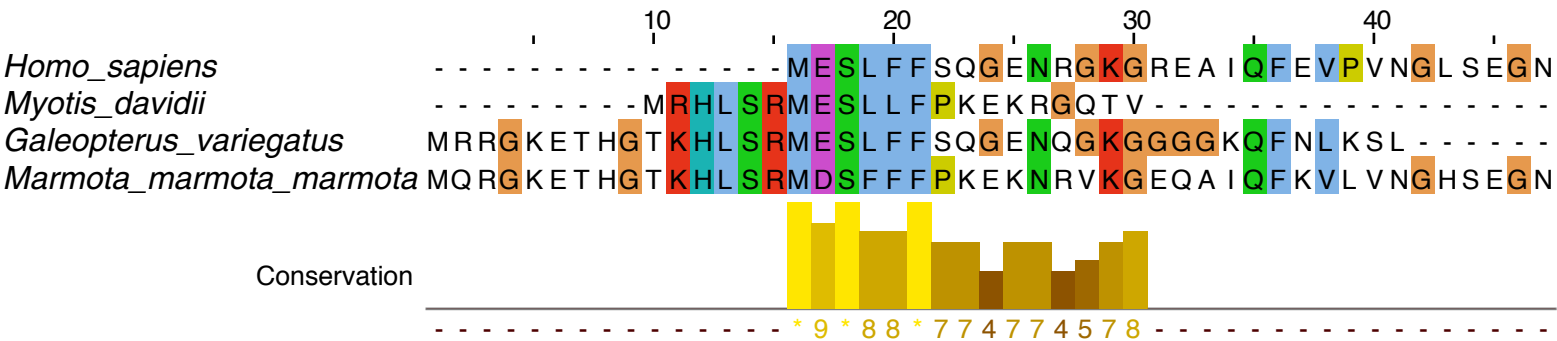


HG1057

ENSG00000131097 (HIGD1B)

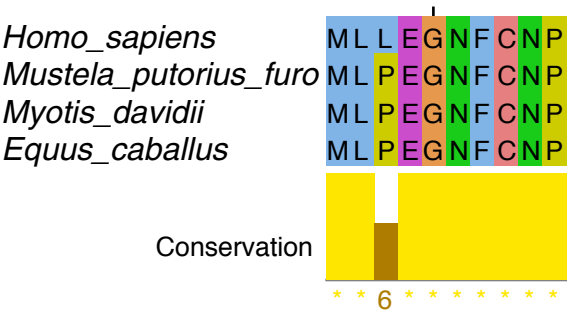


HG1058
 ENSG00000131386 (GALNT15)



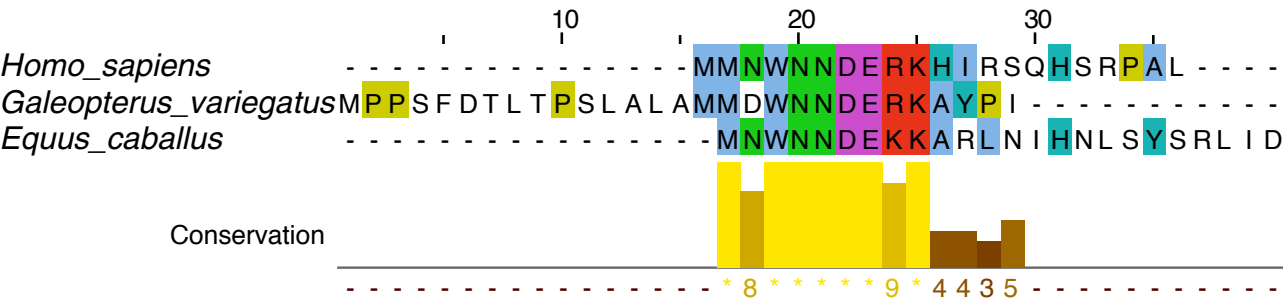
HG1059.1

ENSG00000132970 (WASF3)



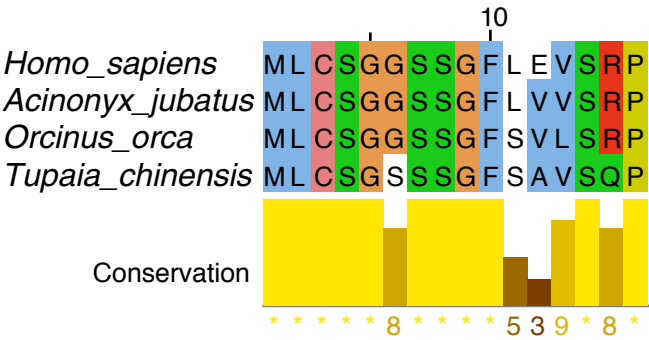
HG1059.2

ENSG00000112290 (WASF1)



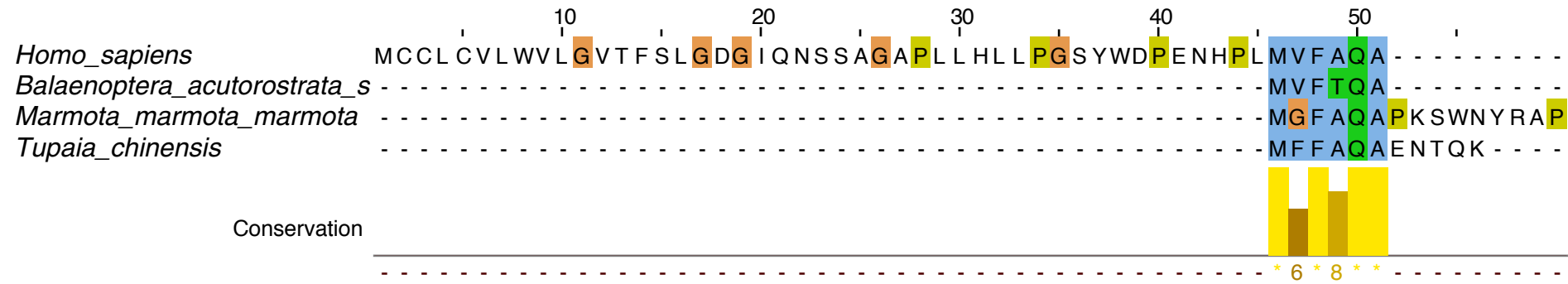
HG1060

ENSG00000134242 (PTPN22)



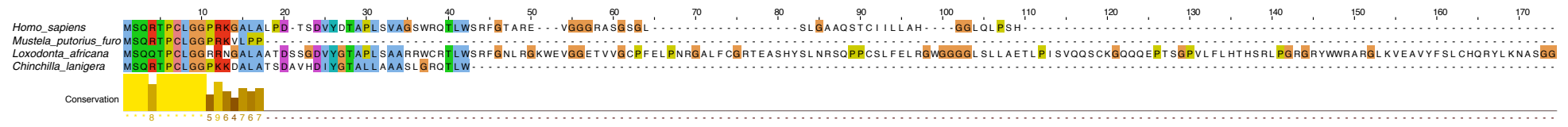
HG1061

ENSG00000134802 (SLC43A3)



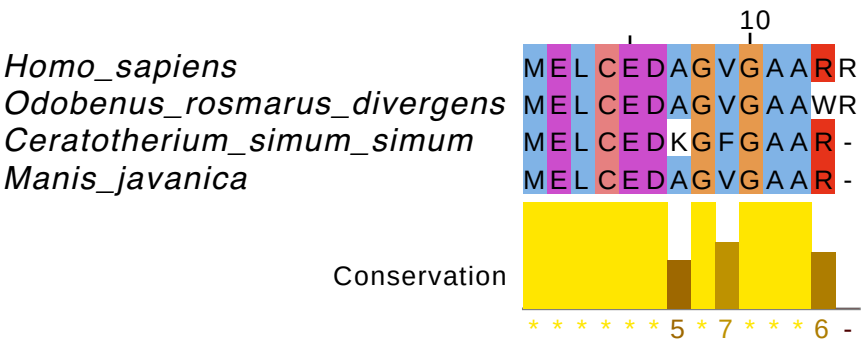
HG1062

ENSG00000137337 (MDC1)



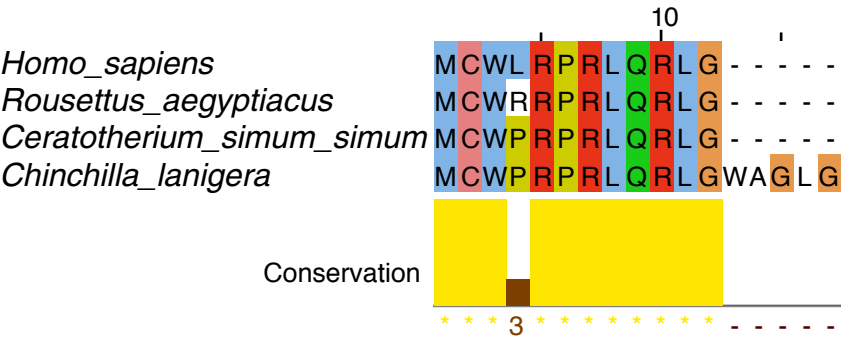
HG1063

ENSG00000138162 (TACC2)



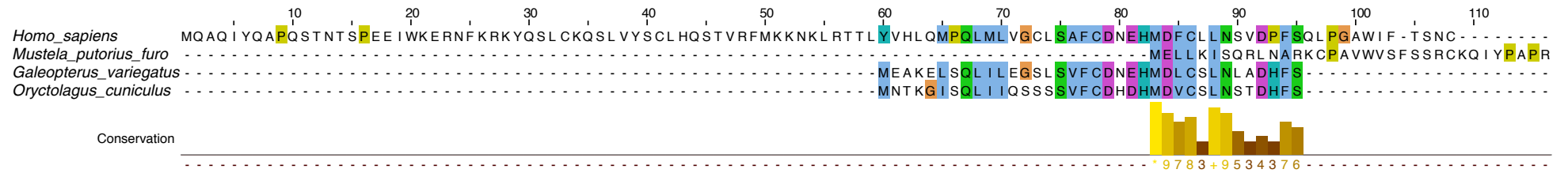
HG1064

ENSG00000139734 (DIAPH3)



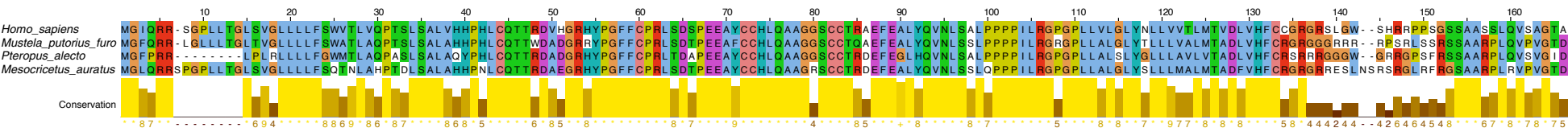
HG1065

ENSG00000140030 (GPR65)



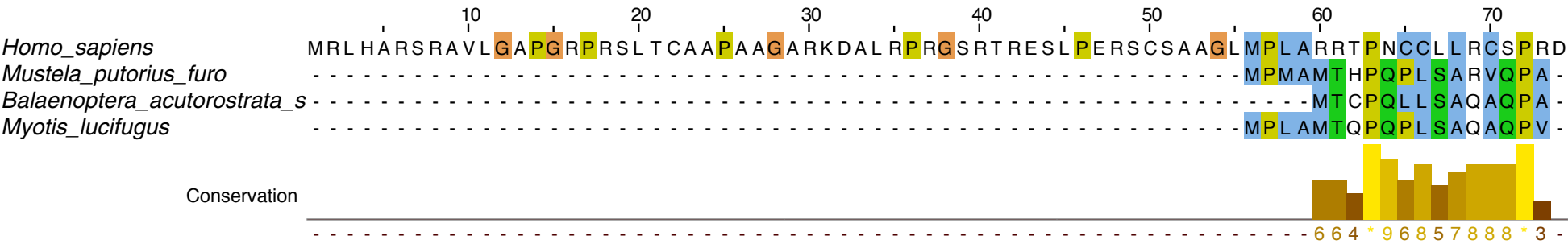
HG1066

ENSG00000140553 (UNC45A)



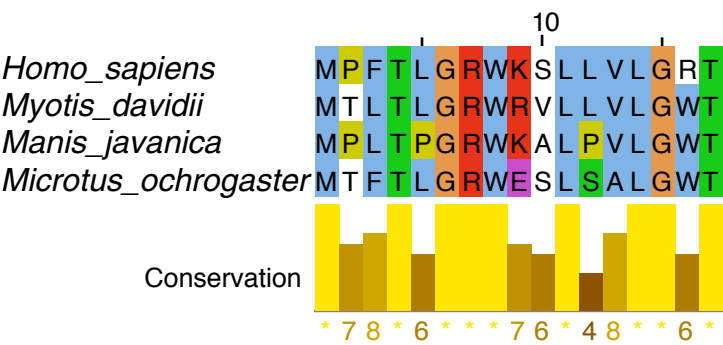
HG1067

ENSG00000143340 (FAM163A)



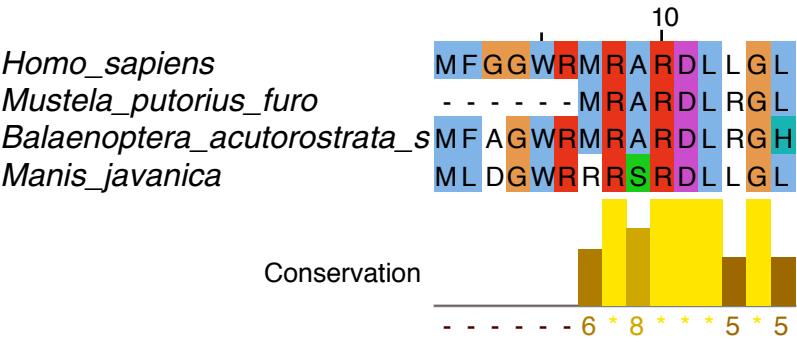
HG1068

ENSG00000144791 (LIMD1)



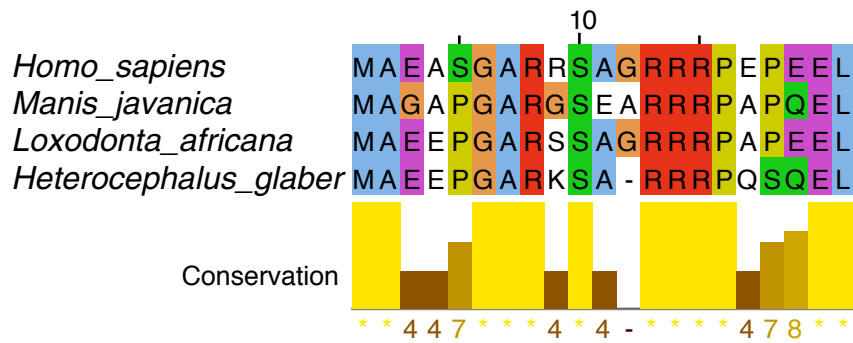
HG1069

ENSG00000146414 (SHPRH)



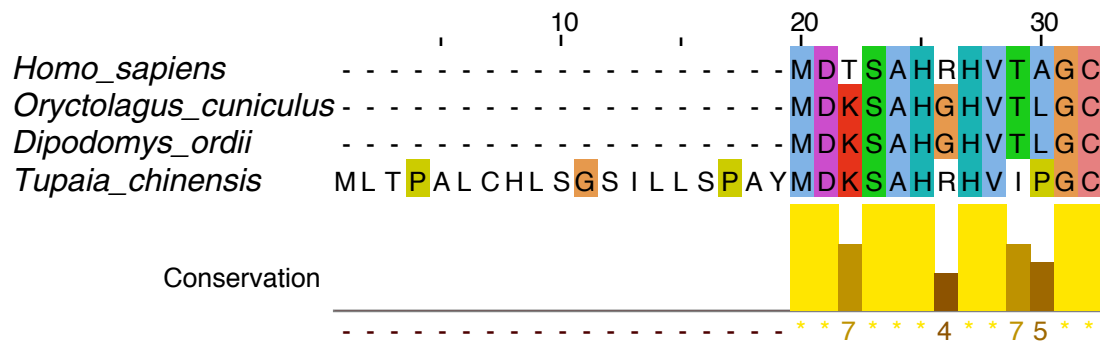
HG1070

ENSG00000147459 (DOCK5)



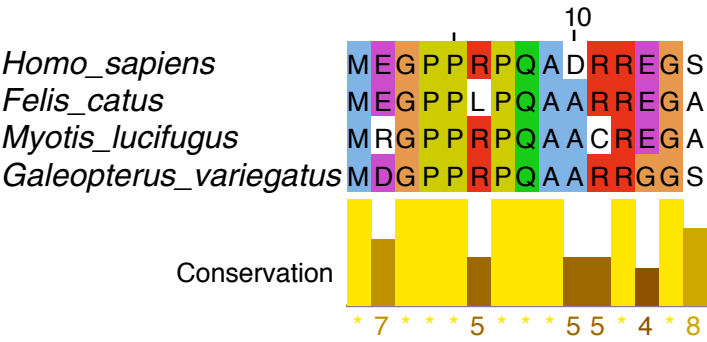
HG1071

ENSG00000147573 (TRIM55)

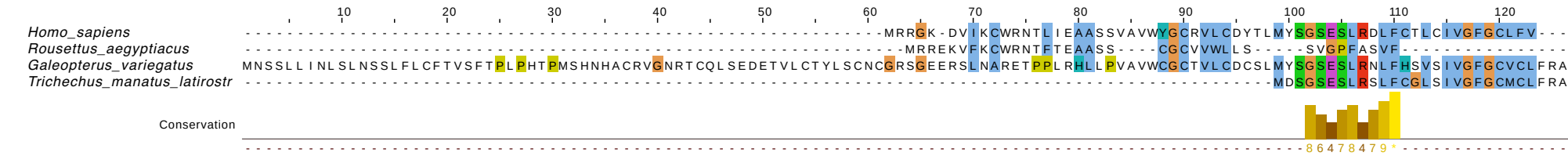


HG1072

ENSG00000147874 (HAUS6)

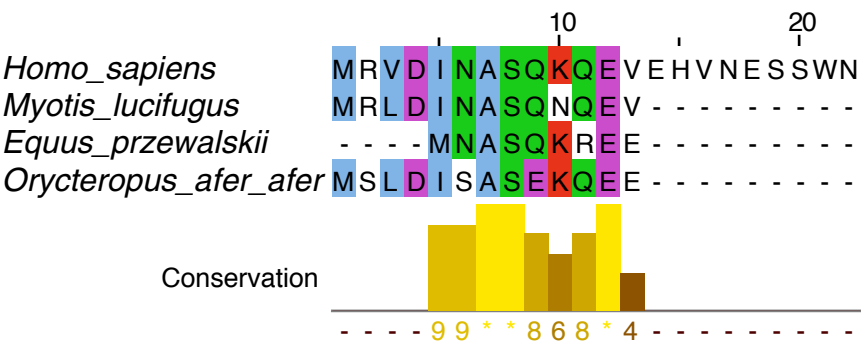


HG1073
 ENSG00000149187 (CELF1)

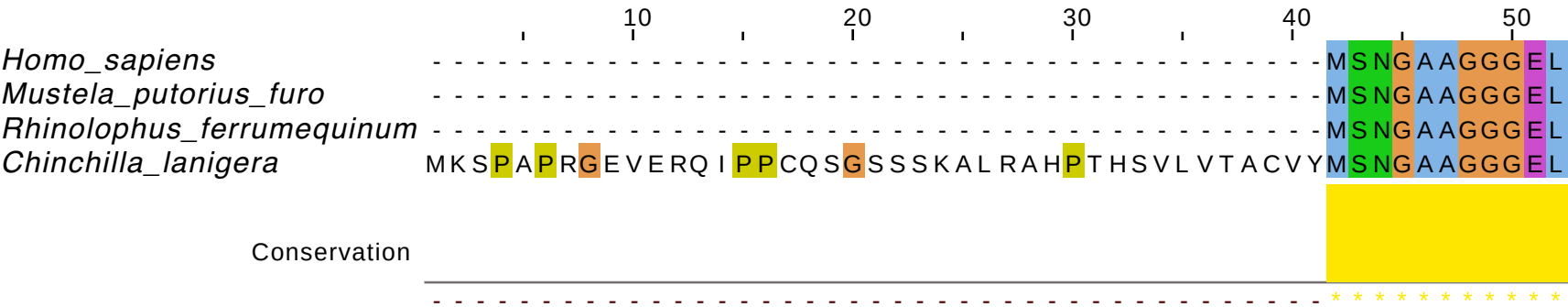


HG1074

ENSG00000150275 (PCDH15)

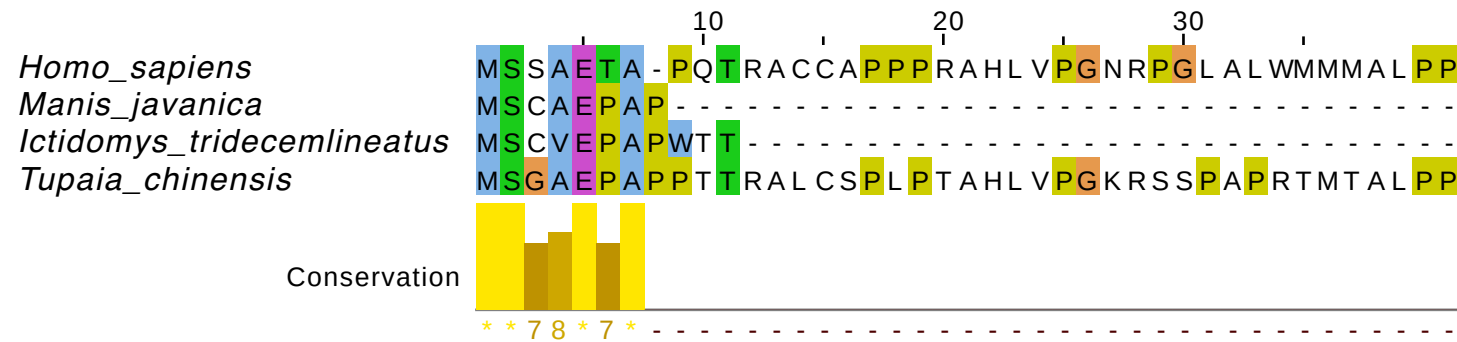


HG1075
 ENSG00000150347 (ARID5B)



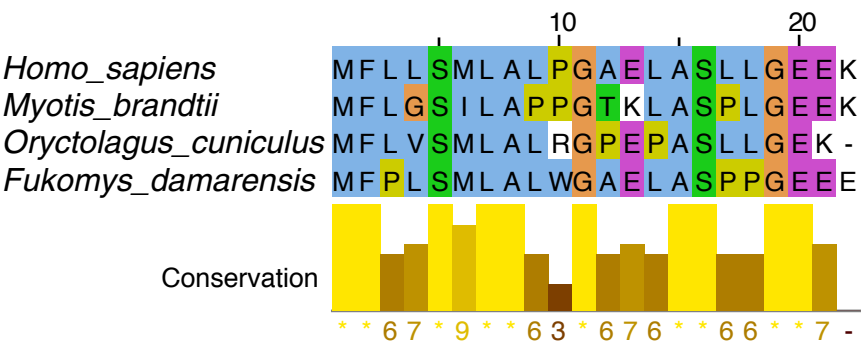
HG1076

ENSG00000150967 (ABCB9)



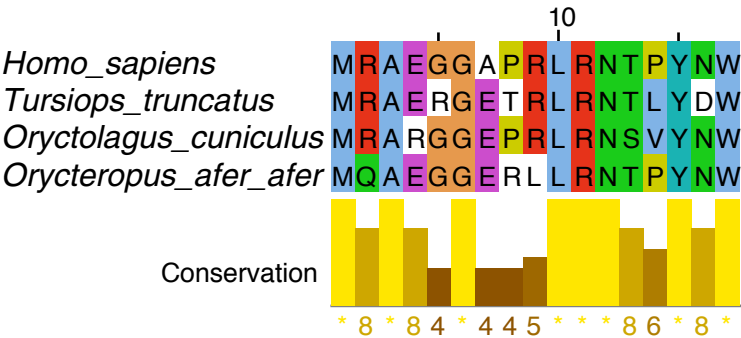
HG1077

ENSG00000151474 (FRMD4A)



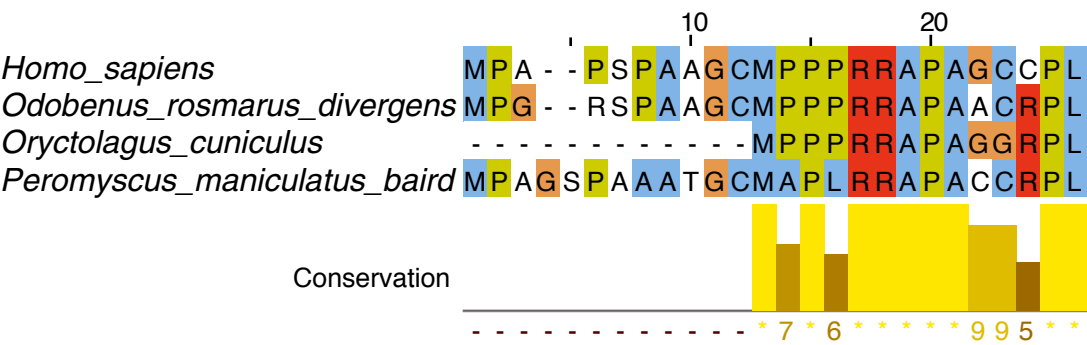
HG1078

ENSG00000162607 (USP1)



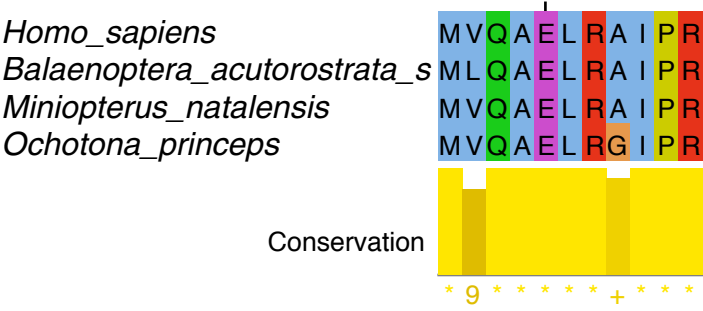
HG1079

ENSG00000162975 (KCNF1)



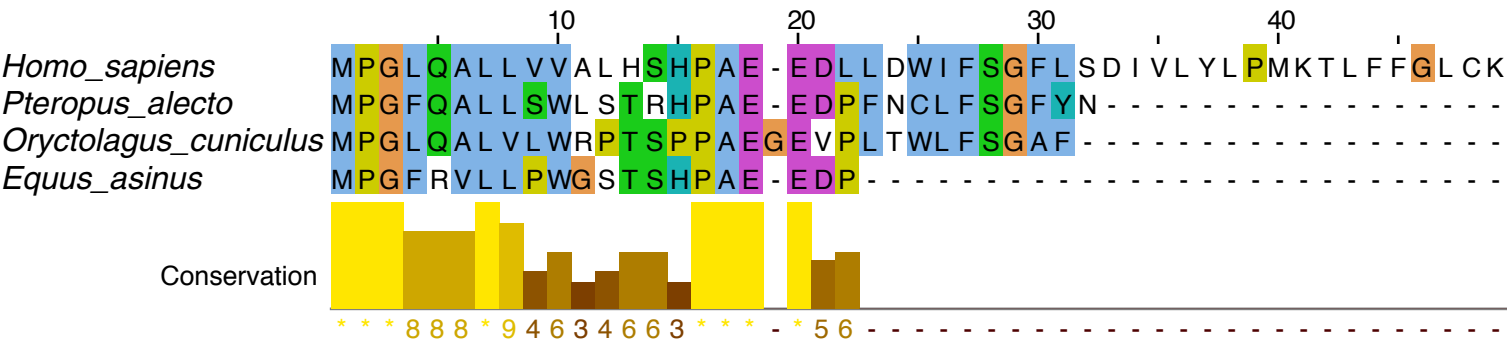
HG1080

ENSG00000164168 (TMEM184C)



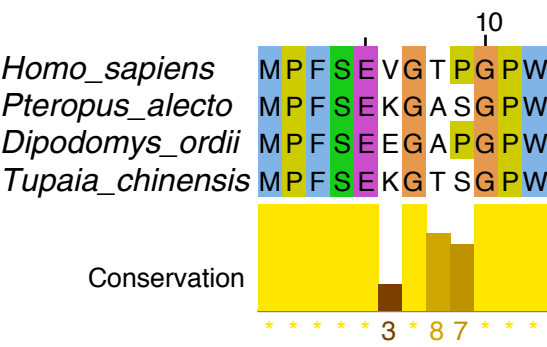
HG1081

ENSG00000165392 (WRN)



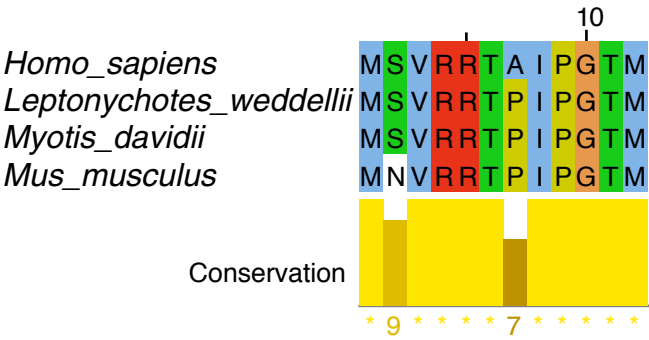
HG1082

ENSG00000165434 (PGM2L1)



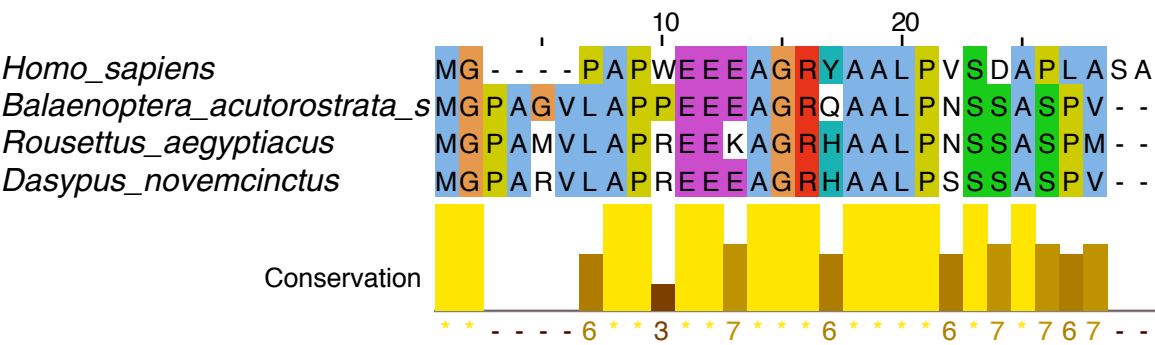
HG1083

ENSG00000165804 (ZNF219)



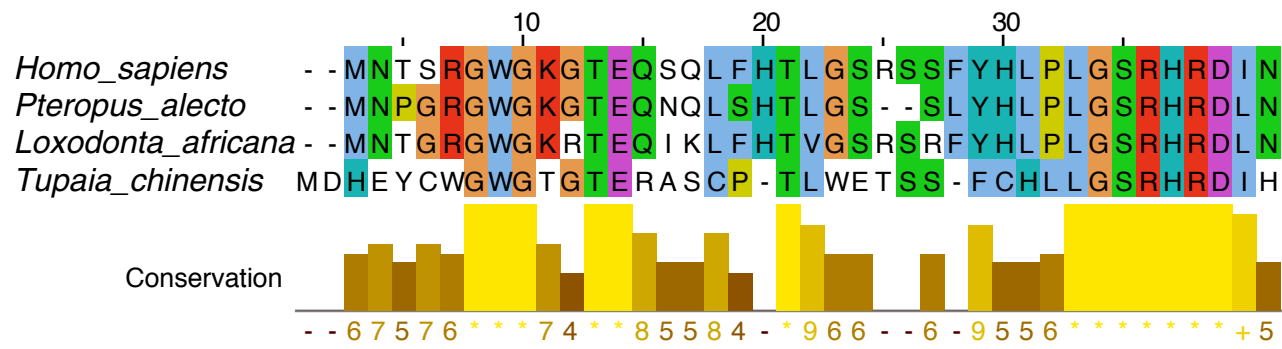
HG1084

ENSG00000165923 (AGBL2)



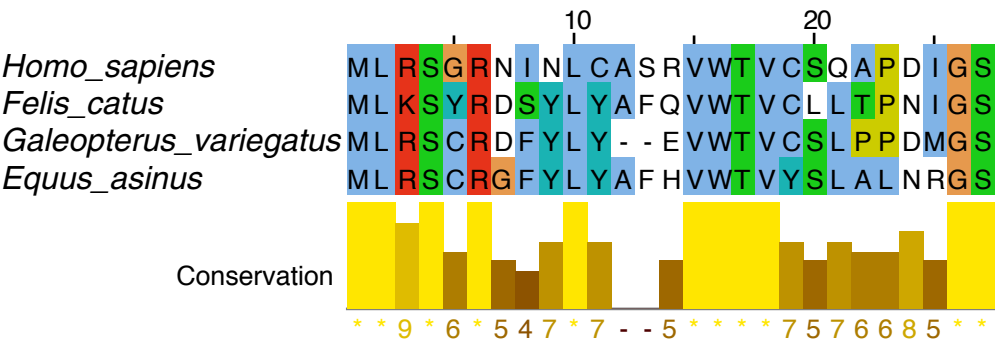
HG1085

ENSG00000166532 (RIMKLB)



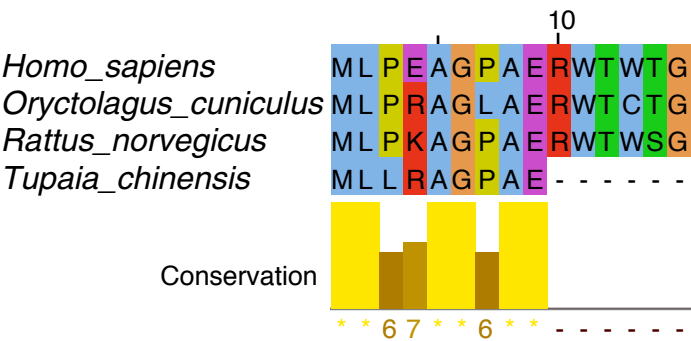
HG1086

ENSG00000167377 (ZNF23)



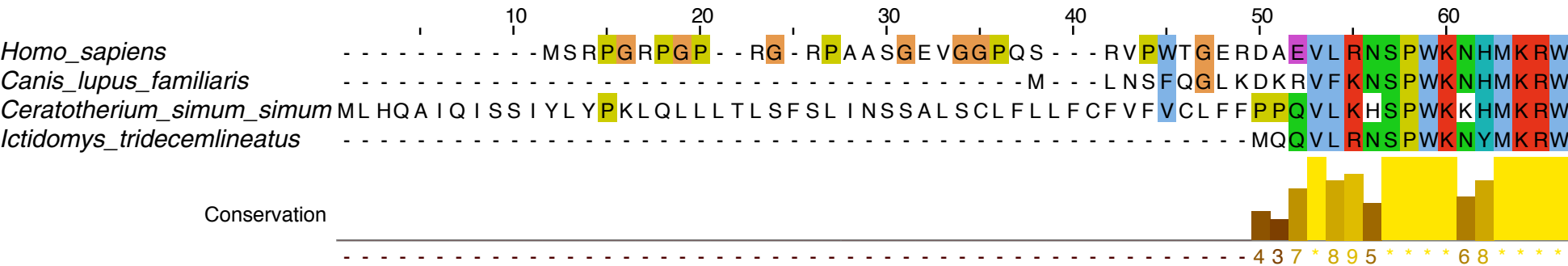
HG1087

ENSG00000168675 (LDLRAD4)



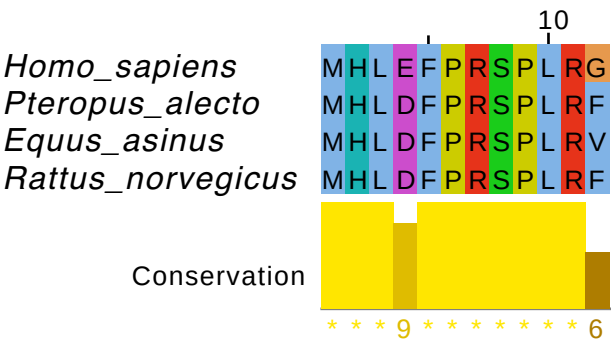
HG1088

ENSG00000169740 (ZNF32)

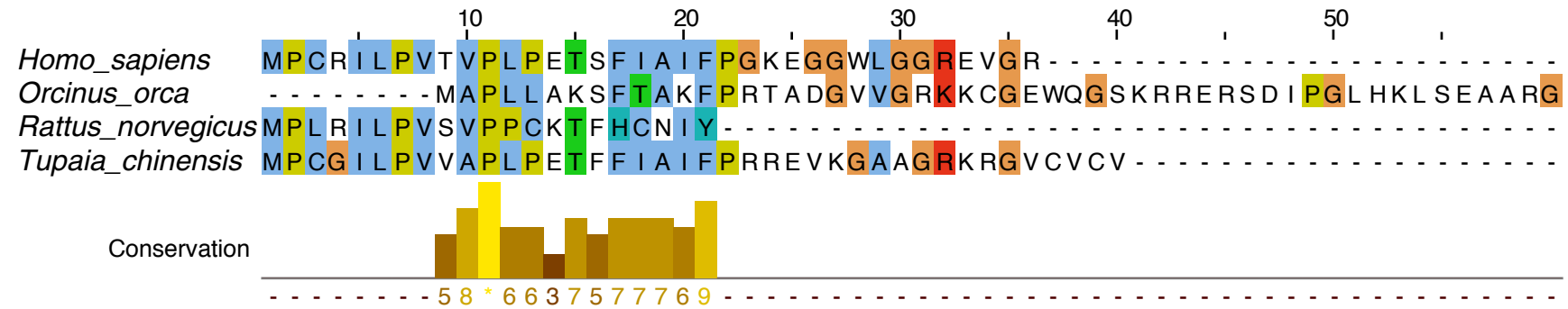


HG1089

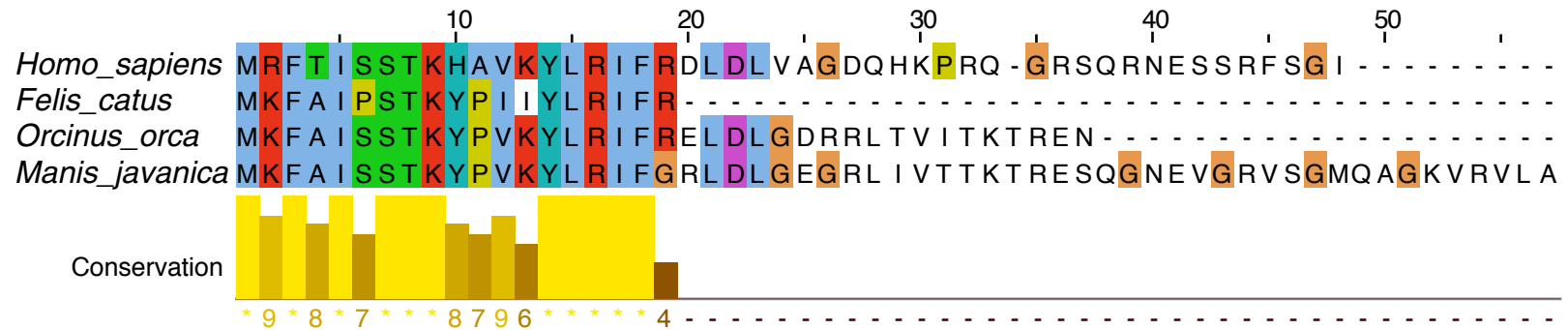
ENSG00000169813 (HNRNPF)



ENSG00000170458 (CD14)

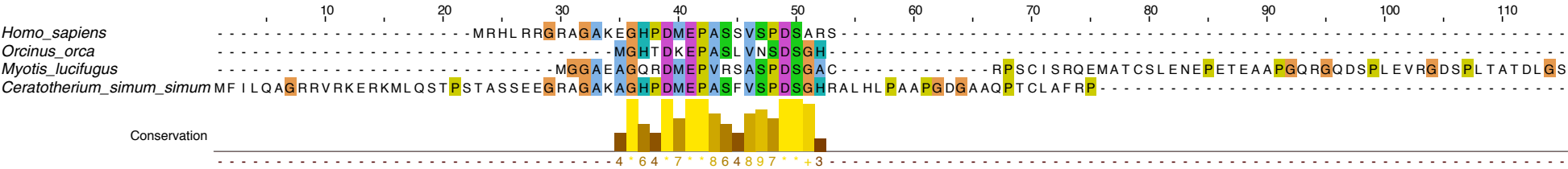


ENSG00000170458 (CD14)



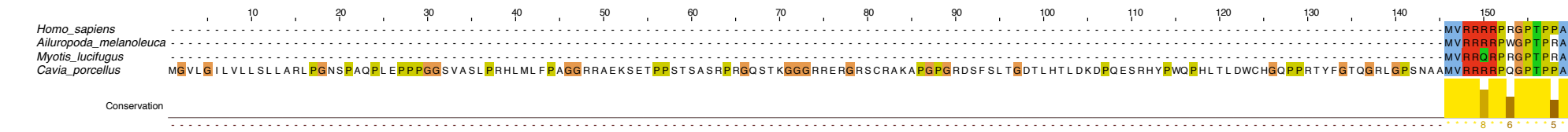
HG1091

ENSG00000172183 (ISG20)

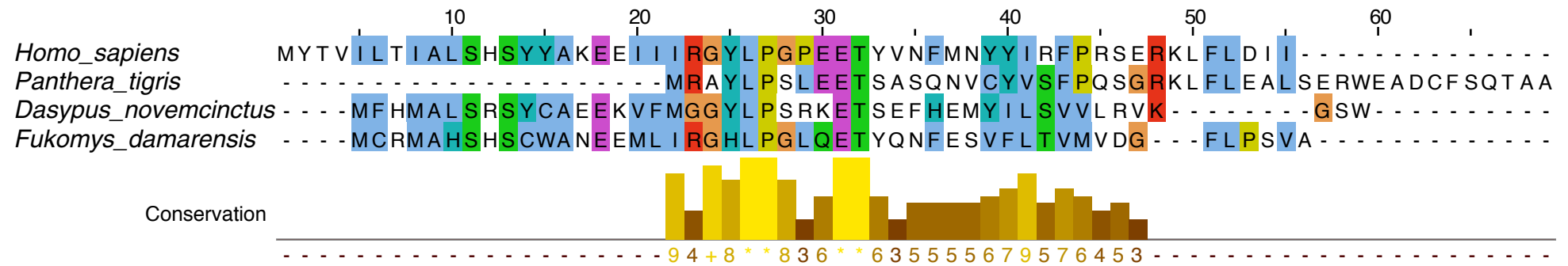


HG1092

ENSG00000173327 (MAP3K11)

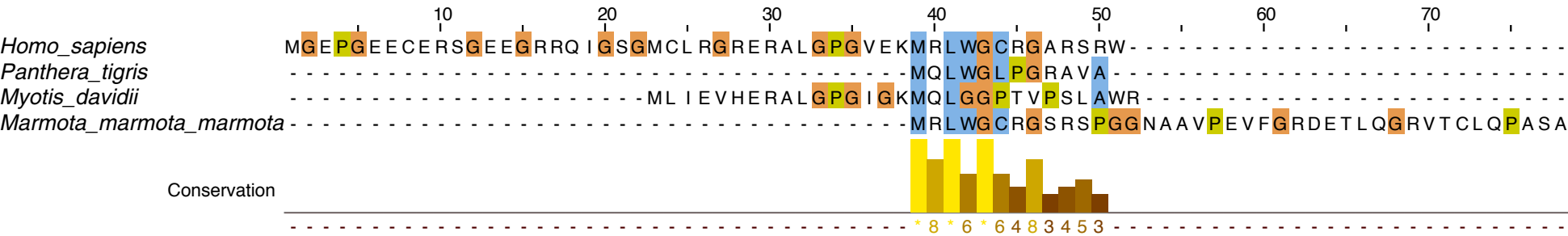


ENSG00000174371 (EXO1)



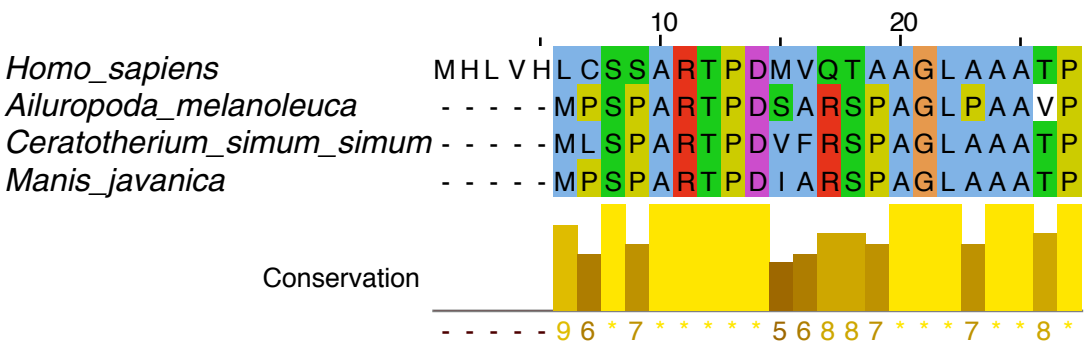
HG1094

ENSG00000177917 (ARL6IP6)



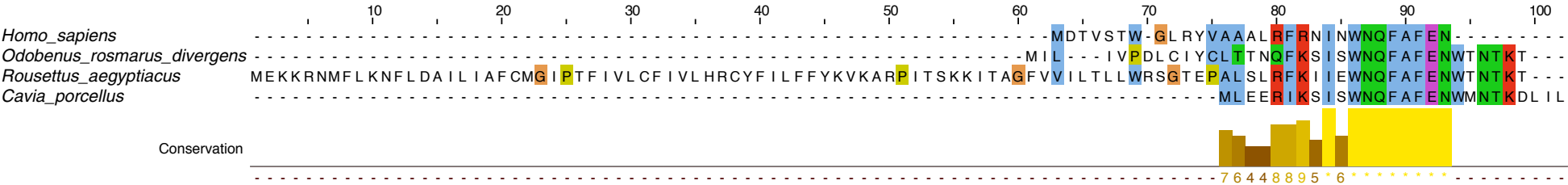
HG1095

ENSG00000179921 (GPBAR1)



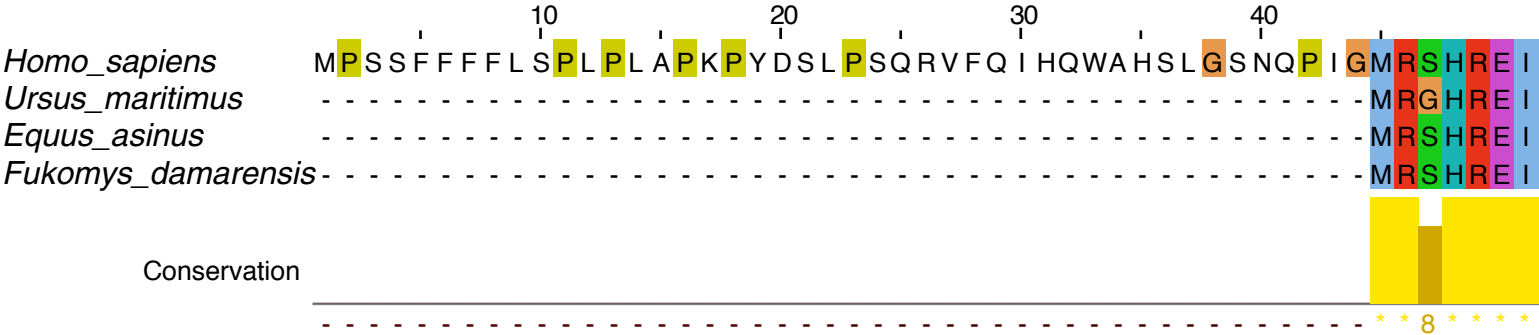
HG1096

ENSG00000181544 (FANCB)



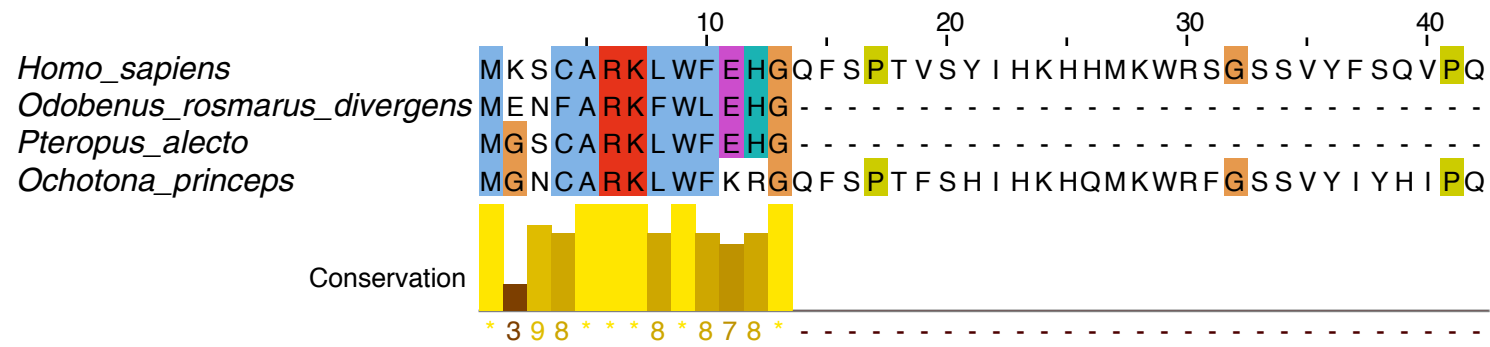
HG1097

ENSG00000182481 (KPNA2)



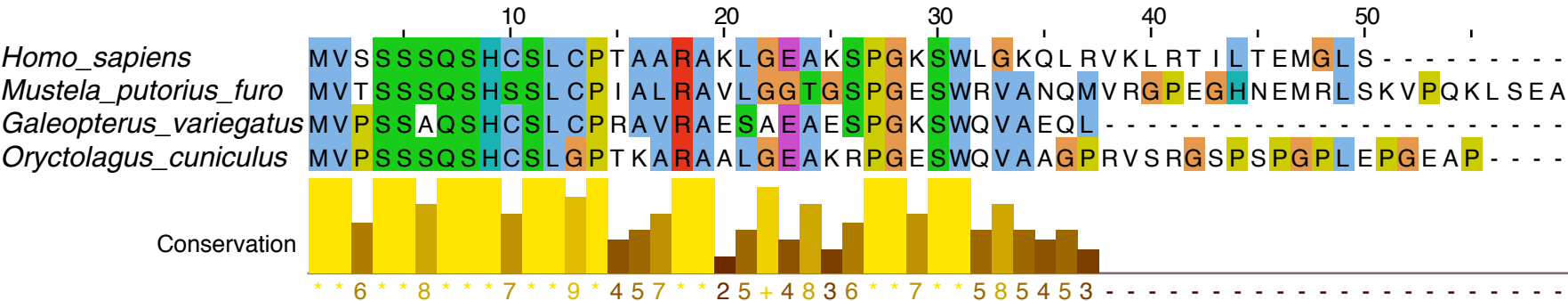
HG1098

ENSG00000183775 (KCTD16)



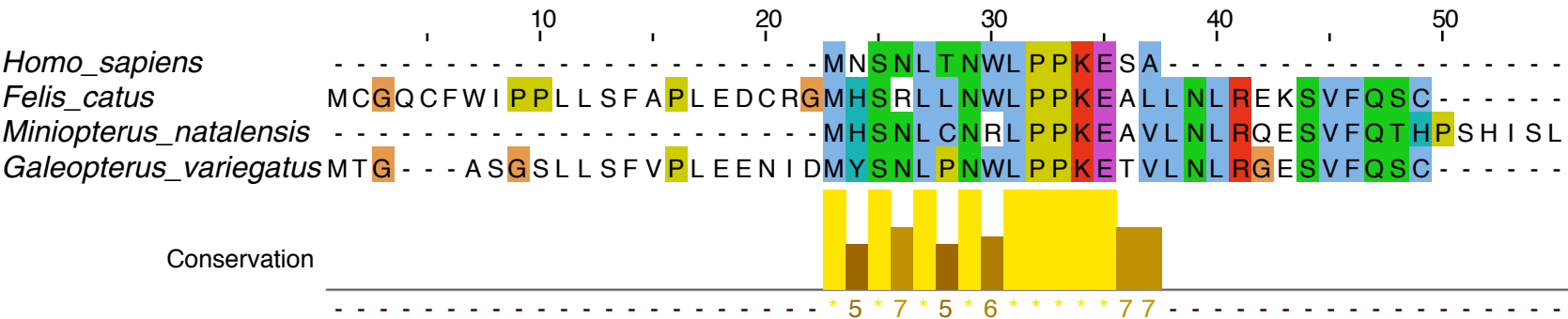
HG1099

ENSG00000186334 (SLC36A3)



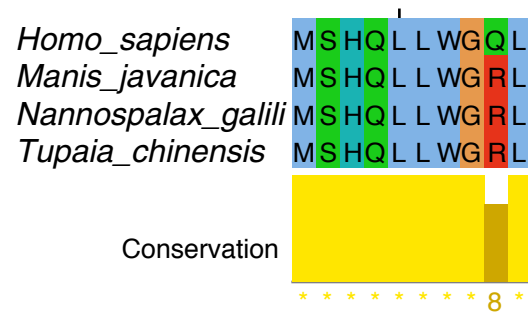
HG1100

ENSG00000187815 (ZFP69)



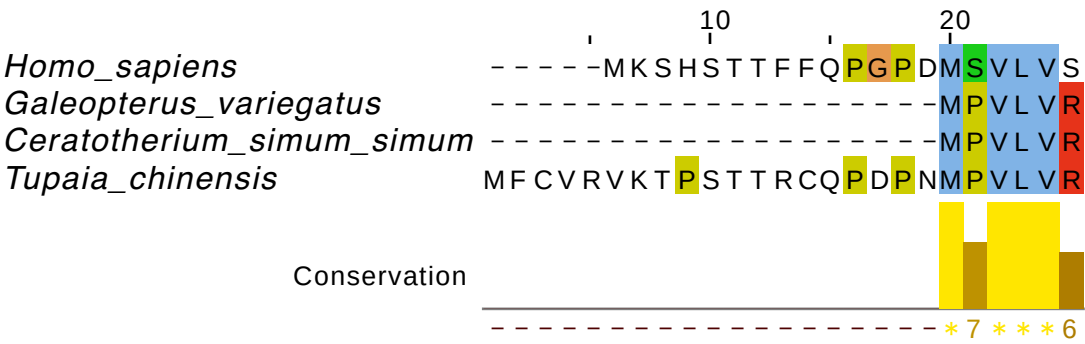
HG1101

ENSG00000189334 (S100A14)



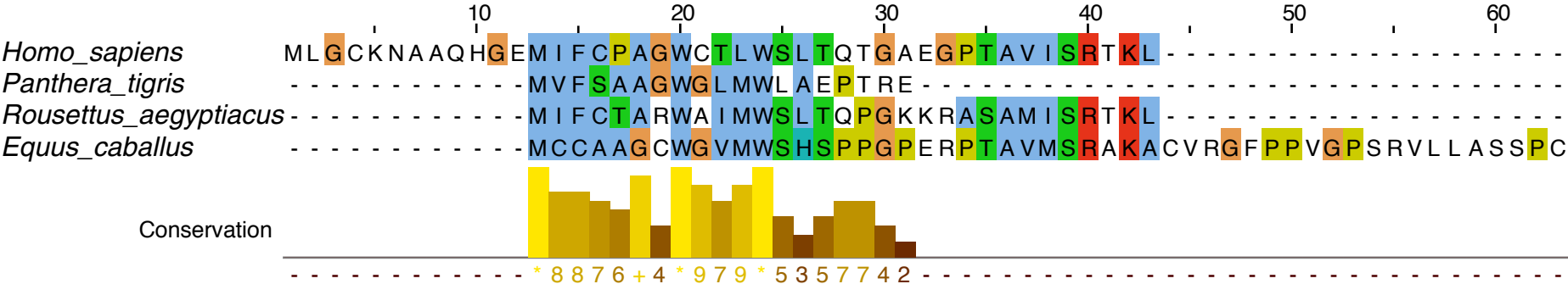
HG1102

ENSG00000196704 (AMZ2)



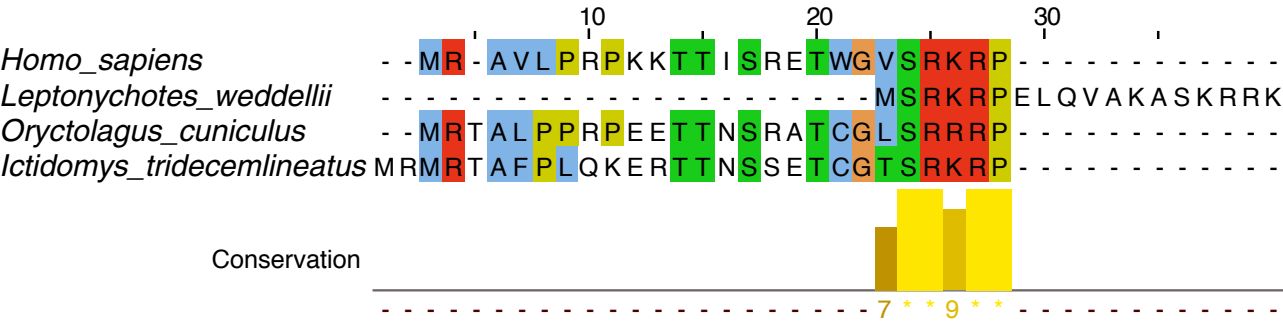
HG1103

ENSG00000197620 (CXorf40A)

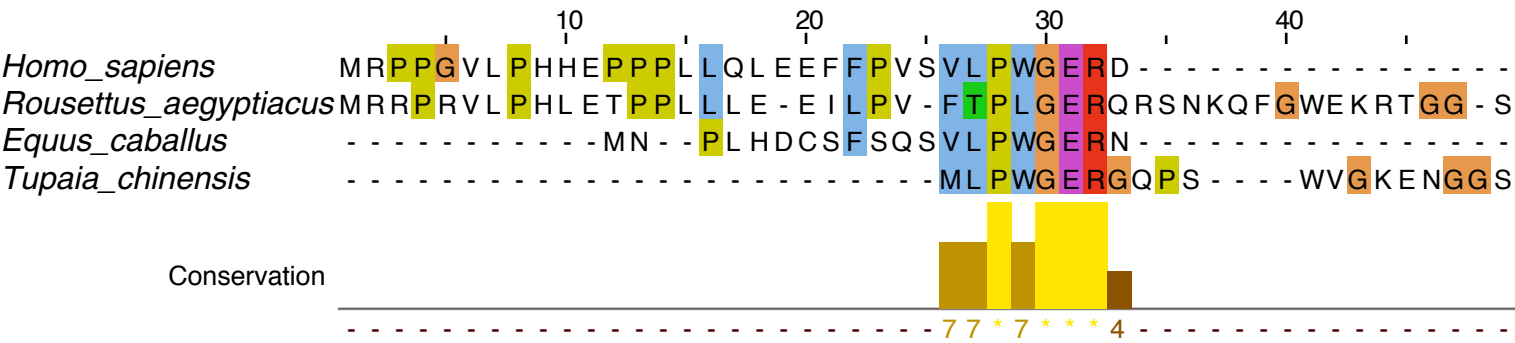


HG1104

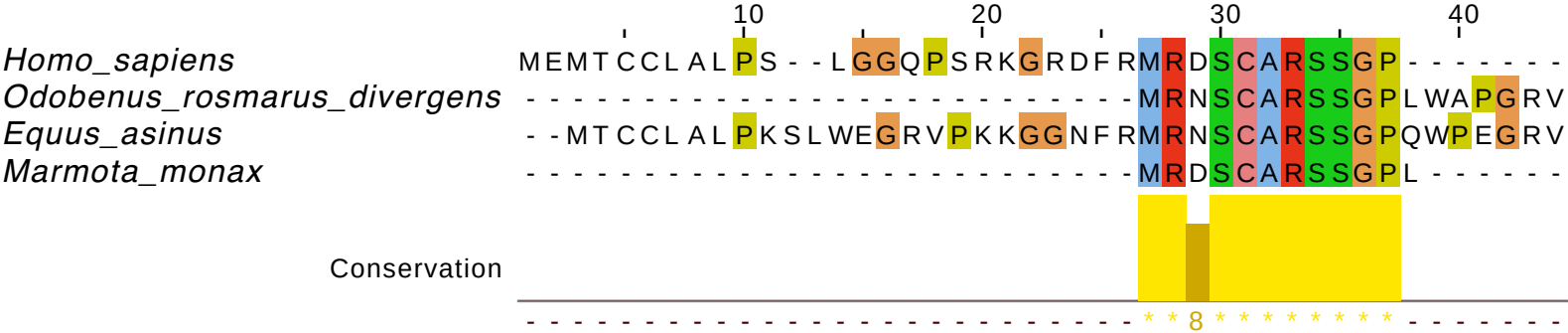
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HG1105
ENSG00000213654 (GPSM3)

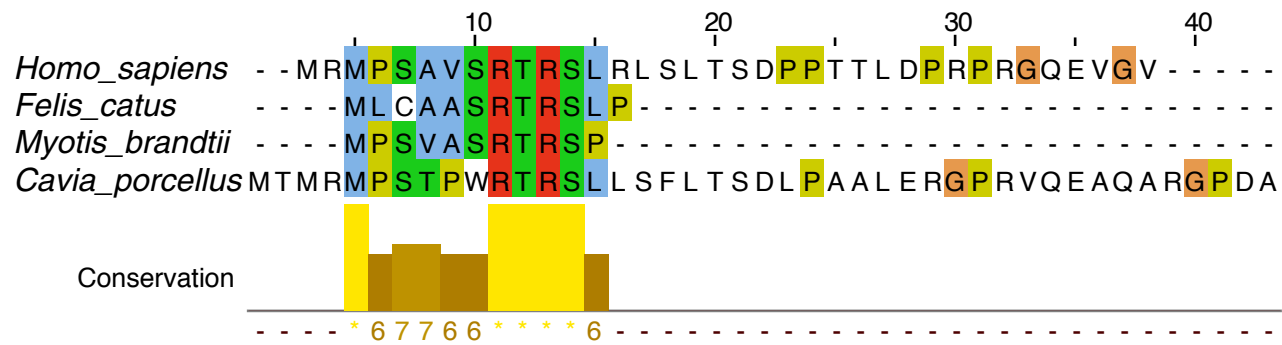


HG1106
 ENSG00000215021 (PHB2)



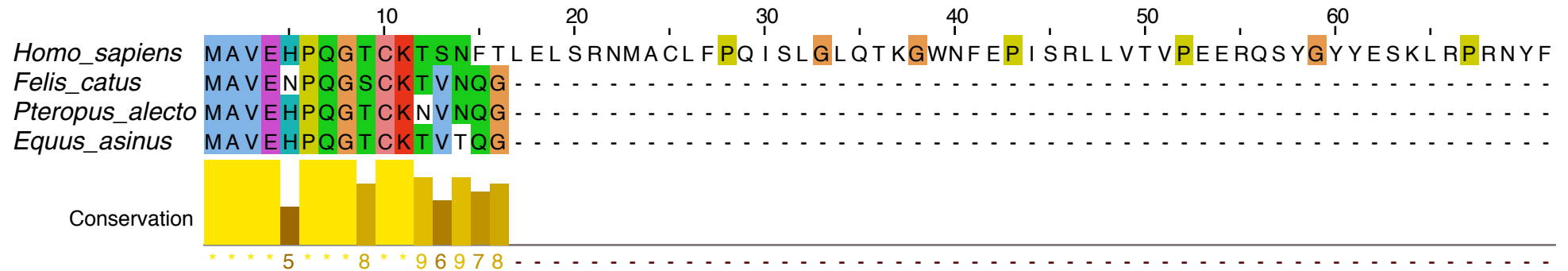
HG1107

ENSG00000217930 (PAM16)

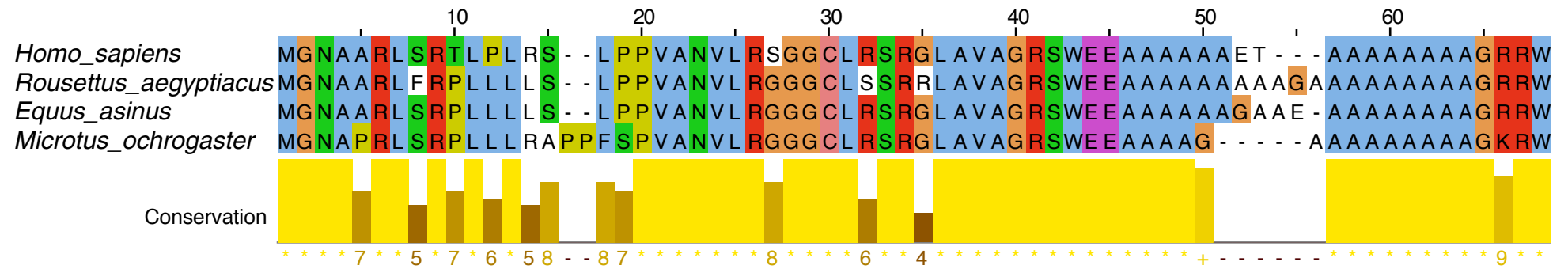


HG1108

ENSG00000251247 (ZNF345)

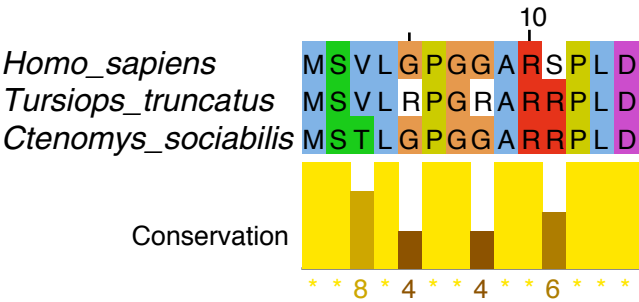


ENSG00000278311 (GGNBP2)



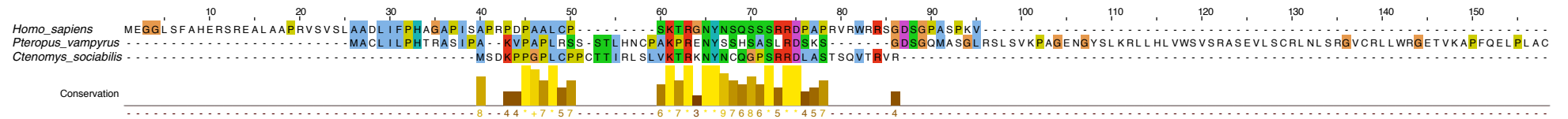
HG1110

ENSG00000034152 (MAP2K3)



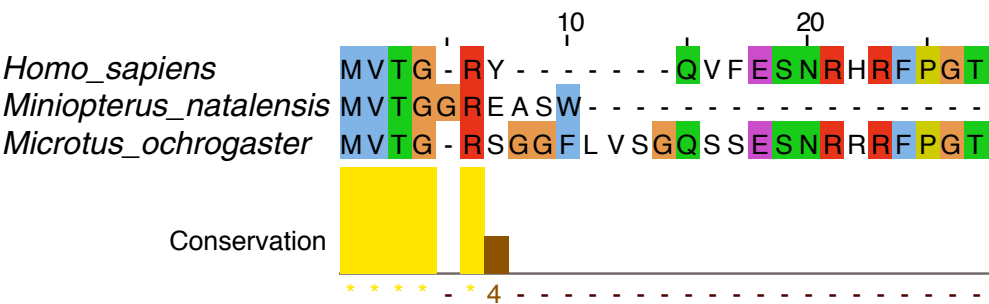
HG1111

ENSG00000040531 (CTNS)



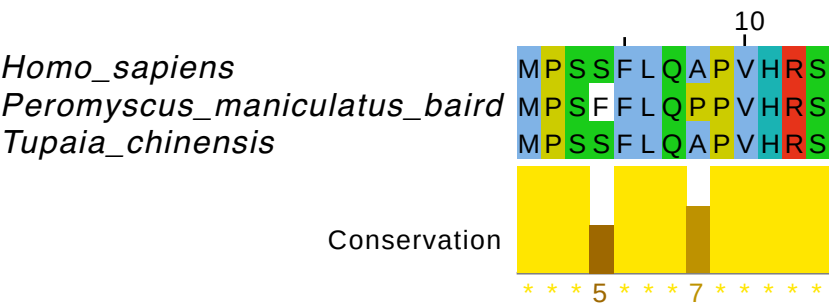
HG1112

ENSG00000068885 (IFT80)



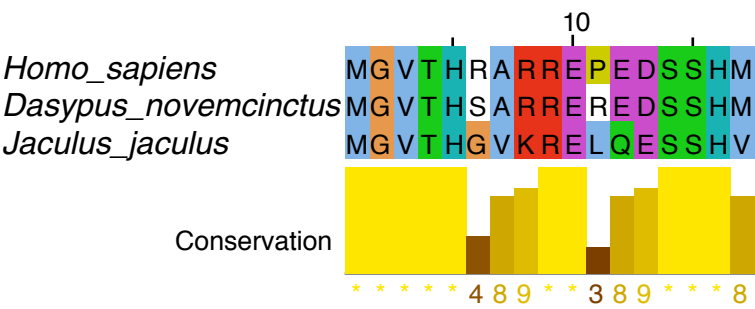
HG1113

ENSG00000072201 (LNX1)



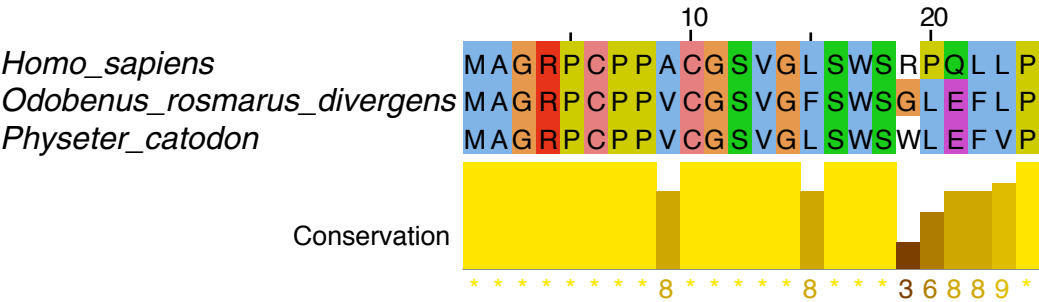
HG1114

ENSG00000073737 (DHRS9)



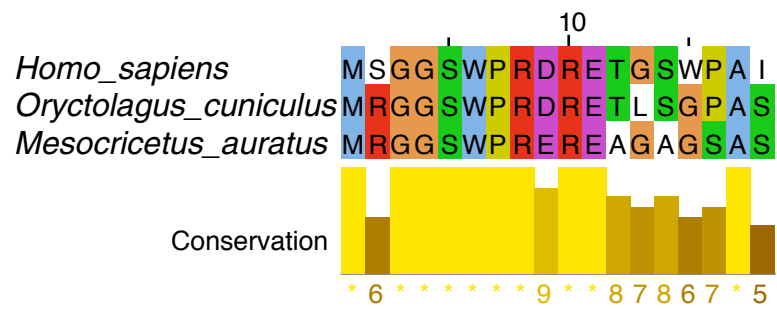
HG1115

ENSG00000074219 (TEAD2)



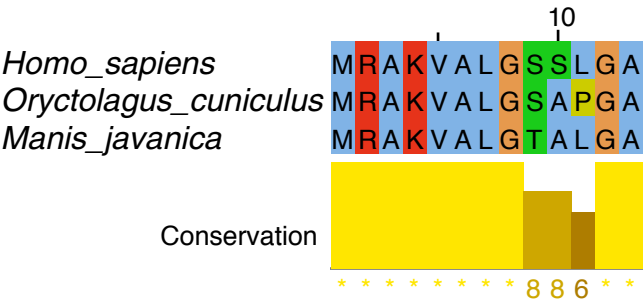
HG1116

ENSG00000084090 (STARD7)



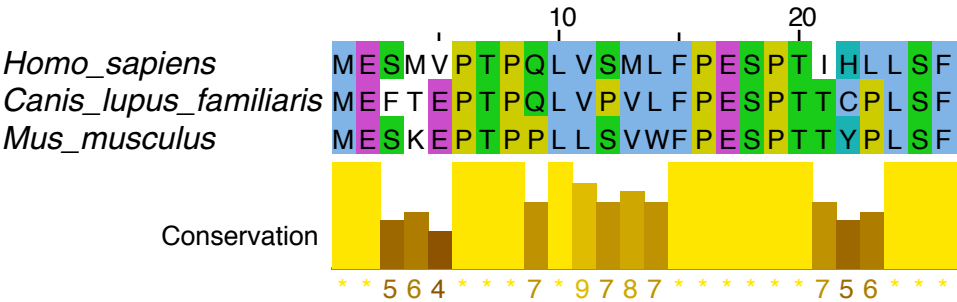
HG1117

ENSG00000089902 (RCOR1)

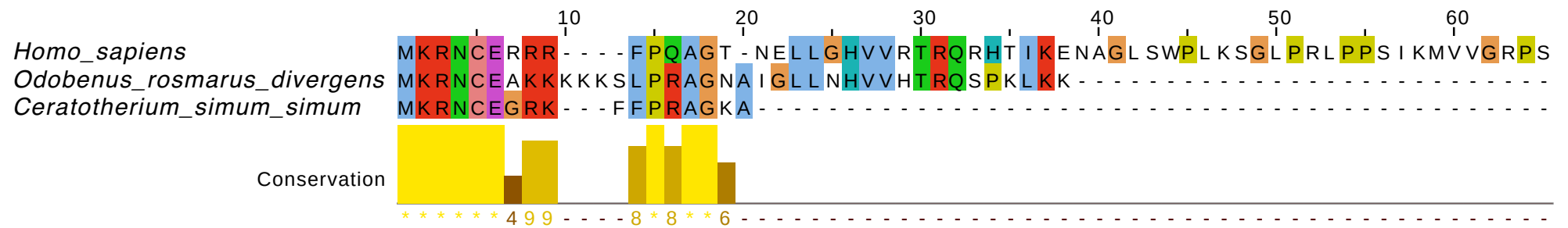


HG1118

ENSG00000090975 (PITPNM2)

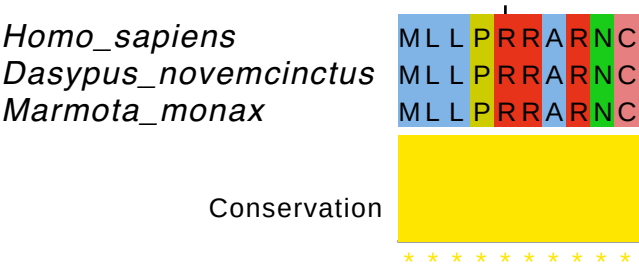


ENSG00000092020 (PPP2R3C)



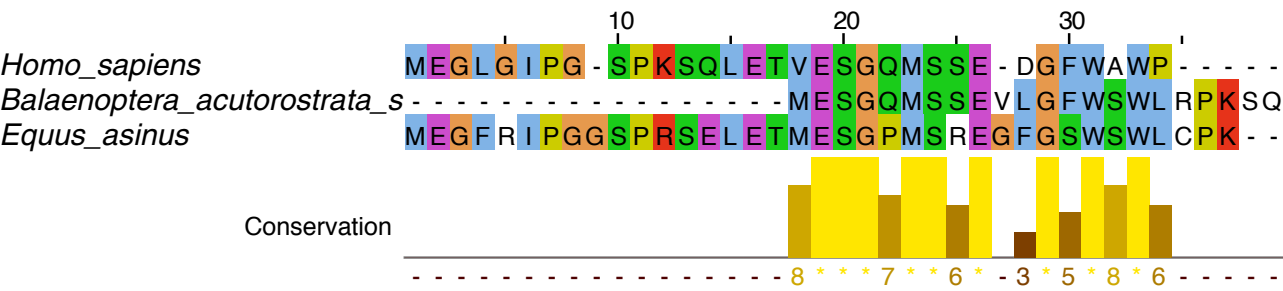
HG1120

ENSG00000095585 (BLNK)



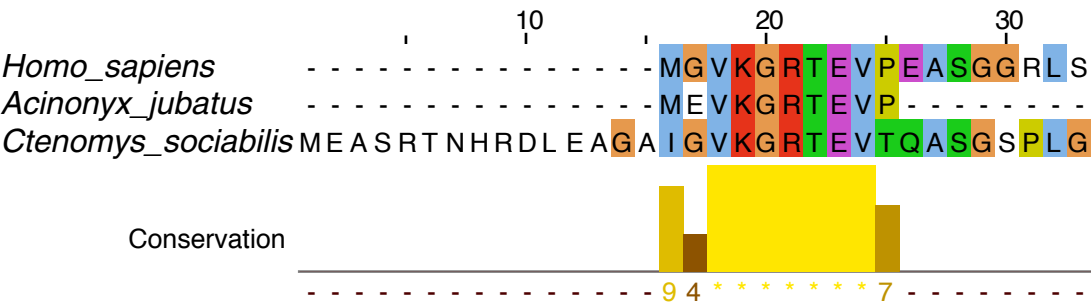
HG1121

ENSG00000100350 (FOXRED2)



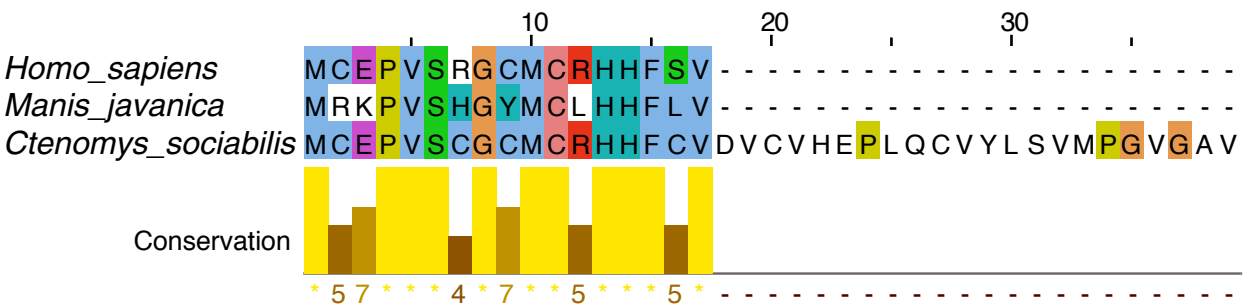
HG1122

ENSG00000100410 (PHF5A)



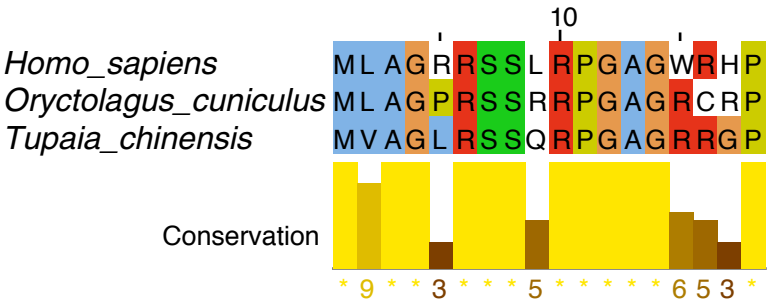
HG1123

ENSG00000100884 (CPNE6)



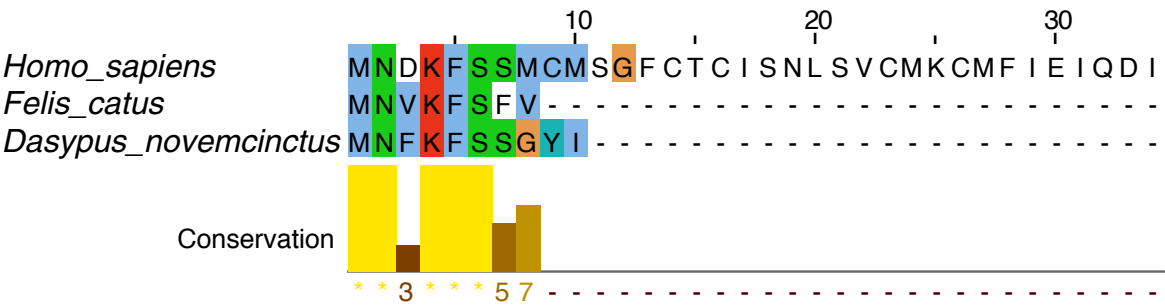
HG1124

ENSG00000100934 (SEC23A)



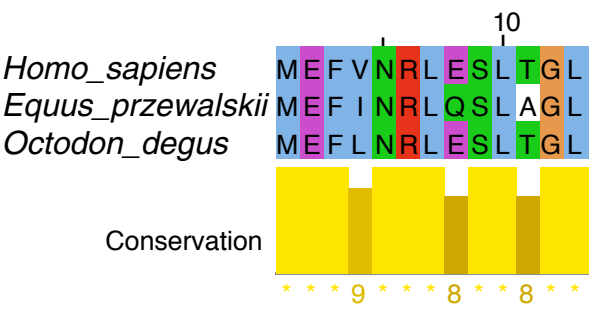
HG1125

ENSG00000101574 (METTL4)



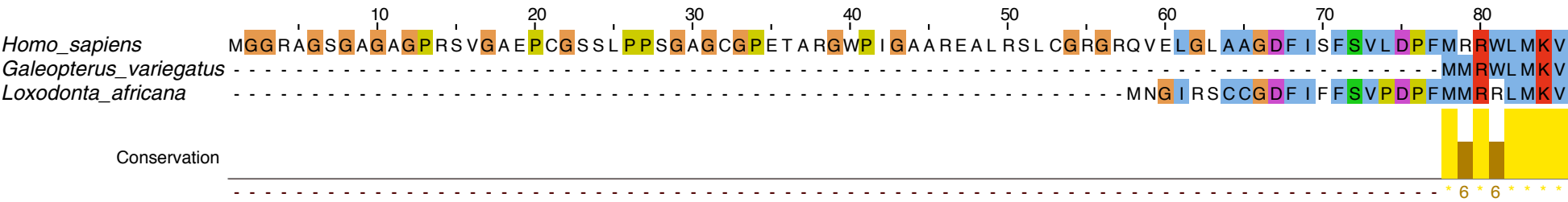
HG1126

ENSG00000101890 (GUCY2F)



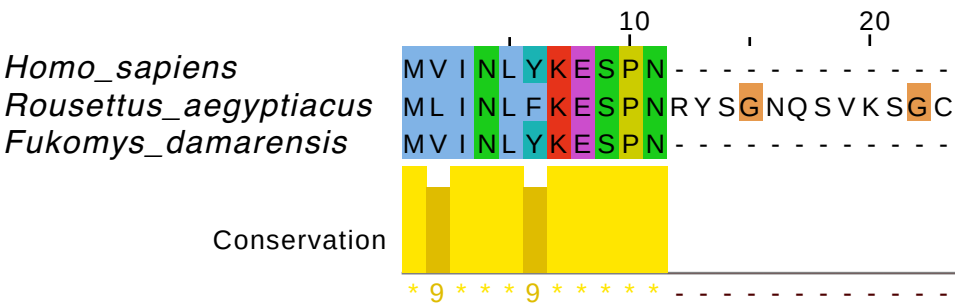
HG1127

ENSG00000103064 (SLC7A6)



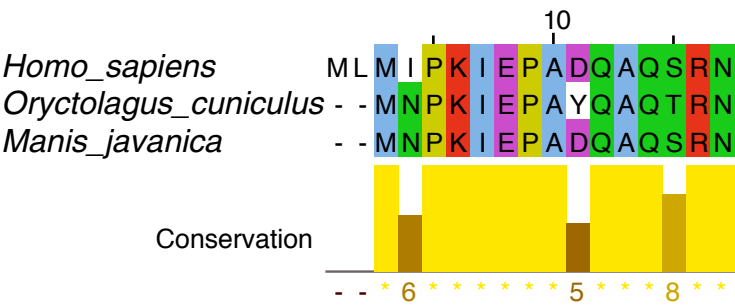
HG1128

ENSG00000103852 (TTC23)



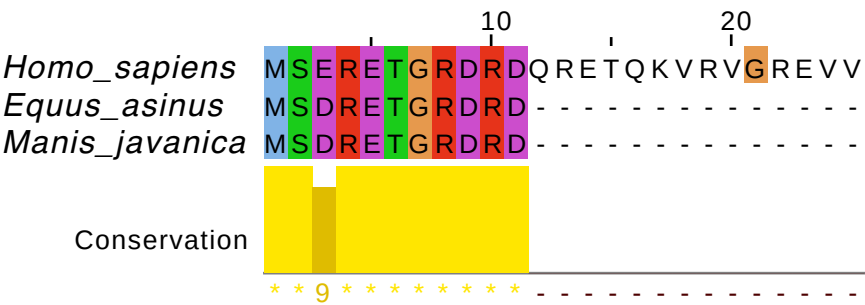
HG1129

ENSG00000104432 (IL7)



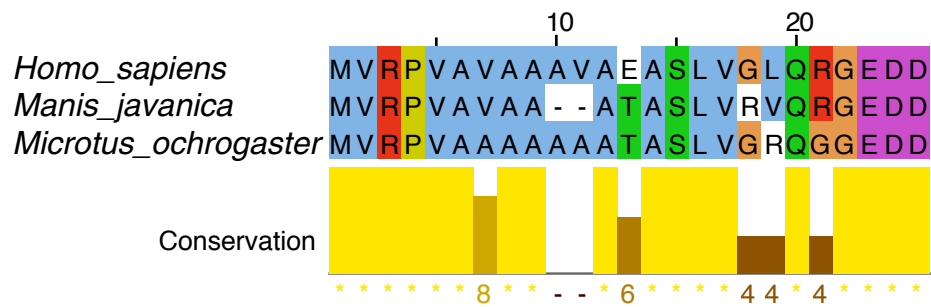
HG1130

ENSG00000105559 (PLEKHA4)



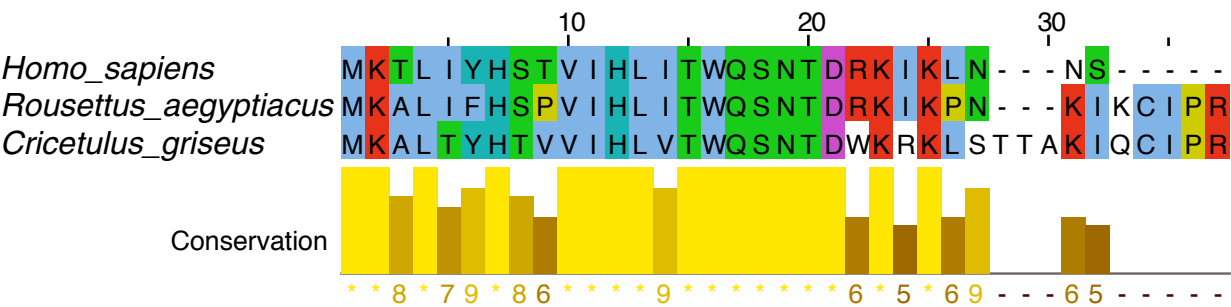
HG1131

ENSG00000106780 (MEGF9)



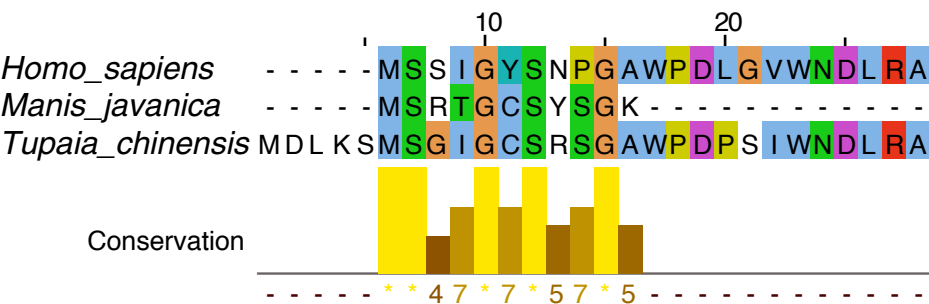
HG1132

ENSG00000109771 (LRP2BP)



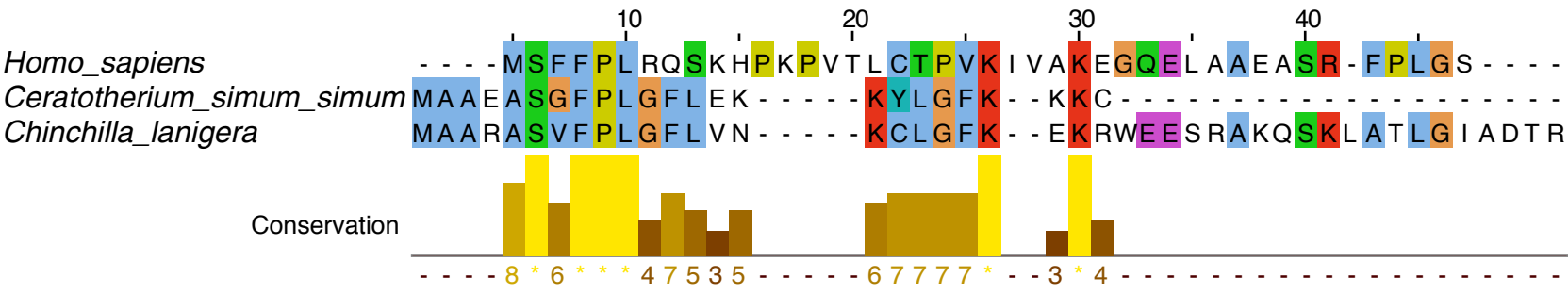
HG1133

ENSG00000111328 (CDK2AP1)

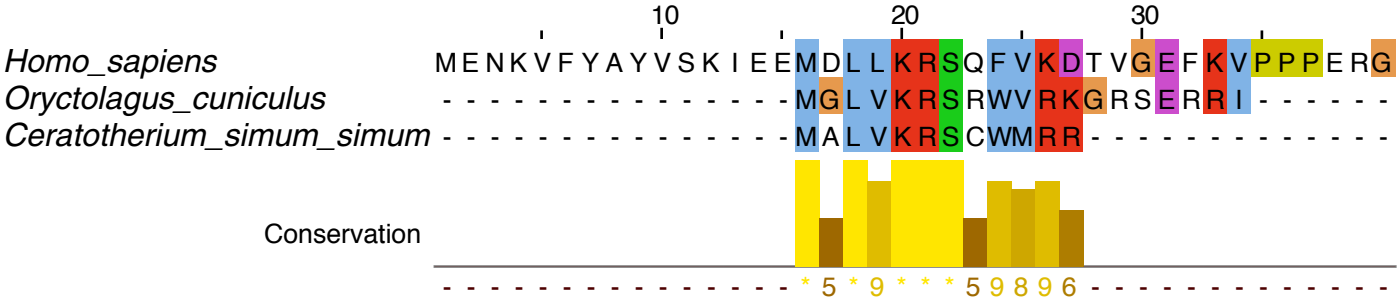


HG1134

ENSG00000112984 (KIF20A)

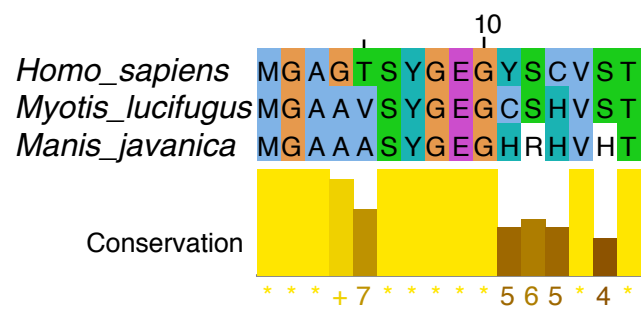


HG1135
 ENSG00000113597 (TRAPPC13)



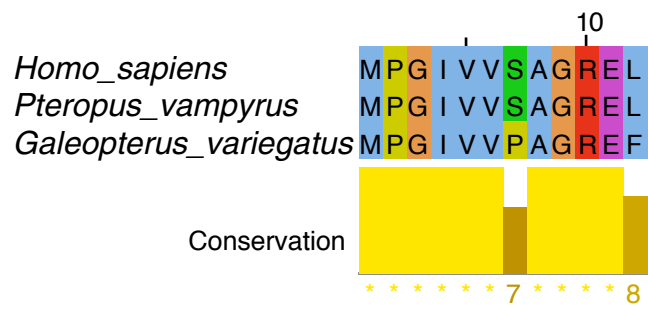
HG1136

ENSG00000113749 (HRH2)



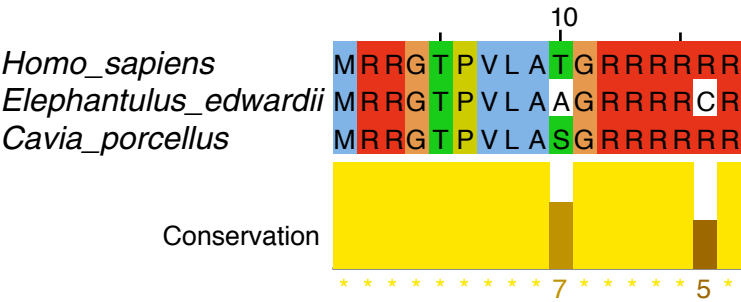
HG1137

ENSG00000115307 (AUP1)

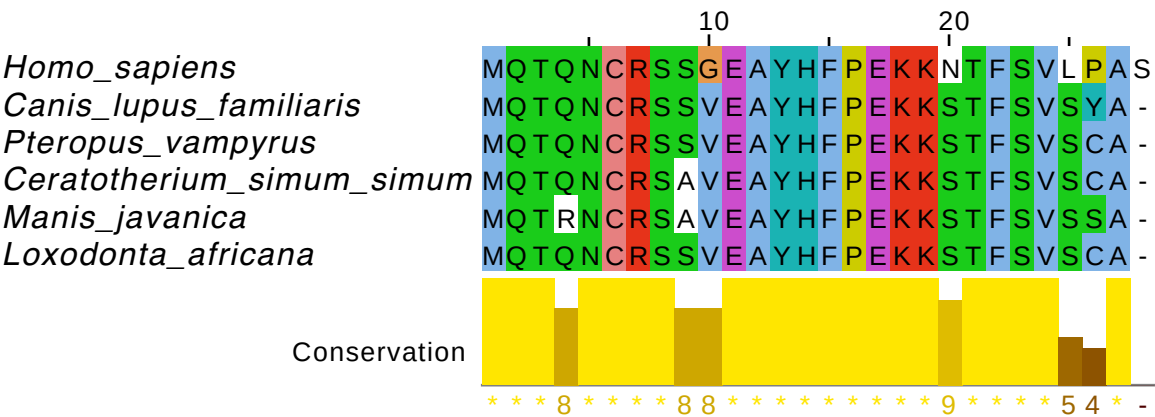


HG1138

ENSG00000116871 (MAP7D1)

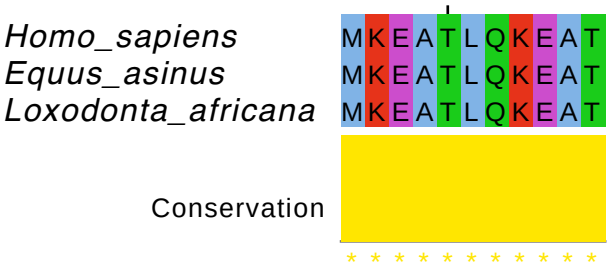


HG1139.1
ENSG00000118308 (LRMP)



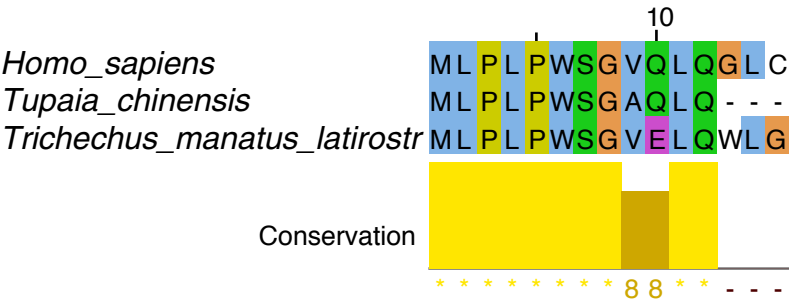
HG1139.2

ENSG00000118308 (LRMP)



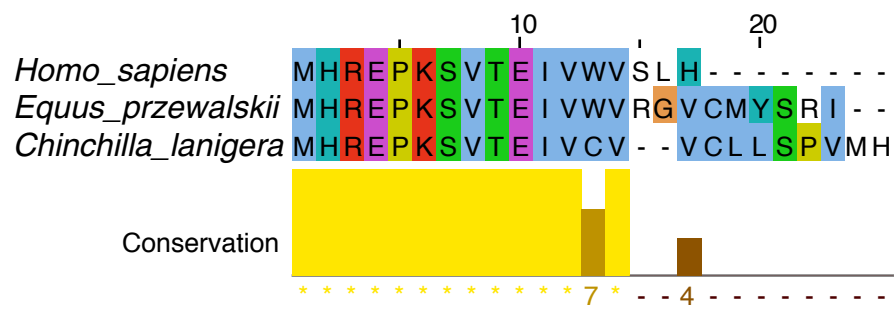
HG1140

ENSG00000118495 (PLAGL1)



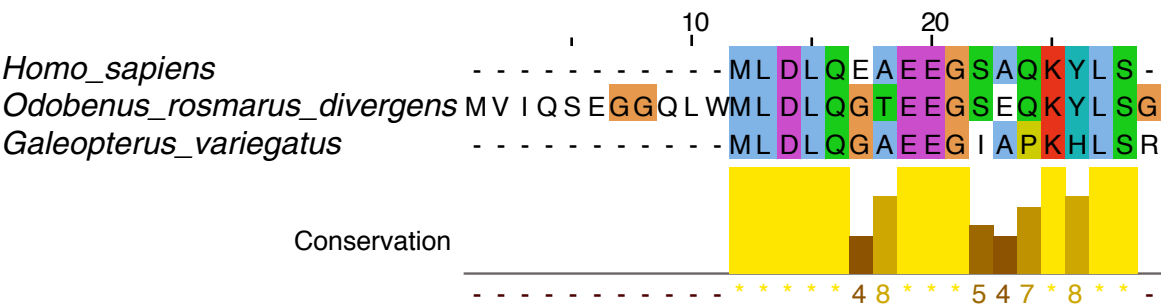
HG1141

ENSG00000121964 (GTDC1)



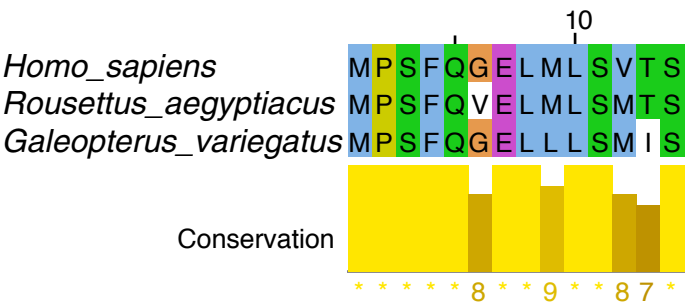
HG1142

ENSG00000124613 (ZNF391)



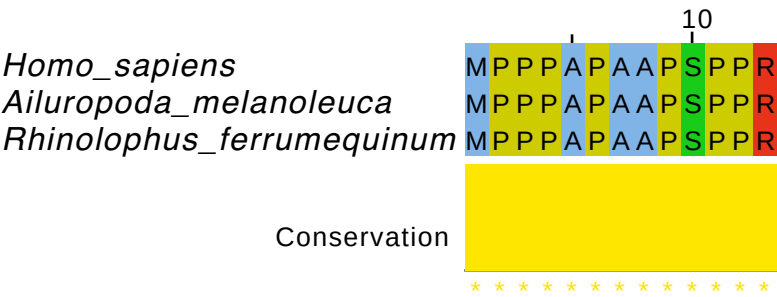
HG1143

ENSG00000125245 (GPR18)



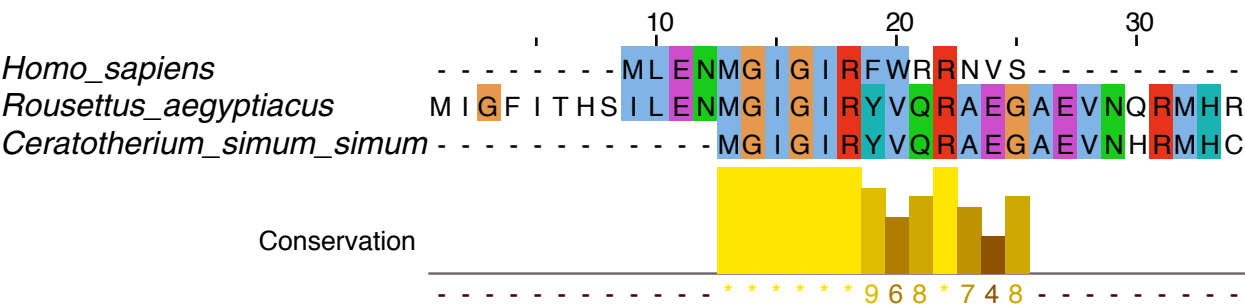
HG1144

ENSG00000128203 (ASPHD2)



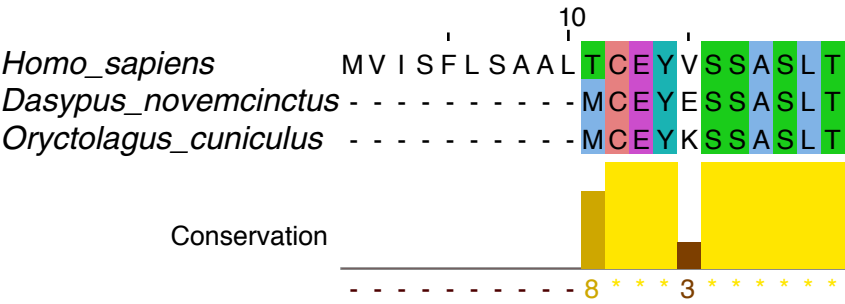
HG1145

ENSG00000128585 (MKLN1)



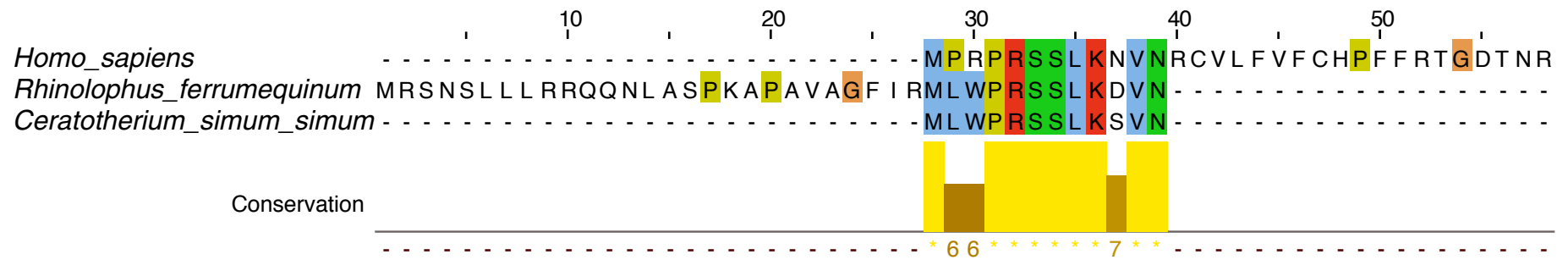
HG1146

ENSG00000130413 (STK33)



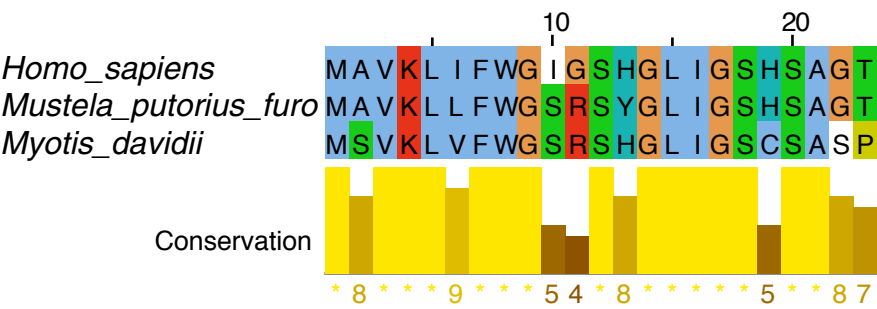
HG1147

ENSG00000131781 (FMO5)



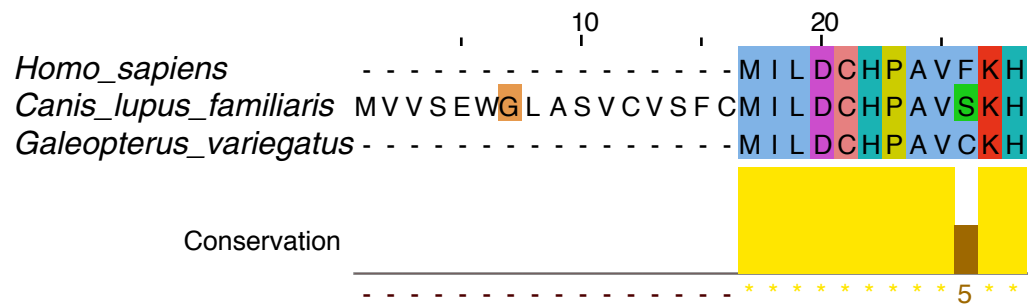
HG1148

ENSG00000132938 (MTUS2)



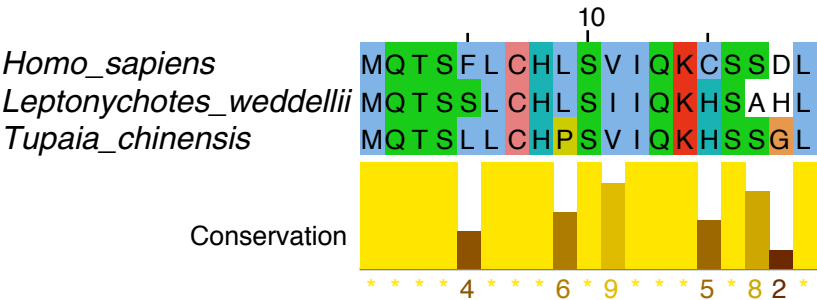
HG1149

ENSG00000132975 (GPR12)



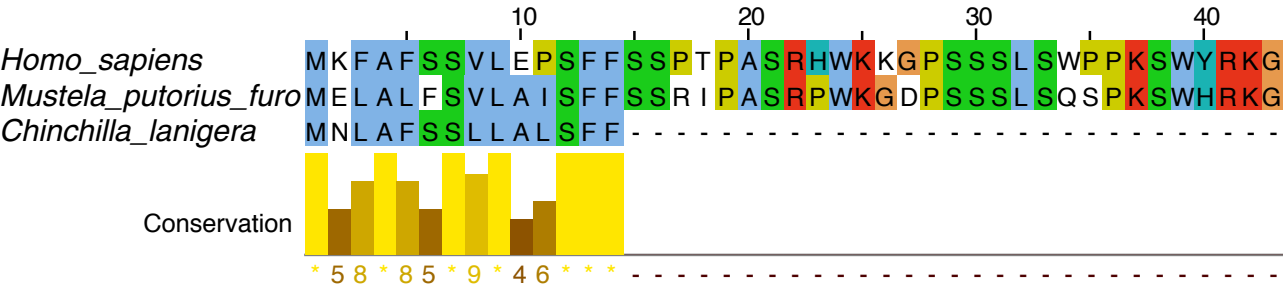
HG1150

ENSG00000135299 (ANKRD6)



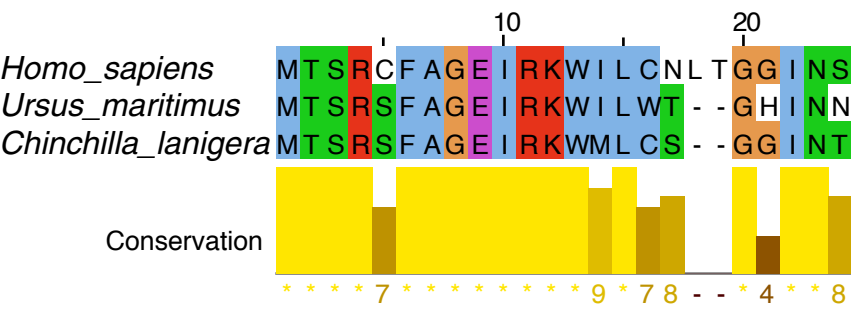
HG1151

ENSG00000137168 (PPIL1)



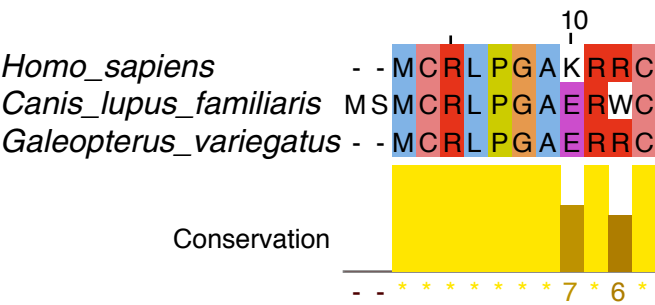
HG1152

ENSG00000138658 (ZGRF1)



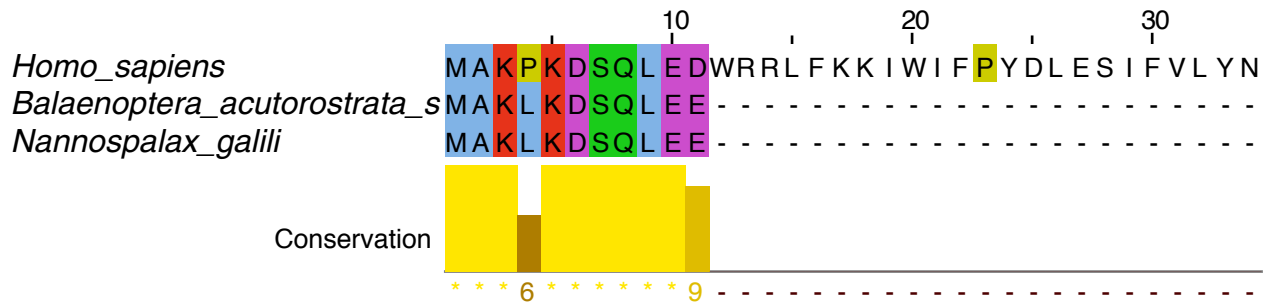
HG1153

ENSG00000138738 (PRDM5)



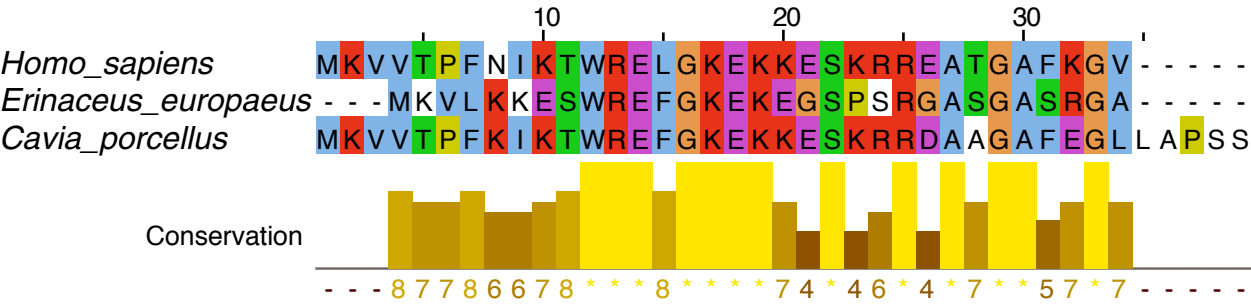
HG1154

ENSG00000139725 (RHOF)



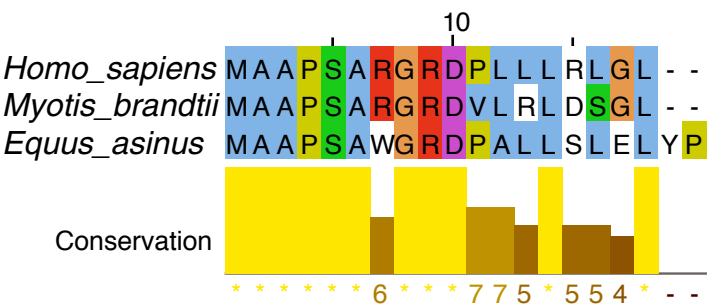
HG1155

ENSG00000141668 (CBLN2)



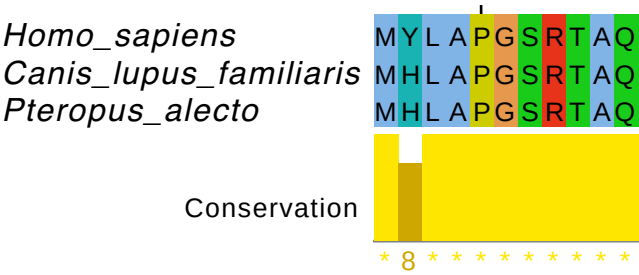
HG1156

ENSG00000144741 (SLC25A26)



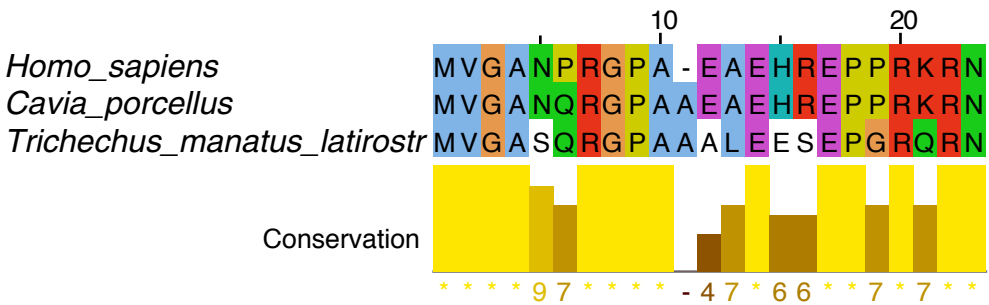
HG1157

ENSG00000148123 (PLPPR1)



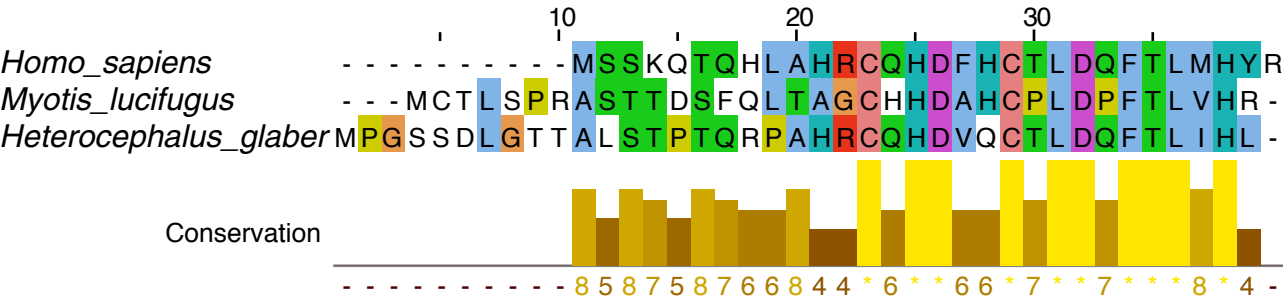
HG1158

ENSG00000149571 (KIRREL3)



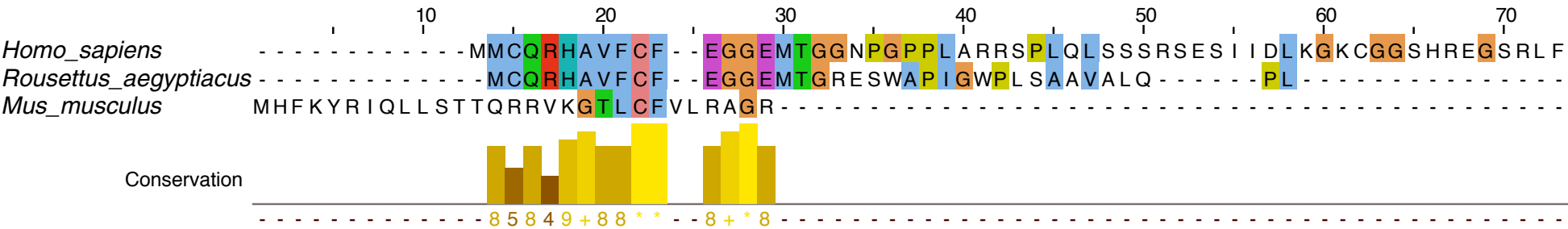
HG1159

ENSG00000152822 (GRM1)



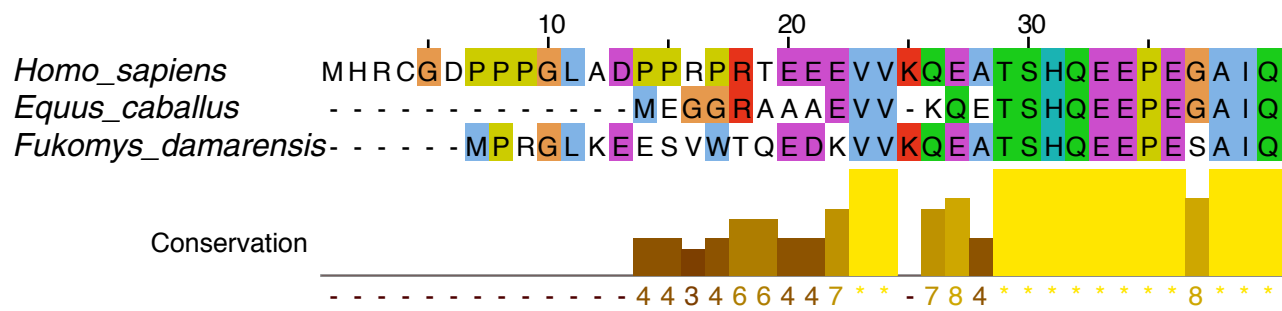
HG1160

ENSG00000154162 (CDH12)



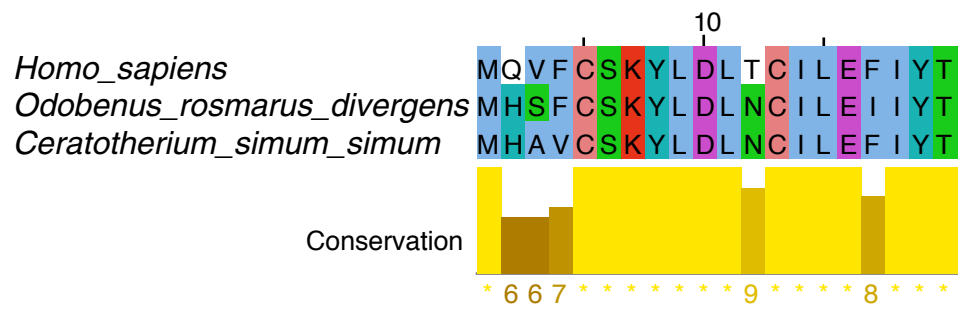
HG1161

ENSG00000154227 (CERS3)



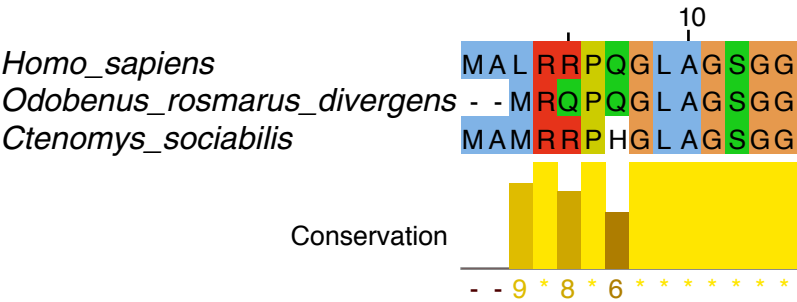
HG1162

ENSG00000155380 (SLC16A1)



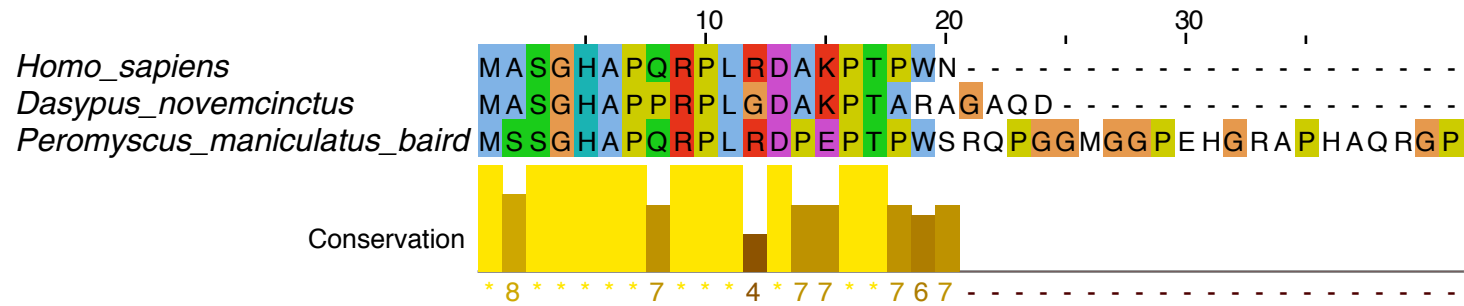
HG1163

ENSG00000157637 (SLC38A10)



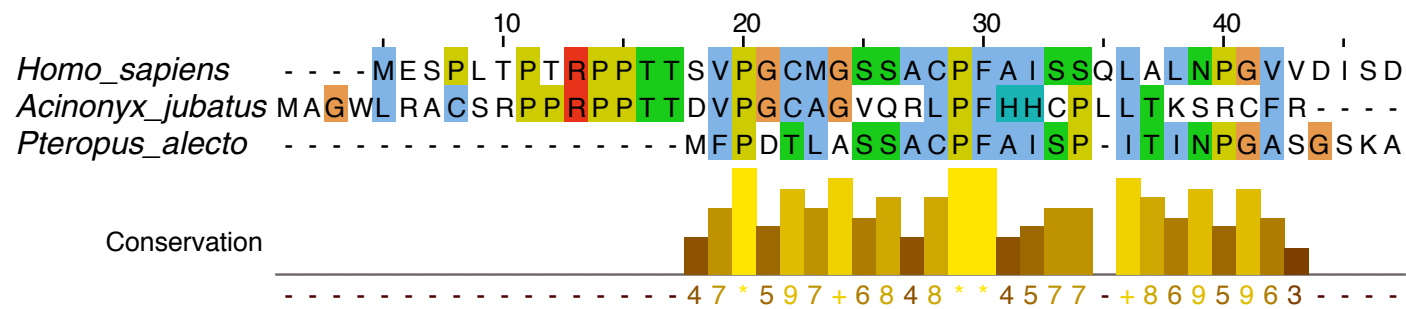
HG1164

ENSG00000162639 (HENMT1)



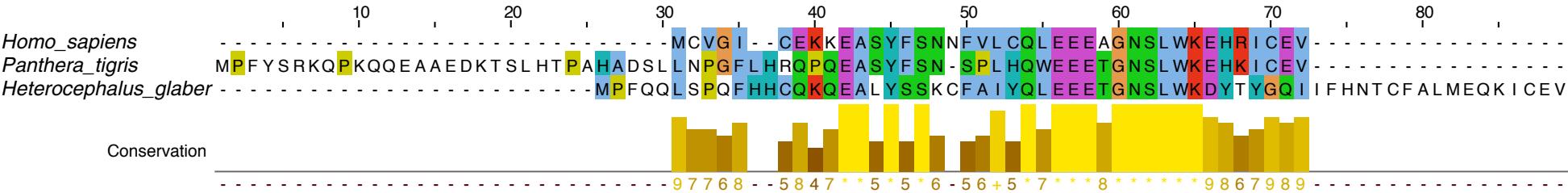
HG1165

ENSG00000162694 (EXTL2)



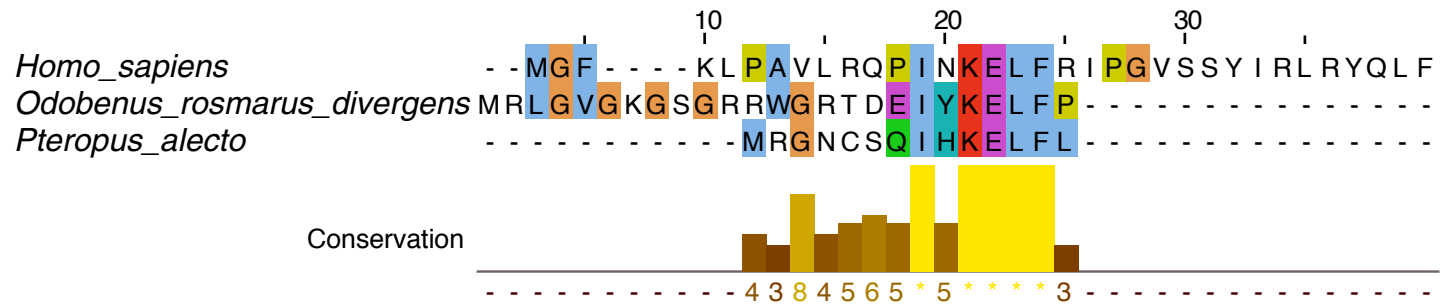
HG1166

ENSG00000165071 (TMEM71)



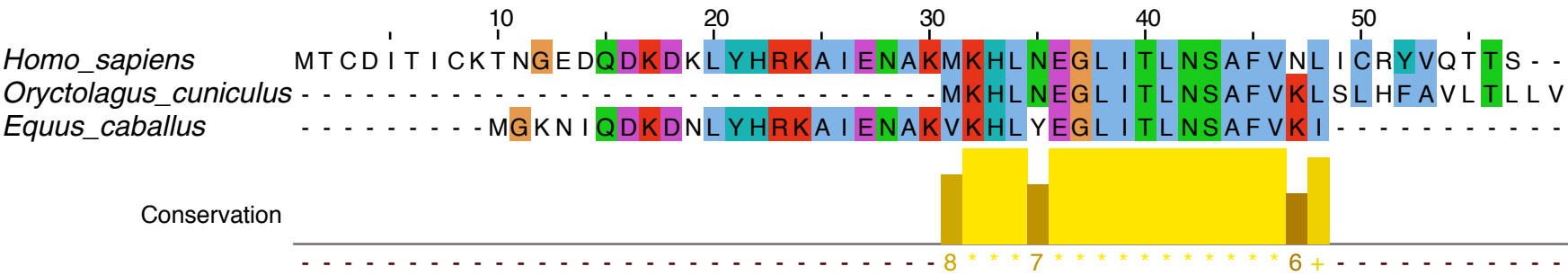
HG1167

ENSG00000165934 (CPSF2)



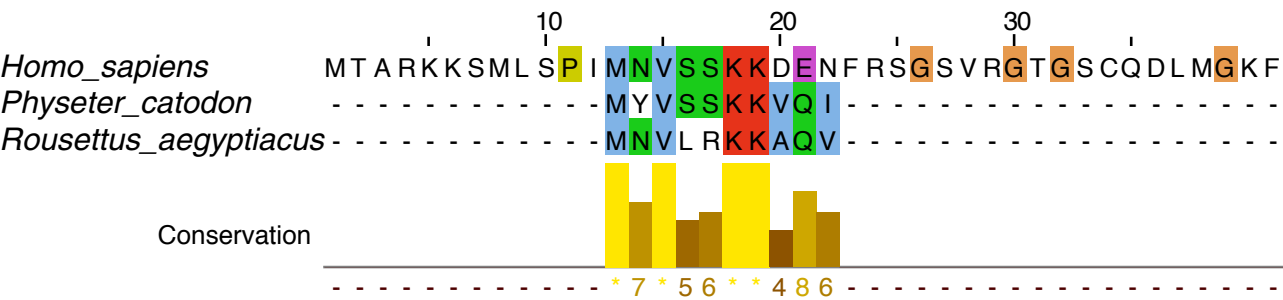
HG1168

ENSG00000166669 (ATF7IP2)



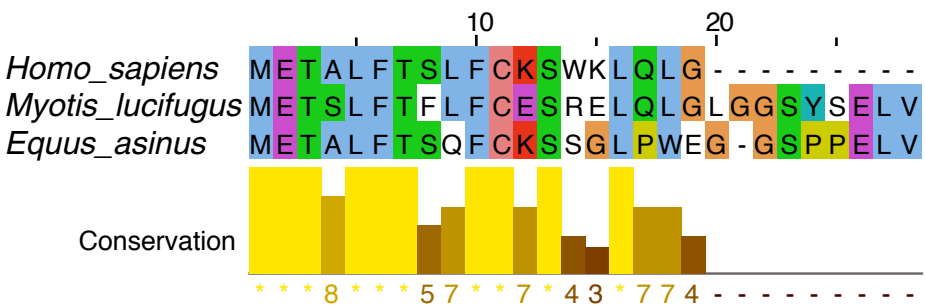
HG1169

ENSG00000167637 (ZNF283)



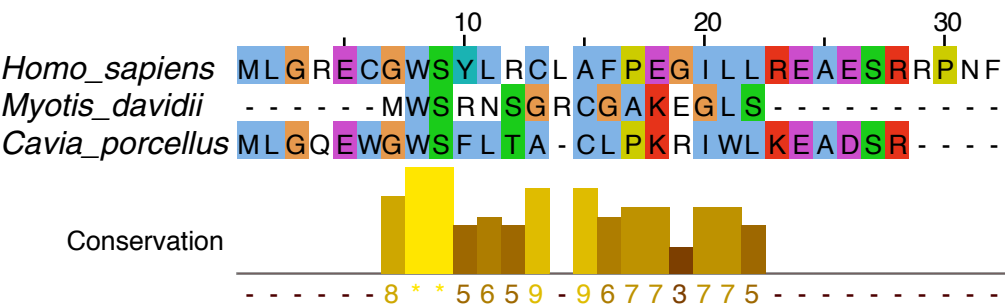
HG1170

ENSG00000167858 (TEKT1)



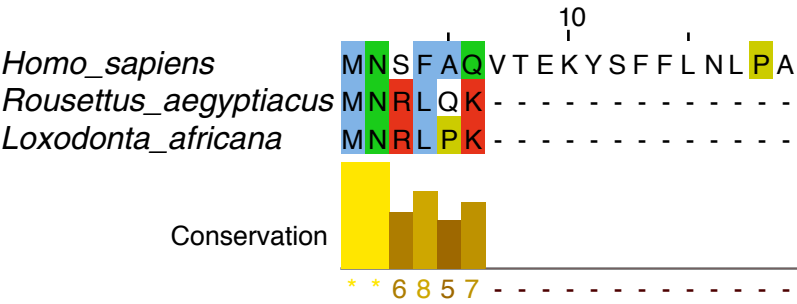
HG1171

ENSG00000167968 (DNASE1L2)



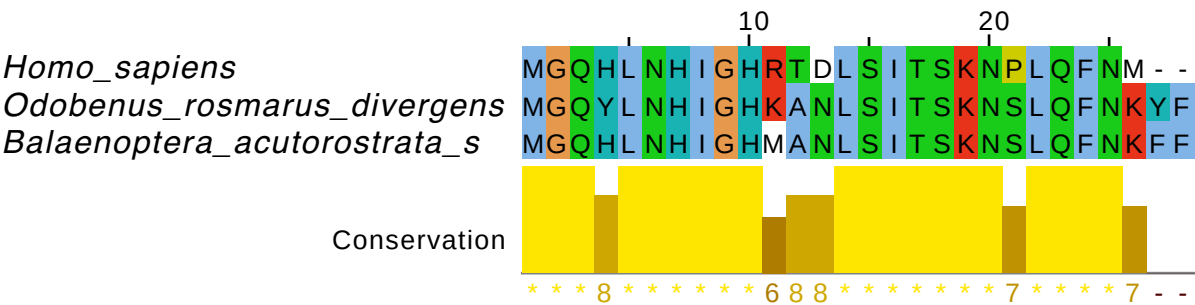
HG1172

ENSG00000170381 (SEMA3E)



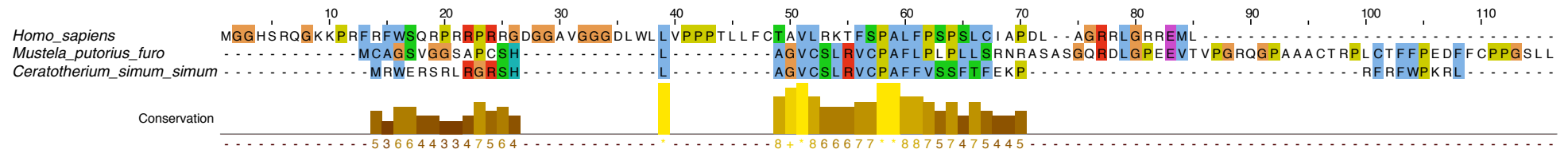
HG1173

ENSG00000170464 (DNAJC18)



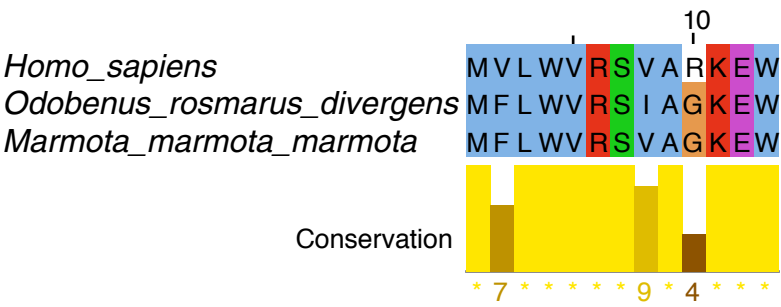
HG1174

ENSG00000173918 (C1QTNF1)



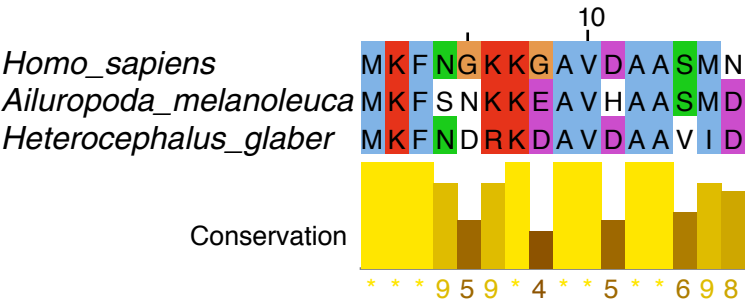
HG1175

ENSG00000174473 (GALNTL6)



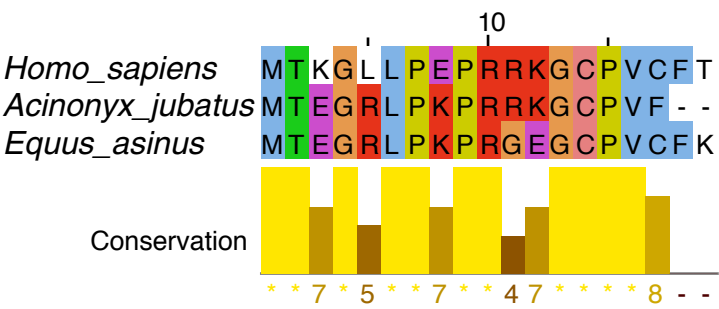
HG1176

ENSG00000176472 (ZNF575)



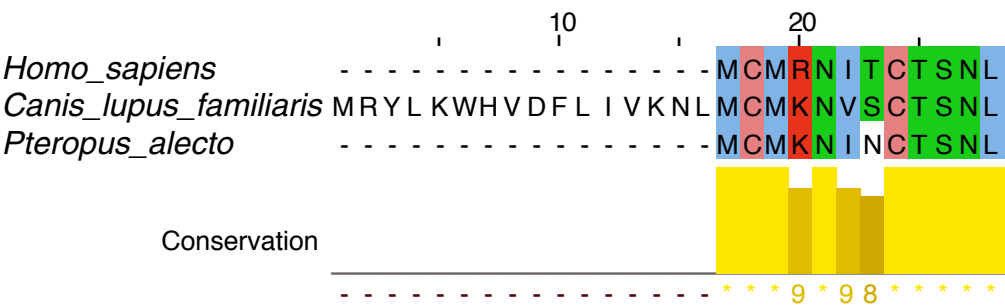
HG1177

ENSG00000178295 (GEN1)



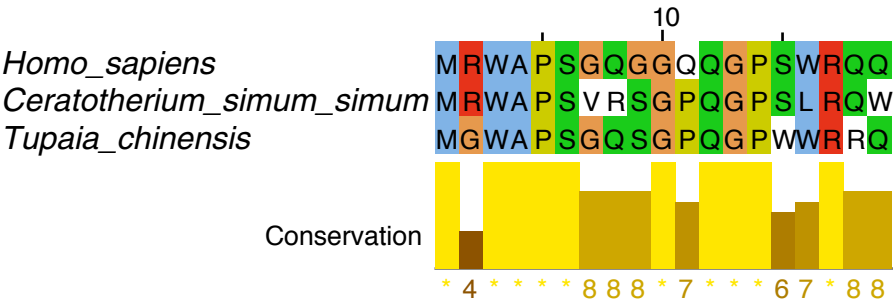
HG1178

ENSG00000182670 (TTC3)



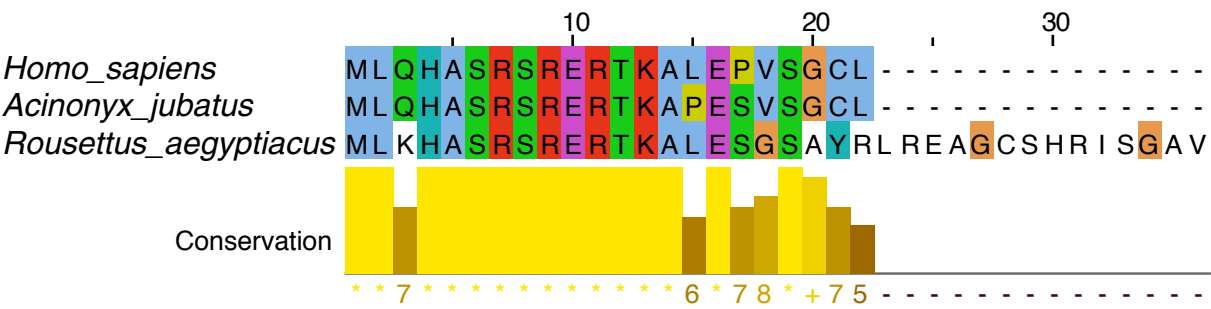
HG1179

ENSG00000185933 (CALHM1)



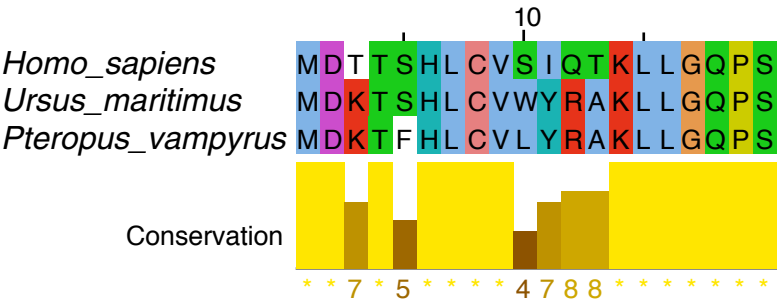
HG1180

ENSG00000188674



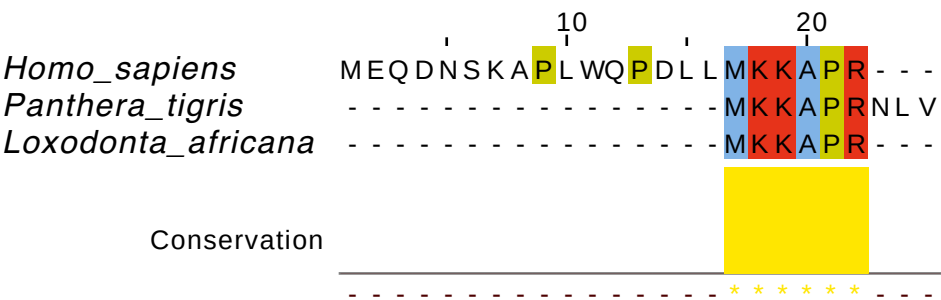
HG1181

ENSG00000189058 (APOD)

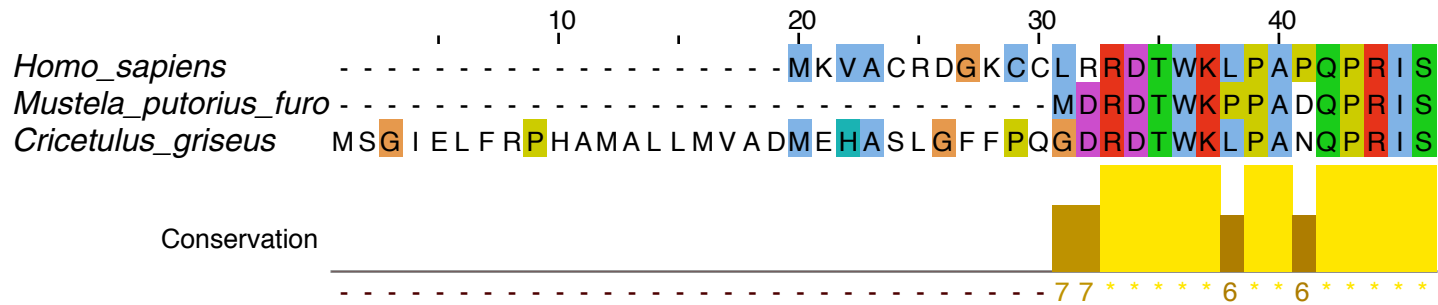


HG1182

ENSG00000196155 (PLEKHG4)

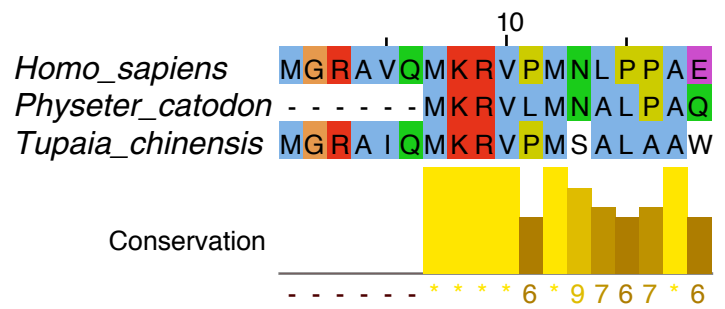


HG1183
ENSG00000198133 (TMEM229B)



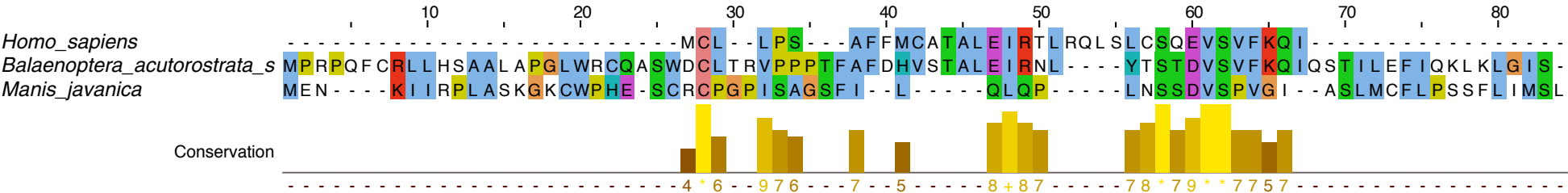
HG1184

ENSG00000198894 (CIPC)

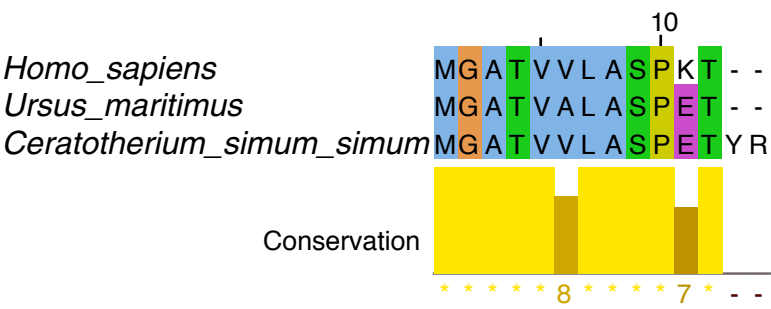


HG1185

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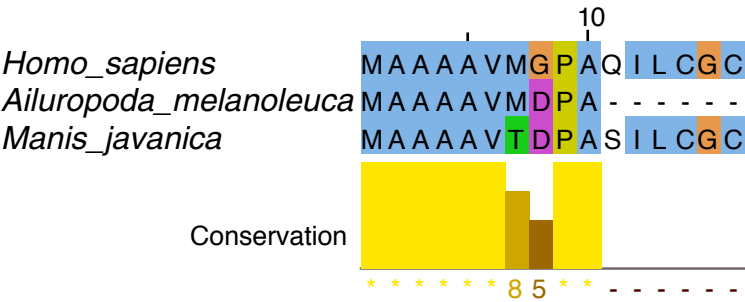


HG1186
ENSG00000204923



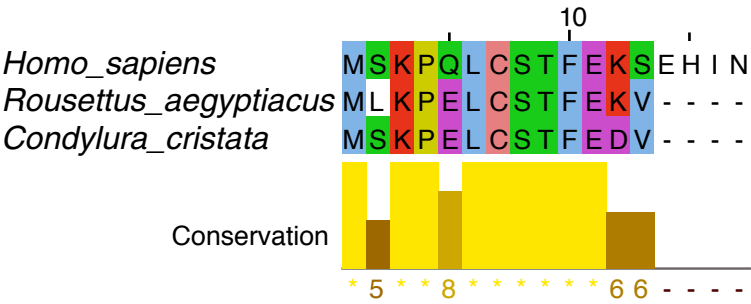
HG1187

ENSG00000213762 (ZNF134)



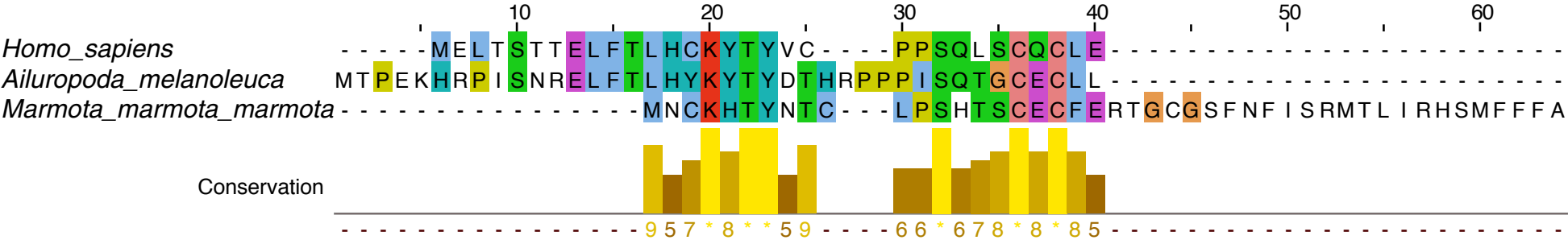
HG1188

ENSG00000214415 (GNAT3)



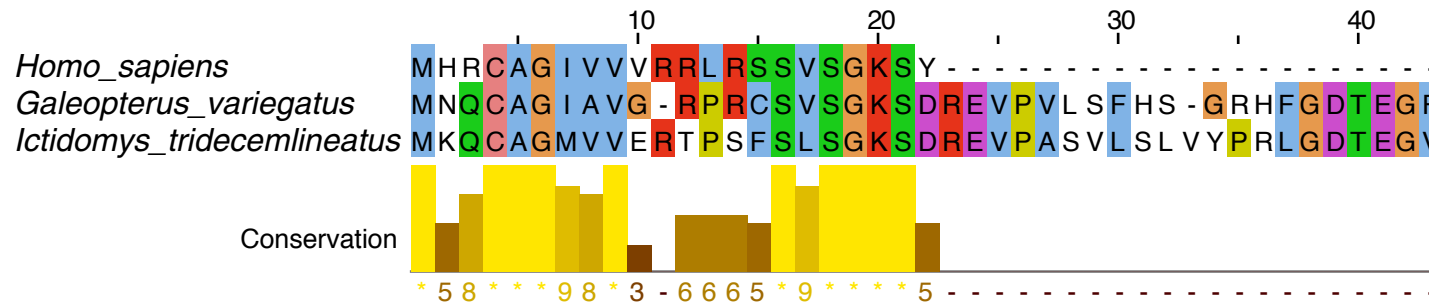
HG1189

ENSG00000279909



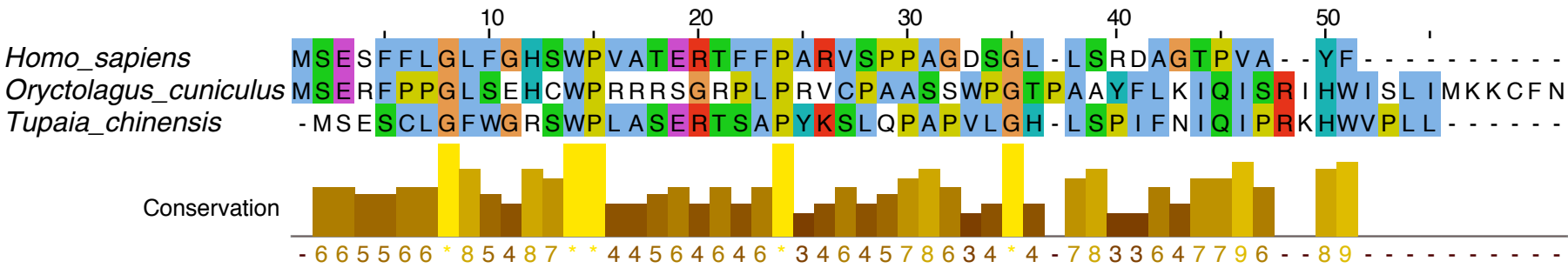
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ENSG00000123684 (LPGAT1)



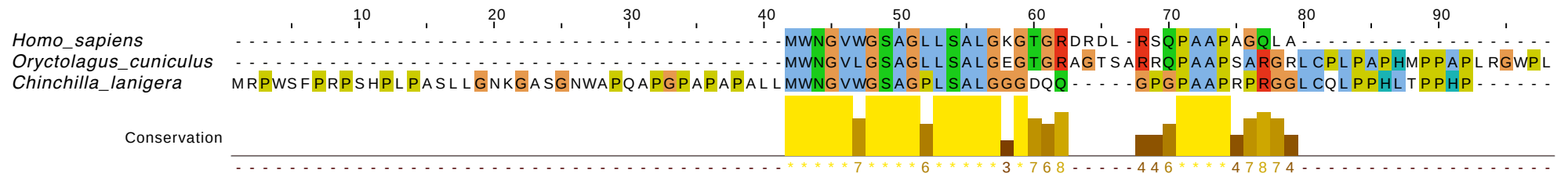
HG1191

ENSG00000164331 (ANKRA2)



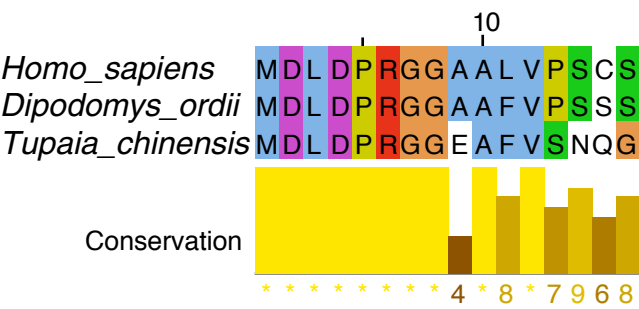
HG1192

ENSG00000168758 (SEMA4C)



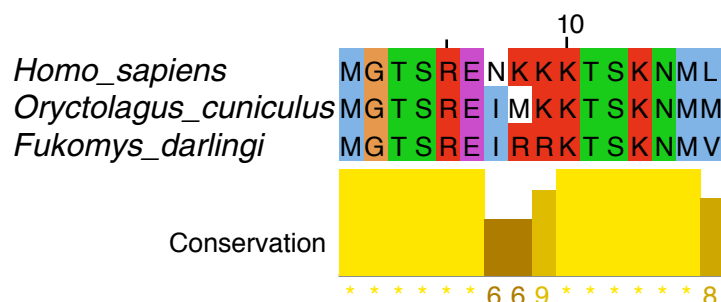
HG1193

ENSG00000177706 (FAM20C)



HG1194

ENSG00000214694 (ARHGEF33)



Supplementary Figure S4. Alignments of the extracted CPuORF sequences by ESUCA. The amino acid sequences of the extracted CPuORFs and their homologous putative uORFs were aligned using Clustal Ω ver. 1.2.2 and displayed using Jalview ver. 2.10.2. For each alignment, a putative uORF sequence was selected from each order in which uORF-tBLASTn and mORF-tBLASTn hits were found. In the alignments of the ENSG00000112245 (HG0001), ENSDARG00000003077 (HG0002), ENSGALG00000041706 (HG0004.1), ENSG00000031003 (HG0004.1), ENSGALG00000009013 (HG0010.1), ENSG00000189266 (HG0018), ENSDARG00000087059 (HG0026), ENSG00000172995 (HG0043), ENSDARG00000061687 (HG0044), ENSG00000139329 (HG0056), ENSG00000280987 (HG0057), ENSDARG00000018060 (HG0059.1), ENSDARG00000040008 (HG0076), ENSG00000164600 (HG0076), ENSG00000204406 (HG0079), ENSGALG00000016176 (HG0105), ENSG00000181690 (HG0125.2), ENSG00000017427 (HG0135), ENSG00000180530 (HG0170), ENSG00000177311 (HG0171.2), ENSG00000023445 (HG0262.1), ENSG00000204256 (HG0274.1), ENSG00000100239 (HG0275.1), ENSG00000175928 (HG0279.1), ENSGALG00000007717 (HG0403.1), ENSGALG00000026736 (HG0436), ENSG00000180008 (HG0460), ENSG00000166444 (HG0484), ENSG00000144460 (HG0504), ENSG00000177853 (HG0506.1), ENSG00000126860 (HG0513), ENSG00000273841 (HG0556), ENSG00000010818 (HG0579), ENSG00000164930 (HG0599), ENSG00000003147 (HG0604.2), ENSG00000074657 (HG0607), ENSG00000122203 (HG0614), ENSG00000259332 (HG0635), ENSG00000100359 (HG0641), ENSG00000166845 (HG0661), ENSG00000111837 (HG0683), ENSG00000085998 (HG0719), ENSG00000104783 (HG0724), ENSG00000115825 (HG0727), ENSG00000163794 (HG0816), ENSG00000127324 (HG0946.2), ENSG00000136235 (HG0956), ENSG00000154319 (HG0968), ENSG00000065357 (HG1022), ENSG00000082175 (HG1030), ENSG00000084453 (HG1032), ENSG00000140030 (HG1065), ENSG00000166532 (HG1085), ENSG00000174371 (HG1093), ENSG00000177917 (HG1094), ENSG00000092020 (HG1119), ENSG00000101574 (HG1125) CPuORFs, some putative uORF sequences were manually removed. After manual removal, K_a/K_s analysis was conducted using the putative uORF sequences shown in the alignments.

Supplementary Figure S5

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

H50003 ENSGAL00000014906 M0C52

>Galus_gallus-----MSCQVTLVYFASKAELVLRSEV-V-SVPRIT-T-SL-Q-----LM-----EEIKVHPRLA-VYRD-----QVFAVRGEYVLLGD-QLLVLGTGDEVAI1PPI500

>Acipenser_sinensis-----MTTEVVLVYFASKAELAVRSEH-I-TYSQVT-SL-Q-----LM-----QELVNRPRLA-AIRD-----QVLAVRGEYVSLSD-ELLTLHPDGEVAI1PPI500

>Adineta_ricciae-----NSTIGWLIYGRRLGVLSSEK-I-DPDSAS-YTGD-----SIL-----DRIIEHPLKSFVYTN-----TFLRANQSVLLGD-----LQFDSKESEVALLPFG00

>Acanthogorgia_aspera----------MLALNEYTDL-EETVLRSTOKIAI1PPI500

>Aiaia_calva-----MTEVYVLYFASKAELADVRES-I-SVQDET-T-SL-Q-----LM-----QELVNRPSLS-VLRD-----QVLAVRGEYVLEGE-QLLSLGGDEVAI1PPI500

>Talitrus_saltator-----MTVOLEIVPKVYFFASKAELVSGSEV-LSLPTTT-----AKK-----LF-----SEVLNMPHLE-KLEK-----SVWVWNGEYTDG-DT-NQVLRAGEVAI1PPI500

>Podocoryna_carnea-----MEESKVPVSLVFAKSELQVKTSD-I-VLEQETL-----LKK-----LL-----EEIHVYPSLK-NQDN-----NFIIAYNKYLE-SE-OCITLKASDEIAI1PPI500

>Megophrys_sanghensis-----MTCEVVLVYFAKSELTVRSEI-I-HVQDET-T-SGN-----LM-----EEVVRHPRLC-TIKD-----QVFAVRGEYVAI-GE-ELLSLRQDEIAI1PPI500

>Nileusium_tardigradum-----MEISWVLVFAKSELVGTGGI-L-TLKGDL-SLOS-----LL-----SNLYSOPFAL-PLGN-----QVLSNKKYTDADLQRPVSNIGDEIAI1PPI500

>Apteryx_australis_pantalli-----MTDVLVYVWK-----QWQVRSRSD-I-SQPELCT-SL-EFKEISMLNMTFLRNLVFLPLR-LA-VYRD-----QVFAVRGEYVLLGD-QLLFLRQDEVAI1PPI500

>Machilia_brahei-----MIALCESEIRLLFAKSELQKSEAS-I-QVPSLHV-VOD-----LL-----DLVIRE-FSLD-LIGN-----MLALANQEVLYRE-QSVNTRTQDEIAI1PPI500

>Scapharca_broughtonii-----MATEPEVQVTLVFAKSELSQLTKSD-L-KTPQTN-VFOG-----LL-----QLVYAFPSLE-IISE-----NIVLSNEDYTK-D-SVNLNSQDEIAI1PPI500

>Oryzias_latipes-----MTADVSVLYFGSAELTQKGE-L-VSVPIT-I-SSRE-----LM-----ELLQGRPHLC-VLRG-----HYVLAAGQYDPAIE-QVLVRDGEVAI1PPI500

>Pterohelosternus_similis-----MADVSVIQLVFAKSELQKQSGC-L-LIP-SVT-SYNN-----LL-----DEIVTK-FSLE-SIRD-----MLLAINNEYTSE-SEVLKAGEVAI1PPI500

>Eurytemora_affinis-----MADVQVWLFAKARELVQSEW-V-REFQELS-SEH-----LK-----SKLISQFVLD-KLGD-----TLLALNEAYTDT-----QRYVLTGDTLAI1PPI500

>Aiatina_alata-----MSENITVTVRFFAKARELVQKTH-V-RTRERIT-AHE-----LI-----SOTIDAFPKLD-VYRD-----CFLAANQEVYSLD-Q-DELNISQDEIAI1PPI500

>Hydrobia_chinensis-----MGESEVLYFASKAELTVRSET-I-SVQDIT-PS-Q-----LM-----DEIVNRPRLA-AIRD-----MVLAVRGEYVLLD-QLLTLQDGEVAI1PPI500

>Siniperca_chuatsi-----MTADVSVLYAGSELTVQKEE-L-VAVPT-I-SSGD-----LM-----RLLLQGRPHLS-LLDG-----QVLAVRQGYVAIG-QPYTLQDGEVAI1PPI500

>Actyanax_mexicanus-----MKSEVLYFASKAELTQKSET-I-SVQSELS-TL-Q-----LM-----QELXHPRLS-AVRD-----QVLAVRGEYVSLGD-QRYVLRQDEVAI1PPI500

>Callinectes_piluli-----MTAESEVLYFASKAELSVRSE-L-SVQDLT-SM-Q-----LM-----EKTVMRPSLI-AIRD-----HYLLAVRGEYLLGD-QILFLQDGEIAI1PPI500

>Dreochromis_niloticus-----MTADQVLYFASVELTVQKEEK-T-VAVPT-I-SSRD-----LM-----ALLVQRPHLC-LLRD-----QVLAVRGEYVPIDG-QVTLQDGEVAI1PPI500

>Alaea_alosa-----MFGSA-VLDPYVISESVLYFASKAELTVQSEV-L-KPSLTI-TI-Q-----LM-----LELXQPHLC-VLRE-----HYVLAVRGEYVLDG-QVLSHGDGEVAI1PPI500

>Latimeria_chalumnae-----MTADISVLYFASKAELTVRSE-I-TVAGDIT-SQ-Q-----LM-----QETVNRPRLA-AIRD-----HYVLAAGQYVLLGD-QFLLLQDGEVAI1PPI500

>Pyrausta_nerata-----MSYTVTLFVAKARELVQSSSS-L-EVPPAL-T-CT-D-----LL-----NTVINE-YSLN-VYRN-----NILLANNEEFCADN-QRLSKTQDEIAI1PPI500

>Coreactis_australis-----MEH-LMSTQVTEVLYFASKRELVEQSEH-L-SLQRLS-GRF-----LI-----ASTVMRPSLS-VLDG-----MLVAVNGEYVEK-E-SEIFEGDEVAI1PPI500

>Quaculus_canorus-----MTAEPLVSVSVLYFASKAELQJREH-L-RVPRVT-AL-Q-----LM-----EETVSLPRLA-VYRD-----QVFAVRGEYVLLGD-QVLAVRQDEVAI1PPI500

>Ctenopharyngodon_idella-----MTEVSVSVLYFASKAELTQKAEH-I-TVPSNT-SL-Q-----LM-----QDLNMRPSLS-VLRD-----QVLAVRGEYVPLGA-QPLTLRQDEVAI1PPI500

>Fundulus_heteroclitus-----MSAQVTLVYFASKAELTQKEEP-V-KVPTPS-S-GD-----LM-----ALLNRQPHLY-ALGD-----HYTLAVRQGYVAIGE-QVTLQDGEVAI1PPI500

>Petrolisthes_cinctipes-----MTCEVSVSVLYFASKAELAVRSEA-I-TLPVIT-T-P-EQ-----LL-----ARVRSPGELD-IIRD-----SVIISLANEYQVPG-QELVLSAGEVAI1PPI500

>Sclerodactylus_braueri-----MFDVQVVOYVAISRDITQREH-L-TVPHVT-L-KQG-----LF-----QDLTERRPQK-QDET-----MOLLAINQDLTEES-QVVELAVRQDEVAI1PPI500

>Fragiella_sauricularia-----M-NDQNLQVTVVLYFASKAELQVKNKA-I-QTPSLTN-S-EE-----LL-----QSLNR-FNLQ-QISS-----CLVLAVNGEVSSE-PLKANSGSIAI1PPI500

>Oocarpus_javanicus-----MUTTEKVLVFAKARELVQKQNAV-LRLDSAG-Q-SQES-----LL-----EQVLSFPQD-RVRG-----SLMLANQVYDL-Q-QVLSYSSQDEIAI1PPI500

>Sarcophaga_crassipalpis-----MNSGLPVNHLVFAKARELSQESN-HQSTPQIIA-S-D-----LL-----EQDG-STNYSL-SYRN-----MLIIATINESEN-LN-TELQDGEIAI1PPI500

>Echiniscus_tentado-----MGTTLFARMLAGRSEILI-DVPADCEVSGV-SSKRL-----QLTIAQCPRLC-EIK-----HYQLAVRQGYVLDG-MLVLOPTSEI1PPI500

>Giona_intestinalis-----MKNQVQVNLVFAKSELVQESGD-L-LPQDIT-SF-Q-----LI-----ETIKNSYPSL-DLGD-----CFLAVNGEYKTQDES-YSLITDQSEIAI1PPI500

>Baetis_sp._AB-2009-----MUPVYVKKLVFASARELSGRSE-I-QVQDET-Y-DT-----LF-----KXVVR-FYLE-KLGN-----SLLAINEEYPMEN-TQLNAPQDIAI1PPI500

>Esca_lucius-----MTEVTVLYFASKAELTQKSET-I-RVPSLT-TL-D-----LM-----LDLVNRPRLS-TVRE-----SVYLAVRGEYVAIGE-LVNSLRQDEVAI1PPI500

>Leptasterias_sp._AB-2014-----MASTCAVNEVLVFAKSELTVQKEGH-L-QWTKNL-PE-E-----LL-----LOLISQYPSL-IIGD-----TVVLSNGEYAKGD-QTLNLRQDEVAI1PPI500

>Gadus_morhua-----MTAVTVLYFASKAELTVRSEV-V-PLAPTS-SC-Q-----LM-----ALLLEHPSLA-ALGD-----QVLAVRGEYVLDG-QLLLAGDGEVAI1PPI500

>Chlamydotis_macqueenii-----MLLGD-QVLAVRQDEVAI1PPI500

>Galioisiana_yuana-----MELNKLISWVLFAKARELVQKSEK-I-QVPSIS-Y-NE-----LL-----DHILE-FSLE-SIKG-----NFILAINNEYTTD-RELDKEGEIAI1PPI500

>Tigriopus_californicus-----MSVSVKVLFAKARELVQKTHET-L-NVMSLS-ASD-----LV-----TQTEAQCPRLC-ILRG-----SPVLANQGYVHN-N-QVLDKSKGEIAI1PPI500

>Acanthosoma_haemorrhoidale-----MDCWIKILVFAKARELSQTKESF-L-SVPSNIS-TPL-----LV-----NKTV-DLFLH-SIGN-----SILLANQEVYVXQGD-QPLNDEGEIAI1PPI500

>Myrmica_ruginodis-----MEETATPIQATVFAKARELVQKQEK-L-QVPSNIS-SA-D-----LL-----DKITHA-FELD-SIGN-----QILLANNEEYVPG-SILVLSKOKIAI1PPI500

>Rhizophthalmus_ependioides-----MEFSFVPLVFLFAKARELVQKSEAS-L-VPAVLR-DVEA-----LK-----EYIFDAPFKLA-SLRG-----SVILANNEYSYDGS-Q-VEYTLQDGEVAI1PPI500

>Oxyerlocania_subpurpurella-----MEGLQVQVNLVFAGREYVQREAS-I-MPSKLS-CA-E-----LL-----DIPYVN-FSLS-AVNN-----NILLANNEQCEGD-NLEIKTQDEIAI1PPI500

>Lutjanus erythropterus-----MTADVSVLYFASVELTQKEED-I-VAVPT-I-SSGD-----LM-----KLLQGRPHLS-VLRD-----QVLAVRQGYVAIG-QVTLQDGEVAI1PPI500

>Mantis religiosa-----MNVSSQVQVQLVFAKARELSQKESD-F-ISETPIS-Y-EL-----LL-----QGVQVK-YSLS-AUKS-----SVILAINEEYCSPS-EHFLNAGEVAI1PPI500

>Nannochlorista_phoebii-----MTEVEVNLVFAKARELVQKNET-L-LTRQIL-CS-E-----LL-----RDITIN-YSL-E-AVNN-----NILLANNEEYCEPN-TELNKADEIAI1PPI500

>Dermasyssus_gallinae-----MVRKVLVFAKARELVQKTAERS-V-DVAKNF-SLDG-----LK-----ELAQLEPSWK-TLLD-----TSILAVOLNIVQSYG-E-EGTQTEIAI1PPI500

>Ornithorhynchus_anatinus-----MVLSPVTLVFAKARELVRSSE-I-SVQDEIK-SL-Q-----LM-----EEIESRPHLA-DVRD-----QVFAVRGEYVLDG-QVLLQDGEIAI1PPI500

>Perna_viridis-----MANKVSVSLVFAKARELSQVNSG-I-KVSSQGS-FTQ-----LF-----ETIVQDPSLS-VISE-----NITLSLANEYISR-D-QSITVQDEIAI1PPI500

>Omelyus_fulvicephalus-----MSVEVRLVFAKADQFARSEST-L-NUPMFI-F-AE-----LL-----TIYVN-YNLQ-AVNN-----TINISLNFQDMD-ATLKFNTEQDEIAI1PPI500

>Haplochaetema_nasutius-----MEH-SFADMDQVNLVFAKARELVQKQSE-V-SITSRYS-ITAG-----LT-----SFLLETFRPLC-PLXG-----SMILANNEEYSGD-ETHLQDGEIAI1PPI500

>Epiplatibus_superstes-----MDCQVTVKVLFAKARELSQIFGD-LKNVAP-S-YTF-----LL-----EEIV-TQFSL-KVNN-----NILLAINNEYYSGS-E-LQNLKQDEIAI1PPI500

>Ooithorichia_felineus-----MGAQVRRVLTQKAEVTFQSAVL-L-LVPYCT-A-AE-----LY-----DLQ-FLPH-LLEK-----SLLLTLDFQVTDIEDNTHLHISQSEGLVAPPI600

>Stenobothrus_lineatus-----MMDKLEKVLVFAKARELVQKSESS-L-KVAGHSI-YEE-----LG-----TLTV-ENFSLA-AUKX-----NFILANNEEYSLS-E-STLQKQDEIAI1PPI500

>Oemerus_mordax-----MTTKVSVLYFASKAELTQKSEV-I-HVQDET-TL-A-----LM-----QELVNRHRLS-AVRE-----QVLAVRGEYVTTIG-QVLSANQGEVAI1PPI500

>Scleropages_ferrousus-----MTEILLVLYFASKAELTQKSEN-V-RVPPDL-T-S-Q-----LM-----EELVTRPHLS-MERT-----QVLAVRGEYVPLDG-QPYVLQDGEVAI1PPI500

>Crassostrea_gigas-----MEQVTVNLVFAKARELVSSGSG-L-VLTANTH-FDT-----LK-----QALLKTPPSL-VYAE-----NITLSLANEYTDG-N-QDLTLRQDEVAI1PPI500

>Hyphalium_djardini-----MDEVNLKMLQKADQVQAT-I-RITAEQPTVQSG-FL-----AKLITTFPRLQ-EIKD-----QLLALNLEYLQNPASAFELKEGEIAI1PPI500

>Teanipopsia_puttata-----MRCQSVLYFASKAELQJREH-L-SVQDET-SL-Q-----LM-----EEIVNRPRLA-LIRD-----QVFAVRGEYVLLGD-QVLAVRQDEVAI1PPI500

>Pecten_maximus-----MADVSVLYFAKARELVQKXTAG-I-IVSEPTN-----LDG-----LI-----STIVSQPPLQ-IIGD-----NLVYSINEDYDGA-D-DEHNLNTQDEVAI1PPI500

>Diisostichus_masoni-----MTADVTVLYFASKAELSQLKEE-L-VAVPT-I-SSGD-----LM-----SLLQGRPHLC-VLRG-----QVLAVRQGYVAIG-ELVALQDGEVAI1PPI500

>Equis_aximus-----MVRPQGVLYFASKAELQJRESE-I-SVQDEIK-AL-Q-----LM-----NEIETHPQMS-----

>Tinea_cristina-----MTNKLKAVKVLFAKARELVQKESD-L-EVCSLT-Y-EC-----LL-----DTLWE-FSLE-LVGN-----HLILANNEYSKAG-QTVLEAGDEIAI1PPI500

>Menopon_gallinae-----MNDSSVSVNLVFAKARELVQKQNEI-V-DVQDNK-Q-AD-----LL-----QFLVSK-FELD-CIRX-----NITILANQGYVLE-CELENSADEIAI1PPI500

>Pernereis_albulbensis-----MADVQVVLFAKSELQATNESE-L-ALPNKS-LAQ-----LK-----EVLQDQNLG-AIEE-----MCLISANNVEE-----QDLNANSGDEIAI1PPI500

>Fasciola_hepatica-----MSTVSVSVLFGAREYVLYRVLC-SLPTTCT-P-AE-----LK-----RELLKHPQLE-LLSS-----SLGLALQVLDQSESTORITLSQSEVYFPPL500

>Colobus_angelensis_pallidus-----MFLQCAEVLVFAKSELTQVRSSE-I-SVQDEIK-AL-Q-----LM-----KEIETHPRLA-DVNN-----QILFAKKEVLELD-QLLQLLPQDEIAI1PPI-----

>Acenotomus_sp._AD-2013-----MADVSVNLVFAKARELVNSEV-L-VLKTETT-QNE-----LL-----SALEKXFPVLS-RIKE-----IHLAVNEAYCED-LS-QSLTNSQDQVAVIPI500

>Meliponettacus_undulatus-----MRCQSVLYFASKAELQJREH-L-SVPRQIT-AI-Q-----LM-----EEIVNRPRLA-VYRD-----QVFAVRGEYVLLGD-QVLAVRQDEVAI1PPI500

>Lipocelia_batrachophylla-----MID-QTEASTQSVKILVFAVQVQKQNR-I-VYPSITV-Q-SA-----LL-----DLIKK-YNL-E-TYNN-----NVLAVNEEDVOLD-SLLTLQDGEVAI1PPI500

>Xanthostigma_xanthostigma-----MSEVKEVLFASASTISLSESL-L-NSQDIA-YDD-----LL-----ELTV-EKYSLO-NIRG-----NILLANNEYSCEK-N-QTLNLSQDEIAI1PPI500

>Rhapiisma_sculentum-----MNAVNEVSVLFFAKSRDVLQHEAH-I-DISSQVT-QGE-----LL-----RAIVTQFPLH-LIRE-----MLLSQNGEYLS-D-QVVELAGEVAI1PPI500

>Marstonia_marstonia-----MVRPQGVLYFASKAELTVRSET-I-SVQDEIK-AL-Q-----LM-----HEIETHPRLA-DVNN-----QVFAVRGEYVLELD-QLLHLQDGEIAI1PPI500

>Coregonus_clupeaformis-----MTEVSVVLYFASKAELTQKSET-I-RVPSLT-TL-E-----LM-----QDVVRPHLS-AVRD-----SVLAVRGEYVALGD-QCVLSRQDEVAI1PPI500

>Favaria_lizardensis-----MEH-FSDTQTEQVTVLFAKARELVQKASG-I-SVQDIT-QTD-----LI-----HYLLNMFPSLA-VIGE-----MLVAVNGEYTEK-D-SEITFEGDEIAI1PPI500

>Sepioididea_lineata-----MLPPL500

>Ictiurus_punctatus-----MTEVTVLYFASKAELTVKSEI-I-RVNSLT-SL-Q-----LM-----QELNRPPLS-AVRE-----QVLAVRGEYYSVE-QVRLRNRQDEVAI1PPI500

>Geratophyllus_gallinae-----MNGEVSIVLYFFASKARELVQSVETS-L-KVNNIS-Q-GE-----LI-----QLQICAI-HOLD-SIGN-----NITILANNEYVQDLA-AILLTKQDEIAI1PPI500

>Stribolopis_benedicti-----MLFLRLMLTLNLKLYLVFLFAKARELVQSSDY-I-MPLQL-ESQ-----LR-----TSVEMRPSLS-PISD-----SPVLANQGYTDE-Q-EEVHSEGEIAI1PPI500

>Squalus_acanthias-----MTADVSVLYFASKAELADVRES-L-SVQDLT-SL-Q-----LM-----QELVRQPRQENREIQRPSVLFHPVPL-----

>Takydromus_sexlineatus-----MRCQSVLYFASKAELQVRET-I-SVQDIT-SL-Q-----LM-----EEIVNRHSLT-AIGD-----QVFAVRGEYVLLGD-QVLAVRQDEVAI1PPI500

>Stylops_mittae-----MNTVTLVFLFAKSRQSKRQEH-I-TLAEVIA-YDD-----LL-----TLIC-MQFQLE-EIKX-----TIFLALNEYLSG-N-TLVLHSGDIAI1PPI500

>Schistosoma_masoni-----MTLQNKVLFGEASSELVQKET-I-QFLSCT-N-KT-----LK-----DIILEDVLYE-PLXG-----SLTVANNKYTDNTLSNOLISEELAEI1PPI500

>Aivinelia_pompejana-----MNAVTVQKTVQKQNDQVNDQVNLKLVYFFAKARELVQKQED-I-DIAPNS-Q-IA-----LY-----KLIVYQPLK-PIGE-----MFLALNEEYDKTD-EEILNSQDQAEI1PPI500

>Pholidoscolus_simensis-----MRCSEVALVFAKARELVRSSE-I-SVQDIT-SL-Q-----LM-----EETVNRPRLA-AIGD-----QVFAVRGEYVLLGD-QVLAVRQDEVAI1PPI500

>Hydroptila_sp._AD-2013-----MEYSKYVNLVFAKARELVQAEKE-L-EVAPRS-Y-SG-----LL-----HLVHT-FKLD-IIGD-----NFVANNQELQDNG-HEIVPENDEIAI1PPI500

>Villosa_lienosa-----MLQHQDEIAI1PPI500

>Sisonovacula_constricta-----MAAMNVQLVFAKARELVQKTN-L-LVNSLT-AHE-----LL-----KXISEPQLQ-VLAD-----TILSLANNEYALQEP-KILNDEQDQVAVIPI500

>Limulus_polyphemus-----MSSQVNLVFLFAKARELVQVTEG-L-VVPMKY-TQOX-----LL-----SIVTEFPVLC-SIGD-----NFVLANNEQDQSG-QSELEKQDQIAI1PPI500

>Palychtha_caribaeorum-----ME-MNDAGQGVTVLFAKARELVQSVTSQ-I-VLARRLS-GQK-----LI-----ETLLMLPPLS-EIER-----MLVAVNGEYTES-D-SEITFEGDEIAI1PPI500

>Thermobia_domestica-----MAESEKVLVFLFAKARELVQKQDIT-I-NLPSITT-YSI-----LV-----SLIA-KEFSL-PIGE-----MLILANNEYTES-D-RDILSNGDEIAI1PPI500

>Drosophila_melanogaster -----MAGQSVYVWHLFFAKSRELANTPR-STVEPTPE---ITA-T-ELLQHLVSK-FGLTS---IR---QNLILANNEYTDL5---QRLTKFEGDELAI1PP1500
>Acipenser_sinensis -----MTTEVVYLFFAKSALEAVRS-ENTYSDP---VTS-L-QLNGELVNRHPLSA---IR---DOVVLAVRGEYVSLD---ELLTLQPGDEVIA1PP1500
>Aemonea_viridis -----MKNKTYGTEPVPVLLFFAKSRELTECAS-KEVGLPRL---VTR-E-QLDSS110DFPSLVO---IE---KTIVVANGEYLDTOK---KVELRKGDTVA11PP1500
>Admetia_ricciae -----MSTIGWAIYVGRRELVLGSS-EKIDFDSA---ISYTDQ-SILDR1DEHPILKSPFLYT---NTRFLANWQVYLLED---L1QFSKESEVALLPP600
>Acanthogorgia_aspera -----MELALNEYITLLEE---TYNLRSTOKIAVPP1500
>Aela_calva -----MNTTEVVYLFFAKSALEADVRS-ETISVQPE---ITS-L-QLNGELVNRHPLSY---LR---DOVVLAVRGEYVALGE---QLLSQSGDEVIAVPP1500
>Talitrus_saltator -----MTQYOLEVYVKNVFFAKSRELSSQSE-VEIDLSPT---TTA-K-KLSEVNRHPELOK---LE---KSVWVANGEYTDQD---TNQVSRANDEVIAVPP1500
>Hydractinia_symboloncarpu -----MKSQSVENLFFAKSRELTKQSV-DVNLKKS---NZL-Q-MALKETIHTYPLALNI---LK---GRFT1ANQYATDQD---KEVLETQDEIA11PP1500
>Xenopus_tropicalis -----MTCEVSVLFFAKSSELADVRS-ETLYSGE---ITS-Q-QLMQDLVGRHPLSA---IR---DOVVLAVRGEYYP10---NELLTNTQDEIAVPP1500
>Milesium_tardigradum -----MEISQSVLFFAKMDLVTDGQ-LITLKED---ILS-LQ-SLLSNLYSQFPALL---LQ---QNVVL5LMOKY1DAQDQPVYSINIDQEAIVLP1500
>Machilia_hrabiei -----MIALCESEIRLLFFAKSRELQACE-ASIQVPSL---VWV-Q-DQLDLTYVE-FGLD---IK---MNLILANWGEYLQEG---SWNRTQDEIAVPP1500
>Scapharca_broughtonii -----MATEVEVOTLLFFAKSRELSQLKT-SQLKTP10---VNF-Q-QLLQLVYVTPSLE1---IS---ENVYLSMEYTDND---SQVNLSSQDEIAVPP1500
>Argulus_siamensis -----MNSLTSLVYLFFAKRELVGARD-TTILTPGS---L1Q-H-KLVALILTYEALKP---IE---QNFILALNEYTDQD---EELSLQSGDEVIAVPP1500
>Oryzias_latipes -----MTADSVYTFQSGAELTQLKGEELVSVTPF---ISS-R-ELNELLOGRHPLAY---LR---GRVVLAAQGYT1AE---QLVYLRODGEVAVVPP1500
>Porphinotermes_simipes -----MADSVSEVTDLFFAKRELQSQGQ-SQLLPSV---TS-YH-MLLDEVTYK-FGLS---IR---QNLILANNEYTTSES---EVQLKSGDEVIAVPP1500
>Tripterygion_dalaisi -----MSARVYLFFAKSRELQKKEE1VAVTPF---ISS-L-QLMKLVGRHPLAY---LR---GRVVLAVRQGYVADQ---EQVALDQDGEVAVVPP1500
>Eurytemora_affinis -----MADQVNLILFAKARELVQASE-VNRPFGPE---LSS-E-HUKSKI1QSPVLQK---LQ---QTLMLALMEAYTQD---RYTLNTQDTLAVPP1500
>Seriola_quinqueradiata -----MTADQVYLFAKSVELTDQKED1VAVTPF---ISS-R-QLMKLLGRHPLSY---LQ---DOVVLAVRQGYVADQ---QVYTLQDGEVAVVPP1800
>Alatina_alata -----MONTVTVVEVFFAKARELAG1OK-THRYTRR---ITA-H-EL1SQ1IDAFPLDY---IR---QSVFLANWGEYSLD---QELN1SQDGEIAVPP1500
>Hyobius_retardatus -----MNSGEVYLFFAKSALTQVRS-ERLSVQPD---ITS-Q-QLNDE1VNRHPLAA---IR---QNVVLAVRGEYVYLQD---QILTQPGDEVIAVPP1500
>Siniperca_chuatsi -----MTADQVYLFAQSVELTQKEELVAVTPF---ISS-Q-QLMKLLGRHPLSA---LQ---DOVVLAVRQGYVADQ---QVYTLQDGEVAVVPP1500
>Actinoptera_mexicanus -----MNSHVLVYLFAKSAELTG1KS-ETISVQGE---LST-L-QLNGELVNRHPLSA---VR---DOVVLAVRGEYVSLD---GRVTLQDGEVIA1PP1500
>Callorhynchus_nili -----MTAEVSVLFFAKSRELQSVRS-ETISVQPD---LTS-H-QLMKETVNRHPLAA---IR---QNVVLAVRGEYVLLQD---QILTQPGDEVIAVPP1500
>Oreochromis_niloticus -----MTAEVSVLFAKSVELTQKEERTVAVTPF---ISS-H-QLMKLVGRHPLCT---LQ---DOVVLAVRGEYYP1QD---QVLTQDGEVAVVPP1500
>Alloea_alosa -----MFGSGLDAPFNVSEVSVLFAKSAELTG1KS-EVTLQPSF---LTT-T-QLMKLEKRNHPLCY---LR---EHVVLAVRGEYVQLDQ---QTVSLQDGEVAVVPP1500
>Latimeria_chalumnae -----MTADSVLFFAKSAELAG1RS-EVITYAGD---ITS-Q-QLNDE1VNRHPLAA---IR---QNVVLAVRGEYVLLQD---QILTQPGDEVIA1PP1500
>Prionace_serrata -----MSVTVTLFFAKARETVQNS-ELSVPPA---LTY-Q-DLNTTIVE-YSLH---IR---MNTILANWEECANQD---RLSKTQDEIAVPP1500
>Micropodus_yunnanensis -----MEYTNHSTQKELNVLFFAKSRELVGRS-AKVLLAKR---LSD-R-ELASLVDSQSPFLY---IR---QNLVYVANGEYVEKET---E1EFGSGEVIA1PP1500
>Oculius_canorus -----MTAGLTVQVSVLFFAKSAGLRLGR-ETLVPRP---VTA-L-QLMEE1VYSLHPLAY---IR---DOVVLAVRGEYVLLQD---QLVLQPGDEVIA1PP1500
>Ctenopharyngodon_idella -----MNTVEVSVLFFAKSALTQKKA-ENTVPSN---ITS-L-QLNGELVNRHPLSY---LR---DOVVLAVRGEYVPLQA---QPLTLQDGEVIA1PP1500
>Fundulus_grandis -----MSADVYLFFAKSELTLQKE-EPVAVTPF---ISS-Q-QLMALLGRHPLAA---LQ---GRVVLAVRQGYVADQ---QVYTLQDGEVAVVPP1500
>Macrobryachium_nipponense -----MNSADVYLFFAKSRELADQVR-SILTVPHF---TTP-E-ELL5QVRSFGEISS---IK---QSVTL5NQGQVPEQD---QDLTSTQDEVIA1PP1500
>Sclerodactylus_briareus -----MNPQVTVQVYV1SRQ1TOTRE-LTQVPHF---VTL-K-QLQGLQTERHPLOK---IE---TNGLLANWDLTEES---QVVELQPGDEVIAVPP1500
>Forficula_auricularia -----MNGDLANDQVTVLFFAKRELQSVNK-A1QTPSL---TNS-E-ELLQSLN1WR-FNLQD---IS---SQLVLAVNWEVSPGQ---LKLNSGSI1AVVPP1500
>Oocarpus_japonicus -----MGTTELVLFFAKSARELVQKMA-AVLRLDQA---QSG-GEELSEVHLSPDQVR---VR---QSLMALNQRVQLD---QRLTSSQDGEIAVPP1500
>Echiniscus_testudo -----MNTVLLFAHNRDAGRSLE1IDVPACDENSYSK-RLQLL1AQCPRLK---IK---HYGLANWQVYVLSN-QNLVLQPTSEIAL1PPY500
>Evechiniscus_chloroticus -----MADQLAGVEYTVLFFAKSRELQAGTKE-ASLQDQD---IKG-E-VLLN1VSEPRDLA---IR---DSVVLNDEYTSSES---SYHSPQDEVIAVPP1500
>Ciona_intestinalis -----MKNQVQVNLFFAKSRELVLQES-QDLTPQD---VTS-F-QL1ET1NCKYPLSD---LQ---GOFTLANWGEY1KTDQ---SYSLTLTQDGEIAVPP1500
>Baetis_sp._AB-2009 -----MNSP1VKNVLLFASARE1SGRE-GE1QVQGE---ETTY-Q-TLYTKVGR-VHLEK---LQ---QNLILANDEYPMEN---NLQPLRQGHIAVPP1500
>Esoc_lucius -----MNTVEVYLFFAKSALTQ1KS-ETIRVQPE---LTT-L-QLMLDLVGRHPLST---VR---ESVVLAVRGEYVANGD---LQVSLRQDGEVIAVPP1500
>Asterias_rubens -----MASCADVVELLFFAKSRELQADVE-QKQVQTH---LXP-E-ELL1TVNHPPLSY---IQ---QTVL5LMGEY1ANG---QDTLNRDQDEVIAVPP1500
>Gadus_morhua -----MTARVTVLFFAKSALTQVRS-EVVPPLAA---TSS-Q-QLMALLGRHPLAA---LQ---DOVVLAVRQGYVADQ---QALLADQDGEVAVVPP1500
>Gallus_gallus -----MNSQVTVLFFAKSAELVGLRS-EVSVPQR---ITS-L-QLMEE1VNLHPLAY---IR---DOVVLAVRGEYVLLQD---QVLQDQDEVIA1PP1500
>Chlamydotis_macqueenii -----MLLQD---QLVLQDQDEVIA1PP1500
>Gallolanius_yassai -----MNLNK1SVNLFFAKARELOKKE-QSLDVVPS---ISY-N-LLLDNE1H-FGLS---IK---QNFILANEEYTTDR---ELQKQDEIA11PP1500
>Tigrionus_callifornicus -----MNSISKVLFFAKARELAGTKE-LTLNVVFN---LSA-Q-QLVTD1EAGPLAI---LR---QSPVLMNDQVYVFN---QVLSKQDGEIAVPP1500
>Trialeurodes_vaporariorum -----MNVSVLFFORAKELAGEEK-VWQVPSF---SSR-Q-HLLNKLVTR-FGLQA---IE---SILLILANNEYLESD---E1KLODGRVIA11PP1500
>Diadromus_collaris -----MTALMNPVFNVRVFFAKARELAGSE-ST1DWDQ1---LSD-Q-QLFARL1OK-FGLQD---IR---QNLILANDEYQVGRGA---TLRQKQDGEIAVPP1500
>Ornithodoros_turicata -----MNSVALNRVLLFFAKARELQKSE-VTLL1PNN---VQD-EKALQDF1FSFPLSY---LY---KCT1LVANWEL1EPQD---ASQVLKQDGEIAVPP1500
>Helicoverpa_armigera -----ME1ENDQVTVLFFAKSRELQAGTKE-STIRLSPF---ISY-Q-KLNL1QDN-NHLQD---IK---QNVILANWEEYQDQ1---Q1D1KQSGDEVIAVPP1500
>Lutjanus erythropterus -----MTADQVTVLFAKSVELTQAKEQ1VAVTPF---ISS-Q-QLMKLLGRHPLSY---LQ---DOVVLAVRQGYVADQ---QVYTLQDGEVAVVPP1500
>Metallyticus_splendendus -----MNDQVQVNLFFAKSRELQSTRE-SQL1SQSV---ISY-E-SLLQD11ET-YQLS---IK---QSVVLANEEYTSAT---MNVLMQDGEVIAVPP1500
>Boreus_hymelalis -----MNTAK1K1FFAKSRELQKATE-DTSVTPFN---ITC-Q-ELL5L1SN-YGLDA---IK---QNVILANWEEYQDNL-QDLTKTQDGEIAVPP1500
>Dermomyssus_gallinae -----MNVKVLFFAKARELAGTAE-RSDVNAER---VTSLD-QLKEL1AGLEPSVKT---LQ---QTSILANDVNVQSV---E1Q-TTQTEIAVPPV500
>Ornithorhynchus_anatinus -----MVLSPVTVLFFAKSALADVRS-ETISVQPE---IKS-L-QLMEE1ESRHPALD---VR---DOVVLAVRGEYVQLDQ---QVLLQDQDEIA11PP1500
>Perma_viridis -----MANNVSVLFFAKSRELQSVFN-SQ1NVSQD---QCF-F-QLFETTVQVPSLVS---IS---ENTILSMEET1SRD---QSTVQSGDEVIAVPP1500
>Osmylus_fulvicephalus -----MSVEVRLFFAKAKQFADKSE-STNL1PNT---LTF-K-ELL1TVQDN-YHGLA---IR---NTIN1SLANFQDGA---TLKFNQTEIAVPP1500
>Haplochromis_moulei -----MNSFADNRQVKNVLFFAKSRELQVQNK-SEV1STR---SVT-TA-QLSP1LTFPPLQK---LK---QGNILALNEEYTSQD---T1HLSQSGDEVIAVPP1500
>Epiplatys_superstes -----MNSQVTVLFFAKSRELQKAGTKE-STIRLSPF---ISY-Q-KLNL1QDN-NHLQD---IK---QNVILANWEEYQDQ1---Q1D1KQSGDEVIAVPP1500
>Opisthorchis_felineus -----MNSQVTVLFFAKSRELQKAGTKE-STIRLSPF---ISY-Q-KLNL1QDN-NHLQD---IK---QNVILANWEEYQDQ1---Q1D1KQSGDEVIAVPP1500
>Oculopholis_sp._AD-2013 -----MADQVQVNLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Osmorus_mordax -----MTTQVSVLFFAKSALTQ1KS-EV1HNPQF---LTT-L-QLNGELVNRHPLSA---VR---EQVVLAVRGEYVY1QD---QVLQVSGDEVIAVPP1500
>Grassostrea_gigas -----MNSQVTVLFFAKSRELQVSSGS-GE1VL1TAN---TNF-Q-DLQKALLKTPPSLQY---IA---ENTILSMEET1DQD---QDLTLRQDGEVIAVPP1500
>Hyphisius_dujardini -----MNSQVTVLFFAKSRELQKATE-DTSVTPFN---ITC-Q-ELL5L1SN-YGLDA---IK---QNVILANWEEYQDNL-QDLTKTQDGEIAVPP1500
>Taeiniopsis_guttata -----MNSQVTVLFFAKARELAGTAE-RSDVNAER---VTSLD-QLKEL1AGLEPSVKT---LQ---QTSILANDVNVQSV---E1Q-TTQTEIAVPPV500
>Pecten_maximus -----MADQVQVNLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Diassotichus_masoni -----MTADQVTVLFFAKSRELQKAGTKE-STIRLSPF---ISY-Q-KLNL1QDN-NHLQD---IK---QNVILANWEEYQDQ1---Q1D1KQSGDEVIAVPP1500
>Equisetum_acinus -----MNSQVTVLFFAKSRELQKATE-DTSVTPFN---ITC-Q-ELL5L1SN-YGLDA---IK---QNVILANWEEYQDNL-QDLTKTQDGEIAVPP1500
>Sepioides_sepioides -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Menopon_gallinae -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Fasciola_hepatica -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Colobus_gongolensis_gallinatus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Acarentomon_sp._AD-2013 -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Meliponini_tasius_undulatus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Liposcelis_butyrophilica -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Inocellia_craspicornis -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Rhaphiella_esculentum -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Maraschia_marcia_marcia -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Oreogonus_clopaformis -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Favosites_lazarensis -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Sepioides_11mollata -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Trichomyces_ceratus_arenolatus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Oreomyza_silantiewi -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Streptopelia_benedicti -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Squalus_squalus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Atractaspis_serrima -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Styllops_mellittae -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Trichobitharia_regenti -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Lathyrus_variegatus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Aivina_vinea_pompejana -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Fraxinus_sorista -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Hydractinia_sp._AD-2013 -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Villosa_11mollata -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Meretrix_meretrix -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Limulus_polyphemus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Protosiphon_venustus -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500
>Tricholopidia_guttata -----MNSQVTVLFFAKARELVQKSE-SNL1TSS---ISY-Q-SLFD1LNT-FGLDA---IK---QNLILANWEEYTSQD---T1HLSQSGDEVIAVPP1500

MS0004.1 ENSMARG0000076779 fam13b

>Danio_rerio	MINVEL.FOHN.KXP
>Acipenser_sinensis	MINVEL.FOHN.KXP
>Meia_calva	MINVEL.FOHN.KXP
>Oanna_punctata	MINVEL.FOHN.KXP
>Anas_platyrhynchos	MINVEL.FOHN.KXP
>Xenopus_laevis	MINVEL.FOHN.KXP
MYTSCDQPLAIVAFKCIHKILITENDQWQELKQLSKRPQWQNS-YHYTAELTELWISD	MINVEL.FOHN.KXP
>Oaetura_pelagica	MINVEL.FOHN.KXP
>Menidia_meniidia	MINVEL.FOHN.KXP
>Porichthys_notatus	MINVEL.FOHN.KXP
>Oryzias_latipes	MINVEL.FOHN.KXP
>Tristerycion_delaissi	MINVEL.FOHN.KXP
>Buceros_rhinoceros_silvestri	MINVEL.FOHN.KXP
>Caprimulgus_carolinensis	MINVEL.FOHN.KXP
>Cerama_cristata	MINVEL.FOHN.KXP
>Canis_lupus_familiaris	MINVEL.FOHN.KXP
>Hyndius_retardatus	MINVEL.FOHN.KXP
>Micropterus_floridanus	MINVEL.FOHN.KXP
>Balanoptera_acutorostrata_s	MINVEL.FOHN.KXP
>Pygocentrus_nattereri	MINVEL.FOHN.KXP
>Callidris_pugax	MINVEL.FOHN.KXP
>Callorhynchus_milli	MINVEL.FOHN.KXP
>Pteropus_vampyrus	MINVEL.FOHN.KXP
>Maylandia_zebra	MINVEL.FOHN.KXP
>Pterocles_gutturalis	MINVEL.FOHN.KXP
>Clupea_harengus	MINVEL.FOHN.KXP
>Latimeria_chalumnae	MINVEL.FOHN.KXP
>Colius_striatus	MINVEL.FOHN.KXP
>Columba_livida	MINVEL.FOHN.KXP
>Merops_rubicus	MINVEL.FOHN.KXP
>Alligator_mississippiensis	MINVEL.FOHN.KXP
>Oculus_cameron	MINVEL.FOHN.KXP
>Kryptolebias_marmoratus	MINVEL.FOHN.KXP
>Sarcophilus_harrisii	MINVEL.FOHN.KXP
>Galeosaurus_variegatus	MINVEL.FOHN.KXP
>Monodelphis_domestica	MINVEL.FOHN.KXP
>Anopheles_funestus	MINVEL.FOHN.KXP
>Esca_lucius	MINVEL.FOHN.KXP
>Falco_cherrug	MINVEL.FOHN.KXP
>Gallus_gallus	MINVEL.FOHN.KXP
>Gavia_stellata	MINVEL.FOHN.KXP
>Balearica_regularis_hibberio	MINVEL.FOHN.KXP
>Erinaceus_europaeus	MINVEL.FOHN.KXP
>Oryctolagus_cuniculus	MINVEL.FOHN.KXP
>Eudarcia_simulatrixcella	MINVEL.FOHN.KXP
>Tauraco_erythrophus	MINVEL.FOHN.KXP
>Opisthocomus_hoazini	MINVEL.FOHN.KXP
>Piecoptes_australis	MINVEL.FOHN.KXP
>Sclerophagus_ferrous	MINVEL.FOHN.KXP
>Lepidodactylus_coronatus	MINVEL.FOHN.KXP
>Nipponia_nippon	MINVEL.FOHN.KXP
>Trematomus_bernacchii	MINVEL.FOHN.KXP
>Geratherium_sinum_sinum	MINVEL.FOHN.KXP
>Menis_javanica	MINVEL.FOHN.KXP
>Glycera_dibranchiata	MINVEL.FOHN.KXP
>Piscoides_pubescens	MINVEL.FOHN.KXP
>Platichthys_stellatus	MINVEL.FOHN.KXP
>Homo_sapiens	MINVEL.FOHN.KXP
>Lusodonta_africana	MINVEL.FOHN.KXP
>Fulmarus_glaucialis	MINVEL.FOHN.KXP
>Nestor_notabilis	MINVEL.FOHN.KXP
>Mus_musculus	MINVEL.FOHN.KXP
>Salmo_salar	MINVEL.FOHN.KXP
>Tupaia_chinensis	MINVEL.FOHN.KXP
>Lepidosteus_osteatus	MINVEL.FOHN.KXP
>Meiurus_nebulosus	MINVEL.FOHN.KXP
>Trichechus_mammatus_latirostr	MINVEL.FOHN.KXP
>Aptenodytes_forsteri	MINVEL.FOHN.KXP
>Crotalus_horridus	MINVEL.FOHN.KXP
>Tyto_alba	MINVEL.FOHN.KXP
>Struthio_camelus_australis	MINVEL.FOHN.KXP
>Chelonia_mydas	MINVEL.FOHN.KXP
>Takifugu_rubripes	MINVEL.FOHN.KXP
>Timamus_guttatus	MINVEL.FOHN.KXP
>Galyte_anna	MINVEL.FOHN.KXP
>Apaloderma_vittatum	MINVEL.FOHN.KXP
>Dryopteris_afer_afer	MINVEL.FOHN.KXP

HG0004.1 ENSG00000001003 FAM138

>Homo_sapiens	-----	MINVEL.FOHNK.KXP
>Acipenser_sinensis	-----	MINVEL.FOHNK.KXP
>Meia_calva	-----	MINVEL.FOHNK.KXP
>Ohamna_punctata	-----	MINVEL.FOHNK.KXP
>Anas_platyrhynchos	-----	MINVEL.FOHNK.KXP
>Xenopus_laevis	-----	MINVEL.FOHNK.KXP
MYTSGSDGDLAIVAFKICIKILITENDQWQELKQLSKRPQWQNS-YHYTAELTELWISD	-----	MINVEL.FOHNK.KXP
>Oaetura_pelagica	-----	MINVEL.FOHNK.KXP
>Menidia_meniidia	-----	MINVEL.FOHNK.KXP
>Porichthys_notatus	-----	MINVEL.FOHNK.KXP
>Oryzias_latipes	-----	MINVEL.FOHNK.KXP
>Tripterygion_delaissi	-----	MINVEL.FOHNK.KXP
>Buceros_rhinoceros_silvestri	-----	MINVEL.FOHNK.KXP
>Caprimulgus_carolinensis	-----	MINVEL.FOHNK.KXP
>Cerama_cristata	-----	MINVEL.FOHNK.KXP
>Canis_lupus_familiaris	-----	MINVEL.FOHNK.KXP
>Hyndrius_retardatus	-----	MINVEL.FOHNK.KXP
>Micropterus_floridanus	-----	MINVEL.FOHNK.KXP
>Balaenoptera_acutorostrata_s	-----	MINVEL.FOHNK.KXP
>Pygocentrus_nattereri	-----	MINVEL.FOHNK.KXP
>Callidris_pugnax	-----	MINVEL.FOHNK.KXP
>Callorhynchus_milli	-----	MINVEL.FOHNK.KXP
>Pteropus_vampyrus	-----	MINVEL.FOHNK.KXP
>Maylandia_zebra	-----	MINVEL.FOHNK.KXP
>Pterocles_gutturalis	-----	MINVEL.FOHNK.KXP
>Clupea_harengus	-----	MINVEL.FOHNK.KXP
>Latimeria_chalumnae	-----	MINVEL.FOHNK.KXP
>Colius_striatus	-----	MINVEL.FOHNK.KXP
>Columba_livida	-----	MINVEL.FOHNK.KXP
>Merops_rubicus	-----	MINVEL.FOHNK.KXP
>Alligator_mississippiensis	-----	MINVEL.FOHNK.KXP
>Ooculus_carnorus	-----	MINVEL.FOHNK.KXP
>Oanio_rerio	-----	MINVEL.FOHNK.KXP
>Xrytolobias_marmoratus	-----	MINVEL.FOHNK.KXP
>Scorophilus_harrisi	-----	MINVEL.FOHNK.KXP
>Galeopterus_variegatus	-----	MINVEL.FOHNK.KXP
>Monodelphis_domestica	-----	MINVEL.FOHNK.KXP
>Esoc_lucius	-----	MINVEL.FOHNK.KXP
>Falco_cherrug	-----	MINVEL.FOHNK.KXP
>Gallus_gallus	-----	MINVEL.FOHNK.KXP
>Gavia_stellata	-----	MINVEL.FOHNK.KXP
>Balearica_regularis_iberico	-----	MINVEL.FOHNK.KXP
>Erinaceus_europaeus	-----	MINVEL.FOHNK.KXP
>Oryctolagus_cuniculus	-----	MINVEL.FOHNK.KXP
>Tauraco_erythrolophus	-----	MINVEL.FOHNK.KXP
>Orithoemus_hoazin	-----	MINVEL.FOHNK.KXP
>Piceoglossus_altivelis	-----	MINVEL.FOHNK.KXP
>Scleropages_fornosus	-----	MINVEL.FOHNK.KXP
>Lepidothrix_coronata	-----	MINVEL.FOHNK.KXP
>Niipponia_nippon	-----	MINVEL.FOHNK.KXP
>Trematomus_bernacchi	-----	MINVEL.FOHNK.KXP
>Ceratotherium_simum_simum	-----	MINVEL.FOHNK.KXP
>Manis_javanica	-----	MINVEL.FOHNK.KXP
>Picooides_pubescens	-----	MINVEL.FOHNK.KXP
>Ptilichthys_stellatus	-----	MINVEL.FOHNK.KXP
>Losodontia_africana	-----	MINVEL.FOHNK.KXP
>Fulmarus_glaucialis	-----	MINVEL.FOHNK.KXP
>Nestor_notabilis	-----	MINVEL.FOHNK.KXP
>Mus_musculus	-----	MINVEL.FOHNK.KXP
>Salmo_salar	-----	MINVEL.FOHNK.KXP
>Tupaia_chinensis	-----	MINVEL.FOHNK.KXP
>Lepidososteus_oculatus	-----	MINVEL.FOHNK.KXP
>Ictalurus_punctatus	-----	MINVEL.FOHNK.KXP
>Trichechus_mammatus_latirostr	-----	MINVEL.FOHNK.KXP
>Aptenodytes_forsteri	-----	MINVEL.FOHNK.KXP
>Orotalus_heroidus	-----	MINVEL.FOHNK.KXP
>Tyto_alba	-----	MINVEL.FOHNK.KXP
>Struthio_camelus_australis	-----	MINVEL.FOHNK.KXP
>Chelonia_mydas	-----	MINVEL.FOHNK.KXP
>Takifugu_rubripes	-----	MINVEL.FOHNK.KXP
>Tinamus_guttatus	-----	MINVEL.FOHNK.KXP
>Gallyste_anna	-----	MINVEL.FOHNK.KXP
>Apaloderma_vittatum	-----	MINVEL.FOHNK.KXP
>Orycteropus_afer_afer	-----	MINVEL.FOHNK.KXP

[illegible]

HS0004.1 FBw0028494

>Drosophila melanogaster
MULTIPLYTHELUP
>Stenotoda grossa
MULTIPLYTHELUP
>Pachinotermes simplex
MULTIPLYTHELUP
>Neoplophora glabripennis
MULTIPLYTHELUP
>Eurylophelia.sp._AD-2013
MULTIPLYTHELUP
>Cimex lectularius
MULTIPLYTHELUP
>Leptoclinus claviger
MULTIPLYTHELUP
>Eudarcia simulatrixcella
MULTIPLYTHELUP
>Metallyticus splendidus
MULTIPLYTHELUP
>Corydalis cornutus
MULTIPLYTHELUP
>Cormentzia graciliformis
MULTIPLYTHELUP
>Medusoides extradentata
MULTIPLYTHELUP
>Tityus serrulatus
MULTIPLYTHELUP
>Drosophila silvaticiwei
MULTIPLYTHELUP
>Amulipalpis.sp._AD-2013
MULTIPLYTHELUP
>Limulus polyphemus
MULTIPLYTHELUP
>Zorotypus caudellii
MULTIPLYTHELUP

HG0004.2 ENSG00000138640 FAM13A
 >Homo_sapiens
 -----MEEAALRLPWELCTGGSPSHRITCAENWFSILLGF
 >Mustela_putorius_furo
 MSKXTSLPNIIGAILRLP-----
 >Procyon_citoides
 -----MEEAALRSPWELRTNSRVSRSISTENSSVLLGF
 >Epitesticus_fuscus
 -----MEEAALRLDWELRTGGSPSNGSIPTONWFSILLGF
 >Lionodonta_africana
 MISTALPRLISTALALPWELWISGRPLNGSISTENWFSILLGF

[illegible]

<i>haliaetus_gallus</i>	MAVVRBARSYS-RCVWFS-RELC
<i>halimene_simensis</i>	MAVVRBARNFA-RCVWFS-RELN
<i>chama_argus</i>	MAVVRBARKY-CVWVFS-RELN
<i>kauaiichthys_hypocoroides</i>	MAVVRBARNFS-RCVWFS-RELY
<i>podocoryna_carnea</i>	MAVVRBARNFA-RCVWFS-RELN
<i>xenopus_tropicalis</i>	MAVVRBARSYS-RCVWFS-RELC
<i>apteryx_australis_mantelli</i>	MAVVRBSRGS-RCVWFS-RELC
<i>stegodyphus_nimosarum</i>	MAVVRBARSFS-RCVWFS-RELC
<i>apostichopus_japonicus</i>	MAVVLARBRY-RCVRFNSRDELC
<i>memidia_memidia</i>	MAVGLIARVTP-GSVTRFS-RELYD
<i>opanus_beta</i>	MAVFLBARKY-RCVWFS-RELC
<i>oryzias_melastigma</i>	MAVFLBARKY-RCVWFS-RELC
<i>prohintonermes simplex</i>	MAVFLBARKY-RCVWFS-RELC
<i>trachinotus_blochii</i>	MAVLRKXGTF-KSVYRFS-RESEA
<i>panthera_tigris</i>	MAVFLBARKY-RCVWFS-RELC
<i>crotoperus_floridanus</i>	MAVVRBARSYS-RCLWVFS-RELC
<i>pygocentrus_nattereri</i>	MAVFLBARKY-CVWVFS-RELC
<i>miniopetrus_natalensis</i>	MAVVRBARKFA-RCVWFS-RELC
<i>ophthalmodon_ventralis</i>	MAVVRBARSYS-RCLWVFS-RELC
<i>clupea_harengus</i>	MAVFLBARKY-RCVWFS-RELC
<i>latimeria_chalumnae</i>	MAVVRBARKTP-KSVYRFS-RELC
<i>alligator_misissippiensis</i>	MAVVRBARNFT-CVWVFS-RELC
<i>neocyttus_lochilus_grahamii</i>	MAVVRBARSYS-RCVWFS-RELC
<i>fundulus_heteroclitus</i>	MAVVRBARKFA-RCVWFS-RELC
<i>sarcophilus_harrisii</i>	MAVFLBARKY-RCVWFS-RELC
<i>homarus_americanus</i>	MAVVRBARSIC-RCLWVFS-RELC
<i>scierodactylus_brianus</i>	MAVVSIRITFT-SVWVFS-RESCIA
<i>macropus_eugenii</i>	MAVVRBARNTH-ONVYRFS-RELC
<i>hapiocombia_palasi</i>	MAVVRBARSIC-RCLWVFS-RELC
<i>esphenia_danica</i>	MAVVLQKQTF-ASVTKYFS-REFMIP
<i>esox_lucius</i>	MAVVRBARKLQAGLVWVFS-RELN
<i>weganyiaphanes_norvegica</i>	MAVFLBYLQFP-RCVWFS-RELC
<i>falco_cherrug</i>	MAVAVSTWTF-ASVYRFS-RESCIA
<i>leptasterias_sp._AR-2014</i>	MAVVRBARSYS-RCVWFS-RELC
<i>gillilichthys_mirabilis</i>	MAVFLRFLFS-KCLWVFS-ROCKA
<i>chanos_chanos</i>	MAVFLBARKY-SVWVFS-RELC
<i>oryziaslatipes_bifurcata</i>	MAVVRBARKFA-RCVWFS-RELC
<i>api_s_cerana</i>	MAVLRKXKYS-TPVTRFS-RELLP
<i>erineaceus_europaeus</i>	MAVVLARLFT-RCVWFS-REYNG
<i>xodops_persulcatus</i>	MAVVRBARSYS-RCLWVFS-RELC
<i>ochotona_princeps</i>	MAVAVKARVR-NCLRFNSRDESCIA
<i>lutjanus erythropterus</i>	MAVVRBARSYS-RCLWVFS-RELC
<i>galopteryx_sp_lendens</i>	MAVFLBARKY-RCVWFS-RELC
<i>ophiocomus_echinata</i>	MAVVLBARKELS-TQVTRFS-RESSA
<i>lousta_migratoria</i>	MAVVLKSLFT-SVWVFS-ROBKA
<i>osmerus_mordax</i>	MAVVRBARKYF-ESVTRFS-REXVP
<i>scieropages_fornus</i>	MAVGRTRVTF-RCVWFS-RELVSYF
<i>corvus_cornix_cornix</i>	MAVVRBARNFA-RCVWFS-RELN
<i>lateolabrax_japonicus</i>	MAVVRBARSOS-RCVWFS-RELC
<i>sebastes_caurinus</i>	MAVFLBARKY-RCVWFS-RELC
<i>braueriothaim_simu_simu</i>	MAVVRBARKY-RCVWFS-RELC
<i>paipio_ambio</i>	MAVVRBARSYS-RCVWFS-RELC
<i>ramus_arteis</i>	MAVVRBARSYS-RCVWFS-RELC
<i>menopon_zalline</i>	MAVLRKXKTF-GSVTRFS-RESLP
<i>perla_marginata</i>	MAVLSKXQTF-GLVTRFS-REFGD
<i>cmoglossus_simeis</i>	MAVVRBARSYS-RCVWFS-RELC
<i>gagadomyces_gagadomyces</i>	MAVVRBARSYS-RCVWFS-RELC
<i>leucoraja_erinacea</i>	MAVVRBARSYS-RCVWFS-RELC
<i>croetus_ochoaster</i>	MAVVRBARNFL-DIVYVFS-RELC
<i>salvelinus_alpinus</i>	MAVVRBARSYS-RCVWFS-RELC
<i>tuqia_chinensis</i>	MAVFLRSLKTP-RCVWFS-RELC
<i>tytus_serrulatus</i>	MAVVRBARSYS-RCLWVFS-RELC
<i>xiphocheilus_poulatus</i>	MAVLRKXKTF-GSVTRFS-RELYA
<i>trichomycterus_aerolatus</i>	MAVVRBARNFA-RCVWFS-RELC
<i>oporus_aurea</i>	MAVVRBARSYS-RCVWFS-RELC
<i>echinaster_spinosus</i>	MAVFLBARKY-RCVWFS-RELC
<i>streblospio_benedicti</i>	MAVFLRFLFA-KCLWVFS-ROBKA
<i>gekko_japonicus</i>	MAVLRBYSFS-SVTCVFS-RELYT
<i>cheiloneus_nydas</i>	MAVVRBARSYS-RCVWFS-RELC
<i>thei flugi_rubripes</i>	MAVVRBARSYS-RCVWFS-RELC
<i>therobia_domestica</i>	MAVVRBARKY-RCVWFS-RELC

HS0006 FBgn0029971 0618624

>Drosophila_melanogaster-----MSSGIVVOLARKYGAVIFFPITVAVGSIYADNHSITRMKRGQLQLAHRAQLKD--QR-----
>Echiropus_macronychus-----MGLVLEIVRRFVVVIFPAFVITCTIADYKHITAEKKRNFLEKQLRDRES-LRN-----
>Machilia_hrabai-----MALWSFGRFGRYQVVIFFPACVTSIYADYSHQKMKAGQLRIQEKLKAE-NHS-----
>Blaberus_atropos-----MAVSQLFRRYVIVLFPFVITAGSIFADLHTKMKKEQKQLQTALEEE--TL-----
>Hymobius_chinensis-----MGQLSNIQVFWRRYVSILFPAFSIGTIYADYAHQKYKSLADFQRKQQLQ-----
>Trypoxylus_dichotomus-----MSFKIGKLVNKYVIVLFPFVASTIYADYHTQEKKSLNKLN-----
>Litopenaeus_vannamei-----MAPRLTALG-FLRKYKVVIFFPVTFSATADILHTRMKKAEKAAALAEASA-----
>Apachys_charteus-----MVLLSIPVISVYSSSIINFCRKYSLSLFPTLSLSIIADFNHSRKMKSLKNE-----
>Daphnia_pulex-----MSVLAFWRRYVSIIFFVLSFSFIYADWSYTRMKGNLKLAEAYDPE--VKA-----
>Camponotus_augens-----MAGS-----RIVTSKLPDAPPVDPISFARCKRANFLWRYRASVLFPVTIVGLILLDYNHTQMKKEGKLEKQAEK-----
>Haploembia_palaui-----MDK-----PPSVLRRTGYLIRKYFIVVALPTALGTAYIADYLHTQMKKGAALQNKPSM-----
>Isomychia_bicolor-----MAVGYYIRYVIGSVLFPFVALSIFADFNHTRMKKEQKQLLTQESNLS-----
>Onuphis_tridescens-----MSGLAYKKYLRNFVSIVFPVGLGLIYADWSRTQKYKASK-----
>Gallioisiana_yuasai-----MASGRLSTINKLWKTYRVVIFPPTFATAAIVADLHTRMKVKASLEAKENN-----
>Aemynthas_koreanus-----MQLSFAYAFVKRNFVSIVFPVCTVMAIYADWSRTRRYKAAELPSTHFQS-----
>Tigriopus_californicus-----MFQKQLALFRKYASVIVFPVVFSSIAQDFNHTGRMKRNGIEFDESQKLIHQ-----
>Adeiphocoris_lineolatus-----MALPIRSFVKRYGPSIVFPVAAFSAIYADYSHITQMKKEQLLKAKTSELL-----
>Lineus_viridis-----MEKE-----VVSAPKVLRFKRNFSIVFPVVAAMAIYSDYSRTGRFKAKARELVYGAVKRELKDSF-----
>Tentredo_koehlerii-----MAAPKVISIGKISRYAAVFFPFIATTFLDNHTRMKKIAESERYSALNSELQ-----
>Armadiillidium_vulgare-----MEGRTHPIKFKRKAGRSIIFSTVISSLTADYLHTRMKKELETKYENFY-----
>Dermacentor_variabilis-----MAATGTA-----LEKVRLLKVCRRYATVLPFTISGMLIYADYSRTGRMKKSKASAE-----
>Triodia_sylvina-----MAGKFLRYGVVIFPPTFAATSIYLDNHSITKMKQKQLFVNKSEIV-----
>Mantis religiosa-----MEV-SRLAGRRFRFKTYWVITLFPVITAGSIFADLHTRMKKKEKELAKADLKR--TLSEEQ-----
>Tanzaniophasma_sp._AD-2013-----MAGVILSSARNFRWYQVILFPFTITITIAADLHTRMKKAKTVAEVLQKTVSEDTVYS-----
>Boreus_hymalis-----MALGKASAIRHFKWYKSVVIFPPTFILTATYADYSHITQMKKAGQSGTK-----
>Siella_tutaria-----MAVRLSTIGSFWRKYVVIFFPVTISSIAADYQHTQMKKASOTNQ-----
>Mytilus_galloprovincialis-----MAGS-----RTISKILIRVRNLSVIFPVLQFGAIVLYDYSRTQKYGRKQLDH-----
>Xibalbanus_tulumensis-----MDVTLVGRVRFRLFKYKVIIFPVAQSGAIFADYNHTRMKKEKARLEALAYQEN-PENIVQ-----
>Euroleon_nostras-----MSVGRKLTYGVWRYYRIVILFPFTITIGTISADLHTRMKKEQQLALENKSKSEF--D-----
>Triops_newberryi-----MALSLAFWRRYNVVIVFPTLTAAGSIYADYSHITQKYKAAKALASRFSELLSE-----
>Epiophlebia_superstes-----MAKGNAAVKFLKKGISIFFPSATVAAYADLSHTKMKKALQVQVAKYSQE-----
>Phalangium_opilio-----MNFKIALRTLKRYKVILFPTITINSIYADYRTLRYKATKLQILGROTVL-----
>Hypochothius_rufulus-----MANESPSLNHKLWYERLVEFRYYRRTILFPVTLLGLVYDFSHITQMKKQKQLSENGSGIVLN-----
>Stenobothrus_lineatus-----MLKATGKFLRYGVVIFPPTVVTAAIITDLSYTRMKKSLKAEKLQKELLTD-----
>Phyllium_ghiilippinicum-----MEVSKLVAANKLVKYYVWVFPFIAAVTISADNHTRMKKLKKAAAEQSGQA--VLAEDGGSNYQ-----
>Glycera_tridactyla-----MSPAAGPLRLKLVNLVITFPTVVAAMAIYADWSRTRRFKAGKALERYKEHT-----
>Cosmiopleria_kuna-----MAAVKEVSAIGKFLRYKVVIFFPFTIATIFADLHTRMKKAGETAGESTVKYTAEKLL-----
>Acerentomon_sp._AD-2013-----MWHGTTTTPHSSSASKYKQFTLVATDAQDANLSFFRRALKATNKYSLVVTFPSIAFAAIIYADYSRTQMKKAEQARLKETE-----
>Ectoposous_briggsi-----MANWRYLLRYSVVVIFPTLTAMSIYADLSHTRMKKAQEEARKKEE-----
>Inocellia_crassicornis-----MAVQKVGFIKAFWRKYGVITFPTLSFSAITLADYHTHYKMKQGAALLQELKDPE--LLKS-----
>Trichomycterus_aeolatus-----MAVAKTPSALGLFNRYKYSIVFPVLVSASIFADYSRTSSMKIKSKFER-----
>Oropsylla_silantiewi-----MAYLASFRLWKYYSIVLFPSPFALGSIYADWSNTQMKKQNTKKQ-----
>Gluvia_dorsalis-----MASSARGILQLYWKYVILFPTGTALSIYADYSHITKORALNNKKE-----
>Stylops_melittae-----NIKIRFRKRSITRHSITLFPVLVAAGLWADYSATQMKKARKGAREAK-----
>Mivineella_pompejana-----MEGGT-----ALNPFQTLVANKLRNFITIIFFPVLTTNAIYADWSHTQKYKAAKALLQASEESQSIG-----
>Gynaikothrips_ficorum-----MWKVANIKRYFLETGFPPVLFPVPIYLDNHSRTQRYKAEKLKESGGSS-----
>Rhyacophila_fasciata-----MGLGKLVKYSVVLFPVTIVTSIVADLRHTYLMKKQKAECLKQ-----
>Zorotypus_caudeilli-----MAVLKTARELSRYFISVLPFTIAISSIVADYKHTQMKKAGQAIIQSS-----
>Atelura_fornicaria-----MAAGVGFLWRRYRVVIFPPTIVAAGISADYHTRMKKAGQAELKSRESVHI-----

HS0007 FBgn0034372 Gint3

>Drosophila_melanogaster
-----MSFNFYVESFNS-----T-----L-----GSIAR-----QVEQAGVALTAAYD-----LRGNLE-----SLTG-----DFRIEN-GP IAFDTQATLLKVLIVLLGTGVLGAGYSMSYGVKITEKVPSPST-LK-EI-EELKLSVAKVLKPKHSPTRI-
>Stegodyphus_lineatus
-----MKSLS-----DII-SNLITPSGVTE-----YLYSVFPEDIPDA-AISLVSFTSNTVDEFQILKILVSLCILLINLFLIHCAMRKYGEKITERFMK-PA-SKSL-EDLKREATELKPKEHTPRI-
>Machilis_hrabai
MS-----S-----VIDFE-----SETSSLFE-----ALHQLFQELTGFICTEF-GLSEVSGEE-----FKSYFWS-----VYHSII-DNLSFDQFQWLLGAFLLILFTNVLVIYIMRVYGERIADRFWYPS-VR-AI-EELKASVORLKPKEHTPRI-
>Argulus_siamensis
-----MFLD-----FD-----NLVLLLYDLY-IQ-LVEKLYE-ELYTNDQFRLTIQCFSFIIQVNIILIIIAWKYGPRIAEKFMVPV-TV-V-EQLSKDIASLKLPEYSPRV-
>Cryptocercus_wrighti
-----MSMKYIGKRISEKFMIPAT-OK-TI-EELKRSVSLKLPKEHSPTRI-
>Moloe_violaceus
MN-----A-----FLNDFSTNSSLFD-----VITYTLTITNIYF-----IDTL-SLDRDPIKH-----KOLLSVF-----DNLP-SLLDFNEFQTLTKTLVLVLANLLFIAMTYGKRIQGRFMIPAT-MK-AI-EELKASVSLKLPKEHTPRI-
>Eucoelops_serrulatus
MNINESLNTFTSSITSLILEDNIQGRETDLLTDLFNFDSSIFSIESLSY-VANSFQNTLVGIFNSTCEISSVFGQVAGSIL-NEATGNIS-SA-VSLTFLESEKLF-DNFMFTFQWLLREFSIIILGNVLVIYAMKYGPRISKFSVSPSRGSGROVI-EOLKSNSELQLPMEHGYLKL
>Apocheilus_charteceus
-----MIPAT-SK-TI-EOLKKSVSLLKLPKEHSPTRI-
>Daphnia_magna
M-----VDEKSGDQGSTLWEL-FVEYFVNLIVYLYT-SVILHTEVL-V-E-YG-EHFLQSFLLLSLSETIVAI-FDLAFSDQIQKLVQVFFQILAIHIIICVAMKYSERIIGRFKPSL-YEISS-EQLKTAIVSELKPAEHTPRW-
>Oocarpus_japyx_japonicus
-----MIPAS-LR-AI-EELKRSVSELKLPKEHSPTRI-
>Aposthonia_japonica
MI-----P-----LFGNYF-NSTVLD-ATTYYVFKLFALA-NEVY-GISSSKTFDGS-ESS-FTI0I-FDLG-TWFAFDQFQITLLKVLQFVLNVLICIIYIMKYGKRISEKFMIPAT-PK-AI-EELKKSVFLKLPKEHSPTRI-
>Isomychia_bicolor
MS-----S-----LSDQVSANST-----VIDSIFQYL-QKQQLLQGL-GLGPVVLPEPLQDL-PHLPTDILTDTFEN-FAFDQFQKLLKGLFVLVTFNIIILFIAMFYGKRISEKFMIPAT-SK-AI-EOLKKSVSLLKLPKEHTPRI-
>Galloisiana_yuasai
MT-----S-----INEDDSNLSFIN-VITNYIYEISTVI-YTAF-GFTSNIKVENN-IPLHFIEGY-YNII-NMLAFDQILKLVGFTFLFANILFIYMSKYGKRISEKFMIPAT-SK-AI-EELKKSVSLLKLPKEHSPTRI-
>Graphocophala_atropunctata
MT-----S-----HVEQLDSSSLMN-LLFYQNDIYFAI-FSNL-NITSMTTSLTSTFIGNEHSNLISYL-RYIA-SLLPYDEFQIELLKGFCAIILTNITQVLAIAMKYGKRIQGRFMIPAT-PK-VI-EELKKSVSLLKLPKEHSPTRI-
>Tentredo_koshleri
MS-----S-SV-ONDVAPGSSGLD-IIMKFAOCLIGLY-FSTI-GITSINNSNLDDTSSHHRTIIQFY-EEPS-AMLAFDEFQILKLVFAFLVSNVLIYAMKYGKRISEKFMIPAT-SK-AI-EELKKSVSRLKLPKEHSPTRI-
>Rhipicephalus_annulatus
-----MFWF-----SASQK-EEEAESPLH-WTSSLLTGPLVEAY-EQDTWLGQZHFERSVADQLLVFAINVLILGVNRGSDQIADQFLNAT-SSSL-EEFGKASSELPEEHSPTRI-
>Enteucha_acetosae
MS-----A-----FFETYIINSTLFE-VLSLTVNDSFGYF-SEL-VIRCF-ESV-KVLESIMKLEKICENTFSKEFL-SSLEFDQFQILKLTLLIIFATFLLICFVWMLYGRISERFMIPAT-SK-AI-EOLKKSVSLLKLPKEHTPRI-
>Empusa_pennata
-----MIPAT-SK-AI-EOLKKSVSLLKLPKEHSPTRI-
>Panorpa_vulgaris
MNILFIYAMFYKDIINEYFMPTTS-VO-ED-AELQKIELLKPKEHTPRI-
>Sialia_lutaria
MT-----S-----YITDNLNTSYTT-D-VILKYSEEWNIYIL-KVIGLFSEHETAIHP-L-IL-FYQS-VVDFAF-SLVHNEFQISILKVLVLIILNLFIQIYMKYGAIGERFMIPAT-SR-AI-EELKASVORLKPKEHTPRI-
>Euroleon_nostras
-----MIPVT-SR-AI-EELKASVORLKPKEHTPRI-
>Triops_newberryi
MK-----FIMPHFDGSLNSHMSAVDSVSLSENKSSVFPWIP-VSLFSLFW-LVES-VTS-AWSSL-TYNLSVVG-ESFSFDQFQILKLVFLVFNQILTLAMRVYGRKITERFMPTSS-DV-LK-EQLKTAIVSELKPAEHTPRI-
>Galopteryx_spelendens
MT-----S-----FNDALFSNSTLDD-YAHYFIHNSNITL-LELL-GIGSEHEIKAD-SNTLHYC-EDLI-QWFADEFQITLLKGFATILSANVLICISMKYGRKISERFMPTTS-TK-AI-EELKKSVSLLKLPKEHSPTRI-
>Nothrus_palustris
-----MIDTLFILLIILVSNLLIYIFWMLYGRIDIVLITREE-KQDIL-DQLREAFELKLPKEHSPTRI-
>Cautophilus_sp_AD-2013
MT-----S-----VAEDA-I-NSSFVD-VIRVYVFLFTAV-TKIF-GLASNIPLQOT-TSTRLFEQY-NSVI-SMLAFDQFQWLLKGVFLICANVLFIYSMKYGRKISERFMPTT-SK-AI-EELKKSVSLLKLPKEHSPTRI-
>Crassostrea_gigas
-----MSSESLSS-A-TTQCAL-VIYDITG-V-GKVIWDFL-VDAFL-LRHEDQVQSKLLVLIIMLFFNLIGIAMOYGNICELMRSKEK-----
>Ramilus_artemis
MT-----S-----VNGDINFWNSFLE-PVLHICELVKSL-NEYL-ADSLNFWNSAP-AYSRVETL-VVLG-SMVTFDQFQILNLLKGFILFFFINILLFIYSMKYGRKISERFMPTT-PK-AI-EELKKSVSLLKLPKEHSPTRI-
>Monopon_gallinae
MD-----QDSSTLGGTTFLD-NLYAGFSKIFQEA-YELL-SSVIOSEI-LSYFEGVSN-LNVL-QYFADELQILKLVGLLIIVFNISVLIITWMLYGRKISERFMPTAS-SK-TI-EOLKKSASMLKLPKEHPTRI-
>Platyneris_dumerilii
MS-----ERAP-I-D-SKIAEFNSTEAEGNTH-VDFG-YD-L-CKEFGKWOKLEFRVLLVLIIGLAVNLNLHCAMRKYGNKITERFMSSGS-SKSS-EN-KEVPEORLIRE-----
>Leuctra_sp_AD-2013
-----MIPPT-SK-SI-EOLKKSVSLLKLPKEHSPTRI-
>Acerentomon_sp_AD-2013
-----MIPAS-LK-VI-EELKRSIAELKLPKEHSPKI-
>Liposcelis_bostrychophila
-----MPTAS-HK-AI-EOLKKSISMLKLPKEHSPTRI-
>Xanthostigma_xanthostigma
MT-----S-----FSYLDVNASYND-IMYAYEYDYIL-QILNLFVWDCST-EH-YLSLYQ-SFIVFNEQWILKSLIIFLCINLLFIYIMKYGHQIGERFMIPAT-SR-AI-EELKASVAKVLKPKVHSPTRI-
>Tityus_serrulatus
-----MV-SHLF-Y-FT-DI-I-YEYLVIPFINIEEFWMLLSLVLFLINLVFIYAMKYGKRISEKFMIPAT-SK-AI-EELKKSVSRLKLPKEHTPRI-
>Trichomycterus_areolatus
-----MIPAT-SK-AI-EELKKSVSRLKLPKEHTPRI-
>Archaeopsylla_erinacei
-----MSLSNYMFTYFNTVYDQL-EYLYVLNENIKLYSTES-EVSFFDPI-GETFE-YLINFQYQLTLKVLVLIQNLFIYAMKYGKVIDNCSIRPTT-LD-ED-YELIERNAKMLPRVHSPTRI-
>Streblospio_benedicti
-----MTEQEL-ONEK-VIHADTLOT-DLE-SLKET-FQL-IVTDFWQSDQIKLFCILTVILLINVLIKIAMSTYGERLSEMFSLTSROTSEERVGEVRAENIQRE-----
>Stylops_melittae
-----MV-NLQNLTWIF-N-EFKQLFVSEI-LYLE-SLTSLSNLQIRIVQVFTLLITLNLTLILVWMLYGRISERFMIPAT-SK-EI-EELKLSVSKLKPKEHSPTRI-
>Frankliniella_cephalica
MS-----T-----FTEESLNTSAL-LMNSLVSSISNTY-LYAI-GLTSNITEG-SHLSALPL-FDMD-ALFSYDQFQVLLKVLFLILAFNLVSGIAMKYGKNIYETFMIPAT-PK-II-EOLKKSVSRLKLPKEHSPTRI-
>Annulipalpia_sp_AD-2013
-----MSHW-RAFSEE-G-LPLP-LSLPSGSLSEFVOVFPPEIPL-GSVQDFQFHALLKTVLFTTLFLIFYSMKLYGKRISEKFMIPAT-SK-AI-EELKKSVSRLKLPKEHTPRI-
>Limulus_polyphemus
MS-----GAVDAA-NOSEL-EXTENSTNAOPONTW-LTSSLGSAREGL-ELWISDNFSDIDEQWILKLTLLTFLCINLTLICLAWKYGKRISEKFMIPAT-SKAL-DOLKREATELKPKEHPTRI-
>Zorotypus_caudealii
-----MFIQIAMKLYGEQISERFMIPAT-AK-FI-EOLKKSVSLLKLPKEHSPTRI-
>Thermobia_domestica
-----MK-PA-STKSF-EDLKASSELKLPKEHSPTRI-

>Homo_sapiens-----MTIRCFVSHPFSMENOGDR-AMTATGSFEEDTFREA-----
>Acipenser_sinensis-----MLVRFVFGRLSMEGRNL--IYTESNFSERDTFREEC-----
>Podocoryna_carnea-----MLVRFVFGRLSMEGRNL--IITESNFSERDTFREEC-----
>Megophrys_sangzhiensis-----MFQHLVLHGFSMEXGGR-IFTASNGDGRDAFREA-----
>Oryzias_latipes-----MILGLSTSEISSMEKGGGT--VKCAANFSQDRTFRES-----
>Acinonyx_jubatus-----MTIRCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Hymnobius_retardatus-----MTITTAGSKPSPMEGGYR-----ERKFNWDTFRET-----
>Micropterus_floridanus-----MILRLITSEKSSMEKGNG--FIAGTNFSQDRTFRES-----
>Orcinus_orca-----MLQEQMALSLLGQPLRSISLKLSSF-----ALTQTHSMITIRCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Astyanax_mexicanus-----MFRCSFSERFSMEGRGNE--IIVESHFNORDAFRES-----
>Miniopterus_natalensis-----MTIRCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Clupea_harengus-----MLLYCLVLERFSMEKGNY--IIVESHFNORDTFRES-----
>Latimeria_chalumnae-----MTIRYSDSAEFSNDQ-EXT--SIKNNFNEDTFRES-----
>Alligator_sinensis-----MVIIRYSDAPMENRNGHR-MVVASCKDGRDAFRES-----
>Sinocyclocheilus_grahami-----MFLICTGSRNFSMEGRGNE--IIVEGHFNORDTFRES-----
>Kryptolebias_marmoratus-----MLKPDVLKYLFLFLLKQLFSRQSMILRLKYSRSSMEKGNG--FIIGTFNORDTFRES-----
>Seiinthispis_crassicaudata-----MTIRCSVSGQFSMENOGDR-TWVARSNFEEDTFREA-----
>Galeopterus_variegatus-----MTFGCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Monodelphis_domestica-----MTIRCSVSGQFSMENOGDR-MNVAVSNFEEDTFREA-----
>Trichosurus_vulpecula-----MTIRCSVSGQLSMENOGDR-MNVAVSNFEQDRTFREA-----
>Esox_lucius-----MFLGHVFERGSMEEKGNG--IIVESNFQORDAFRES-----
>Acanthopobius_hasta-----MENWRTQ--FIAGTNFSQORDAFREA-----
>Ohanos_ohanos-----MFMCPVFKHFSMEGRGNE--IIAESTFNORDTFRES-----
>Condylura_cristata-----MTVRGFSQPFVSMENOGDR-AMLTADSFEEADAFREA-----
>Oryzotylagus_cuniculus-----MNVRCFVSGPFSMENOGDR-QMTATGSFEEDAFREA-----
>Elephantulus_edwardii-----MTIRYSVSGPFSMENOGDR-IMTATGSFKNDFVREA-----
>Sclerophagus_fornosus-----MFLKQYTLKRVSMEDQNE--IIAESQFSERDTFREA-----
>Lateolabrax_japonicus-----MILRLITSKRSSMEKGYO--FIAGTNFSQDRTFRES-----
>Sebastes_caurinus-----MILKLLITSESCSMERGGNG--CIAGTNFSQORDAFRES-----
>Equus_asinus-----MTIRCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Manis_javanica-----MTIRCFVSGPFSMENOGDR-AMTATGSFEEDAFREA-----
>Loxodonta_africana-----MTIRCSVSGPFSMENOGDR-IMTATGSFEEDVREA-----
>Leucoraja_ocellata-----MII--WRFISELSMEGRGSG--TVVKRYNEDRTFRESSPARL-----
>Psammomys_obesus-----MIFKCFVSKPFSMENOGDR-AMTATGSFEEDTFREA-----
>Oncorhynchus_tshawytscha-----MFLRYIVFERFSMEKGGNG--IIVESNFQORDAFRES-----
>Tupaia_chinensis-----MTIRCSVSGPFSMENOGDR-AMTATGSFKNDFVREA-----
>Lepisosteus_oculatus-----MLFTSLVLGIFSMEOGGTQ--IIVESNFNEDTFRES-----
>Ictalurus_punctatus-----MFLKCPFSLSFSMEKGGNE--IIVDSHFNORDAFREA-----
>Trichechus_manatus_latirostr-----MTIRCSVSGPFSMENOGDR-IMTATGSFEEDVREA-----
>Squalus_acanthias-----MII--RRFISELSME--RUGO--IIVKKSYNEDTFRES-----
>Gekko_japonicus-----MTIRORLSAAFMSKSGSR-AAVALSNFDERDTFRES-----
>Oryzomys_picta-----MILKCLVSKRVSMENOGDR-IIVVALSNFDERDTFRES-----
>Oryzotropus_afer_afer-----MTIRCFVSGPFSMENOGDR-IMTATGSFEEDVREA-----

>Drosophila_melanogaster
-----MWQVQPSROGILRLYKHLIRYGNHLKLTOKNYFLGRVHREFRDNRSLTNPVEVFSFKRGETLLKKGRLL
>Talitrus_saltator
-----MELSDRRFFEKRIIRREFTKQRNS--PEELDTAVQRAEAFLEKGRLL
>Latrodectus_geometricus
-----MTYSRQKVLSLYKELLYKSNLKYTDKSYLLMRLLKNEFLNRNLQNAEIDFQIRQGNFLEKGRLL
>Meimetus_sundmacheri
-----MGIIPKQGVQLYKSLLYRGELRLTDKYFTRVRSFEFQNKSSDQKEIFQYKRGALKVNSKRL
>Blattella_germanica
-----MSNPTAREVRLKYDILKYGRQLQTDKNYFGRIIRNEFKAGKSLKNGEDINHFQRGSEALLKXKRVV
>Gelanus_fimbricus
-----MSQATLLYKSLLYRGRLQMTDKYFYRRVRFEFKNSYLLEKQEVQQLDKRGFLKXKRLV
>Photinus_pyralis
-----MPPKMDILKLYKNLLRYGGELQYTDKNYFRRIRKNEFRNRDITDEADIFQYKRGISLLEKXRVV
>Apocheus_chertseus
-----MASTLPWTRGILSLYKNLMRYGKLFKTNQYFYERVRSFEFNKTIPEQ--KREFYYKGLSLEKXRVV
>Daphnia_pulex
MNTIFIIMNVPKMTQIFELFRSCIRYSGQLKSDKRLVSKRIKSEFNKNTLSNPEEIOKAYENGGSFLSKRLL
>Oocae_jappa_japonicus
-----MAATNSQSPQVQLRYSLVRYGRLKYTRDFYQRIIRNEFRRHRLTQDEDIRFQYKGLAFISRKRII
>Haploembia_palaui
-----MSQPSASEVRLYRELLRFGRQLQTDKNYFRRIRKQFQENKHLKDEQIEFQYKGSLLKXKRVV
>Beetle_sp._Ad-2013
-----MSVASEVRLYSLILKYGQILKLTOKYFYRRIRQEFRRNKSDNPKEIFQYKGLALKXKRVV
>Glomeris_pustulata
-----MTIQSGSVLKYRELLRYGGLOYTDKNYFRRIRKNEFEQNRSLTAPADIQYKRGITFLTNKRLI
>Gallioisena_yuaeai
-----MTIIGSGRIILKLYRLRYGRLQFTDINYNRRIRKTEFLKNSLADDEIQFQYKRGISLXKXRVV
>Tigriopus_californicus
-----MSQRSEALRYKSLLYGGSLRLTDSYLRRRTAEFTPRST--PAQTERALAGARALLSQRRLL
>Ceroopis_vulnerata
-----MNPFTKQIVOLYRLRYGNLKYTDKDYFRRIRKQEFQNRSLTAPADIQYKRGISLXKXRVV
>Argochrysis_armilla
-----MSAIIRLKYELRYGELTKYTDKYFRRIRRTFFNNKNTLNEQIDFQYKGSVFLKXRVV
>Rhhipiocephalus_appendiculatus
-----MSQFQKQVQLRYSLVRYGRLKELSDKNYFYRRIRKEEFARKLTLPKELQFYKRGISLXKXRVV
>Papilio_machaon
-----MSTIRSEILNLYKLMQYSGQLTQDKYFTRVSNFRNKLTQPEDISFAYKRGSEALLKXGSL
>Mantis religiosa
-----MSTPSPQVQLYKSLILRYGELKFTDKYFYRRIRKQEFQNRSLTAPADIQYKRGISLXKXRVV
>Panorpa_vulgaris
-----MSVPMCSHILRYKLLRYGGQLQTLKYFSKIRKNEFNKNTLENKQISFYKRGISLXKXRVV
>Dermanyssus_gallinae
-----MSQYSSAFQVQMSLRYKQLARYGGQLVTDNRERQRLKEFKAPRYVT--AEQMFAYKRGISLXKXRVV
>Omlyus_fulvicoephalus
-----MLIPWQGVNRLYRHLRYGGRLRYTDKYFYRRVRRNEFNKSLTOPADIVFNKRGSEALLKXKTVG
>Triops_newberryi
-----MSQSPQVQLYKSLLYSSLTQYTDKSFYIKRIIRSEFKKKKLTNEEIRKAFKGLSFLSKXRIV
>Calopteryx_sp.undens
-----MDDPSPSQVQLRYSLLYGNLKYTDKDYFIRKIRKQEFESNRNLTIP--KERGFQYKGLVLLXKXRVV
>Hypochthonius_rufulus
-----MSVSRVHLRLYKNLLRYGSLVYTDKSYLQVRKREFRNLQTDSDIRFYKRGITFLTNKRLI
>Prosarthritis_tetretirostris
-----MNPATAREVRLYKLLQYKQLKLTOKYFYRRIRKQEFKNTKLTNGEDVTFQYKRGISLXKXRVV
>Ramulus_artemis
-----MNPAPQVQLRYDLRYGNLQTLTDKYFQVRVREFRNRVLENKNDLLHFHNGESLKTIXRVV
>Menopon_gallinae
-----MNPVITREVLTKYRLLYRGRLKYTDQYYSKIRKQEFQSNQKQGN--EAIHFYKGLQLLKXKRVV
>Perla_marginata
-----MSQPTAKQVQLYRLRYSKHLKFTDKNFFTKRVKFEKTNKSLNEEDIQFYKGLISLXKXSVI
>Polydesmus_angustus
-----MSASVYKQSDILHLYRQLRYGRILTYTDKNYFYRRIRAEFEKQREALE--KTLQFYKQKGLLENKRLI
>Acerentomon_sp._Ad-2013
-----MCKWQWIPYNSDILKLYRLRYGRILQYTDKQFRRKQVQDEFRRNGAITAPNEIFQYKGLSFLSKXRLV
>Liposcelis_bostrychophila
-----MSAFSRTQVRLYKQILRYGEELTYTNKYFNRVKNNEFLSASAKQNKETDNLQYKGVALLMRRRVV
>Xanthostigma_xanthostigma
-----MSVPSSTQVRLRYRLRYGQLQYTDKNYFYRRIRAEFRNRNLEDQKEIKFQYKGSLLKXKSVI
>Trichomycterus_arenolatus
-----MPSRSEILKLYKQLLYGGQLRLTDKSYQERIRKQEFQNKSLASKNDITFNFQKGLLEKGLVM
>Otenocephalides_felis
-----MNTFSAQVRLYKNLLRYGNLQYTDKDYFQRIIRKNEFRNKTCSTRTEQLIFNFVQCI-----
>Stylops_melittae
-----MRLKVLNLYKSLMRYGKSLRLTDNEYFLERIRSEFRNRKSLYNGEIDYHFYKGETLLXKXKLV
>Symphylella_vulgaris
-----MNPTRVQILSLYKTLRYADNLKYSDTYLKQVRVFSQHRSLTAKNDIEFYKRGISFLERKRLV
>Frankliniella_ophelica
-----MSTLNSQVQLYSLIRYGGSLKLTOKYLYKRVKREFRANKLOQPEKIEFNYKGVSLDRKRLI
>Philopotamus_ludificatus
-----MPSKREILKLYKQLRYGGQLQTLTDKYFGQRIIRKQEFQNRSLTAPADIVFNKRGISLXKXRVV
>Zorotypus_candilli
-----MNPQKPGILLYKSLIRYGNLKYTDKDYFERIRKQEFQNRKLENEEDINFAFQYKGVLLXKXRII
>Atelura_Fornicaria
-----MVPSPQVQLYRLMRYGRLKYTDKDYKRVREFRNRKSLNDEKXIFHFYKGLALLSKXRIV

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>Homo_sapiens-----MSLRLNRDYYKLVVWVPLVGLIHLGWYRIKSSPVFQIPK---N-DQIPEQSLGLSNLQ-KSQIQG---K-----
>Neia_calva-----MGLSSVMKNYKVLIVMGTSLGLIHGWYRIKSNPFIKSE---T-NYFPEPGIVSFYSSEP-QHPKPG---K-----
>Micrurus_glaber-----MVFRMGVIESLKTNYVLVWVPAIVVHLGWRLQDNPLVQPMKRE---IPPVGFSYLVKLVEELFTTIDK-----
>Anas_platyrhynchos-----MGLKTFMKNYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-DVPEPAIVAYWQK-DKNQKE---K-----
>Xenopus_laevis-----MGLGLMKNYKVLIVMGTSLGLIHGWYRIKSNPAFGPAK---EDSLEPAISAEKNTM---KKKG---K-----
>Apteryx_australis_mantelli-----MGLKTFMKNYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---EENFVPEPGIVAYWQK-EHKNQKE---KQD-----
>Mastotermes_darwiniensis-----MSGKHGFFNRNAVTVVWIPALVHLGWYRIKQDEVLVKKEEKE---LPVVVGARYLVHLEELQSFRRGSSGSGEK-----
>Acinonyx_jubatus-----MSFQMFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFGMPK---K-DQISEPQSLGLSPQ-KSHIQG---K-----
>Hymobius_retardatus-----MGLKMLMKNYKVLIVMGTSLGLIHGWYRIKSNPLFHPKR---D-EFVPEPSIVTVYLOG-NQDTKA---K-----
>Physeter_catodon-----MSFQMFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFQIPK---K-DQISEPQSLGLTSP-KSHLPG---K-----
>Calidris_pugnax-----MGLKTIIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-DIVPEPGIVAYWQD-DHKSKE---K-----
>Miniopterus_natalensis-----MSFGSFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFGVPS---K-DNVPEPSLALASLQ-KKHLDK---K-----
>Echinarachnius_parna-----MGPNPKXNFFNRNRVLFQSLISLTFIHGWYRIANDPVFNRDVSGGASR---KLESVPAYIKS-KTGASAE---KSS-----
>Laternia_chalumae-----MGLKLSNSNYKVLIVGTSLGLIHGWYRIKSNPVFKMR---E-DYAPEPGIATSIQDQ-KQPKG---KQD-----
>Columba_livia-----MGLKTIIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-KFVPEPGIVAYWQD-DQKNKE---K-----
>Alligator_sinensis-----MGLKTIIMKNYKVLIVMGTSLVLIHGWYRIKSNPFIQVKT---E-DLDQEPGIVTHWQD-DKQNGD---K-----
>Callinectes_sapids-----MTGTGMRAREFLRNVLVWVPLVGVHFGWQKIQDEVFVFKQRIQ---LPVIEGARYLREGVEKLLGLKKEE-----
>Sclerodactyla_briareus-----MTKPSFIRRYKVLIVAGLSLIHLGWYRLSKNPFTGIavgAE---PEIKPSYKQ-KS-GKG---TSA-----
>Monodelphis_domestica-----MSLKTFNRDYYKVLWIPSLGLIHGWRIKSNPFIQTAN---ANEDSIPEPGIVAHMIPQ-KNQNDV---K-----
>Strongylocentrotus_purpuratus-----MNPKNKFFVRNKVLFQSLISLTFIHGWYRIANDPVFNKGEK---KT---VSOLLPSYIKS-KALKAPAE---KSN-----
>Megamycophanes_norvegica-----MHWGRVSEAKRNLWIVWPLFLGLHLGLKLIQDEAFVFKQKME---LPAVTAARLGEIEKRVKQNDQD-----
>Aquila_chrysaetos_canadensis-----MGLKTIIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-DVPEPGIVAYWQD-DHKNKE---K-----
>Marthasterias_glacialis-----MSFFARYKVLTVAAVGLTWVFGYRIKSSPVFNPK---K-VLGIITPEYIKS-KQAQKKA---AVEGVTKSQ-----
>Numida_meleagris-----MMSLKLIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-EIVPEPGIVAYWQK-DKNQKE---K-----
>Meocus_pallidipennis-----MWNKQKQFFKHLWIVFPLPLGLIHYSHLQDNEILWKNKQNE---LPIITIFKRLTQGRES-----
>Oryctolagus_cuniculus-----MNLQMFNRDYYKLVVWVPLVGLIHLGWRIKSSPFIQVPM---K-DNISEPQSLALASLP-KGPPQG---K-----
>Ornithorhynchus_anatinus-----MSLKTIIMKDYKVLIVWVPLVGLIHLGWRIKSNPFIQIPK---K-DTIPEPAIVTHWQD-EASQKG---K-----
>Octopus_bimaculoides-----MLKQLKAFKNYTVLLWIPSVVALHYGWYRIKSNPLVEPEKGEI---RILSKIFPK-T-PKE-----
>C euthophilus_sp_AD-2013-----MLDKGMQGFINRLVSIWVPSLILLHWYRIQDIEVFVKKEEKN---LPVFLGWYI/QE---KFLKWEQDGVHPDE-----
>Scleropages_formosus-----MGLGWVNRDYYKVLIVMSASLGLIHGWYRIKSNPLHSGQREDEYIPEPAIVSYVASG-RQSG-G---K-----
>Lepidothrix_coronata-----MGLKTIIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-DVPEPGIVTVWQD-DQKNKE---K-----
>Ceratotherium_simum_simum-----MSFQMFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFQIPK---K-DVPEPQNLALASSQ-KSHIQE---K-----
>Manis_javanica-----MSFQTFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFQIPK---K-DQSEPSLVLASPD-KKHLDG---K-----
>Glycera_dibranchiata-----MMSVAFLRKNVILVVCIPSLALIHGWYRIKSNPFIQDGRHI---RIA-GIDIDP---EKR-RTTTSQE-----
>Leuctra_sp_AD-2013-----MTGASSKFAFINRLVAVWVPLVGLIHWYRIQDEVFVTKEEKDQ---LPIILGARYLEQKIEEKVATWQDQKAYTKE-----
>Chinchilla_lanigera-----MSFQMFNRDYYKLVVWVPLVGLIHWYRIKSSPVFRVPT---K-DQISEPQSLGLASP-KSQIQG---K-----
>Taupa_chinensis-----MRRVARGAKVPMRGGSGRRFLWGLLSVAAAGGAAGGVHQCCITMSFQMFNRDYYKLVVWVPLVGLIHLGWRIKSSPVFQIPK---K-DQISEPQSLALASSQ-KSQIQG---K-----
>Aptenodytes_forsteri-----MGLKTIIMKDYKVLIVMGTSLGLIHGWYRIKSSPFIQVKT---E-DVPEPGIVAYWQD-DHKNQKE---K-----
>Henricia_sp_AR-2014-----MSFSRYRVLTIGVGLAAIHGWYRIKSNPFIQVKT---E-VVNIITPEYIKS-KRSLGAT---TASSDAKNI-----
>Takydromus_sexlineatus-----MGLKTIIMKNYKVLIVWVPSLGLIHGWYRIKSNPFGPKR---E-DIVPEPGIVTVYLOG-DHKSNG---K-----
>Pelodiscus_sinensis-----MILQYSHGQVC---RTQVDSMSLKTIIMKNYKVLIVMGTSLGLIHGWYRIKSNPFIQVKT---E-DVPEPGIVTVWQD-EQKNKG---K-----
>Zorotypus_caudeilli-----MGQKGLREFVNRNIVTLVWVPLVGLIHWYRIKSNPFIQVKT---FYIFRSFRMKNLNEERYRSIVQNSKD-----
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>Gallus_gallus-----MMSLKTLMQYKYLIVMGISLGLVHGIFHIKSSPLFOVK---TE-EIVPEPGIVTYWGSQHNKKEK-----
>Ania_caeva-----MGLSSVMKNYKYLIVMGTSGLLTHGIRYSIKSNPIFKKS---ET-NYFPEPGIVSFYSEPDHDKGK-----
>Anas_platyrhynchos-----MGLKTFHKSYKYLIVMGTEGLVHGIFHIKSSPIFOVK---TE-DYVPEPAIVAYWGSQHNKKEK-----
>Xenopus_tropicalis-----MGLGNLMKNYKYLIVMGTEGLLTHGIRYNIKSNPIFOPE---REDTLEPEPAITGYAYEKNTAKKAK-----
>Apteryx_australis_mantelli-----MAGRCQFTMGLKTFHKYKYLIVMGPSLGLVHGIFHIKSSPIFOVK---TEENFYPEPGIVAYWGSQHNKKEGQ-----
>Canis_lupus_familiaris-----MSFQMFHKDYKYLIVMVPLVGLLTHGIRHIKSSPVFGMPN---KQNVSEPENPELGGPPKNHLOGK-----
>Hymobius_retardatus-----MGLKNLMKNYKYLIVMGTEGLLTHGIRYHKTNPFLHFK---RD-EFYPEPSIVTYLQGNQKQTKAK-----
>Orcinus_orca-----MSFQKFNRODYKYLIVMVPLVGLLTHGIRHIKSSPVFGQPN---KQDLPEPGIVAVTSPKXNLPGK-----
>Calidris_pugnax-----MGLKTIIMQDYKYLIVMGTSGLVHGIFHYKSSPIFOVK---TE-DIVPEPGIVAYWGSQHNKKEK-----
>Mniotiltus_natalensis-----MSFQSFNRDYKYLIVMVPLVGLLTHGIRHIKSSPVFGVPS---KQNVPEPSLALASLQDNHLOGK-----
>Echinarachnius_pama-----MQPNPKXNFVRNRYLVGLISLTLHYGIRFIANDPVFNDAVSGQ---ASRKLESVPAYIKSKTGSASAEEKSS-----
>Latimeria_chalumnae-----MGLKTSNSYKYLIVMGTEGLLTHGIRYSIKSNPVFHKN---RE-DYAPEPGIATSIWQDQKPKGQKQ-----
>Columba_livia-----MGLKTIIMQDYKYLIVMGTEGLLTHGIRFYKSSPIFOVK---TE-KFYPEPGIVAYWGSQHNKKEK-----
>Alligator_mississippiensis-----MGLKTIIMKNYKYLIVMGPSVLTHGIRYNIKSNPIFKMK---RE-DLDGEPGIVTHWGSQHNKKGK-----
>Sclerodactyla_briareus-----MTKPSFIRRYRYLVIVAFAGLSLHLGIRYLSKNPDFGTAY---GAEPENKPSYLSKQSKGKTSK-----
>Monodelphis_domestica-----MSLKTFRNDYKYLIVMPSLGLTHGIRYSIKSNPIFOANA---NEGSIPEPGIVAHMIPQKNGQVK-----
>Strongyloentrotus_purpuratu-----MNPCKXNFVRNRYLVGLISLTLHYGIRFIANDPVFNKGEK---KTVSDLLPSYIKSKALKAPAEKSN-----
>Aquila_chrysaetos_canadensis-----MGLKTIIMQDYKYLIVMGTSGLVHGIRFYIKSSPIFOVK---TE-DYVPEPGIVAYWGSQHNKKEK-----
>Marthasteria_glacialis-----MSFARYRYLVIVAAVGLTMVHFGRYYIASDPVFNPK---KVLGITPEYFKSGQAGQKAAVEGVTKSQ-----
>Oryctolagus_cuniculus-----MNLQKFNRODYKYLIVMVPLVGLLTHGIRHIKSSPIFOVPN---KQNIPEPSLALASLPGKPGQK-----
>Ornithorhynchus_anatinus-----MSLKTIIMRODYKYLIVMPSLGLTHGIRYSIKSNPIFOQPN---KDTIPEPAIVTHWGSQHNKKGK-----
>Octopus_bimaculoides-----MLKQLKAFKNTYLLVMIPSVVALHYGIRYNGFNPLVEPEK---QEIRILGKIF-KXTPKK-----
>Laupala_kohalensis-----MISGKIRKFNRLNLMVIMIPSLIFVHGIRLQGGKQIFWKEE---RKLPLIIGMAKIVMKLMP-AEKEDSTPTQPE-----
>Scleropages_formosus-----MGLGNVNRDYRYLVIVSASLGLTHHGIRFQKGPALHGKQDDEYIPEPAIVSYVYASGROSSGK-----
>Manacus_vitellinus-----MGLKTIIMQDYKYLIVMGTEGLLTHGIRFYIKSSPLFOVK---TE-DYVPEPGIVTYWGSQHNKKEK-----
>Ceratotherium_simum_simum-----MSFQMFNRDYKYLIVMVPLVGLLTHGIRHIKSSPVFGQPN---KQNVPEPDLALASSQKSHLOGK-----
>Manis_javanica-----MSFQTFNRDYKYLIVMVPLVGLLTHGIRHIKSSPVFGQPN---KQDSEPSLVLASPKQKHLOGK-----
>Glycera_dibranchiata-----MMSVAAFLKNNILVVICPSLALIHYGIRYNGKQNFIPDQ---RNIIRIAGIDIDPEKRRITTSQE-----
>Nomasus_leucogenys-----MSLNLIMQDYKYLIVMVPLVGLLTHGIRYIKSSPVFGQPR---NDIPEQDGLSLNLQKSOLOGK-----
>Fukomya_darlingi-----MSLQKFNRODYKYLIVMVPLVGLLTHGIRHIKSSPIFOPT---KQNIPEPSLALASSPKRQLOGK-----
>Tupaia_chinensis
MRRVARGAKVPMRRGSSRRFLWGLLSVAAAGGAAAGGVHQCCITMSFQNFNRDYKYLIVMVPLVGLLTHGIRHIKSSPVFGQIPS---KQDISEPSLALASSQKSOLOGK-----
>Sepia_pharaonis-----MASRLTAFLEKTYKLLMLPAAVAGIHYVYKMGKSPVMEGEK---TKI---FGKDLVSDSPK-----
>Aptenodytes_forsteri-----MGLKTIIMQDYKYLIVMGTSGLVHGIRFYIKSSPIFOVK---TE-DYVPEPGIVAYWGSQHNKKEK-----
>Henricia_sp._AR-2014-----MSFSRYRYLVITGVVGLAAIHAGIFYIAHNPFGKEK---EVNITPEYFKSKRSKLGAATASSDAANI-----
>Takydromus_sexlineatus-----MGLKTIIMKNYKYLIVMVPSLGLTHGIRYNIKSNPWFQPK---RE-DIVPVPGIVTYALQGNKSKGK-----
>Pelodiscus_sinensis-----MSLKTIIMKNYKYLIVMGTSGLLTHGIRYIKSNSIFQTK---RE-DYVPEPGIVTYWGHESQNKKGK-----

HS0010.2 ENSG00000125863 MKKS

>Homo_sapiens-----MKNTSIRKXNILLVAGISF1GVHLGTYFLORSAGQSVFGSGSKOKSIEE-----
>Meia_calva-----MKRSIRLXKNILLIAGLSF1GHLGTYVWKTWKSVRSDLO--LKRQDASE-----
>Anser_cygnoides-----MKKASIRKXNILLVAGLSF1GVHFGTMLVNFVAKKSVRSHSEKKQDRSE-----
>Xenopus_tropicalis-----M1KKGTWLRKNILLVAGISF1GHLGTYFF1QKLAKGSAKSNLQKESKQSE-----
>Apteryx_australis_mantelli-----MKTSIRKXNILLVAGLSL1GVHFGSMLVNLVAKKSVQSHSE1KKQDRRE-----
>Ursus_maritimus-----MLKEEMKNTSIRLXKNILLVAGVSF1GVHLGTYFF1QRAAKGSVKSGSGSKQKQNIIE-----
>Aebystoma_mexicanum-----MKSKSIRLXKNILLVAGISFVLHG1GTY11QVAKTSARSGSELKQKQDYDE-----
>Physeter_catodon-----MKNSNIRLXKNILLVAGISF1GHLGTYFF1QRAAKGSVKSGPEKOKSLNDELK-----
>Calidris_pugnax-----MKTSIRKXNILLVAGLSV1AHFGSMLVNFVAKKSARSHSEAKKQDRRE-----
>Miniopterus_natalensis-----MKNTSIRLXKNILLVAGVSF1GVHLGTYFF1QRAAKGSVKSGSGKQK--SIRE-----
>Dasypus_noveboracensis-----MKISIRLXKNILLVAGLSF1GHLGTY11QRTAKGSVKSGGVPKHIEE-----
>Latimeria_chalumnae-----MKNSINIRKXNILLVAGLSF1GHLGTY1MOKSVKSTKSTENTYLKAND1-----
>Columba_livia-----MKTTWNRKNILLVAGLSV1GVHFGSMLVNFVAKKSARSHSEAKKQDRRE-----
>Alligator_mississippiensis-----MKTSIRLXKNILLVAGLSF1GVH1GTYL1QRAAKGSVKSTVE1KHNLDE-----
>Sarcophilus_harrisii-----MKQTSIRRRKNILLVAGLTF1GVHFGTYFLQ1AAKHSKQSL1EYKQK1KE1K-----
>Galeopterus_variegatus-----MKNTSIRLXKNILLVAGVSF1GVHLGTYFF1QRTAKGSVKSGSNK-----
>Monodelphis_domestica-----MKQTSIRLXKNILLVAGLTF1GVHLGTYFF1QVAAKHSKSGSGSKKX1KEMK-----
>Aquila_chrysaetos_canadensis-----MKKASIRKXNILLVAGLSL1GVHFGSMLVNFVAKKSVRSHSEAKKQDRHE-----
>Asterias_rubens-----MKLPWVAVKXNILLVAGLSL1H1LT1Y1VKTALATKSTKRLR--GMDQETERK-----
>Meleagris_gallinapavo-----MKKASIRKXNILLVAGLSL1GVHLGTYL1VNFVAKKSARSHSEAKKQDRRE-----
>Condylura_cristata-----MKNTSIRLXKNILLVAGVSF1GVHLGTYFLQNSAGSVKSG1QKQKQIEE-----
>Dryctolagus_cuniculus-----MKNTSIRLXKNILLVAGVSF1GVHLGTYFF1QRAAKGSVKSGSGSKOKSIEE-----
>Ornithorhynchus_anatinus-----MKKSTIRRRKNILLVAGLSF1GVHLGTY11Q1TAOKNSAKSVLETOKK1QDE-----
>Sclerophagus_ferrousus-----MTMKNSIRLXKNILLVAAAASFLGIHVGTLMKAKNSAKHSQTRTKQKS--VDE-----
>Ficedula_albicollis-----MKTTWNRKNILLVAGLSL1GVHLGSMVNVVYAKKSAGSGSKRSS-----
>Ceratotherium_simum_simum-----MKNLSIRLXKNILLVAGVSF1GVHLGTYFF1QRTAKGSVKYSGGNVLLNNEVK-----
>Manis_javanica-----MKNTSIRLXKNILLIAGVSF1GVHLGTYFF1QRAAKGSVKSGSGSKQKQNIIEE-----
>Melopsittacus_undulatus-----MKKAMNIRKXNILLVVLGVSV1GVHFGSMLVNFVAKKSARSHSEAKKQDRHE-----
>Marmota_marmota_marmota-----MKSTSIRLXKNILLVAGVSF1GVHLGTYFF1QRAAKGS1KSGSVKOKSIEE-----
>Tapalia_chinensis-----MKRVAKSVKPNQSGSGRFG1MGLLSVAAAGGAAGGXKATLNL1L1LKEDMNTSIRLXKNILLVAGVSF1GVHLGTY11QRTAKHSVKSGSKQKQNIIEE-----
>Lepisosteus_oculatus-----MNSRSMLQKNILLVAGLSF1GHLGTYLLQKTVKSTSRDLA--LKKQDKVK-----
>Pygoscelis_adeliae-----MKKASIRKXNILLVAGLSL1GVHFGSMLVNFVAKKSVRSHSEAKKQDRHE-----
>Echinaster_spinosus-----MKLPWVAVKXNILL1G1ALATLH1LT1Y1QKMAHSTSKSRSLTPPPQHSRE-----
>Takydromus_sexlineatus-----MKKLSIRLXKNILLVAGLSF1GVHLGTYFF1QRAAKSSAKSGLNKS1KGLDE-----
>Struthio_camelus_australis-----MLQKEEMKTSIRKXNILLVAGLSL1GVH1GSTL1VNLVAKKSVHSHSE1KKQDRRE-----
>Pelodiscus_sinensis-----MKKT SIRLXKNILLVAGSF1GVHLGTYFF1QRAAKNSAKSALEWQKQNIIEE-----
>Patiria_minitata-----MKLPWVAVKXNILLVAGL1ALT1H1LT1Y1VKTALSTSKTRRSLTPSPPADKED-----

HS0010.2 ENSGAL00000009013 MKKS

>Gallus_gallus
-----MKKASMSKKNFLLVAGLSLIGVHFGTMLVNFVAKKSARGHSEIK--RDMHRE---
>Anas_cailva
-----MKNSKMLKKNMLLIAGLSFLGIHLGTYYMKTMMKNSKVSRSQDLQ--LKSKDASE---
>Anser_cygnoides
-----MKKASMSKKNLFLVAGLSF IGVHFGTMLVNFVAKKSVRSHSEIK--KDRSE---
>Xenopus_tropicalis
-----MIKKQTMLKKNMLMVAGLSF LIGHFGTYFIDKLAKGSAKSNLQK--ESKNE---
>Apteryx_australis_mantelli
-----MKTSMSKKNFLLVAGLSLIGVHFGSMLVNLVAKKSVDGHSIEK--KDRRE---
>Mastella_putorius_furo
-----MKNSMLKKNMLLVAGVSF IGVLHGTYYIDRAAKGSVKSGSGK--QESIKE---
>Aebystoma_mexicanum
-----MKSKSMLKKNMLLVAGLSFVQLHIGTYIIDKAKTSARGSGSELK--QKQDYDE---
>Belienoptera_austrostrata_s
-----MKNSMLKKNMLLVAGLSF LIGHLGTYYIDRAAKGSVKSGSGK--QKSLNMLK
>Calidris_pugnax
-----MKTSMSKKNFLLLAGLSVIAVHFGSMLVNFVAKKSARGHSEAK--KEDRRE---
>Eptesicus_fuscus
-----MKTTSLKKNMLLVAGVSF IGVLHGTYYIDRAAKGSVKSGSGK--QKSIKE---
>Dasypus_noveboracensis
-----MKLSMLKKNMLLVAGLSF LIGVLHGTYYIDRTAKGSVKSGSGK--PKHIEE---
>Latimeria_chalumnae
-----MKNSMSKKNMLLVAGLSFLGIHLGTYYIMKSKVSKSTKSTENTVLKADII---
>Columba_livia
-----MKKTTMKNKMLLVAGLSVIGVHFGSMLVNFVAKKSARGHSEAK--KDMHRE---
>Alligator_misissippiensis
-----MKKTSMLKKNMLLVAGLSFLGIHLGTYYIDRAAKGSVKSTVEIK--HMLDE---
>Sarcophilus_harrisii
-----MKGTSMLKKNMLLVAGLSF IGVHFGSTYFLIDAAKHSAGSDIEYR--QKNIKEIK--
-----MKNTSLKKNMLLVAGVSF IGVLHGTYYIDRTAKGSVKSGSGK-----
>Monodelphis_domestica
-----MKGTSMLKKNMLLVAGLSF IGVLHGTYYIDAAKHSAGSGSGK--QKNIKEIK--
>Aquila_chrysaetos_canadensis
-----MKKASMSKKNFLLVAGLSLIGVHFGSMLVNFVAKKSVRSHSEAK--KEDRHE---
>Condylura_cristata
-----MKNTSLKKNMLLVAGVSF IGVLHGTYYLQWSAKGSVKSGSIOK--QKNIEE---
>Oryzotylagus_cuniculus
-----MKNTSLKKNMLLVAGVSF IGVLHGTYYIDRAAKGSVKSGSGK--KSTEE---
>Ornithorhynchus_anatinus
-----MKKSSMLKKNMLLVAGLSF IGVLHGTYYIDTANKSAKSVLETK--KKSIOE---
>Sceloporus_formosus
-----MTMNSMLKKNMLLVAGLSFLGIHVGTMKMKAKSSAHSOTRTKQKS--VDE---
>Corvus_brachyrhynchus
-----MKKTTMSKKNFLLVAGLSLIGVHFGSMLVNFVAKKSAGHSEAK--RDRHE---
>Equus_asinus
-----MKNTSLKKNMLLVAGVSFLGVHLGTYYIDRAAKGSVKSGSGH--KVLNDEVK
>Manis_javanica
-----MKNTSLKKNMLLVAGVSF IGVLHGTYYMDRAAKGSVKSGSRNK--QENIEE---
>Microcebus_murinus
-----MKNTSLKKNMLLVAGLSLIGVLHGTYYIDRAAKGSVKSGSAK--QKSIEE---
>Melopittacus_undulatus
-----MKKAMNKKNFLLVGLSVIGVHFGSMLVNFVAKKSAGHSEAK--KDRHE---
>Dipodomys_ordii
-----MKKPSMLKKNMLLVAGVSF IGVLHGTYYMQRIDAGSVRSQSAK--QNNVEE---
>Tupaia_chinensis
-----MKNTSLKKNMLLVAGVSF IGVLHGTYYIDRTAKHSVKSGSGK--QKNIEE---
>Leposteus_oculetus
-----MKNSMLKKNMLLVAGLSFLGIHLGTYYLQKTVKSSSTRDLA--LKQDKK---
>Pygocellia_adellae
-----MKKASMSKKNFLLVAGLSLIGVHFGSMLVNFVAKKSVRSHSEAK--KEDHIE---
>Anolis_carolinensis
-----MKLSMLKKNMLLVAGLTFVGVHLGTYYIDRAAKSAGSDIDK--SKLDE---
>Struthio_camelus_australis
-----MLQKEEMKTSMSKKNFLLVAGLSLIGVHIGSTLVNLVAKKSVMHSEIK--KDRRE---
>Trachomys_scripta
-----MKKTSMLKKNMLLVAGLSFLGVHLGTYYIDRAAKSAGSALEIK--QKDLGE---

>Homo_sapiens
-----MLISFINIELFDFIATMLHHTLIPKE-----
>Canis_lupus_familiaris
-----MSLSHYMLISFINIELFSFIATLLHVDFHS-----
>Miniopterus_natalensis
-----MSLNHYMLISFINMKLFNFITTLRLIQTVPEEYFKMLNRKLWLT-----
>>Ossypus_hovemoictus
-----MNNKLFNFITPMLHVOTFILRVFLNVRTHONYIYAKGV-----
>Galeopterus_variegatus
-----MSLNHFVLFNFINIELFNFIDTMLHA-----
>Condylura_cristata
-----MSLNLYLLTTFINMELFNFATYLDGCS-----
>>Oryctolagus_cuniculus
MNNHGVIKSLSVSISFIIIEPPHFLASVLHIQTFPKE-----
>Equus_caballus
-----MSLNHYMLISFINIELFNFATMLHIQTFPEE-----
>Manis_javanica
-----MEPPNFIAIVPHIPFIIP-----
>Fukomys_damarensis
-----MLLSHYVLSFIDTESYNFIAATLNIPEEYFKYKTHGK-----
>Tupaia_chinensis
-----MSLNHYLLISFINIELFNFIAMLHVALSVLQNNFKC-----

>Drosophila_melanogaster-----MVRERMRKANGGDYDSSAASRRFDY-----
----->Euphrynichus_bacillifer-----MVKSLVKNTINAMVIATIGISFSLAKSSVDNRYEAMKVRERMRKANVGEYEPSYRNFYS-----
----->Stegodyphus_tentoriicola-----MALSKLTKNINIGATLAIIGLISFFVVKLVITQRYEAMKARMAKSNVGEYEVKRF-----
----->Machilia_habea-----MLQLDKIGIGMTILVVGVSFGFTYSKTSDKKRYDNMVRERMRKSNGLYEATERFVGGETNKSQ-----
----->Prorhinotermes_simplex-----MPLGNVTKIAYGMVAVITAAGLYSFVLSKGSVDKRYEAMKVRERIRSNSEGEYDGPKNFTG-----
----->Hymobius_chinensis-----MLQLDKIGIGMTILVVGVSFGFTYSKTSDKKRYDNMVRERMRKSNGLYEATERFVGGETNKSQ-----
----->Dascillus_cervinus-----MLLNKTKAKIGIGWGFVVSAGIYGFYLSKENITKKRYEAMKVRERMRKANFGEYEPSRKNFD-----
----->Scylla_parmamosia-----MLTSKNARIAYGMSAVIVIGVGGFVFTKQTEQORRESMKVRERMRNANTGDYEPSRKNFTG-----
----->Forficula_auricularia-----MLILGTHAKVALGSLIVATGITYSFVLAKKSEKNRYEAMKVRERMRNNSNIGETYSTEKNKF-----
----->Aposthia_japonica-----NSIKSLGHWKIAIGMTILVVGSLYAVIWARDISIKSRYEAMKSRERMRKSNIGDYEVQDKY-----
----->Isomyia_bicolor-----MPLTKYTKVIGIMAIITFAGISGFLSKKSEKRYEAMKVRERMRKSNVGEYAGSERKF-----
----->Meganyctiphanes_norvegica-----MFSTKATLVIGIMAAISGSGGFTLTKISVEDORDAMKVRERMRNANTGEYAKRTFTG-----
----->Grylloblatta_bifratrilecta-----MWNVSLMPLGNNAKIGIGMTIIVSGLYSFVLSKRSIDKRYEAMKVRERMRKSNAGDYETARTFTG-----
----->Mecurus_pellucidipennis-----MFNVTIKIGIGMSLIVAGIYSFVLSKRSIERKRYEAMKVRERMRKSNVITASERKNFTG-----
----->Cephus_cinctus-----MLNNHCKIAIGMLVVISGLYGFVLSKQRYEAMKVRERMRKANAGPOGLSTRVUSST-----
----->Ixodes_persulcatus-----MNVSTVMSITLIMAILVTYVAGISGFVYAKLVQKRYEAMKVRERMRKSNIGDYEPSRKNFT-----
----->Biston_suppressaria-----MPLGKFKITLSMLAVTISLSLFFVAKHINQRLKNMVRERMRKSNAGDYEDVYNL-----
----->Lithobius_forficatus-----MLIGRMKSNSEYEGSPRHS-----
----->Mantis religiosa-----MVRERMRKANVGEYETTRKFSG-----
----->Tanzaniophana_sp._AD-2013-----MKPSISMKVYIGMTVTIVGLYGFVLSKSSVDNRYEAMKVRERMRKANESGYETERKNFTG-----
----->Nannochorista_philipotti-----MLQLTKATKIGIGNSVITVSSLFGFVKSKEIDKRYEAMKVRERMRKSNAGDYDKSTGRYI-----
----->Corydalinae_sp._KMSFPM-2012-----MVRERMRKSNFGEYESSRKNFNG-----
----->Metaseiulus_occidentalis-----MLNKSPFKIGIGVIGIAVVGGLGAFVARDKIIAORYEAMKSRERMRKANAGSYGNRVFRKDGITTEKIQNFK-----
----->Xibalbanus_tulumensis-----MALSNVAYVIGMTIVISAGVGFVLAKISIDKRFASMKARERIRKANEGDVPVRYKTYT-----
----->Conwentzia_psociformis-----MLGKVAKIGIGMTIITIASLIFYFLSKGSIDKRYEAMKVRERMRNANI GDYKSSSRNF-----
----->Triops_newberryi-----MNVTVYNGIMAILISVIGISGFVAKNLVDTRLHMRSERMRKANVGEYEPSRKNFYD-----
----->Epiplatia_superstes-----MVLNNAKIAIGMTIVITVIGISFVLSKGSIEQRLKNMVRERMRKANAGDYEPSYRKNFNG-----
----->Prosarthria_teretirostris-----MPLNNAKIGIGSNFIVAKSLTFVLKRYVDNRYEAMKVRERMRKANISGDYEPSRKNFTG-----
----->Phyllium_philippinicum-----MVRQRIRDMKGVYESSRKNFD-----
----->Cosmioperla_kuna-----NSIMPLKRYAKIGIGNSFITAAGLYGFVLSKRSVDKRYDSMKVRERMRNNSYQKYDTSARKFTG-----
----->Ectoposocus_briggsi-----MPLKLRDAKVAIGMAVVVVGGLYSFVLSKGSIDKRYDNMKIRERMRNANVGEYEPSRFSH-----
----->Raphidia_ariadne-----MVLGNSKTLIGIGNSVITFAGIFYFLSKRSIEKRYEAMKIRERMRKSNVGDYQITGRYSKSS-----
----->Titius_serrulatus-----MPLNLTAKIGIGWVLSIAGIGGFVAKNSVNMRYESMKVRERMRKANAGPXPSPRFSR-----
----->Trichomycterus_areolatus-----MLSNVGVGVIGMTIFVILGISGFAASKNSVDKRYDSMKVRERMRKANEGYQIPETRFEA-----
----->Geratophyllus_gallinae-----MVAIGKFAKIGLSMAALTFASISAFVLSKQHIDAGRYENMKIRERIRNSNTGEYKSYRIFD-----
----->Hydroptila_sp._AD-2013-----MLSNFAKITISMAFLGVAGISGFLSKNSVHRREDMVIKVRERMRNNSYGEYASSRNF-----
----->Tricholepidion_gertschi-----MPYSKVAKIGIGMAIATAGVSFGIFOKHIEKORHESMKVRERMRKSNKGEYEPSYRNFTE-----

>Drosophila_melanogaster
 MATAAAAVKYSVIRIFVGNLPWTVGHRELGRYFREFGRVISA--NVIFDKRTGSKGYGVSFNSLTALEXIENEQKHILEGNVNIQKS-----
 >Boeckmannila_carpentarii
 -----MSMSFSKIFTGNLPSVSGNRELGRYFSQFGRVLSA--DVHFDKXLGKSKYGFVTFKDRQSAEASLKHQNHILEGNLTIVQRTENF-----
 >Machilia_hrabei
 -----MAARNLQKIFVGNLPWTVGHRELGRYFSEFGHVITA--NVVFDNNTGMSRGYGFVQFGRDGYNSASNKQGHILEGNVNIQPASN-----
 >Blaberus_atropos
 -----MATKIRKIFVGNLPWTVGHRELGRYFSEFGHVISA--NVIFDNTGMSRGYGFVVFSTPGGFENASNKQGHILEGSKLTTHPASN-----
 >Gyrinus_marinus
 -----NAVTSRLYRLFVGNLPWTVGHRELGRYFSEFGHVITA--SVVFDNTGLSRNYGFVTFNSQNGFDSATNVQTHLEGNLTIVQVPAAS-----
 >Macrorhabdium_roseipetii
 -----MAARSILKLFVGNLPWTVGHRELGRYFSQFGRVITA--NVVFDKSGMSKGYGFVQFGRNRYEAALNKSPQFLEGNLTIVQPLHP-----
 >Forficula_auricularia
 -----MANLRKQKIFVGNLPWTVGHRELGRYFSEFGPVHVS--KVIFNNITGLSKGYGFVEFDSKESIPKVLG-QKHILEGNLTISTEININGN-----
 >Camposoa_augens
 -----MASSKLKLFVGNLPWTVGHRELGRYFSEFGHVITS--NVVFDNNGLSKGYGFVTFSSQGFENALNKQTHLEGNVNIQPASTT-----
 >Aposthia_japonica
 -----MASRAIRKLFVGNLPWTVGHRELGRYFSEFGHVISA--YVVFDRNTGLTRYGFVFGSPSEYTNADVQNHILEGNLVQNSAN-----
 >Eurylophella_sp._AD-2013
 -----MAARSILKLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVQFGRNRYEAALNKSPQFLEGNLTIVQSSAN-----
 >Meganyctiphanes_norvegica
 -----MAARNLQKIFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVQFGRNRYEAALNKSPQFLEGNVNIQDANSK-----
 >Gallioisiana_yuasei
 -----MASRAIRKLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVTFSTGSGYSAASKQGHILEGNLTIVQVASN-----
 >Xenophysella_greeniadeae
 -----MASAARSAGKLFVGNLPWTVGHRELGRYFSEFGHVISA--VVFDRDGLSRGYGFVTFGTSGADSVARQKHVLEGNLTITQPAST-----
 >Tenthrredo_koehlerii
 -----MSKNGIIGKLVGNLPWTVGHRELGRYFSEFGHISRA--VVFQKNSGMSKGYGFVTFSTGKSINTVQKSHVHLEGNLTIGSDVDSQDTE-----
 >Metaphatus_ochraceus
 -----MASSGRALNRLFVGNLPWTVGHRELGRYFSEFGPVISA--NVVFDKSTGLSKGYGFVTFATKSAADATNKQVTHVEGNLTIVQPIN-----
 >Mantis religiosa
 -----MAARLIRKLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVTFGTSGYSAASKQGHILEGNLTIVQVASN-----
 >Tanzaniophasma_sp._AD-2013
 -----MAANATGRAIRKLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVTFSTGGLDSATIKQNHILEGNLTIVQVAA-----
 >Boreus_hymalia
 -----MASSVIRKLFVGNLPWTVGHRELGRYFSEFGPVISA--NVVYKSSGVSRGYGFVFGSGRSGFENATNKQTHALEGNLTIVQPASN-----
 >Corydalus_cornutus
 -----MATLPRGSINTYKRLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDNNTGMSRGYGFVTFGTSGYSAASKQGHILEGNLTIVQVASN-----
 >Chrysopa_pallens
 -----MSIRKATATAMLRVFNLPWTVGHRELGRYFSEFGVLSQV--NVVFDKNGFSGYGFVFQKESQJLLTETPHNLEGNLTIVQATF-----
 >Triops_newberryi
 -----MASRSAGRLFVGNLPWTVGHRELGRYFSEFGVADA--NVVFDNNTGMSRGYGFVTFGTSGYSAASKQGHILEGNLTIVQVASN-----
 >Cordulegaster_boltonii
 -----MASRLYKRLFVGNLPWTVGHRELGRYFSEFGHVISA--NVVFNRETGILSRGYGFVFGKSGIAAMDRGNHLEGNLTIVQASN-----
 >Stenobothrus_lineatus
 -----MAARAANKLFVGNLPWTVGHRELGRYFSEFGPVISA--VVVFDNNTGLSRGYGFVLLGNKSGFVKYTNKQTHVLEGNLTIVQAAH-----
 >Rhamulus_artemia
 -----MASKYNKLFVGNLPWTVGSRKLYFSEFGHVISA--NVVFDNNTGILSRGYGFVIFSAQRGLSVLEKQGHILEGNLTIVQAAH-----
 >Menopon_gallinae
 -----MSLLNAPIRKLFVGNLPWTVGDKLTSYFVRFGGVKS--QVEVDKTFGSKGYGVFFSRFL--SGDINSQPHILLENEVLEVPVNL-----
 >Leuctra_sp._AD-2013
 -----MAARNLIRKLFVGNLPWTVGHRELGRYFSEFGVISA--RVVFDNNTGMSKGYGFVFNKSGALDNLGRQNHVLEGNLTIVQSTD-----
 >Acerentomon_sp._AD-2013
 -----MSKITTTFVAVLSNYSRLEGRFSEFGVLA--DVVFDKTFGSKRYGFVRFADRSIAERALQTNVTFIDGLAVKVPSSGGSSA-----
 >Liposcelis_bostrychophila
 -----MASRVSRPLVGNLPWTVGSRKLYFSEFGHVISA--DVVFDNNTGILSRGYGFVIFSAQRGLSVLEKQGHILEGNLTIVQAAH-----
 >Xanthostigma_xanthostigma
 -----MARFPRALNRLFVGNLPWTVGKELRYFSEFGVNSY--NVVFDKDTGFSKNGFYVYSKQGFENALNKPHLEGSTLIVFPVSNPWN-----
 >Trichomycterus_areolatus
 -----MASTVIRKLFVGNLPWTVGSRKLYFSEFGVISA--KVVFDRSSGLSRGYGFVTFASRTGYDTANQPHVLEGNLTIVQAAH-----
 >Ceratophyllus_lineatus
 -----MASTARLNLVGNLPWTVGHRELGRYFSEFGHVISA--NVVFDKSTGILSRGYGFVFSKSGLEKALNQZHVLEGNLTIVQVSN-----
 >Gynaikothrips_ficorum
 -----MESTYLKLVGNLPWTVGAKLSAYCSSFQPVHVS--RVVFDYSTGFGYGFVHVFANADSKSRLE-KKHTLEGNLTIVQSRSKIE-----
 >Rhyacophila_fasciata
 -----MASQVGRSVKLFVGNLPWTVGHRELGRYFSEFGHVISA--KVVFDRSTGVSRGYGFVEFSSKATAYENAINQMSHLEGNLTIVQVSN-----
 >Zorotypus_caudei
 -----MAARVNFVGNLPWTVGKELRYFSEFGVISA--NVVFDNNTGFSKGYGFVTFSGNSEAIAKQKQFVLEGNLTIVQVPAE-----
 >Atelura_fornicaria
 -----MAARAVNKLAVNLPWTVGHRELGRYFSEFGHVISA--NVVFDKNTGMSRGYGFVTFATQDANSATDKRNHILEGNLTIVQVAAH-----

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>Drosophila_melanogaster-----MSASEDQPKIKYGE--SAPKLDKAQLDFMKLIEEQNLDRVQKLRIRRNLLTAGALGVSVLAITYGYSIFSVOGEKFLDOFEEPKVYSS-----
>Artemia_franciscana-----MAGNDQMPKVDLAK--DRPKFSQAQLDMRLVEKLNALRYTELGRKRNWYITAGVATQVLGIYGYSIMFVAVGEKFLDOFDEPAKXISASS-----
>Meinertellus_cundinamarcensis-----MQVDLEK--DKAKLSRAQLDMRLVEKQMAERVQKLRIRRNWITGSLLGVDVLGIYFYSIFVAVGEKFLDOFDEPAKXISASS-----
>Argulus_siamensis-----MANQVMPKLNLO--DQQLKQIQLEYIKKIERENLIRVNRKKLKQWVYAGQLLGFVLGVYTYTLVSVKGEKFLDQLEEPSHV-----
>Mastotermes_darwiniensis-----MGNDQMPKVDLVK--DRANISRTTLDYMKIVERENLRVQALGRKQWRTGLMLGAGVLGIYTYTIVSVKGEKFLDOFDEPATTSN-----
>Wymobilus_chinensis-----MYAVGEKFLDOFEEPAKEELTQKL-----
>Dastarcus_helophoroides-----MNSQPKAP-----KL--DYSKLKEAELKFVLVEQMFERVQKLRKIRRNLLTAGAVGAVLGIYGYTLFAVHGESFLDOFDEPAKTVQ-----
>Forficula_auricularia-----MSQMPKVDFVK--DKELKNTAVDYIKHLEKLDIRAKKTYIRIRRNWITGQLLGLGITSIFKFTIIGVKGKFLDOFDEPAKISS-----
>Camptodea_augens-----MESAEMPKLDLQK--DKPLHQAGLYWQWIEKNILERVQKLRKIRRNLLTAGILGIAVVSIFSVMIAVGEKFLDEVFDETEAKTLKQ-----
>Haploembia_palai-----MADSEQMPKVDFAK--DKAELKHTADYVKLINWVNEERALKFGRIRKSNWITGVLGVAALGIYSYTIYAVKGEKFLDOFEEPERINIAN-----
>Eurylophella_sp._AD-2013-----MFKVDFVK--DKANLKPASLDYIRLIEQNMREVLKLRKIRRNLLTAGILGVSVFGIYFYSIMFVAVGEKFLDOFDEPERSSNPW-----
>Grylloblatta_bifratrilecta-----MGSQMPKVDFVK--DKDKLKFATVYKVEILEKXNLERVQKLRIRRNWITGILLGGVFGIYLSIMFVAVGEKFLDOFNEPKTED-----
>Anoploemmis_curvipes-----MGADQMPKLNLAK-----DKVDKNVLDYIRLIEQNMRSVEXLRIRRNLLTAFGLGIVLSIYGYSIFAVRGEKFLDOFDEPAIKE-----
>Neodiprion_sertifer-----MADQMPKHGEK--NFKRLTVEGEVWRLIEERNLERYTLKRNQFNWRYTLALGALVLSIYGYSIMFVAVRGEKFLDOFEEPKITTE-----
>Acanthopoctetes_unifascia-----MGNDVMPKLNLDK--EKPEKLKFELEYMKVINQNLERVQKLRIRRNWITGSLLGVDVLGIYFYSIMFVAVGEKFLDOFNEPEKIRRN-----
>Empusa_pennata-----MKDQMPKVDLVK--DKANISRVVVDYMKMEKENLERYVSLKRLRKIRRNLLTGLLGGAVFGVYTYTLVSVKGEKFLDOFEPPELVEKN-----
>Tanzaniophasma_sp._AD-2013-----MFVAVGEKFLDOFEEPAKIVE-----
>Boreus_hymalis-----MSGDVMPKLNLS--KSQKLOPTELDYMKIEKQNLARVQKLRIRRNLLTAGILATGVFGIYGYSIFAVGEKFLDOFKEPEKLTNN-----
>Corydalus_cornutus-----MNNQMPKVNLKS-----SNITGSDIDFMYIEKQNIERVQKLRKIRRNLLTAGLLGGVFGIYLSIMIAVGEKFLDOFNEPAKYVE-----
>Conwentzia_psociformis-----MLD--EEKKLTPTQLRFWQIEEQNLDRVQKLRIRRNWITVGSIGLSVLAITYGYSIFSVOGEKFLDOFNPPSKVGS-----
>Triops_cancriformis-----MASQMPKVDLVK--DATKLQPLDYMKLIEKQNLERVQKLRIRRNLLTGAALFASVFGIYYSIAAVGEKFLDOLETPSSKPSH-----
>Cordulegaster_boltonii-----MAGDKNSMFKVDFEK--DRQLGRAELGYIRQIEQTRTRAERLKKRRGNLLTGAFALTAGVLGIYTYIYAVKGEKFLDOFEPKLEPKQ-----
>Schistoceora_gregaria-----MENQDPK-----NKEFISKSMAEYMKLIEKQNLERVQKLRIRRNLLTAGILGAATGIYFYSIMYSVKGEKFLDOFEEPKLISG-----
>Timema_cristinae-----MAKESMPKVDFEK--DKAKFNTAVDYIKLIEKLNLERVQKLRIRRNWITGVLGGSVLGIYYSIMYSVKGEKFLDOFDEPATTSN-----
>Menopon_gallinae-----MTSSEDMPRADLS--EKLN--AQAYAKYLEKQWYMSLQKRLRRKRFMAGFCAFVGVGYOTLFRVQGEKFLDOFEEPRVNRDEKN-----
>Perla_marginata-----MGNEEMPKVDFTK--DKENIKLSDYMKLVEKQNLERVEKLRIGRRNLLTGCLIGVDVLGIYYSIMFVAVGEKFLDOFDEPAKTEALS-----
>Acerentomon_sp._AD-2013-----MALTEKPGDVPEVDLK--DAADINQVHLYMKLLEAKNTKRAHYVWIKKXKLLGSSLFGVASIYYSIMFVAVGEKFLDOFEPDANIPPPQ-----
>Liposcelis_bostrychophila-----MAKEMPEVDFKD--IDKNNKRGAYIYAKQLEERNVFRALIGARNLKRSRIIGITGLFAAGVYSLTINRVQGETFLDNWEEPEIPGRS-----
>Inocellia_crassicornis-----MGSQMPKVYSGT-----SKINKTELDYMKFIEKQNLERVEKLRIRRNWITGVLGAGILSIYAYSILSVKGEKFLDOFEEPKYVYAEQ-----
>Ceratophyllus_gallinae-----MAGNLALRAPSRNFRGAKTKQWVDSDSETRAKLSIQMDLIHRAEKMSRRATQFSKYRRHVVVGVGYFSMAIATYTYTIFAIXGEKFLDOFDMPOMLPVQSGE-----
>Stylops_melittae-----MVDG-----AKVMPD-----KEFTPEQLFQFQDNKLRRLRLRNSNNKKIGLQGFVAAFYAYSIMFVAVGEHFLDOFKPEIVGD-----
>Gynaikothrips_ficum-----MDKNEAMVYDLK-----ADVPTTLEHMKIMEKYNLARVQMKRIRKKSFNLSGLVSLAVGTYLSIMFVAVGEKFLDOFEEPKLTK-----
>Platycentropus_radiatus-----MSTEDGKGI--VS--TSKPAFSKGDIDYMKVVENLNLERVEKLRIRRNWITGSLGIVLGIYAYSIFSVMGEKFLDOFIEPTVHWKET-----
>Astelura_formicaria-----MGDERMPKYNLQK-----DHMKOTELDYMKLVEKQNLERVQKLRIRRNWITGSLGLGAVVGIYGYSIYAVKGEKFLDOFDEPKTYEQK-----

>Drosophila_melanogaster
MNDLSPNNDIEDRKPIILADGLVOTSNSPFETISGETOTSG---IGGGCHLTVDOLDIELPLIYDIVROVEKDPLEN-AVKLRESQSDNMKIFELQKRFESAREQIRQLPGIDFNKEEQGRLELLRNQGLAKQDLIRKYVDTEF-----
>Echinogammarus_veneris
-----MSITGATVAEDIDLDLLPLIYOYLRQLEKQD---QTDLNRVALDATQKLTENMKITLAREQVWKLAGEVYSPADQLQKLSALRAQLTLKKQLAKYYSK-ASADG-----VTTRO-----
>Reticulitermes_Flavipes
-----MDSSEQNG---AALTCXLTVDVDIEFLPLIYEIIRSVKRDPH-DTSQKTRESQDTSQKVELOKXLDGARNQIRRLPGIENVSKEEQGLQKLETLRNQGLQKQELLKYRN-MCTFDIPKS-----
>Agrilus_planipennis
-----MDSNNESN---SDLQKMTYVDLNIETLVPFYEIIRSVKRDHQN-TAKTRESQDSCQKVELOKRFQDARSQISLLPGIDYYSKEEQGLQHEALKTQGLHKQELLKYYSF-WYFFQMKQ-----
>Petroliastes_cinctipes
-----MSSPYYAAEDVDVDFLPVIYIYLRQLEKQ-----TDLGRVSGESSQKVELOKRIQTAREQVWKLPGVEYSREEQGLRLEALRNQGLAKKRLLIKYYSK-SEATH-----
>Apachys_charteus
-----MDISEST-S-QSLIQNLTVDDLVDFLPPIYDIIRSVKRDPL-DPSQKNRESQDSSQKVELOKXLDGARNQVQLDGIIEYSKAEQGLKKVEILRNQGLQKRDLLNKYRT-MCTFDIPK-----
>Daphnia_pulex
-----MAQLVEGGDFDILLSTIYDIIRSVKEQEG-DNAQKQKSDGAGQKVELOKXLDHAREVVKLPGIEYSKEQGLQKLETLRNQGLQKRDLLNKYRL-ITSFDRAGSEFQIHGH-----
>Campodea_augens
-----MAASNPTEQIDVEFLPTIYDIIRNIERDSG-DTTQKTRLDQAGQKVELOKXLDGAREQIKKLPGIEYNKEEQGLRLETLRNQGLQKRELLKYRN-WCSFEVPKA-----
>Haploembia_palaui
-----MEEQDNLNGS-VAASLTVDLDLEFLPLIYEILRSIEKDPH-DSSQKVRESQDLSQKILELOKXLDTARSQDVLPGVEYSKEEQGLQKLETLRNQGLQKQELLKYRN-WCSFEVPK-----
>Batetis_sp._AD-2013
-----MDSAEOP---TYNGLQSAEYDVEFLPLIYELMRSIERESI-ETAKQPRESQDTSQKVDLHKQLNLLREGIKRLPGIEYNREDQLDHLRNQGLQKRELLKYRN-WCSFEMPKA-----
>Tigriopus_californicus
-----MRTGIYGLSGIENSKEEQGLQKLETLRNQGLRNMKKLIIHKYKE-LNLKVFGLSGTY-----
>Guerna_arida
-----MDVH---ATINDGQEG-QPTDYKPLTVENLDVDFLPDIYDIIRSVKRDPH-DNAQKSSQSDQISQKVIETLHNKLEQAKKVRRLPGVEYSKEEQGLQKLETLRNQGLQKRELLKYRN-IDSPKVP-----
>Tenthrredo_koshleri
-----MMEVETAE-ETPARSQFTVDOLDIELPLIYEIIRSVKRDPH-DNTQAKESQDTSQKILELOKXLDGARSQIKRLPGIEYSKEEQGLQKLETLRNQGLQKRELLKYRN-MCTFDIPKV-----
>Armadillidium_vulgare
-----MSSHTIAEAEVDVDFLPVIYIYLRQLEKQD---MDLNRISVSSQKILEIQKXIDIAREQVGRLPVEYSKEEQGLRLEALRNQGLSLKKILLPKYYSK-AGPEQ---SH-----
>Plutella_xylostella
-----MENNTDAE---QNSCAPLVDVDVDFLPVIYEIIRSVKRDHQN-SAKVRESQDSCQKVELOKXLDGARNQIRRLPGIEYSKEEQGLQKLETLRNQGLQKRELLKYRN-MCTFDIPKST-----
>Empusa_pennata
-----MF-----SEDQNSGAG---SALPAQLTVDDVDVDFLPVIYEIIRSVKRDPH-DTSQKTRESQDTSQKVELOKXLDGARNQIRRLPGIEYSKEEQGLQKLETLRNQGLQKRELLKYRN-MCTFDIPKST-----
>Tanzaniophasma_sp._AD-2013
-----MVGEGQNG---TSMPTQLTVDDVDVDFLPVIYEIIRSVKRDPH-DTSQKTRESQDTSQKVELOKXLDGARSQISRLPGVQVYSKEEQGLQKLETLRNQGLQKRELLKYRN-WCSFDIPKS-----
>Panorpa_vulgaris
-----ME-----PWDTQSE---LXNNTLTVDQVEIDILPTIYDIIRSVKRDPHSG-AGKLRESQDCAKVELOKXLDKARNQIKQLPGIDLNPEEQGLRVDTLRNQLQKKEELLHYRN-WYSFDSKIK-----
>Corydalus_cornutus
-----ME-----VSEQDQSN---NRSQEPLTVEEVDIELPIIYDIIRSVKRDHQN-AAKARESQDSCQKVELOKXLEFSRDQIRRLTGINCSEEQGLAKLTSRLTQGLQKQDLRKYRE-WYSLSESTKS-----
>Pseudomallada_prasinus
-----ME-----VSESNELN---NRNSTQLNTEELDFELPIYIYEIIRSVKRDHQN-AAKARESQDSCQKVELOKXLDGARNQIRRLPGIEFSREEQGLRLEALKTQGLQKRELLKYRN-WCSLDSIKA-----
>Triops_newberryi
-----MTATSEEVDFELPLIYDIIRSVFERDPV-DNTQKLDQSETYQKVELOKXLDHAREQIKKLPGEVFSKEEQGLQKLETLRNQGLQKRELLKYRN-LGFFDLPK-----
>Epiophlebia_superstes
-----MDSSEQKT---GLSPSQLSAEYDVEFLPLIYEIIRSVKRDPH-DATQKPRESQDTAGKILELOKXLDGAREQVWKLPGVDLSREEQGLKLEFLRTQGLQKRELLKYRT-TCTFEIPSNPTGKNSGSSPQLSSSTQDQDQDINTNSLPTSNSQPIVNTGKA-----
>Locusta_migratoria
-----MESIEQNGS-TATPSQLTVDDVDVDFLPDIYDIIRSVKRDPH-DSTQKTRESQDLSQKILELHKXFDARSQIGRLPGVEYSKEEQGLRLEFLRNQGLQKQDLRKYRE-MCTFEIPK-----
>Phyllium_philippinicum
-----MDEGNATDSCDH---DMEGEGQNS---STHASELSYVDVDVDFLPDIYDIIRSVKRDPH-DTSQKRSQDQTSQKVDLHKXLDGARNQIRRLTGIEYSKEEQGLQKLETLRNQGLQKQELLKYRN-WCSFDIPKV-----
>Cosmioperla_kuna
-----ME-----ASDQSNQEG---SSIPTLYTVNDVDVDFLPVIYEIIRSVKRDPH-DTSQKTRESQDTSQKVELOKXLDGARSQIGRLPGVEYSKEEQGLQKLETLRNQGLQKRELLKYRN-WCSFEIPKV-----
>Acerentomon_franzi
-----MDADVETDIEDTDFLPDIYDIIRSVIEREPTQLSAKPKEQPDANKILDLNKKLEQAREQIRQFPGIEQNKVEQGLRRFDALKQDLTKEQILAKYRT-LCSFELO-----
>Ectopseocus_briggsi
-----MAEQDLSNAVKIEM---NLPGKNT---DLVANNSTNMKEFDPEFLPIYEVIXSVGPQD---DPTQKGRESQDASIKILELERKNEARQDILVLPGIEHSKEEQGLRQLEGRKQVILKQKILAKYRS-FQNFSLAD-----
>Xanthostigma_xanthostigma
-----ME-----VTD---QSE---TLNKKQLSVEELDIDILPIIYIYEIIRSVKRDHQN-TAKTREAGQDSQKVELOKXLDGARSQIRQLPGIEYSREEQGLQKLEALRTQGLQKQELLKYRN-MCTLDPNKS-----
>Trichomycterus_areolatus
-----ME-----SVEEGE---GEGVGYAESPLQLELLPALYDVRVSVEREYSEGGANKARESQDSCSLKVEILHRQLEAARDQVRSLAGISQTKREQLRQFEILRTQLFLKRLKKYRA-MQLETSSEFX-----
>Oropsylla_silantiewi
-----ME-----SMNTESEQ---QTNANPLTVDDQVEIDILPTIYDIIRSVKRDHQN-ASKARESQDSCSTKVELOKXLDKIRTQVALLPGIDYNNKEEQGLQDLNRQGLQKQELLHYRT-WYSFDSMKIK-----
>Mengenilla_moldrzyki
-----MD-----ISN-----TEIEQGSAGEQITSEILPAVVEYIRSLKDSYD-----ISFKIHQCSQKILLHKQDFDARQILIEDFPGIRYISIDONKALMKSRLRQGLQKRELLKYRN-IRDFGTTQVP-----
>Platycentropus_radiatus
-----MD-----VINLMDNEP---QNNFSLPTVDVDVDIDILPIIYDIIRSVKRDHQN-SAKARESQDSCSLKVELOKXLDGARSQIKRLPGIDYNNKEEQGLRQFEILRNQGLQKRELLKYRN-WCSFDAPFK-----
>Zorotypus_caudelli
-----MDSNDQPAVPTIYINNPATYDDIDVDFLPVIYEIIRSVKRDPH-DTSQKSRESYDTSQKVELOKXLDARSQVRLPGVELSKSEQLAHDTLYKQLQKRDLLHYRN-WCSFDISQVQ-----
>Atelura_formicaria
-----ME-----SVEQNPVPTV-APSPSTITVDQDVDFLPVIYIYEILRSIERDPH-DSTQKRESQDTSQKVELOKXLDGAREQIKLPGIEYSKEEQGLKXLDLNRQGLQKQELLKYRN-MCTFELPKV-----

>Denio_rerio
MRFKNQGLREV----HTGQGLAAYLKGFNF-TGEPPWLSIC
>Acipenser_siemensi
MLFKMAPFKVYNGFSEGGLALYLKGFNF-TGEPPW----
>Ameia_calva
MLFKNTFRSKAHNGFLGDFAFYLYKGFNF-KGEPPWL----
>Oreana_altrivata
MLFKNNHKSXSVTAYSSGQLESYLKGFNF-TGEPPWLLCT-
>Podocoryna_carnea
MLFKMAPFKVYNGFSGVGLGLALYLKGFNF-TGEPPW----
>Xenopus_laevis
MLFKNTNSRTAGSSGLESGVGLVLYLPGFYF-TGEPPWNE----
>Basilichthys_microlepidotus
MLFKNPNHRSKSHSGSGTGPQLESYLKGFNF-TGEPPWLLCT-
>Parichthys_notatus
MLVKTHHCRTHASDYSAGQLESYLKGFNF-TGDPWWLLCT-
>Oryzias_latipes
MLFQNLHRSKSYHSSSTGPTSESYLKGFFTEGPPWQRDL
Hynobius_chinensis
MLFKNSGSTSYHSSSGSLRLSLYLPGFYF-TGEPPWQDS--
>Micropterus_floridanus
MLFKNNPLKTHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Actynanax_mexicanus
MLFKNTSLBKATHT-ASQGLAAYLKGFNF-TGEPPWLL--
>Gallorhinchus_millii
MFKYNNQIRKLYNGTSEGRLFLYLKVSF-TGEPPWRRS--
>Haplochromis_burtoni
MLFKNLHRSKSHGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Alosa_alosa
MLLXNNHLRTLHT-YSEGQLESYLKGFNF-TGEPPWLLYT-
>Latimeria_chalumnae
MLFKNTYDRLYNGTSEGSLALYKGFNF-AGAPPWHS--
>Poecilia_reticulata
MLFKNLHRSKSHSGSGTGPQLELYLKGFNF-TGEPPWLLCT-
>Esox_lucius
MLFKNNHFKAHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Gadus_morhua
MLFKINMFRKWHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Acanthopobius_hasta
MLFKNLHLRS----ETGPGLAAYLKGFNF-TGEPPWLLCT-
>Apteronotus_leptorhynchus
MLFKTTOLBKAHITGYSAGQLELYLKGFNF-TGEPPWVI--
>Erinaceus_europaeus
MFKPGLRNCHTSSG-----CTSEV-TGDP-----
>Lutjanus_erythropterus
MLFKNHSRQAHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Osmorus_mordax
MLFKNTNFKAHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Scleropages_formosus
MLFKNSRLRKAFRYSTGGQLESYLKGFNF-TGEPPWLLCT-
>Lateolabrax_japonicus
MLFKNNHRSKTHIT--GAPQLESYLKGFNF-TGEPPWLLCT-
>Perca_flavescens
MLFKNNHRSKTHIT----GPQLESYLKGFNF-TGEPPWLLCT-
>Paralichthys_olivaceus
MLFKNPNHRSKSHGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Leucoraja_erinacea
MFKNIERNVRVHFHYTESPVLTYLRGFNS-VGKPPWRTS--
>Salmo_salar
MLFKNNHFKAHITGYSAGQLESYLKGFNF-TGEPPWLLCT-
>Lepisosteus_oculatus
MLFKNAHFRKADIFLEGGLASYLKGFNF-TGEPPWLSG--
>Trichomycterus_oreolatus
MLFKTSRLSKAH----TPQLELYLKGFNF-TGEPPWGL--
>Squalus_acanthias
MFKNEDARKVYNGVESPDALYLRGFNS-VGKPPWRGS--
>Taki_fugu_rubripes
MLFQNPFRFKTHITGYSAGQLESYLKGFNF-TGEPPWALYS-

>Gallus_gallus-----MAYATGPLLKFQIQVS
>Acipenser_sinensis-----MAKTIWL,SF SVLFLGVFYL-S-AVADNG--APQKRLKMGFATGPLLKFQIQVS
>Kaupichthys_hyoproroides-----MQRWLSFQLLFLGVF-FLSCA-SADNNG--VKKLKMGFATGPLLKFQIQIS
>Podocoryna_cornua-----MAKRWLSFSLFLGVFYL-S-ALADNG--APQKRLKMGSTGPLLKFQIQVS
>Xenopus_laevis-----MDYTAGPLLKFQIQVS
>Acinonyx_jubatus-----MRF--LLVLL--VAASAVIRSDASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Aebystoma_mexicanum-----MNYTSGPLLRFQIQVS
>Tursiops_truncatus-----MRLLLFLLVAA SAVVRSDASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Eptesicus_fuscus-----MRLLLFLLVAA SALVRSDASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Desypus_noveboracensis-----MRLLLLLLAASAVVRSEASANLGG-LPSKRLKMDYATGPLLKFQIQVS
>Alligator_mississippiensis-----MAYATGPLLKFQIQVS
>Mitsurnus_anguillicaudatus-----MQRWLSV LILWAG-SLVS-VSADNNG--LKKMKMGFATGPLLKFQIQVS
>Galeopterus_variegatus-----MRLLLLLLVAA SAMVRSEASANRGG-VPSKRLKMDYATGPLLKFQIQVS
>Monodelphis_domestica-----MRFLLLL-LMAAALRGEASADTGG-VPSKRLKMDYATGPLLKFQIQVS
>Trichosurus_vulpecula-----MRFLLLL-LMAAALRGEASADTGG-VPSKRLKMDYATGPLLKFQIQVS
>Aegypius_monachus-----MRAVLLLLLLALAAPGG--SAEGGG-LPAKKLRMAYATGPLLKFQIQVS
>Gadus_morhua-----MASSRWLRFSLFLGVF-SLYCATSDNNG--VKMKMGFATGPLLKFQIQIS
>Condylura_cristata-----MRLLLLLLVAA SAVVGT DASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Oryctolagus_cuniculus-----MRLLLLLLVAA SAVRSEASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Pseudopodoces_humilis-----MRAQLRLLLLLLLAGLAAPGGGAAAEDEGG-LPAKKLRMAYATGPLLKFQIQVS
>Trematomus_bernacchi-----MKWLQFSL-LVGLS-SLLCASSDNG--VKMKMGFANGPLLKFQIQIS
>Geratherium_simum_simum-----MRLVLLLVAA SAVVRSDASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Manis_javanica-----MRLLLLLLVAA SAMIRSDASANLGG-MPSKRLKMDYATGPLLKFQIQVS
>Platichthys_stellatus-----MQRWMPRFLLALGAF-SLOCATSDISG--VKMKMGFATGPLLKFQIQIS
>Aotus_nancymae-----MRLLLLLLVAA SAVRSEASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Loxodonta_africana-----MRLLLLLLVAA SAVRSEASANLGG-MPSKRLKMDYATGPLLKFQIQVS
>Melopsittacus_undulatus-----MRAVLLLLLLALAAPGG--SAEGGG-LPAKKLRMAYATGPLLKFQIQVS
>Marmota_marmota_marmota-----MQRWLEFVWVWREITRKRLLLLLLVAA SAVRSEASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Oncomerychus_mykiss-----MKMGFATGPLLKFQIQIS
>Tupaia_chinensis-----MRLLLFLLVAA SAVVRSEASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Trichechus_manatus_latirostr-----MRFLLLLLVAA SAVVRSEASANLGG-VPSKRLKMDYATGPLLKFQIQVS
>Gekko_japonicus-----MKQALALL-LLSV--GLDWASAPGGLPPAKKLRMAYATGPLLKFQIQVS
>Mauremys_reevesii-----MAYTTGPLLKFQIQVS
>Orycteropus_afer_afer-----MRLLLLLLVAA SAVVRSEASANLGG-VPMKRLKMDYASGPLLKFQIQVS

>Denio_rerio-----MFFICTSSGRFSMEERGDKI-QVESHFNGDAFRES-----
>Acipenser_sinensis-----MLVORVVFGRLSMEGRGNLI-VTESNFSEROTFREEQ-----
>Podocoryna_carnea-----MLVORVVFGRLSMEGRGNLI-ITESNFSEROTFREEQ-----
>Oryzias_latipes-----MILGLSTSEISMEKGGDTY-KAANFSQROTFRES-----
>Micropterus_floridanus-----MILRLITSEKSSMEKGGNGF-IAGTKFSQROTFRES-----
>Astyanax_mexicanus-----MFFRCFSSERFSMEDRGNEI-IVESHFNGDAFRES-----
>Gallorhinchus_millii-----MII-QRFISGFSMEGPETOI-IVKXSFNERDIFRES-----
>Neolamprologus_brichardi-----MILRLI-AVKKSMKGGKLF-IAGTKFSQRODAFRES-----
>Alosa_alosa-----MILYQLVLERFSMEGGDNVI-IVESHFNGROTFRES-----
>Latimeria_madaoensis-----MIIYSOSAGFSMDGE-KTS-IWKNFNERDIFRES-----
>Kryptolebias_marmoratus-----MIKPYDLKYYLLFFFLLLK-----CLFSRSMIMILRLKYSERSSMEKGGNGF-IGSTFNGROTFRES-----
>Serrinthis_crassicauda-----MIIICSVSQQFSMEKGGKCTWARSNFEEROTFREA-----
>Galeorhinus_variegatus-----MITGCFVSQFSMEKGGDNMIATGSFEERDAFREA-----
>Monodelphis_domestica-----MIIICSVSQQFSMEKGGKMMWAVSNFEEROTFREA-----
>Trichosurus_vulpecula-----MIIICSVSQQFSMEKGGKMMWAVSNFEEROTFREA-----
>Esox_lucius-----MFLGHI VFERCSMEEGGQI-IVESNFORDAFRES-----
>Acanthopobius_hasta-----MENKRTOI-IAGTKFSQRODAFREA-----
>Chanos_chanos-----MFWCPVFVKHFSMEEGONEI-IAESTFNGROTFRES-----
>Dryptolagus_cuniculus-----MNFRCQFSQFSMEKGGDNMIATGSFEERDAFREA-----
>Osmorus_mordax-----MFFGYTVFEACSMEE-QKQI-IGESNFORDTFRES-----
>Scleropages_formosus-----MFLKCYTLKRVSMEDQVNEI-IAESQFSEROTFREA-----
>Lateolabrax_japonicus-----MILRLITSKRSSMEKGGYQF-IAGTKFSQROTFRES-----
>Trematoma_bernaoalii-----MILRLNTSEKSSMEKGGNLF-KAGTFNGROTFRES-----
>Equus_asinus-----MITRCQVSQFSMEKGGDNMIATGSFEERDAFREA-----
>Propithecus_coquereli-----MITRCQVSQFSMEKGGDNMIATGSFEERDAFREA-----
>Leucoraja_ocellata-----MII-MFISSELSMEGGQSOI-VVWGTNERDITRESSPARL-----
>Otenomys_sociabilis-----MFAAPPALKSSASRADRIASPAALFGHRRHWPLTADORPLSRVLPAAGTSMIFKQLVSQFSMEKGGDNMIATGNFEEROTFREA-----
>Salmo_salar-----MFFGYVVFERFSMEEGQNGI-IIESNFORDAFRES-----
>Lepisosteus_oculatus-----MLFTSLVLGI FSMEGGTOI-IVESHFNERDIFRES-----
>Ictalurus_furcatus-----MFLKQPSSELSFMEERGNEI-IVESHFNGDAFREA-----
>Squalus_acanthias-----MII-RRFISELSME-RQSOI-IVKXSYNERDIFRES-----
>Gekko_japonicus-----MIIICRLSAAFSSKSGSRAVALSNFDERDIFRES-----
>Chrysemys_picta-----MILKQLVSKRVSMKGGQIVVALSKFDERDIFRES-----

>Denio_rerio	-----MFNSVPRQNN-----AHHHMKTSOLA-----GHGCAARSR-S-TTSRTWSPIGEEKLKSEKXNA-----LNFFTTKR-----
>Acipenser_sinensis	-----MYDSSSTREN-----TNFRHMKTKTTA-----GLTRSESRSGEI-PTSPRTWSPGDKVSRKEEANK-----SCYFTITTKR-----
>Aeolia_calva	-----MFSSAARPD-----TAVRHWSAPSPA-----GPTRAIRSGFI-STSRTWSPVGEELKKRPD-----FCTTKR-----
>Ohamia_striata	-----MFNSAPRENN-----AHHHMKTSQFA-----GHGCAARSROK-TTSRTWSPIGGERLKKD-LCF-----VDFQTKR-----
>Anguilla_japonica	-----MFSSASRQNC-SYFHHMKTPKLA-----GLRRTERSGPT-PTSRTWSPIGEEKLVEEVRT-----RYFLTTKR-----
>Podocoryna_carnea	-----MYDSSSTREN-----TNFRHMKTKTTA-----GLRRSESRSGEI-PTSPRTWSPGDKVSRKEEVNK-----PCFFTITTKR-----
>Basillichthys_microlepidotus	-----MFSSASRENN-----ALHHHMKTSOLA-----GHGSAARSROK-ATSRTWSPIGGERLKKD-LCF-----DNFLTTKR-----
>Opsanus_beta	-----MFSSAPREND-----AHHHMKTSICT-----HKGROK-AASRTWSPIGGERLKKD-LCSV-----TTKR-----
>Oryzias_melastigma	-----MFSSVPRENI-----AHHHMKTSOLA-----GOKSAVRSROK-ATSRTWSPIGGERLKKD-LCF-----VNIPPTTKR-----
>Tripterygion_delsaisi	-----MFYSAPRDIN-----AHHHMKTSOLA-----GHNTSAARSRLRTTSRTWSPVGEELKKD-LCSVFTT-----KR-----
>Trachinotus_blochii	-----MFSSAPRENN-----AHHHMKTSOLA-----GHKSAARSROK-ATSRTWSPIGGERLKID-LCF-----INFLTTKR-----
>Mistela_putorius_furo	-----MLASAPRLNS-----ADHPMKTSVLR-----GRKGSVRQKH-----LLSNAMQGRGOVVEILOSE-----KOTER-----
>Micropterus_dolomieu	-----MFSPAPRENN-----ALHHHMKTSOLA-----GNKTAARSROK-TTSRTWSPIGGERLKKD-HCF-----FNFLTTKR-----
>Pygocentrus_nattereri	-----MFNSASRQNI-----AHHHMKTSQTV-----GLKRAVRSRA-ATSRTWSPIGEEKLRMDIYAVIFN-----TKR-----
>Miniopterus_natalensis	-----MLASAPRLNS-----ADHPMKTSVLR-----GRKGSVRQKH-----LLSNAMQGRGOVVEILOSE-----KOTER-----
>Haplochromis_burtoni	-----MFSSASRENN-----AHHHMKTSQFA-----GHGCAARSROK-TTSRTWSPIGGERLKKD-LCF-----VNFFLTTKR-----
>Aloosa_alosa	-----MFSSVTROYT-----AHHHMKTSOLA-----GHGCAARSRS-PTSRTWSPVGEELKSEI IHH-----LNFFLTTKR-----
>Poecilia_mexicana	-----MFSSASRQNI-----AHHHMKTSOLA-----GHGSAARSROK-TTSRTWSPIGGERLKKD-LTV-----FSLTTKR-----
>Esox_lucius	-----MFSSASLENN-----AHHHMKTSOLA-----GLKSAARSROK-TTLRTWSPIGEEKLRNH-LCT-----FNILITTKR-----
>Acanthopobius_hasta	-----MFSSVPRQNI-----ALHHHMKTSVLA-----GHKSAVRSRR-TTSRTWSPIGGVRLLKRA-HCNT-----FLTTKR-----
>Chanos_chanos	-----MKTSQLA-----GRKCAARSR-T-TTSRTWSPIGEEKLRKSIDDE-----LNLVTTTKR-----
>Plecoglossus_altivelis	-----MNTSFTROPDYLTGDPYPSQKSRFSSSRSTVFGELMFSSGTRENI-----ADRHMKTAOLA-----GHKSAARSRSK-TTLRTWSPIGEEKLRKXALCS-----FNFLTTKR-----
>Lateolabrax_japonicus	-----MFSSAPRENN-----AHHHMKTSOLA-----GHGSAARSROK-TTSRTWSPIGGERLKKD-HCF-----VDFLTTKR-----
>Sebastes_caurinus	-----MFSSVPRENNSTTHHMKTSOLA-----GHSTARSROK-TTSRTWSPIGGERLKKD-LSFYFNFFLTTKR-----
>Omyglossus_semihaevis	-----MFSSAARVNN-----AHHHMKTSQFA-----GHLSAVRSROK-TTSRTWSPIGGERLKED-SCS-----TNFLTTKR-----
>Microcebus_murinus	-----MLASAPRLNS-----ADHPMKTSVLT-----GRKGSVRQKH-----LLSNAMQGRGOVVEILOSE-----KOTER-----
>Ictidomys_tridomilineatus	-----MLASAPRLNS-----ADHPMKTSVLR-----GRKGSVRQKH-----LLSNAMQGRGOVVEILOSE-----KOTER-----
>Oncorhynchus_tshawytscha	-----MFYSASREND-----AHHHMKTPOLA-----GPKSAARSROK-TTSRTWSPIGEEKLRKYLCT-----FNFLTTKR-----
>Lepisosteus_oculatus	-----MFSSASRYG-----PDFRHMKTPMLA-----GLTPSERSGLR-PTSRTWSPVGEELKRKESNR-----LCFSTAKR-----
>Ictalurus_punctatus	-----MFSSASRQNA-----AFHHHNTINTITINIELNTCAVRSRR-----TTSRTWROISQETVRRRLCT-----GNFTTITER-----
>Trichechus_manatus_latirostr	-----MLASAPRLNS-----ADHPMKTSVFR-----GRKGSVRQKH-----LLSNAMQGRGOVVEILOSE-----KOTER-----
>Taki_fugu_rubripes	-----MFSSVPRQNI-----ALHHHMKTLGLA-----GHGSAVRSRSR-AAPRTSPVDEPSKIGS-----AHFATTKR-----

>Homo_sapiens
-----MLASAPRLNSADRPWKT SVLRQRKGSVRKHLLSWAIQOGRGQVVEILOSEKQTER
>Araa_platyrhynchus
MQLDFFPWFSAENPWLGSAPILNTADHPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Chaetura_pelagica
-----MLGSATWILDTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Apteryx_austalis_mantelli
-----MLGSATWILKAAVDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Buceros_rhinoceros_silvestri
-----MLGSAMILKSADDPWNT SVSRQRGSEKRGHLLFOAIKQERGGHELVSESEKTER
>Caprimulgus_carolinensis
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGEMSEVESEKTER
>Ceriama_cristata
-----MLGSATWILNTADHPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Odobenus_rossmarcus_divergens
-----MLASAPRLNSADRPWKT SVLRQRKGSGRKHLLSWAIQOGRGQVVEILOSEKQTER
>Orcinus_orca
-----MLASAPRLNSADRPWKT SVLRQRKGSIRKHLLSWAIQOGRGQVVEILOSEKQTER
>Charadrius_vociferus
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Eptesicus_fuscus
-----MLASAPRLNSADHPWKT SVLRQRGSEKRGHLLSWAIQOGRGQVVEILOSEKQTER
>Pterocles_gutturalis
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Dasypus_noveboracensis
-----MLTSAPRLNSADDPWKT SVFRQRGSEKRGHLLTWAIQOGRGQVVEILOSEKQTER
>Colius_striatus
-----MLGSAPILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Columba_livia
-----MLGSAPILNTADHPWKT SIPSRKESSEKRGHLLFOAIKQERGGELERAISEKTER
>Merops_nubicus
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Alligator_mississippiensis
-----MWSASILDTADRPWKT SIPSRKESSEKRGHLLFOAIKQERGGREVAASEKTER
>Oculous_canorus
-----MLTSAPRLNTADDPWKT TYICSPRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Sarcophilus_harrisii
-----MLNSADDPWKT SILRQRNRSGRKHLLSWAIQOGRGQVVEILOSAKQTER
>Galeopterus_variegatus
-----MLASAPRLNSTDHPWKT SVLRQRKGSRRKHLLSWAIQOGRGQVVEILOSEKQTER
>Monodelphis_domestica
-----MLNSVDDPWKT SILRERNRSGRKVLLSWAIQOGRGQVVEILOSAKQTER
>Macropus_eugenii
-----MLNSADDPWKT SILRQRNRSGRKHLLSWAIQOGRGQVVEILOSAKQTER
>Falco_cherrug
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Gallus_gallus
-----MLGSAMILNTADRPWKT SVPSQRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Gavia_stellata
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Balearica_regularis_gibberica
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Condylura_cristata
-----MLASAPRLNSADRPWKT SVLRQRKGSVRKHLLSWAIQOGRGQVVEILOSEKQTER
>Oryctolagus_cuniculus
-----MLASAPRLNSADRPWNT SVLRQRGSEKRGHLLSPWAIQGRGQVGTIHSQOQTER
>Ornithorhynchus_anatinus
-----MLGSASILNTADDPWKT STRRQRSEKRGHLLFOAIQOGRGQVVEILWSEKQTER
>Tauraco_erythrolophus
-----MLGSATWILNTADRPWKT SIPSRKESSEKRGHLLFOAIKQERGGELTVESEKTER
>Opisthocomus_hoazini
-----MLGSAPILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Sturnus_vulgaris
-----MLGSAPILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Phaethon_lepturus
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGALSEVESEKTER
>Ceratotherium_simum_simum
-----MLASAPRLNSADRPWKT SVLRQRKGSVRKHLLSWAIQOGRGQVVEILRSKQTER
>Manis_javanica
-----MLASAPRLNSADRPWKT SVLRQRKGSVRKHLLSWAIQOGRGQVVEILRSKQTER
>Picooides_pubescens
-----MLGSAPILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Loxodonta_africana
-----MLASAPRLNSADRPWKT SVFRQRKGSVRKHLLWAIQOGRGQVVEILRSEKQTER
>Fulmarus_glaucialis
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Melospittacus_undulatus
-----MLGSAPRLNTADDPWNT SVLSQRKESSEKRGHLLFOAIKQERGGELSEGESEKTER
>Ictidomys_tridactylus
-----MLASAPRLNSADHPWKT SVLRQRKGSVRKHLLSWAIQOGRGQVVEILOSEKQTER
>Tupaia_chinensis
-----MLASAPRLNSADRPWKT YALRQRKGSVRKHLLPWAIQOGRGQVVEILOSEKQTER
>Trichechus_manatus_latirostris
-----MLASAPRLNSADHPWKT SVFRQRKGSVRKHLLSWAIQOGRGQVVEILOSEKQTER
>Aptenodytes_forsteri
-----MLGSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Gekko_japonicus
-----MLGSASILNTADRPWKT ITIPKQRKGSNRSQHLLFQVWQOGRGQVETVQSEKTER
>Tyto_alba
-----MWSATWILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Struthio_camelus_australis
-----MLGSATWILNAADDPWKT SIPSRQRGSEKRGHLLFOAIWQERGGELSEVESEKTER
>Trachemys_scripta
-----MLGSASILNTADDPWKT SILSRQRKGSNRRKHLLFOAIQOGRGGREVAESEKTER
>Tinamus_guttatus
-----MLGSATWILNAADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGQELSEVESEKTER
>Calypte_anna
-----MLGSAMILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGHELVSESEKTER
>Apaloderma_vittatum
-----MLGSAMILNTADDPWKT SIPSRKESSEKRGHLLFOAIKQERGGELSEVESEKTER
>Orycteropus afer
-----MLASAPRLNSADRPWKT SVLRQRRLVRKHLLSWAIQOGRGQVVEILOSEKQTER

>Gallus_gallus	MLGSAAILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Anas platyrhynchos	MLGSAAILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKAT
>Chaetura pelagica	MLGSAAILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Apteryx australis mantelli	MLGSAAILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
MCF0KSVQERHGGACDARGMLDGEGRLSAGVSRGPVIMLRLLPWSLCAENPMLGSAITILKAYDPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT	
>Buceros rhinoceros silvestri	MLGSAAILKSADRPWKT SVPSORKESSERQHLLFQAMKQERGHELESVSEKTTT
>Caprimulgus carolinensis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Ceriama cristata	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Odobenus rosmarus divergens	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
.....MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Balaenoptera acutorostrata s	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Charadrius vociferus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Eptesicus fuscus	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Pterocles gutturalis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Dasypus novemcinctus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
.....MLTSAPRLNSADRPWKT SVFRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Colinus striatus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Columba livia	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Merops nubicus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Alligator mississippiensis	MLGSAAILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Oculus canorus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Sarcophilus harrisii	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
.....MLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Galeopterus variegatus	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Monodelphis domestica	MLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
.....MLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Macropus eugenii	MLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
.....MLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Aquila chrysaetos canadensis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Gavia stellata	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Mesitornis unicolor	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Condylura cristata	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Dryctolagus cuniculus	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
.....MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Ornithorhynchus anatinus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Tauraco erythrophus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Opisthocomus hoazin	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Serinus canaria	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Phalacrocorax carbo	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Ceratotherium simum simum	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
.....MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Manis javanica	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
.....MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT	
>Picooides pubescens	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Nomascus leucogenys	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
.....MLASAPRLNSADRPWKT SVFRORKESSERQHLLSINAMQGRGDDVEILQSEKOT	
>Loxodonta africana	MLASAPRLNSADRPWKT SVFRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Fulmarus glacialis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Nestor notabilis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Ictidomys tridactylus	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Tupaia chinensis	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Trichechus manatus latirostris	MLASAPRLNSADRPWKT SVFRORKESSERQHLLSINAMQGRGDDVEILQSEKOT
>Aptenodytes forsteri	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Gekko japonicus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Tyto alba	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Struthio camelus australis	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Trachemys scripta	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Tinamus guttatus	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Galypte ana	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Apaloderma vittatum	MLGSAITILNTADRPWKT SVPSORKESSERQHLLFQAMKQERGDELESVESEKTTT
>Dryopteris afer	MLASAPRLNSADRPWKT SVLRORKESSERQHLLSINAMQGRGDDVEILQSEKOT

>Homo_sapiens
-----MAA-----ALSGLAARLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Canis_lupus_familiaris
-----MAA-----ALSGLAARLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Hymobius_retardatus
-----MA-----ALAVLAARYSOSAARSYGVSFCKGLSRILLIFFDMAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Balaenoptera_acutorostrata_s
-----NNLNVRLQVHIEIH-----
>Pteropus_vampyrus
-----MAA-----ALSGALRLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Echineraechinus_perna
MAATYSSPILLSDYQERERRLKLAALQTGVP-FPLLTRTLNFFNLAYQGRIPITIFVGLLAFDVRQLQINNVQI
>Latimeria_menadoensis
-----MA-----QLTALVRFSSGAARSYGVSCKLNRILLIFFDLAARLRINFPYLYITLSMLNVRLQVHIEIH--
>Scorophilus_harrisi
-----MAA-----ALSALALRLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Monodelphis_domestica
-----MAA-----ALSALALRLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Arachnocampa_luminosa
-----MIFNYLAKSLLNITYPSVSGRLSPLMLFCNFAMRAFTLPYINFLATINATGQIRVEIEFE-----
>Strongylocentrotus_purpuratu
-----MAPWMIYSRFQRHERNLTAVIRTPPP-FPLLTRTLNFFNLAYQGRIPITIFVGLLAFDVRQLQINNVQI
>Marthasterias_glacialis
-----MFXNLQNRGDSQNTQVGSMPV-RPFLSRTLTFFDMAFRCHFLPSIVAFVLFADTQLQLQINNVNH--
>Condyliura_cristata
-----NNLNVRLQVHIEIH-----
>Oryctolagus_cuniculus
-----NNLNVRLQVHIEIH-----
>Lingula_anatina
-----MLE-----NYIP-----GRMGPSLSDVOMFFFXLANGRSLRPVILTVFVILDTROLEINININ
>Crassostrea_gigas
-----MVLQTLNDSYASFARLSRILLFFRFAMQTKFSLPYLLNSTMLALDFRVRVIVILL-----
>Equus_asinus
-----MAA-----ALSGLAARLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Manis_javanica
-----NNLNVRLQVHIEIH-----
>Brachionus_manjavacas
-----MIFNYLAKSLLNITYPSVSGRLSPLMLFCNFAMRAFTLPYINFLATINATGQIRVEIEFE-----
>Heterocephalus_glaber
-----MAA-----VLSGLAARLRSAAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Tupaia_chinensis
-----NNLNVRLQVHIEIH-----
>Echinaster_spinosus
-----MLKISDPSQSIQVCTVLPV-RNVMSRTLTFDDMAFRCHFLPSIVAFVLFADTQLQLQINNVNH--
>Takydromus_sexlineatus
MAVTAAT-----LLSALVARFSGAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Sphaerechinus_granularis
-----MMAPMLBYLYQSSQSRVQ-----TVSP-FPLLTRTLNFFNLAYQGRIPITIFVGLLAFDVRQLQINNVQI
>Pelodiscus_sinensis
-----MAA-----DLSAARLSGAARSYGVFCKGLTRILLIFFDLAARLRINFPYLYIVASNNLNVRLQVHIEIH--
>Villosa_tenosia
-----MLKLSALNSTYSNTRNLTPILMFFFRAMLSPFLPQLITVFLALNIRVTVIHH-----

>Drosophila_melanogaster-----MASNAQLGKIIILISAIAVFFYFFWVAVLPFNLIDGNPRLRFFPPLKYAFIVPTVGVIFLGGIAAFSFYHNSLRVKRD-----
>Meinertellus_cundinamarcensi-----MISDAAGRLAIYVGSSIFSYYTLWIVLFPYDREHA--VRGFFPDVTYALVPLNLGVVFIGSLVYYACASLKERCTS-----
>Macrobrachium_nipponense-----MYGDRYIGKVL SVTGVALLYLTWVCLPFADGSS--IRLLFPDLVALIVPTIVFVFLITLTGFIYGHSLYDYITTSISS-----
>Forficula_auricularia-----MSDPYIGKVLIVISSVIVLIVFSQWFLTFADATDY--FFKVFPSRLRYALIIPAVSGLIFGGLISLFLGSVI-----
>Daphnia_pulex-----MAYGHDLIGKILLFLCVIFVLYYTFWITGLPLEPNFF--AHQVFPDSFYAIGVPLSVLWVTVLSYALNLMKFO-----
>Aposthonia_japonica-----MEDATLGKVLFCQGLFFIYYSMWVLFPYDENNV--IRRFPPNWFHIFTPAVLGLSFSSLIFFTIYAMTFQS-----
>Eurylophella_sp._AD-2013-----MVHTRTVGGLILLISLILLYYTLWVVALPFADSDHF--LVQLFPSRRYAIIVPAISGLTFIGSLAVFTWISMYSC-----
>Meganyctiphanes_norvegica-----MLGCDLIGKVLGVFLSLSLYIIVWVGLPFTDEDSF--LBALFPDPIYAIIVGPTLVFVALLNGVYMLKAYFKVQKLKAO-----
>Grylloblatta_bifratrilecta-----MVVTDATGKAILILLTLFPYYTVWVILPFTDAEDV--LNAVFPNRYALVPALAGLQFVGLVAFTLYSLAS-----
>Xenophysella_greeniadeae-----MGALTDTLGLILLTASVFLYYTLWVILSPFYEP-----ISSLPPIRYALLVPAFTGLTFISSLIFFTIWALLSS-----
>Sceliphron_caementarium-----MFDSDREKGLILIVTIILFLYYTIWIIIGLPIIDGRL--RSLFCSHDFALVPAYSGLQFIGSLVFLTYHVRPYLLSDRASKIQ-----
>Asellus_aquaticus-----MYGQYMLGVLLISSIVFYTYLWNTILLPFVQDQSV--IRIFFPPLALIPTSLFLVYTFGVLTYAVNKKELL-----
>Pararge_aegeria-----MSFTLYHIYPYL-----
>Metallyticus_splendius-----MINDSALGKILLIASQLFFCYTTWIVLFPSDRHH--INILFPVQHALLVPAGNVAFIGSLIITYVNIQO-----
>Tanzaniophasma_sp._AD-2013-----MINDTLGTFWIFSVLFFWYTFWVLPFVGDHV--IHTIFTSVDFALVMPAVAGLFFIGSLVIFTLFLALRH-----
>Euroleon_nostras-----MKQVILGRLLIFSGLFVLYTFWVVLPLPLADDTFLFFPDVTYALLPLILGTLFIGLSAFTLYHLPHLKLKK-----
>Calopteryx_splendens-----MGISDAQLGKIIILVLSASLFVYTLNLMWPPFISPFSPNTEPTVFPPTRYALIPAISGLFIGLLVFTIAALQNA-----
>Gryllotalpa_sp._AD-2013-----MLSDATLGKIIILFSSCSFFIYTAIVWFLPFADNIQV--IKS-FPPITWIALVPAIMGLLVGALMNYTVAIRRK-----
>Ramulus_artemis-----MILLCLLKLRLSLKKSILSVHQLLHFFLYQGLFNFINDTEYVIMVSDSVGKLVATCIGFTTYSFVWVLPFTDSEK--INSPFSPVWYALVPAMGLFFIGSLVFTLCVETRGRS-----
>Cosmioperla_kuna-----MSDALIGKVLIASCTFFCYTANTLLPFADGDT--INSLFPSIWYALVPAYMGLAFIGSLMFTLYALRT-----
>Liposcelis_bostrychophila-----MLAKLILALAVSFSRYTFQIALPFEPETHL--IVSYFPGRYTLIIPALFGLTFGSLIFTIAVLNKEKP-----
>Trichomycterus_areolatus-----MILPORILGKSVLITTFAFVYLVMILLPFTDFEKDHMLYKGLDREYALICISNGFFIGSLMLFTLYQIYPYL-----
>Thrips_palmi-----MNDKTVGSLILALSASFYSYVWVGLPFFDSDHF--IHSLFPAVEFALLVPALMGLTFIGSLIFCIIELRKAGAASK-----
>Hydroptila_sp._AD-2013-----MIISSQNLGKLVLAAYSIFTYLVIMLTLPTDFQEDHMLYKGLPREYALFICIGKGLFIGSLNGFTLYHLYFLK-----
>Thermobia_domestica-----MTIABETLGKLLIGSLFLTYTFWIIILPFDQPHI--LHDLFPVTVGVMTPAWMLQFIGSLFVTVQFQSEK-----

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>Denio_rerio
MYRSKSNIGIAFNITFLTVPLEYQTQKHYSKNWSIG

>Menidia
MORFRSGITGIAFYSYLLTVPLDGFHLERDYSKNWSIG

>Gnana_punctata
MYRCSGGFSRIAFAFDFLSTVQREYHFTRDYNKWSIG

>Anguilla_japonica
MYRFRPGITGIAFNSYLLTLLKKGFLKHKTRNWSIG

>Podocoryna_carnea
MORFGSPITRIFAFTSLLAVPFEDQLMRHYKNQLSVG

>Menidia_menidia
MYRLGGTISFKIAFDFLSTVPREHFHTRDYNKWSIG

>Opsanus_beta
MYRLGLQLAKITFTSIFQTVPREYHFTRDYSKNWSIG

>Oryzias_latipes
MYRLGGAFISKIAFDYFLSTVPREHFTTRDYNKWSIG

>Tripterygion_delaiei
MYRLGGGFSRIAFAFSLPTVPREYFLTRDYNKWSIG

>Astyanax_mexicanus
MYRFRSGALIGIAFNSLLFTVPLDDIGFKRYSKNWSIG

>Neolamprologus_birchardi
MYRLPGSISKIAFDFLSTVPREYHFTRDYNKWSIG

>Clupea_harengus
MYRLRSKSFISKIAFNITFFAIVPLEEIVFRDYSKNWSIG

>Fundulus_heteroclitus
MYRLGROSISKIAFNFLSTVPREHFHTRDYNKWSIG

>Esox_lucius
MYRFRITLISRIAFAFNSFLTIVPREDDQFWDFNKNWSIG

>Gadus_morhua
-----MYDYNKWSIG

>Acanthopoma_hasta
MYRLAGDVSKIALISLPAVPREYHFTRDYNKWSIG

>Apterontus_leptorhynchus
MYRFRLOAFIGIAFYSLPTVLEDGFKRHYSKNWSIG

>Plecoglossus_altivelis
MYRLGGGFSRIAFAFSLSTVPREDLHFTRDYNKWSIG

>Perca_flavescens
MYRLGGGCPKIAFNSFLSAVPREYHFTRDYNKWSIG

>Osmoglossus_semiilevis
MYRLGGGFSRIAFAFSLSTVPREYHFTRDYNKWSIG

>Coregonus_clupeaformis
MYRLPGGFSRIAFAFNSFLSTVPREDDQFWDFNKNWSIG

>Lepidotus_oculeus
MORFRITLIGIAFYSLSTVPGDGFHLERDYSKNWSIG

>Ictalurus_punctatus
MYRSRSGAFIGIAFNPLFTVVPFEDQKHYSKNWSIG

>Sperus_aurata
MYRLGGGFSRIAFAFDFLSTVPREYHFTRDYSKWSIG

>Takifugu_rubripes
MYRLGLTISKIAFNSFLSAVPREYHFTRDYNKWSIG

HS0021.1 ENSG0000000652 IFD1

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>Homo_sapiens-----MYRFRSQLFTGISAAATAHSYP---RRFSTLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Xenopus_laevis-----MYRLHSQAFGVSV---TSTF---RHVYPIPIEDS---KLIPERR-FS---KKCSSIG
>Apteryx_australis_mantelli-----MHFRSRAFTGISAFATDSS-FACFRGSPPLPRSGK---SASQRR-CSKKRSCSSIG
>Laptonychotes_weddellii-----MYRFRPQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Aebystoma_mexicanum-----MYRFRSQALIGFPWSRRRCSPA---RRCSPPLGLGL---NLIPERR-FS---KKCSSIG
>Physeter_catodon-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLVENSPLSRPPHRR-TS---KKCSSIG
>Rhinolophus_ferrumequinum-----MYRFRSQLFTGISAAATAHSYP---RRSSPLLLAEASPLSRPPHRR-TS---KKCSSIG
>Desypus_noveboracensis-----MCRFRSQLFTGISATATHSYP---RRFSPLLLVEDSPLSRPPHRR-TS---KKCSSIG
>Latimeria_menadoensis-----MIRSGSQTIVRIA---SCY---HILLAVPF---GDLHVPERR-YS---KKCSSIG
>Sarcophilus_harrisii-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSLSDPPHRR-TS---KKCSSIG
>Galeopterus_variegatus-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
MCRDILVVRVVPFTGDDRRRSCYLRRLDRPALAPALERMYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Monodelphis_domestica-----MYRFRSQLFTGISAAATAYSSP---RRFSPLLLAEDSLSDPPHRR-TS---KKCSSIG
>Coturnix_japonica-----MHRLSRAFTGISAIAGSS-FACLRGSPPLPRPK---SASQRL-MNKKRSCSSIG
>Sorex_araneus-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Ochotona_princeps-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Elephantulus_edwardii-----MHFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSDPPHRR-TS---KKCSSIG
>Equus_przewalskii-----MYRFRQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Manis_javanica-----MCRFRSQLFTGISAAATHFYP---RRCSPLLAEDGFSRPPHRR-TS---KKCSSIG
>Loxodonta_africana-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLVEDSPLSRPPHRR-TS---KKCSSIG
>Marmota_monax-----MYRFRSQLFTGISAAATAHFYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Tupaia_chinensis-----MYRFRSQLFTGISAAATAHSYP---RRFSPLLLAEDSPLSRPPHRR-TS---KKCSSIG
>Trichechus_manatus_latirostr-----MYRFRSQTFTGISAAATAHSYP---RRFSPLLLVEDSLNLRPHRR-TS---KKCSSIG
>Anolis_carolinensis-----MYRFRSRASTGISAAATAPLIIARLPQSHPLPRSGK---PASQRRFYSKKKRSCSSIG
>Struthio_camelus_australis-----MHFRSRAFTGISAFATDSS-FACFRGSPPLPRSGK---SASQRR-CSKKRSCSSIG
>Chelonis_mydas-----MHFRCSRAFTGISATATLS-FACLRGSPPLPRSGK---SAPQRR-CSKKRSCSSIG
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>Gallus_gallus	-----MRLRSRAFTGISATIASSSFACLRGSPPLPRPEKS-----ASGRRW-MKXKSCSSIG
>Xenopus_laevis	-----MYRLHSQAFTGVSVTS-----T-FRHYPPIPIED-----SKLIPERRF-----SKKGCSSIG
>Apteryx_australis_mantelli	-----MHLFRSRAFTGISAFATDSSFACFRGSPPLPRSGKS-----ASGRRC-SKKKSCSSIG
>Canis_lupus_familiaris	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Hymobius_chinensis	-----MHLFRSQALTGVSSRC-----PPIHTAPLPLGD-----LHLIPERRF-----SKKGCSSIG
>Lipotes_vexillifer	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLVENSPLSRPPHRRF-----SKKGCSSIG
>Calidris_pugnax	-----MHLRSRAFTGISAFAGSSSACFRGSPPLPRPEKS-----ASLTHW-MKXKSCSSIG
>Rousettus_aegyptiacus	-----MCRFRSQFLTGISAAAARSH-----PRRSSPLSLATAESPLSRPPHRRF-----SKKGCSSIG
>Desmodus_novemcinctus	-----MCRFRSQFLTGISATATHSY-----PRRFSPLLLVEDSPLSRPPHRRF-----SKKGCSSIG
>Alligator_mississippiensis	-----MHLFRSRASTGISAAS-ASSIACRRGSPPLPRPTKP-----AAHGRW-SKKKSCSSIG
>Quouius_canorus	-----MHLRSRASTGISAFAGSSSACFRGSPPLPRPGKS-----TSQKRW-MKXKSCSSIG
>Sarcophilus_harrisii	-----MYFRRSQFLTGISAAAIAHSS-----PRRFSPLLLAEDLSLQPPHRRF-----SKKGCSSIG
>Galeopterus_variegatus	-----MCRDWLVRVVRVPTGDDRRRSCYLRRGLDRPALAPALENMVFRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Monodelphis_domestica	-----MYFRRSQFLTGISAAAIAVSS-----PRRFSPLLLAEDLSLQPPHRRF-----SKKGCSSIG
>Falco_peregrinus	-----MHLRSRASTGISAFAGSSSACFRGSPPLPRPGKS-----ASGRRW-SKKKSCSSIG
>Sorex_araneus	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Ochotona_princeps	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Elephantulus_edwardii	-----MHLFRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSLQPPHRRF-----SKKGCSSIG
>Junco_hyemalis	-----MHLRSRASTGISAFAGSPSACRQSPPLPRPEKS-----ASGRRW-MKXKSCSSIG
>Ceratotherium_simum_simum	-----MHLRSRASTGISAFAGSSSACFRGSPPLPRPEKS-----ASGRRW-SKKKSCSSIG
NSPAMKNSGCEGYWLGSRVVRVPTGDDRRRSCYLRRGLDRPALAPALKXNMVFRQLQLFTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG	
>Picooides_pubescent	-----MHLRSRASTGISAFAGLSSVCFRGSPPLPRTPGKS-----TSGRRW-SKKKSCSSIG
>Otolemur_garnettii	-----MYFRRSQFLTGISATATAHSY-----PRRFSPLLLTEDSPLSRPPHRRF-----SKKGCSSIG
>Melopittacus_undulatus	-----MHLRSRASTGISAFAGSSSACFRGSPPLPRTPAKS-----TSGRRW-SKKKSCSSIG
>Marmota_monax	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Tupaia_chinensis	-----MYFRRSQFLTGISAAATAHSY-----PRRFSPLLLAEDSPLSRPPHRRF-----SKKGCSSIG
>Takydromus_sexlineatus	-----MYFRSRASTGISAAATALPIACFPGSNPLRSQKP-----ASGRFYNMKXKSCSSIG
>Struthio_camelus_australis	-----MHLFRSRAFTGISAFATDSSFACFRGSPPLPRSGKS-----ASGRRC-SKKKSCSSIG
>Trachemys_scripta	-----MHLFRCSRAFTGISATATDSSFACLRGSPPLPRSGKS-----APGRRC-SKKKSCSSIG

HS0021.2 ENSDARG00000036811 ifrd2

>Denio_rerio
NVEGSAATCTLLRPKHFKHILPSQPGIRHRLPGDNHR
>Acipenser_sinensis
WVEFTRATCSQIG--LLQACLSQPRIRYILPGDNHR
>Menidia_menidia
NVDLATVACSELRPKHFEKYLPSQPGVRYRLPGDNHR
>Oryzias_latipes
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>Trachinotus_blochi
NVDFATAACSKLRPHFKHYLSQPGSRYRLPGDNHR
>Pogoncentrus_nattereri
WVESAAATCTLLRPKHFEKSLPSQPGIRYRLPGDKHR
>Oreochromis_niloticus
NVDLATTACSKLRPHKFEKSLPSHPSIRYRLPGDNHR
>Alopias_alosae
WVESAAATCTIPRPKLSEKYLSSQPGIRYRLPGDNHR
>Oxyrinodon_variegatus
NVDLATAACSKLRPHKFEKYLPSQPGVRYRLPGDNHR
>Esox_lucius
WVEFATATCSLLLPKHFKYCIQSQPGIRYRLPGDNHR
>Gadus_morhua
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>Acanthopagrus_haeta
WVLSSETAACSKLRPHKPRISLSQPGIRYRLPGDNHR
>Pleuroglossus_altivelis
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>Sclerogobius_ferrousus
WVEFAATATLLRPKHFEKYLPSQPGIRYRLPGDNHR
>Lateolabrax_japonicus
NVDFATTSCSELRPKHFKDILLPSQPGIRFRLPGDTHR
>Trematomus_bernacchi
NVDLATTACSKLRPHKFKYFISQPGIRYRLPGDNHR
>Oxyglossus_semihaevis
NVDFVTAACSKLRPKLSEKISLSQPGIRYRLPGDNHR
>Salmo_gairdneri
WVEFETVWKSLLCPKHFEKYLPSQPGIRYRLPGDNHR
>Lepisosteus_oculatus
NVDLGAAAGTLLRPKRSEKYLPSQPGIRYRLPGDNHR
>Ictalurus_punctatus
WVESAAATCTLLRPKHFKYLSQPGIRYRLPGDKHR
>Takifugu_rubripes
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>Drosophila_melanogaster
MSKYDSKYLEEKLEKLEOTETYSVYVDESOGGGAFFSAIVSPAFS-GKLLGRHRLVNSTLAEEKLTHAFSQKSYTPEQWEKVKAAQ-----
>Talitrus_saltator
MSYTAETIKAKLEKELDSTHYSVVDESOGGGAFFSAIVSSAFQ-GKPLLGRHRLVNSTLAEEKLTHAFSMKTYTPEQWEQOGSKQD-
>Meinertellus_cundinamarcensis
-MVFTEEDYIREKLVELEASHVVEYVDESOGGGAFFNVLVSLFE-GKPLLGRHRLVNSTLEELKTHAFSQKTLTPEQWEKQKSS-----
>Purpurostomus_xanthurus
-MSYADYIKSKLLEKLEAYVVEYVDESOGGGAFFSVIVSDKF-GKPLLGRHRLVNSTLEELKTHAFSQKTLTPEQWEKQKSS-----
>Leptinotarsa_decemlineata
-MTYTEEHLRMLIKLELASHVVEYVDESOGGGAFFSOVIVSEVFK-GKPLLGRHRLVNSVLEELKTHAFSQKTYTPEQWEQKQ-----
>Farfantepenaeus_aztecus
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>Meganyctiphanes_norvegica
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>Asyrtosiphon_pisum
-MTINELLKSKLTVALDASYSVNDOSOGGGAFFSVVVSDFN-GKLLGRHRLVNSVLAEEKLTHAFSQKTLTPEQWNLNKV-----
>Gnaspis_sp._G1
-MPTYAEHIRMLITELKAHVEYVDESOGGGAFFSAIVSEDFK-GKPLLGRHRLVNSVLAEEKLTHAFSQKTLTPEQWEKEQS-----
>Triodia_sylvina
-MVFTEEYIKELTKELDAHNSVVEYVDESOGGGAFFSVVVSDFN-GKPLLARHRLVNSVLEELKTHAFSQKTYTPEQWEKQNTAVNE
>Mantis religiosa
-MPLTEEYIKNMLMELEATHVEYVDESOGGGAFFNVLVSDKFE-GKPLLGRHRLVNSVLEELKTHAFSQKTLTPEQWEKQKAA-----
>Boreus_hymelii
-MVFTEEYIKELIKELMAHVEYVDOSOGGGAFFSAIVASIFQ-GKLLARHRLVNSVLAEEKLTHAFSQKTLTPEQWEKQKNTS-----
>Corydalus_cornutus
-MSVTEEQIKQKLLRELDAHNVVDESOGGGAFFSVIVSDKFV-GKSLGRHRLVNTLQELKNTHAFSQKTLTPEQWEKQKSSN-----
>Gonwentzia_pisciformis
-MVFTEEYIKELTKELDAHNSVVEYVDESOGGGAFFSAIVSDKFN-GKPLLGRHRLVNSVLEELKTHAFSQKTLTPEQWEKQKQSH-----
>Cordulegaster_boltonii
MSVYTTNYIKELRTGVEATHVEYVDOSOGGGAFFSVLVSPKFE-GLPLLGRHRLVNSVLAEEKLTHAFSQKTLTPEQWEKQKNDAN
>Teleogryllus_commodus
-MVFTEEYIKNMLMELEATHVEYVDOSOGGGAFFNAIVSSKFE-GKPLLGRHRLVNSTLEELKTHAFSQKTLTPEQWEKQKQSG-----
>Gasterosteus_aculeatus
-----MLQNTSKIKSRROYKLTILQINSTLEELKTHALTLKTLTPHWEKTRQK-----
>Menopon_palline
-MPTYKDYIGSKLEKLOPVYIVVEDESOGGGAFFSAIVSPKFQ-GKPLLGRHRLVNSTLEELKTHAFSQKTLTPEQWEKQKSS-----
>Perla_marginata
-MPTYENDIKTKLLEKLEATHVVDOSOGGGAFFSVIVSEKFE-GKPLLARHRLVNSVLEELKTHAFSQKTLTPEQWEKQKSSA-----
>Liposcelis_bostrychophila
-MVFTEEYIKNMLMELEADYVVEYVDESOGGGAFFSAIVSPKFE-GKPLLGRHRLVNSVLEELKTHAFSQKTLTPEQWEKQKSS-----
>Ctenocephalides_felis
-MSYTKQYLEEKLTQLQAEHVEYVDLSDOGGGAFFSAIVSSVFE-GKPLLARHRLVNSTLAEEKLTHAFSQKTLTPEQWEKQKQD-----
>Thrips_palmi
-MSLVQVHVKMLSKELQPHVHVEYVDESOGGGAFFNVIVSDKF-GKPLLGRHRLVNSTLEELKYTHAFSQKTLTPEQWEKQKSSQ-----
>Hydroptila_sp._AD-2013
-MVSSEEEIRSKLLTQLEAHVEYVDESOGGGAFFSAIVSDKFI-GKPLLARHRLVNSVLAEEKLTHAFSQKTLTPEQWEKQKSKAL-----
>Thermobia_domestica
-MVFTEEYIKNMLMELEATHVEYVDESOGGGAFFNAIVSPKFE-GKPLLGRHRLVNSVLEELKTHAFSQKTLTPEQWEKQKQGT-----

>Homo_sapiens
-MLKNSGII---GRQ-----SONGSNLRREGCSRRKCI F IHHHT
>Xenopus_laevi s
-M I N S F K S L N V G P T S S ---RQRF I R Q K R T D P T W R K C W R R K T I F I H H H T
>Ursus_americanus
-MLKNSGII---QPO-----SONGSNLRREGCSRRKCI F IHHHT
>Hymobius_retar datus
-M V N K S L R S P S E -P S T A A R P P P R A L Q R P Q A G O R R R K C W R K T K I F I H H H T
>Tursiops_truncatus
-MLKNSGII---GRQ-----SONGSNLRREGCSRRKCI F IHHHT
>Raoulttus_egyptiacus
-MLKNSGII---GRQ-----SONGSRLRREGCSRRKCI F IHHHT
>Dasypus_noveincinctus
MLKNSGII---GRQ-----SUSGSNLRREGCSRRKCI F IHHHT
>Alligator_mississippiensis
MQAKNSGII-----GQNRSS-GEERWPRRKSRRKCI F IHHHT
>Sarcophilus_harrisii
MMMKNTWII---GRQ-----SONGSRDPRREGCSRRKS I F IHHHT
>Galeopterus_variegatus
-MLKNSGII---GRQ-----SONGSNLRREGCSRRKCI F IHHHT
>Haliaeetus_leucoccephalus
MPSRMNSG-----GQRSGNSRGEGPPPRKASRRKCVLVDHHT
>Oryctolagus_cuniculus
-----MANNVCVSPQCSRRKCI F IHHHT
>Egystia_hippohaecolus
-MLKNSGII---GRQ-----SONNSNLRREGCSRRKCI F IHHHT
>Parus_major
-----GQRPERRGRGEGPPPRKASRRKCVLADHHT
MRTTNRG
>Ceratotherium_simum_simum
-MLKNSGII---QPO-----SONGSNLRREGCSRRKCI F IHHHT
>Manis_javanica
-MLKNSGII---GRQ-----SONGSNMPREGCSRRKCI F IHHHT
>Loxodonta_africana
-MLKNSGII---GRQ-----SUSGSNLRREGCSRRKCI F IHHHT
>Chinchilla_lanigera
-MLKNSGII---QPO-----SUSGSNLRREGCSRRKCI F IHHHT
>Trichechus_manatus_latirostr
-MLKNNQWII---GRQ-----SONGSNLRREGCSRRKCI F IHHHT
>Trachemys_scripta
MFAARKSR-----RQRGSRGDEGQPPRRKSRRKCVF IHHHT

>Denio_rerio
MVNNISQPSLQKHTITLNDKQPSKRNKKRSYWDKISPTTHGT
>Aeta_calva
MVNNISYHGSTPEKNTANPQSGSKRNKKRRCWGTPSPPTHROT
>Kaupichthys_hyoproroides
MVNNISYHGSQKYIHTPTPTKRNKKRRCWDKLSPTAHRGT
>Gryllus_melastigma
MVNNISYQGFLKYLHS-SSQSGSRANKRKNYWDKLSPTHFOT-
>Pygocentrus_nattereri
MVNNISYQGPQKYIHTPSPRETAKRNKKRNFWDKISPTTHNT
>Haplochromis_burtoni
MVNNISYHFLKYLHS-NSQSGSRANKRKNYWDKLSPTNCGT-
>Aloosa_alosa
MVNNISYHGSQKYIHTPMPQSGSKRNKKRNWDLSPTTHROT
>Austrofundulus_limasa
MVNNISDHFLKYLHS-ASSQSGSRANKRKNYWDKLSPTLFOT-
>Esox_lucius
MVNNISYHGSQKYIHTPMPROTAKRNKKRRCWDKLSPTPNCOT
>Aptereronotus_leptorhynchus
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>Scleropages_formosus
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>Motothemis_coriacea
MVNNISYHFLKYLHS-SSQSGSRRTNKRKRDWDKLSPTNWT-
>Oncorhynchus_mykiss
MVNNISYHGSQKYIHTPMPQSGSKRNKKRRCWDKLSPTNCGT
>Lepisosteus_oculatus
MVNNISYHSTPEKNSPMPQSGSKRNKKRRLVSDTPTPPNHRGT
>Trichomycterus_areolatus
MVNNISYQGSQKYIHTSPSLQSGSKRNKKRKNYWDLSPTTHNT

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>Denio_rerio
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>Acipenser_sinensis
MGPPGSRNCVTFERMDOFQILVSL
>Amlia_calva
MGPPGSKPRVSVFERMEDFGIFVSL
>Ohamma_argus
MGPPGDRTOHMTERTEDSSNIVOL
>Podocoryna_carnea
MGPPGSRNCVTFERMEDFGILVSL
>Mendia_mendia
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>Oryzias_latipes
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>Astyarex_mexicanus
MGPPRGSKLLTERRGMSIFVHL
>Haplochromis_burtoni
MGPPGDRKLHMTERTEDSNIVOL
>Allosa_alosa
MGPPRGSRLLSPERTEDFGIFVTL
>Kryptolebias_marmoratus
MGPPGDRTRHMTKRTEDSRNIVOL
>Esoc_lucius
MGPPGDKPRVVSERTEDFGIFVSL
>Plecoglossus_altivelis
MGPPGDKPRVSTERTEDGIFVSL
>Trematomus_bernachii
MGPPGDRTOHMTERTEDFGNIVOL
>Oymoglossus_semilaevis
MGPPGDRRRHLLTERTEDSNIVOL
>Salmo_salar
MGPPGDMPRVVSERTEDGIFVSL
>Lepisosteus_oculatus
MGPPGSKPRVSVFERMEDFGIFVSL
>Ictalurus_punctatus
MGPPRGSKLLSERKLNHIFVSL
>Takifugu_rubripes
MGPPDRTOHMTERTEDGIFVSL

>Homo_sapiens
 M0F0-M0GVSVLLHT
 >Mustela_putorius_furo
 M0F0-M0GVSVLLHT
 >Tursiops_truncatus
 M0F0-M0GVSVLLHT
 >Pteropus_vampyrus
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 >Dasypus_noveboracensis
 M0F0-M0GVSVLLHT
 >Sarcophilus_harrisii
 M0K0-M0GVSVLLHT
 >Galeopterus_variegatus
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 >Monodelphis_domestica
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 >Erinaceus_europaeus
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 >Oryctolagus_cuniculus
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 >Elephantulus_edwardii
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 >Phalacrocorax_carbo
 ---M0-M0GVSVLLHT
 >Equus_asinus
 M0K0-M0GVSVLLHT
 >Manis_javanica
 M0F0-M0GVSVLLHT
 >Loxodonta_africana
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 >Didymys_ordini
 M0F0-M0GVSVLLHT
 >Oryzomys_sfer_sfer
 M0F0FMTGVSVLLHT

>Gallus_gallus
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>Anser_cynoedes
NONACASFLLYT
>Apteryx_australis_mantelli
NONACASFLLYT
>Buceros_rhinoceros_silvestri
NONACASFLLYT
>Caprimulgus_carolinensis
NONACASFLLYT
>Gariusa_cristata
NONACASFLLYT
>Gallidris_pugnax
NONACASFLLYT
>Pterocles_gutturalis
NONACASFLLYT
>Colius_striatus
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>Columba_livida
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>Leptosomus_discolor
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>Alligator_sinensis
NONACASFLLYT
>Aquila_chrysaetos_canadensis
NONACASFLLYT
>Gavia_stellata
NONACASFLLYT
>Balearica_regulorum_gibberic
NONACASFLLYT
>Tauraco_erythrophus
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>Opisthocomus_hoazin
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>Taeniopygia_guttata
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>Pelecanus_crispus
NONACASFLLYT
>Picaoides_pubescens
NONACASFLLYT
>Fulmarus_glaucialis
NONACASFLLYT
>Melopittacus_undulatus
NONACASFLLYT
>Aptenodytes_forsteri
NONACASFLLYT
>Tyto_alba
NONACASFLLYT
>Struthio_camelus_australis
NONACASFLLYT
>Chrysemys_picta
NONACASFLLYT
>Tinamus_guttatus
NONACASFLLYT

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>Gallus_gallus
-----MAGOLLILFLDPSNTTFP-
>Anser_cygnoides
WVKPVCGPAMAGOLL-LFLDPSDITFS-
>Apteryx_australis_mantelli
-----WVGOLLILFLDPSNKAFS-
>Buercus_thimoceros_silvestri
-----MAGOLFSFLDPSNTTFS-
>Caprimulgus_carolinensis
-----MAGOLLTLVFDPSTTTSS-
>Carima_cristata
-----MAGOLLRLFLDPSDITTFs
>Calidris_pugnax
-----MAGOLLTLFLDPSNTTFS-
>Pterocles_gutturalis
-----MAGOLLTLFRGSPDITFS-
>Colius_striatus
-----MAGOLLTLFRGSPDITVS-
>Columba_livis
-----MAGOLLTLFGPSDITFS-
>Leptosomus_discolor
-----MTGOLLTLFLDPSDITFS-
>Alligator_mississippiensis
-----WVGORLLFLDPSNMIVS-
>Quouius_canorus
-----MAGOLLTLFLDPSNTMFS-
>Falco_cherrug
-----MAGOLLTLFLDPSNTTFS-
>Gavia_stellata
-----MAGOLLSLFLDPSDITFS-
>Chlamydotis_macqueni
-----MAGOLLTLFLDPSDITFS-
>Tauraco_erythrophus
-----MAGOLLTLFLDPSDITFS-
>Opisthocomus_hoazin
-----MAGRLTLFLDPSNATFS-
>Corvus_cornix_cornix
-----MAGOLLSLFLDPSNTTFS-
>Pelecanus_crispus
-----MAGOLLTLFLDPSNTTFS-
>Picoides_pubescens
-----MAEOLLSNLFDPSTITFS-
>Fulmarus_glaucialis
-----MAGOLLTLFLDPSDITFS-
>Nestor_notabilis
-----MAGOLLTLFLDPSERFFS-
>Aptenodytes_forsteri
-----MAGOLLTLFLDPSDITLS-
>Anolis_carolinensis
-----WVGRLLLFLYDPSNMKIVS-
>Tyto_alba
-----MAGOLLTLFLDPSDITFS-
>Struthio_camelus_australis
-----WVGOLLILFLDPSNTTFS-
>Chelonia_mydas
-----WVGOLSLFLDPSNMILAS-
>Tinamus_guttatus
-----WVGOLLILFLDPSNTTFS-
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>Denio_rerio	-----MRTLIGPAGNIRGSDRFMLHLEL
>Anguilla_anguilla	-----MRTKTGKVVNFRGSDRFMLHLEL
>Podocoryna_carnea	-----MITQAGTVLNRGSDRFMLHLEL
>Oryzias_latipes	-----MKAPLGTVVNIRRSORFILLQLEL
>Pygocentrus_nattereri	-----MTALIGSVVNIIRRSORFMLHLEL
>Haplochromis_burtoni	-----MKAPLGTVVNIRRSORFILLHLEL
>Clupea_harengus	-----MRTKICTVNRGSDRYMLHLSL
>Kryptolebias_marmoratus	-----MRTSRPAVNLRSRDFMLHLLL
>Esox_lucius	-----MRTQISTVVHLRRSDFMLHVL
>Acanthopagrus_hasta	-----MRTLIGSVVNIIRRSORFMLHLEL
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>Apterionotus_leptorhynchus	-----MTTLIGSVVNIIRRSORFMLHLEL
>Scleropages_formosus	-----MRTLIGTVLNRGSDRFILLHLEL
>Notothenia_coriiceps	-----MKAPLGTVVNIRRSORFILLHLEL
>Salvelinus_alpinus	-----MKAPLGTVVNIRRSORFILLHLEL
>Lepisosteus_oculatus	-----MKQLETVNLRSDRFMLHLEF
>Takifugu_rubripes	-----MRAQTGTVVNFRGSDRFMLHLEI
	-----MKALLGTVVNIRRSORFILLHLEL

>Denio_rerio
-----MELY-----TRAVGSGVLTV--IEA-LRSF--TELFITQPGV-ATLTQLADTDLRLTD-----GD-DRYFKARELWESSGAVIMAVRRPG
>Oxyacanthus_purpuratus
-----MSLVPEMLGSNIGMLTGGTLA-GIITTYCN.PRRWFQGHVSKNDIELLDAPLQRL-----PAEGSVWFGQQLMKDGTAVVMAIRRRPG
>Scapharca_broughtonii
-----MALIS-----PTLLGIAGLTA--GAAILLNL--PASWLFSTKK--STLSYLESAKLOTLH-----SSNNRNFSARELWOKDPAVIMAVRRPG
>Micropterus_dolomieu
WTFLEGEGLYNN-----WY-GALAFVATLMVVVALAN-TDLFLTKSAP--ASLEELGATDLOTTT-----GD-GKTVKGQLWERSGAVILAVRRPG
>Rhodactis_indosinensis
-----MA-----WFLGAGGAVA--IAG-IYLA-HNDWYNSNSAR-PDLAYLSSIKLKALN-----GT-NKDVWASELWRESSGAVIMVVRRRPG
>Strongylocentrotus_purpuratus
-----MALLNSGAAAAAY--GG-LLVAN-MDFWLPFRGGAATTEAYLAGAVLQLLGETKLGAQLSLVDEAVRTFKAKOLWKTGAVILAVRRPG
>Meganyctiphanes_norvegica
-----MLLDGGLSIMALSTMLPNWPLVTGALT--GFVAYCN--PAYWLNAPQK--ATTEYLSGAPLMKLD-----GS-GGQILSNELWOKNGALVMAVRRPG
>Perna_viridis
-----WIFS-----KALLGVAGFTA--GAAILLNL--PTRFFWASEX--ATLSYLTTAKLOTID-----EA-KKNFSASQLWKNNGIWMVVRRRPG
>Octopus_bimaculoides
-----MAEK-ATLAYLGATLKTGL-----DD-PKEFGAGELWKNNGAIWMVVRRRPG
>Sacostrea_glomerata
-----MIS-----PVLVGFAGLTA--GIAYIGNL--PVTWTTVEK--ATLKYLEKGLOTIE-----AS-PRIFSVQOLWKNHGVIIMAVRRPG
>Pecten_maximus
-----MGVT-----KALLGMAGVTA--MAATLON-PVSWFWMSSEK--ATLNYLENARVOTLD-----SQ-PKNITASELWKNNGVIMAVRRPG
>Anoplopoma_fimbria
-----M-----MEIIAAGGFJ--TDV-MNFF--TDKFLTPPLK--ATLKHLEAEALTK-----GE-TRTLKGRSLWERSGAVIMAVRRPG
>Montastraea_faveolata
-----MA-----WFLGAGGVA--LTG-VIIA-HNDWYKNSPR-PDLAYLSSIKLKALD-----GT-SKEVWASELWKSAGAVIMVVRRRPG
>Sepia_officinalis
-----MAEK-ATVGYLAGATLKTGL-----DD-PKEFGAELWKSAGAVIMVVRRRPG
>Sepioloidea_lineolata
-----MAEK-ATVGYLAGATLKTGL-----DD-PKEFGAELWKNKTGAVIMVVRRRPG
>Doryteuthis_pealeii
-----MAEK-ATVGYLAGATLKTGL-----DD-PKEFGAELWKNKTGAVIMVVRRRPG

>Homo_sapiens	-----MERNNRYOPLOKHAKL-----
>Chama_argus	MLREFYTTIRPALDELMEALINGGGVGRGRKNHNPLOKHTKVERPLAL-----
>Millepora_albicornis	-----MERKNWYQLOKHTKI-----
>Latrodectus_hesperus	-----MERNNWYQLOKHTKL-----
>Hymobius_retardatus	MLREFITTRPALDELLKALN-----MERKNHYOPLOKHTEVHRPVTL-----
>Chironomus riparius	MLRDFYTTIRPALDELLKALN-----MERNNWYQLOKHKCKHRRHYEETASTNGKITTS

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>Chama_argus	-----MEDSFDCDQGELEPPDH
>Kaupichthys_hyoproroides	-----MEDCFDCDQGELEPPDH
>Anas_platyrhynchos	-----MDGSFDCDQGELEPPDH
>Microhyla_fissipes	-----MDASFDCDQGELEPPDH
>Chaetura_pelagica	-----MDGSFDCDQGELEPPDH
>Apteryx_australis_mantelli	-----MDGSFDCDQGELEPPDH
>Porichthys_notatus	-----MFWDIDL-----FSLFLRLSRNWDGSFDCDQGELEPPDH
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>Oryzias_latipes	-----MEDSFDCDQGELEPPDH
>Buceros_rhinoceros_silvestri	-----MDGSFDCDQGELEPPDH
>Caprimulgus_carolinensis	-----MDGSFDCDQGELEPPDH
>Trachinotus_blochii	-----MEDSFDCDQGELEPPDH
>Gariama_cristata	-----MDGSFDCDQGELEPPDH
>Canis_lupus_familiaris	-----MDGSFDCDQGELEPPDH
>Hymnibus_retardatus	-----MDGSFDCDQGELEPPDH
-----	-----MDGSFDCDQGELEPPDH
>Micropterus_floridanus	-----MEDSFDCDQGELEPPDH
>Tursiops_truncatus	-----MDGSFDCDQGELEPPDH
>Pygocentrus_nattereri	-----MDGSFDCDQGELEPPDH
>Charadrius_vociferus	-----MEDSFDCDQGELEPPDH
>Gallinorhynchus_millii	-----MDGSFDCDQGELEPPDH
>Rousettus_aegyptiacus	-----MDGSFDCDQGELEPPDH
-----MPLKYS-LD-----INFFLINVQDQLRE-----KINSQG-NGAQTASGLYRSKMEDSFDCDQGELEPPDH	
>Haplochromis_burtoni	-----MLYPSKMEDSFDCDQGELEPPDH
>Pterocles_gutturalis	-----MDGSFDCDQGELEPPDH
>Dasypus_noveboracensis	-----MDGSFDCDQGELEPPDH
>Clupea_harengus	-----MEDSFDCDQGELEPPDH
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>Colinus_striatus	-----MDGSFDCDQGELEPPDH
>Columba_livia	-----MDGSFDCDQGELEPPDH
>Leptosomus_discolor	-----MDGSFDCDQGELEPPDH
>Alligator_mississippiensis	-----MDGSFDCDQGELEPPDH
>Oculus_canorus	-----MDGSFDCDQGELEPPDH
>Kryptolebias_marmoratus	-----MEDSFDCDQGELEPPDH
>Sarcophilus_harrisii	-----MDGSFDCDQGELEPPDH
>Galeoceratus_variegatus	-----MDGSFDCDQGELEPPDH
>Monodelphis_domestica	-----MDGSFDCDQGELEPPDH
>Esox_lucius	-----MEDSFDCDQGELEPPDH
>Haliaeetus_albicilla	-----MDGSFDCDQGELEPPDH
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>Balearica_regularis_gibberis	-----MDGSFDCDQGELEPPDH
>Apterodactylus_leptorhynchus	-----MEDSFDCDQGELEPPDH
>Condylura_cristata	-----MDGSFDCDQGELEPPDH
>Oryctolagus_cuniculus	-----MDGSFDCDQGELEPPDH
>Elephantulus_edwardii	-----MDGSFDCDQGELEPPDH
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>Tauraco_erythrophys	-----MDGSFDCDQGELEPPDH
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>Sclerophagus_ferrous	-----MEDSFDCDQGELEPPDH
>Lepidodactylus_coronatus	-----MDGSFDCDQGELEPPDH
>Egretta_garzetta	-----MDGSFDCDQGELEPPDH
>Mothia_coriacea	-----MEDSFDCDQGELEPPDH
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-----MAATA-KREPRRRRRQHSRRPEPT-----LGAV-----R-----GPSR-RSPVSVQVLYGSKMDGSFDCDQGELEPPDH	
>Manis_javanica	-----MDGSFDCDQGELEPPDH
>Picooides_pubescens	-----MDGSFDCDQGELEPPDH
>Oryzomys_somaliensis	-----MEDSFDCDQGELEPPDH
>Actus_nancyensis	-----MAATA-KREPRRRRRQHSRRPEPT-----LGAV-----GLR-----TLNMR-RSPVSVQVLYGSKMDGSFDCDQGELEPPDH
-----MAATA-KREPRRRRRQHSRRPEPT-----LGAV-----GLR-----TLNMR-RSPVSVQVLYGSKMDGSFDCDQGELEPPDH	
>Loxodonta_africana	-----MDGSFDCDQGELEPPDH
>Fulmarus_glaucialis	-----MDGSFDCDQGELEPPDH
>Melospiza_undulatus	-----MDGSFDCDQGELEPPDH
>Mus_musculus	-----MAATA-KREPRRRRRQHSRRPEPT-----LRAVR-----GPC-----TLNMR-RSPVSVQVLYGSKMDGSFDCDQGELEPPDH
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>Oncomelasma_kiutich	-----MEDSFDCDQGELEPPDH
>Tupaia_chinensis	-----MDGSFDCDQGELEPPDH
>Lepidosteus_oculatus	-----MEDSFDCDQGELEPPDH
>Ictalurus_punctatus	-----MEDSFDCDQGELEPPDH
>Trichostema_mantatus_latirostris	-----MEDSFDCDQGELEPPDH
>Pygoscelis_adeliae	-----MDGSFDCDQGELEPPDH
>Squalus_acanthias	-----MDGSFDCDQGELEPPDH
>Hypsiglena_sp._JMS-2014	-----MDGSFDCDQGELEPPDH
>Tyto_alba	-----MDGSFDCDQGELEPPDH
>Struthio_camelus_australis	-----MDGSFDCDQGELEPPDH
>Pelodiscus_sinensis	-----MDGSFDCDQGELEPPDH
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>Takifugu_rubripes	-----MEDSFDCDQGELEPPDH
>Tinamus_guttatus	-----MDGSFDCDQGELEPPDH
>Galypte_anna	-----MDGSFDCDQGELEPPDH
>Apaloderma_vittatum	-----MDGSFDCDQGELEPPDH
>Oryzomys_afer_afer	-----MDGSFDCDQGELEPPDH

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>Homo_sapiens	MDGSFDCDGGELLEPPDH
>Chama_argus	MDGSFDCDGGELLEPPDH
>Kaupichthys_hyoproroides	MDGSFDCDGGELLEPPDH
>Anas_platyrhynchos	MDGSFDCDGGELLEPPDH
>Xenopus_laevis	MDGSFDCDGGELLEPPDH
>Chaetura_pelagica	MDGSFDCDGGELLEPPDH
>Apteryx_australis_mantelli	MDGSFDCDGGELLEPPDH
>Porichthys_notatus	MDGSFDCDGGELLEPPDH
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>Oryzias_latipes	MDGSFDCDGGELLEPPDH
>Buceros_rhinoceros_silvestri	MDGSFDCDGGELLEPPDH
>Caprimulgus_carolinensis	MDGSFDCDGGELLEPPDH
>Trachinotus_blochii	MDGSFDCDGGELLEPPDH
>Gariama_cristata	MDGSFDCDGGELLEPPDH
>Alliurapoda_melanoleuca	MDGSFDCDGGELLEPPDH
>Hymobius_retardatus	MDGSFDCDGGELLEPPDH
>Micropterus_floridanus	MDGSFDCDGGELLEPPDH
>Tursiops_truncatus	MDGSFDCDGGELLEPPDH
>Pygocentrus_nattereri	MDGSFDCDGGELLEPPDH
>Charadrius_vociferus	MDGSFDCDGGELLEPPDH
>Callorhynchus_millii	MDGSFDCDGGELLEPPDH
>Miniopterus_natalensis	MDGSFDCDGGELLEPPDH
>Haplochromis_burtoni	MDGSFDCDGGELLEPPDH
>Pterocles_gutturalis	MDGSFDCDGGELLEPPDH
-----MLYPSKMDGSFDCDGGELLEPPDH	
>Dasypus_noveboracensis	MDGSFDCDGGELLEPPDH
>Clupea_harengus	MDGSFDCDGGELLEPPDH
>Latimeria_chalumnae	MDGSFDCDGGELLEPPDH
>Colius_striatus	MDGSFDCDGGELLEPPDH
>Columba_livia	MDGSFDCDGGELLEPPDH
>Leptosomus_discolor	MDGSFDCDGGELLEPPDH
>Alligator_mississippiensis	MDGSFDCDGGELLEPPDH
>Coccyzus_corymbosus	MDGSFDCDGGELLEPPDH
>Sinuocyclocheilus_rhinocerosus	MDGSFDCDGGELLEPPDH
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>Poecilia_formosa	MDGSFDCDGGELLEPPDH
-----MTKSXTSHGNS-----TEYHRLYPSKMDGSFDCDGGELLEPPDH	
>Sarcophilus_harrisii	MDGSFDCDGGELLEPPDH
>Galeoceratus_variegatus	MDGSFDCDGGELLEPPDH
>Monodelphis_domestica	MDGSFDCDGGELLEPPDH
>Esox_lucius	MDGSFDCDGGELLEPPDH
>Halimaeetus_albicollis	MDGSFDCDGGELLEPPDH
>Gortynix_japonica	MDGSFDCDGGELLEPPDH
>Gavia_stellata	MDGSFDCDGGELLEPPDH
>Acanthopneuste_hasta	MDGSFDCDGGELLEPPDH
>Balearica_regularis_gibberis	MDGSFDCDGGELLEPPDH
>Apterodactylus_leptorhynchus	MDGSFDCDGGELLEPPDH
>Condylura_cristata	MDGSFDCDGGELLEPPDH
>Oryzotylagus_cuniculus	MDGSFDCDGGELLEPPDH
>Elephantulus_edwardsii	MDGSFDCDGGELLEPPDH
>Ornithorhynchus_anatinus	MDGSFDCDGGELLEPPDH
>Tauraco_erythrophys	MDGSFDCDGGELLEPPDH
>Opisthocomus_hoazin	MDGSFDCDGGELLEPPDH
>Sclerophagus_ferrous	MDGSFDCDGGELLEPPDH
>Manacus_vitellinus	MDGSFDCDGGELLEPPDH
>Egretta_garzetta	MDGSFDCDGGELLEPPDH
>Notonecta_coriacea	MDGSFDCDGGELLEPPDH
>Equus_asinus	MDGSFDCDGGELLEPPDH
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>Picooides_pubescens	MDGSFDCDGGELLEPPDH
>Platichthys_stellatus	MDGSFDCDGGELLEPPDH
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>Ictalurus_punctatus	MDGSFDCDGGELLEPPDH
>Trichechus_manatus_latirostris	MDGSFDCDGGELLEPPDH
>Aptenodytes_forsteri	MDGSFDCDGGELLEPPDH
>Squalus_acanthias	MDGSFDCDGGELLEPPDH
>Python_bivittatus	MDGSFDCDGGELLEPPDH
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>Tyto_alba	MDGSFDCDGGELLEPPDH
>Struthio_camelus_australis	MDGSFDCDGGELLEPPDH
>Oryzomys_pictus	MDGSFDCDGGELLEPPDH
>Takifugu_rubripes	MDGSFDCDGGELLEPPDH
>Timamus_mammillatus	MDGSFDCDGGELLEPPDH
>Gallus_gallus	MDGSFDCDGGELLEPPDH
>Apaloderma_vittatum	MDGSFDCDGGELLEPPDH
>Oryzomys_leucogaster	MDGSFDCDGGELLEPPDH

H50028.1 ENSGAL000000031448 MAPK6

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>Chama_argus	MDGSFDCDGGELLEPPDH
>Kaupichthys_hyoproroides	MDGSFDCDGGELLEPPDH
>Anas_platyrhynchos	MDGSFDCDGGELLEPPDH
>Xenopus_laevis	MDGSFDCDGGELLEPPDH
>Chaetura_pelagica	MDGSFDCDGGELLEPPDH
>Apteryx_australis_mantelli	MDGSFDCDGGELLEPPDH
>Porichthys_notatus	MDGSFDCDGGELLEPPDH
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>Buceros_rhinoceros_silvestri	MDGSFDCDGGELLEPPDH
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>Hymobius_retardatus	MDGSFDCDGGELLEPPDH
>Micropterus_floridanus	MDGSFDCDGGELLEPPDH
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>Pygocentrus_nattereri	MDGSFDCDGGELLEPPDH
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>Callorhynchus_millii	MDGSFDCDGGELLEPPDH
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>Apaloderma_vittatum	MDGSFDCDGGELLEPPDH
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>Anser_cygnoides
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>Channa_punctata	MHLVDVNDCCGSHASVFVITPLINTO.....
>Xenopus_tropicalis	MHLVDVNEHCGNHAPVFVNIPIWQRTPT.....
>Apteryx_australis_mantelli	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Menidia_menidia	MHLVDVNECCGSHASVFVITPFLINTQLDXN.....
>Porichthys_notatus	MHLVDVNECCGSHASVFVITSILINTO.....
>Oryzias_melastigma	MHLVDVNDCCGSHASVFVITPFLINTO.....
>Canis_lupus_familiaris	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Hymobius_retardatus	MHLVDVNEHCGSYLVLIPIWHRTP.....
>Micropterus_dolomieu	MHLVDVNDCCGSHASVFVITPLINTO.....
>Orcinus_orca	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Pygocentrus_nattereri	MHLVDVNECCGSHASVFVITV-LINTO.....
>Charadrius_vociferus	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Callorhynchus_millii	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Maylandia_zebra	MHLVDVNECCGSHASVFVITPFLINTO.....
>Desmopus_novemcinctus	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Alosa_alosa	MHLVDVNECCGSHASVFVITPLINTO.....
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>Esox_lucius	MHLVDVNECCG.....
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>Gadus_morhua	MHLVDVNECCG.....
>Acanthopobius_hasta	MHLVDVNDCCGSHASVFRTALINTO.....
>Chlamydotis_macqueenii	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Condyura_cristata	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Ornithorhynchus_anatinus	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Aotus_nancymaeae	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Leucoraja_erinacea	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Mesocricetus_aureatus	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Salmo_salar	MHLVDVNECCGSHASVFVITPMLINTO.....
>Tupaia_chinensis	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Trichechus_manatus_latirostr	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Squalus_acanthias	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
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>Chelonia_mydas	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Takifugu_rubripes	MHLVDVNDCCGSHASVFVITPLINTO.....
>Tinamus_guttatus	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Galypte_anna	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Apeloderma_vittatum	MHLVDVNEHCGNHAPVFVNIPIWHRTP.....
>Orycteropus_afer_afer	MGLMHLVDVNEHCGNHAPVFVNIPIWHRTP.....

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>Aelia_calva-----MHLDVONEHCGRHAPVFNI1QMLRTO-----
>Channa_punctata-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Anser_cygnoides-----MHLDVONEHCGRHAPVFNI1PMWRTL-----
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>Apteryx_australis_mantelli-----MGLWMHLDVONEHCGRHAPVFNI1PMWRTP-----
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>Porichthys_notatus-----MHLDVONECGGRHASVFNI1SLMTO-----
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>Buceros_rhinoceros_silvestri-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Caprimulgus_carolinensis-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Cariama_cristata-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
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>Orcinus_orca-----MGLWMHLDVONEHCGRHAPVFNI1PMWRTP-----
>Pygocentrus_nattereri-----MHLDVONECGGRHASVFNI1V-LMTO-----
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>Callorhynchus_millii-----MHLDVONEHCGRHAPVFNI1MPWRTP-----
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>Manis_javanica-----MGLWMHLDVONEHCGRHAPVFNI1PMWRTP-----
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>Trichomycterus_aeolatus-----MHLDVONDCGGRHASVFNI1PLMTO-----
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>Xenopus_tropicalis	MSWKCLSRLOGSP- SVNSVAAIPTP
>Apteryx_australis_mantelli	MSVTCMPRLGGSPSPSERPVAALWTP
>Menidia_menidia	MTVSGAVRLGGAPP- LEKSAAGVWTL
>Buceros_rhinoceros_silvestri	MSVTCMPRLGGSPSPSERPVAALWTP
>Caprimulgus_carolinensis	MSVTCMPRLGGSPSPSERPVAALWTP
>Gariama_cristata	MSVTCMPRLGGSPSPSERPVAALWTP
>Genia_lupus_familiaris	MSITQILRLCSPPLSENVPVINWTP
>Physester_catodon	MSITQILRLCSPPLSENVPVSDNWTP
>Charadrius_vociferus	MSVTCMPRLGGSPSPSERPVAALWTP
>Pteropus_vampyrus	MSITQILRLCSPPLSENVPVINWTP
>Pterocles_gutturalis	MSVTCMPRLGGSPSPSERPVAALWTP
>Dasypus_novemcinctus	MSITCOLLCSAPPSENVSILNWTP
>Latimeria_chalumnae	MSMKQIRSRHGGSP- LVNSVAAIWTP
>Colius_striatus	MSVTCMPRLGGSPSPSERPVAALWTP
>Columba_livia	MSVTCMPRLGGSPSPSERPVAALWTP
>Leptosomus_discolor	MSVTCMPRLGGSPSPSERPVAALWTP
>Alligator_mississippiensis	MSVTCMPRLGGSPSPSERPVAALWTP
>Pooecilia_mexicana	MSVTCMPRLGGSPSPSERPVAALWTP
>Sarcophilus_harrisii	MSLSRQLRDGAPL- LENSVAISWTL
>Monodelphis_domestica	MSLTCMSRLGSGAPLSENVPVINWTP
>Aquila_chrysaetos_canadensis	MSVTCMPRLGGSPSPSERPVAALWTP
>Gallus_gallus	MSVTCMPRLGGSPSPSERPVAALWTP
>Gavia_stellata	MSVTCMPRLGGASPPSGRPVAALWTP
>Mesitornis_unicolor	MSVTCMPRLGGSPSPSERPVAALWTP
>Condylura_cristata	MSITQILRLCSPPLSENVPVINWTP
>Oryctolagus_cuniculus	MSVTCMPRLCSPPLSENVSINWTP
>Ornithorhynchus_anatinus	MLTRSSESAAM- IF-RRRWQRYW-DETSIGYKGLMSVTCMLMGGSPPLSENVSINWTP
>Opisthocomus_hoazii	MSVTCMPRLGGSPSPSERPVAALWTP
>Plecoglossus_altivelis	MSVSRRLGGAPP- LENSVAAVRTP
>Zonotrichia_albicollis	MSVTCMPRLGGSPSPSERPVAALWTP
>Egretta_garzetta	MSVTCMPRLGGSPSPSERPVAALWTP
>Equus_asinus	MSITQILRLCSPPLSENVPVINWTP
>Manis_javanica	MSITQILRLCSPPLSENVPVINWTP
>Picoides_pubescens	MSVTCMPRLGGSPSPSERPVAALWTP
>Loxodonta_africana	MSVTWMSRLCSPPLSENVSINWTP
>Fulmarus glacialis	MSVTCMPRLGGSPSPSERPVAALWTP
>Meleptotus_undulatus	MSVTCMPRLGGSPSPSERPVAALWTP
>Cricetulus_griseus	MSAGFLMSITQILRLCSPPLSENVSINWTP
>Tupaia_chinensis	MSITQILRLRSSPLSENVPVINWTP
>Trichechus_manatus_latirostr	MSITQILRLCSPPLSENVSINWTP
>Aptenodytes_forsteri	MSVTCMPRLGGSPSPSERPVAALWTP
>Anolis_carolinensis	MSVTCMPRLGGSPSPSERPVAALWTP
>Struthio_camelus_australis	MSVTCMPRLGGSPSPSERPVAALWTP
>Trachemys_scripta	MSVTCMPRLGGSPSPSERPVAALWTP
>Timimus_guttatus	MSVTCMPRLGGSPSPSERPVAALWTP
>Galypte_anna	MSVTCMPRLGGSPSPSERPVAALWTP
>Apeloderma_vittatum	MSVTCMPRLGGSPSPSERPVAALWTP
>Orycteropus_afer_afer	MSISQILRLCSPLPENSINWTP

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>Gallus_gallus	-----MHLDVONEHCGRHAPVFNI1PMWRTL-----
>Acipenser_sinensis	-----MHLDVONEHCGRHASVFNI1PMLRTP-----
>Aelia_calva	-----MHLDVONEHCGRHAPVFNI1QMLRTO-----
>Ohamna_punctata	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Anser_cygnoides	-----MHLDVONEHCGRHAPVFNI1PMWRTL-----
>Xenopus_tropicalis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Chaetura_pelagica	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Apteryx_australis_mantelli	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Menidia_menidia	-----MHLDVONEHCGRHASVFNI1PFLMTOLDKN-----
>Porichthys_notatus	-----MHLDVONEHCGRHASVFNI1SLMTO-----
>Oryzias_latipes	-----MHLDVONDCGGRHASVFNI1PFLMTO-----
>Buceros_rhinoceros_silvestri	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Caprimulgus_carolinensis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Cariama_cristata	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Mustela_putorius_furo	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
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>Aebystoma_mexicanum	-----MHLDVONEHCGRHASVFNI1PMWRTP-----
>Micropterus_dolomieu	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Orcinus_orca	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Pygocentrus_nattereri	-----MHLDVONEHCGRHASVFNI1LWTO-----
>Callidris_pugnax	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Callorhynchus_millii	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Myotis_brandtii	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Haplochromis_burtoni	-----MHLDVONEHCGRHASVFNI1PFLMTO-----
>Pterocles_gutturalis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Dasypus_noveboracensis	-----MHLDVONDCGGRHASVFNI1PMWRTP-----
>Clupea_harengus	-----MHLDVONEHCGRHASVFNI1PLMTO-----
>Latimeria_chalumnae	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Columba_livia	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Merops_nubicus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Alligator_mississippiensis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Oculus_canorus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Sinocyclocheilus_grahami	-----MHLDVONECGG-----
>Austrofundulus_limaensis	-----MHLDVONDCGGRHASVFNI1PFLMTO-----
>Sarcophilus_harrisii	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Galeoceratus_variegatus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Monodelphis_domestica	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Esax_lucius	-----MHLDVONECGG-----
>Falco_cherrug	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Gadus_morhua	-----MHLDVONECGG-----
>Acanthopobius_hasta	-----MHLDVONDCGGRHASVFNI1ALMTO-----
>Chlamydotis_macquensis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Aptereronotus_leptorhynchus	-----MHLDVONDCGGRHASVFNI1AVLWTO-----
>Condyliura_cristata	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Ochotona_princeps	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Elephantulus_edwardii	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Ornithorhynchus_anatinus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Pleoglossus_altivelis	-----MHLDVONEHCGRHASVFNI1PMLMTO-----
>Sclerophagus_fermeus	-----MHLDVONECGGRHASVFNI1PTLWTL-----
>Manacus_vitellinus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Nipponia_nippon	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Lateolabrax_japonicus	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Sebastes_caurinus	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Ceratotherium_simum_simum	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Manis_javanica	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Ptilinopus_pudens	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Platichthys_stellatus	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Pan_peniculus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Loxodonta_africana	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Leucoraja_erinacea	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Mesocricetus_aureatus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Salmo_salar	-----MHLDVONECGGRHASVFNI1PMLMTO-----
>Tupaia_chinensis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Lepisosteus_oculatus	-----MHLDVONEHCGRHAPVFNI1PMLMTO-----
>Ictalurus_punctatus	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Trichechus_manatus_latirostris	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Aptenodytes_forsteri	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Squalus_acanthias	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Thammodon_sibiricus	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Tyto_alba	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Struthio_camelus_australis	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Chelonia_mydas	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Takifugu_rubripes	-----MHLDVONDCGGRHASVFNI1PLMTO-----
>Tinamus_guttatus	-----MHLDVONEHCGRHAPVFNI1SMWRTP-----
>Calypte_anna	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Apeloderma_vittatum	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----
>Oryzopsis_eperua	-----MHLDVONEHCGRHAPVFNI1PMWRTP-----

>Homo_sapiens	-----MSSLLLTQEDTKKLSKISSSY-----
>Acipenser_sinensis	-----MSSLLLTQEDTKKLSKISSSY-----
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>Kaupichthys_hyoproroides	-----MSSLLLTQEDTKKLSKISSSY-----
>Anser_cygnoides	-----MSSLLLTQEDTKKLSKISSSY-----
>Megophrys_sangzhiensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Chaetura_pelagica	-----MSSLLLTQEDTKKLSKISSSY-----
>Apteryx_australis_mantelli	-----MSSLLLTQEDTKKLSKISSSY-----
>Porichthys_notatus	-----MSSLLLTQEDTKKLSKISSSY-----
>Oryzias_latipes	-----MSSLLLTQEDTKKLSKISSSY-----
>Buceros_rhinoceros_silvestri	-----MSSLLLTQEDTKKLSKISSSY-----
>Caprimulgus_carolinensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Seriola quinqueradiata	-----MSSLLLTQEDTKKLSKISSSY-----
>Gariama_cristata	-----MSSLLLTQEDTKKLSKISSSY-----
>Mustela putorius_furo	-----MSSLLLTQEDTKKLSKISSSY-----
>Hymobius_chinensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Siniperca_chuatsi	-----MSSLLLTQEDTKKLSKISSSY-----
>Lipotes_vexillifer	-----MSSLLLTQEDTKKLSKISSSY-----
>Astyanax_mexicanus	-----MSSLLLTQEDTKKLSKISSSY-----
>Callidria_pugnax	-----MSSLLLTQEDTKKLSKISSSY-----
>Callorhynchus_milli	-----MSSLLLTQEDTKKLSKISSSY-----
>Miniopterus_natalensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Haplochromis_burtoni	-----MSSLLLTQEDTKKLSKISSSY-----
>Pterocles_gutturalis	-----MSSLLLTQEDTKKLSKISSSY-----
>Dasypus_noveboracensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Latimeria_chalumnae	-----MSSLLLTQEDTKKLSKISSSY-----
>Colius_striatus	-----MSSLLLTQEDTKKLSKISSSY-----
>Columba_livia	-----MSSLLLTQEDTKKLSKISSSY-----
>Merops_nubicus	-----MSSLLLTQEDTKKLSKISSSY-----
>Alligator_mississippiensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Cuculus_canorus	-----MSSLLLTQEDTKKLSKISSSY-----
>Ctenopharyngodon_idella	-----MSSLLLTQEDTKKLSKISSSY-----
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>Fundulus_heteroclitus	-----MSSLLLTQEDTKKLSKISSSY-----
>Sarcophilus_harrisii	-----MSSLLLTQEDTKKLSKISSSY-----
>Galeoscoptes_variatus	-----MSSLLLTQEDTKKLSKISSSY-----
>Monodelphis_domestica	-----MSSLLLTQEDTKKLSKISSSY-----
>Eoosoma_lucius	-----MSSLLLTQEDTKKLSKISSSY-----
>Aquila_chrysaetos_canadensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Gallus_gallus	-----MSSLLLTQEDTKKLSKISSSY-----
>Savia_stellata	-----MSSLLLTQEDTKKLSKISSSY-----
>Chanos_chanos	-----MSSLLLTQEDTKKLSKISSSY-----
>Chlamydotis_macquensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Apterodactylus_leptorhynchus	-----MSSLLLTQEDTKKLSKISSSY-----
>Condylura_cristata	-----MSSLLLTQEDTKKLSKISSSY-----
>Oryzias_latipes	-----MSSLLLTQEDTKKLSKISSSY-----
>Elephantulus_edwardsii	-----MSSLLLTQEDTKKLSKISSSY-----
>Ornithorhynchus_anatinus	-----MSSLLLTQEDTKKLSKISSSY-----
>Tauraco_erythrophthalmus	-----MSSLLLTQEDTKKLSKISSSY-----
>Opisthocomus_hoazin	-----MSSLLLTQEDTKKLSKISSSY-----
>Omeisaurus_mordax	-----MSSLLLTQEDTKKLSKISSSY-----
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>Scioperosaurus_formosus	-----MSSLLLTQEDTKKLSKISSSY-----
>Xanthocephalus_chloris	-----MSSLLLTQEDTKKLSKISSSY-----
>Nipponia_nippon	-----MSSLLLTQEDTKKLSKISSSY-----
>Nototheria_coriacea	-----MSSLLLTQEDTKKLSKISSSY-----
>Geratherium_simum_simum	-----MSSLLLTQEDTKKLSKISSSY-----
>Manis javanica	-----MSSLLLTQEDTKKLSKISSSY-----
>Picooides_pubescens	-----MSSLLLTQEDTKKLSKISSSY-----
>Loxodonta_africana	-----MSSLLLTQEDTKKLSKISSSY-----
>Fulmarus_glaucialis	-----MSSLLLTQEDTKKLSKISSSY-----
>Melospiza_cinnerea	-----MSSLLLTQEDTKKLSKISSSY-----
>Leucoraja_erinacea	-----MSSLLLTQEDTKKLSKISSSY-----
>Jaanus_janus	-----MSSLLLTQEDTKKLSKISSSY-----
>Salmo_salar	-----MSSLLLTQEDTKKLSKISSSY-----
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>Tupaia_chinensis	-----MSSLLLTQEDTKKLSKISSSY-----
>Lepisosteus_oculatus	-----MSSLLLTQEDTKKLSKISSSY-----
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>Ictalurus_nebulosus	-----MSSLLLTQEDTKKLSKISSSY-----
>Trichechus_manatus_latirostris	-----MSSLLLTQEDTKKLSKISSSY-----
>Aptenodytes_forsteri	-----MSSLLLTQEDTKKLSKISSSY-----
>Gekko_japonicus	-----MSSLLLTQEDTKKLSKISSSY-----
>Tyto_alba	-----MSSLLLTQEDTKKLSKISSSY-----
>Struthio_camelus_australis	-----MSSLLLTQEDTKKLSKISSSY-----
>Chrysomys_pictus	-----MSSLLLTQEDTKKLSKISSSY-----
>Tinamus_guttatus	-----MSSLLLTQEDTKKLSKISSSY-----
>Calyptra_anna	-----MSSLLLTQEDTKKLSKISSSY-----
>Apaloderma_vittatum	-----MSSLLLTQEDTKKLSKISSSY-----
>Oryzias_latipes	-----MSSLLLTQEDTKKLSKISSSY-----

>Gallus_gallus-----MSSRLLOTEDTKKLOSKI5SSY-
>Acipenser_sinensis
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>Kaupiochthys_hyoproroides-----MSSLLOTEDTKKLOSKI5FLSC-
>Anas_platyrhynchos-----MSSRLLOTEDTKKLOSKI5SSY-
>Leptobrachium_boringii-----MSSLLQTEDTKKLOSKI5FSY-
>Chaetura_pelagica-----MSSRLLOTEDTKKLOSKI5SSY-
>Apteryx_australis_mantelli-----MSSRLLOTEDTKKLOSKI5SSY-
>Oryzias_latipes-----MSSPFFQTEDPKKSPTKILLPY-
>Buceros_rhinoceros_silvestri-----MSSRLLOTEDTKKLOSKI5SSY-
>Caprimulgus_carolinensis-----MSSRLLOTEDTKKLOSKI5SSY-
>Seriola quinqueradiata-----MSSPLFQTEDPKKSPTKILLSY-
>Gariama_cristata-----MSSRLLOTEDTKKLOSKI5SSY-
>Mustela putorius_furo-----MSSLLLOTEDTKKLOSKI5SSY-
>Hynobius_chinensis-----MSSPLLQTEDTKKLSQIF5SY-
>Siniperca chuatsi-----MSSPLFQTEDPKKSPTKILLSY-
>Lipotes_vexillifer-----MSSLLLOTEDTKKLOSKI5SSY-
>Astyanax_mexicanus-----MSSLLLOTEDTKKSPSKI5FLSC-
>Calidris_pugnax-----MSSRLLOTEDTKKLOSKI5SSY-
>Callorhynchus_millii-----MSSLLOTEDTKKFKGKIFSLYS-
>Miniopterus_natalensis-----MSSLLLOTEDTKKLOSKI5SSYR-
>Oreochromis_niloticus-----MSSPLFQTEDPKKSPTKILLSY-
>Pterocles_gutturalis-----MSSRLLOTEDTKKLOSKI5SSY-
>Dasypus novemcinctus-----MSSLLLOTEDTKKLOSKI5SSY-
>Latimeria_chalumnae-----MSSLLOQTEDTKKLOSKI5FSY-
>Colius_striatus-----MSSRLLOTEDTKKLOSKI5SSY-
>Columba_livia-----MSSRLLOTEDTKKLOSKI5SSY-
>Merops_nubicus-----MSSRLLOTEDTKKLOSKI5SSY-
>Alligator_sinensis-----MSSRLLOTEDTKKLOSKI5SSY-
>Coccyzus_canorus-----MSSRLLOTEDTKKLOSKI5SSY-
>Bario_rerio
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>Cyprinodon_variegatus-----MSSPLFQTEDPKKSPTKILLSY-
>Sarcophilus_harrisii-----MSSLLOTEDTKKLOSKI5SSY-
>Galeopterus_variegatus-----MSSLLOTEDTKKLOSKI5SSY-
>Monodelphis_domestica-----MSSLLOTEDTKKLOSKI5SSY-
>Esax_lucius-----MSPPLQTEDTKKLOSKI5FLSY-
>Aquila_chrysaetos_canadensis-----MSSRLLOTEDTKKLOSKI5SSY-
>Gavia_stellata-----MSSRLLOTEDTKKLOSKV5SSY-
>Chanos_chanos-----MSSSLLQTEDTKNGRSIF5SC-
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>Apteronotus_leptorhynchus-----MSSLLOTEDTPKSPSKI5FLFC-
>Condylura_cristata-----MSSLLOTEDTKKLOSKI5SSY-
>Oryctolagus_cuniculus-----MSSLLOTEDTKKLOSKI5SSY-
>Elephantulus_edwardii-----MSSLLOTEDTKKL-----
>Ornithorhynchus_anatinus-----MSSLLOTEDTKKLOSKI5SPY-
>Tauraco_erythrophus-----MSSRLLOTEDTKKLOSKI5SSY-
>Opisthocomus_hoazin-----MSSRLLOTEDTKKLOSKI5SSY-
>Pleoglossus_altivelis-----MSSPLQTEDTKNGOSKIFLSY-
>Sclerophages_formosus
-MFGYLSLAYLATSPVFKLQAVAGLLEPVWDTNRLQARSPQPRGQNLFHVDRVHLQPFMSSTLLOTEDTKKSPSKI5FLPY-
>Serinus_carnaria-----MSSLLOTEDTKKLOSKI5SSY-
>Nipponia_nippon-----MSSRLLOTEDTKKLOSKI5SSY-
>Notothernia_coriiceps-----MSSPLFQTEDPKKSPTKILLSY-
>Equus_asinus-----MSSLLOTEDTKKLOSKI5SSY-
>Manis javanica-----MSSLLOTEDTKKLOSKI5SSY-
>Picooides_pubescens-----MSSRLLOTEDTKKLOSKI5SSY-
>Macaca_nemestrina-----MSSLLOTEDTKKLOSKI5SFY-
>Loxodonta_africana-----MSSLLOTEDTKKLOSKI5SSY-
>Fulmarus_glaucialis-----MSSRLLOTEDTKKLOSKI5SSY-
>Melopittacus_undulatus-----MSSRLLOTEDTKKLOSKI5SSY-
>Leucoraja_erinacea-----MSSLLOTEDTKKFKSKIFSLHS-
>Jaoulus_jaoulus-----MSSLLOTEDTKKLOSKI5SSY-
>Salmo_salar
MSLFQENGEYPQDSDSGMERAVAQLLEPVWGELNLDARS.LQPHWQLFHVDRVHLQSFMSSTLLOTEDTKKLOSKI5FLSY-
>Tupaia_chinensis-----MSSLLOTEDTKKLOSKI5SSY-
>Leposteus_oculatus
MSLFYENGEPYDQSDSGMERAVAQLLEPVWGLSLDARS.LQPQWRKLFHVDRVHLQSFMSSTLLOTEDTKKLOSKI5FLSC-
>Ictalurus_punctatus-----MSSRLLOTEDTOKSPSRIFLFC-
>Trichechus_manatus_latirostr-----MSSLLOTEDTKKLOSKI5SSY-
>Aptenodytes_forsteri-----MSSRLLOTEDTKKLOSKI5SSY-
>Gekko_japonicus-----MSSRLLOTEDTKKLOSKI5ASY-
>Tyto_alba-----MSSRLLOTEDTKKLOSKI5SSY-
>Struthio_camelus_australis-----MSSRLLOTEDTKKLOSKI5SSY-
>Oryzomys_picta-----MSSRLLOTEDTKKLOSKI5SSY-
>Tinamus_guttatus-----MSSRLLOTEDTKKLOSKI5SSY-
>Calypte_anna-----MSSRLLOTEDTKKLOSKI5SSY-
>Apeloderma_vittatum-----MSSRLLOTEDTKKLOSKI5SSY-
>Orycteropus afer_afer-----MSSLLOTEDTKKLOSKI5SSY-

>Drosophila_melanogaster

-----MNSKRTKNRTSSNRHKKLOPFRT-----
>Hyalella_azteca-----MIP-EGG-FSRVV-----YDYPRACYSPFLHMCANNDSPINIRNFSSNRHKKLOPFRTS-----
>Meinertellus_cundinamarcensi-----MTVLSMKP-----LLRGGS-----GIDHTS-REHIFASGSPAVRCMTS-PKR-----QHPL-----SYRTSKFSSNRHKKLOPFRET-----
>Argulus_siamensis-----MNLYSMDL-----LLSPNP-----ASFRRQ-LVA-----SGQPPSGQWFA-AKK-----YEP-----SYRTSKFSSNRHKKLOPFRTS-----
>Ooptotermes_gestroi-----MIS-SKR-----DEPI-----SYRTSKFSSNRHKKLOPFRET-----
>Agrilus_planipennis-----MT-SGR-----DEL-----HCNRTTKSSSNRHHKKLOPFRET-----
>Callinectes_sapida-----MTLFSMK-----GHISPGNCLSVEPFGLLT-----QS-----CMACASDPLDIRNRFSSNRHKKLOPFRTS-----
>Apachys_chartreus-----MTLLSTCRET-----TLSRKS-----GSFH-----ALEP-----IRGLDSRWISS-SKK-----DEPI-----NHRPYRTSKFSTNRHKKLOPFRET-----
>Oocajapyx_japonicus-----MIF-FGR-----DEPI-----SFRTSKFSSNRHKKLOPFRET-----
>Haploembia_palaui-----MTLNTCRET-----TLTRKS-----GSFH-----SLEP-----FRGLDSTOMIS-SKR-----DEPI-----TYRTSKFSSNRHKKLOPFRET-----
>Isomychia_bicolor-----MTFRHCNEI-----SLSRGS-----GRLIH-----ALEP-----IFGLDPRMSS-SKN-----QNP1-----SGRTSKFSSNRHKKLOPFRET-----
>Meganyctiphanes_norvegica-----MTLFSMK-----GHISPGHISLLVEPLGGLT-----KS-----CMACASDPLDIRNRFSSNRHKKLOPFRTS-----
>Galloisiana_yuasai-----MTLLSTCRET-----TLSRKS-----GSFH-----SLEP-----IRGLDSRWISS-SKR-----DEPI-----SYRTSKFSTNRHKKLOPFRET-----
>Tupiooia_notatus-----MIS-SKL-----QNPV-----SYRTSKFSSNRHKKLOPFRET-----
>Copidosoma_floridanum
MTFLRQRETSRISRRAGTYINTGGGGSTSSLRRTSRAY-DGLLSRRTIATTTSPDVKITIGQRNININLVSSGKEEGQDYRRRCSPFL-----SSSCSAPAAMII-EGRGLSSRSSSSSSSGGASHKQLODEDDHCMAA-----LRVILNRLLLVDHRTAKFSSNRHKKLOPFRET-----
>Eudarcia_simulatrixella-----CGKSCCIE-----RVGR-----AADCAR-----QNTLYGPTTGBRTAKFSSNRHKKLOPFRET-----
>Metalliytus_splendius-----MTLLPTCRET-----TLSRGS-----GSFH-----ALEP-----VRGLDSRWISS-SKR-----DEPI-----SYRTSKFSSNRHKKLOPFRET-----
>Tanzaniophasma_sp._AD-2013-----MTLLTLTR-----IGR-----FSRKFSGGYI-SPKPSFG-----LEI-----SRNILLKQELLVHRTAKFSSNRHKKLOPFRET-----
>Panorpa_vulgaris-----MTLERYETS-VLRGVPR-----SPTALSPRGTKOMI-----PPRRHLSYRTSKFSSNRHKKLOPFRET-----
>Corydalis_cornutus-----MTLAGCIE-----LLSRKP-----GITQYS-VLEP-----VLGIDTRMIS-SKF-----DEPI-----SYRTSKFSTNRHKKLOPFRET-----
>Pseudomallada_prasinus
-MRQRAETFRISRRAGSYGSGGGGRTLSRRRNMTTIIISYICRNSL-----RWCQGR-----LSTWCSEIIE-----TRYGPAACMI-ENYPLPTRSRINSN-----QDT-----TQHFLNMLVLPKRTSKFSSNRHKKLOPFRET-----
>Calopteryx_splendens-----MT-LLSKGI-----SLSRGS-----GFTSI-----ALEP-----ILGLDSRWISS-SKR-----DEPI-----SYRTSKFSSNRHKKLOPFRET-----
>Gryllotalpa_sp._AD-2013-----MTLLPTCRET-----TLTRKS-----GSFH-----ALAP-----IRGLDSRWISS-SKR-----DEPI-----SYRTSKFSSNRHKKLOPFRET-----
>Ciliatarchus_hookeri-----MTLLTCRET-----TLSRGS-----GSFH-----AEEP-----ARGDSRWISS-TNR-----DEPI-----CYRTSKFSSNRHKKLOPFRET-----
>Menopon_gallinae-----MTLXIFKE-----ASLTRKCRPNLSP-----GRGF-----RQMSHKGQPSYRKSKLSTNRHKKLOPFRET-----
>Leuctra_sp._AD-2013-----MTLLPTCRET-----TLTRKS-----GSFH-----ALEP-----VRGLDSRWISS-YKR-----RDP1-----SHRTSKFSTNRHKKLOPFRET-----
>Polydemus_angustus-----MTLLSLK-----ELLL-----LRGLNCCOKLT-O-----PMIESVLSRC-----MFSTKFKPVSHRTPKFGSNRHHKKLOPFRTS-----
>Acerentomon_sp._AD-2013-----MTLINSKEKRSKDGSKLYIRLQ-TFCQPGFINQWNLQPHS-----SASPLSALCCT-----EPSKSHYSSSHQIRKLLPFREES-----
>Liposcella_hostychophila-----MTLTHFKE-----ASLTRKCRPNLSP-----GRGF-----RQMSHKGQPSYRKSKLSTNRHKKLOPFRET-----
>Inocellia_crassicornis-----MTLVHTEI-----LLSRGS-----GSSRYS-ALEP-----ALGIDTRMSS-SKR-----QGP1-----SYRTSKYSTSRHKKLOPFRET-----
>Ctenocephalides_felis-----MTLERYETS-VLRGVPR-----SACAPSSHSKQMT-----PTRRRHCYRQSKFSSNRHKKLOPFRET-----
>Thrips_palmi-----MTFRSCKETW-----TVSRGS-----GSSPI-----AQEP-----GRQPGSRWISS-YQP-----HGP1-----SHRTSKFSSNRHKKLOPFRET-----
>Zorotypus_caudehilli-----MTLLPLQRE-----TLTRKS-----GNFH-----ALVP-----TGGLDSRWISS-SKR-----KDP1-----CYRTSKFSSNRHKKLOPFRET-----
>Tricholepidion_gertschi-----MTLLSMKEI-----SLSRGS-----GSFH-----TLEP-----ILGLDTRMIS-SKR-----DEPI-----SYRTSKFSSNRHKKLOPFRET-----

H50031 ENSDARG0000000540 esnsl

>Denio_rerio-----MSKN|QRT-E-----PGASEEADKEELNKK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADKGETL.SSOKDLNMKEYQD|-----

>Acipenser_sinensis-----NST-K-SGQDN-----TSEV-NTKQKEELNKK|KEGKVLVDEL.SNLKKNRRVY|YQOPNSN|FFLGDKSETL.SSEKNLDMKKYQDL-----

>Aelia_calva-----MSNKS-QAKDD-Q|NG-KAKQKEELNKK|KEGKVY|DEL.SNLKKNRRVY|YQOPNSN|FFLEDKSETLAKSLDHMKYQDL-----

>Chama_striata-----MKKELQDM-----

>Anser_cygnoides-----MAARGEEEEKKEEG-----EGESAVLRPQDL.SRR|KEGK|V|DEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQK|VLDELKKAHJEMENSEKTK|KK|-----

>Polypedates_megacephalus-----MSDVG-VVLGE-DQSRNTQKKEEYANKFREGVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRAKTL.SQOKTLDELKHTH|ENSEN|QD|TD-----

>Porichthys_notatus-----MSKL-HDIDA-SFG-GTSP|EVLNKK|SEGVVLDEL.SNLKKNRRVY|YQOPNSN|FFLADRKOTL.SSOKKELDMKRLQDS-----

>Oryzias_latipes-----MKNSSKK-VYMSD-MSGE-Q|TYKEEL.SKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRSOTL.STRKDYLLKKELQD|-----

>Trachinotus_blochii-----MSKN-RMDSD-HFEG-GSALKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLGRSOTL.SSOKKELDMKKELQDM-----

>Carania_cristata-----ML.SQOKNTLDELKKAHJEMENSEKTKVKK-----

>Phoca_large-----MPSRGSPEDGAGL-----SADNSTLHKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Hymbios_refartatus-----MSGTKPM-KEDSSSAINTKEELDTK|REGTVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRTATL.SESKTLDDLKTAHDEL.EKSKARVK-----

>Micropterus_salmoides-----MKNSSK1-RMDSD-NCEG-RCALKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRSOTL.SQOKREDMKKQDLQDM-----

>Lipotes_vexillifer-----MPSRGAPPEDGSLV-PTNSTQHKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSD|FFLADRTML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Astayanax_mexicanus-----MSIRSESPED-PAGE-ERPTREELNTK|KEGKVLVDEL.SNLKKNRRVY|YQOPNSN|FFLSDKGETL.SSOKKELDMKKYQDM-----

>Calidris_pugnax-----MSGRAARDEEEEEKREESAKHKEEL.SRR|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQOKNTLDELKKAHJEMENSEKTKVKK-----

>Callorhynchus_milii-----MEAEETRAPEGEE-RETROATRQELNKK|KEGKVA|NEL.SNLKETRRVY|YQOPNSN|FFLADTKALTALTEKRAFDELKHEQLENPKMK-----

>Myotis_lucifugus-----MEWPAAREAPEDAGRA-APGREEL.SSR|KEGK|V|VDEL.SNLKKNRTVY|YQOPNSN|FFLADRTLEL.SESKN|LDELKKEYQ|E|ENSEKTK|TK|-----

>Oreochromis_niloticus-----MSKG-CSSDE-QFEG-QAAVKEELNKK|KEGKVLVDEL.SNLKKNRRVY|YQOPNSN|FFLVGORSOTL.SSOKKELDMKKELQD|-----

>Clupea_harengus-----MTTKNLPAAN-TVG-DETQKEEL.SKK|KEGK|L|VDEL.SNLKKNRRVY|YQOPNSN|FFLTDRGOTL.SSKTELDMLKKDYQDM-----

>Latimeria_chalumnae-----MSGRY-QEEDN-ESQ-LRTSHKEELNKK|KEGKVLVDEL.SNLKKNRRVY|YQOPNSN|FFLADRSKTL.SDOKKLDLMKREYQEL-----

>Columba_livia-----MSGRPRDEE-GGDSAKRHKEEL.SRK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQOKNTLDELKKAHJEMENSEKTK|KK|-----

>Alligator_sinensis-----MSRERARVWPMFAMWGGASCAEGVILGGAEVRSQSGAARLVSGMSGRAPR-DEEARLRRKEELNKK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTLSQOKNLDLKKAHJEMENSEKSK|KK|-----

>Xyptolebias_marmoratus-----

>Sarcophilus_harrisii-----MSLKS-POSSD-NISAE-GSALKEELNKK|KEGK|L|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRSOTL.SSQOKLDVLKKELQDV-----

>Monodelphis_domestica-----MPSRGTRVEDGPEPA-ISAKPLMKELNSK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENTENKMK|SK|-----

>Trichosurus_vulpecula-----MPGKGTREDAPEG-TFASPLNKEELNSK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLSDRTML.SESKN|LDELKKEYQ|E|ENTENKMK|KK|-----

-----ML.SESKN|LDELKKEYQ|E|ENTENKMK|KK|-----

>Eoax_lucius-----MSV-KNE-IFDEESALVKEELNKK|KEGKVVDEL.SNLKKSRRVY|YQOPNSN|FFLADRGOTL.SSQKRRAGHEGSPKYV|F-----

>Aquila_chrysaetos_canadensis-----MSGRAPDEEG-ESAKLRRKEEL.SRR|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQOKNTLDELKKAHJEMENSEKAK|KK|-----

>Gadus_morhua-----MTSN-SREDE-ISEA-HSA|KEELNKK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRGOML.GTNKELD|LKKELQDM-----

>Numida meleagris-----MSRREEEGAGVCRKEEL.SRR|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQOKNTLDELKKAHJEMENSEKTKVKK-----

>Acanthopobius_hasta-----MS-INTED-INEG-L.SALKEENKK|REGKVLDEL.SNLKKNRRVY|YQOPNSN|FFLADRSOTL.SAKKELDMKKELQD|-----

>Condyura_cristata-----MPSG-QFEGEARLV-SSONSLLKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENLDTK|KK|-----

>Oryctolagus_cuniculus-----MPSRGVHPEDSAPV-PAGRTLHKEELCNK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENSEKSS|KK|-----

>Lutjanus erythropterus-----MKKELQDM-----

>Ornithorhynchus_anatinus-----ML.SESKN|LDELKKEYQ|E|ENTENKMK|KK|-----

>Pleoglossus_altivelis-----MSKKQDLN-LFAGGESKKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRGQTL.SSYNVKNOMKKELD|-----

>Scleropages_formosus-----MSVRE-QEKEG-ASLG-DTSLKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADKAEATL.GSGRRTLDMKKKEYQDL-----

>Pseudopodoces_humilis-----MSGRPPREDG-ESALRHKEEL.SRR|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SQOKNTLDELKKAHJEMENSEKAK|KK|-----

>Lateolabrax_ japonicus-----MSS-K-SQNSD-WFG-GSAAKEELNTK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRGOTL.GSOKKELDMKKELQDM-----

>Anoplopoma_fimbria-----MSK1-HMED-NCEG-TSALKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRGOTL.GSOKKELDMKKHLQDM-----

>Ceratotherium_simum_simum-----MPSRGTRPEDGAGLV-PTDGSAPHKEEL.SNK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Manis javanica-----MPSGSPPEDGAAPV-PTENSTLHKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Hippoglossus_hippoglossus-----MSKG-RMED-SFEW-GSALKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRGOTL.GSOKKELDMKKELQDM-----

>Pongo_abelii-----MPSRGTRPEDSIVL-PTNSTPHKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENLDTK|KK|-----

>Loxodonta_africana-----MEWPSRAWPEDSAEV-PSONSTPHKEEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENLDTK|KK|-----

>Callispermophilus_lateralis-----MLRGVEMPIRGTRSDSAPV-STDYSTAKEEL.SNK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLSDRTML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Oncorhynchus_mykiss-----MSKNQREN-E-NIDEEESTLKEELNKK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRGOTL.SQOKKELDMKKOM-----

>Tupaia_chinensis-----MEWPSRGARLEDSAVRG-PTDOSTPHREEL.HSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRAELL.SESKNVLDELKKEYQ|E|ENSEKTK|KK|-----

>Lepisosteus_oculatus-----MSKN-QWDD-VVGA-KAKQKEELNKK|REGK|V|DEL.SNLKKTTRVY|YQOPNSN|FFLANKAETL.SASKNLDMKKKEYQDV-----

>Ictalurus_punctatus-----MSTN-LVHE-ERATKEELNKK|KEGKV|DEL.SNLKKNRRVY|YQOPNSN|FFLADKGM.LSTOKKLDNMKEYQDM-----

>Trichechus_manatus_latirostr-----MEWPSRAWPEDESTVL-PSONSTPHREEL.SSK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADRTML.SESKN|LDELKKEYQ|E|ENLDTK|KKSSS-----

>Squalus_acanthias-----MEGTD-KVGSSEADKEELNKK|KEGKV|DEL.SNLKKSRRVY|YQOPNSN|FFSADRTOTL.SQOKALEMKKEYQDLENSEKMK-----

>Thamophis_sirtalis-----TQEQWSS-QALLREGGSSKLPOKEELNKK|KEGK|V|VDEL.SNLKKNRRVY|YQOPNSN|FFLADKTOTL.SCKTLDELKKAHJEMENPEKTK|KK|-----

>Tyto_alba-----ML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

>Trachemys_scripta-----MSGREPR-EEEGAKPHKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLVDRETLSQOKNTLDELKKAHJEMENSEKTK|KK|-----

>Takifugu_rubripes-----MAFND-HFDE-QSTLKEELNKK|KEGKVVDEL.SNLKKNRRVY|YQOPNSN|FFLADRAETL.SSNKKLDFMKVEQNMKD-----

>Orycteropus_afer_afer-----ML.SESKN|LDELKKEYQ|E|ENSEKTK|KK|-----

HS0031 ENSG00000138381 ASNSD1

>Homo_sapiens-----MPSRGTRPE-----DSSVLPTDNTSPHKEDLSSKIKEQKIVVDELSNLKKNRTEQKCOLBARIYWNH-----

>Acipenser_sinensis-----M-----STK-----SGGD--NTSEVNTKQKEELNKKIKEQKVLVDELSNLKKNRKYYIQDPNSNIFFLGDKSETLSSEKMLDNMKKEYQDL-----

>Aelia_calva-----MS-----NKS-----QAKD--DQINGKAKQKEELNKKMKQKVVIDELSNLKKNRKYYVQDQNSNIFFLEKDSKSETLATOKSLDNMKKEYQDL-----

>Ochama_argus-----MT-----SKT-----QDNDINVEGQ--CGLKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSGOKELDNNMKKELDQM-----

>Anser_cygnoides-----MAARGEEEEKEEEEGEGESAVLRPDQLSRRIKEQKVIIDELSNLKKNRKYYKQDPNSNIFFLVORTETLSQKIVLDELKKAHGENSEKTKIKK-----

>Nanorana_parkeri-----MSD-----TVAGEDCRGNTDKQKEDFYTKFREQKVIIDELTNLKKORKYYRQDPNSNIFFVADKQTKLSECKTLADLEHTYQILENSEKLGDKK-----

>Porichthys_notatus-----MS-----SKL-----HDDI--ASFGG--TPSIEVLNKKIASEQVVLDELSNLKKNRKYYIQDQNSNIFFLADKOTLSGOKELDNLKROLQDS-----

>Oryzias_latipes-----MK-----MS-----SKK-----YNNSSNSGEG--TTYKEELSKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSRKELDYLLKELDQI-----

>Trachinotus_blochii-----MS-----SKN-----RNDONFEGQ--SALKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLGRSOTLSGOKELDNNMKKELDQM-----

>Acinonyx_jubatus-----MPSRSGSPE-----DGAALSSADNSTPHKEELSSKIKEQKIVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKNILDCLKKEYQIEENSEKTKIKK-----

>Hymibius_chinensis-----MSGTKPXNK-----EAGSDSAANTKEEDLTKIREGTVVVDELSNLKKNRKYYIQDPNSNIFFLADRTATLSSEKNTLDLKTARGELKSUEVVRVK-----

>Micropodus_salmoides-----MNK-----MS-----SKI-----RNDONCEGR--CALKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSGOKELDNMKKELDQM-----

>Orcinus_orca-----MPSRGARPE-----DGSGLVPTDNTGKKEELSSKIKEQKIVVDELSNLKKNRIT-----YHNS-----

>Aetyanax_mexicanus-----MS-----IRSS-----EGPE--DPAGEERTPEELNKKIKEQKVLVDELSNLKKNRKYYLQDPNSNIFFLSQKGETLSGOKELDNNKKEYQDM-----

>Calidria_pugnax-----MSGRAA--RDEEEEEKREESAKARKEELSSRIKEQKIVVDELSNLKKNRKYYRQDPNSNIFFLVADRTETLSQKNTLDLKAHGENSEKTKYNNK-----

>Callorhynchus_milii-----NEAAETRAAP--GGE--RETRODATHRQELNKKIKEQKVAIINELSKETBRYYKQDPNSNIFFLTOKTTALTECRAFDELKKEHDELNPDKNNK-----

>Rousettus_aegyptiacus-----MEMFFCETRPE-----NGAELVPTDNTSAPHKVDLSKIKEQKVVVDELSNLKKNRIT-----YHNS-----

>Neolamprologus_burcharadi-----MS-----SKS-----YSNDEGEGQ--AAVKEELNKKIKEQKVLVDELSNLKKNRKYYIQDPNSNIFFVGRSOTLSGOKELDNNKKELDQI-----

>Clupea_harengus-----MT-----TKNN--LPAANTVDE--TPKEELSKIKEQKILLVDELSNLKKNRKYYLQDPNSNIFFLTORGQMLTSCKELDNLKKYQDM-----

>Latimeria_chalumnae-----MS-----GRV-----QGED--NESQLRTSHKEELNKKIKEQKVLVDELSNLKKNRKYYQDQNSNIFFLADRSOTLSGOKELDNMKKEYQEL-----

>Colubra_livia-----MSGRRP--RDEE-----GDGSAKLKHDELSRKIKEQKVVVDELSNLKKNRKYYRQDPNSNIFFLVORTETLSQKNTLDLKAHGENSEKTKIKK-----

>Alligator_sinensis-----MPSRGARVPMFAMVGSACAEVNLGGAEVRSQSGAARLVSG--MSGRAP--RRD-----EEEARLRKEELNKKIKEQKIVVDELSNLKKNRKYYRQDPNSNIFFLADRTETLSQKNTLDLKAHGEENSEKTKIKK-----

>Ombio_rerio-----MS-----SKNI--ORTE--PGASERAQKEELNKKIKEQKIVVDELSNLKKNRKYYIQDPNSNIFFLADGETLSGOKELDNMKKEYQDI-----

>Xyptolebias_marmoratus-----MS-----LKS-----POSSNSAEQ--SALKEELNKKIKEQKIVLDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSGOKELDNLKKEYQDV-----

>Sarcophilus_harrisii-----MPSRGTRVE--DGPEPAISAKPLNKEELNSKIKEQKVVVDELSNLKKNRTEQKCSLKXTH-----

>Monodelphis_domestica-----MPSGKTRRE--DATEPGTFASPLNKEELNSKIKEQKVVVDELSNLKKNRTEQKCSLKXTH-----

>Exocoetidae-----MS-----VWNEIFDEE--SALKVELNKKIKEQKVVVDELSNLKKSRRYYVQDPNSNIFFLADRGOTLSGOKARQHEEGSPKYVIF-----

>Aquila_chrysaetos_canadensis-----MSGRAP--RDEEG-----ESAKLRKEELSSRIKEQKVVVDELSNLKKNRKYYRQDPNSNIFFLVORTETLSQKNTLDLKAHGENSEKTKIKK-----

>Meleagris_gallinapavo-----MGRREEEESAEGLKEELSSRIKEQKVVVDELSNLKKNRKYYRQDPNSNIFFLVORTETLSQKNTLDLKAHGEENSEKTKYNNK-----

>Acanthopobius_hasta-----MS-----RNTEDNNEGL--SALKEELNKKIKEQKVLVDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSGOKELDNNMKKELDQI-----

>Condyura_cristata-----MPSQ-----GPE-----EGARLVSSDSSSLIKEELSSKIKEQKIVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKNILDCLKKEYQIEENSEKTKIKK-----

>Oryzotylagus_cuniculus-----MPSRGVHPE--DSAVPPAGRTLIKEDLONKIKEQKVVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKNILDCLKKEYQIEENSEKTKIKK-----

>Pileoglossus_altivelis-----MS-----SKQD--LDLENLFAGGSKRKEELNKKIKEQKVVVDELSNLKKNRKYYQDQNSNIFFLADRGQDLSYNNKYNNMKKELDQI-----

>Scleropages_formosus-----MS-----VRE-----GEKE--GASLGDTSKEELNKKIKEQKVVVDELSNLKKNRKYYVQDPNSNIFFLADKNETLGSORNTLDNNMKKEYQDL-----

>Zonotrichia_albicollis-----MSGRRP--RDE-----GDGSAKLKHKEELSSRIKEQKVVVDELSNLKKNRKYYQDPNSNIFFLADRTETMLSESKNTLDLKAHGEENSEKTKIKK-----

>Lateolabrax_japonicus-----M-----SSK-----SDNSDFDGO--SAAKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRGOTLSGOKELDNNMKKELDQM-----

>Perca_flavescens-----MS-----SKS-----RNDONFEGQ--SAHKEELNKKIKEQKIVVDELSNLKKNRKYYIQDPNSNIFFLADRSOTLSGOKELDNNMKKELDQM-----

>Ceratotherium_simum_simum-----MPSRGTRPE-----DGAELVPTDNTSAPHKEELSSKIKEQKIVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKNILDCLKKEYQIEENSEKTKIKK-----

>Manis_javanica-----MPSGGSRPE--DGAAPVPTENSLIKEELSSKIKEQKIVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKILFPSLHRYIG-----

>Hippoglossus_hippoglossus-----MS-----SKG-----RNDNSFENG--SALKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRGOTLSGOKELDNNMKKELDQM-----

>Loxodonta_africana-----MEMPSRRAMPE--DGAELVPSDNTSPHKEELNSKIKEQKIVVDELSNLKKNRTEQKCOLKAKIYWNH-----

>Ictidomys_tridactylus-----MLRGVEMP1RGRSD--DSAVSYSTDNTAHKEELSSKIKEQKIVVDELSNLKKNRKYYRQDQNSNIFFLADRTETMLSESKNILDCLKKEYQIEENSEKTKIKK-----

>Oncomerycinus_mykiss-----MS-----AKNQ--RENNIDEEE--STLKEELNKKIKEQKIVVDELSNLKKNRKYYVQDPNSNIFFLADRGOTLSGOKELDNNMKKQM-----

>Tupaia_chinensis-----MEMPSRGARLE--DSAVRPTDNTSPHREDLNSKIKEQKIVVDELSNLKKNRKYYVQDQNSNIFFLADRAELSSKNVLDCLKKEYQIEENSEKTKIKK-----

>Lepisosteus_oculatus-----MS-----NNN-----QVQD--DVQAKAKQKEELNKKIKEQKIVVDELSNLKKTBRYYVQDPNSNIFFLADKNETLSASKNSLENMKKEYQDV-----

>Ictalurus_punctatus-----MS-----HST--HLVHEERATKEELNKKIKEQKVVVDELSNLKKNRKYYVQDPNSNIFFLADGEMLSTOKDLDNNMKKEYQDM-----

>Trichechus_manatus_latirostris-----MEMPSRRAMPE--DSTELVPSDNTSPHREDLSSKIKEQKIVVDELSNLKKNRKYYVQDQNSNIFFLADRTETMLSESKNTLDLCLKKEYQIEENSEKTKIKKSSS-----

>Squalus_acanthias-----ME-----GTSD--KYGSEADRKKEELNKKMKQKVVVDELSNLKKSRRYYVQDPNSNIFFSADRTOTLSGOKALEMKKEYQDENSEKNNK-----

>Protothrips_mucronatus-----MSSPA-----LLGEGGEEKSLPKKEELNKKIKEQKIVVDELSNLKKNRKYYRQDPNSNIFFLADRTOTLSGORTLDLKAHGEENSEKTKIKK-----

>Trachemys_scripta-----MSGREP--RRE-----EEGAKPHKEELNKKIKEQKVVVDELSNLKKNRKYYVQDPNSNIFFLVORTETLSGOKNTLDLKAHGEENSEKTKIKK-----

>Takifugu_rubripes-----MAFNHFDQD--STLKEELNKKIKEQKVVVDELSNLKKNRKYYIQDPNSNIFFLADRAETLSNNKKLDFNNKKEYQNNKD-----

H50031 ENSGALG00000041666

>Gallus_gallus	MSRREEETAEI GYGEELSRRIKEQKVYVDEL.SNLKKNRKVYVGDPNSNIFFLVORTEAL.SQKNTLDLKKAHGELENSEKTKVKK
>Acipenser_sinensis	MTK-SGGD-----NTS-EVNTKQKEELNKIKEQVLVDEL.SNLKKNRKVYIIGDPNSNIFFLGDKSETLSEKEMLDNMKKEYODL
>Aelia_calva	MSKSGAKD-----DGI-NGKAKGKEELNKMKKEQVVIDEL.SNLKKNRKVYVGDPNSNIFFLDEKSETLATORSLDHHMKKEYODL
>Chama_striata	-----MKKELGDM-----
>Anas_platyrhynchos	-----MENSEKTKDK-----
>Pelophylax_nigromaculatus	MTDV-----EVEKREDKRAMTKGEEFYTKFREQVYVDEL.SNLKQDRKVYVGDPNSNIFFLADRAKTLSEKKTLDLKKTSQIENSEKTKDQK
>Porichthys_notatus	MSKLDHID-----ASFGGTPIEVLNRKISEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRKTLSSKKELDNLKKRQDS
>Oryzias_latipes	MMSSKKYNNIS-----DMS-DEQITTEYELSKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRSQTLSTRKELDYLKKELDGI
>Caprimulgus_carolinensis	-----MENSEKTKDK-----
>Trachinotus_blochii	MSKMRDND-----DNF-EGSALKEELNKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLGDRSQTLGSKKELDNMKELGDM
>Gariama_cristata	-----MLSQKNTLDLKKAHGEMENSEKTKVKK-----
>Acinonyx_jubatus	MPSRGGSPED-----GAALSADNSTPKKEELSSKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENSEKTKDK
>Hymbius_retdatus	MSGTKPK-----NKEDGSDSAANTKEELDTKIREQTVVDEL.SNLKKNRKVYIIGDPNSNIFFLADRTATLSEKNTLDLKTAHGELEKSKARVKK
>Micropterus_salmoides	MMMSKLRDND-----DNC-EGRCALKEELNKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRSQTLASCKKELDNMKKQDGLDM
>Lipotes_vexillifer	MPSRGARPED-----GSGLVPTDNTQIKDELSSKIKEQKIVDEL.SNLKKNRKVYVGDPNSDIFFLADRTMLSEKNTLDLKKKEYOEIENSEKTKDK
>Pygocentrus_nattereri	MSVRSSEQT-----DGLADGSAAREELNRRIKEQVVIDEL.SNLKKNRKVYIIGDPNSNIFFLTKGSETLSSKKELDNMKHYGDM
>Calidria_pugnax	MSGRAARGEEEEKEREESAKARKEELSRRIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLVORTEAL.SQKNTLDLKKAHGEMENSEKTKVKK
>Callorhynchus_millii	MEAAETRAAPGS-----EERETRDGATRRDELHNKIKEQNVATNELSNKJETRIRVYVGDPNSNIFFLTKDTATLGEORAFDELKKGDELNPQKNNKK
>Myotis_lucifugus	MEMPARAEARPED-----GAGRA-----APGRELSSRIKEQKIVDEL.SNLKKNRTYVGDPNSNIFFLADRTLLSEKNTLDLKKKEYOEIENSEKTKTKK
>Oreochromis_niloticus	MSSKGGSSD-----EGF-EGGAAKEELNKIKEQVVLVDEL.SNLKKNRKVYIIGDPNSNIFFLVDRSQTLSSKKELDYMKKELDGI
>Pterocles_gutturalis	-----MENSEKTKDK-----
>Allosa_alosa	MGIQDVNIS---YIVLFLTTMTKMLPA-----ADTVEQTEETKEELSKQIKEQNTLVDEL.SNLKKNRKVYIIGDPNSNIFFLDREQMLSTOKKDLNLKKKEYGDM
>Latimeria_chalumnae	-----MKREYDEL-----
>Columba_livia	MSGRPPR-----QEEGDSAKLRKQDEL.SRIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLVORTETLSQKNTLDLKKAHGEMENSEKTKDK
>Alligator_sinensis	MSRERARVRNMPAMVGGASCAEGVILGGAEVRSQSGAARLYSG-----MSGRAPR-----RD-----EEEARLRKEELNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTETLSQKNTLDLKKAHGEIENSEKSKDK
>Oculus_cancrus	-----MENSEKTEKK-----
>Pimephales_promelas	MSKXNHQP-----EPGTQEEALKEELNKIKEQKTLVDEL.SNLKKNRKVYIIGDPNSNIFFLADGESLSSKKDLDNMKKEYODI
>Pocilia_formosa	MSGTNGSS-----DNV-SKYSALKEELNRKVEQKIIVDEL.SNLKKNRKVYIIGDPNSNIFFLADRSQTLSSKQGLDYMKKEGDL
>Sarcophilus_harrisii	MPGRGTRVED-----GPEPAISAKPLNKEELNSKIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKHGEIENETKNNSSK
>Monodelphis_domestica	MPSKGTRRED-----ATEPGTFASLPLNKEELNSKIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLSRTMELSEKNTLDLKKHYGGEIENETKNNKK
>Trichosurus_vulpecula	-----MLSEKNTLDLKKHGEIENETKNNKK-----
>Eoos_lucius	MSVKN-----EIFDEESALKVLELNKIKEQVYVDEL.SNLKKSRRVYVGDPNSNIFFLADRGQTLSSCKARHGEGSPKYVIF
>Aquila_chrysaetos_canadensis	MSGRAPR-----QEE-GEASAKLRKEELSRRIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLVORTETLSQKNTLDLKKAHGEMENSEKATDK
>Gadus_morhua	MTSNS-RED-----EIS-EHSAIKKEELNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADGQMLGTNKKELDILKKELGDM
>Gavia stellata	-----MENSEKTKDK-----
>Acanthopobius_hasta	MSRNTTE-----DMN-EGLSALKEELNKIKEQVYVDEL.SNLKKGGRVYIIGDPNSNIFFLAERSQTLGCKKELDNMKKELDGI
>Balearica_regularis_gibberica	-----MENSEKTKDK-----
>Condyura_cristata	MPSQ--GFEE--CARLVSSDSSLIKEELSSKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENLQNTQDK
>Oryctolagus_cuniculus	MPGRGWPED-----SAVPVPAGGRTLKKEELCNKIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENSEKSSDK
>Lutjanus erythropterus	-----MKKELGDM-----
>Ornithorhynchus_anatinus	-----MLSEKNTLDLKKTHGEMSEKTKVKK-----
>Plecoglossus_altivelis	MSXKQULDL-----ENLFAGDESKRKEELNKIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADROUGLSYNNKVDNMKELDGI
>Sierapages_fornosus	MSVREDEK-----EGASLDGSLKEELNKIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADRAQTLGSKRRTLDMNKKEYODL
>Taeniopygia_guttata	MSGGPA-----RQEDGESAALRKEELSRRIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSQKNTLDLKKAHGELENSEKAKDK
>Nilipponia_nippon	-----MENSEKTRNNK-----
>Lateolabrax_japonicus	MSKX-SDMS-----DNF-DGGSAAKEELNTKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRGQTLGSKKELDNMKKELLDN
>Perca_flavescens	MSKSRDND-----DNF-EGGSAHKEELNNKIKEQKIVDEL.SNLKKNRKVYIIGDPNSNIFFLADRSQTLGCKKELDNMKKQDGLDM
>Geratotherium_simum_simum	MPSRGTRPED-----GAGLVPTDQSAPIKDEL.SNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENSEKTKDK
>Manis javanica	MPSGGSRPED-----GAAPVPTENSILLKKEELSSKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENSEKTKDK
>Picoidea_pubescens	-----MENPEKTKDK-----
>Hippoglossus_hippoglossus	MSXKGRONE-----DSF-ENQGSALKEELNKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRGQTLGSKKELDNMKKELGDM
>Microcebus_murinus	MPSRATHPED-----SAVLVSTDESTPYGQDLSNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSGKNTLDLKKKEYOEIENSEKTKDK
>Loxodonta_africana	MEMPSRRAMPED-----SAELVPSDNTSPHKEELNSKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENLTKDK
>Fulmarus glacialis	-----MENSEKTKDK-----
>Melopittacus_undulatus	-----MENSEKTKTEK-----
>Galluspermophilus_lateralis	MLRGVEMP1RGTRSDD-----SAVLFTDYSTAQKEELSNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLSRTMELSENNLDELKKKEYODIENSEKTKDK
>Oncomerychus_mykiss	MSKNGREN-----ENIDEEESTLKEELNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRGQTLASCKKELDNMKKQDM
>Tupaia_chinensis	MEMPSRGARLED-----SAVRGPTDOSTPHREDLSHKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRAELLSEKNTLDLKKKEYOEIENSEKTKDK
>Lepisosteus_poulatus	MSKNNKVD-----DVGAKAKGKEELNKIKEQKIVDEL.SNLKKTTRVYVGDPNSNIFFLANKAETLSASKNSLENMKKEYODV
>Ictalurus_punctatus	MT-----MLV-HEERATKEELNQIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADGEMLSTOKKDLDMKKEYODM
>Trichechus_manatus_latirostr	MEMPSRRAMPED-----STELVPSDNTSPHREDLSNKIKEQKIVDEL.SNLKKNRKVYVGDPNSNIFFLADRTMLSEKNTLDLKKKEYOEIENLTKDKSSS
>Aptenodytes_forsteri	-----MENSEKTKDK-----
>Squalus_acanthis	ME-----G-T-----SDKVSSSEADRKEELNQMKKEQNVVIDEL.SNLKKSRRVYVGDPNSNIFFLSADRTOTLSECKALEEMKKEYODLENSEKMKKX
>Anolis_carolinensis	MSQMPQ-----REEEGEAGLGDKEELSRRIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLADRTOTLSEKNTLDLKKAHGEMENSEKTKDK
>Tyto_alba	-----MLDELKKAHGEMENSEKTKSKX-----
>Chelonia_mydas	MSGREPR-----REE-EGAKLHKDELTKRIKEQVYVDEL.SNLKKNRKVYVGDPNSNIFFLVORTEMLSEKNTLDLKRHGEIENSEKTKDK
>Taki fugu_rubripes	MAF-----NDNF-DEGSTLKEELNNKIKEQVYVDEL.SNLKKNRKVYIIGDPNSNIFFLADRAETLSSNNKGLDMKKEYQMMND
>Calyptra_anna	-----MENSEKTKVKK-----
>Oryzteropus_afer_afer	-----MLSEKNTLDLKKKEYOEIENSEKTKDK-----

>Denio_rerio
MGILRFQFSGSRSPSLGLPS---TLY-----STASIQIMKVLVLTENQIWIIFTVSSRG
>Acipenser_siemisia
MGINRGAPTQVAFPSLCSGP---TLF-----STGSIQIMKVLVLTENQIWIILWCSRG
>Ameia_calva
MGIFRGAPTQVAFRPLLHCSF---SLF-----STSSSEIMKVLVLTENQIWIIFTNCSRG
>Osmia_aurus
MGIFRGAPTAAAGPPPSH-----CTPTHSIQPSIQPFLYKMTLELTKSSIWIFTACNRG
>Pseudacris_regilla
MGINSASPVQVAFACSRKT---ENF-----TSSSEIMKVLVLTENQIWIIFNCSG-
>Chaetura_pelagica
-----MKVLVLTENQIWIIFNCSG-
>Oryzias_melastigma
MGIFRGAPPVAVITOPPSRP-FCSLLPAPPTVIEPSIQPHRWITLELTKSSIRIFTACNRG
>Mastelia_putorius_furo
MSGNGSPSDVAFPLCSRT---NNF-----STASIMMVLVLTENQIWIIFNCSG-
>Hymobius_retdardatus
MGINSGAPLQVAFTRCSGT---NNF-----TSSSEIMKVLVLTENQIWIIFNCSG-
>Pygocentrus_nattereri
MGIFRGAPTQVAFPPACRLP---SLY-----NTSSSEIMKVLVLTENQIWIIFTVSSRG
>Calidris_pugnax
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Gallinula_mellie
MSGNSGAPQVAFALYKQ---NL-----NTSSIKIMKVLVLTENQIWIIFNCSRG-
>Myotis_brandtii
MSGNGAPSRVAFPLCSRP---NHA-----CTPSVMKMLVLTENQIWIIONCSG-
>Haplochromis_burtoni
MGIFRGAPTAAAFPPPTPPRDLIAPHSVIQPSIQPSIKMTLELTKSSIWIFTACNRG
>Pterocles_gutturalis
-----MKVLVLTENQIWIIFNCSG-
>Beypus_novemcinctus
MGINSPPFQVAFSPPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Aloua_aloua
MGIFRGAPTQVAFPPRRLP---SLY-----RTSISQIMKVLVLTENQIWIIFTNFSRG
>Latimeria_chalumnae
MGINSGAPLQVAFPLCSK---NLF-----NTSSIKIMKVLVLTENQIWIIFNCSRG
>Colius_striatus
-----MKVLVLTENQIWIIFNCSG-
>Columba_livia
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Leptosomus_discolor
-----MKVLVLTENQIWIIFNCSG-
>Alligator_mississippiensis
MGINSGAPLQVAFPLCSK---NF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Oculous_canorus
-----MKVLVLTENQIWIIFNCSG-
>Pecilia_formosa
MGIFAGAPALATSPSPS---HSLSPVPTHTI---IQPRHKMTLELTKSSIWIFTACNRG
>Sarcophilus_harrisii
MGINSPPFQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Monodelphis_domestica
MGINSPPFQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Esor_lucius
MGIFRGALPQASGPPRRLP---SLF-----CTSTQIMKVLVLTENQIWIIFTSSRG
>Aquila_chrysaetos_canadensis
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Coturnix_japonica
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Eurypyga_helias
-----MKVLVLTENQIWIIFNCSG-
>Condylura_cristata
MSGNRGAPLQVAFPLRGTE---SSF-----STASIMKVLVLTENQIWIIFNCSG-
>Oryctolagus_cuniculus
MGISRAPVQVAFPLCSK---RAG-----STGSMKMLVLTENQIWIIFNCSRG
>Opisthocomus_hoazini
-----MKVLVLTENQIWIIFNCSG-
>Sclerogages_formosus
MGIFRGAPTQVAFPLRLP---PLF-----STSTSEIMKVLVLTENQIWIIFTNFSRG
>Acanthitta_chloris
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFTNCSG-
>Phaethon_lepturus
MGINSGAPLQVAFPLCSKN---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Equus_asinus
MSGNGPPFQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Manis_javanica
MSGNGPPFQVAFPLCSK---SNF-----STTSVIMKVLVLTENQIWIIFNCSG-
>Picaoides_pubescentis
-----MKVLVLTENQIWIIFNCSG-
>Platichthys_stellatus
MGIFRGAPTAAQPPAFS-PR-----APTLSV---IQPSIKMTLELTKSSIWIFTACNRG
>Macaca_fascicularis
MGITSGTQVQVAFPLCSK---IHF-----STSSVIMKVLVLTENQIWIIFNCSG-
>Loxodonta_africana
MGINSGLSFQVAFPLYSK---NNF-----STSSVIMKVLVLTENQIWIIFNCSG-
>Meleopithecus_undulatus
-----MKVLVLTENQIWIIFNCSG-
>Cavia_porcellus
MGIFRGALPWFVAFPLCSK---SDC-----SASSVMKMLVLTENQIWIIFNCSGLD-
>Oncorhynchus_mykiss
MGIFRGALTVASGPPRRLP---SLF-----CTSTTHIMKVLVLTENQIWIIFTSSRG
>Tupaia_chinensis
MSGYSAAAVGAA-SKPLCSK---HHR-----STSSVMKMLVLTENQIWIIONCSG-
>Leptosomus_souletus
MGIFRGAPTQVAFPLRLP---SLF-----RTSTSEIMKVLVLTENQIWIIFTNCSRG
>Ictalurax_punctatus
MGIFHRAPSDVAFPAARLP---SLF-----NTSTSEIMKVLVLTENQIWIIFTVSNRG
>Aptenodytes_forsteri
-----MKVLVLTENQIWIIFNCSG-
>Anolis_carolinensis
MGITSGAANDVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Tyto_alba
MGINSGAPLQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Struthio_camelus_australis
MGINSGAPLQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Oryzomys_picta
MGINSGAPQVAFPLCSKN---NNF-----STLSIIMKVLVLTENQIWIIFNCSG-
>Takifugu_rubripes
MGIFRGAPPNGTACGPPSP-PSGLYFTPTTSDIQPTILPSIKMTLELTKSSIWIFTATNRG
>Tinnius_guttatus
MGINSGAPLQVAFPLCSK---NNF-----STSSIIMKVLVLTENQIWIIFNCSG-
>Galypte_anne
-----MKVLVLTENQIWIIFNCSG-

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>Homo_sapiens-----MYLGDSHVLNLTLCNCOHRK1WLHSGEDCYHCRTEPLRP-----
>Anser_cygnoides-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Apteryx_australis_mantelli-----MQLKLPEDGGLSDRRLSLENIIPAT1HTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Menidia_menidia-----MSPPA---LPTV-FCOCHRK1WLHSGAGREIRICFPFN-----
>Oryzias_melastigma-----MTPPA---LPPG-FCOCHRK1WLHSAAGEEHVGFVLSKHVVDG-----
>Buceros_rhinoceros_silvestri-----MIPATVHTVLSALYLCOHRKNMLHEEKQTKR-----
>Caprimulgus_carolinensis-----MIPAT1HSVLSALYLCOHRKNMLHSEEK-HK0H-----
>Gerania_cristata-----MIPATVHTVLSALYLCOHRKNMLDSEEK-HK0H-----
>Odobenus_rossmarus_divergens-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACRLCRITPPRP-----
>Physeter_catodon-----MYLGDSHVINLTLCNCOHRK1WLHSGEVGYCGRDPPRP-----
>Charadrius_vociferus-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Pteropus_vampyrus-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACQCRTEPPRP-----
>Pterocles_gutturalis-----MIPATVHTVLSALYLCOHRKNMLHSEEK-YEHKKR-----
>Colius_striatus-----MIPATVHTVLSALYLCOHRKNMLHSEEK-H-----
>Columba_livia-----MIPATVHTVLSALYLCOHRKNMLHSEEK-H-----
>Merops_nubicus-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HRKHGLKCACS-----
>Alligator_mississippiensis-----M1LAAFHVL SALYLCOHRKNMLHSEEHREYVPKD-----
>Oculous_canorus-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HKHGELKCACS-----
>Xiphophorus_maculatus-----MNTPA---QPIV-FCOCHRK1WLHSAVEGEHKCFSS-----
>Sarcophilus_harrisii-----MYLRDCHD1SNTLCNCOHRK1WLHSGEKFHRRGSSD-----
>Galeopterus_variegatus-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACQCRTEPPRP-----
>Monodelphis_domestica-----MYLRKCP1PMTLCNCOHRK1WLHSGEDCCSHRKGSSD-----
>Esox_lucius-----MSPPA---VPV-FCOCHRK1WLHSTAARGLPFVFSSSP-----
>Aquila_chrysaetos_canadensis-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Gallus_gallus-----MYORLSLENIIPATVDTVLSALYLCOHRKNMLDSEKH-----
>Gavia_stellata-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Eurypyga_helias-----MIPATVHTVLSALYLCOHRKNMLHSEEE-HK0H-----
>Erinaceus_europaeus-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACQCRTEPPRP-----
>Oryctolagus_cuniculus-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACTHCRTEPPRP-----
>Ornithorhynchus_anatinus-----MYLRDHHVSDSLFCOHRK1WLSRSGRRVLGN-----
>Tauraco_erythrolophus-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Pileocolossus_altivelis-----MNPST---LPAY-HCCOHRK1WLHSAAGSHLSLFLVPAMPHLOFAE-----
>Parus_major-----MSRAPPALGRSCSAGRGRGGA1PGLSAGRAGRIYRDRLSLENIIPATVHTVLSALYLCOHRKNMLHSEKHRRGLKCACS-----
>Egretta_garzetta-----MIPATVHTVLSALYLCOHRKNMLHSEEK-H-----
>Latteolabrax_japonicus-----MSPPA---LPVVQLCCOHRK1WLHSAARGISRD-----
>Ceratotherium_simum_simum-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACQCRTEPPRP-----
>Manis_javanica-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACFCGTAPRRL-----
>Picaoides_pubescens-----MIPATVDTVLSALYLCOHRKNMLHSEKH-HRKH-----
>Oynoglossus_semilaevis-----MSPPA---WPSV-SCCOHRK1WLHSAAGHHSDAFNS-----
>Loxodonta_africana-----MEQTSLSVFIJRRLIFENMYLGDSGVLMPLCNCOHRK1WLHSGEACTHCRTEPPRP-----
>Fulmarus_glacialis-----MIPATVHTVLSALYLCOHRKNMLHSEEK-RK0H-----
>Nestor_notabilis-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Mus_musculus-----MYLGDNHVLNLTLCNCOHRK1WLHSGEACTHCRTEPPRP-----
>Oncorhynchus_nerka-----MSPTA---VPVY-HCCOHRK1WLHSDAGGKFPATSVFLLA1VI-----
>Tupaia_chinensis-----MYLGDSHVLNLTLCNCOHRK1WLHSGEACQCRTEPPRP-----
>Trichechus_manatus_latirostr-----MYLRDSHVLTLCNCOHRK1WLHSGEACTHCRTEPPRP-----
>Pygoscelis_adeliae-----MIPATVHTVLSALYLCOHRKNMLHSEEK-HK0H-----
>Anolis_carolinensis-----MSPENHAALETLGLCOHRKNMLHSEKCFSS-----
>Tyto_alba-----MIPATVHTVLSALYLCOHRKNMLHSEKH-Y-----
>Struthio_camelus_australis-----MYMVI1CHRDQLQLNSLSKRLRLNIIPATVHTVLSALYLCOHRKNMLHSEKH-HK0H-----
>Oryzomys_picta-----MTLVA1HAVLSTVLCOHRKNMLHSEKHVSREAFTKD-----
>Galypte_anna-----MIPATVHTVLSALYLCOHRKNMLHSEEK-LK0H-----
>Apaloderma_vittatum-----MIPATVHTVLSALYLCOHRKNMLHSEKFPNTKD-----
>Orycteropus afer afer-----MYLGDRIY-LNLTLCNCOHRK1WLHSGGACTHCRTEPPRP-----

>Gallus_gallus-----MIPATVDTVLSALQLCOHRNNMLGSEKHQI-----
>Anas_platyrhynchos-----MWNISGGADQRLSLENIWIPATVDTVLSALYLCOHRNNMLGSECHKNKSH-----
>Apteryx_australis_mantelli-----WQL-----KLPEGGGLSGNDQRLSLENIWIPATHVTVLSALYLCOHRNNMLHSEKHKNH-----
>Buceros_rhinoceros_silvestri-----MIPATVHTVLSALYLCOHRNNMLHEEKQTKR-----
>Caprimulgus_carolinensis-----MIPATHSVLSALYLCOHRNNMLHSEKHKKQI-----
>Cariama_cristata-----MIPATVHTVLSALYLCOHRNNMLGSEKHKKI-----
>Ailuropoda_melanoleuca-----WYLGDSHVLNLTLOWCCHRKIWLHSEACRLQRTAPPP-----
>Balaenoptera_acutorostrata_s-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Ocharadrius_vooiferus-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Pteropus_alecto-----WYLGDSHVVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Pterocles_gutturalis-----MIPATVHTVLSALYLCOHRNNMLHSEKYEKHKR-----
>Latimeria_madaoensis-----NSTVLPVLLCYWYCCCHRKIWLHSEK-----
>Colius_striatus-----MIPATVHTVLSALYLCOHRNNMLHSEKHQI-----
>Columba_livia-----MIPATVHTVLSALYLCOHRNNMLHSEKHQI-----
>Leptosomus_discolor-----MIPATVHTVLSALYLCOHRNNMLYSEKHQI-----
>Alligator_mississippiensis-----WTLAAMHGVLSALYLCOHRNNMLHSEEHREYVPO-----
>Oculous_canorus-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKHKEGLKAGS-----
>Sarcophilus_harrisii-----WYLRDCHDI SMTLOWCCHRVNLHSEKCFHGRREGSD-----
>Galiopterus_variegatus-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Haliaeetus_leucoccephalus-----MIPATVHTVLSALYLCOHRNNMLHSEKHQI-----
>Gavia_stellata-----MIPATVHTVLSALYLCOHRNNMLHSEKHKNH-----
>Balearica_regulorum_gibberic-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Erinaceus_europaeus-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Oryctolagus_cuniculus-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Tauraco_erythrophus-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Opisthocomus_hoazin-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKHKEGLKAGS-----
>Lepidothrix_coronata-----MIPATVHTVLSALYLCOHRNNMLGSEKHKKI-----
>Nisponia_nippon-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Equus_asinus-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Manis_javanica-----WYLGDSGVVLNLTLOWCCHRKIWLHSEACGCGTAPPR-----
>Picooides_pubescens-----MIPATVDTVLSALYLCOHRNNMLHSEKHKKI-----
>Homo_sapiens-----MGTYSFFPSSGSLLPQRLLIFQWYLGDSHVLNLTLOWCCHRKIWLHSEDCYHCRTEPLRP-----
>Loxodonta_africana-----MEQTSLSVFI SRRLLIFENWYLGDSGVVLNPLWCCHRVNLHSEACYHCRTEPPPP-----
>Fulmarus_glaialis-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Nestor_notabilis-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Orioctulus_griseus-----WYLGDSHVLNLTLOWCCHRKIWLHSEACYCRTEPPPP-----
>Tupaia_chinensis-----WYLGDSHVLNLTLOWCCHRKIWLHSEACGCRTEPPPP-----
>Trichechus_manatus_latirostr-----WYLRDSHVVLNLTLOWCCHRVNLHSEACYHCRTEPPPP-----
>Aptenodytes_forsteri-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Anolis_carolinensis-----NSPENHAAL EILQLCOHRNNMLHSEKHQI SCS-----
>Tyto_alba-----MIPATVHTVLSALYLCOHRNNMLHSEKHQI-----
>Struthio_camelus_australis-----WYHVV IOWDOLQLNSLHQRLRLNWI PA-VHTVLSALYLCOHRNNMLHSEKHKKI-----
>Oryzomys_picta-----WTLVAIHAVLSTYLCOHRNNMLHSEKHVSCOREAF TKD-----
>Galypte_anna-----MIPATVHTVLSALYLCOHRNNMLHSEKHKKI-----
>Apaloderma_vittatum-----MIPATVHTVLSALYLCOHRNNMLHSEKXPNTKD-----
>Orycteropus_afer_afer-----WYLGDRHY-VLNTLOWCCHRKIWLHSGGACYHCRTEPPPP-----

>Denio_rerio-----MGWSRSQAVLQLYRALLRAGQLQYTDYDYYRVVYTRFRRQGT-LSAPAEKEDALKRGGFFLNSRLGGLV

>Acipenser_sinensis-----MGWSRSQAVLQLYRALLRAGRLQHTDRNYRRAALSRFFRRQGG-LREEGARELALKRGLVFLHSKLGGLV

>Channa_punctata-----MLHVQLYSLAVNVPYTSRQGGVPLHVWSLMGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQD-LTIPQDKEEALKRGGFFLSSRLGGLM

>Xoser_oygnoides-----MAAWSRAVNLVSLYRALLRGRRLQYTDYDYYRAVAREFRRCQD-LORPEDEKEREKGGAFLLRSKLGGLI

>Rhacophorus_omeimontis-----MAGWSREAVLKLRYRALLREGRLQYTDYDYYSSYIRREFRKNQK-LANLEEKEXQLAKGGFFLOTKLGGLV

>Basillichthys_microlepidotus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQGT-LTVPDEKKEALKRGGFFLNSRLGGLM

>Porichthys_notatus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRVVAREFRRCQA-LTAPQDKEEALKRGGFFLSSKLGGLM

>Oryzias_melastigma-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRVVAREFRRCQA-LTVPDEKKEALKRGGFFLNSRLGGLM

>Tripterygion_delaiei-----MGWSRSQAVLELYRALLRAGRLQHTERYGYRRAVAREFRRCGT-LTLPDQKEDALRRGGFFLSSRLGGLM

>Trachinotus_blochii-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPADKEDALKRGGFFLNSRLGGLM

>Ailuropoda_melanoleuca-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Aebystoma_mexicanum-----MAAWSRAVNLVSLYRALLRGRRLQYTDYDYYFATVRREFRRNQD-LTEPDEKEREKGGAFLOTRLGGLV

>Micropterus_floridanus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPDEKEDALRRGGFFLRSRLGGLM

>Orcinus_orca-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Astyanax_mexicanus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPGEKEDALRRGGFFLTSRLGGLV

>Callidris_pugnax-----MAAWSRAVNLVTLYRALLRGRRLQYTDQDFYLASIRREFRKNQK-LDQLDEEKERQLEKGGAFLLGSKLGGLV

>Callorhynchus_millii-----MATWSRTAVLNLVYRALLRAGRLQYTDREYTYTYNVREFRKNQK-LTEEQRTQQLKGGIYFLNMLKGGLV

>Pteropus_vampyrus-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Haplochromis_burtoni-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPDEKKEALKRGGFFLSSRLGGLM

>Aloosa_alosa-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LSAPQEKEDALRRGGFFLNSRLGGLV

>Latimeria_chalumnae-----MAGWSRTAVLNLVYRALLREGRLQYTDYDYYTYNVREFRKNQK-LSDPEKEREKQLEKGGFFLQNLKGGLI

>Alligator_mississippiensis-----MAAWSRQAVLSLYRTLRRGRRLQYTDYDYLATIRREFRKNQK-LDQLDEKERQLEKGGAFLLGSKLGGLV

>Cyprinodon_variegatus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPDEKKEALKRGGFFLSSRLGGLM

>Sarcophilus_harrisii-----MAEPGRQAVLGLYRTLRRARELRLTDYDFYETIRREFRRPLPPGAGDAVQRQLEKGRAFLRGERGLV

>Galeoceratus_variegatus-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLAFIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Monodelphis_domestica-----MAEPGRQAVLGLYRALLRRARLQYTDYDFYEAIVAREFRRRPLPPGVQPEAVQRQLEKGRAFLRGERGLV

>Esox_lucius-----MGWSRSQAVLDLYRALLRAGRLQYTDYDYYRAVAHAREFRRCGT-LTAPSDKEEDALKRGGFFLHSRLGGLM

>Numida_meleagris-----MAAWSRQAVLTLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LQRLDEKERQLEKGGAFLLGSKLGGLV

>Acanthopobius_hasta-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LSSGDEKEDALKRGGFFLNSKLGGLM

>Aptereronotus_leptorhynchus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LNAPQEKEDALNRGGFFLSSRLGGLV

>Condyura_cristata-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLV

>Ochotona_princeps-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEPGEKEREKGLVFLRSKLGGLV

>Plecoglossus_altivelis-----MGWSRSQAVLDLYRALLRAGRLQHTDRNYRRAVAREFRRCQA-LSAPSDKEEDALKRGGFFLSSRLGGLV

>Scleropages_formosus-----MGWSRTAVLELYRALLRAGRLQYTDYDYYRHTLAREFRRCQA-LTNPDAREEALKRGGFFLRSRLGGLV

>Zonotrichia_albicollis-----MAAWSRQAVLTLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LQRLDEKERQLEKGGAFLLRSSLGGLV

>Lateolabrax_japonicus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTIPDEKEDALKRGGFFLSSRLGGLM

>Anoplocoma_fimbria-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAHAREFRRCQA-LTIPDEKKEALKRGGFFLNSRLGGLM

>Ceratotherium_simum_simum-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Oryzogllossus_semi-laevis-----MGWSRSQAVLKYKALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTIPDEKKEALKRGGFFLSSRLGGLM

>Pongo_abelii-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLNKGKGLRI

>Jaoulus_jaculus-----MAAWSRAVNLVYRSLLRGRRLQYTDREYTYTFIKREFRKNQK-LSGEEEKAQQLEKGLVFLGSKLGGLV

>Jaoulus_jaculus-----MAPWSRQAVLSLYRALLRGRRLQYTDYDYLASIRREFRKNQK-LQDPVAREKQLEKGLVFLHSKLGGLV

>Salvelinus_alpinus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTVPQDEKEDALKRGGFFLSSRLGGLM

>Lepisosteus_oculatus-----MGWSRTAVLELYRALLRAGRLQHTDRNYRRAVAREFRRCQD-LTAPQDKERALKRGGFFLSSRLGGLV

>Ictalurus_punctatus-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRTIAREFRRCQD-LSEPREKKEALKRGGFFLNSRLGGLI

>Trichechus_manatus_latirostr-----MAPWSRQAVLSLYRTLRRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

>Squalus_scanthias-----MATWSRAVNLVYRALLRGRRLQYTDREYTYTFIKREFRKNQK-LTGEDEKYNQLEKGIYFLKSKLGGLV

>Grotalus_adamanteus-----MATWSRQAVNLVYRALLRGRRLQYTDYDYLSSIKREFRKNQK-LTSPDEKERNLKKGGTFLHSKLGGLI

>Ohrysomys_picta-----MAAWSRQAVNLVYRALLRGRRLQYTDYDYLASIRREFRKNQK-LERLEDERERQLEKGGAFLLHSRLGGLV

>Takifugu_rubripes-----MGWSRSQAVLELYRALLRAGRLQYTDYDYYRRAVAREFRRCQA-LTAPDEKKEALKRGGFFLKSRLGGLM

>Oryzeteropus_afer_afer-----MAPWSRAVLSLYRTLRRGRRLQYTDYDYLASIRREFRKNQK-LLEDPEAREKQLEKGLVFLHSKLGGLI

HS0034 ENSG00000100335 WIEF1

>Homo_sapiens-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDAEAREKQLEKGLVFLHSGKLGRII
>Acipenser_sinensis-----MGWSRSQAVLQLYRALLRAGRPLQHTDRNYRRAALSREFFRQDG-L-REEGARELALKRGLVFLHSGLGGLV
>Channa_punctata-----MLHVQLYSIAVNVPTSRDGVPLHVLSLWGWSRSQAVLELYRALLRAGRLYOTDRNYRRAVAREFRQDG-L-TIPDQKEALKRGDFLSSRLGGLM
>Xoser_cygnoides-----MAAWSREAVLSLYRALLRGRRLRYTDRDYFASVRSSEFRQDG-LORPEDEKEREKQLEKGLFRLTQGLGLI
>Xenopus_tropicalis-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDAEAREKQLEKGLVFLHSGKLGRII
>Basillichthys_microlepidotus-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQGT-L-TVPEDKEEALKRGDFLNSRLGGLM
>Porichthys_notatus-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDG-L-TAPDQKEALKRGDFLSSRLGGLM
>Oryzias_latipes-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDG-L-TVAEDKEEALKRGDFLNSRLGGLM
>Tripterygion_delaiei-----MGWSRSQAVLELYRALLRAGRRLQHTERYGYRRAVAREFRQGT-L-TLPDQKEDALKRGDFLSSRLGGLM
>Trachinotus_blochii-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TVPADKEDALKRGDFLNSRLGGLM
>Brus_maritimus-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Hymobius_chinensis-----MAAWSRSQAVLSLYRALLRGRRLYOTDRDYFASVRSSEFRQDG-LTRPEDKERQLEKGLFRLTQGLGLI
>Micropterus_floridanus-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TVPEDKEDALKRGDFLRSRLGGLM
>Orcinus_orca-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Pygocentrus_nattereri-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-SAPAEKEDALKRGDFLSSRLGGV
>Calidris_pugnax-----MAAWSRQAVLTLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-DQLDEKERQLEKGFALQSKLGGLV
>Callorhynchus_millii-----MATWSRTAVLNLRYRALLRGRRLRYTDRDYFASVRSSEFRKNQK-L-TTEEQRTQQLKGGIYFLHMKLGGLV
>Pteropus_vampyrus-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Haplochromis_burtoni-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TVPEDKEEALKRGDFLSSRLGGLM
>Aloosa_alosa-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-SAPQEKEDALKRGDFLNSRLGGV
>Latimeria_chalumnae-----MAGWSRTAVLNLRYRALLRGRRLRYTDRDYNYNYNREFRKNQK-L-SQPEKEREKQLEKGFALQMLGGLI
>Alligator_mississippiensis-----MAAWSRQAVLSLYRLLRGRRLRYTDRDYFALATIRREFRKNQK-L-EQLDEKERQLEKGFALQSKLGGLV
>Sinuocyclocheilus_rhinoceros-----MGWSRSQAVLQLYRALLRAGRLYOTDRDYRRAVAREFRQGT-L-SAPAEKEDALKRGDFLNSRLGGV
>Kryptolebias_marmoratus-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TGAEDKEEALKRGDFLRSGLGGLM
>Sarcophilus_harrisii-----MAEPGRQAVLGLYRLLRARELRLTORQYVETIRREFRRLPPGAGFQAVQKLEKGFALRGERGLV
>Galeopterus_variegatus-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFALAFIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Monodelphis_domestica-----MAEPGRQAVLGLYRALLRARELRYTDRDYVEAVREFRRLPPGVQFQAVQKLEKGFALRGERGLV
>Esox_lucius-----MGWSRSQAVLDLYRALLRAGRRLYOTDRDYRRAVAREFRQGT-L-TAPSDREKDALKRGDFLHSLRGGLM
>Numida meleagris-----MAAWSRQAVLTLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-ORLEDEKERQLEKGFALQSKLGGLV
>Acanthopneuste_hasta-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-SGQEKEDALKRGDFLNSRLGGLM
>Apterontotus_leptorhynchus-----MGWSRSQAVLELYRALLRAGRRLYOTDRSYGRAVAREFRQDA-L-NAPEEKEDALKRGDFLSSRLGGV
>Erinaceus_europaeus-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPAAREKQLEKGLVFLHSGKLGII
>Ochotona_princeps-----MAPWSRQAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EEPEGREKQLEKGLVFLRSKLGGLV
>Plecoglossus_altivelis-----MGWSRSQAVLDLYRALLRAGRRLQHTDRNYRRAVAREFRQDA-L-SAPQEKEDALKRGDFLSSRLGGV
>Sclerophagus_ferrous-----MGWSRTAVLELYRALLRAGRRLYOTDRNYRRLAREFRQDA-L-TNPQAREEALKRGDFLRSRLGGV
>Sturnus_vulgaris-----MAAWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-ORLEDEKERQLEKGFALQMLGGV
>Latotabrax_japonicus-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TIPEDKEDALKRGDFLSSRLGGLM
>Trematomus_bernaohii-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDG-L-XKAQKEEALKRGDFLDSRLGGLM
>Equis_asinus-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Oryzias_latipes-----MGWSRSQAVLGLYKALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TIPEDKEEALKRGDFLSSRLGGLM
>Leucoraja_erinacea-----MAAWSRQAVLNLVRSLLRGRRLRYTDRDYFTIRREFRKNQK-L-SGEDEKQLEKGLVFLHSGKLGGLV
>Psammomyobes-----MAPWSREAVLSLYRALLRGRRLRYTDRDYFASIRREFRKNQK-L-EDLEAREKQLEKGLVFLHSGKLGII
>Salmo_salar-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TVSROKEEALKRGDFLSSRLGGLM
>Lepisosteus_oculatus-----MGWSRTAVLELYRALLRAGRRLQHTDRNYRRAVAREFRQDG-L-TAPDQKEREALKRGDFLSSRLGGV
>Trichomycterus_aeolatus-----MGWSRSQAVLQLYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TEPEDKEEALKRGDFLSSRLGGV
>Trichechus_manatus_latirostr-----MAPWSREAVLSLYRLLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPEAREKQLEKGLVFLHSGKLGII
>Squalus_acanthias-----MATWSRQAVLNLVRSLLRGRRLRYTDRDYFTIRREFRKNQK-L-GEDEKQLEKGFALQSKLGGLV
>Gekko_japonicus-----MAAWTREAVLNLVRSLLRGRRLRYTDRDYFTIRREFRKNQK-L-ERLEDEKERQLEKGFALQSKLGGLV
>Oryzias_picta-----MAAWSREAVLNLVRSLLRGRRLRYTDRDYFASIRREFRKNQK-L-ERLEDEKERQLEKGFALQSKLGGLV
>Takifugu_rubripes-----MGWSRSQAVLELYRALLRAGRRLYOTDRNYRRAVAREFRQDA-L-TAPEDEEALKRGDFLKSRLGGLM
>Oryzias_picta-----MAPWSREAVLSLYRLLRGRRLRYTDRDYFASIRREFRKNQK-L-EDPAAREKQLEKGLVFLHSGKLGII

>Homo_sapiens
MKTNTIEWVLNFKRG0PPD
>Anser_sylvaticus
MKTNVKMACPINFKRG0PPD
>Leptobrachium_boringii
MKSNAEKSRIKQFKRG0PPD
>Chaetura_pelagica
MKTNVKMACPINFKRG0PPD
>Buceros_rhinoceros_silvestri
MKTNVKMACPINFKRG0PPD
>Caprimulgus_carolinensis
MKTNVKMACPINFKRG0PPD
>Gariama_cristata
MKTNVKMACPINFKRG0PPD
>Acinonyx_jubatus
MKTNTIEWVLNFKRG0PPD
>Aebystoma_mexicanum
-----MOCIRKFKRG0PPD
>Physeter_catodon
MKTITEVLNFKRG0PPD
>Charadrius_vociferus
MKTNVKMACPINFKRG0PPD
>Myotis_ricketti
MKTNTIEWVLNFKRG0PPD
>Pterocles_gutturalis
MKTNVKMACPINFKRG0PPD
>Oesypus_novemcinctus
MKTNTIEWVLNFKRG0PPD
>Colius_striatus
MKTNVKMACPINFKRG0PPD
>Columba_livia
MKTNVKMACPINFKRG0PPD
>Merops_nubicus
MKTNVKMACPINFKRG0PPD
>Alligator_misissippiensis
MKANAKMACPINFKRG0PPD
>Oculus_canorus
MKANVNMACPINFKRG0PPD
>Sarophyllus_harrisii
MKTAEIWLNFKRG0PPD
>Galeopterus_variegatus
MKTNTIEWVLNFKRG0PPD
>Monodelphis_domestica
MKTAEIWLNFKRG0PPD
>Macropus_eugenii
MKTAEIWLNFKRG0PPD
>Aquila_chrysaetos_canadensis
MKTNVKMACPINFKRG0PPD
>Ooturnix_japonica
MKTNVKMACPINFKRG0PPD
>Gavia_stellata
MKTNVKMACPINFKRG0PPD
>Balearica_regularum_gibberic
MKTNVKMACPINFKRG0PPD
>Condyliura_cristata
MKTNTIEWVLNFKRG0PPD
>Oryctolagus_cuniculus
MKONTIEWVLNFKRG0PPD
>Elephantulus_edwardii
MKTNTIEWVLNFKRG0PPD
>Tauraco_erythrolophus
MKTNVKMACPINFKRG0PPD
>Opisthocomus_hoazin
MKTNVKMACPINFKRG0PPD
>Acanthis_flammea
MKTNVKMACPINFKRG0PPD
>Egretta_garzetta
MKTNVKMACPINFKRG0PPD
>Geratotherium_sinum_sinum
MKTNTIEWVLNFKRG0PPD
>Menia_javanica
MKTNTIEWVLNFKRG0PPD
>Ptiloides_pubescens
MKTNVKMACPINFKRG0PPD
>Loxodonta_africana
MKTNTIEWVLNFKRG0PPD
>Megalopterus_undulatus
MKTNVKMACPINFKRG0PPD
>Nannospalax_galili
MKTNSIWLNFKRG0PPD
>Tupaia_chinensis
MKTNTDVLNFKRG0PPD
>Trichechus_manatus_latirostr
MKTNTIEWVLNFKRG0PPD
>Aptenodytes_forsteri
MKTNVKMACPINFKRG0PPD
>Gekko_japonicus
MKTVMKMLNFKRG0PPD
>Tyto_alba
MKTNVKMACPINFKRG0PPD
>Struthio_camelus_australis
MKTNAKMACPINFKRG0PPD
>Chryseops_picta
MKINAKMACPINFKRG0PPD
>Tinamus_guttatus
MKTNAKMACPINFKRG0PPD
>Gallus_gallus
MKTNVKMACPINFKRG0PPD
>Apaloderma_vittatum
MKTNVKMACPINFKRG0PPD
>Orycteropus afer_afer
MKTNTIEWVLNFKRG0PPD

>Gallus_gallus
-----MKTNVVMACPRNFKRCRPPD
>Anser_cygnoides
-----MKTNVVMACPRNFKRCRPPD
>Leptobrachium_boringii
-----MKSNAEMSRIKHFKRCRPPD
>Chaetura_pelagica
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>Cariama_cristata
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>Felis_catus
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-----MKTITTEVVLRFNFKRCRPPD
>Charadrius_vociferus
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>Myotis_ricketti
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>Pterocles_gutturalis
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>Dasypus_noveboracensis
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>Colinus_striatus
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>Alligator_mississippiensis
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>Otocolus_canorus
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>Sarcophilus_harrisii
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>Galeopterus_variegatus
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>Gavia_stellata
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>Balearica_regularis_gibberic
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>Oryzotylagus_cuniculus
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>Elephantulus_edwardii
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>Melospittacus_undulatus
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>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Tinamus_guttatus
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>Calypte Anna
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>Apaloderma_vittatum
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>Oryzotylagus_afer_afer
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>Xerus_cynoides
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Cariacus_cristata
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>Lipotes_vexillifer
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>Pterocles_gutturalis
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>Oxyechus_novaezelandiae
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>Columba_livia
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>Colaptes_aerophilus
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>Anser_cygnoides
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>Chaetura_pelagica
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Canis_lupus_familiaris
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>Hymobius_chinensis
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>Eptesicus_fuscus
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>Pterocles_gutturalis
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>Oxyechus_hemionus
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>Columba_livia
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>Leptotomus_dioscori
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>Gallinago_vulgans
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>Monodelphis_domestica
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>Macropus_eugenii
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>Aquila_chrysaetos_canadensis
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>Colaptes_aerophilus
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>Apaloderma_vittatum
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>Chaetura_pelagica
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Gariema_cristata
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>Felis_catus
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>Hydrobius_retdatus
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>Ornithorhynchus_anatinus
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>Tauraco erythrophus
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>Opisthocomus_hoazin
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>Corvus_brachyrhynchus
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Gariema_cristata
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>Tyto_alba
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>Pelodiscus_sinensis
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>Apeloderm_vittatum
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>Anas_platyrhynchos	MSVTCWPRLCGSSPPSERPVAALWTP
>Xenopus_tropicalis	MSVKCLSLRCGSPP-SVMSVAI1PTP
>Apteryx_australis_mantelli	MSVTCWPRLCGSSPPSERPVAALWTP
>Buceros_rhinoceros_silvestri	MSVTCWPRLCGSSPPSERPVAALWTP
>Caprimulgus_carolinensis	MSVTCWPRLCGSSPPSERPVAALWTP
>Cariama_cristata	MSVTCWPRLCGSSPPSERPVAALWTP
>Ailuropoda_melanoleuca	MSITCWLRLCSSPPLSEWPVSINWTP
>Orcinus_orca	MSITCWLRLCSSPPLSEWPVSINWTP
>Charadrius_vociferus	MSVTCWPRLCGSSPPSERPVAALWTP
>Rousettus_aegyptiacus	MSITCWLRLCGSPPLSEWPVSINWTP
>Pterocles_gutturalis	MSVTCWPRLCGSSPPSERPVAALWTP
>Dasypus_novemcinctus	MSITCCLRLCSAPPLSEWSVSLN1IP
>Latimeria_chalumnae	MSMKCWSRHCGSP-LVMSVAA1WTP
>Colius_striatus	MSVTCWPRLCGSSPPSERPVAALWTP
>Columba_livia	MSVTCWPRLCGSSPPSERPVAALWTP
>Merops_nubicus	MSVTCWPRLCGSSPPSERPVAALWTP
>Alligator_mississippiensis	MSVTCWPRLCGSSPPSERPVAALWTP
>Sarcophilus_harrisii	MSVTCWPRLCGSSPPLERPVA1LWTP
>Monodelphis_domestica	MSLTCWLRLCGSPPLSEWPVSINWTP
>Aquila_chrysaetos_canadensis	MSLTCWSRLCGSAPLSEWPVSINW1P
>Gavia_stellata	MSVTCWPRLCGSSPPSERPVAALWTP
>Chlamydotis_macqueenii	MSVTCWPRLCGSSPPSERPVAALWTP
>Condylura_cristata	MSITCWLRLCSSPPLSEWPVSINWTP
>Oryctolagus_cuniculus	MSVTCWPRLCSSPPLSEWSVSINWTP
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>Opisthocomus_hoazin	MSVTCWPRLCGSSPPPERPVAALWTP
>Ficedula_albicollis	MSVTCWPRLCGSSPPSERPVAALWTP
>Nipponia_nippon	MSVTCWPRLCGSSPPSERPVAALWTP
>Equus_asinus	MSITCWLRLCSSPPLSEWPVSINWTP
>Manis_javanica	MSITCWLRLCSSPPLSEWPVSINWTP
>Picoides_pubescens	MSVTCWPRLCGSSPPSERPVAALWTP
>Callithrix_jacchus	MCSSMLFF-SILICVSTFSRSELL-ADNF-GGLHIQKSIKVTDAFLMSVTCWMRLCSSPPLSEWSVS1KWTP
>Loxodonta_africana	MSVTWWSRLCSSPPLSEWSVSINWTP
>Fulmarus_glacialis	MSVTCWPRLCGSSPPSERPVAALWTP
>Melopsittacus_undulatus	MSVTCWPRLCGSSPPSERPVAALWTP
>Fukomys_darlingi	MSVTCWLRICGSPPLSEWSVSISWTP
>Tupaia_chinensis	MSITCWLRLRSSPPLSEWSVSINWTP
>Trichechus_manatus_latirostr	MSITCWLRLCSSPPLSEWSVSINWTP
>Aptenodytes_forsteri	MSVTCWPRLCGSSPPSERPVAALWTP
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>Struthio_camelus_australis	MSVTCWPRLCGSSPPSERPVAALWTP
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>Calypte_anna	MSVTCWPRLCGSSPPSERPLAALWTP
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>Orycteropus_afer_afer	MSISCWLRCLSLPPLPEWSISINWTP

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>Amia_calva
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>Anser_cygnoides
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>Xenopus_tropicalis
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Ursus_maritimus
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>Orcinus_orca
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>Gallorhinchus_millii
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>Columba_livia
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>Galeopterus_variegatus
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MIIWINYRLLA VLSV1IHDSGLGKRPTAYVPKGGQSLMELGVLLC-AIFLYT--
>Callospermophilus_lateralis
MIIWINYRLLAGLSV1IHDSGLGKRPTAYVPKGGQSLMELGGLFY-AIQLHT--
>Salmo_salar-----MELCALMF-AIIHT--

>Tupaia_chinensis
MIIWINYRLLAGLSV1IHDSGLGKRPTAYVPKGGQSLMELGGLFY-AIQLLT--
>Lepisosteus_oculatus
MIIWINYRLVLSV1IHDSGLGKRPRSYVPKGGQSLMELVPLLH-AISLHT--
>Trichechus_manatus_latirostris
MIIWINYRLLAGLSV1IHDSGLGKRPTAYVPKGGQSLMELGGLFY-AIQLRT--
>Pygoscelis_adeliae
MIIWINYRLLA VLSV1IHDSGLGKRPTAYVPKGGQSLMELGVLLC-AIFLHT--
>Squalus_acanthias
MIIWINYRLLA VLSV1IHDSGLGKRPTAQRAKRGEEKI-----
>Struthio_camelus_australis
MIIWINYRLLA VLSV1IHDSGLGKRPTAYVPKGGQSLMELGVLLC-AIFLHT--
>Trachemys_scripta
MIIWINYRLLA VLSV1IHDSGLGKRRTAYVPKGGQSLMELGVLLY-AIFLHT--
>Tinamus_guttatus
MIIWINYRLLA VLSV1IHDSGLGKRPTAYVPKGGQSLMELGVLLC-AIFLHT--
>Calypte_anna
MIIWINYRLLA VLSV1IHDSGLGKRPTAYVPKGGQSLMELGVLLC-AIFLHT--
>Oryzopsis_eperouensis
MIIWINYRLLAGLSV1IHDSGLGKRPTAYVPKGGQSLMELGGLFY-AIQLRT--

HG0039.2 ENSG00000077092 RARB

>Homo_sapiens
MPRTRAIIRAGFVWAPSG
>Odobenus_rosmarus_divergens
MPRTRASRAGFVWAPSG
>Orcinus_orca
MPRTRASRAGLVWAPSG
>Rousettus_aegyptiacus
MPRTRASRAGLVWAPSG
>Galeopterus_variegatus
MPRTRAIIRAGFVWAPSG
>Condylura_cristata
MPRTRASRAGFVWAPSG
>Ochotona_princeps
MPRTRATQAGSLWAPSG
>Elephantulus_edwardii
MRRTRASRAGVWAPSG
>Equus_przewalskii
MPRTRASRAGFVWAPSG
>Marmota_marmota_marmota
MPRTRASRAGFVWAPSG
>Tupaia_chinensis
MPRTRASRAGLVWAPSG
>Trichechus_manatus_latirostr
MPRTRAIIRAGFVWAPSG
>Orycteropus_afer_afer
MPRTQTIIRAGFVWAPSG

>Homo_sapiens	-----MGSNDSIWHLN
>Anser_cygnoides	-----MGSNDSIWHLN
>Xenopus_laevis	-----MGSNDSIWHFN
>Chaetura_pelagica	-----MGSNDSIWHLN
>Apteryx_australis_mantelli	-----MGSNDSIWHLN
>Buceros_rhinoceros_silvestri	-----MGSNDSIWHLN
>Caprimulgus_carolinensis	-----MGSNDSIWHLN
>Gariama_cristata	-----MGSNDSIWHLN
>Felis_catus	-----MGSNDSIWHLN
>Balaenoptera_acutorostrata_s	-----MGSNDSIWHLN
>Calidris_pugnax	-----MGSNDSIWHLN
>Miniopterus_natalensis	-----MGSNDSIWHLN
>Pterocles_gutturalis	-----MGSNDSIWHLN
>Dasypus_novemcinctus	-----MHKYSVWEMGSNDSIWHLN
>Columba_livia	-----MGSNDSIWHLN
>Leptosomus_discolor	-----MGSNDSIWHLN
>Cuculus_canorus	-----MGSNDSIWHLN
>Sarcophilus_harrisii MVDNWRNWCISRGKQIPRSISVSSAGASGLLQSIIIPKQKVCITYYRCIIISKLQIFLKIWHHLVARRSPENPIESRGYPKSGHPPAAFPKSGEKGHRSHPI SFILHPSGPLRF SRERGRRLGKPPNAFLWSPSREARRRPKLRSSHFPHSRLGLQLPTSDNADSPSVWEMGSNDSIWHLS	-----MGSNDSIWHLS
>Geleopteris_variegatus	-----MGSNDSIWHLN
>Monodelphis_domestica	-----MGSNDSIWHLS
>Haliaeetus_leucoccephalus	-----MGSNDSIWHMN
>Otornix_japonica	-----MGSNDSIWHLN
>Gavia_stellata	-----MGSNDSIWHLN
>Chlamydotis_macqueenii	-----MGSNDSIWHLN
>Condylura_cristata	-----MGSNDSIWHLN
>Oryctolagus_cuniculus	-----MGSNDSIWHLN
>Elephantulus_edwardii	-----MGSNDSIWHLN
>Ornithorhynchus_anatinus	-----MGSNDSIWHLN
>Tauraco_erythrolophus	-----MGSNDSIWHLN
>Opisthocomus_hoazin	-----MGSNDSIWHLN
>Lepidothrix_coronata	-----MGSNDSIWHLN
>Nipponia_nippon	-----MGSNDSIWHLN
>Equus_przewalskii	-----MGSNDSIWHLN
>Picooides_pubescens	-----MGSNDSIWHLN
>Loxodonta_africana	-----MGSNDSIWHLN
>Melopsittacus_undulatus	-----MGSNDSIWHLN
>Peromyscus_maniculatus_baird	-----MGSNDSIWHLN
>Tupaia_chinensis	-----MGSNDSIWHLN
>Aptenodytes_forsteri	-----MGSNDSIWHLN
>Gekko_japonicus	-----MGSNDSIWHLN
>Tyto_alba	-----MGSNDSIWHLN
>Pelodiscus_sinensis	-----MGSNDSIWHLN
>Tinamus_guttatus	-----MGSNDSIWHLN
>Calypte_anna	-----MGSNDSIWHLN
>Apaloderma_vittatum	-----MGSNDSIWHLN
>Orycteropus_afer_afer	-----MGSNDSIWHLN

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>Homo_sapiens
MFPALRRRKRSRSHPPSRPGL-----
>Apteryx_australis_mantelli
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Mustela_putorius_furo
MFPALRRRKRSRSHPPSRPGL-----
>Physeter_catodon
MFPALRRRKRSRSHPPSRPGL-----
>Miniopterus_natalensis
MFPALRRRKRSRSHPPSRPGL-----
>Alligator_mississippiensis
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Galeopterus_variegatus
MFPALRRRKRSRSHPPSRPGL-----
>Aquila_chrysaetos_canadensis
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Coturnix_japonica
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Condylura_cristata
MFPALRRRKRSRSHPPSRPGL-----
>Oryctolagus_cuniculus
MFPALRRRKRSRSHPPSRPGL-----
>Elephantulus_edwardii
MFPALRSRKRSRSHPPSRPGL-----
>Ficedula_albicollis
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Equus_caballus
MFPALRRRKRSRSHPPSRPGL-----
>Loxodonta_africana
MFPALRRRKRSRSHPPSRPGL-----
>Melopsittacus_undulatus
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Chinchilla_lanigera
MFPALRRRKRSRSHPPSRPGL-----
>Trichechus_manatus_latirostr
MFPALRRRKRSRSHPPSWPGL-----
>Anolis_carolinensis
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSSAAQRRIL-----
>Pelodiscus_sinensis
MFAALRR-RRKRSQPPSRPGLLLYYLPSSSCSAAAAAQRRRL-
>Orycteropus afer afer
MFPALRRRKRSRSHPPSRPGL-----

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>Danio_rerio-----MTAIPQSIFPAP~SLYYF
>Acipenser_sinensis-----MTAIPQSIFPAP~SLYYF
>Anser_cygnoides-----MTAIPQIFPAP~SLYYF
>Pelophylax_nigromaculatus-----MTAVPQIFPAP~SLYYF
>Chaetura_pelagica-----MTAIPQIFPAP~SLYYF
>Apteryx_australis_mantelli-----MTAIPQIFPAP~SLYYF
>Oryzias_melastigma-----MSGVRRPOPVDQVRRRHVRALELAQLEGGGEGEGKGGFCHFFP~FSLSTHLSLTLSLSLFSL-----LSFLKKAMTAIPRSIFASAQSLYYF
>Tripterygion_delaiei-----MTAIPRSIFASAPSLYYF
>Mustela_putorius_furo-----MTALPQIFPAP~SLYYF
>Lipotes_vexillifer-----MTALPQIFPAP~SLYYF
>Pygocentrus_nattereri-----MSVHWFCHFSLLPLPGFALPMFCMSVSIHLTFKFAGTSRP~HL-----NLQLRGAFATFS~SLS-----LSLFKKAMTAIPQSIFPAP~SFYYF
>Calidris_pugnax-----MFCMSLSIQAPDVQVRRDVT~AL-----ELAAQGGFCHFFH~LSLSLTLSP~PSLSLFFFC-----TKKKKKAMTAIPQIFPAP~SLYYF
>Rousettus_aegyptiacus-----MTALPQIFPAP~SLYYF
>Dasypus_novemcinctus-----MTALPQIFPAP~SLYYF
>Alosa_alosa-----MTAIPQSIFPAP~SLYYF
>Latimeria_chalumnae-----MTAIPQSIFPAP~SLYYF
>Alligator_mississippiensis-----MTAIPQIFPAP~SLYYF
>Sarcophilus_harrisii-----MTALPQIFPAP~SLYYF
>Galeopterus_variegatus-----MTALPQIFPAP~SLYYF
>Esox_lucius-----MTAIPQSIFPAP~SLYYF
>Haliaeetus_leucocephalus-----MFCMSLSIQAPDVQVRRDVT~AL-----ELAAQGGFCHFFH~LSLSFSLSLPL~PLSLFFFP-----HKKKKKAMTAIPQIFPAP~SLYYF
>Gallus_gallus-----MSLSIQAPDVQVRGDVT~AL-----ELAAQGGFCHFFH~LALFL~PSFPLSP~LSPSLFFPR-----TQKKKKAMTAIPQIFPAP~SLYYF
>Erinaceus_europaeus-----MTALPQIFPAP~SLYYF
>Ochotona_princeps-----MTALPQIFPAP~SLYYF
>Elephantulus_ewardii-----MTALPQIFPAP~SLYYF
>Ornithorhynchus_anatinus-----MTALPQIFPAP~SLYYF
>Sclerophagus_formosus-----MSAVPQSIFSAP~SLHYP
>Geospiza_fortis-----MSLSIQAPDVQVRRDVT~AL-----ELAAQGGFCHFFH~LSLSPSLSPSLP~LPLSLFLAQKKKKKKKKKKAMTAIPQIFPAP~SLYYF
>Egretta_garzetta-----MTAIPQIFPAP~SLYYF
>Ceratotherium_simum_simum-----MTALPQIFPAP~SLYYF
>Manis_javanica-----MTALPQIFPAP~SLYYF
>Callithrix_jacchus-----MCVHWCELPSPSPSLLLALPMFCVSLSIQTPDVQVRRDVT~AL-----ELAAQGGFCHFFSSLSLSLSPPLSLFSLSLFFFFF-----LLKKKKAMTALPQIFPAP~SLYYF
>Loxodonta_africana-----MTALPQIFPAP~SLYYF
>Melopsittacus_undulatus-----MSLSIQAPDVQVRRDVT~AL-----ELAAQGGFCHFFH~LSLSFSPSLSLSL~SFFFFPFSL-----HKKKKKAMTAIPQIFPAP~SLYYF
>Mus_musculus-----MTALPQIFPAP~SLYYF
>Salmo_salar-----MTAIPQSIFPAP~SLYYF
>Lepisosteus_oculatus-----MTAIPQSIFPAP~SLYYF
>Ictalurus_punctatus-----MTAIPQSIFSAP~SLYYF
>Trichechus_manatus_latirostr-----MTALPQIFPAP~SLYYF
>Thamnomphis_sirtalis-----MFCMSLSIQPLDVQVRRDVT~AL-----ELAAQGGFCHFFH~LSLSLTLSPPTVS-----PSLAQKGKKEKAMTAIPQIFPAP~SLYYF
>Pelodiscus_sinensis-----MTAIPQIFPAP~SLYYF
>Calypte_anna-----MTAIPQIFPAP~SLYYF
>Orycteropus_afer_afer-----MTALPQIFPAP~SLYYF

```

>Homo_sapiens	-----MTALPQFIFF-APSLYYF
>Acipenser_sinensis	-----MTAIPQSIFP-APSLYYF
>Anser_cygnoides	-----MTAIPQFIFF-APSLYYF
>Pelophylax_nigromaculatus	-----MTAVPQFIFF-APSLYYF
>Chaetura_pelagica	-----MTAIPQFIFF-APSLYYF
>Apteryx_australis_mantelli	-----MTAIPQFIFF-APSLYYF
>Tripterygion_delaiei	-----MTAIPRSIFASAPSLYYF
>Canis_lupus_familiaris	-----MTALPQFIFF-APSLYYF
>Lipotes_vexillifer	-----MTALPQFIFF-APSLYYF
>Astyanax_mexicanus	-----MTAIPQFIFF-APSLYYF
>Calidris_pugnax	-----MTAIPQFIFF-APSLYYF
MFCMSLSIQAPDVQVRRDVTSALELAAOGGCHFFHLSL LLSLPLSPSPSLSLFFFPC T K K K K K A M T A I P Q F I F F - A P S L Y Y F	
>Rousettus_aegyptiacus	-----MTALPQFIFF-APSLYYF
>Dasypus_novemcinctus	-----MTALPQFIFF-APSLYYF
>Alosa_alosa	-----MTAIPQSIFP-APSLYYF
>Latimeria_chalumnae	-----MTAIPQSIFP-APSLYYF
>Alligator_mississippiensis	-----MTAIPQFIFF-APSLYYF
>Sinocyclocheilus_rhinoceros	-----MTAIPQSIFP-APSLYYF
>Sarcophilus_harrisii	-----MTALPQFIFF-APSLYYF
>Galeopterus_variegatus	-----MTALPQFIFF-APSLYYF
>Esox_lucius	-----MTAIPQSIFP-APSLYYF
>Haliaeetus_leucocephalus	-----MTAIPQSIFP-APSLYYF
MFCMSLSIQAPDVQVRRDVTSALELAAOGGCHFFHLSL SFSLSLSLPL-PLSLFFFPLH K K K K K A M T A I P Q F I F F - A P S L Y Y F	
>Gallus_gallus	-----MTAIPQSIFP-APSLYYF
---MSLSIQAPDVQVRRDVTSALELAAOGGCHFFHLALFL-PSFPLSPS-LSPSLFFPRTQ K K K K A M T A I P Q F I F F - A P S L Y Y F	
>Erinaceus_europaeus	-----MTALPQFIFF-APSLYYF
>Ochotona_princeps	-----MTALPQFIFF-APSLYYF
>Elephantulus_edwardii	-----MTALPQFIFF-APSLYYF
>Ornithorhynchus_anatinus	-----MTALPQFIFF-APSLYYF
>Scleropages_formosus	-----MSAVPQSIFS-APSLHYP
>Sturnus_vulgaris	-----MTAIPQFIFF-APSLYYF
>Egretta_garzetta	-----MTAIPQFIFF-APSLYYF
>Ceratotherium_simum_simum	-----MTALPQFIFF-APSLYYF
>Manis_javanica	-----MTALPQFIFF-APSLYYF
>Loxodonta_africana	-----MTALPQFIFF-APSLYYF
>Melopsittacus_undulatus	-----MTAIPQSIFP-APSLYYF
---MSLSIQAPDVQVRRDVTSALELAAOGGCHFFHLSL SFSPSLSLSLSSFFFFPFS L H K K K K K A M T A I P Q F I F F - A P S L Y Y F	
>Dipodomys_ordii	-----MTALPQFIFF-APSLYYF
>Salmo_salar	-----MTAIPQSIFP-APSLYYF
>Lepisosteus_oculatus	-----MTAIPQSIFP-APSLYYF
>Ictalurus_punctatus	-----MTAIPQSIFS-APSLYYF
>Trichechus_manatus_latirostr	-----MTALPQFIFF-APSLYYF
>Thamnophis_sirtalis	-----MTAIPQSIFP-APSLYYF
MFCMSLSIQPLDVQVRRDVTSALELAAOGGCHFFHLSL SLSLLSPPT---VSPSLAQKGKKEKEK A M T A I P Q F I F F - A P S L Y Y F	
>Pelodiscus_sinensis	-----MTAIPQFIFF-APSLYYF
>Calypte_anna	-----MTAIPQFIFF-APSLYYF
>Orycteropus afer afer	-----MTALPQFIFF-APSLYYF

>Gallus_gallus	MTAIPQFIFF-APSLYYF
>Acipenser_sinensis	MTAIPQSIFP-APSLYYF
>Anser_cygnoides	MTAIPQFIFF-APSLYYF
>Pelophylax_nigromaculatus	MTAVPQFIFF-APSLYYF
>Chaetura_pelagica	MTAIPQFIFF-APSLYYF
>Apteryx_australis_mantelli	MTAIPQFIFF-APSLYYF
>Tripterygion_delaisi	MTAIPRSIFASAPSLYYF
>Mustela_putorius_furo	MTALPQFIFF-APSLYYF
>Lipotes_vexillifer	MTALPQFIFF-APSLYYF
>Astyanax_mexicanus	MTAIPQFIFF-APSLYYF
>Calidris_pugnax MFCMSLSIQAPDVQVRRDVTSALELAAOGGFCHEFFHL-SLSLLLSLPLSP-SPSLSLFFFCTKHKKKAMTAIPQFIFF-APSLYYF	MTALPQFIFF-APSLYYF
>Rousettus_aegyptiacus	MTALPQFIFF-APSLYYF
>Dasypus_novemcinctus	MTALPQFIFF-APSLYYF
>Alosa_alosa	MTAIPQSIFP-APSLYYF
>Latimeria_chalumnae	MTAIPQSIFP-APSLYYF
>Alligator_sinensis	MTAIPQFIFF-APSLYYF
>Catla_catla	MTAIPQSIFP-APSLYYF
>Sarcophilus_harrisii	MTALPQFIFF-APSLYYF
>Galeopterus_variegatus	MTALPQFIFF-APSLYYF
>Esox_lucius	MTAIPQSIFP-APSLYYF
>Haliaeetus_leucocephalus MFCMSLSIQAPDVQVRRDVTSALELAAOGGFCHEFFHL-SLSFSLSLPL-PLSLSFFPLHKKKKAMTAIPQFIFF-APSLYYF	MTALPQFIFF-APSLYYF
>Erinaceus_europaeus	MTALPQFIFF-APSLYYF
>Ochotona_princeps	MTALPQFIFF-APSLYYF
>Elephantulus_edwardii	MTALPQFIFF-APSLYYF
>Ornithorhynchus_anatinus	MTALPQFIFF-APSLYYF
>Sclerophages_formosus	MSAVPQSIFS-APSLHYP
>Sturnus_vulgaris	MTAIPQFIFF-APSLYYF
>Egretta_garzetta	MTAIPQFIFF-APSLYYF
>Ceratotherium_simum_simum	MTALPQFIFF-APSLYYF
>Manis_javanica	MTALPQFIFF-APSLYYF
>Callithrix_jacchus MFCVSLSIQTDPDVQVRRDVTSALELAAOGGFCHEFFSSLSLSLSPPLSLFSLSLSFFFFFLHKKKKAMTALPQFIFF-APSLYYF	MTALPQFIFF-APSLYYF
>Loxodonta_africana	MTALPQFIFF-APSLYYF
>Melopsittacus_undulatus ---MSLSIQAPDVQVRRDVTSALELAAOGGFCHEFFHL-SLSFSPSLSLSL-SFFFFFPFLHKKKKAMTAIPQFIFF-APSLYYF	MTALPQFIFF-APSLYYF
>Mus_musculus	MTALPQFIFF-APSLYYF
>Salmo_salar	MTAIPQSIFP-APSLYYF
>Lepisosteus_oculatus	MTAIPQSIFP-APSLYYF
>Ictalurus_punctatus	MTAIPQSIFS-APSLYYF
>Trichechus_manatus_latirostr	MTALPQFIFF-APSLYYF
>Gekko_japonicus	MTAIPQFIFF-APSLYYF
>Chrysemys_picta	MTAIPQFIFF-APSLYYF
>Calypte_anna	MTAIPQFIFF-APSLYYF
>Orycteropus afer afer	MTALPQFIFF-APSLYYF


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>Homo_sapiens
----MGG-VCYRNWQVSNQ
>Anas_platyrhynchos
----MCG-ICYVNWQVSSG
>Chaetura_pelagica
----MCG-ICYENWQVSSG
>Apteryx_australis_mantelli
----MCG-ICYVSWQVSSG
>Buceros_rhinoceros_silvestri
----MCG-ICYINWQVSSG
>Caprimulgus_carolinensis
----MCG-ICYINWQVSSG
>Acinonyx_jubatus
----MGG-VCYRNWQVSNQ
>Balaenoptera_acutorostrata_s
MTNQMGGLRLRYRNWQVSNQ
>Charadrius_vociferus
----MCG-ICYINWQVSSG
>Eptesicus_fuscus
----MGG-VCYRNWQVSNQ
>Pterocles_gutturalis
----MCG-ICYINWQVSSG
>Dasypus_noveboracensis
----MGE-LSYRNWQVSSG
>Columba_livia
----MCG-ICYINWQVSSG
>Leptosomus_discolor
----MCG-ICYINWQVSSG
>Alligator_mississippiensis
----MGG-ICYINWQVSNQ
>Galeopterus_variegatus
----MGG-VCYRNWQVSNQ
>Monodelphis_domestica
----MGG-VCYRNWQVSNQ
>Falco_cherrug
----MCG-ICYINWQVSSG
>Coturnix_japonica
----MCG-ICYINWQVSSG
>Gavia_stellata
----MCG-ICYINWQVSSG
>Chlamydotis_macqueenii
----MCG-ICYINWQVSSG
>Sorex_araneus
----MGG-VCYRNWQVSNQ
>Oryctolagus_cuniculus
----MGG-VCYRNWQVSNQ
>Tauraco_erythrolophus
----MCG-ICYINWQVSSG
>Opisthocomus_hoazini
----MCG-ICYINWQVSSG
>Pseudopodoces_humilis
----MCG-ICYINWQVSSG
>Phaethon_lepturus
----MCG-ICYINWQVSNQ
>Ceratotherium_simum_simum
----MGG-VCYRNWQVSNQ
>Manis_javanica
----MGG-VCYRNWQVSNQ
>Picoides_pubescens
----MCG-ICYINWQVPSG
>Loxodonta_africana
----MGG-VYRNWQVSNQ
>Fulmarus_glaucialis
----MCG-ICYINWQVSSG
>Melopsittacus_undulatus
----MCG-ICYINWQVSSG
>Heterocephalus_glaber
----MGG-VCYRNWQVSNQ
>Tupaia_chinensis
----MGG-ICYRNWQVSNQ
>Aptenodytes_forsteri
----MSG-ICYITWQVSSG
>Takydromus_sexlineatus
----MGG-ICYFNWQVSSG
>Struthio_camelus_australis
----MCG-ICYRSWQVSSG
>Chelonia_mydas
----MGG-ICYINWQVSSG
>Tinamus_guttatus
----MCG-ICYISWQVSSG
>Calypte_anna
----MCG-ICYINWQVSSG
>Apaloderma_vittatum
----MCG-ICYINWQVSSG
>Orycteropus afer afer
MTNQMGRL-VCYRNWQVSNQ
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HG0042.2 ENSGALG00000039985

>Gallus_gallus
MHSRCGGSVCAEHFI
>Anas_platyrhynchos
MHSMCGGNLCAEHFI
>Charadrius_vociferus
MCLMCGGILCAEHFI
>Columba_livia
MCLMCGGILCAEHFI
>Falco_cherrug
MCLMCGGILCAEHFI
>Balearica_regulorum_gibberio
MCLMCGGILCAEHFI
>Opisthocomus_hoazin
MCLMCGGILCAEHFI
>Phalacrocorax_carbo
MCLMCGGILCAEHFI
>Fulmarus_glaucialis
MGSVCGGILCAEHFI
>Melospittacus_undulatus
MHLMCGGILCAEHFI
>Aptenodytes_forsteri
MCLMCGGILCAEHFI
>Struthio_camelus_australis
MHFMCGAILCAEHFI
>Tinamus_guttatus
MHFMCGGILCAEHFI
>Apaloderma_vittatum
MCLMCGGILCAEHFI

HG0042.3 ENSG00000140937 CDH11

>Homo_sapiens
MPRGPLAAAAADL
>Leptonychotes_weddellii
MPRGPLAAAAADL
>Orcinus_orca
MPRGPLAAAAADL
>Rousettus_aegyptiacus
MPRGPLAAAAADL
>Manis_javanica
MPRGPLAAAAADL
>Loxodonta_africana
MPRGPLAAAAADL
>Octodon_degus
MPRGPLAAAAADL
>Orycteropus_afer_afer
MPRGPLAAAAADL

HG0042.4 ENSG00000140937 CDH11

>Homo_sapiens
MSSTSRDIPSQERSA
>Mustela_putorius_furo
MYSVSRDIPFQERSA
>Pteropus_vampyrus
MCSASRDIPFQERSA
>Condylura_cristata
MLSASRDIPLQDRSA
>Geraotherium_simum_simum
MCSASRDIPLQERSA
>Octodon_degus
MCSESKDIPLQERSA

HG0042.5 ENSG00000140937 CDH11

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>Homo_sapiens
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>Leptonychotes_weddellii
MGPGLGSLTPLRSSCARDRRPVARAHPPGPQKSLYFRLSGPV-TLYPVVIG
>Eptesicus_fuscus
-----MIIPVAVG
>Erinaceus_europaeus
MGPGLGPGVPPLRSP-RDRPPEARAHPLGPQSFPPWLSGPE-AFSPVGIG
>Peromyscus_maniculatus_baird
-----MTKSLCFWLGGPVKTFISVVIG
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>Homo_sapiens	-----MLFNEGASASLSNKRSMREDRAVHGYYWTRIFGKVD-DVSHCVRESHGDGHSSELLMGTWDSSCL-----
>Anas_platyrhynchos	MLTQHSKCAVQFNICYFPFIFYRLSORGEHTIQGSFLCARCVLAPLLI-----LLSLRFQVCAVLFQFIPLLLCHIQVDDLSNSLKNQHDWHAELLMGTWDSSCH-----
>Chaetura_pelagica	-----MGTWDSGCH-----
>Buceros_rhinoceros_silvestri	-----MGTWDSRCH-----
>Caprimulgus_carolinensis	-----MGTWDSRCH-----
>Cariama_cristata	-----MGTWDSRCR-----
>Mustela_utorius_furo	-----MLHWGVLCSLFL-MLFNEGASASLSNKRSMREDRAVHGYYWRRIFYEKVD-DVSNRVRESHGDGHSSELLMGTWDSSCL-----
>Hynobius_retardatus	-----MGTWDSSHCH-----
>Lipotes_vexillifer	-----MGTWDSRCL-----
>Callorhinchus_milii	-----MRTWDSLCCYCSAVLISQVNSIR-----
>Rousettus_aegyptiacus	-----MKEQAPHLANKRSMREDRAVHGYYWRRIFYGKVD-DVSNVRESHGHGRDLLMGTWDSSFL-----
>Pterocles_gutturalis	-----MGTWDSRRH-----
>Dasypus_novemcinctus	-----MGTWDSSCR-----
>Latimeria_chalumnae	-----MGTWDSRCH-----
>Colius_striatus	-----MGTWDSSHCH-----
>Columba_livia	-----MGTWDSRCHLSLAWT-----
>Leptosomus_discolor	-----MGTWDSSHCH-----
>Alligator_sinensis	-----MGTWDAHCLS-----
>Cuculus_canorus	-----MGTWDSRCH-----
>Galeopterus_variegatus	-----MLHRGVLCSLFL-MLFNEGASASLSNKRSMREDRAVHGYYWRTIFYGKVDVSKCVKESHGDGHSSELLKGTWDSSCL-----
>Aquila_chrysaetos_canadensis	-----MKHSLPSPFLLRRQVDYDPSNSLKDQHDWHSSELLMGTWDSRCH-----
>Gallus_gallus	-----MGTWDSSCR-----
>Balearica_regulorum_gibberic	-----MGTWDSRCH-----
>Erinaceus_europaeus	-----MGTWDSSCL-----
>Oryctolagus_cuniculus	-----MGTWDSSCL-----
>Elephantulus_edwardii	-----MGTWDSGHP-----
>Tauraco_erythrolophus	-----MRTWDSRCH-----
>Opisthocomus_hoazin	-----MGTWDSRCH-----
>Parus_major	-----MGTWDSRCR-----
>Egretta_garzetta	-----MGTWDSRCH-----
>Equus_asinus	-----MLHWGVLCSLFL-MLFNEGASASLSNKRSMREDRAVHGYYWRRISGKVD-DVSNVRESHGDGRSELLMGTWDSSCL-----
>Manis_javanica	-----MVDDVSHCVRKPHGDEHSELLVGTWDPSCLCSLVWILLVHDSRR-----
>Picoides_pubescens	-----MGTWDSRCH-----
>Loxodonta_africana	-----MGTWDSSCL-----
>Fulmarus_glacialis	-----MGTWDSRCH-----
>Nestor_notabilis	-----MGTWDSRCH-----
>Heterocephalus_glaber	-----MLRWGVLCSLFL-MPFNERASTLSNKRMRKDSVHGYSWRRIFYGKVDVSKCVREPHGDGHSALLMGTWDSSCF-----
>Pygoscelis_adeliae	-----MGTWDSRCH-----
>Python_bivittatus	-----MGSWDSSHCH-----
>Tyto_alba	-----MGTWDSRCH-----
>Tinamus_guttatus	-----MGTWDSHCR-----
>Calypte_anna	-----MGTWDSRCH-----
>Orycteropus_afer_afer	-----MGTWDSGCL-----

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>Acipenser_sinensis	-----MIPHEVPGSLSDS-----RCDFQCI-----RLRSVTSDEASQ-----
>Amia_calva	-----MIPHEVHGSLSES-----RRDFPSL-----RLRSMVLVRH-----
>Anser_cygnoides	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Rhacophorus_dennysi	-----MIPHEVVGVPsGI-----KCDFFPT-----RLKSVSVRQ-----
>Apteryx_australis_mantelli	-----MIPHEVTGSLSEI-----KCDFFPI-----RLKSKPARQ-----
>Oryzias_latipes	-----MIPHEVHGAFRS-----WSNSIFS-----CVKPGAGGQ-----
>Canis_lupus_familiaris	-----MIPHEEPGSPTIEI-----KCDFFPI-----RLKPEPARQ-----
>Hynobius_retardatus	-----MIPHEVSGSSGI-----KCDFLSL-----RLKP IPARQ-----
>Balaenoptera_acutorostrata_s	-----MIPHEEPGSPTIEI-----KCDFFPI-----RLKAEPARE-----
>Pygocentrus_nattereri	-----MIPHEPQQLFCG-----RHVFCF-----RLRSASIQP-----
>Calidris_pugnax	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Miniopterus_natalensis	-----MIPHEEPGSPTIEI-----KCDFFPI-----RLKSEPARQ-----
>Dasypus_noveboracensis	-----MIPHEAPGAPAAV-----PCDFPCS-----RLKSQPARQ-----
>Latimeria_chalumnae	-----MIPHEVPGSPSEN-----QCDFTF-----RLKSEQKRH-----
>Columba_livia	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Alligator_mississippiensis	-----MIPHEVTGSPSEI-----KCDFFPI-----RLKSEPARQ-----
>Sarcophilus_harrisii	-----MIPHEVSGSPSEI-----KCDFFPT-----RLKPELARQ-----
>Monodelphis_domestica	-----MIPHEVSGSPSEI-----KCDFFPT-----RLKSELARQ-----
>Aquila_chrysaetos_canadensis	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Coturnix_japonica	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Eurypyga_helias	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Condylura_cristata	-----MIPHEPGSPTEI-----KCDFFPI-----RLKSEPARQ-----
>Oryctolagus_cuniculus	-----MIPHEPGSPTEI-----KCDFFPI-----RLKSEPASQ-----
>Opisthocomus_hoazini	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Sclerophages_formosus	-----MIPHEVCGPLTNS-----RRCLPFF-----RLRPAPIRR-----
>Lepidothrix_coronata	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPDRO-----
>Egretta_garzetta	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Equus_asinus	-----MIPHEEPGSPTDI-----QCDFPI-----RLKSEPARQ-----
>Manis_javanica	-----MIPHEPGSPTEI-----KCDFFPI-----RLKSEPARQ-----
>Cercopithecus_atys	-----MIPHEPGSPTEI-----KCDFFPI-----RLKSEPARQ-----
>Loxodonta_africana	-----MIPHEPGSPTEI-----KCDFFPI-----RLKPEPASQ-----
>Melopsittacus_undulatus	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Ictidomys_tridecemlineatus	-----MIPHEEPGSPTIEI-----KCDFFPI-----RLKSEPARQ-----
>Salmo_salar	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
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>Tupaia_chinensis	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
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>Lepisosteus_oculatus	-----MIPHEVHGSHDS-----RRDFPCI-----RLRSVPVRH-----
>Ictalurus_punctatus	-----MIPHELVQVLSHS-----RHVFCF-----QLRSVSIQP-----
>Aptenodytes_forsteri	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
>Anolis_carolinensis	-----MRCLQRFLVTEMIPHEVSGASQI-----KCDFFPLS-----RLKPEPARQ-----
>Struthio_camelus_australis	-----MIPHEVTGSLAEI-----KCDFFPI-----RLKSEPARQ-----
MLF-----SSLKPFVQWSSSTKMAPNPEELSKGCAHGEMIPHEVTGSLSEI-----KCDFFPI-----RLKSEPARQ-----	
>Pelodiscus_sinensis	-----MIPHEVTGSLSEI-----KCDFFPI-----RLKSEPARQ-----
>Tinamus_guttatus	-----MIPHEVTGSLSDI-----KCDFFPI-----RLKPEAARQ-----

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>Acipenser_sinensis-----MIPHEVPGSLSDSRCDFOCI|RLRSVTSDEASQ-----
>Amia_calva-----MIPHEVHGSLSESRRDFPSL|RLRSMVLRH-----
>Anser_cygnoides-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Pelophylax_nigromaculatus-----MIPHEVVGVPSCI|KCDFFI|RLKSVSVRQ-----
>Apteryx_australis_mantelli-----MIPHEVTGSLSE|KCDFFI|RLKSKPARQ-----
>Felis_catus-----MIPHEEPGSPTI|KCDFFI|RLKPEPARQ-----
>Hynobius_retardatus-----MIPHEVSGSSSGI|KCDLFL|RLKPPIPARQ-----
>Balaenoptera_acutorostrata_s-----MIPHEEPGSPTI|KCDFFI|RLKAEPARE-----
>Calidris_pugnax-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Pteropus_vampyrus-----MIPHEEPGSPTI|KCDFFI|RLKSEPAKQ-----
>Dasypus_novemcinctus-----MIPHEAPGAPAAVPCDFPCS|RLKSQPARQ-----
>Latimeria_chalumnae-----MIPHEVPGSPSENQCDFTFTFRLKSEQKRH-----
>Columba_livia-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Alligator_mississippiensis-----MQDSQAEQEMENPEQLLEDCAHKEMIPHEVTGSPSE|KCDFFI|RLKSEPARQ-----
>Sinocyclocheilus_anshuiensis-----MAS-LSTKVLPAVLETHSQREMI|PHELHGPLSHSRCDFHCL|RLKSVSIRP-----
>Sarcophilus_harrisii-----MIPHEVSGSPSE|KCDFFI|RLKPELARQ-----
>Monodelphis_domestica-----MIPHEVSGSPSE|KCDFFI|RLKSELARQ-----
>Aquila_chrysaetos_canadensis-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Coturnix_japonica-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Eurypyga_helias-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Condylura_cristata-----MIPHEPGSPTI|KCDFFI|RLKSEPARQ-----
>Oryctolagus_cuniculus-----MIPHEEPGSPTI|KCDFFI|RLKSEPASQ-----
>Opisthocomus_hoazin-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Scleropages_formosus-----MIPHEVCGPLTNSRRCLPFF|RLRPAPIRR-----
>Corvus_brachyrhynchos-----MIPHEVTGSPAE|KCDFFI|RLKSEPARQ-----
>Egretta_garzetta-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Equus_asinus-----MIPHEEPGSPTD|QCDFFI|RLKSEPARQ-----
>Manis_javanica-----MIPHEPGSPTI|KCDFFI|RLKSEPARQ-----
>Loxodonta_africana-----MIPHEEPGSPTI|KCDFFI|RLKPEPASQ-----
>Melopsittacus_undulatus-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Marmota_monax-----MIPHEEPGSPTI|KCDFFI|RLKSEPARQ-----
>Tupaia_chinensis-----MLFPGADVSI|SLPSFLSSLFPAPSLPSSFSQKPELLSADCTHGMVPHPEPGSPTI|KCDFFI|RLKAESARQ-----
>Lepisosteus_oculatus-----MIPHEVHGSHDSRRDFPCI|RLRSVPVRH-----
>Aptenodytes_forsteri-----MIPHEVTGSLAE|KCDFFI|RLKSEPARQ-----
>Thamnophis_sirtalis-----MLVEDCGHKEMIPHEVSGSTQEI|KCDFFLGL|RLKSEPARQ-----
>Struthio_camelus_australis-----MIPHEVTGSLSE|KCDFFI|RLKSEPARQ-----
>Chrysemys_picta-----MVLWNPEQLLEHCAHREMIPHEVTGSPSE|KCDFFI|RLKSEPARQ-----
>Tinamus_guttatus-----MIPHEVTGSLSDI|KCDFFI|RLKPEAARQ-----
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>Anser_cygnoides
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>Apteryx_australis_mantelli
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>Canis_lupus_familiaris
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>Physeter_catodon
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>Tinamus_guttatus
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>Orycteropus_ afer_ afer
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HG0047 ENSGALG00000015422 NRG1

Gallus gallus
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Anser cygnoides
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Xenopus laevis
MVLNLSLP-----RLFLPFLLLAFLLLLHDSY-FLP-NRYHLQMLQVREQTFLGYWFT-----
Oaetura pelagica
MLLLSLLP-----LP-L-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Buceros rhinoceros silvestri
-----MLKVRVMPFALGYWFT-----
Caprimulgus carolinensis
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Mustela putorius furo
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Hynobius retardatus
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Physeter catodon
-----MLEVRNMPFSLGYWFT-----
Calidris pugnax
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Eptesicus fuscus
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Pterocles gutturalis
-----MLKVRVLPFALGYWFT-----
Dasypus novemcinctus
-----MLGLL-SPPLPPPPPLVLLLLAPLPHSDC-FRHLSDQQLGLESGPLPFLSGSWFT-----
Columba livia
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Leptosomus discolor
-----MLKVRVLPFALGYWFT-----
Cuculus canorus
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Galeopterus variegatus
-----MLEVRNMPFLGYWFT-----
Haliaeetus leucocephalus
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Gavia stellata
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Balearea regulorum gibberic
-----MLKVRVLPFALGYWFT-----
Condylura cristata
MLLLSLLPPLLPPLPPP-PPVPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Oryctolagus cuniculus
MLLLSLLPPLLPPLLP-----PPPLFLLLLLLHSDC-FLHLSRHQLQMLEVRNIPFSLGYWFT-----
Elephantulus edwardii
MLLLSLLPPLLPPLPPP-PPVPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Ornithorhynchus anatinus
MLLLSLLYLLLL-LLLL-LPLLLLLLLLLLRDSC-FLHLSDQQLQMLEVRNIPFLGYWFT-----
Opisthocomus hoazin
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOTLKVRVLPFALGYWFT-----
Parus major
MLLLSLLP-----LPLLL-----EILLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Egretta garzetta
MLLLSLLP-----LPLML-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Ceratherium simum simum
MLLLSLLPPLLPPLPPP-PPPLILLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Manis javanica
ML-----VLPAFLPPLPP-PPVPLLLLLPHSDG-FLHLSDPQLQMLEVRNIPFSLGYWFT-----
Mandrillus leucophaeus
MLLLSLLPPLLPPLPPP-PPALVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Loxodonta africana
MLLLSLLPPLLPPLPPP-PPVPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Melopittacus undulatus
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Chinchilla lanigera
MLLLSLLPPLLPPLPPPPPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Trichechus manatus latirostr
MLLLSLLPPLLP-----LPPPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Pygoscelis adeliae
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Anolis carolinensis
MLVLSSL-----LPLPLPFLFLLLLLHSDGVFLHLSHQOMLKVRYPFLTGWFT-----
Chrysomys picta
MLLLSLLP-----LPLPLLPFLFLLLLLHSDNC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----
Calypte anna
MLLLSLLP-----LPLLL-----QILLLLLLPHDNC-FPRLSRYQPOMLKVRVLPFALGYWFT-----
Apaloderma vittatum
-----MLKVRVLPFALGYWFT-----
Orycteropus afer afer
MLLLSLLPPLLPPLPPP-PPPLVLLLLLLLLLHSDC-FLHLSDQQLQMLEVRNIPFSLGYWFT-----

>Homo_sapiens	-----MGYILCCDLMV
>Anser_cygnoides	-----MGCVLCCDLMV
>Chaetura_pelagica	-----MGCVLCCDLMV
>Apteryx_australis_mantelli	-----MGCVLCCDLMV
>Cariama_cristata	-----MGCVLCCDLMV
>Acinonyx_jubatus	-----MGYILCCDLMV
>Lipotes_vexillifer	-----MGYILCCDLMV
>Charadrius_vociferus	-----MGCVLCCDLMV
>Myotis_brandtii	-----MGYILCCDLMV
>Colius_striatus	-----MGCVLCCDLMV
>Columba_livia	-----MGCVLCCDLMV
>Leptosomus_discolor	-----MGCVLCCDLMV
>Alligator_sinensis	-----MGYILCCDLMV
>Cuculus_canorus	-----MGCVLCCDLMV
>Sarcophilus_harrisii	-----MGYILCCDLMV
>Galeopterus_variegatus	-----MGYILCCDLMV
>Monodelphis_domestica	-----MGYILCCDLMV
>Aquila_chrysaetos_canadensis	-----MGCVLCCDLMV
>Coturnix_japonica	-----MGCVLCCDLMV
MTFSCSLFGSAWKGROTCYLRMRHSASPLCGKRHLKGKLLHINALPMGCVLCCDLMV	
>Balearica_regulorum_gibberic	-----MGCVLCCDLMV
>Condylura_cristata	-----MGYILCCDLMV
>Oryctolagus_cuniculus	-----MHQQOQLVIGGTGYSAVSHINALPMGYILCCDLMV
>Tauraco_erythrolophus	-----MGCVLCCDLMV
>Opisthocomus_hoazin	-----MGCVLCCDLMV
>Corvus_cornix_cornix	-----MGCVLCCDLMV
>Phaethon_lepturus	-----MGCVLCCDLMV
>Ceratotherium_simum_simum	-----MGYILCCDLMV
>Picoides_pubescens	-----MGCVLCCDLMV
>Fulmarus_glacialis	-----MGCVLCCDLMV
>Melopsittacus_undulatus	-----MGCVLCCDLMV
>Cricetulus_griseus	-----MGYILCCDLMV
>Tupaia_chinensis	-----MGHVLCCGLMV
>Trichechus_manatus_latirostr	-----MGYILCCDLMV
>Pygoscelis_adeliae	-----MGCVLCCDLMV
>Anolis_carolinensis	-----MGYILCRDLMV
>Tyto_alba	-----MGCVLCCDLMV
>Struthio_camelus_australis	-----MGCVLCCDLMV
>Chelonia_mydas	-----MGYILCRDLMV
>Orycteropus_afer_afer	-----MGYILCCDLMV

HG0048 ENSGALG00000039182

>Gallus_gallus
-----MGCVLCDDLNV
>Anser_cygnoides
-----MGCVLCDDLNV
>Chaetura_pelagica
-----MGCVLCDDLNV
>Apteryx_australis_mantelli
-----MGCVLCDDLNV
>Cariama_cristata
-----MGCVLCDDLNV
>Ailuropoda_melanoleuca
-----MGYILCCDLNV
>Lipotes_vexillifer
-----MGYILCCDLNV
>Calidris_pugnax
-----MGCVLCDDLNV
>Rousettus_aegyptiacus
-----MGYILCCDLNV
>Colius_striatus
-----MGCVLCDDLNV
>Columba_livia
-----MGCVLCDDLNV
>Leptosomus_discolor
-----MGCVLCDDLNV
>Cuculus_canorus
-----MGCVLCDDLNV
>Sarcophilus_harrisii
-----MGYILCCDLNV
>Galeopterus_variegatus
-----MGYILCCDLNV
>Monodelphis_domestica
-----MGYILCCDLNV
>Aquila_chrysaetos_canadensis
-----MGCVLCDDLNV
>Balearica_regulorum_gibberic
-----MGCVLCDDLNV
>Condylura_cristata
-----MGYILCCDLNV
>Oryctolagus_cuniculus
MH000QLVIGGTGYSAVSHJNALPMGYILCCDLNV
>Tauraco_erythrolophus
-----MGCVLCDDLNV
>Opisthocomus_hoazin
-----MGCVLCDDLNV
>Acanthisitta_chloris
-----MGCVLCDDLNV
>Egretta_garzetta
-----MGCVLCDDLNV
>Equus_asinus
-----MGF ILCCDLNV
>Picoides_pubescens
-----MGCVLCDDLNV
>Coccothraustes_atys
-----MGYILCCDLNV
>Fulmarus_glaucialis
-----MGCVLCDDLNV
>Melospiza_undulatus
-----MGCVLCDDLNV
>Chinchilla_lanigera
-----MGYILCCDLNV
>Tupaia_chinensis
-----MGHVLCCGLNV
>Trichechus_manatus_latirostr
-----MGYILCCDLNV
>Aptenodytes_forsteri
-----MGCVLCDDLNV
>Gekko_japonicus
-----MGCILRCDDLNV
>Tyto_alba
-----MGCVLCDDLNV
>Struthio_camelus_australis
-----MGCVLCDDLNV
>Apaloderma_vittatum
-----MDCVLCDDLNV
>Orycteropus_afer_afer
-----MGYILCCDLNV

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>Danio_rerio
-----MINRNALLIIIIITLTCAFLLEGLEISPNLENF-----
>Channa_argus
MCEPLDWSQSAVRGTVINRNALLIIIIITLTCAFLLEGLEIFRGEQFVEEAEEN-----
>Anser_cygnoides
-----MINRNALLIIIIITLTCAFRPMGVISQL-----
>Xenopus_laevis
-----MGGSII-----QQLLEFFFFGGGERE-----
>Oryzias_latipes
MCEPSGLEPISQGLVINRNALLIIIIITLTCAFPTRGANFSPRRICRRRAGKLSATLCS-----
>Cyprinodon_variegatus
MCEPLDRSQSAVREPAINRNALLIIIIITLTCAFLLEREGG-----
>Coturnix_japonica
-----MINRNALLIIIIITLTCAFRPMGVISQL-----
>Plecoglossus_altivelis
-----MINRRALLII--ITGTCAVDGL--DFRNFELIFLV--IFYSFLADV-----
>Ficedula_albicollis
-----MINRNALLIIIIITLTCAFRPKFPNSRNLL-----
>Cebus_capucinus_imitator
-----MSRIAGTCAFLKGGNFRTPGIQCVK-----
>Rattus_norvegicus
-----MINRNALLIIIIITGTCAFLPKGGKIS-----
>Lepisosteus_oculatus
-----MINRNALLIIIIITLTCAFLLEGLEISQL-----
>Ictalurus_punctatus
-----MINRNALLIIIIITLTCAFLLEGLEISADLENLLRRRSKACYLPQMVV-----
>Chrysemys_picta
-----MINRNALLIIIIITLTCAFRPRGVISQL-----

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>Gallus_gallus
MINRNALLIIIIAGHMRGARRTGEAGGRLDFRNFE----KIFF-----
>Acipenser_sinensis
MINRNALLIIIIIEGHMRGGWARFP-----
>Anser_cygnoides
-----MRGARRIGEVGGRLDFRNFE----KIFF-----
>Xenopus_tropicalis
MINRNALLIIIIIMAGHMRAGWSLPAIGSTFWE-----
>Chaetura_pelagica
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Apteryx_australis_mantelli
MINRNALLIIIIAGHMRGARRIGEVGGRLDFRNFE----KIFF-----
>Menidia_menidia
MINRRALLII--ITGHMRGGWARFT-----
>Oryzias_latipes
MINRRALLII--ITGHMRGGWARFT-----
>Charadrius_vociferus
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Pteropus_vampyrus
MINRNALLIIIIAGHMRGAAPGAGEPGRGRAGRAGGAAAAAARFP-----
>Haplochromis_burtoni
MINRNALLII--ITGHMRGGCSRFT-----
>Alosa_alosa
MINRKALLII--ITGHMRGGWARFS-----
>Columba_livia
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Cuculus_canorus
MINRNALLIIIIAGHMRGARRIGEAGGGSISVILR-----RFFFSNFLFCPS
>Ctenopharyngodon_idella
MINREALLII--ITGHMRGGWARFP-----
>Kryptolebias_marmoratus
MINRTALLII--ITGHMRGWSIY----EIFEVL-----
>Monodelphis_domestica
MINRNALLIIIIAGHMRARRAGESGRGAGREGGATA--AARFP-----
>Esox_lucius
MINRNALLII--ITGHMRGGWARFP-----
>Falco_cherrug
MINRNALLIIIIAGHMRGARRIGEAGGEARFP-----
>Chanos_chanos
MINRKALLII--ITGHMRGGWARFP-----
>Apteronotus_leptorhynchus
MINREALLII--ITGHMRGGWTRYF-----
>Plecoglossus_altivelis
MINRNALLII--ITGCAVDGLDFRNFEIFLVIFYSF-----LADV-----
>Scleropages_formosus
-----MRAGWAPLGRALS-----EKVCGNFP-----
>Corvus_brachyrhynchus
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Egretta_garzetta
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Trematomus_bernacchii
MINRNALLII--ITGHMRGGWARFT-----
>Picoides_pubescens
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Cynoglossus_semihaevis
MINRTALLII--ITGHMRGGWARFF--T-----
>Cebus_capucinus_imitator
MINRNALLIIIIIEGHMRGAAPGAGEPGRGRAGRAGGAAAAAARFP-----
>Melopsittacus_undulatus
MINRNALLIIIIAGHMRGARRTGEAGGGSISVILR-----RFFFSNFLFCPS
>Peromyscus_maniculatus_baird
MINRNALLIIIIAGHMRVAPGAGEPGRGRAGRAGGAAAA--AARFP-----
>Salvelinus_alpinus
MINRKALLII--ITGHMRGGWTRFS-----
>Ictalurus_punctatus
MINRNALLIIIIITLTCAFLLEGLISADLENLL----RRRSKACYYPQMVV---
>Aptenodytes_forsteri
MINRNALLIIIIAGHMRGARRIGEAGGEARFP-----
>Struthio_camelus_australis
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----
>Chelonia_mydas
MINRNALLIIIIAGHMRGAANLGE--GGGSISVILR-----RFFFSNFLFCPS
>Tinamus_guttatus
MINRNALLIIIIAGHMRGARRTGAVGGGEARFP-----
>Calypte_anna
MINRNALLIIIIAGHMRGARRIGEAGGRLDFRNFE----KIFF-----

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>Homo_sapiens-----MVHCCHSPDCIFETQALS--NLQRT--KRQPPRYVCWEGV----IVTAL-----
>Amia_calva-----MLHCCHTPACISILQPLC--DLQRI--SQQPLG-----
>Anser_cygnoides-----MVHCCHSQNCIFETQTLS--NLHRT--KRPPASVRGGICRTVCPLAFLLLVLCF--
>Rhacophorus_dennysi-----MVNCCHSQDCIFDQALR--KLFQTSDDH--EEVIC-----
>Apteryx_australis_mantelli-----MVHCCHSRNCIFETQTLS--NLHRT--KRPPAYVCRRIFWTCCPLAFLLLVLYF--
>Ailuropoda_melanoleuca-----MVHCCHSPDCIFETQALS--NFQRT--KRQPPGYVYWEGV----TLTAL-----
>Hynobius_retardatus-----MLNCFHSPHCILGTQHSIRNLHRT--KRPRGYDC-----PLAFIVVLDW
>Tursiops_truncatus-----MVHCCHSPDCISETQALS--NLQQT--KRPPPGDACWEGV----TPTAL-----
>Pygocentrus_nattereri-----MVHCCHSQACIPKAQPLA--SLRCT-----
>Calidris_pugnax-----MVHCCHSQNCIFETQTLS--NLHRT--KRPPAYVYRGIFRTYCPAFLLLVLYF--
>Callorhinchus_milii-----MLHCCRSQDCICSPRPLD--NLQET--DRRPLG-----
>Rousettus_aegyptiacus-----MVHCCHSPDCIFETQALS--NLYRT--NRQPPGYVYWEGV----TLTAL-----
>Dasypus_novemcinctus-----MVHCCHSPDCIFETQALS--NLWRARATRQPPGHVYQEGSS-----
>Columba_livia-----MVHCCHSQNCIFETQTLS--NLHRT--KRPPAYVYRGIFRTYCPAFLLLVLYF--
>Alligator_mississippiensis-----MVHCCHSQNCIFETQAFS--NLHRT--KRQPTGFCRGIFPTCCPLASFSLVLYL
>Sarcophilus_harrisii-----MVHCCHSPDCIFETKALS--NLQYT--QRQPPGSLPSGRFSLTAL-----
>Galeopterus_variegatus-----MVHCCHSPDCIFETQALS--NLQRT--KRQPPRYVYWEGV----ILTAL-----
>Monodelphis_domestica-----MVHCCHSPDCISETKALS--NLQQT--KRQPPGSLPSKEIQPDCPLAFFGLCCCI--
>Aquila_chrysaetos_canadensis-----MVHCCHSQNCIFETQTLS--NLHRT--KRQPPAYVYRGIFRTYCPAFLLLVLYF--
>Coturnix_japonica-----MVHCCHSQNCIFETQALS--NLH-----
>Condylura_cristata-----MVHCCHSPDCIFETQTLS--NLQRT--KRQPPGSFYLEGV----TLTAL-----
>Oryctolagus_cuniculus-----MVHCCHSPDCIFETQALS--NLQQT--KRQLPRYGYWEGV----ILTAL-----
>Elephantulus_edwardii-----MYDILLPLTSSSRYLNTWFIQPAALQTHMVHCCHSPDCIFETQALG--NSQQT--KROLLGSVYREGV----VLTAL-----
>Taeniopygia_guttata-----MVHCCHSQNCIFETQALS--NLHRR--KRPPAYICRGSFWPCCLAFWLLLYF--
>Ceratotherium_simum_simum-----MVHCCHSPDCIFETQALS--NLQQT--KRQPPRYVYREGV----TLTAP-----
>Manis_javanica-----MVHCCHSLDCIFEQAALS--NLQQT--KRQPPGHVYWEGV----TLTAL-----
>Loxodonta_africana-----MVHCCHSLDCIFETQTLS--NLLQT--KR-----
>Dipodomys_ordii-----MVHCCHSPDCIFETQALS--NLQRT--KRPPPGLYREGV----ILTAL-----
>Tupaia_chinensis-----MVHCCHSPDCIFETQALS--NLQRT--KRQPPGYIYREGV----ILTAL-----
>Lepisosteus_oculatus-----MVHCFHSQACISVLQPLS--NLQHI-----
>Trichechus_manatus_latirostr-----MVHCCHSPDCIFETQTLS--NLQQT--KRQPPGSLYQEGV----ILTAL-----
>Aptenodytes_forsteri-----MVHCCHSQNCIFETQTLS--NLH-----
>Squalus_acanthias-----MVHCCRSRDRICSPELLS--NLQQA--DORPLG-----
>Anolis_carolinensis-----MVHCCHSQNHIFEIQALG--NLHOT--KRPRGSS--RRTAQTCRPLASLLPVLLF
>Struthio_camelus_australis-----MVHCCHSQNCIFETQTLS--NLHRT--KRQPPYVCRGIFWTCPLAFLLLVLYF--
>Chelonia_mydas-----MVHCCHSQNCIFETQALS--NLHRT--KRRTGYIYSGVSOTYCPALFSPVL.YF
>Tinamus_guttatus-----MVHCCHSQNCIFEIQTLS--NLHRT--KRPPPAYSCRGIF-----
>Orycteropus_afer_afer-----MVHCCHSPDYIFETQALS--NLQQT--KRQPPGSVYQEGN----ILTAL-----
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HG0050.2 ENSG00000074054 CLASP1

>Homo_sapiens
MKYFRPSS-RTSLCHSLLYLLLV
>Acinonyx_jubatus
MKNFRPKS-RTSLCHSLLYLLLV
>Tursiops_truncatus
MKYSRPRR-RTSLCHSLPSPLPV
>Myotis_brandtii
MKYFRPNT-RTSLCHSLLYRLLV
>Dasypus_novemcinctus
MKYFRPNS-VASLCHSLLYRLLV
>Galeopterus_variegatus
MKYFRPNS-RTSLCHSLLYLLLV
>Condylura_cristata
MKYFRANS-RTSLCHSLLYLLLV
>Oryctolagus_cuniculus
MKYFKPSSRRSLCHSLLYLLLV
>Elephantulus_edwardii
MKYFRPLC-MTSFCHSLHLLDI-
>Ceratotherium_simum_simum
MKYFRPNS-RTSLCHSLLYLQLV
>Fukomys_darlingi
MKYFRPSS-RTSLCHSLLYLLLV
>Orycteropus_afer_afer
MKYFRHNS-IASLCHSLLYLLLDI

HG0051 ENSG00000116679 IVNS1ABP

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>Homo_sapiens
-----MNVSISSEMNOIMMHYHRRNSCL
>Anas_platyrhynchos
-----MMHDYHRRNSCL
>Apteryx_australis_mantelli
-----MH DYHRRNSCL
>Ailuropoda_melanoleuca
-----MSFISISSEMNOIMMHYHRRNSCL
>Hynobius_chinensis
-----MSLTVCAQRNQIMIDYHRRNSCL
>Physeter_catodon
-----MSFISISSEMNOIMMHYHRRNSCL
>Callorhynchus_millii
-----MMQHHSRNSCL
>Rousettus_aegyptiacus
-----MSFISISSEMNOIMMHYHRRNSCL
>Dasypus_noveboracensis
-----MMHDYHRRNSCL
>Latimeria_menadoensis
-----MRMNFIVYSTRNQIMMDYHSRKQSL
>Alligator_sinensis
-----MSSLVRADRHQFMHYYHRRNSCL
>Sarcophilus_harrisii
-----MNFVVSAQRNQIMIDYHRRNSCL
>Galeopterus_variegatus
-----MMHYYHRRNSCL
>Macropus_eugenii
-----MNFVFLSQRNQIMMHYHRRNSCL
>Aquila_chrysaetos_canadensis
-----MNSIVYAEHQIMMHYHRRNSCL
>Numida_meleagris
-----MSCIVRAERQKIMMHYHRRNSCL
>Erinaceus_europaeus
-----MSFPISEMNOIMMHYHRRNSCL
>Oryctolagus_cuniculus
MRSWRTANSDEKHGTQRSPGVQIMMHSRNSCL
>Elephantulus_edwardii
-----MNFSTERNQIMMHYHRRNSCL
>Ornithorhynchus_anatinus
-----MMHDYHRRNSCL
>Pseudopodoces_humilis
-----MFTAVRAQRHQVMMHDYHRRNSCL
>Ceratotherium_simum_simum
-----MSFISISSEMNOIMMHYHRRNSCL
>Manis_javanica
-----MSVSTISEMNOIMMHYHRRNSCL
>Loxodonta_africana
-----MNFVSVAERSQTMMDYHRRNSCL
>Heterocephalus_glaber
-----MSFISISSEMNOIMMHRYHRRNSCL
>Tupaia_chinensis
-----MNFISISSEMNOIMMYHYHRRNWCL
>Trichechus_manatus_latirostris
-----MNFSTERNQIMMHYHRRNSCL
>Aptenodytes_forsteri
-----MMHDYHRRNSCL
>Anolis_carolinensis
-----MSAVVOGERDOSMMNDYHRRNSCL
>Struthio_camelus_australis
-----MMHDYHRRNSCL
>Chrysemys_picta
-----MNGVVCAERHQIMMHYHRRNSCL
>Tinamus_guttatus
-----MMHDYHRRNSCL
>Calypte_anna
-----MMHDYHRRNSCL
>Orycteropus afer afer
-----MNFSTERNQIMMHYHRRNSCL
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>Gallus_gallus
-----MSCIIRAERQKIMMHDYHRRNSCL
>Acipenser_sinensis
-----MSTVVYSHRNQVIMRDYHRTTFL
>Anas_platyrhynchos
-----MMHDYHRRNSCL
>Apteryx_australis_mantelli
-----MMHDYHRRNSCL
>Ailuropoda_melanoleuca
-----MSFSISSEMNOIMMHDYHRRNSCL
>Cynops_pyrhogaster
-----MSLIVCAERNQIMIDYHKRSSCL
>Physeter_catodon
-----MSFSISSEMNOIMMHDYHRRNSCL
>Rousettus_aegyptiacus
-----MSFSISSEMNOIMMHDYHRRNSCL
>Dasypus_noveboracensis
-----MMHDYHRRNSCL
>Latimeria_chalumnae
-----MRMNSIVYSTRNQIMMDYHSRKQSL
>Alligator_sinensis
-----MSSLVRADRHQFMHYYHRRNSCL
>Rutilus_rutilus
-----MSTIVNRQPDQVIMHDQHRKGLSL
>Sarcophilus_harrisii
-----MNFVVSQRNQIMMHDYHRRNSCL
>Galeopterus_variegatus
-----MMHYYHRRNSCL
>Macropus_eugenii
-----MNFVLSQRNQIMMHDYHRRNSCL
>Aquila_chrysaetos_canadensis
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>Erinaceus_europaeus
-----MSFPISEMNOIMMHDYHRRNSCL
>Oryctolagus_cuniculus
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>Elephantulus_edwardii
-----MNFSTERNQIMMHDYHRRNSCL
>Ornithorhynchus_anatinus
-----MMHDYHRRNSCL
>Sturnus_vulgaris
-----MFSTVRAQRHQMHDYHRRNSCL
>Ceratotherium_simum_simum
-----MSFSISSEMNOIMMHDYHRRNSCL
>Manis_javanica
-----MSVSTSEMNOIMMHDYHRRNSCL
>Pan_paniscus
-----MNVISSEMNOIMMHHYYHRRNSCL
>Loxodonta_africana
-----MNFVSAERSQTMMDYHRRNSCL
>Mus_musculus
-----MNFATISEMTQIMMHDYHRRNSCL
>Salmo_salar
-----MSTTTTCQKQVIMHDQHRKSLTL
>Tupaia_chinensis
-----MNFISSEMNOIMMYHYHRRNWCL
>Trichechus_manatus_latirostris
-----MNFSTERNQIMMHDYHRRNSCL
>Aptenodytes_forsteri
-----MMHDYHRRNSCL
>Squalus_acanthias
-----MIYIVRFVPRKDNQDHHNRNSCL
>Anolis_carolinensis
-----MSAVVCGERDQSMMDYHRRNSCL
>Struthio_camelus_australis
-----MMHDYHRRNSCL
>Pelodiscus_sinensis
-----MSGVVCAERHQIMMHDYHRRNSCL
>Tinamus_guttatus
-----MMHDYHRRNSCL
>Calypte_anna
-----MMHDYHRRNSCL
>Orycteropus_ afer_ afer
-----MNFSTERNQIMMHDYHRRNSCL

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>Homo_sapiens
MNLNCVCGEGDGCYFVMRSGMNC SL
>Anser_cygnoides
-----MKSGMNC SV
>Apteryx_australis_mantelli
MNWNCFRCEEDGCCYFVMRSGMNR SV
>Buceros_rhinoceros_silvestri
MNWNCFPCEEDGCCYFVMRSGMNC SV
>Caprimulgus_carolinensis
MNWNSFPCEEDGCCYFVMRSGMNC SV
>Ailuropoda_melanoleuca
MNLNCVCGEGDGCYFVMRSGMNC SL
>Lipotes_vexillifer
MNLNCVCGEGDGCYFVMRSGMNC SL
>Calidris_pugnax
MNWNCFPCEEDGCCYFVMRSGMNC SV
>Miniopterus_natalensis
MNLNCVCGEGDGCYFVMRSG-----
>Pterocles_gutturalis
MNWNCFPCEEDGCCYFVMRSGMNC SV
>Columba_livia
MNWNSFPWEEDGCCYFVMRSGMHCV
>Leptosomus_discolor
MNWNCFPREEDGCCYFVMRSGMNC SV
>Galeopterus_variegatus
MNLNCVCGEGDGCYFVMRSGMNC SL
>Monodelphis_domestica
MNLNCVCGCGDDCCYFVMKSGMNC SV
>Falco_cherrug
MNWNCFPCEKDGCCYFVMRSGMNC SV
>Coturnix_japonica
MNWNCFPREEDGCCYFVMRSGMNC SV
>Balearica_regulorum_gibberio
MNWNCFPFEEDGCCYFVMRSGMNC SV
>Erinaceus_europaeus
MNLNCVCGEGDGCYFVMRSGMNC SL
>Oryctolagus_cuniculus
MNLNCVCGEGDGCYFVMRSGMNC SL
>Elephantulus_edwardii
MNLDCVCGEGDGCYFVMKSGMNC SL
>Tauraco_erythrolophus
-----MRSGMNC SV
>Lepidothrix_coronata
MNWNCFPCEEDGCCYFVMRSGMNC SV
>Egretta_garzetta
MNWNCFPCEEDGCCYFVMRSGMNC SV
>Geratherium_simum_simum
MNLNCVCGEGDGCYFVMRSGMNC SL
>Manis_javanica
-----MRSGMNC SL
>Picoides_pubescens
-----MRSGMNC SV
>Loxodonta_africana
-----MRSGMNC SL
>Melopsittacus_undulatus
MNWNCFPCEEDGCCYFVTRSGMNC SV
>Jaculus_jaculus
MNLNCVCGEGDGCYFVMRSGMNC SL
>Tupaia_chinensis
MNLNCVCGEGDGCYFVMRSGMNC SL
>Trichechus_manatus_latirostr
-----MRSGMNC SL
>Aptenodytes_forsteri
MNWNCFPCEEDGCCYFVMRSGMNR SV
>Struthio_camelus_australis
MNWNCFRCEEDGCCYFVMRSGMNR SV
>Chrysemys_picta
MNWNCFRCEEDGCCYFVMTSGMNC SV
>Tinamus_guttatus
MDWNCFRYEEDGCCYFVMRSGMNC SV
>Apaloderma_vittatum
MNWNCFPCKEDGCCYFVMRSGMNC SV
>Orycteropus_afer_afer
MNLNCVCGEGDGCYFVMRSGMNC SL
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>Homo_sapiens
---MVNYMQSQHSQHSCEVCREf
>Anser_cygnoides
-----MQKSQHSCEVCCEf
>Chaetura_pelagica
-----MQKSQHSCEVCCEf
>Buceros_rhinoceros_silvestri
MLQTVNYMQSQHSQHSCEVCREf
>Caprimulgus_carolinensis
-----MQKSQHSCEVCCEf
>Cariana_cristata
-----MQKSQHSCEVCCEf
>Acinonyx_jubatus
---MVNYMQSQHSQHSCEVCREf
>Charadrius_vociferus
-----MQKQSQHSCEVCCEf
>Eptesicus_fuscus
---MVNYMQSQHSQHSCEVCPEf
>Pterocles_gutturalis
-----MQKSQHSCEVCCEf
>Colius_striatus
-----MQKSQHSCEVCSEf
>Columba_livia
-----MQTQHSCEVCCEf
>Merops_nubicus
-----MQKSQHSCEVCCEf
>Cuculus_canorus
-----MQKSQHSCEVCCEf
>Falco_cherrug
-----MQKSQHSCEVCCEf
>Gallus_gallus
-----MRKSQHSCEVCCEf
>Gavia_stellata
-----MQKSQHSCEVCCEf
>Mesitornis_unicolor
-----MQKSQHSCEVCCEf
>Condylura_cristata
---MVNYMQTQHSCEVCCEf
>Ornithorhynchus_anatinus
---MVNYMQSQHSQHSCEVCCEf
>Tauraco_erythrophus
-----MQKSQHSCEVCCEf
>Opisthocomus_hoazin
-----MQKGQHSCEVCCEf
>Acanthisitta_chloris
-----MQKSQHSCEVCCEf
>Pelecanus_crispus
-----MQKSQHSCEVCCEf
>Equus_caballus
---MVNYMQSQHSQHSCEVCCEf
>Manis_javanica
---MVNYMQSQHSQHSCEVCCEf
>Picoides_pubescens
-----MQKSQHSCEVCCEf
>Loxodonta_africana
---MVNYMQSQHSQHSCEVCCEf
>Fulmarus_glaucialis
-----MQKSQHSCEVCCEf
>Nestor_notabilis
-----MQTSQHSCEVCCEf
>Marmota_marmota_marmota
---MVNYMQSQHSQHSCEVCCEf
>Trichechus_manatus_latirostr
---MVNYMQSQHSQHSCEVCCEf
>Aptenodytes_forsteri
-----MQKSQHSCEVCCEf
>Chelonia_mydas
---MVNYMQSQHSQHSCEVCCEf
>Calypte_anna
-----MQKSQHSCEVCCEf
>Apaloderma_vittatum
-----MQTQHSCEVCCEf
>Orycteropus afer afer
---MVNYMQSQHSQHSCEVCCEf
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>Homo_sapiens
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>Canis_lupus_familiaris
-----MKQWDLPKSDI-----
>Physeter_catodon
-----MLSLSLTRGFNFIKRWDLPKSDI-----
>Rousettus_aegyptiacus
-----MLSLGLTRGFHFIK-----
>Galeopterus_variegatus
-----MLSVLSLTRGFNFMKLDLTKSDI-----
>Condylura_cristata
-----MLSLSLNRGFNFMKQRCQKVI FQKKMHSGLWCFLF
>Oryctolagus_cuniculus
-----MLSIFSWTRSLNFMMLGNTPOS DI-----
>Equus_asinus
MHSARNIFNEMLSLSLTKGFNFMKQWDLPKSDI-----
>Manis_javanica
-----MLSLSLTRGFNFMKQWDLPKSDI I-----
>Loxodonta_africana
MHSARNIFSEMLSLSLIGAVNFRKLDLTKSDI-----
>Fukomys_darlingi
-----MLSLSLTRDFNFMKLDLTKSDI-----
>Tupaia_chinensis
-----MLSLVSLTRGFNFMKLDLTKSDI-----
>Orycteropus_afer
-----MLSLSLTGVFNFKKLDMPKSDI-----

HG0054 ENSG00000124479 NDP

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>Homo_sapiens
-----MTTRKLQDPDPALSLNGTGS-----
>Anser_cygnoides
-----MTAKRLKPDFSLSWRGTSHDLEFF
>Leptonychotes_weddelii
-----MTTRKLQDPDPALCLKGTGS-----
>Balaenoptera_acutorostrata_s
-----MTTRKLQDPDPALSLKGTGA-----
>Miniopterus_natalensis
-----MTTRKLQDPDPALSLGEGTS-----
>Dasypus_novemcinctus
-----MTTRKLQSDPALSLRGTRS-----
>Galeopterus_variegatus
-----MTTRKLQDPDPALSLKGTGS-----
>Meleagris_gallopavo
-----MTTRKLKPDFSLSWRGTSQYLVFF
>Gavia_stellata
-----MTAKRLKPDFLWSWKGTCQYLEFF
>Sorex_araneus
-----MTARKLQDPDPALSLGEGTS-----
>Oryctolagus_cuniculus
-----MTTRKLQDPDPALSLKSGGA-----
>Ceratotherium_simum_simum
-----MTTRKLQDPDPALSLKGTGS-----
>Loxodonta_africana
-----MTTRKLQDPDPALSLKGTGS-----
>Ctenomys_sociabilis
-----MTTKLQDPDPALALKGTGS-----
>Tupaia_chinensis
-----MTTRKLQDPDTLSLKGTGS-----
>Trichechus_manatus_latirostr
-----MTTRKLQDPDPALSLKGTGS-----
>Python_bivittatus
MSNPKPAMTTWRKTDPLLWQGTGPQSLEGF
>Orycteropus_ afer_ afer
-----MTTRKLQDPDTLSLKGTGS-----
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HG0054 ENSGALG00000016222 NDP

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>Gallus_gallus
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>Anser_cygnoides
-----MTAKRLKPDFSLSWRGSGHDLEFF
>Apteryx_australis_mantelli
-----MTAKRPPKPDFSPSWKETGSOYLEFF
>Cariama_cristata
-----MTAKRLKPDFSPSWKGTGCOYLEFF
>Felis_catus
-----MTTRKLRPDRALCWEGTGS-----
>Balaenoptera_acutorostrata_s
-----MTTRKLQDPDPALSLKGTGA-----
>Calidris_pugnax
-----MTAKRLKPDFSPSWKGTGCOYLEFF
>Pteropus_vampyrus
-----MTTRKLQDPDPALSLKGTGS-----
>Pterocles_gutturalis
-----MTAKRLKPDFSPSWKGTGCOYLEFF
>Colius_striatus
-----MTSKRLKPVFSPSWEGTGGQYLEFC
>Leptosomus_discolor
-----MTAKRLKPDFSPSWKGTGCGCLEFF
>Cuculus_canorus
-----MPAKRLKPGFSPSWKGTDCOYLEFF
>Galeopterus_variegatus
-----MTTRKLQDPDPALSLKGTGS-----
>Haliaeetus_albicilla
-----MTAKRLKPDFSPSWRGTCOYLEFF
>Gavia_stellata
-----MTAKRLKPDFLLSWKGTGCOYLEFF
>Balearica_regulorum_gibberic
-----MTAKRLKPDFSPSWKGTGCOYLEFF
>Sorex_araneus
-----MTARKLQDPDPALSLLEGTS-----
>Oryctolagus_cuniculus
-----MTTRKLQDPDPALSLKSGGA-----
>Tauraco_erythrolophus
-----MTAKRLKPDFSPSWKGTGCGDLEFF
>Opisthocomus_hoazin
-----MTAKRLKPDFSPSWKGTGCPYLEFF
>Nipponia_nippon
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>Ceratotherium_simum_simum
-----MTTRKLQDPDPALSLKGTGS-----
>Aotus_nancymae
-----MTTRKLQDPDPALSLKGTGS-----
>Loxodonta_africana
-----MTTRKLQDPDPALSLKGTGS-----
>Fulmarus_glaucialis
-----MTAKRLKPDFSPSWKGTGCOYLEFF
>Nestor_notabilis
-----MTAKALKPDFSPSWKGTGCHYLEFF
>Heterocephalus_glaber
-----MTTKLRPDPALTLLKGTGS-----
>Tupaia_chinensis
-----MTTRKLQDPDTLSLKGTS-----
>Trichechus_manatus_latirostr
-----MTTRKLQDPDPALSLKGTGS-----
>Pygoscelis_adeliae
-----MTAKRLKPDFSSSWKGTGCOYLEFF
>Gekko_japonicus
-----MSTPKLAMITQRLKTDLSLSSKGTGPOSLECF
>Struthio_camelus_australis
-----MTAKRLKPDFSPSWKGTGSRYLEFF
>Chrysemys_picta
-----MTTRKLKPGFSSSLKGTESQYLEFF
>Tinamus_guttatus
-----MTVKRTNPDFSLSWKMGSGOYLEFF
>Calypte_anna
-----MTAKRLKPDSSPSWKGTDCQVLEFF
>Orycteropus afer_afer
-----MTTRKLQDPDTLSLKGTS-----
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>Gallus_gallus
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>Anser_cygnoides
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>Chaetura_pelagica
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLSLFDVSRGCKGPSL
>Apteryx_australis_mantelli
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSGTVRRNVSFYITFFLLTL-----
>Caprimulgus_carolinensis
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Canis_lupus_familiaris
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLPWAAL-----
>Hynobius_retardatus
MLH1VFQVRSCHDLIKRGGGLYVLQRIYVYDL-LHRWAAVL-----
>Lipotes_vexillifer
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Calidris_pugnax
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Myotis_lucifugus
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Dasypus_noveboracensis
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Oculus_canorus
MLH1VFQVRSCHDLIKRGGGVYVLQCLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Galeopterus_variegatus
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Aquila_chrysaetos_canadensis
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Balearica_regulorum_gibberica
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Condylura_cristata
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Oryctolagus_cuniculus
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>Elephantulus_edwardii
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Opisthocomus_hoazini
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Corvus_brachyrhynchos
MLH1VFQVRSCHDLIKRGGGLYVLQCLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Egretta_garzetta
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Ceratotherium_simum_simum
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>Manis_javanica
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>Aotus_nancymae
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>Loxodonta_africana
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>Fulmarus_glaucialis
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>Melospiza_undulatus
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>Dipodomys_ordii
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>Trichechus_manatus_latirostris
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----
>Aptenodytes_forsteri
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Anolis_carolinensis
MLH1VFQVRSCHDLIKRGGGLYVYQRLVYADL-LHRWAAVL-----
>Tyto_alba
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSAVRRNVSFYITLFLLLTL-----
>Struthio_camelus_australis
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSGTVRRNVSFYITFFLLTL-----
>Chelonia_mydas
MLH1VFQVRSCHDLIKRGGGLYVLQRLVYVDF-VASLGSGTVRRNVSFYITFFLLTL-----
>Tinamus_guttatus
MLH1VFQVRSCHDLIKRGGGSCVLRRLVYVDF-VASLGSGTVRRNVSFYITLSLLPTL-----
>Orycteropus afer
MLHLVFQVRSCHDLIKRRRLVCVAVPGVLSCCFLWAAAL-----

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>Gallus_gallus
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>Anser_cygnoides
-----MSILLHRWAAAL
>Chaetura_pelagica
MCCSANYMSILLHRWAAAL
>Apteryx_australis_mantelli
-----MSILLHRWAAVL
>Caprimulgus_carolinensis
-----MSILLHRWAAAL
>Galidris_pugnax
-----MSILLHRWAAAL
>Cuculus_canorus
-----MSILLHRWAAAL
>Aquila_chrysaetos_canadensis
-----MSILLHRWAAAL
>Balearica_regulorum_gibberic
-----MSILLHRWAAAL
>Opisthocomus_hoazin
-----MSILLHRWAAAL
>Corvus_brachyrhynchos
-----MSILLHRWAAAL
>Egretta_garzetta
-----MSILLHRWAAAL
>Fulmarus_glaucialis
-----MSILLHRWAAAL
>Melopsittacus_undulatus
-----MSILLHRWAAAL
>Aptenodytes_forsteri
-----MSILLHRWAAAL
>Tyto_alba
-----MSILLHRWAAAL
>Struthio_camelus_australis
-----MSILLHRWAAAL
>Pelodiscus_sinensis
-----MSILLHRWAAVL
>Tinamus_guttatus
-----MSILLHRWAAVL
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>Homo_sapiens
-----MSWAVLSPHVHLHFVREGQSHAT---PQDPHNDITPFRDWRDAG-SHPHPSALVSLRIWQPVPS-----
>Ursus_maritimus
-----MSGAVLAPHVHLHFVREQNAHMP---PCK-----IPTMT-----
>Hynobius_chinensis
-----MGWPFLS---IHLHFVREGYFHMP---HHK-----FTMT-----
>Orcinus_orca
-----MP---HHK-----IPTMT-----
>Calidris_pugnax
MSTSIKNNRWVLVGNMVSTCT-----SLESCIFGHATPDHDDIAASENSVTRAFF---FFFLFVTERIWQFTS-----
>Myotis_ricketti
-----MYWAVLAHQSTQTSLESRAFTCH---TTRSHNDITPFRVWRDAG-SPPFSSCITKNLAASSALTEFTAYIGGCLSIHLHL
>Haliaeetus_leucocephalus
-----MGCPCTKYGIHLHFIRESCIFVHATPDHDDIAASENSVTRAFF---FF-FSLVTQRIWQFTS-----
>Mesitornis_unicolor
-----MVSTCT-----SLESYIFVHATPDHDDIAAASQNSVTRAFF---F---SLVTQRIWQFTS-----
>Ficedula_albicollis
-----MVSTCT-----SLESCIFVHATPDHDDIAASENSVTRAFF---FF-SPLVTQRIWQSFTS-----
>Ceratotherium_simum_simum
-----MSWADFHHVHLHFVREGSVHMP---HHK-----IPTMT-----
>Picoides_pubescens
-----MGSTCT-----SLELHFFVHATPDHDDIAASHNSLTRAFLSFFFFPPAVTQRIWQIFTS-----
>Loxodonta_africana
-----MSRAVLSLHVHLHFVRELSFYTP---HHE-----IPTMK-----
>Nestor_notabilis
-----MVSTCT-----SLESCIFVHATPDHDDIAASENSVTRAFF---F---SLVTQRIWQCTS-----
>Marmota_marmota_marmota
-----MSWAVVAQHVLHFVREGSVNMP---HHK-----SPTMT-----
>Tupaia_chinensis
-----MSRAVLVHHVHLHFVREGQVHMP---HHK-----LPTMT-----
>Pygoscelis_adeliae
-----MGCPCTKYGIHLHFIRELHFCTCHTRSP-----
>Python_bivittatus
-----MGRIDGLSFTIFS---LHLHLIRQQQFHIP---HAR---IP-----
>Orycteropus afer_afer
-----MSWAVLALHVHLHFVREGSFHMP---HHK-----IPTMK-----

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HG0056 ENSGALG00000011271 LUM

>Gallus_gallus
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>Anser_cygnoides
-----MPHHK1TMMT
>Apteryx_australis_mantelli
-----MPHHK1TMMT
>Caprimulgus_carolinensis
-----MPHHK1TMMT
>Cariama_cristata
-----MPHHK1TMMT
>Hynobius_chinensis
MGWPF--LSTHLHFVRE-QYFHMPPHKKFTMMT
>Charadrius_vociferus
-----MPHHK1TMMT
>Myotis_ricketti
-----MPHHK1PQ--
>Pterocles_gutturalis
-----MPHHK1TMMT
>Latimeria_chalumnae
-----MHLHLVKE-LCFF1PHHKL1TMMT
>Colius_striatus
MDCPYTKYGIHLHFIRE-LHFCSCHTT1SMMT
>Columba_livia
-----MPHHK1TMMT
>Merops_nubicus
-----MPHHK1TMMT
>Alligator_sinensis
-----MPHHK1TMMT
>Haliaeetus_leucocephalus
MVS-----TCTSLERAFLYMPHHR1TMMT
>Gavia_stellata
-----MPHHK1TMMT
>Chlamydotis_macqueenii
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>Gondylura_cristata
-----MPHHK1PTMT
>Ficedula_albicollis
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>Nipponia_nippon
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>Equus_przewalskii
-----MPHHK1PTMT
>Picoides_pubescens
MGCPYTKYGIHLHFIRA-AFFCPCHTRSP--
>Propithecus_coquereli
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>Loxodonta_africana
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>Fulmarus_glaucialis
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>Nestor_notabilis
-----MPHHK1TMMT
>Tupaia_chinensis
MSRAVLVHVHLHFVRE-QCVHMPHKLPTMT
>Pygoscelis_adeliae
-----MPHHK1TMMT
>Gekko_japonicus
-----MPHHQNPMMT
>Tyto_alba
-----MPHHK1TMMT
>Struthio_camelus_australis
-----MPHHK1TMMT
>Pelodiscus_sinensis
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>Tinamus_guttatus
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>Apaloderma_vittatum
-----MPHHK1TMMT
>Orycteropus_afer_afer
MSWAVLALHVHLHFVRE-QSFHMPHHK1PTMK

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>Homo_sapiens-----MLGAQWRRNOPSPRAAESCLLVLSLKK1LQSLILFLGVTIFEAKLT
>Anas_platyrhynchos-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Apteryx_australis_mantelli-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Buceros_rhinoceros_silvestri-----MMHK---LNC1CLKGL-MTK---TACFSTELSGVSQL EEDLQSLILFLGVTLLVEVKFA
>Caprimulgus_carolinensis-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEKFA
>Cariama_cristata-----MTK---PACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Odobenus_rossmarus_divergens-----MLGAQWRRNOPSPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Calidris_pugnax-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTVEVKFA
>Miniopterus_natalensis-----MLGAQWRRNOPSPRAAESCLLVLSLKK1LQSLILFLGVTIFEAKLT
>Pterocles_gutturalis-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Colius_striatus-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTVEVKFA
>Columba_livia-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Merops_nubicus-----MTK---PACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Cuculus_canorus-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTILK-----
>Monodelphis_domestica-----MLGTQW-----
>Gallus_gallus
MLAVQGRPPRCRFALLFFTLP EHXIAPRGPGARS---HRRXRAELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Gavia_stellata-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Chlamydotis_macqueenii-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Condylura_cristata-----MLGAQWRRNOPSPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Oryctolagus_cuniculus-----MLGAQWRRRQSPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Tauraco_erythrolophus-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTVLK-----
>Opisthocomus_hoazin-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTVF-----
>Acanthisitta_chloris-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTVEVKFA
>Egretta_garzetta-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Ceratotherium_simum_simum-----MLGAQWRRKQPLRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Picoides_pubescens-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Loxodonta_africana-----MLGAQGRRSQPPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Fulmarus_glaialis-----MTK---TACFSTELSGVSQL EEDLRSLLILFLGVTIFEVKFA
>Melopsittacus_undulatus-----MTK---PACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Jaculus_jaculus-----MRA-SRSAAAMLGAQWRRRQPPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Trichechus_manatus_latirostr-----MLGAQWRRSQPPRAAESCLLVLSLKK1LQSLILFLGVTIF-----
>Aptenodytes_forsteri-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Tyto_alba-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Struthio_camelus_australis-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
>Tinamus_guttatus-----MTK---TACFSTELSGVSQL EEDLQSLILFLGVTIFEVKFA
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>Homo_sapiens-----MLPAFPFHHQAGAE-----
>Anser_cygnoides-----MLAAFPFOHRAGAEERCF--
>Xenopus_laevis
MQIVFFPAVLVISCLHSSYATYCKSELRAHAMLAAFPFFHHRGAG-----
>Apteryx_australis_mantelli-----MPAAFPFOHRAGAE-----
>Caprimulgus_carolinensis-----MRAAFPFOHRAGAE-----
>Cariama_cristata-----MLAAFPFOHRAGAE-----
>Ailuropoda_melanoleuca-----MLPAFPFHHQAGAE-----
>Charadrius_vociferus-----MLAAFPFOHRAGAE-----
>Miniopterus_natalensis-----MLPAFPFHHQAGAE-----
>Colius_striatus-----MLAAFPFOHRAGAE-----
>Columba_livia-----MLAAFPFOHRAGAE-----
>Leptosomus_discolor-----MLAAFPFOHRAGAE-----
>Galeopterus_variegatus-----MLPAFPFHHQAGAE-----
>Haliaeetus_albicilla-----MLAAFPFOHRAGAE-----
>Gavia_stellata-----MLAAFPFOHRAGAE-----
>Chlamydotis_macqueenii-----MLAAFPFOHRAGAE-----
>Erinaceus_europaeus-----MLPAFPFHHQAGAE-----
>Ochotona_princeps-----MLPAFPFPRQAGTE-----
>Tauraco_erythrolophus-----MLAAFPFF-----
>Opisthocomus_hoazin-----MLAAFPFOHRAGAE-----
>Manacus_vitellinus-----MLAAFPFOHRGAE-----
>Egretta_garzetta-----MLAAFPFOHRAGAE-----
>Ceratotherium_simum_simum-----MLPAFPFHHQAGAE-----
>Manis_javanica-----MLPAFSFHHQAGLNKGVFVW-----
>Fulmarus_glaucialis-----MLAAFPFOHRAGAE-----
>Nestor_notabilis-----MLAAFPFOHRAGAE-----
>Ictidomys_tridecemlineatus-----MLPAFPFHRQAGTE-----
>Tupaia_chinensis-----MLPAFPFHHQAGAE-----
>Trichechus_manatus_latirostr-----MLPAFPFHHQAGTE-----
>Pygoscelis_adeliae-----MLAAFPFOHRAGAE-----
>Tyto_alba-----MLAAFPFOHRAGAE-----
>Trachemys_scripta-----MLAALPFHHRAGAE-----
>Calypte_anna-----MLSAFPFOHRAGAE-----
>Apaloderma_vittatum-----MLAAFPFOHRAGAE-----
>Orycteropus afer afer-----MLPVFPFHQAGAE-----
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>Danio_rerio
-----MLHSLCSIIWLNRGFKLRKVACTANTGOV-----
>Acipenser_sinensis
-----MLVKLSLCSIIWLNRGFKRRGVLLTMGLGHH-----
>Amia_calva
-----MLPTSSLCSIIWLNRGFKLRKVLSS-NTGQN-----
>Channa_punctata
-----MLPTLSLCSIIWLNRGIKLRKVHRSTNTGOV-----
>Anas_platyrhynchos
MPSRERWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Xenopus_tropicalis
M1PEKSWIMFVSFLCSIIWLNRGFKLRITGT-----
>Menidia_menia
-----MLPTLSLCSIIWLNRGIKLRKVHRTNTDOV-----
>Tripterygion_delaiei
-----MLPTRSLCSIIWLNRGIKLRKVHQSANTGOV-----
>Carriama_cristata
MPAHQGWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Hynobius_chinensis
-----MIVAPSLCSIIWLNRGFKLRKGGT-----
>Micropterus_salmoides
-----MLPTLSLCSIIWLNRGIKLRKVHQTNTGOV-----
>Calidris_pugnax
MPARQGWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Haplochromis_burtoni
-----MLPTLSLCSIIWLNRGIKLRKVHQSNTGOV-----
>Clupea_harengus
-----MFPTLSLCSIIWLNRGFKLRKVLCVANTGOI-----
>Latimeria_menadoensis
MVVVKQWSML-ALSLCSIIWLNRGFKLRKGVPLQDCALLPMWTEELDITSASKIELPVIWGRGPP1
>Columba_livia
MPAHKQWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Poeciliopsis_prolifica
-----MLPTLSLCSIIWLNRGIKLRKVQSSNTGQL-----
>Monodelphis_domestica
-----MVRRALCSIIWLSRGFKLRKSG-----
>Esox_lucius
-----MLPTLSLCSIIWLNRGIKLRKVLHCANTGQL-----
>Aquila_chrysaetos_canadensis
MPAHKQWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Coturnix_japonica
MPTRECWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Lutjanus_erythropterus
-----MLPTLSLCSIIWLNRGIKLRKVHQATNTGOV-----
>Scleropages_formosus
-----MLPTLSLCSIIWLNRGIKLRKVLVSANTGOF-----
>Lepidothrix_coronata
MPAHQGWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Lateolabrax_japonicus
-----MLPTLSLCSIIWLNRGIKLRKVHQSNTNTGOV-----
>Sebastes_caurinus
-----MLPTLSLCSIIWLNRGIKLRKVHQTNTGOV-----
>Cynoglossus_semilaevis
-----MLPSLSLCSIIWLNRGIKLRKHLSTNTGOI-----
>Salmo_salar
-----MLPTLSLCSIIWLNRGIKLRKVLHCANTGQL-----
>Lepisosteus_oculatus
-----MLPTLSLCSIIWLNRGFKLRKALLS-NTGOH-----
>Aptenodytes_forsteri
MPAHQGWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Gekko_japonicus
-----MLLTFSLCSIIWLNRGFKLRERGCT-----
>Struthio_camelus_australis
MPARNQWIMFVSFSLCSIIWLNRGFKLRKRGCT-----
>Chrysemys_picta
MPSHECWIMFVAFSLCSIIWLNRGFKLRKRGCTSACGSLSVCGA1LTRLR--STWLVRW-----
>Takifugu_rubripes
-----MLPTLSLCSIIWLNRGFKLRKVHQSNTNTGOV-----

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>Gallus_gallus
MPTHECWI MFVSFSLCSIIWLNRGFKLRKR-GCT-----
>Acipenser_sinensis
-----MLVKLSLCSIVWLNRGFKRRGVLLTMGLGHH-----
>Amia_calva
-----MLPTSSLCSIVWLNRGFKLRKVLSSNTG-QN-----
>Channa_argus
-----MLPTLSLCSIIWLNRGIKLRKMYRSTNTGOV-----
>Anas_platyrhynchos
MPSRERWIMVVSFSLCSIIWLNRGFKLRKR-GCT-----
>Megophrys_sanghiensis
MVPVKSWIMFVSFLCSIIWLNRGFKLRIR-GT-----
>Menidia_menia
-----MLPTLSLCSIIWLNRGIKLRKVHFTNTGOV-----
>Ambystoma_mexicanum
MCGGKCWIMFVALSLCSIIWLNRGFKLRKG-GT-----
>Micropterus_salmoides
-----MLPTLSLCSIIWLNRGIKLRKVHQFTNTGOV-----
>Haplochromis_burtoni
-----MLPTISLCSIIWLNRGIKLRKVHQSTNTGOV-----
>Clupea_harengus
-----MFPTLSLCSIIWLNRGFKLRKVLCAVANTGOI-----
>Latimeria_chalumnae
MVVVKCWSML-ALSLCSIIWLNRGFKLRKGVLPDCCALLSMWTEELDITSASKIELPVIWGRGPP1
>Danio_rerio
-----MLHSLCSIIWLNRGFKLRKVACTANTGOV-----
>Poecilia_mexicana
-----MLPMLSLSCSIIWLNRGIKLRKVQGSTTLVSSEAAATTV-IT-AATL-----
>Monodelphis_domestica
-----MVRRALCSIVWLSRGFKLRKS-G-----
>Esox_lucius
-----MLPTLSLCSIVWLNRGIKLRKVLHCANTGQL-----
>Falco_cherrug
MPTHKCWIMFVSFSLCSIIWLNRGFKLRKR-GCT-----
>Lutjanus_erythropterus
-----MLPTLSLCSIIWLNRGIKLRKVHQATNTGOV-----
>Scleropages_formosus
-----MLPTLSLCSIVWLNRGIKLRKVLYSANTGQF-----
>Lateolabrax_japonicus
-----MLPTLSLCSIIWLNRGIKLRKVHQSTNTGOV-----
>Sebastes_caurinus
-----MLPTLSLCSIIWLNRGIKLRKVHPTNTGOV-----
>Platichthys_stellatus
-----MLPTISLCSIIWLNRGIKLRKSHQSTNTGOV-----
>Oncorhynchus_mykiss
-----MLPTLSLCSIIWLNRGIKLRKVLHSANTGLL-----
>Lepisosteus_oculatus
-----MLPTLSLCSIVWLNRGFKLRKALLSNTG-QH-----
>Crotalus_adamanteus
-----MLVTFCLCFIIWLNRGFKLRERRGCT-----
>Takifugu_rubripes
-----MLPTLSLCSIIWLNRGFKLRKVHQSSNTGOV-----

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>Homo_sapiens
-----MDSVTKVSEIRIGPRCESQPGFKVLTSC
>Canis_lupus_familiaris
MDLGGNHWEFGEARVRSDTVQIRQMDSVTRVSEIRIGPRCENQPGGQVLTSC
>Balaenoptera_acutorostrata_s
-----MDSVTRASERIGPRCESQPRVWVLTSC
>Myotis_brandtii
-----MDSVTRVSEIRIGPRCESQPGVQVLTSC
>Dasypus_novemcinctus
-----MDSVTRASERIGPRCESQPGGQVLTSC
>Erinaceus_europaeus
-----MDSVTGVSEIRIGPRCENQPGVKMLTSC
>Oryctolagus_cuniculus
-----MDSVARASERIGPRERQPRVWVLTSC
>Equus_asinus
-----MDSVTGVSEIRIGPRCESQPGVKVLASC
>Manis_javanica
-----MDSVTRVSEIRIGPRCESQSEVQVLTSC
>Loxodonta_africana
-----MDSVTRASERIGPRCESQPGVKC-----
>Mus_musculus
-----MDSVTGTSEIRIGPRCESQPGVKVLTSC
>Tupaia_chinensis
-----MDSVTRASERIGPRCESRPGVRVLTSC
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HG0059.3 ENSG00000105647 PIK3R2

>Homo_sapiens
MVAACLTGSLVWCSQGSQRPWAPMALRVRA-----
>Felis_catus
MVTACALGPLVWRSRKSRQPRAPMAPRVRE-----
>Balaenoptera_acutorostrata_s
MVTACALGPLAWRSWKSRQPREPMAPHVRE-----
>Rousettus_aegyptiacus
MVTACALGSLVWRSRKSRQRPWAPMAPRVRE-----
>Condylura_cristata
MVTSSALGPLVWRSWKSRQSRAPMAPHVKE-----
>Equus_asinus
MVTACVLGPLIWRSWKRRQRPWEPMAAHVRE-----
>Manis_javanica
MVTACALGPLVWRSWKSRQPRAPMAHHVRE-----
>Chinchilla_lanigera
MVAALTLCSLVWRSWKSNQRPVPMALYHRRMANPVAK

HG0059.4 ENSG00000145675 PIK3R1

>Homo_sapiens
MDSRMASHLSS
>Dasypus_novemcinctus
MDSRMASHLSS
>Equus_asinus
MDSRMASHLSS
>Loxodonta_africana
MDSRMASHLSS
>Nannospalax_galili
MDSRMASHLSS
>Tupaia_chinensis
MDSRMASHLSS

HG0059.5 ENSDARG00000038524 pik3r1

>Danio_rerio	-----MGRVCMKHLEGAPNHWTSFT
>Astyanax_mexicanus	-----MGKLCVKHREGALDHWRTSFT
>Alosa_alosa	-----MGSLCLKHHAGAMEHWPINMT
>Apteronotus_leptorhynchus	
MLNCIFKLTPLVSCDSYRKERFSRADFDGFLNLAIYQSRGCFGQSTGADFSQMTLCLKHREGAQEHWRIRLT	
>Ictalurus_punctatus	-----METLCLKHHEAPLDHWRTSFT

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>Homo_sapiens-----MNPDI EESAGC WIKVAKQWNIQ
>Anser_cygnoides-----MTADIEESTGCWKRI PVKKWNVQ
>Chaetura_pelagica-----MTADVEESTGCWKRI PVKKWNI-
>Buceros_rhinoceros_silvestri-----MTADIEESTGCWKRI LVKKWNNQ
>Caprimulgus_carolinensis-----MTADIEESTGCWKRI PVKKWNIQ
>Cariama_cristata-----MTDIEESTGYWKRI PVKKWNIQ
>Odobenus_rossmarus_divergens-----MKILHHSFFPGLKKMNPDI EESTGCWKVPVKQWNI-
>Lipotes_vexillifer-----MKILPSLSFSFWTEKMNPDTEESTGCWKRI PVKKWNI-
>Charadrius_vociferus-----MTADIEESTGCWKRI PVKKWNIQ
>Pteropus_alecto-----MLKNGHTLVNQPNALMKILPSLIFSFWIEKMNPDIEESTGCWKVPVKQWTD-
>Dasypus_novemcinctus-----MKTKMNGDTEESMGWTKVPVKQRNI-
>Columba_livia-----MTADIEESTGCWKRI PVKKWNIQ
>Leptosomus_discolor-----MTADIEESTGCWKRI PVEKKWNVQ
>Sarcophilus_harrisii-----MNPERGESTGCWKRAPAKKWNI-
>Galeopterus_variegatus-----MNPDI EESMGCKV LVKQWNT-
>Monodelphis_domestica-----MNPERGESTGCWKRAPAKKWNI-
>Aquila_chrysaetos_canadensis-----MTADIEESTGCWKRI PVKKWNIQ
>Gallus_gallus-----MTADIEE---SCWKRPVKKWNIQ
>Eurypyga_helias-----MTADLEENTGCWKRI PVKKWNVQ
>Sorex_araneus-----MNPVIEESMGCKKVSIIQWNI-
>Oryctolagus_cuniculus-----MNPDI EESTGCWKLLVKQWNI-
>Tauraco_erythrolophus-----MTADIEESTGCWKRI PVKKWNIQ
>Opisthocomus_hoazin-----MTADIEEGTFWKRI PVKKWNIQ
>Nipponia_nippon-----MTADIEESTGCWKRI PFKKWNIQ
>Ceratotherium_simum_simum-----MKILPSLFFSFWIEKMNPDIEESMGCKVPVKQ----
>Manis_javanica-----MNPHEESMGCKVPKQWNI-
>Loxodonta_africana-----MNPDT EESMGCKEKPVKQWNIY
>Fulmarus_glacialis-----MTADIEESTGCWKRI PVKKWNIQ
>Ictidomys_tridecemlineatus-----MNPDI EESAGCKKEPVKQWNI-
>Tupaia_chinensis-----MNPDMDDSMGFVKVPVKQWKM-
>Pygoscelis_adeliae-----MTADIEESTGCWKRI PVKKWNLQ
>Struthio_camelus_australis-----MTADIEESTGCRKRI PVKKWNIQ
>Chrysemys_picta-----MTADIEESTGCWKRPVKKWNIQ
>Orycteropus_afer_afer-----MNPDT EEST EYWEKI PVKQWNI-
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HG0060.1 ENSGALG00000014751

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>Gallus_gallus-----MTADIEE--SCWKRPVKKNW1Q
>Anser_cygnoides-----MTADIEESTGCKWKRI PVKKWNVQ
>Chaetura_pelagica-----MTADVEESTGCKWKRI PVKKWNI-
>Buceros_rhinoceros_silvestri-----MTADIEESTGCKWKRI LVKKWNNQ
>Caprimulgus_carolinensis-----MTADIEESTGCKWKRI PVKKWNIQ
>Cariama_cristata-----MTDIEESTGYWKRI PVKKWNIQ
>Odobenus_rossmarus_divergens-----MKILHHSFFPGLKKNPDIEESTGCKWKVPVKQWNI-
>Lipotes_vexillifer-----MKILPSLSFSFWTEKMNPDIEESTGCKWKRI PVKKWNI-
>Charadrius_vociferus-----MTADIEESTGCKWKRI PVKKWNIQ
>Pteropus_alecto
MLKNGHTLYTNQPNALLMKILPSLIFSFWIEKMNPDIEESTGCKWKVPVKQWTD-
>Dasypus_novemcinctus-----MKTMMNQDTEESMGWTKVPVKQRNI-
>Columba_livia-----MTADIEESTGCKWKRI PVKKWNIQ
>Leptosomus_discolor-----MTADIEESTGCKWKRI PVEKWNVQ
>Sarcophilus_harrisii-----MNPERGESTGCKWRAPAKKWN1-
>Galeopterus_variegatus-----MNPDI EESMGCKVKLVKQWNT-
>Monodelphis_domestica-----MNPERGESTGCKWRAPAKKWN1-
>Aquila_chrysaetos_canadensis-----MTADIEESTGCKWKRI PVKKWNIQ
>Eurypyga_helias-----MTADLENTGCKWKRI PVKKWNVQ
>Oryctolagus_cuniculus-----MNPDI EESTGCKWKL LVKQWNI-
>Tauraco_erythrolophus-----MTADIEESTGCKWKRI PVKKWNIQ
>Opisthocomus_hoazin-----MTADIEESTGFWKRI PVKKWNIQ
>Nipponia_nippon-----MTADIEESTGCKWKRI PFKKWN1Q
>Equus_asinus-----MKILPSLFSFWIEKMNPDIEESMRCKWKVPVKQWNI-
>Manis_javanica-----MNPHLEESMGCKVKVPKQWNI-
>Cerocebus_atys-----MKTFTIIIFSWIEKMNPDIEESAGCWI KVPLKQWNIQ
>Loxodonta_africana-----MNPDI EESMGCKWKVPVKQWNIY
>Fulmarus_glaucialis-----MTADIEESTGCKWKRI PVKKWNIQ
>Ictidomys_tridecemlineatus-----MNPDI EESAGCKWKVPVKQWNI-
>Pygoscelis_adeliae-----MTADIEESTGCKWKRI PVKKWNLQ
>Struthio_camelus_australis-----MTADIEESTGCKWKRI PVKKWNIQ
>Chrysemys_picta-----MTADIEESTGCKWKRPVKKNWNIQ
>Orycteropus afer-----MNPDI EESTEYWEKIPVKQWNI-
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>Homo_sapiens
MLRFWYGIDSLAHR
>Anas_platyrhynchos
MVRFWSGVSSIAHR
>Chaetura_pelagica
MVRFWSGVNSVSHR
>Canis_lupus_familiaris
MLRFWYGIDSLAHR
>Physeter_catodon
MLRFWHGIDSLAHR
>Charadrius_vociferus
MVGFWSGVNSVAHR
>Dasypus_novemcinctus
MLRFWYGVDLSAHR
>Columba_livia
MVRWWSGANSIAHR
>Leptosomus_discolor
MVRFWSGVNFIAHR
>Galeopterus_variegatus
MLRLWYDIDSLTHR
>Aquila_chrysaetos_canadensis
MVRFWSGVNSVAHR
>Gallus_gallus
MVGFWSGVNP1AHR
>Eurypyga_helias
MVRFWSGVNSVAHR
>Sorex_araneus
MLRFWYDIDSLAHR
>Oryctolagus_cuniculus
MLRFWYGIDSLAHR
>Tauraco_erythrolophus
MVPFWSGVNSIAHR
>Opisthocomus_hoazin
MVRFWSGVNSIAHR
>Acanthisitta_chloris
MVRFWSGVNSIAHR
>Phaethon_lepturus
MVRFWSGVNSLAHR
>Ceratotherium_simum_simum
MLRFWYGIDSLAHR
>Manis_javanica
MLRFWYGIDSLAHR
>Loxodonta_africana
MLRFWYGIDSLAHR
>Fulmarus_glacialis
MVRFWSGVNSTAHR
>Nannospalax_galili
MLRFWYGIDSLAHR
>Tupaia_chinensis
MLRFGYDSDSLAHR
>Pygoscelis_adeliae
MVRFWSGVNSVAHR
>Thamnophis_sirtalis
MVGFWSGVKA1AHR
>Struthio_camelus_australis
MVRFWSGVKSIAHR
>Chrysemys_picta
MVRFWSGVNSIAHR
>Orycteropus afer_afer
MLRFWHGVDSLAHR

HG0060.2 ENSGALG00000014751

>Gallus_gallus
MVGFWSGVNPIAHR
>Anser_cygnoides
MVRFWSGVSSIAHR
>Chaetura_pelagica
MVRFWSGVNSVSHR
>Buceros_rhinoceros_silvestri
MVLFWSGVNFIAHR
>Caprimulgus_carolinensis
MVRFWSGVNSIAHR
>Gariama_cristata
MVRFWSGVNSVAHK
>Charadrius_vociferus
MVGFWSGVNSIAHR
>Dasyus_novemcinctus
MLRFWYGVDSLAHR
>Columba_livia
MVRFWSGVNSIAHR
>Leptosomus_discolor
MVRFWSGVNFIAHR
>Aquila_chrysaetos_canadensis
MVRFWSGVNSIAHR
>Eurypyga_helias
MVRFWSGVNSIAHR
>Tauraco_erythrolophus
MVPFWSGVNSIAHR
>Opisthocomus_hoazin
MVRFWSGVNSIAHR
>Manacus_vitellinus
MVGFWSGVNSIAHK
>Nipponia_nippon
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>Microcebus_murinus
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>Loxodonta_africana
MLRFWYGIDSLAHR
>Fulmarus_glacialis
MVRFWSGVNSTAHR
>Chinchilla_lanigera
MLRFWYGINSIAHR
>Pygoscelis_adeliae
MVRFWSGVNSIAHR
>Thamnophis_sirtalis
MVGFWSGVKAIHR
>Struthio_camelus_australis
MVRFWSGVKSIAHR
>Chrysemys_picta
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>Orycteropus_afer_afer
MLRFWHGVDSLHR

HG0061.1 ENSG00000166398

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>Homo_sapiens
----MVTCLMEMPFCLKLRFaelHYFYT
>Anas_platyrhynchos
-----MPFVKPMYTVLHCYCT
>Xenopus_laevis
-----MPFTKPVFADFYYLT
>Caprimulgus_carolinensis
-----MPFVKLMYTVLHCYCT
>Felis_catus
----MVTCLMEMPFCLKLRFaelHYFYT
>Hynobius_retardatus
-----MPFTKPSYPVPHYTY-
>Physeter_catodon
----MVTCLMEMPFCLKLRFaelHYFYT
>Cynopterus_sphinx
----MVTCLMEMPFCLKLRFaelHYFYT
>Columba_livia
-----MPFVKPMYAVLHCYCT
>Alligator_mississippiensis
-----MPFMKPAYAVLHYTYT
>Sarcophilus_harrisii
-----MPFMELLFAVLYCYTYT
>Galeopterus_variegatus
----MATCLMEMPFCLKLGLaelHYFYT
>Monodelphis_domestica
-----MPFMELLFAVLHYTYT
>Condylura_cristata
----MVTCLMKMPFCLKLRFaelHYFYT
>Oryctolagus_cuniculus
----MVICLEMSFLKLTFAEVHYFYT
>Phaethon_lepturus
-----MPFVKPMATVLHCYTYT
>Ceratotherium_simum_simum
----MVICLMEMPFCLKLRFaelHYFYT
>Manis_javanica
----MVTFLMEMPFCLKLRFaelHYFYT
>Melopsittacus_undulatus
-----MPFVKPTYTVLHFYCT
>Ctenomys_sociabilis
MFDHMTCLMEMPFCLKLQFAELHYFYT
>Tupaia_chinensis
-----MEMPFCLKHRFAELQYFYT
>Tyto_alba
-----MPFVKLMYMLHCYCT
>Struthio_camelus_australis
-----MPFVKPMYAVLHCYCT
>Pelodiscus_sinensis
-----MPFLKRMVTVLHCYTYT
>Galypte_anna
-----MPFVKPMYTVLHCYCT
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>Gallus_gallus
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>Anser_cygnoides
MPFVKPMYTVLHCYCT-----
>Leptobrachium_boringii
MPFTKPMYVALLCYLT-----
>Chaetura_pelagica
MPFVKPMYTVLHCYCT-----
>Apteryx_australis_mantelli
MPFVKPMYTVLHCYCT-----
>Buceros_rhinoceros_silvestri
MPFVEPMYTVLHCYCT-----
>Caprimulgus_carolinensis
MPFVKLMYTVLHCYCT-----
>Cariama_cristata
MPFVKPMYTVLHCYCT-----
>Charadrius_vociferus
MPFVKPMYTVLHCYCTKLYI
>Pterocles_gutturalis
MPFVKPMYTVLHCYCT-----
>Colius_striatus
MPFVKPMYTVHHCYCT-----
>Columba_livia
MPFVKPMYAVLHCYCT-----
>Merops_nubicus
MPFVKPMYTVLHCYCT-----
>Alligator_sinensis
MPFMKPAYAVLHYYT-----
>Cuculus_canorus
MPFVKPMYTVLHCYCT-----
>Falco_cherrug
MPFVKPMYTVLHCYCT-----
>Gavia_stellata
MPFVKPMYTVLHCYCT-----
>Balearica_regulorum_gibberic
MPFVKPMYTVLHCYCT-----
>Ornithorhynchus_anatinus
MPFVKPGFTVLRHYHT-----
>Tauraco_erythrolophus
MPFVKPMYTVLHCYCT-----
>Opisthocomus_hoazin
MPFVKRMCAVLDYCTELYI
>Corvus_brachyrhynchos
MPFVKPMYTVLHCYCT-----
>Egretta_garzetta
MPFVKPMYTVLHCYCT-----
>Picoides_pubescens
MPFVTPMYTAPHRRCT-----
>Fulmarus_glaucialis
MPFVKPMYTVLHCYCT-----
>Nestor_notabilis
MPFVKPVYTVLHCYCT-----
>Aptenodytes_forsteri
MPFVKPMYTVLHCYCT-----
>Tyto_alba
MPFVKLMYVVLHCYCT-----
>Struthio_camelus_australis
MPFVKPMYAVLHCYCT-----
>Pelodiscus_sinensis
MPFLKRMYTVLHCYTYT-----
>Tinamus_guttatus
MPFVKPMYTVLHCYCT-----
>Calypte_anna
MPFVKPMYTVLHCYCT-----
>Apaloderma_vittatum
MPFVKPMYTVLHCYCT-----

>Gallus_gallus	-----MLQRKQLPQQTRKGEEGLQ-----
>Anas_platyrhynchos	-----MLQRKQLPQQTRKGEEGLQ-----
>Calidris_pugnax	-----MLQRKQLPQQRKGGKGGKACNNK-HSNF-----
>Columba_livia	-----MLQRKQLPQQTRKGEEGLQ-----
>Sarcophilus_harrisii	-----MLQRKQLPQKTKGEEAAEQLEITNTPNF-----
>Monodelphis_domestica	-----MLQRKQLPQKTEGKEEAPWQLEITNTPVFNNLTCEKRRHF1FFSCS1KKKHYY-----
>Aquila_chrysaetos_canadensis	-----MLQRKQLPQQTRKGEEGLQ-----
>Corvus_brachyrhynchos	-----MLQRKQLPQQTKGEEGLQ-----
>Aptenodytes_forsteri	-----MLQRKQLPQQTRKGEEGLQ-----
>Struthio_camelus_australis	-----MLQRKQLPQQTRKGEEGLQ-----
MNLLLLKYSKPVNSLESLLTEHRSCGNDLEALQIHLCIFVPSLRLRANA1WKHHFLTQRKQLPQQTRKGEEGLQ-----	

>Homo_sapiens
MLOGNRYLSKQKEWRRRLTTNA-I-----
>Pteropus_lecto
MLOGNRYLSKQKERRRLITNA-IF-----
>Galeopterus_variegatus
MLOGNRYLSKQKERRRLITNGIFKKTG--FRKTLEE-I-----
>Condylura_cristata
MLOGNRYLSKQKERRRLIYNMPFF-----
>Oryctolagus_cuniculus
MLOGNRYLSKQKERRRLKITNDIFTKQTCFQKTLIEWTFLASGRFVSKWI
>Ceratotherium_simum_simum
MLOGSHYLNKQKERRRLITNAIFKKLG-FRKY-----
>Nannospalax_galili
MLOGNRYLSKEKERRRRTVDAM-FKENL--FSENPTGDL-----
>Tupaia_chinensis
MLOGNRYLSKQKERRRLTTTNAIFKQTNSEFPNIEE-I-----

HG0062.1 ENSDARG00000075569 gbp111

>Danio_rerio
MPPSTDGRHWT
>Pygocentrus_nattereri
MPRSTDGRHWT
>Clupea_harengus
MPRSTEGRHWT
>Poecilia_formosa
MPPSTDQKHWT
>Apteronotus_leptorhynchus
MPRSTDGRHWT
>Salmo_salar
MPRSTDGRHWT
>Trichomycterus_areolatus
MPRSTDGRHWT

HG0062.1 ENSGALG00000010276 GPBP1L1

>Gallus_gallus
MPHFIEGRHWT
>Anser_cygnoides
MPHFIEGRHWT
>Chaetura_pelagica
MPHFIEGRHWT
>Apteryx_australis_mantelli
MPHFIEGRHWT
>Buceros_rhinoceros_silvestri
MPHFIEGRHWT
>Caprimulgus_carolinensis
MPHFVEGRHWT
>Cariama_cristata
MPHFIEGRHWT
>Physeter_catodon
MPHLVEKRHWT
>Charadrius_vociferus
MPHFIEGRHWT
>Pterocles_gutturalis
MPHFIEGRHWT
>Colius_striatus
MPHFIEGRHWT
>Columba_livia
MPHFIEGRHWT
>Leptosomus_discolor
MPHFIEGRHWT
>Alligator_mississippiensis
MPHFIEGRHWT
>Cuculus_canorus
MPHFIEGRHWT
>Falco_cherrug
MPHFIEGRHWT
>Eurypyga_helias
MPHFIEGRHWT
>Tauraco_erythrophus
MPHFIEGRHWT
>Opisthocomus_hoazin
MPHFVEGRHWT
>Geospiza_fortis
MPHFIEGRHWT
>Egretta_garzetta
MPHFIEGRHWT
>Picoides_pubescens
MPHFIEGRHWT
>Fulmarus_glacialis
MPHFIEGRHWT
>Melopsittacus_undulatus
MPHFIEGRHWT
>Oncorhynchus_mykiss
MPHSTDGRHWT
>Aptenodytes_forsteri
MPHFIEGRHWT
>Gekko_japonicus
MPRFIEGRHWT
>Tyto_alba
MPHFIEGRHWT
>Struthio_camelus_australis
MPHFIEGRHWT
>Pelodiscus_sinensis
MPHFIEGRHWT
>Tinamus_guttatus
MPHFIERRHWT
>Calypte_anna
MPHFVEGRHWT
>Apaloderma_vittatum
MPHFIEGRHWT

HG0062.2 ENSGALG00000010276 GPBP1L1

>Gallus_gallus
MSCPADLGVSVQY
>Anser_cygnoides
MNYPAELGVSVQY
>Caprimulgus_carolinensis
MNYPADLSVSVQY
>Charadrius_vociferus
MNYPADLSVSVQY
>Pterocles_gutturalis
MNYPADLSVSVQY
>Colius_striatus
MSYPADLGVSAQY
>Columba_livia
MNDPADLSVSVQY
>Cuculus_canorus
MNYPADLSVSVQY
>Haliaeetus_leucocephalus
MNYPADLSVSVQY
>Gavia_stellata
MNYPADLSVSVQY
>Chlamydotis_macqueenii
MNYPADLSVSVQY
>Opisthocomus_hoazin
MNYPADLSVSVQY
>Acanthisitta_chloris
MNCPAALSVSVQY
>Phaethon_lepturus
MNYPADLSVSVQY
>Fulmarus_glacialis
MNYPADLSVSVQY
>Melopsittacus_undulatus
MNYPADLGVSVQY
>Pygoscelis_adeliae
MNYPADLSVSVQY
>Tyto_alba
MNYPADLSVSVQY
>Struthio_camelus_australis
MNYPADLGASVQY
>Tinamus_guttatus
MNYPADLGASVQY
>Calypte_anna
MNYPADLSVSVQY

HG0062.3 ENSG00000159592 GPBP1L1

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>Homo_sapiens
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>Leptonychotes_weddellii
MSMYLFFKQHHSAITQGS
>Balaenoptera_acutorostrata_s
MSMYLFFKQHHRAITQGS
>Rousettus_aegyptiacus
--MYLFFKQHHSAITQGS
>Dasypus_novemcinctus
MSMYLFFKQHHSTITQGS
>Galeopterus_variegatus
MSMYLFFKQHHSAITQGS
>Condylura_cristata
MSLNYLFFKQHHSDITQGS
>Oryctolagus_cuniculus
MPMYLFFKQHHSAITQGS
>Ceratotherium_simum_simum
MSMYLFFKQHHSAITQGS
>Loxodonta_africana
MSMYLFFKQHHSAITORS
>Marmota_marmota_marmota
MSMYLFFKQHHSAITQGS
>Trichechus_manatus_latirostr
MSMYLFFKQHHSTITQGS
>Orycteropus_afer_afer
MSMYLFFKQHHSAITORS
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>Homo_sapiens
-----MCACSTIASFLLK-----
>Anas_platyrhynchos
-----MCACSTIASFLLK-----
>Chaetura_pelagica
-----MCACSTIASFLLK-----
>Buceros_rhinoceros_silvestri
-----MCACSTIASFLLK-----
>Caprimulgus_carolinensis
-----MCACSRASFLLK-----
>Cariama_cristata
-----MCACSTIASFLLK-----
>Mustela_putorius_furo
-----MCACSTIASFLLK-----
>Charadrius_vociferus
-----MCACSTIASFLLK-----
>Pterocles_gutturalis
---MGYREGQGPQEADGWMACACSTIASFLLK-----
>Dasypus_noveboracensis
-----MCACSTIASFWLK-----
>Colinus_striatus
-----MCACSTIASFLLK-----
>Columba_livia
-----MCACSTIASFLLK-----
>Cuculus_canorus
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>Galeopterus_variegatus
-----MCACSTIASFLLK-----
>Monodelphis_domestica
-----MCACSTIASFLLK-----
>Macropus_eugenii
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>Aquila_chrysaetos_canadensis
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>Gallus_gallus
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>Gavia_stellata
-----MCACSTIASFLLK-----
>Mesitornis_unicolor
-----MCACSTIASFLLK-----
>Condylura_cristata
-----MCACSTIASFLLK-----
>Ornithorhynchus_anatinus
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>Tauraco_erythrolophus
-----MCACSTIASFLLK-----
>Opisthocomus_hoazini
-----MCACSTIASFLLK-----
>Phalacrocorax_carbo
MDRLDTYKKQSQEAGCGWMACACSTIASFLLK-----
>Ceratotherium_simum_simum
-----MCACSTIASFLLK-----
>Manis_javanica
-----MCACSTIASLTK-----
>Loxodonta_africana
-----MCACSLTSFLLK-----
>Fulmarus_glaucialis
-----MCACSTIASFLLK-----
>Nannospalax_galili
-----MCACSTIASFLLK-----
>Aptenodytes_forsteri
-----MCACSTIASFLLK-----
>Chelonia_mydas
-----MCACSTIASFLLK-----
>Apaloderma_vittatum
-----MCACSTIASFLPKRWRAKTIIFWGYNPRTINGLTKEVSHLOTTTQHKQRKMNTKE

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>Gallus_gallus
-----MCACSTIASFLLK-----
>Anas_platyrhynchos
-----MCACSTIASFLLK-----
>Chaetura_pelagica
-----MCACSTIASFLLK-----
>Buceros_rhinoceros_silvestri
-----MCACSTIASFLLK-----
>Caprimulgus_carolinensis
-----MCACSRASFLLK-----
>Cariama_cristata
-----MCACSTIASFLLK-----
>Mustela_putorius_furo
-----MCACSTIASFLLK-----
>Charadrius_vociferus
-----MCACSTIASFLLK-----
>Pterocles_gutturalis
---MGYREQQPQEAQGWGMCACSTIASFLLK-----
>Dasypus_noveboracensis
-----MCACSTIASFLLK-----
>Colinus_striatus
-----MCACSTIASFLLK-----
>Columba_livia
-----MCACSTIASFLLK-----
>Cuculus_canorus
-----MCACSTIASFLLK-----
>Galeopterus_variegatus
-----MCACSTIASFLLK-----
>Monodelphis_domestica
-----MCACSTIASFLLK-----
>Macropus_eugenii
-----MCACSTIASFLLK-----
>Aquila_chrysaetos_canadensis
-----MCACSTIASFLLK-----
>Gavia_stellata
-----MCACSTIASFLLK-----
>Mesitornis_unicolor
-----MCACSTIASFLLK-----
>Condylura_cristata
-----MCACSTIASFLLK-----
>Ornithorhynchus_anatinus
MDGSDTGEEPSREAERWGMACSMASF-----
>Tauraco_erythrolophus
-----MCACSTIASFLLK-----
>Opisthocomus_hoazin
-----MCACSTIASFLLK-----
>Phalacrocorax_carbo
MDRLDTYKKGQEAAGQWGMACSTIASFLLK-----
>Ceratotherium_simum_simum
-----MCACSTIASFLLK-----
>Manis_javanica
-----MCACSTIASFLLK-----
>Cercopithecus_atys
-----MCACSTIASFLLK-----
>Loxodonta_africana
-----MCACSTIASFLLK-----
>Fulmarus_glaucialis
-----MCACSTIASFLLK-----
>Nannospalax_galili
-----MCACSTIASFLLK-----
>Aptenodytes_forsteri
-----MCACSTIASFLLK-----
>Chelonia_mydas
-----MCACSTIASFLLK-----
>Apaloderma_vittatum
-----MCACSTIASFLPKRWRAKTIKFWGYNPRTINGLTKEVSHLOTTTQHKQRKMNTKE-----
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HG0063.2 ENSG00000162630 B3GALT2

>Homo_sapiens
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>Anser_cygnoides
MDTEEKRTQHCIVRQGHOM
>Canis_lupus_familiaris
MD-TEKRIQHCIVRPGKQOM
>Balaenoptera_acutorostrata_s
MD-TEKRIQHCIVRPGKQOM
>Rousettus_aegyptiacus
MD-TEKRTQHCIVRPGKQOM
>Dasypus_novemcinctus
MD-TEKRTQHCIVQPGKQOM
>Galeopterus_variegatus
MD-TEKRTQHCIVQPGKQOM
>Monodelphis_domestica
MD-TEKRIQHCIVRQGHYKM
>Macropus_eugenii
MD-TEKRIQHCIVRQGHYEM
>Aquila_chrysaetos_canadensis
MDTGKRTQHCIVRQGHOM
>Gallus_gallus
MDTGERTQHCIVRQGHOM
>Erinaceus_europaeus
MD-TQKRIQHCIVRPGKQOM
>Oryctolagus_cuniculus
MD-TEKRTQHCIVQPGKQOM
>Lepidothrix_coronata
MDTGERTQHCIVRHGHOM
>Ceratotherium_simum_simum
MD-TEKRTQHCIVRPGKQOM
>Manis_javanica
MD-TEKRIQHCIVRPGKQOM
>Loxodonta_africana
MD-TEKRIKHCIVRPGKQOT
>Dipodomys_ordii
MD-TEKRTQHCIVQPGKQOM
>Tupaia_chinensis
MD-TGKRTQHRIVQPGKQOL
>Trichechus_manatus_latirostr
MD-TEKRIQHCIVQPGKQOM
>Gekko_japonicus
MD-TEKRTQHCIVQGHQOL
>Chelonia_mydas
MD-TEKRIQHCIVRQGHQOM
>Orycteropus afer afer
MD-TEKRIQHCIVQPGKQOM

>Homo_sapiens
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>Anas_platyrhynchos
MVILILNOMEKLRIFFFITVGWAEDLIAC
>Chaetura_pelagica
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Canis_lupus_familiaris
MVILISNOMEKLRIFFPYY-GRMG-----
>Balaenoptera_acutorostrata_s
MVILISNOMEKLRIFFPYY-GRMG-----
>Charadrius_vociferus
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Rousettus_aegyptiacus
MVIPINWOMEKLRIFSLMTASWDEDLPVC
>Dasypus_noveboracensis
MVILISNOMEKLRIFFLITVGWDEDLTAC
>Leptosomus_discolor
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Cuculus_canorus
MVILTLNOMEKLRIFFFITVGWAEDRIAC
>Galeopterus_variegatus
MVILISNOMEKLRIFFLITVGWDEDLPAY
>Macropus_eugenii
MVILISNOMEKLRIFFLITVGWDEDLTAC
>Aquila_chrysaetos_canadensis
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Coturnix_japonica
MVILFLNOMEKLRIFFLYY-GWVG-----
>Eurypyga_helias
MVILILNOMEKLRIFFLITVGWAEDRIAC
>Condylura_cristata
MVILISNOMEKLRIFFPYY-GRMG-----
>Oryctolagus_cuniculus
MVILISKOMEKLRIFFPYY-GRMG-----
>Elephantulus_edwardii
MVILISNOMEKLRIFFLIMAGWDEDLTAC
>Opisthocomus_hoazini
MVILVLNOMEKLRIFFLDY-GWVG-----
>Lepidothrix_coronata
MVILILNOMEKLRIFFLYY-SWVG-----
>Egretta_garzetta
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Equus_przewalskii
MVILISNOMEKLRIFFPYY-GRMG-----
>Manis_javanica
MVILISNOMEKLRIFFLITVGWDEDLSAC
>Picoides_pubescens
MVILILNOMEKLRIFFLITVGWAEDRIAC
>Loxodonta_africana
MVILISSOMEKLRIFFLITVGWDEDLTAC
>Peromyscus_maniculatus_baird
MVILISKOMEKLRIFFPYY-GRMG-----
>Tupaia_chinensis
MVILISNOMEKLRIFFPYY-GRMG-----
>Aptenodytes_forsteri
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Struthio_camelus_australis
MVILILNOMEKLRIFFFITVGWAEDLIAC
>Chelonia_mydas
MVILILNOMEKLRIFFLIAGWAEDLTAC
>Tinamus_guttatus
MVFLILNOMEKLRIFFLYY-SWVG-----
>Calypte_anna
MVILILNOMEKLRIFFFITVGWAEDRIAC
>Orycteropus afer
MVILISNOMEKLRIFFLITVGWDEDFTAC

>Homo_sapiens	MVCGFTQFFSWGFSELHSYQKGSRRTSGSNSLRSGIRASPPFLGGHSLLMVWGNSLPPAAACLQLSW-----
>Panthera_tigris	-----MENGNSLPPAAACLQHSR-----
>Myotis_brandtii	-----MANGNSLPAAAAGLPCSW-----
>Galeopterus_variegatus	-----MVWGNSLLPAAACLRCSWRGSDTAPEKKLLRAKAKSKSATTSS-----
>Condylura_cristata	-----MENGNSLPPAAASPQRSW-----
>Ceratotherium_simum_simum	-----MENGNSLPPAAACLQRSC-----
>Nannospalax_galili	-----MVWGNSLPQSL---LAASW-----
>Orycteropus afer_afer	-----MGNGNSLPPAPACLK-----

>Gallus_gallus	-----MKRFQAKQLLSKTPRRREKEKERES-----
>Anser_cygnoides	-----MKRFQAKQRLAKTPRRREKEKGREKLKH-----
>Chaetura_pelagica	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Apteryx_australis_mantelli	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Buceros_rhinoceros_silvestri	-----MKRFCQTKQCLAKTPRRREKEKGRERELKH-----
>Caprimulgus_carolinensis	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Cariama_cristata	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Balaenoptera_austrorotata_s	-----MKRYCHRKQCLVKTTTRKREKDXGRRS-----
>Charadrius_vociferus	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Colius_striatus	-----MKRFYQAKQCLAKTPRRREKEKGRERELKH-----
>Columba_livia	-----MKRFCQTKQGLAKTPRRREKEKGRESELKH-----
>Merops_nubicus	-----MKRFQAKQCLAKTPRRREKEKGREKELKH-----
>Alligator_mississippiensis	-----MRRFQAKQCLAKTPRRREKEKGEGERS-----
>Cuculus_canorus	-----MKRFQAKQCLAKTPRRREKEKRRRRRELKH-----
>Monodelphis_domestica	-----MRRFCLTKQGPLKTTTRKREKRGKS-----
>Aquila_chrysaetos_canadensis	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Gavia_stellata	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Balearica_regulorum_gibberic	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Condylura_cristata	-----MKRYCHTKQCLVKTPRKRQGDHRKKLKLTL-----
>Tauraco_erythrolophus	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Zonotrichia_albicollis	-----
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>Picoides_pubescens	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Otolemur_garnettii	-----MKRYCHTKQCLVKTTTRKREKDREKS-----
>Fulmarus_glaucialis	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Melopsittacus_undulatus	-----MKRFQAKQCLAKTPRRREKEKGRERELKH-----
>Aptenodytes_forsteri	-----MKRFQAKQCLAKTPRRREKEKGREKELKH-----
>Anolis_carolinensis	-----MGARGAVTWGPERRLA-----AVELPERSERRDGEDAAAAGVLOSRI PGASVPLL RDLLSRQETERHMRSSWQAKSLAKTPRRREKEKADRRRS-----
>Struthio_camelus_australis	-----MKRFQAKQCLAKTPRRREKEKGREKELKH-----
>Chrysemys_picta	-----MRRFQAKTVPSKDTFEEGKGEGGGGAELRL-----
>Tinamus_guttatus	-----MKRFCQTKQCLAKTPRRREKEKGGRDOLKH-----
>Calypte_anna	-----MKRLQAKQCLAKTPRRREKEKGREKELKH-----
>Apaloderma_vittatum	-----MKRFQAKQCLAKTPRRREKEKGWERELKH-----


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>Homo_sapiens
----MDCCSLLISPFQAQFPAS
>Anser_cygnoides
----MDCCSLLISPLILFPAS
>Mustela_putorius_furo
----MDCCSLLISPFQAQFPAS
>Orcinus_orca
----MDCCSLLISPFQAQFPAS
>Charadrius_vociferus
----MDCCSLLISPLILFPAS
>Eptesicus_fuscus
----MDCCSLLISPFQAQFPAS
>Dasypus_novemcinctus
----MDCCSLLISPFQAQFSAS
>Columba_livia
----MDCCSLLISPLILFPAS
>Alligator_mississippiensis
----MDCCSLLISPTQFPAS
>Cuculus_canorus
----MDCCSLLISPLIPFPAS
>Sarcophilus_harrisii
----MDCCNLLISPTQFPAS
>Monodelphis_domestica
----MDCCSLFISPTQFPAS
>Macropus_eugenii
----MDCCSLLISPTQFPAS
>Falco_cherrug
----MDCCSLLISPLILFPAS
>Gallus_gallus
----MDCCSLLISPLILFPAS
>Mesitornis_unicolor
----MDCCSLLISPVILFPAS
>Condylura_cristata
----MDCCSFLISPFQAQCPAS
>Oryctolagus_cuniculus
----MDCCSLLISPFQAQSPAS
>Elephantulus_edwardii
----MDCCSLLISPFQAQFPAS
>Opisthocomus_hoazini
----MDCCSLLISPLILFPAS
>Pseudopodoces_humilis
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>Equus_asinus
----MDCCSLLISPFQAQFPAS
>Manis_javanica
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>Heterocephalus_glaber
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>Trichechus_manatus_latirostris
----MDCCSLLISPFQAQFPAS
>Aptenodytes_forsteri
----MDCCSLLISPLILFPAS
>Gekko_japonicus
----MDCCKLLISPFVHFLVS
>Struthio_camelus_australis
----MDCCSLLISPLILFPAS
>Chrysemys_picta
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>Tinamus_guttatus
----MDCCSLFISPLIPFPAS
>Orycteropus afer afer
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>Homo_sapiens	METGDNFRKRD-----
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>Anser_cygnoides	METGDNFRKRD-----
>Microhyla_fissipes	METGDNFRKRD-----
>Oryzias_latipes	METGDNFRKKKKRSC-----
>Canis_lupus_familiaris	METGDNFRKRD-----
>Balaenoptera_acutorostrata_s	METGDNFRKRD-----
>Astyanax_mexicanus	MESGDNFRKKEN-----
>Calidris_pugnax	METGDNFRKRD-----
>Rousettus_aegyptiacus	METGDNFRKRD-----
>Maylandia_zebra	METGDNFRKKENLSG-----
>Dasypus_novemcinctus	METGDNFRKRD-----
>Alosa_alosa	METGDNFRKKEN-----
>Sinocyclocheilus_anshuiensis	METGDNFRKKDI-----
>Poecilia_mexicana	METGDNFRKKENLSG-----
>Galeopterus_variegatus	METGDNFRKRD-----
>Monodelphis_domestica	METGDNFRKRD-----
>Aquila_chrysaetos_canadensis	METGDNFRKRD-----
>Meleagris_gallopavo	METGDNFRKRD-----
>Apteronotus_leptorhynchus	METGDNFRKKDIYQLFILNFRFHFSVY-----
>Zonotrichia_albicollis	METGDNFRKRD-----
>Ceratotherium_simum_simum	METGDNFRKRD-----
>Manis_javanica	METGDNFRKRD-----
>Melopsittacus_undulatus	METGDNFRKRD-----
>Nannospalax_galili	METGDNFRKRD-----
>Salmo_salar	METGDNFRKKKI-----
>Tupaia_chinensis	METGDNFRKRD-----
>Ictalurus_punctatus	METGDNFRKKLN-----
>Thamnophis_sirtalis	METGDNFRKRD-----
>Struthio_camelus_australis	METGDNFRKRD-----
>Chelonia_mydas	METGDNFRKRD-----
>Takifugu_rubripes	METGDNFRKKENPCVSFGFSF-----SSCVPTRTI-----
>Tinamus_guttatus	METGDNFRKRD-----

>Danio_rerio	-----MRFFRL-TFKCFVDCF
>Amia_calva	-----MRFFRL-TFKCFVDCF
>Xenopus_tropicalis	-----MRFFRL-TFKCFVDCF
>Menidia_menidia	-----MRFFRL-TFKCFVDCF
>Porichthys_notatus	-----MRFFRL-TFKCFVDCF
>Oryzias_melastigma	-----MRFFRL-TFKCFVDCF
>Hynobius_chinensis	-----MRFFRL-TFKCFVDCF
>Micropterus_floridanus	-----MRFFRL-TFKCFVDCF
>Astyanax_mexicanus	-----MRFFRL-TFKCFVDCF
>Rousettus_aegyptiacus	-----MRFFRL-TFKCFVDCF
>Haplochromis_burtoni	-----MRFFRL-TFKCFVDCF
>Clupea_harengus	-----MRFFRL-TFKCFVDCF
>Latimeria_chalumnae	-----MRFFRL-TFKCFVDCF
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>Cyprinodon_variegatus	-----MRFFRL-TFKCFVDCF
>Monodelphis_domestica	-----MRFFRL-TFKCFVDCF
>Ciona_intestinalis	-----MRFFRL-TFKCFVDCF
>Esox_lucius	-----MRFFRL-TFKCFVDCF
>Gallus_gallus	-----MRFFRL-TFKCFVDCF
>Erinaceus_europaeus	-----MRFFRL-TFKCFVDCF
>Scleropages_formosus	-----MRFFRL-TFKCFVDCF
>Notothenia_coriiceps	-----MRFFRL-TFKCFVDCF
>Platichthys_stellatus	-----MRFFRL-TFKCFVDCF
>Papio_anubis	-----MRFFRL-TFKCFVDCF
>Leucoraja_erinacea	-----MRFFRL-TFKCFVDCF
>Psammomys_obesus	-----MRFFRL-TFKCFVDCF
>Salmo_salar	-----MRFFRL-TFKCFVDCF
>Lepisosteus_oculatus	-----MRFFRL-TFKCFVDCF
>Macropisthodon_rudis	-----MRFFRL-TFKCFVDCF
>Botryllus_schlosseri	-----MHYFKLTTFKCFIDCF
>Tetronarce_californica	-----MRFFRL-TFKCFVDCF

>Homo_sapiens	-----MRFFRL-TFKCFVDCF
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>Tripterygion_dalaisi	-----MRFFRL-TFKCFVDCF
>Hynobius_chinensis	-----MRFFRL-TFKCFVDCF
>Micropterus_floridanus	-----MRFFRL-TFKCFVDCF
>Pygocentrus_nattereri	-----MRFFRL-TFKCFVDCF
>Rousettus_aegyptiacus	-----MRFFRL-TFKCFVDCF
>Haplochromis_burtoni	-----MRFFRL-TFKCFVDCF
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>Botryllus_schlosseri	-----MHYFKLTTFKCFIDCF
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>Xenopus_tropicalis	-----MRFFRL-TFKCFVDCF
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>Ciona_intestinalis	-----MRFFRL-TFKCFVDCF
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>Macropisthodon_rudis	-----MRFFRL-TFKCFVDCF
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>Tetronarce_californica	-----MRFFRL-TFKCFVDCF

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>Lipotes_vexillifer
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>Astyanax_mexicanus
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>Myotis_davidii
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>Alligator_sinensis
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>Lepisosteus_oculatus
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>Ictalurus_punctatus
MRHDSLVTCRLLMGRL
>Python_bivittatus
MRHDSLVTCGLLTGRS
>Struthio_camelus_australis
MRHDSLVTCGLLTGRS
>Takifugu_rubripes
MRHDSLVTCRLLMGRL
>Tetronarce_californica
MRDDSFVTCGLLTGRS
>Orycteropus_afer_afer
MKHDSSVTCGLLTGRS

HG0071.2 ENSG00000143995 MEIS1

>Homo_sapiens
MLSDSGALLQVP
>Panthera_tigris
MLSDSGALLQVP
>Balaenoptera_acutorostrata_s
MLSDSGALLQVP
>Myotis_davidii
MLSDSGALLQVP
>Galeopterus_variegatus
MLSDSGALLQVP
>Condylura_cristata
MLSDSGALLQVP
>Ochotona_princeps
MLSDSGALLQVP
>Equus_caballus
MLSDSGALLQVP
>Manis_javanica
MLSDSGALLQVP
>Loxodonta_africana
MLSDSGALLQVP
>Mus_musculus
MLNDAGALLQVP
>Tupaia_chinensis
MLSDSGALLQVP

HG0072 ENSG00000104435 STMN2

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>Homo_sapiens
---MGGADREGLISISNCILVLCTPAPLADQYLMLGSDSAGVMSGDLGSQSA---
>Chaetura_pelagica
-----MPRDSGSAGVMSGDL-----
>Odobenus_rosmarus_divergens
-----MLGSDSAGVMSGDLGSQSA-----
>Hynobius_retardatus
-----MSGDLWSQSAGAEP-----
>Tursiops_truncatus
-----MLGSDSAGVMSGDLGSQSA-----
>Charadrius_vociferus
-----MPGDSGSAGVMSGDL-----
>Myotis_davidii
-----MLGSDSARVMSGDLGSQSARASG-----
>Dasypus_novemcinctus
-----MSGDLGSQSA-----
>Columba_livia
-----MPRDSGSAGVMSGDL-----
>Cuculus_canorus
-----MPRDSGSAGVMSGDL-----
>Galeopterus_variegatus
---MGGAAAREGLISISNCILVLCTPAPLADQYLMLGSDSAGVMSGDLGSQSA---
>Falco_cherrug
-----MPGDSGSAGVMSGDL-----
>Gallus_gallus
-----MPGDSGSAGVMSGDL-----
>Condylura_cristata
-----MLGSDSAGVMSGDLGSQSA-----
>Ochotona_princeps
---MGGAAAREGLISISNCILVLCTPAPLADQYLMLRSDSAGVMSGDLGSQSA---
>Opisthocomus_hoazini
-----MPGDSGSAGVMSGDL-----
>Sturnus_vulgaris
-----MPGDSGSAGVMSGDLSSQSAWVEE-----
>Egretta_garzetta
-----MPGDSGSAGVMSGDL-----
>Ceratotherium_simum_simum
-----MLGSDSAGVMSGDLGSQSA-----
>Picoides_pubescens
-----MPGDSGSAGVMSGDL-----
>Loxodonta_africana
---MGGAAAREGLISISNCILVLCTAPLADQYLMLGSDSAGVMSGDLGSQSA---
>Melopsittacus_undulatus
-----MPGDSGSAGVMSGDL-----
>Marmota_marmota_marmota
---MGGAAAREGLISISNCILVLCTPAPLADQYMLLGSDSAGVMSGDLGSQSA---
>Tupaia_chinensis
-----MLGSDSAGVMSGDLGSQSA-----
>Aptenodytes_forsteri
-----MPGDSGSAGVMSGDL-----
>Squalus_acanthias
MFHWKKRGGPILICISNCILALCTLASLVDQYMLMPGDPENAPVMSRDLFSQSALLGR
>Anolis_carolinensis
-----MLADSGSAGVMSGELWSQSAWLEE-----
>Struthio_camelus_australis
-----MPGDSGSAGVMSGDL-----
>Chelonia_mydas
-----MLGDSSSAGVMSGDL-----
>Tinamus_guttatus
-----MPGDSGSAGVMSGDL-----
>Calypte_anna
-----MPGDSGSAGVMSGDL-----
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>Gallus_gallus	-----MPGDSGSAGVMSGDL-----
>Chaetura_pelagica	-----MPRDSGSAGVMSGDL-----
>Canis_lupus_familiaris	-----MLGSDSDSAGVMSGDLGSQSA-----
>Lipotes_vexillifer	-----MLGSDSDSAGVMSGDLGSQSA-----
>Charadrius_vociferus	-----MPGDSGSAGVMSGDL-----
>Cynopterus_sphinx	-----MPGSDSDSAGVMSGDLGSQSAWVSE-----
>Columba_livia	-----MPRDSGSAGVMSGDL-----
>Cuculus_canorus	-----MPRDSGSAGVMSGDL-----
>Galeopterus_variegatus	-----MPGDSGSAGVMSGDLGSQSA-----
MGGAAREGLISTISNCILVLCTPAPLADQYMLGSDSDSAGVMSGDLGSQSA-----	
>Haliaeetus_leucocephalus	-----MPGDSGSAGVMSGDL-----
>Opisthocomus_hoazin	-----MPGGSGSAGVMSGDL-----
>Pseudopodoces_humilis	-----MPGDSGSAGVMSGDLGSQSAWVEE-----
>Egretta_garzetta	-----MPGDSGSAGVMSGDL-----
>Ceratotherium_simum_simum	-----MLGSDSDSAGVMSGDLGSQSA-----
>Picoides_pubescens	-----MPGDSGSAGVMSGDL-----
>Cebus_capucinus_imitator	-----MPGDSGSAGVMSGDLGSQSA-----
MGGAAREGLITISNCILVLCTPALLADQYMLGSDSDSAGVMSGDLGSQSA-----	
>Loxodonta_africana	-----MPGDSGSAGVMSGDLGSQSA-----
MGGAAREGLISTISNCILVLCTPLADQYMLGSDSDSAGVMSGDLGSQSA-----	
>Melopsittacus_undulatus	-----MPGDSGSAGVMSGDL-----
>Ictidomys_tridecemlineatus	-----MLGSDSDSAGVMSGDLGSQSA-----
>Tupaia_chinensis	-----MLGSDSDSAGVMSGDLGSQSA-----
>Aptenodytes_forsteri	-----MPGDSGSAGVMSGDL-----
>Anolis_carolinensis	-----MLADSGSAGVMSGELWSQSAWLEE-----
>Struthio_camelus_australis	-----MPGDSGSAGVMSGDL-----
>Chelonia_mydas	-----MLGDSSSAGVMSGDL-----
>Tinamus_guttatus	-----MPGDSGSAGVMSGDL-----
>Calypte_anna	-----MPGDSGSAGVMSGDL-----

>Danio_rerio-----MSTASKVVLGLSIVLTI STVAGVHIKQNWDRQRLREGVVRDLERLERKKENLRALLEEQIQLTRELVTERNRQAEASETHDS-----
>Amia_calva-----MSTTSKVVLGVS LALTLGT VAGVHIKQSLDRERLREGVVRDLERQARKKENLRLEEQIALTREL EKERQRAAGTOGS-----
>Channa_striata-----MSTTSKVVLGLSVSLTLTTVAGVHLKQALDRQLHEGVVDLERLERKKENLRLLQEQVLT RHL EEERQRREAE LHPQDHN-----
>Xenopus_laevis-----MSTISKVVLGISVVL SVGT VGVVHKQRLDRERLREGVLDLERQSRKKENLRLEEQIHLTKRLEAEREKILLTEGSSKF-----
>Porichthys_notatus-----MSRVSKVVLGLSVVLT LTGT VGVHLQARDQRRLHDGVLRLERVQKKDNLRRLQDQKVL SRRL EAERQRREAELOTTGHTHTD-----
>Tripterygion_delaiei-----MSTTSKVVLGVS VLSLSTIVAGVHLKQNDQRRLHEGVIRDLERLAKKKENLRLEEQIILTQL EEERQQAQLSSQES-----
>Odobenus_rossmarus_divergens-----MSRSSKAVLGLSVVLTAA TVAGVHLKQRDQRRLHDGVI RDIERQNRKKENIRLLGEQIILTQL EAEREKMLLAKGSQKT-----
>Hynobius_chinensis-----MSASKVVLGVS VLASVATVAGVHLKQKLDRERLREGVFRDIERQHRKKENLRLEEQIVLTQL EEVERKMLMTKGSQKS-----
>Pygocentrus_nattereri-----MSTASKVVLGVS VLTSTVTVGVVHKQNWDRQRLREGVLRDLERLERKKENLRALLEEQIQLTRELVAEQAYQAAEAAAGS-----
>Calidris_pugnax-----MEERDKALMAKGSQOP-----
>Callorhinchus_milii-----MSAVSKVVLGVS VAYTAGTVAGVHLRQQLDREKLREGVFRDLERQEHKKENLRLEEQIILTQL EADRVASEIQSEKHKSDF-----
>Rhinolophus_ferrumequinum-----MSRTSKVVLGLSVVLTVA TVAGVHLKQRDQQRRLDGVIR DIERQNRKKENIRLLGEQIILTQL EAEREKTL LAKDLKKH-----
>Maylandia_zebra-----MSAVSKVVLGVS VLTSTVVA VHLKQAWDRERLREGVVRDLERLERKKENLRMLEEQRLLTQL EERRRREARLHPQDT-----
>Alosa_alosa-----MSTASKVVLGLSVLTI STVAGVHIKQNWDRQRLHEGVLRLERVERKKENLRLEEQIQLTQELTERQORREASAASGATQSP-----
>Merops_nubicus-----MEERDKALMEKGSQQS-----
>Cuculus_canorus-----MSRKKQRLHDGVLRLERQHKKENIRLLGEQIALTQQL VEERDKGLMSKGSQES-----
>Nothobranchius_furzeri-----EVRPNVMSAASKVVLGVS VLTTLGTVA VHLNQAWDRERLREGVVDLERVERKKENLRLEEQIILTRHLE EERRRGEERLQSDT-----
MNIADSSVVG IWL-----
>Numida meleagris-----MSRSSRAVLVVTALLSAATIAA VHVQRRERERLHSGVLRDIERQNGKKENIRLLGEQIALTQQL TEERDKMLMEKGSQQS-----
>Acanthogobius_hasta-----MSRASRAVLGVS VLTLTSTVAGVHLKQAWDRERLHOGVVRDLERLQKKENLQLEEQR LTRILQQDRDQGRDQGGQGRDQDQGGQGGQGGQGRD-----
>Apteronotus_leptorhynchus-----MTVVSKVVLGISVVLTI GSVGVVHIKQNWDRERLREGVLRDLERLERKKENLQDLEDQIQLTKVLVAERERRETQTANSAQGS-----
>Plecoglossus_altivelis-----MSKTSKLVLGVS VLTLTSTVAGVHLKQWDRERLHOGVLRDLERMERKKENLRVLEEQR LTKEL EAERDRRTTALQSPDQPH-----
>Zonotrichia_albicollis-----MSRGSRLALAVSALLSAAI VAAVHIQORRELERLHSGVVRDLERQKQKKENVRLLGEQIALT KRL TEERDKALMEKRSQOP-----
>Gasterosteus_aculeatus-----MTTVSKVVLGVS VLTLTSTVA VHLNQSWDRQRLHOGVVRDLERLERKKENLRLEEQIILTSQL EERLRREAEERRPDH-----
>Ceratotherium_simum_simum-----MSRSSKVVLGLSVVLTAA TVAGVHLKQRDQQRRLDGVIR DIERQNRKKENIRLLGEQIILTQL EAEREKMLLAKGSQKT-----
>Papio_hamadryas-----MSRTSKVVLGLSVLLTAATL AGVHVKQWDRQRLDGVIR DIERQIRKKENIRLLGEQIILTQL EAEREKTL LAKGSQKS-----
>Mus_musculus-----MSRSSKAVLGLSVLLTAATVAGVHLKQRDQRRLDGVIR DIERQNKKENIRLLGEQIILTQQL EAEREKMLKGSQNT-----
>Salmo_salar-----MSTTSKVVLGVS VILTVSTVAGVHLKQNWQERLHAGVLRDIERLERKKENLRVLEQQRSLTKELKAERDRRESGQGSQDQDQ-----
>Ictalurus_punctatus-----MSTASKVVLGLSVLTVGT VAGVHIKQNWDRQRLREGVLRDLERVERKENQRALEEQIRLTTTELVAHREQQEAGETAGSN-----
>Takydromus_sexlineatus-----MSAASKAVLAASVAVSGAVVA VHLQOSRVRERLREGVLDFERQNRKKENLRLEEQIALTQL EMERSKMLMGKESPH-----
>Trachemys_scripta-----MHHPLELCGSR SANGPVGEGMSTASKVALGISVLT SAGTVA VHIQORRVKERLHEGVIRDLERQSRKKENIRLLGEQIILTQQL EAERDKMLMEKGSQQS-----
>Takifugu_rubripes-----MLSVSSWLA-----KTNRNVMRSRASKVVLGVS VLTLTSTVAVHLKQWDRQRLHDGVLRLERLEKKENLRLEEQRVLTQL EYERQGRE-----

>Danio_rerio	-----MTLDVQTVAVFTVIAIILLVNVILIFFMGSS
>Maylandia_zebra	-----MALDVQTCAVFTVIAVLVLNVLLMFILGTR
>Fundulus_heteroclitus	-----MALDVQTCAVFTVIAVLVLNVLLMFILGTR
>Esox_lucius	-----MVDAIWTVKFKQPRSRAEQTSNANLPSSRQSTHRR-GSGVLLALQHCTMALDVQTFVFTVIAVLVLNVLLMFILGTR
>Cynoglossus_semihaevis	-----MALDVQTCVFTVIAFLVLNVLLMFILGTR
>Salmo_salar	
MSCNSACRVKTRSVAWAEAVFPAVFFFSICSQMVDVWTVKFKQSRSRPEQSSSARLPSSGQAHRHRSRIYLALQHYTMALDVQTFVFTVIAVLVLNVLLMFILGTR	

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>Homo_sapiens
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Anser_cygnoides
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Nanorana_parkeri
-----MDSFAEQ-----RLTP-QNLPAPR-----LDHYNVHLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Apteryx_australis_mantelli
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Oryzias_latipes
-----MARGGGGAGR-----WSRQRMGFLNTVLR CNLPPETQKVVVFFIMMLLII INVVL MFLLAQ
>Panthera_tigris
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Hynobius_retardatus
-----MDSFTEQ-----RLTT-QNLQAPH-----LEQYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Orcinus_orca
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Calidris_pugnax
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Myotis_brandtii
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Neolamprologus_brichardi
-----MARGGGGSGR-----WSRQRMGFFNTMLRCNLPPETQKVVVFLIMMLLII INVVL MFLLAQ
>Danio_rerio
-----MTLDVQTVAVFTVIAI LLL VNVILIFFMGSS
>Fundulus_heteroclitus
-----MARGNGSGR-----WSROKMGFFNTLLRCNLPPDTQKVVVFIIMMLLII INVVL MFLLAQ
>Monodelphis_domestica
-----MA-----KGPD-----CSR PQWSILHTFLRCNMNPETQRVVVFILLFLII INVVL MFLLAFR
>Macropus_eugenii
-----MTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Esox_lucius
MVDAIWTVKFKQPRSRAEOTSNANLPSSRQSTHRRSGVLLALQHCTMALDVQTFVVFVIAVLVL VNVILMFI LGTR
>Aquila_chrysaetos_canadensis
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Meleagris_gallopavo
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Condylura_cristata
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Ochotona_princeps
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Elephantulus_edwardii
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Pseudopodoces_humilis
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Ceratotherium_simum_simum
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Cynoglossus_semi_laevis
-----MALDVQTCVVFVIAFLVL VNVILMFI LGTR
>Gricetulus_griseus
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Salmo_salar
-----MARGG-GAH-----RARQRLGYLNTLLRCNLHPETQKVVVFIMMLLVI INVVL MFLLA F-
>Lepisosteus_oculatus
-----MDSYTEP-----RLTSENNLP AQH-----LEYYSLLHCTMTLDVQTVVVFVAVIVVLL VNVILMFFLGSR
>Trichechus_manatus_latirostr
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Struthio_camelus_australis
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR
>Pelodiscus_sinensis
-----MDSLTEQ-----RLTS-PNLPAPH-----LEHYSVLHCTMTLDVQTVVVFVAVIVVLLL VNVILMFFLGTR

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>Homo_sapiens-----MKDTRLTALETEVPVVRTVW-----
>Anas_platyrhynchos-----MKGVWLTALQTEAQR IHRTVW-----
>Apteryx_australis_mantelli-----MKGVWLI AVETEARL IRR TAW-----
>Leptonychotes_weddellii-----MKDTRLTALETEVP IVPRTVW-----
>Balaenoptera_acutorostrata_s-----
MATCGGCAVGKRWKPNAPLPLLLGSHFIVRLVLTDAFFSSVTMKDTRLTALETEVP IVPRTVW-----
>Calidris_pugnax-----MKGVWLTALQTEARLVHRTVW-----
>Miniopterus_natalensis-----MKDTRLTALETELP IVPRTVW-----
>Dasypus_noveboracensis-----MKDTRLTALETEVFPVPTVW-----
>Columba_livia-----MKGVWLTALQTEAQL IHRTVW-----
>Alligator_mississippiensis-----MKGARLTALKTEALLVHRTVW-----
>Sarcophilus_harrisii-----MKDTRLTALETEVLI VHRTVW-----
>Galeopterus_variegatus-----MKDSRLTALETEVPI IPR TAW-----
>Monodelphis_domestica-----MKDTRLTALETEVLI VHRTVW-----
>Haliaeetus_leucocephalus-----MKGVWLTALQTEAQL VHRTVW-----
>Coturnix_japonica-----MKGVWLTALQTEAQL IHRTVW-----
>Condylura_cristata-----MRDTRLTALETDPVVPRTGWSRR-----
>Oryctolagus_cuniculus-----MRDNKLAALGTEAPVVHRAVYSNPQ-----
>Elephantulus_wardi-----MKDTRLTALETEVSVVPTV-----
>Ornithorhynchus_anatinus-----MKVSRLTTLETEGPI IYRTVW-----
>Parus_major-----MKGVWLTALQTEAQL IHRTVW-----
>Ceratotherium_simum_simum-----MKDTRLTALETEVPVVPRTVW-----
>Manis_javanica-----MKDTRLTALETEVPVVPRTV-----
>Loxodonta_africana-----MKDTRLTALETEI SIVPRAVL-----
>Mesocricetus_auratus-----MKDTRLTALETDPVTPRTVW-----
>Tupaia_chinensis-----MRDTGLTALETEI SIVPRTVW-----
>Trichechus_manatus_latirostr-----MKDTRLTALETEVSI VPRAVW-----
>Aptenodytes_forsteri-----MKGVWLTALQTEARLVHRTVW-----
>Struthio_camelus_australis-----MDVQTRMKFLIMKGVWLIALETEAQL IHRTVW-----
>Chrysemys_picta-----MKGARLTALTEVLLVHRTVW-----
>Orycteropus afer_afer-----MKETRLTALETEVSI VPQSSLVAPMKSLWSL-----
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>Danio_rerio
MGTS^{SGSWH}QCHFS-----
>Anser_cygnoides
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSRRRC^DIQTEKIWKAKNEN-----
>Microhyla_fissipes
MGTS^{SGSWH}QCHFF-----
>Canis_lupus_familiaris
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RYK}---MKTDY
>Hynobius_retardatus
MGTS^{SGSWH}QCHFL^EINEIVQLH---TDPDSWRRRG^IQTEQWPKKWKLIID-
>Lipotes_vexillifer
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLETSGDDATLSLKRGR^{SK}---MKTDY
>Calidris_pugnax
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLSRRRC^DIQTEKIWKAKNEN-----
>Pteropus_allecto
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RSK}---MKTDY
>Sarcophilus_harrisii
MGTS^{SGSWH}QCHFL^EINEIVQRSIPRSRDSRRRC^DIRTEKIWKTKK-----
>Galeopterus_variegatus
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RPK}---MKTDY
>Macropus_eugenii
MGTS^{SGSWH}QCHFL^EINEIVQRSIPRSRDSRRRC^DIRTEKIWKTKK-----
>Aquila_chrysaetos_canadensis
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSRRRC^DIQTEKIWKAKNEN-----
>Gallus_gallus
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSRRRC^DIQTEKIWKAKNEN-----
>Condylura_cristata
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RSK}---MKTDY
>Ochotona_princeps
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RPK}---MKTDY
>Elephantulus_edwardii
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETRGDDATLSLKRFG^{RPK}---MR^{TDY}
>Ficedula_albicollis
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSSRRRC^DIQTEKIWKAKNEN-----
>Geraotherium_simum_simum
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RSK}---MKTDY
>Pongo_abelii
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RPK}---MKTDY
>Loxodonta_africana
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLETPGDDATLSLKRFG^{RPK}---MR^{TDY}
>Peromyscus_maniculatus_baird
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLEAPGDDATLSLKRFG^{RSK}---MKTDY
>Tupaia_chinensis
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLETPGDDATLSLKRFG^{RPK}---MKTDY
>Trichechus_manatus_latirostr
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETPGDDATLSLKRFG^{RPK}---MR^{TDY}
>Anolis_carolinensis
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSRRRC^DIQIEKIWKAKK-----
>Struthio_camelus_australis
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLSRRRC^DIQTEKIWKAKNEN-----
>Chrysemys_picta
MGTS^{SGSWH}QCHFL^EINEIVQRY---TDLSRRRC^DIQTEKIWKAKNEN-----
>Tinamus_guttatus
MGTS^{SGSWH}QCHFL^EINEIVQIH---TDLSRRRC^DIQTEKIWKAKNEN-----
>Calypte_anna
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLSRRRC^DIQTEKIWKAKNEN-----
>Orycteropus_afer_afer
MGTS^{SGSWH}QCHFL^EINEIVQIY---TDLETSGDDATLSLKRFG^{RPK}---MR^{TDY}

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>Homo_sapiens
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RPKMKTDY
>Anser_cygnoides
-----MGTSSGSWHQCHFLEINEIVQI--YTDLDSRRRCDIQTEKIWKAKNEN-----
>Microhyla_fissipes
MHHVVLCPVTSQADMGMTSSGSWHQCHFF-----
>Panthera_tigris
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RPKMKTDY
>Hynobius_retardatus
-----MGTSSGSWHQCHFLEINEIVQL--HTDPDSWRRRGIQTEQWPKKWLIIID-
>Orcinus_orca
-----MGTSSGSWHQCHFLEINEIVQIH--TDLETPGDDATLSLKRFG--RSKMKTDY
>Calidris_pugnax
-----MGTSSGSWHQCHFLEINEIVQI--HTDLDSRRRCDIQTEKIWKAKNEN-----
>Pteropus_allecto
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RSKMKTDY
>Sarcophilus_harrisii
-----MGTSSGSWHQCHFLEINEIVQRSIPRSRDSRRRCDIRTEKIWKTKK-----
>Galeopterus_variegatus
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RPKMKTDY
>Macropus_eugenii
-----MGTSSGSWHQCHFLEINEIVQRSIPRSRDSRRRCDIRTEKIWKTKK-----
>Aquila_chrysaetos_canadensis
-----MGTSSGSWHQCHFLEINEIVQI--YTDLDSRRRCDIQTEKIWKAKNEN-----
>Gallus_gallus
-----MGTSSGSWHQCHFLEINEIVQI--YTDLGSRRRCDIQTEKIWKAKNEN-----
>Condylura_cristata
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RSKMKTDY
>Ochotona_princeps
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATFSLKRFG--RPKMKTDY
>Elephantulus_edwardii
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETRGDDATLSLKRFG--RPKMRTDY
>Scleropages_formosus
-----MGTSSGSWHQCHCSKREEQGETERK-----DGPGTQRVYGT-----
>Lepidothrix_coronata
-----MGTSSGSWHQCHFLEINEIVQI--YTDLDSRRRCDIQTEKIWKAKNEN-----
>Ceratotherium_simum_simum
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RSKMKTDY
>Loxodonta_africana
-----MGTSSGSWHQCHFLEINEIVQIH--TDLETPGDDATLSLKRFG--RPKMRTDY
>Ictidomys_tridecemlineatus
-----MGTSSGSWHQCHFLEINEIVQIY--TDLEAPGDDATLSLKRFG--RPKMKTDY
>Tupaia_chinensis
-----MGTSSGSWHQCHFLEINEIVQIH--TDLETPGDDATLSLKRFG--RPKMKTDY
>Trichechus_manatus_latirostr
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETPGDDATLSLKRFG--RPKMRTDY
>Anolis_carolinensis
-----MGTSSGSWHQCHFLEINEIVQI--YTDLDSRRRCDIQIEKIWKAKK-----
>Struthio_camelus_australis
-----MGTSSGSWHQCHFLEINEIVQI--HTDLDSRRRCDIQTEKIWKAKNEN-----
>Chrysemys_picta
-----MGTSSGSWHQCHFLEINEIVQR--YTDLDSRRRCDIQTEKIWKAKNEN-----
>Tinamus_guttatus
-----MGTSSGSWHQCHFLEINEIVQI--HTDLGSRRRCDIQTEKIWKAKNEN-----
>Calypte_anna
-----MGTSSGSWHQCHFLEINEIVQI--YTDLDSRRRCDIQTEKIWKAKNEN-----
>Orycteropus afer afer
-----MGTSSGSWHQCHFLEINEIVQIY--TDLETSDDATLSLKRFG--RPKMRTDY
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>Gallus_gallus
-----MIP-QPDPTTKEKRIVHLKLGRRHN
>Chaetura_pelagica
MLQRFDLTSSSSPEAAVAMIP-QPDPTTKDKRIVRLKLGRRCN
>Apteryx_australis_mantelli
-----MIP-QPDPTTKEKRIVRLKLGRRHN
>Buceros_rhinoceros_silvestri
-----MIP-QPDPTTKEKRIVRLKLGRRCN
>Caprimulgus_carolinensis
-----MIP-QPDPTTKEKRIVCLKLGRRCN
>Cariama_cristata
-----MIP-QPDPTTKEKRIVCLKLGRRCN
>Charadrius_vociferus
-----MIP-QPDPTTKEKRIVHLKLGRRCN
>Pterocles_gutturalis
-----MIP-QPDPTTKEKRIVCLKLGRRHN
>Colius_striatus
-----MTP-QPDPTTKEKRIVRLKLGRRHN
>Columba_livia
-----MIP-QPDPTTKEKRIVRLKLGRRHN
>Leptosomus_discolor
-----MIP-QPDPTTKEKRVVRLKLGRRCN
>Alligator_mississippiensis
-----MIP-QPDPTTSERRASYFEAEOSLN
>Cuculus_canorus
-----MIP-QPDPTTKEKRIVRLKLGRRCN
>Falco_cherrug
-----MIP-QPDPTTKEKRIVRLKLGRRCN
>Gavia_stellata
-----MIP-QPDPTTKEKRIVRLKLGRRCN
>Chlamydotis_macqueenii
-----MIP-QPDPTTKEKRIVCLKLGRRCN
>Opisthocomus_hoazin
-----MIP-QPDPTTKEKRIVCLKLGRRCN
>Manacus_vitellinus
-----MIP-QPDPTTKEKRIVRLKLGRRHN
>Phaethon_lepturus
-----MIP-QPDPTTKEKRIVHLKLGRRCN
>Picoides_pubescens
-----MIP-QPDPTTKEKRVVCLKLGRRCN
>Fulmarus_glacialis
-----MIP-QPDPTTKEKRIVRLKLGRRCN
>Melopsittacus_undulatus
-----MIP-QPDPTTKEKRIVCLKLGRRCN
>Pygoscelis_adeliae
-----MIP-QPDPTTKEKRIVHLKLGRRCN
>Tyto_alba
-----MIP-QPDPTTKEKRIVHLKLGRRHN
>Struthio_camelus_australis
-----MIP-QPDPTTKEKRIVHLKLGRRHN
>Chrysemys_picta
MFQRFRTLSSSSPEACQGNDSTARSDHQREKRIVHLKLGRRHN
>Tinamus_guttatus
-----MTP-QPDPTTKEKRIVRLKQGRHON
>Calypte_anna
-----MIP-QPDPTTKEKRIVHLKLGRRHN
>Apaloderma_vittatum
-----MIP-QPDPTTKEKRIVCLKLGRRHN

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>Gallus_gallus
MPSGGVLLKLGHCHNL
>Caprimulgus_carolinensis
MLSGGVVLKTEHCSL
>Callidris_pugnax
MLSGGVVLKTEHCNL
>Pterocles_gutturalis
MLSGGVVLKTEHCSL
>Columba_livia
MLSGGVVLKTEHCNL
>Aquila_chrysaetos_canadensis
MLSGGVVLKTEHCSL
>Manacus_vitellinus
MLSGGVVLKTEHCSL
>Nipponia_nippon
MLSGGVVLKTEHCSL
>Nestor_notabilis
MLSGGVVLKTEHCSL

>Gallus_gallus
MVNNTDPQEAL
>Anas_platyrhynchos
MVNNTDPQEAL
>Chaetura_pelagica
MVNNTDPQEAL
>Apteryx_australis_mantelli
MVNNTDPQEAL
>Buceros_rhinoceros_silvestri
MVNNTDPQEAL
>Cariama_cristata
MVNNTDPQEAL
>Charadrius_vociferus
MVNNTDPQEAL
>Pterocles_gutturalis
MVNNTDPREAL
>Colius_striatus
MVNNTDLOEAL
>Leptosomus_discolor
MVNNTDPQEAL
>Alligator_mississippiensis
MVNNTDPHEAF
>Cuculus_canorus
MVNNTDPQEAL
>Falco_cherrug
MVNNTDPQEAL
>Gavia_stellata
MVNNTDPQEAL
>Chlamydotis_macqueenii
MVNNTDPQEAL
>Tauraco_erythrophus
MVNNTDPQEAL
>Opisthocomus_hoazin
MVNNTDPQEAL
>Zonotrichia_albicollis
MVNNTDPQEAL
>Egretta_garzetta
MVNNTDPQEAL
>Picoides_pubescens
MRNNTDPQEAL
>Fulmarus_glacialis
MVNNTDPREAL
>Melopsittacus_undulatus
MVNNTDPQEAL
>Aptenodytes_forsteri
MVNNTDPQEAL
>Tyto_alba
MVNNTDPQEAL
>Struthio_camelus_australis
MVNNTDPQEAL
>Pelodiscus_sinensis
MVNNAEDPQAF
>Tinamus_guttatus
MVNNTDPYEAL
>Calypte_anna
MVNNTDPQEAL
>Apaloderma_vittatum
MVNNTDPQEAL

>Homo_sapiens
MVDNADHLWKGY
>Felis_catus
MINNADHL-----
>Pteropus_alecto
MVNNADHL-----
>Dasypus_novemcinctus
MINYANHLWKGY
>Erinaceus_europaeus
MVDNTDHLWKGY
>Oryctolagus_cuniculus
MINHIDHLWKGY
>Equus_asinus
MVNNADHL-----
>Loxodonta_africana
MVNIADHLWKGY
>Heterocephalus_glaber
MVNNADHLWKGY
>Trichechus_manatus_latirostr
MVNNADHLWKGY
>Orycteropus_afer_afer
MINNADHLWKGY

>Homo_sapiens
MSTIFWREKRYSLIGTRKDI EHLEINCLHYTAESHTLLVMFSSLLSRRLHYWNFEV MKTSDEPTCN TLDSDWIKIRKFKKECGL---
>Anas_platyrhynchos
-----MKETQE---ESLDNERKIKRKQKECGI---
>Xenopus_laevis
-----MKSPGKHCLNLSTDWIKIRRKQEECDK---
>Odobenus_rosmarus_divergens
-----MKTSDEPTYNILDSDWIMKKKFKKECGL---
>Ambystoma_mexicanum
-----MV--SSPEAGSSDLPSL--YTEE--PSSSEFVSLETERLCNQDLGIMRIIQEKASEVFVMDWIKIRKCLKESGF---
>Orcinus_orca
-----MLCFY-QFLCRRLHYWNFEDMKTSDEPTCNILDSDWIMKKKFKKECGL---
>Calidris_pugnax
-----MKETQE---DNLDNERKIKRKQKECGI---
>Eptesicus_fuscus
MSTVFWREKRYSHIGIHKDIEQLIECCLHYAAGSHSTCYVF-KFLSRRLQYWNFEDMNTSDEPTCNILDSDWIMKKKFKKECGL---
>Dasypus_noveboracensis
-----MKTSNEPTCNALDSDWIKIRKYKCDL---
>Columba_livia
-----MKETQE---DNLDHEWKIKRKQKECGI---
>Alligator_sinensis
-----MKESQE---ETLDNEWKIKRKQKECGI---
>Galeopterus_variegatus
-----MKTSDEPTCN TLDSDWIKIRKFKKECGL---
>Monodelphis_domestica
-----MVKSEERIYNLTNIKKI---KLKECGI---
>Falco_cherrug
-----MKETQE---DNLDNERKIKRKQKECGI---
>Gallus_gallus
-----MKGTQE---ENLDNERKIKRKQKECGI---
>Condylura_cristata
-----MKTSSEPTCNILNSVIMKKKFKKECGL---
>Oryctolagus_cuniculus
-----MKTSDEPTCN TLDSDWIKIRKFKKECGL---
>Manacus_vitellinus
-----MKESQE---DNLDSEGIKSKQKEGGMGRV---
>Equus_przewalskii
-----MKTSDEPA CNILNSDWIMKKKFKKECGL---
>Manis_javanica
-----MKTSDEPTCSILNSDWIMKKKFKKECGL---
>Loxodonta_africana
-----MKTSSEPA CNILNSDWIKIERKFKECGQ---
>Tupaia_chinensis
-----MKTSDEPTCN TLDSDWIKI---FKGCGL---
>Trichechus_manatus_latirostris
-----MKTSDEPTCN TLDSDWIKIERKFKECGQ---
>Aptenodytes_forsteri
-----MKETQE---DNLDNERKIKRKQKECGI---
>Python_bivittatus
-----MRKQKECGI---
>Struthio_camelus_australis
-----MKESQE---ENLDNEWKIKRKQKECGI---
>Chrysemys_picta
-----MKESQEDTLSTLDNEWKIKRKQKECGI---
>Tinamus_guttatus
-----MKESQE---ENLDNEWKIKRKQKECGI---
>Orycteropus_afer_afer
-----MKTSDEPTCN TLDSDWIKIERKFKECGQ---

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>Homo_sapiens-----MGPDGS LQKVQPQVVP LLLWQE
>Anser_cygnoides-----MVL YYLLGTDGSLQKVLQMVN L IL---
>Canis_lupus_familiaris-----MGPDGS LQKVQPLVVP LLLWQE
>Orcinus_orca-----MGPDGS LQKVQPQVVP LLLWQE
>Calidris_pugnax-----MIL YYLLGTDGSLQKVQLQMVN L IL---
>Myotis_lucifugus
MEIKLNL RGLTVTFQSRKLA EAHRAFLRGP DGS LQKVRPQVVP LLLWQE
>Dasypus_noveboracensis-----MGPDGS LQKVQPQVVP LLLWRE
>Galeopterus_variegatus-----MGPDGS LQKEQPQVVP LLLWRE
>Monodelphis_domestica-----MGPDGS LQKV-----
>Aquila_chrysaetos_canadensis-----MVL YYLLGTDGSLQKVQRMVN L IL---
>Coturnix_japonica-----MVL YHLLGTDGSLQKVQRMVN L SL---
>Sorex_araneus-----MGP DGR LQTVEPQVVL FLLWQE
>Oryctolagus_cuniculus-----MGPDGS LQKVQPQVVP LLLWQE
>Elephantulus_edwardii-----MGPNGSLQQTQPQVVL LLLWQE
>Ornithorhynchus_anatinus-----MGP DTRW KVR LQTV P LLLQQE
>Lepidothrix_coronata-----MVL YHLLGTDGSLQKVQLQMVSL IL---
>Equus_asinus-----MGPDGS LQKVQPQVVP LLLWQE
>Manis_javanica-----MGPDGS LQKVQALVVP LLLRQK
>Loxodonta_africana-----MGPDGS LQKVQPQVVP LFLWQE
>Mus_musculus-----MGPDGS LQKVQPQVVP LLLWQE
>Tupaia_chinensis-----MGPDGS LQKVQAGVVP LLLWQE
>Trichechus_manatus_latirostris-----MGPDGS LRKVQPQVVP LFLWQE
>Anolis_carolinensis-----MVL YSASLGTDGSLQKGLQIVHFL L---
>Struthio_camelus_australis-----MVL YYLLGTDGSLQKVQLQMVN L IL---
>Trachemys_scripta-----MVHLL F---
>Tinamus_guttatus-----MVL YYLLGTDGSLQKVQLQMVNFT L---
>Calypte_anna-----MVN L IL---
>Orycteropus afer afer-----MGPDGS LQKVQPQVVP LLLWQE
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>Gallus_gallus
-----MVLY-HLLGTDGSLQKVQFQMVNLLNL---
>Anser_cygnoides
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>Leptonychotes_weddelii
-----MGPDGSLQKVQPLVVPVLLLWQE
>Orcinus_orca
-----MGPDGSLQKVQPVVPLLLWQE
>Calidris_pugnax
-----MVLY-YLLGTDGSLQKVQLQMVNLLIL---
>Dasypus_novemcinctus
-----MGPDGSLQKVQPVVPLLLWRE
>Galeopterus_variegatus
-----MGPDGSLQKEQPVVPLLLWRE
>Aquila_chrysaetos_canadensis
-----MVLY-YLLGTDGSLQKVQRMVNLIL---
>Oryctolagus_cuniculus
-----MGPDGSLQKVQPVVPLLLWQE
>Lepidothrix_coronata
-----MVLY-HLLGTDGSLQKVQLQMVSLIL---
>Equus_asinus
-----MGPDGSLQKVQPVVPLLLWQE
>Aotus_nancymae
MG1HCDVQ1KKTCCGQSLFPMGPDGSLQKVQPVVPLLLWQE
>Loxodonta_africana
-----MGPDGSLQKVQPVVPLFLWQE
>Fukomys_damarensis
-----MGPDGSLQKVQPVVPLPLCQO
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
-----MGPDGSLRKVPVVPVPLFLWQE
>Anolis_carolinensis
-----MVLYSASLGTGSLQKGLQIVHFLL---
>Struthio_camelus_australis
-----MVLY-YLLGTDGSLQKVQLQMVNLLIL---
>Tinamus_guttatus
-----MVLY-YLLGTDGSLQKVQLQMVNFTL---
>Calypte_anna
-----MVNLLIL---
>Orycteropus_afer_afer
-----MGPDGSLQKVQPVVPIILLWQE
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>Homo_sapiens	MTRNNSATRLISRT
>Odobenus_rosmarus_divergens	MTRNNSATGLTSRT
>Myotis_brandtii	MPRNNSAAGLSRTWIVDLIPTSEPRRLF
>Condylura_cristata	MTRNNSATGLTSRT
>Oryctolagus_cuniculus	MTRNNSATGLTSRT
>Chinchilla_lanigera	MTRNNSATGLTSRT
>Tupaia_chinensis	MTRNNSATGLTSRT
>Trichechus_manatus_latirostr	
MGDPRTVTRGGARLGCSDGADRGRILEHSFSDCLPQVTSWTCPPGGTRTCPAEMTRNNSATGLTSRT	

>Homo_sapiens	-----MEETWRLLGQLSPLSPEISHKCGRCARLTRRRRRRRR-----
>Mustela_putorius_furo	-----MEDTWRRPGQLSPLSPETSHKCGRGACLARRRRR-----
>Erinaceus_europaeus	-----MEATWGWPAQLCPLGPQISHKCGRGAGARRRRRHGSAGFL--TAPSAQSRE-----
>Oryctolagus_cuniculus	-----MEETWRRLGQLSPLNPESSHKCGRGARLARGGGGGGGADMELRAPQRASSPRPLRGAGNNSATGLTSRT-----
>Mus_musculus	MVGAKRLVIPGAIPAAAPRAAWGEWPRAEGREAPGVDQSRPPVGVFVTHMEETRWLGRLSPLSPETSHKCGRGARLSRWPRRRQR-----

>Danio_rerio				
MMSEQLTGCHPPVFSSNAQTGS				
>Anser_cygnoides				
MMSEQLTACHPSAFYSNTQTGS				
>Xenopus_laevis				
MMSEQLTACHPSAFYSNTQTGS				
>Apteryx_australis_mantelli				
MMSEQLTACHPSAFYSNTQTGS				
>Canis_lupus_familiaris				
MMSEQLTACHPSAFYSNTQTGS				
>Balaenoptera_acutorostrata_s				
MMSEQLTACHPSAFYSNTQTGS				
>Astyanax_mexicanus				
MMSEQLTGCHPPVFSSTAQTGS				
>Calidris_pugnax				
MMSEQLTACHPSAFYSNTQTGS				
>Miniopterus_natalensis				
MMSEQLTACHPSAFYSNTQTGS				
>Dasyus_novemcinctus				
MMSEQLTACHPSAFYSNTQTGS	SCVR-SCAGGGI	SFLSNIIIS	TLHLSS	
>Columba_livia				
MMSEQLTACHPSAFYSNTQTGS				
>Kryptolebias_marmoratus				
MMSEQLTGCHPPHLLHRLHPSPVLYCESQRQPGRVVSALCVCVCVVRVFAAADQRLQEGGGRRGGGGRWYLVPPPTSPPLGICPSQFEQRGFFLFVCLFSLPLSLSFFFFFAYLPSSSALLFYPLIDSE				
>Monodelphis_domestica				
MMSEQLTACHPSAFYSNTQTGS				
>Esox_lucius				
MMSEQLTGCHPPVFYSNTQTGS				
>Coturnix_japonica				
MMSEQLTACHPSAFYSNTQTGS				
>Erinaceus_europaeus				
MMSEQLTACHPSAFYSNTQTGS				
>Oryctolagus_cuniculus				
MMSEQLTACHPSAFYSNTQTGS				
>Corvus_brachyrhynchos				
MMSEQLTACHPSAFYSNTQTGS				
>Geratherium_simum_simum				
MMSEQLTACHPSAFYSNTQTGS				
>Manis_javanica				
MMSEQLTACHPSAFYSNTQTGS				
>Cercopithecus_atys				
MMSEQLTACHPSAFYSNTQTGS				
>Cricetulus_griseus				
MMSEQLTACHPSAFYSNTQTGS				
>Salmo_salar				
MMSEQLTGCHPPVFYSNAQTGS				
>Tupaia_chinensis				
MMSEQLTACHPSAFYSNTQTGS				
>Ictalurus_punctatus				
MMSEQLTGCHPPVFSSAAQTAS				
>Anolis_carolinensis				
MMSEQLTACHPSAFYSNTQTGS	ECVCRSVCKEGI	SFLSNIIIS	TLHLSL	
>Chelonia_mydas				
MMSEQLTACHPSAFYSNTQTGS				
>Tinamus_guttatus				
MMSEQLTACHPSAFYSNTQTGS				

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>Danio_rerio
MIVP!VSYFFFPPLSVVQRVSKMNDGNGAASEP
>Astyanax_mexicanus
-----MNDGNGAASEP
>Esox_lucius
-----MNDGNGEGSEP

>Danio_rerio-----MAEDKDPYTKLDLVHLKDQLEEIQKRVENEVOAGVPQGGSLLASPFLLKGLAGYVVSRLRSSAVLGVALGTLSGIFAAQNYOVVNIETLRDILNSLKKRPGE

>Acipenser_sinensis-----MADDKDALSKLDLAHLKNQLEDIQKRVEEVQAGIPQGGSLLASPFLLKGLAGYVVARLRSSAVMGVLIGTCTGIIAAQSFDPVNIETVKDYFNSIKKGP-

>Amia_calva-----MAGDKDPLSKLDLAQLKDQLEDIQKRVENEVOAGIPQGGSLLASPFLLKGLAGYVVARLRSSAVLGVVVGCTGIIAAQNFDPVNIETSVKDYNSMKKRP-

>Odorrana_margaretae
MVAISTCSRPQSVSCSPAVILSVR--LPWLDNMA-DDKGTPKLDLAFLKDQLEGLQKRLNEVOAGVSGQGSLLSSPFLKGLAGYII SKLRASAVLGFVAGFTGIIAAQYAVPNVEKTIKDYLSLRKGP-

>Porichthys_notatus-----MANDKDPKQLKDQLTLRKNQLEIQRVENELSVGIPQGGTVMGSPFLKGLAGYVVARLRSSAVIGVLLGTVTGMVYAQNYQVPIDKTFKEYMNHVKNAPK-

>Oryzias_melastigma-----MTIREYMNLSLKGPK-

>Trachinotus_blochii-----MADDKDPLKQLKDQLTLRKNQLEEIQRRVENEVSIGIPQGGSVLGSFLLKGLAGYVVARLRSSAII GVLLGTITGMVYAQNYOVVNIERTVKEYLNMMKKGPK-

>Ursus_maritimus-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYLSLRKGP-

>Micropterus_floridanus-----MVAKLRSSAIIAGVLLGTITGMVYAQSYOVVNIERTVRDYLNMMKKGPK-

>Pteropus_vampyrus-----MAGALDIRWEGCACATSSGTGMADDKDSLPLKLDLAFLKNQLEHLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYLSLRKGP-

>Maylandia_zebra-----MADDKDPLKQLKDQLTLRKNQLEDEIQRRVEHVSAGIPQGGSVLGSFLLKGLAGYVVARLRSSAVLGVLLGTVTGMVYAQNYOVVNIERTFKEYMNNLKKGP-

>Dasyatis_novemcinctus-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVMGFVVGCTGIIIAQYAVPNVEKTLRDYLSLRKGP-

>Latimeria_chalumnae-----MADDKDTRLKLDLAQLKDQLEDIQKRVEEVQAGIPQGGSLLASPFLLKGLTGYVVARLRSSALLGVVGCTGIIAAQNYKVPNIETVKDYISSLKGGS-

>Fundulus_grandis-----MADNKDPLKQLKDQLTLRKNQLEAIIQRRVENEVSIGIPQGGSVLGSFLLKGLAGYVVARLRSSAVLGVLLGTVTGMVYAQNYOVVNIERTVKDYMSLTKKGP-

>Sarcophilus_harrisii-----MADDKDPLKQLKDQLTLRKNQLEAIIQRRVENEVSIGIPQGGSVLGSFLLKGLAGYVVARLRSSAVLGVLLGTVTGMVYAQNYOVVNIERTVKDYMSLTKKGP-

>Esox_lucius-----MADDKDPFKQMKDLNQLKNQLESIIQKRVESFATGIPQGGSVLGSFLLKGLAGYVVARLRSSAII GVLLGTFGTGIIAAQNYOVVNIERTLDYMSLTKKGP-

>Gallus_gallus-----MADDKDSLPLKLDLALLKGQLESLORRVEDEVHAGVQDGSLLSSPFLKGLAGYLVAKLRFSAVLGFVAGTCTGIIAAQNYAVPDVEKTVRDYLSALRKGGE-

>Acanthis_flammea-----MADDKDSLPLKLDLAFLKGQLESLORRVEDEVQAGVQDGSLLASPLLLKGLAGYLVAKLRFSAVLGFVAGTCTGIIAAQNYAVPNVEKTI RDYVNSLKKGRD-

>Lateolabrax_japonicus-----MIIAAQNYOVVNIERTMKDCMNNLRKGP-

>Trematomus_bernacchii-----MAGDKDPLKQLKDQLTKLKSQLEEIQRRVENEVTGIPQGGSVLGSFLLKGLAGYVVARLRSSAFLGLLVGTATGIIAAQNYVVPNIERTVKDYINSLKKGP-

>Equus_asinus-----MADDKDSLPLKLDLAFLKDQLESLORRVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYLSLRKGP-

>Manis_javanica-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYLSLRKGP-

>Platichthys_stellatus-----MADDKDPLKQLRDQLTHLKSQLEEIQRRVESEASGIPQGGSVLGSPLLLKGLAGYVVARLRSSAII GVLLGTLTGIIAAQSYOVVNIERTVKDYMTFKKGP-

>Nomascus_leucogenys-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYLSLRKGP-

>Marmota_monax-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVQDGSLLSSPFLKGLAGYVVARLRASAVLGFVAGTCTGIIAAQYAVPNVEKTLRDYFRSLRKGPD-

>Salmo_salar-----MAGDKDPFKQMKDLNQLKNQLEDIQKRVETEFAGIPQGGSVLASPFLLKGLAGYVVARLRSSAII GVLLGTFGTGIIAAQNYOVVNIESTLDYMSLFRKGP-

>Trichomycterus_areolatus-----MANDKDPKQLKDQLADLAFLKNQLEAIIQRRVENEVOAGIPQGGSLLASPFLLKGLAGYVVARLRASAVLGVALGTLTGIIAAQNYEVVNIERTIKDYLSLKKGP-

>Gekko_japonicus-----MADDKDSLPLKLDLAFLKDQLANLQORVENEVGTGVQDGSLLASPFLLKGLAGYVVARLRSSAVLGVLGTCGIVVYAQTYAIPNVEKTIKEFFSSFRKGP-

>Homo_sapiens-----MADDKDSLPKLDLAFLKNQLESLQRRVEDEVNSGVGDGSLSSPFLKGLAGYVVAKLRSASVLGFVGTCTGIIAAQAYAVPNVEKTLRDYLLRKGPD-
>Acipenser_sinensis-----MADDKDALSPLKDLAHLKNQLEDIQKRVEEEVQAGIPQGGSLLASPFLKGLAGYVVAKLRSASVGLIGTCTGIIAAQSFVDPNIEKSVKDYNSMKKRPN-
>Amia_calva-----MAGDKDPLSKLDLAQLKDQLEDIQKRVEDEVQAGIPQGGSLLASPFLKGLAGYVVAKLRSASVGLGVVGTCTGIIAAQNFVDPNIEKSVKDYNSMKKRPN-
>Pelophylax_nigromaculatus-----MADD-KGSPKLDLAFLKNQLEGLQKRLENEVQAGVSGFLSSPFLKGLAGYIVSKLRASAVLGFVGAFTGIIAAQAYAVPNVEKTIKDYLGSRLKGPD-
>Porichthys_notatus-----MADDKDSLKQLDQLTQLRNQLEIQQRVENELSVGIPQGSTVWGSFPLKGLAGYVVAKLRSASVIGVLLGTVTGMYYAQNYQVPIIDKTFKEYMNHVKNAFK-
>Oryzias_melastigma-----MTITREYMNSLKKGGPK-
>Trachinotus_blochii-----MADDKDSLKQLDQLTQLRNQLEEQRRVEDEVSVGIPQGGSVLGSFPLKGLAGYVVAKLRSASVIGVLLGTITGMYYAQNYQVPIERTVKEYLNNMKKGPK-
>Ursus_maritimus-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVSSGVSDGSLSSPFLKGLAGYVVAKLRSASVLFVGTCTGIIAAQAYAVPNVEKTLRDYLSRLKGPD-
>Micropterus_floridanus-----MIVAKLRSSAIGVLLGTITGMYYAQSYQVPIERTVRDYLNMMKGPK-
>Rhinolophus_ferrumequinum-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVNSGMGDGSLSSPFLKGLAGYVVAKLRSASVLFVGTCTGIIAAQAYAVPNVEKTLRDYLSRLKGPD-
>Maylandia_zebra-----MADDKDSLKQLDQLTQLRNQLEIQRRVEHEVSAGIPQGGSVLGSFPLKGLAGYVVAKLRSASVLFVLLGTVTGMYYAQNYQVPIERTFKEYMNNLKKGPK-
>Dasypus_novemcinctus-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVNSGVGDGSLSSPFLKGLAGYVVAKLRSASVGMGFVGTCTGIIAQAYAVPNVEKTLRDYLSRLKGPD-
>Latimeria_chalumnae-----MADDKDTLRLKDLAQLKDQLEDIQKRVEEEVNAGIPQGGSLASPFLKGLTGYVVAKLRSALLGVVGTCTGIIAAQNYKVPNIENTVKDYISSLKKGSN-
>Pimephales_promelas-----MRSSAIGVALGTLTGIIYAVQNYQVPIEQTVRDFLNSLKKGPRD
>Fundulus_grandis-----MADNKDPLKQLDQLTQLKNQLEAIQRRVEDEVSSGIPQGGSVLGSFPLKGLAGYVVAKLRSASVLFVLLGTVTGIIAAQNYQVPNVERTVKDYMSTLRKGPK-
>Sarcophilus_harrisii-----MADDKEGSFLSSPFLKGLAGYVVAKLRSASVGMFVGLCTGIIAAQSYAVPNVEKTLQDYLSRLKGPD-
>Esox_lucius-----MADDKDPFKQMKDLNQLKNQLESLQKRVESEFATGIPQGGSVLGSFPLKGLAGYVVAKLRSASVIGVVLGTFGTGIIAAQNYQVPIERTLKDYMSLFKKGP-
>Gallus_gallus-----MADDKDSLPLKLDLALLKGQESLQRRVEDEVHAGVGGGSLASPFLKGLAGYLVAKLRFSAVLGFVGTCTGIIAAQNYAVPDVEKTVRDYLSALRKGGE-
>Acanthis_flammea-----MADDKDSLPLKLDLAFLKGQESLQRRVEDEVQAGVGDGSLASPLKGLAGYLVAKLRFSAVLGFVGTCTGIIAAQNYAVPNVEKTIIRDYVNSLKKGRD-
>Lateolabrax_japonicus-----MYAAQNYQVPIERTMKDCMNNLKKGPK-
>Trematodus_bernacchii-----MAGDKDPLKQLDQLTKLKSQLEEQRRVEDEVTLGIPQGGSVLGSFPLKGLAGYVVAKLRSASVLFLLVGTATGIIAAQNYQVPIERTVKDYINSCLKKGPK-
>Equus_asinus-----MADDKDSLPLKLDLAFLKNQLESQRRVEDEVNSGVGDGSLSSPFLKGLAGYVVAKLRSASVLFVGTCTGIIAAQAYAVPNVEKTLRDYLSRLKGPD-
>Manis_javanica-----MADDKDSLPLKLDLAFLKNQLERLQORVEDEVNSGVSDGSLSSPFLKGLAGYVVAKLRSASVLFVGTCTGIIAAQAYAVPNVEKTLRDYLSRLKGPD-
>Cynoglossus_semihaevis-----MSRIPSTPPSKMANDKPLKQLDQLTQLKNQLEEQRRVENEISAGIPQGGSVLGSFPLKGLAGYVVAKLRSASVILGLVIGTCTGIIAAQNYQVPIEQTVKEYMRNLIKKGPK-
>Heterocephalus_glaber-----MADDKDSLPLKIDLAFLKNQLERLQORVEDEVNSGVGDGSLSSPFLKGLAGYVVAKLRSASVLFVGTCTGIIAAQAYALPNVEKTLRDYFQSLRKGPD-
>Salmo_salar-----MLLSTPGIRVDHRAFNRKAMADDKDPFKQMKNLNQLKNQLEEQKRVESEFAEGIPQGGSVLASPFLKGLAGYVVAKLRSASVIGVVLGTFGTGIIAAQNYQVPIESTLKDYMSLFRKGPK-
>Ictalurus_punctatus-----MANGKDPLTQLKDLAQLKDQLEDIQKRVEDEVQIGIPQGGSLASPFLKGLAGYVVAKLRSASVLFVLLGTVTGTGIIYAAQNYQVPIETTIKDYLNSLKKGPNN
>Gekko_japonicus-----MADDKDSLPLKLDLAFLKNQLANLQORVEDEVQTVGGQEGSLASPFLKGLAGYVVAKLRSASVLFVLTGTCGVYVAAQTYAIPNVEKTIKEFFSFRKGPD-

>Gallus_gallus
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>Anser_cygnoides
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>Chaetura_pelagica
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>Apteryx_australis_mantelli
MDWPOQRCRCWEKTSHLKWR
>Buceros_rhinoceros_silvestri
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>Gariama_cristata
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>Charadrius_vociferus
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>Pterocles_gutturalis
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>Colius_striatus
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>Columba_livia
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>Gavia_stellata
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>Eurypyga_helias
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>Tauraco_erythrolophus
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>Opisthocomus_hoazin
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>Sturnus_vulgaris
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>Egretta_garzetta
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>Picooides_pubescens
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>Fulmarus_glaucialis
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>Nestor_notabilis
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>Aptenodytes_forsteri
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>Tyto_alba
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>Struthio_camelus_australis
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>Chelonia_mydas
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>Calypte_anna
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>Balaenoptera_acutorostrata_s
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>Dasypus_noveboracensis
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>Geratherium_simum_simum
MARLLVAMSAPRCFWG
>Cavia_porcellus
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>Gallus_gallus
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>Anser_cygnoides
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>Chaetura_pelagica
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Caprimulgus_carolinensis
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>Pterocles_gutturalis
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>Colius_striatus
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>Merops_nubicus
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>Cuculus_canorus
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>Aquila_chrysaetos_canadensis
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>Gavia_stellata
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>Balearica_regulorum_gibberic
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>Tauraco_erythrolophus
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>Opisthocomus_hoazin
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>Lepidothrix_coronata
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>Picoides_pubescens
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>Fulmarus_glacialis
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>Melopsittacus_undulatus
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>Tyto_alba
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>Struthio_camelus_australis
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>Chelonia_mydas
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>Tinamus_guttatus
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>Calypte_anna
MMVCSGLLRNCSSVPARILSSALH-
>Apaloderma_vittatum
MMVCSFGLLRNCSSVPARILSSALH-

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>Homo_sapiens
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>Canis_lupus_familiaris
MSHFKGCTEL
>Equus_asinus
MNHFKGCTQL
>Nannospalax_galili
MNHFKGCTQL
>Orycteropus_afer_afer
MSHYKGCTQL

>Homo_sapiens
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>Polypedates_megacephalus
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>Chaetura_pelagica
MHFHNTTFELMKWKYR-----
>Odobenus_rossmarus_divergens
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>Orcinus_orca
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>Calidris_pugnax
MHFHNTTFELMKWKYR-----
>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
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>Alligator_mississippiensis
MHCYNIILELMKKWKYR-----
>Monodelphis_domestica
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>Falco_cherrug
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>Gallus_gallus
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>Gavia_stellata
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>Chlamydotis_macqueenii
MHCHSITFELMKWKYR-----
>Erinaceus_europaeus
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>Oryctolagus_cuniculus
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>Ornithorhynchus_anatinus
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>Opisthocomus_hoazini
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>Parus_major
MHFHNTTFELMKWKYR-----
>Equus_asinus
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>Manis_javanica
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>Picoides_pubescens
MHFHNTTFELMKWKYR-----
>Loxodonta_africana
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>Melopsittacus_undulatus
MHFHNTTFELMKWKYR-----
>Marmota_monax
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>Tupaia_chinensis
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>Trichechus_manatus_latirostris
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>Tinamus_guttatus
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>Gallus_gallus
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>Anas_platyrhynchos
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>Chaetura_pelagica
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>Calidris_pugnax
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>Alligator_mississippiensis
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>Melopsittacus_undulatus
-----MHFHNTTFELMKWKYR-----
>Struthio_camelus_australis
-----MQFHNTTFELMKWKYR-----
>Chrysemys_picta
-----MHCYNIILELMKWKYR-----
>Tinamus_guttatus
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HG0086 ENSGALG0000009835 XPOT

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>Gallus_gallus
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>Anser_cygnoides
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>Rana_clamitans
-----MLVDSAVPERGKPIVRNRELEV-
>Chaetura_pelagica
-----MIVASPLEEVGKPVSRKQRI-
>Apteryx_australis_mantelli
-----MIVVSPLEEVGKPVNRKQQRV-
>Buceros_rhinoceros_silvestri
-----MIVVSPLEEVGKPVSRKQQRV-
>Caprimulgus_carolinensis
-----MIVVSPLEEVGKPVESRKRVRVQ-
>Cariama_cristata
-----MIVVSPLEEVGKPVSRKQQRV-
>Hynobius_chinensis
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>Charadrius_vociferus
-----MIVVSLLEEVGKPVSRKQQRV-
>Colius_striatus
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>Columba_livia
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>Gavia_stellata
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>Mesitornis_unicolor
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>Tauraco_erythrolophus
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>Opisthocomus_hoazin
-----MIVASPLEEVGKPVTCRKQQRVQ-
>Manacus_vitellinus
-----MIVVSPLEEVGKPVSRKQQRV-
>Phaethon_lepturus
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>Fulmarus_glaucialis
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>Melopsittacus_undulatus
-----MMVVPLEEVGKPVSRKQQRV-
>Pygoscelis_adeliae
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>Tyto_alba
-----MFVSPLEEVGKPVSRKQQRV-
>Struthio_camelus_australis
-----MIVVSPLEEVGKAVNRKQQRV-
>Chrysemys_picta
-----MFVSTIGEGGKPVKNRKQKV-
>Apaloderma_vittatum
-----MIVVSPLEEVGKPVSRKQKAEQ
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>Homo_sapiens-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Xenopus_tropicalis-----MSDVEGRVNVREEMEEFFPRILKIKQDKRRLMKSFQDKKSI EWGNFLNRRLGR-----
>Canis_lupus_familiarisMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Orinus_orcaMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Galidris_pugnaxMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Myotis_brandtiiMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Haplochromis_burtoni-----MKTYTEQNIELEREVEVYRNGVR-----
>Dasypus_noveboracensisMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Latimeria_chalumnaeMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Columba_liviaMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Sarcophilus_harrisii-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Aquila_chrysaetos_canadensisMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
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>Ochotona_princepsMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
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>Parus_majorMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Lateolabrax_japonicus-----MKTCTEQNIEVEREEM-----
>Anoplopoma_fimbria-----MKTCTEQNIEVEREEM-----
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>Manis_javanicaMSDIEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Cynoglossus_semilaevis-----MKTCTEQNIEVQRVENVTEEWQIEALVV-----
>Marmota_marmota_marmotaMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Trichechus_manatus_latirostris-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Pygoscelis_adeliaeMSDVEENNFEGRVNVREEIEEFFPRMWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Struthio_camelus_australis-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Pelodiscus_sinensis-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----
>Tinamus_guttatus-----MWKINQDKRRLMKSIKDQKIKIEWGKKLNRRLVR-----

>Homo_sapiens	-----MQARRRDWTF-----PTCSLP
>Anas_platyrhynchos	-----MQARRGDWTF-----PTCSLP
>Chaetura_pelagica	-----MQARRGDWTF-----PTCSLP
>Apteryx_australis_mantelli	-----MQARRGDWTF-----PTCSLP
>Canis_lupus_familiaris	-----MPARRGDWTF-----PTCSLP
>Orcinus_orca	-----MLFLLFILRLSYVDMQARRHDWLY-----PTCSLP
>Charadrius_vociferus	-----MQARRGDWTF-----PTCSLP
>Eptesicus_fuscus	-----MQARRGAWTF-----PTCSLP
>Columba_livia	-----MQARRGDWTF-----PTCSLP
>Cuculus_canorus	-----MQARRGDWTF-----PTCSLP
>Haliaeetus_leucocephalus	-----MQARRGDWTF-----PTCSLP
>Coturnix_japonica	-----MQARRGAWTF-----PTCSLP
>Condylura_cristata	-----MQARREDWTF-----STCLLP
>Ochotona_princeps	-----MITLSRSLCLPYVDMQARRGDCTFPTSFPPTCSLP
>Elephantulus_edwardii	-----MITLSFTLRLSYVDMQARRGDWTS-----PTCSLP
>Opisthocomus_hoazin	-----MQARRGDWTF-----PTCSLP
>Manacus_vitellinus	-----MQARRGDWTF-----PTCSLP
>Nipponia_nippon	-----MQARRGDWTF-----PTCSLP
>Manis_javanica	-----MQARRGDWTP-----PPCSLP
>Ctenomys_sociabilis	-----MQARRGDWTF-----PTCSLP
>Tupaia_chinensis	-----MISRSFILRLSYVDMKARRGDWTS-----PTCPLP
>Trichechus_manatus_latirostr	-----MITLSFILRLSYVDMQARRGDWTF-----PTCSLP
>Aptenodytes_forsteri	-----MQARRGDWTF-----PTCSLP
>Thamnophis_sirtalis	-----MQARRGDWTF-----PTCSLP
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>Struthio_camelus_australis	-----MQARRGDWTF-----PTCSLP
>Chrysemys_picta	-----MQARREVWIV-----PTCSLL
>Tinamus_guttatus	-----MQARRGDWTF-----PTCSLP
>Orycteropus_afer_afer	-----MITLSFTLRLSYVDMQARRGDWTF-----PTCSLP

>Homo_sapiens
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>Chaetura_pelagica
MTKDCKGET--GSSFPERSP-----
>Canis_lupus_familiaris
MTKACRGESAA--RGPERSPR----
>Hynobius_retardatus
MTKDCCGESAAAGSRFPERSP-----
>Balaenoptera_acutorostrata_s
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MTKDCKGES--GSSFPERSP-----
>Miniopterus_natalensis
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>Columba_livia
MTKDCKGES--GSSFPERSP-----
>Cuculus_canorus
MTKDCCGES--GSSFPERSP-----
>Galeopterus_variegatus
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>Monodelphis_domestica
MTKDCCGESGP--RSPERSPI-----
>Falco_cherrug
MTKDCKGES--GSSFPERSP-----
>Coturnix_japonica
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>Sorex_araneus
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>Oryctolagus_cuniculus
MTKACGGESAA--RGPERAPR----
>Lepidothrix_coronata
MTKDCKGES--GSSFPERSPKM-DY
>Egretta_garzetta
MTKDCKGES--GSSFPERSP-----
>Geratherium_simum_simum
MTKACEGESAA--RGPERSPR----
>Manis_javanica
MTKACEAESAA--RGPRESSPR----
>Picooides_pubescens
MTKDCKGES--GSSFPERSP-----
>Loxodonta_africana
MTKACEGESAA--RSPERSPSIMDY
>Heterocephalus_glaber
MTKACKAESAA--RGPCKSPR----
>Trichechus_manatus_latirostr
MTKACEGESAA--RGPERSPR----
>Python_bivittatus
MTKDCKGES--GSSFAERSP-----
>Struthio_camelus_australis
MTKDCKGES--GSSFPERSP-----
>Chrysemys_picta
MTKDCKGES--GSSFPERSP-----
>Orycteropus_ afer_ afer
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>Gallus_gallus
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>Nanorana_parkeri
MTKDCQRPV-TGSAFPERSLSV—DY-----
>Chaetura_pelagica
MTKDCKGET—GSSFPERSP-----
>Odobenus_rossmarus_divergens
MTKACKGESAA—CGPERSPR-----
>Hynobius_retardatus
MTKDCQGESAAAGSRFPERSP-----
>Lipotes_vexillifer
MTKACEGESAA—RGPERSPR-----
>Calidris_pugnax
MTKDCKGES—GSSFPERSP-----
>Miniopterus_natalensis
MTKACEGESAA—RGPERSPR-----
>Columba_livia
MTKDCKGES—GSSFPERSP-----
>Alligator_mississippiensis
MTKDCTGERGGV—PRAVPGHLLNGTLPQLGLSSGCR
>Cuculus_canorus
MTKDCQGES—GSSFPERSP-----
>Monodelphis_domestica
MTKDCEGSGP—RSPERSPI-----
>Falco_cherrug
MTKDCKGES—GSSFPERSP-----
>Sorex_araneus
MTKACKGESAA—RGPERSPSI—MDY-----
>Oryctolagus_cuniculus
MTKACGESAA—RGPERSPR-----
>Ficedula_albicollis
MTKDCKGES—GSSFPERSPKM—DY-----
>Egretta_garzetta
MTKDCKGES—GSSFPERSP-----
>Equus_caballus
MTKACKGESTA—RGPERSPR-----
>Picoides_pubescens
MTKDCKGES—GSSFPERSP-----
>Cebus_capucinus_imitator
MTKACEGESAA—RGPERSPR-----
>Loxodonta_africana
MTKACEGESAA—RSPERSPSI—MDY-----
>Heterocephalus_glaber
MTKACKAESAA—RGPERSPR-----
>Trichechus_manatus_latirostr
MTKACEGESAA—RGPERSPR-----
>Takydromus_sexlineatus
MTKDCKGES—GSSFAERSP-----
>Struthio_camelus_australis
MTKDCKGES—GSSFPERSP-----
>Chrysemys_picta
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>Orycteropus_ afer
MTKACKGESEA—RCPERSPR-----

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>Homo_sapiens
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>Balaenoptera_acutorostrata_s
MNTARLHPRK
>Rhinolophus_ferrumequinum
MNTERLHPRK
>Galeopterus_variegatus
MNTARLHPRK
>Sorex_araneus
MNTARLHPRK
>Oryctolagus_cuniculus
MNTARLHPRK
>Equus_asinus
MNTARLHPRK
>Manis_javanica
MNTARLHPRK
>Jaculus_jaculus
MNTARLHPRK
>Trichechus_manatus_latirostr
MNTARLHPRK

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>Gallus_gallus
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>Chaetura_pelagica
MNKLHLQFRK
>Calidris_pugnax
MNKLHLQFRK
>Columba_livia
MNKLHLQFRK
>Falco_cherrug
MNKLHLQFRK
>Egretta_garzetta
MNKLHLQFRK
>Picoides_pubescens
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>Struthio_camelus_australis
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>Mustela_putorius_furo
----MKPPSHSCMCSYC
>Balaenoptera_acutorostrata_s
----MKPSSQSCMCSYC
>Miniopterus_natalensis
----MKPSSHSCMCSYC
>Dasypus_novemcinctus
----MKPPSYSCMCSHC
>Sorex_araneus
----MKPSSHSCMCSQW
>Ceratotherium_simum_simum
----MKPPSHSCMCSYC
>Loxodonta_africana
MK1GMKPSSHSCMRSHC
>Chinchilla_lanigera
----MKPPSHSCMHSHC
>Tupaia_chinensis
MK1GMKPSSHSCMCSHY
>Trichechus_manatus_latirostr
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>Gallus_gallus
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>Anser_cygnoides
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>Apteryx_australis_mantelli
-MEISMRSPIWHSOMCSH-
>Buceros_rhinoceros_silvestri
-MEISMRSPIWHSOMCSHS
>Mustela_putorius_furo
-----MKPPSHSOMCSYC
>Galidris_pugnax
-MEISMRSPIWHSOMCSHS
>Eptesicus_fuscus
-----MKPPSHSOMCSYY
>Merops_nubicus
-MEISMRSPIWHSOMCSHS
>Alligator_mississippiensis
-----MRSPWHSCMRSHS
>Cuculus_canorus
-----MRSPWHSCMRSHS
>Sarcophilus_harrisii
MEEISMRSSSHSCMRSHS
>Aquila_chrysaetos_canadensis
-MEISMRSPIWHSOMCSHS
>Mesitornis_unicolor
-MEISMRSPIWHSOMCSRS
>Condylura_cristata
-----MKPPSHSCMSCYW
>Tauraco_erythrolophus
-----MRSPWHSCMRSHS
>Opisthocomus_hoazin
-MEISMRSPIWHSOMCSHS
>Geospiza_fortis
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>Phaethon_lepturus
-MEISMRSPIWHSOMCSHS
>Ceratotherium_simum_simum
-----MKPPSHSOMCSYC
>Picoides_pubescens
-MEISMRSPIWHSOMCSHS
>Nestor_notabilis
-----MRSPWHSCMYSHS
>Trichechus_manatus_latirostr
-----MKPPSHSCMSCNC
>Aptenodytes_forsteri
-----MRSPWHSCMRSHC
>Takydromus_sexlineatus
-----MRPPWHSCMCIHS
>Tyto_alba
-MEISMRSPIWHSOMCSHS
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>Chrysemys_picta
-MEISMRRPPIWHSOMCSRS

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>Channa_argus-----MTLSQVTDACPL-----
>Basilichthys_microlepidotus-----MTSMTLSQATDACPLKRPN-----
>Oryzias_melastigma-----MTSMTLSQATDACPLKGSD-----
>Trachinotus_blochii-----MTSMTLSQATDACPLKRPN-----
>Micropterus_floridanus-----MTSMTLSQATDACALKRPN-----
>Pygocentrus_nattereri-----MDRAIPELRARGGQAGLMTSMTLSQSADACTLAEST-----
>Maylandia_zebra-----MTSMTLSQATDACPLKRPN-----
>Austrofundulus_limnaeus-----MTSMTLSQATDACPLKRPN-----
>Esox_lucius-----MTSMTLSQSADACTGSK-----
>Gadus_morhua-----MTSMTLRQTDDACTLV-----
>Apteronotus_leptorhynchus-----MSMTLSQSADACTLTEST-----
>Plecoglossus_altivelis-----MTSMTLSQSSDACTLAVPI-----
>Lateolabrax_japonicus-----MTSMTLSQATDACPLKRPN-----
>Notothenia_coriiceps-----MTSMTLSQATDACPLKRPN-----
>Ictalurus_punctatus-----MNGHSAQSSQGSPIPELRARGGRAGPMTSMTLSQSTDACTLTESTRVPSPLLPGF-----
>Takifugu_rubripes-----MTSMTLSQATDACPHKGH-----

>Gallus_gallus
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>Anas_platyrhynchos
-----MSAMKKGK
>Apteryx_australis_mantelli
-----MSAMLKDN
>Charadrius_vociferus
-----MORDELASAILSFVQWRDCCMSAMKKGK
>Merops_nubicus
-----MSAMKKGK
>Cuculus_canorus
-----MSTMLKGK
>Aquila_chrysaetos_canadensis
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>Tauraco_erythrolophus
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>Opisthocomus_hoazin
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>Nipponia_nippon
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>Nestor_notabilis
-----MSAMKKGK
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>Struthio_camelus_australis
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>Homo_sapiens	MAHYRHIFSLRSFSKRCL
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>Chaetura_pelagica	MAQYRHKFSLRSFFEDMLITLFPFYSANK
>Caprimulgus_carolinensis	MAQYRHKFSLRSFFEDMLITLFLSLLC
>Odobenus_rossmarus_divergens	MAQYRHIFSLRSFLKRCL
>Hynobius_retardatus	MAQHRHIFSLRSFSEEMLMALFPWYSAYK
>Orcinus_orca	MYFQMLIDSTVGRVDCSSLOALHPYISSTAETMAQYRHTFSLRSFSKRCL
>Calidris_pugnax	MAHYRHKFSLRSFLEDMLITLFPFYSANK
>Rousettus_aegyptiacus	MAQYRHIFSLRSFQDVYEPLQVL
>Pterocles_gutturalis	MAHYRHKFSLRSFLEDMLITLFPFYSANK
>Colius_striatus	MAQYRHKFSLRSFFEDMLITIFPFYSANK
>Merops_nubicus	MAQYRHKFSLRSFLEDMLITLFPFYSANK
>Galeopterus_variegatus	MAQYRHIFSLRSFLKRCL
>Aquila_chrysaetos_canadensis	MAQYRHKFSLRSFFEDMLITLFPFYSANK
>Coturnix_japonica	MAHYRHKFSLRSFFEDVLTLPFFFSANK
>Erinaceus_europaeus	MAQYRHIFSLRSFRDVPDPLPILY
>Oryctolagus_cuniculus	MAQYRHIFSLRSFLKRCL
>Tauraco_erythrolophus	MAQYRHKFSLRSFFEDMLITLTKNSANK
>Zonotrichia_albicollis	MAQYRHKFSLRSFFEDMLITLFPFYSANKVNKMNPNSNLELLHLHREFTKSLVEGMOQLIQFYY
>Phaethon_lepturus	MAQYRHKFSLRSFFEEMMLITLFSFYSANK
>Ceratotherium_simum_simum	MAQYRHIFSLRSFSKRCL
>Manis_javanica	MAQYRHIFSLRSFPKRCL
>Melopsittacus_undulatus	MAQYRHKFSLRSFFEDMLITLFPFYSANK
>Ictidomys_tridecemlineatus	MAQYRHIFSLRSFLKRCL
>Aptenodytes_forsteri	MAQYRHKFSLRSFFEDMLITLFPFYSANK
>Calypte_anna	MAHYRHKFSLRSFFEDMLITLLPFYSANK
>Apaloderma_vittatum	MAQYRHKFSLRSFFGDTLITLFPFYSANK

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>Orcinus_orca
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>Pteropus_alecto
-----MSKYILGARNLMFPFLFSHVLENKCTL-----
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>Dasypus_novemcinctus
-----MAKYIFETRNLMYPFLLSRILENKETL-----
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>Galeopterus_variegatus
-----MSKYILEARNLMFPFLFSHILENKETLSYIPSKGNIIISII-----
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>Monodelphis_domestica
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>Oryctolagus_cuniculus
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>Ornithorhynchus_anatinus
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>Manis_javanica
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>Heterocephalus_glaber
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>Chrysemys_picta
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>Lipotes_vexillifer
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>Pteropus_allecto
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>Galeopterus_variegatus
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>Monodelphis_domestica
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>Oryctolagus_cuniculus
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>Gallus_gallus
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-----MRHVILV-----
>Apteryx_australis_mantelli
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>Charadrius_vociferus
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>Pteropus_alecto
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>Colius_striatus
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>Alligator_mississippiensis
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>Gavia_stellata
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>Calypte_anna
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>Homo_sapiens
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>Rousettus_aegyptiacus
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>Fukomys_damarensis
-----MKQSI~~CH~~KIRCSGFSTRLEQNYI~~CF~~SQKRIPQ-----
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>Apteryx_australis_mantelli
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>Struthio_camelus_australis
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>Chelonia_mydas
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>Orycteropus afer
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>Chaetura_pelagica
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>Apteryx_australis_mantelli
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>Struthio_camelus_australis
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>Mustela_putorius_furo
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>Balaenoptera_acutorostrata_s
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>Gallidris_pugnax
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>Pteropus_allecto
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>Columba_livia
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>Anolis_carolinensis
MLCTGMPASTNQ--VLVFCISHVEKTVMTVENWKSEFQLS
>Struthio_camelus_australis
-----MPSADK--ILVFCISNAEKTITTVENWKSEFQLS
>Pelodiscus_sinensis
-----MPSADK--ILVFCISNAEKAITTVENWKSEFQLS
>Tinamus_guttatus
-----MSRSADK--ILVFCISNAEKTITTVENWKSEFQLS
>Orycteropus_ afer_ afer
-----MQQKLLTTVDNWKYEFQLS
```

>Homo_sapiens
MDLQEGFQVNSGKHIYLNSTT-----
>Ailuropoda_melanoleuca
MDLQEGFQVNSGKHIYLNSTTSLILH-----
>Pteropus_vampyrus
MDLQEGFQVNTGKHIYLNSTTSLILH-----
>Dasypus_noveboracensis
MDLQEGFQVNSGKHIYLNSTTSLILH-----
>Galeopterus_variegatus
MDLQEGFQVNSGKHIYLNSTTSLILH-----
>Monodelphis_domestica
MDFREGLVNSGKHIYFTSTILSFILH-----
>Sorex_araneus
MDLKEGFQVNSGKHIYLNSTLNLVLH-----
>Oryctolagus_cuniculus
MDLQEGFQVNSGKHIYLNSTTSLILH-----
>Ceratotherium_simum_simum
MDLQEGFQVNSGKHIYLNSTTSLILH-----
>Manis_javanica
MDLQEGFQVNSGKHIYLNSTTSLILHDDTKDVKVITKLDPKYISQHGGADEHRSVIQKSGSVLERTQGLRRTQEQVKITLITQFIRRSTLLNSNTKGLIINSYRNA
>Loxodonta_africana
MDLQEGFQVNSGKHIYLNSTSLILH-----
>Ictidomys_tridecemlineatus
MDLQEGFQVNSGKHIYLNSTSLILH-----
>Trichechus_manatus_latirostris
MDLQEGFQVNSGKHIYLNSTSLILH-----
>Chelonia_mydas
MDLQKFFQVNSGKHIN-----
>Orycteropus afer afer
MDLQEGFQVNSGKHIYLNSTTSLILH-----

>Danio_rerio
 MEERSSSLIGYAMVSATYPVQVVLSSLSEVCRFSVA-----PEE-----KLISSGVPAT
 >Amia_calva
 -----MVSAKHPVLQVVLSYTDVCFVSI-----VEE-----AIISSLTTTT
 >Channa_argus
 -----MVSAAHPDLQVLVSLSCVFG--FSSRCSTAEVA-----VSSLACAP
 >Microhyla_fissipes
 -----MVSAKRSVFELCKADICRLAF-----LEG-----TIISSLVTAT
 >Menidia_menidia
 -----MVSAAHPDLQVLVSLSRAFG--LSSLCSTAEVA-----VISLLVASP
 >Porichthys_notatus
 -----MVSAAHPDLQVLVSLSRVLG--LDSLCSAEVA-----VISLLASAP
 >Oryzias_melastigma
 -----MVSATHPDLQVLVSLSCVFG--LSSLCSTAEVA-----VISLLASAP
 >Ambystoma_mexicanum
 -----MVSACGQVHEVLLCPHTCWYVY-----IKG-----SPISSLTLAT
 >Pygocentrus_nattereri
 -----MVSAAHPDLQVVLSSLSDVCRFSIS-----PEE-----AVIFSCPTAT
 >Callorhynchus_milii
 -----MVSARQPELEVLLCTDLNWFIF-----TEE-----AIHSSLATTT
 >Haplochromis_burtoni
 -----MVSAAHPDLQVLVSLSRVFR--LSSLCSTAEVA-----VISLLASAP
 >Dasyatis_novemcinctus
 -----MVSARWFI LDELFTDICYVVF-----YKW-----TII SFFKTTT
 >Alosa_alosa
 -----MVSATPPVLQVVLSSLRACRLSVS-----LEE-----AVISPRAPAT
 >Latimeria_chalumnae
 -----MLSAKQSVLEVLLYTDTCWFAIF-----TEG-----VIISLKTITT
 >Poeciliopsis_prolifica
 -----MVSAVHPDLQVLATLSRVFR--LSFLRCTAEVA-----VISLLASAP
 >Sarcophilus_harrisii
 -----MVSARWFI LDELFTDICYVFI-----YKR-----TLISPLTTTT
 >Esox_lucius
 -----MVSAAHPDLQVVLSSLAPRQCSSLRSVSEVAEAPPVISLLASAP
 >Gadus_morhua
 -----MVSAAHPDLQVLVSLSCVFG--LVYLCSTAEVA-----VIPLVASAP
 >Apteronotus_leptorhynchus
 -----MVTATQPKQVLLSCLLALWIRPA-----ALQ-----AVISRLAPTT
 >Ornithorhynchus_anatinus
 -----MVAATWLALFELFKTDTCRYCIV-----SKR-----TII PSLPTTT
 >Scleropages_formosus
 -----MVAASRPALQLVLSHTDVCWFSVT-----TDE-----ALISSPAIAT
 >Trematodus_bernacchii
 -----MVSAAHPDLQVLVSLSRAFG--LSSLCSTAEVA-----VISLLASAP
 >Platichthys_stellatus
 -----MVSAAHPDLQVLVSLSRVFG--LSSLCSTAEVA-----VISLLASAP
 >Macaca_nemestrina
 -----MVSARWFI LELDFKTDKCYVFI-----YKW-----TII SFLKTTT
 >Oncorhynchus_mykiss
 -----MVSAAHPDLQVVLSSLVPRLLSSLCSSEVAEAPPVISLVVSA
 >Lepisosteus_oculatus
 -----MVSAKHPVLQVVLSSDQACWFSII-----VEE-----AIISSLTTTT
 >Ictalurus_punctatus
 -----MVS-----ASALASAVCYFSIS-----PEE-----AVISRAPVT

>Gallus_gallus	-----MVFSCRCRKIADMTA
>Anas_platyrhynchos	-----MVFFHRCRKIADMTA
>Chaetura_pelagica	-----MVFFRGCRKIADMTA
>Apteryx_australis_mantelli	-----MVFFCRCRKIADMTA
>Buceros_rhinoceros_silvestri	-----MVFFHRSRKIAEMTA
>Caprimulgus_carolinensis	-----MVFFCRCRKIADMTA
>Cariama_cristata	-----MVFFHRCRKIADMTA
>Calidris_pugnax	-----MVFFHRCRKIADMTA
MLVVSQPLMQEENPRLKGFSEGSVLIRSGDVMVFFRRCRKIADMTA	
>Pterocles_gutturalis	-----MVFFHRCRKIAAMTA
>Colius_striatus	-----MVFFHRCRKIADMTA
>Columba_livia	-----MVFFHRCRKIADMTA
>Leptosomus_discolor	-----MVFFRRCRKIADMTA
>Cuculus_canorus	-----MVFFRRCRKIADMTA
>Haliaeetus_albicilla	-----MVFSRRRCRKIADMTA
>Gavia_stellata	-----MVFFHRCRKIADMTA
>Mesitornis_unicolor	-----MVFFHRCRKIADMTA
>Tauraco_erythrolophus	-----MVFSRRRCRKIADMTA
>Opisthocomus_hoazin	-----MVFFRRCRKIADMTA
>Acanthisitta_chloris	-----MVFFHRCRKIADMTA
>Nipponia_nippon	-----MVFFRRCRKIADMTA
>Fulmarus_glacialis	-----MVFFHRCRKIADMTA
>Nestor_notabilis	-----MVFFRRCRKIADMTA
>Aptenodytes_forsteri	-----MVFFHRCRKIADMTA
>Tyto_alba	-----MVFFRRCRKIADMTA
>Struthio_camelus_australis	-----MVFFRRCRKIADMTA
>Chrysemys_picta	-----MVFFCRCRKIAQMTI
>Tinamus_guttatus	-----MVFFCRYRKIADMTA

HG0097 ENSGALG00000037496

>Gallus_gallus	
MELOPRAGAADTPSAFLRSSHHERGRFHLVKMAVWDRCNL	
>Ailuropoda_melanoleuca	
-----MAVRDRCNL	
>Orcinus_orca	
-----MAVRDRCNL	
>Calidris_pugnax	
-----MAVWDRCNL	
>Rousettus_aegyptiacus	
-----MAVRDRCNL	
>Dasypus_novemcinctus	
-----MAVRGRCHL	
>Columba_livia	
-----MAVWDRCNL	
>Alligator_mississippiensis	
-----MAVGDRCNL	
>Sarcophilus_harrisii	
-----MAVRDHCNL	
>Galeopterus_variegatus	
-----MAVRDRCNL	
>Monodelphis_domestica	
-----MAVRDHCNL	
>Falco_peregrinus	
-----MAVWDRCNL	
>Erinaceus_europaeus	
-----MAVRDRCNL	
>Elephantulus_edwardii	
-----MAVRDRCNL	
>Lepidothrix_coronata	
-----MAVWDRCNL	
>Nipponia_nippon	
-----MAVWDRCNL	
>Ceratotherium_simum_simum	
-----MAVRDRCNL	
>Manis_javanica	
-----MAVRDRCNL	
>Pongo_abelii	
-----MAVRDRCNL	
>Loxodonta_africana	
-----MAVRDRCNL	
>Melopsittacus_undulatus	
-----MAVRDRCNL	
>Microtus_ochrogaster	
-----MAVCDRCNL	
>Trichechus_manatus_latirostr	
-----MAVRDRCNL	
>Aptenodytes_forsteri	
-----MAVWDRCNL	
>Gekko_japonicus	
-----MAVWDRCNL	
>Pelodiscus_sinensis	
-----MAVWDHCNL	
>Calypte_anna	
-----MAVWDRYNL	

HG0098 ENSG00000198739 LRRTM3

>Homo_sapiens
MOKRNIHEDPIT
>Anser_cygnoides
MOKRNIHEDPIT
>Panthera_tigris
MOKRNIHEDPIT
>Tursiops_truncatus
MOKRNIHEDPIT
>Galidris_pugnax
MOKRNIHEDPIT
>Pteropus_alecto
MOKRNIHEDPIT
>Dasypus_novemcinctus
MOKRNIHEDPIT
>Galeopterus_variegatus
MOKRNIHEDPIT
>Monodelphis_domestica
MOKRNIHEDPIT
>Aquila_chrysaetos_canadensis
MOKRNIHEDPIT
>Coturnix_japonica
MOKRNIHEDPIT
>Condylura_cristata
MOKRNIHEDPIT
>Oryctolagus_cuniculus
MOKRNIHEDPIT
>Elephantulus_edwardii
MOKRNIHEDPIT
>Ornithorhynchus_anatinus
MOKRNIHEDPIT
>Lepidothrix_coronata
MOKRNIHEDPIT
>Ceratotherium_simum_simum
MOKRNIHEDPIT
>Manis_javanica
MOKRNIHEDPIT
>Loxodonta_africana
MOKRNIHEDPIT
>Marmota_marmota_marmota
MOKRNIHEDPIT
>Tupaia_chinensis
MOKRNIHEDPIT
>Trichechus_manatus_latirostr
MOKRNIHEDPIT
>Anolis_carolinensis
MOKRNIHEDPIT
>Struthio_camelus_australis
MOKRNIHEDPIT
>Chrysemys_picta
MOKRNIHEDPIT
>Tinamus_guttatus
MOKRNIHEDPIT
>Orycteropus_afer_afer
MOKRNIHEDPIT

>Homo_sapiens	-----MRKT-----NGSEKYRRIIGGDIITAFPDREEKYGMCFAD-----
>Anas_platyrhynchos	-----MCFTADREQANEQYL-----
>Mustela_putorius_furo	-----
MFLTAPLLTOLLCCIIFELLSSTAIAGSPLMNRVL FHVDELVATRRN-----GKGYRNQLQLGGDIITAFPDWEEKYGMCFAD-----	
>Balaenoptera_acutorostrata_s	-----MCFTAD-----
>Miniopterus_natalensis	-----MRENPSFSMSSVEIKEPGGDIITAFPDREEKYGMCFAD-----
>Dasypus_novemcinctus	-----MCFTAD-----
>Cuculus_canorus	-----MCFTADRRQPNEQYL-----
>Sarcophilus_harrisii	-----MCFTAD-----
>Galeopterus_variegatus	-----MCFNAD-----
>Monodelphis_domestica	-----
-----MCQK-----KLITIEQV-----QSLDFLQPRKKDACKRGY-----HSVSSLREKYGMCFAD-----	
>Haliaeetus_albicilla	-----MCFTADRRQPNEQYL-----
>Condylura_cristata	-----MCFTAD-----
>Oryctolagus_cuniculus	-----MHFPAD-----
>Elephantulus_edwardii	-----MCFTTDCQPNELD-----
>Ornithorhynchus_anatinus	-----MCFTAD-----
>Sturnus_vulgaris	-----MCFTADRRQPNEQYL-----
>Equus_asinus	-----MCFTAD-----
>Manis_javanica	-----MCFNAD-----
>Loxodonta_africana	-----MCFTAD-----
>Cavia_porcellus	-----MCFTAD-----
>Tupaia_chinensis	-----
-----MGCSILELIRPLTG-----TDSORHVHPQAP-----PSSDVGSCMAGGDIITAFPDWEEKYGMCFAD-----	
>Trichechus_manatus_latirostr	-----MCFTAD-----
>Struthio_camelus_australis	-----MPSCAGGSFIPGLLVTG-----HHSCTSLGAKYGMCFADRTQPNQYL-----
>Chrysemys_picta	-----MTGHCSCTSFEEKYGMCFAD-----
>Tinamus_guttatus	-----MCFTADRRQPNEQYL-----
>Orycteropus_afer_afer	-----MCFTADRTQPNELY-----

HG0099.2 ENSG00000144136 SLC20A1

>Homo_sapiens
MNLRPFSPPWNSAPCF
>Leptonychotes_weddellii
MNLRPFSPPWNS-PCF
>Tursiops_truncatus
MNLRPFSPPWNSAPCF
>Condylura_cristata
MNLRPFSPPWNSAPC-
>Oryctolagus_cuniculus
MNLRPFSPPWNFAPCF
>Equus_przewalskii
MNLRPFSQPWNSAPCF
>Manis_javanica
MNRPPCSSKPWNSAPLL
>Rattus_norvegicus
MNLRPFSNPWNSAPCF
>Tupaia_chinensis
MNLRPFSPPWNSAPCF
>Trichechus_manatus_latirostr
MNLRPSSLPWNSAPCF
>Orycteropus_afer_afer
MNLRPFSRPWNSAPCF

>Homo_sapiens-----MMLCIVHOGTPLGRISH-----
>Leptonychotes_weddelii-----MMLCIVQOSTPLGQISH-----
>Eptesicus_fuscus-----MMLCIVHOGTPLGQISH-----
>Galeopterus_variegatus
MPVAKKSLFLFVSTCKNHLKEDRVIGPNSIISIIVMLCIVH-----
>Erinaceus_europaeus
MPVVKKLALFSLVLAKTTYKKLVVLGLNSVICIIMMLCIVHONTPLSQISH-----
>Elephantulus_edwardii
MPVVKGAYYSIFVSTCKSNLKEVSAVGLTSIISIIVMLCIVHOSTPLCQISH-----
>Ceratotherium_simum_simum
MPVVKKSLFLFVSTCKNNLKEVSIIGLKSIISIIMMLCIVHRARPLARFPIKRTPTLS
>Heterocephalus_glaber-----MGIIMMLCIVHOGTPLGHISH-----
>Tupaia_chinensis
MPVVKELTL---SVSTCKINLKEVSIIGLHSVSIISIIVMLCIVHOGTPLGQISH-----
>Orycteropus_afer_afer-----MMLCIVHOGTPLCQISH-----

HG0099.4 ENSDARG00000010641 slc20a1b

>Danio_rerio
MDVRCICLIVQAKTNRNRSSLFRG
>Trachinotus_blochii
MAVHSLCLIAQDPKKSNRSSIITG
>Astyanax_mexicanus
MDVRSVCLITQTKTHCSSTSLFRG
>Clupea_harengus
——MGCLIHQSQTNCSSLLRG
>Apteronotus_leptorhynchus
MDVCSVGLIAQTKTHCSRYSLFRG
>Lutjanus_erythropterus
MAVCSLCLIAQHQSNSNRSSIITG
>Sebastes_caurinus
MAVCSICLISEHORNRNRSSLITG
>Platichthys_stellatus
MAVMSLCLIAQRSKNSNRSSLILG
>Trichomycterus_areolatus
MDVRSVCLIGQTKTHCSSTSLFRG

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>Danio_rerio-----MRVLGVGLSWGWRWRSGALLSRV-----
>Acipenser_sinensis-----MVLGVGLSWGWRWRSVATFLRFFVA-----
>Channa_punctata-----MVLGVGLSWGWRWRSGALLHLF-----
>Menidia_menidia-----MIMVLGVGLSWGWRWRSGALLHFF-----
>Porichthys_notatus-----MVLGVGLSWVDLRRSVALLPFF-----
>Oryzias_latipes
MKKFDVTQNGYVEHLAIAARLPKCCSVPDFLNGRFETRPVHGDRCSWGYLMTIMVLGVGLTWGWRWRSGALLHLF-----
>Trachinotus_blochii-----MVLGVGLSWGWRWRSGALLHLF-----
>Micropterus_floridanus-----MLGHLTIIMVLGVGLSWGWRWRSGALLHLF-----
>Pygocentrus_nattereri-----MVLGVGLSWGWRWRAALLLF-----
>Maylandia_zebra-----MVLGVGLSWGWRWRSGALLHLF-----
>Alosa_alosa-----MIMVLGVGLSWGWRWRSGALLLF-----
>Nothobranchius_furzeri
MKKFDVTQNGYFEHLELRLYPRNAEIHNLIPDRHLKARFLHGDPFISGYLMTIMVLGVGLSWGWRWRSGALLHLF-----
>Esox_lucius-----MVLGVGLSWGDCQWRVALLPFF-----
>Acanthogobius_hasta-----MIMVLGVGLSWGWRWRSGALLHLF-----
>Apteronotus_leptorhynchus-----MVFGLSWGWRWRSGALLLV-----
>Lutjanus_erythropterus-----MVLGVGLSWGWRWRSGALLHLF-----
>Plecoglossus_altivelis-----MVLGVGLSWGWRWRSGALLHLF-----
>Scleropages_formosus-----MVLGVGLSGWRWRSGALLLF-----
>Lateolabrax_japonicus-----MVLGVGLSWGWRWRSGALLHLF-----
>Trematomus_bernacchii-----MVLGVGLSWGWRWRSGALLHLF-----
>Cynoglossus_semiolaenis-----MLSNCRAEVGS LHGEYFIVRYLTIIMVLGVGLSWGWRWRSGALLHLF-----
>Salvelinus_alpinus-----MVLVVGLSWWRWRSGALLHLF-----
>Lepisosteus_oculatus-----MVLGVGLSWGWRWRS GAL-----
>Trichomycterus_areolatus-----MSVIGVDLSWVWWRWRSGALLLVF-----
>Takifugu_rubripes
MNTFDVTQNDFFTH-LDITFFLGNAAVHLTSLDCHPEVRF LHGEYFILGYLTIIMVLGVGLSWGWRWRSGALLHLF-----

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>Danio_rerio-----MIMVVLGVGLSWGELWWRGALLLFF----
>Acipenser_sinensis-----MVVLGVGLSWGELWWRGAVATFLRFFVA
>Channa_punctata-----MVVLGVGLSWGELWWRSGALLHLF----
>Menidia_menidia-----MIMVVLGVGLSWGELWWRSGALLHFF----
>Porichthys_notatus-----MVVLGVGLSWVDLRRRSVALLPFF----
>Oryzias_latipes
MKTFDVTQNGYVEHLAIALPKCCSVPDFLNGRFETRPVHGDRCSWGYLMTIMVVLGVGLTWGELWWRSGALLHLF----
>Trachinotus_blochii-----MVVLGVGLSWGELWWRSGALLHLF----
>Micropterus_floridanus-----MLGHLTIIMVVLGVGLSWGELWWRSGALLHLF----
>Pygocentrus_nattereri-----MVVLGVGLSWGELWWRRAALLLFF----
>Maylandia_zebra-----MVVLGVGLSWGELWWRSGALLHLF----
>Clupea_harengus-----MIMVVLGVGLSWGELWWRSGALLLFF----
>Latimeria_chalumnae-----MKCVLTVGFLSAIMVVLGVLSGGDRWWRGALLLLH----
>Nothobranchius_furzeri
MKKFDVTQNGYFEHLELRLYPRNAEHLNIPDRHLKARFLHGDPFISGYLMTIMVVLGVGLSWGELWWRSGALLHLF----
>Esox_lucius-----MVVLGVGLSWGDCQWRVALLPFF----
>Acanthogobius_hasta-----MIMVVLGVGLSWGELWWRSGALLHLF----
>Apteronotus_leptorhynchus-----MMVFGVGLSWGELWWRSGALLLVL----
>Lutjanus_erythropterus-----MVVLGVGLSWGELWWRSGALLHLF----
>Plecoglossus_altivelis-----MVVLGVGLSWGELWWRSGALLHLF----
>Scleropages_formosus-----MVVLGVGLSWGELWWRSGALLLFF----
>Lateolabrax_japonicus-----MVVLGVGLSWGELWWRSGALLHLF----
>Sebastes_caurinus-----MVVLGVGLSWGELWWRSGALLHLF----
>Cynoglossus_semi-laevis-----MLSNCRAEVGSLHGEYFIVRYLTIIMVVLGVGLSWGELWWRSGALLHLF----
>Oncorhynchus_kisutch-----MMVLVVGLSWVEWWRSGALLHLF----
>Lepisosteus_oculatus-----MVVLGVGLSWGELWWRSGAL-----
>Trichomycterus_areolatus-----MSVIGVDLSWVEWWRSGALLLVF----
>Takifugu_rubripes
MNTFDVTQNDFFTHLDITFFLGNAAVHLTSLDCHPEVRFHGEYFILGYLTIIMVVLGVGLSWGELWWRSGALLHLF----

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>Danio_rerio	-----MAEKTDASSEDKRENCs-----VAEEAT
>Channa_punctata	-----MADRTECSIEDGSWDNFC-----VAEEAT
>Micropterus_floridanus	-----MADRTECSTEDGSWDSFC-----VAEEAT
>Pygocentrus_nattereri	-----MAVKMDPALEERSRHQVS-----VAHEAT
>Pundamilia_nyererei	-----MPGRTEYSPEDRSWDGFC-----VAEEAT
>Clupea_harengus	-----MAEKTDAMEDRSWDNVS-----VTEEAK
MRRTPERRYRGAGLHSLSCFPSSLTRYDALAQRNRTLLISPPTMAEKTDTAMEDKSWDNLp-----VAEEAT	
>Esox_lucius	-----MAEKTDAMEDRSWDNVS-----VTEEAK
>Apteronotus_leptorhynchus	-----MAENTDTAIEDKSRDNVF-----VADEAT
>Plecoglossus_altivelis	-----MAEKTDATMEDSSWDNFS-----VAEEAT
>Scleropages_formosus	-----MAEKTDAPAEDRSWDNLNFTVAEEAT
>Notothenia_coriiceps	-----MAERTESSTEDGSWDSFC-----VAEEAT
>Salmo_salar	-----MAEKTDAMEDRSWDNFS-----AAKEAK

HG0101 ENSG00000099250 NRP1

>Homo_sapiens
MARAVAPRGTSVGKGRGSRs
>Apteryx_australis_mantelli
MVGAVAPGEGTSVGKGRGSLs
>Odobenus_rosmarus_divergens
MARAVAPRGTSVGKGRGNRS
>Orcinus_orca
MARAVAPRGTSVGKGRGNRS
>Calidris_pugnax
MAGAAAPGEGTSVGKGRGSRs
>Rousettus_aegyptiacus
MARAVAPRGTSVGKGRGNRS
>Dasypus_novemcinctus
MARAVAPRGTSVGKGRGNRS
>Monodelphis_domestica
MARAAALSGGTSVGKGRGNRS
>Aquila_chrysaetos_canadensis
MAGAAAPGEGTSVGKGRGSRs
>Coturnix_japonica
MAGAAALGAGTSVGKGRGSRs
>Condylura_cristata
MARAVAPRGTSVGKGRGNRS
>Oryctolagus_cuniculus
MARAVAPRGTSVGKGRGSRs
>Elephantulus_edwardii
MARAVAPRGTSVGKGRGNRS
>Ornithorhynchus_anatinus
MARAASSRGTSVGREIGNRS
>Geospiza_fortis
MARAAPGEGTSVGKGRGSRs
>Ceratotherium_simum_simum
MARAVAPRGTSVGKGRGNRS
>Manis_javanica
MARAVAP-----
>Loxodonta_africana
MARAVALRGTSVGKGRGNRS
>Melopsittacus_undulatus
MAGAAAPGEEtsVGKKGKGNRS
>Microtus_ochrogaster
MARAVAPRGTSVGKGRGNRS
>Tupaia_chinensis
MARAVAPRGTSVGKGRGNRS
>Lepisosteus_oculatus
-MATPAPRGTSVGKGRGNQs
>Aptenodytes_forsteri
--MAGAPGEGTSVGKGRGSRs
>Anolis_carolinensis
MAKAVTPKGTSVGKGRGNWS
>Struthio_camelus_australis
MVGAVAPGEGTSVGKGRGSRs
>Pelodiscus_sinensis
MAGAATPGKATVGKGRGNQs

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>Homo_sapiens
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVLSPrVQVK
>Acipenser_sinensis
-----MISNRRHPhLTrAPiHQOT----HRIDVTLTSEAALPhTQA-
>Anser_cygnoides
MLAPCKAAVLGLKFQHGRCGSSSLQKLGMISNHRHLHLTrAPiHQOT----HRIDATLTyrVLPNLOVK
>Apteryx_australis_mantelli
-----MISNHRHLHLTrAPiHQOT----RRIDATLTyrVLPNLOVK
>Acinonyx_jubatus
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVFAPrVQVK
>Physeter_catodon
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVFAPrVQVK
>Calidris_pugnax
-----MISNHRHLHLTrAPiHQOT----HRIDATLTyrVLPNLOVK
>Rousettus_aegyptiacus
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVFAPrVQVK
>Dasypus_novemcinctus
-----MISNHRHLHLTrASIHQOT----HRIDATLTyrVLARrVQVK
>Alligator_mississippiensis
MLAPCKAAVLGLKFQHGRCGSSSLQKLGMISNHRHLHLTrAPiHQOT----HRIDAILTyrVLIpNLOVK
>Galeopterus_variegatus
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVLAPrVQVK
>Gallus_gallus
MLAPCKAAVLGLKFQHGRCGSSSLQKLGMISNHRHLHLTrAPiHQOT----HRIDAALTyrVLEpNLOVK
>Apterionotus_leptorhynchus
-----MVSNRMHLRLTRTTiHQR-----NRIDVALTSEVILSYTQV-
>Ochotona_princeps
-----MISNKHHLHLTLASIHQOT----QRIDATLTyrVLPAPrVQVK
>Ornithorhynchus_anatinus
-----MISNHRHLHLTrAPiHQOT----HRIDATLTyrVPGPrIQVK
>Scleropages_formosus
-----MVSNKGHPRLTRAaVHQKKIQHSGIDVTLTCEAALSHTQV-
>Manacus_vitellinus
-----MISNHRHLHLTrAPiHQOT----HRIDATLTyrVLPNLOVK
>Equus_asinus
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVFAPrVQVK
>Manis_javanica
-----MISNHRHLHLTrASIHQOT----HRIDATLTyrVFAPrVQVK
>Ictidomys_tridecemlineatus
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVLPAPrVQVK
>Tupaia_chinensis
-----MISNHRHLHLTLASIHQOT----HRIDATLTyrVLPAPrVQVK
>Lepisosteus_oculatus
-----MISNRRHPhLTLAPiHQOT----YRIDVTLTSEAALPhTQA-
>Trichechus_manatus_latirostr
-----MISNHRHLHLTrASIHQOT----HRIDATLTyrVLPPrVQVK
>Struthio_camelus_australis
-----MISNHRHLHLTrAPiHQOT----PRIDATLTyrVLPNLOVK
>Chrysemys_picta
MLAPCKAAVLGLKFQHGRCGSSSLQKLGMISNHRHLHLTrAPiHQOT----QRIDATLTyrVLPNLOVK
>Tinamus_guttatus
-----MISNHRHLHLTrAPVHQOT----RRIDATLTyrVLLPNLOVK

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>Homo_sapiens	-----MPFETIFSSCLMSTA-
>Canis_lupus_familiaris	-----MPFETVFSSCLMSTAW
>Orcinus_orca	-----MPFEPVCSSCLRSTAW
>Rousettus_aegyptiacus	-----MPFETVFSSCLMSTSW
>Dasypus_novemcinctus	-----MPFDTIFSSCLTSTA-
>Sorex_araneus	-----MPFETVFSSCLMSTAW
>Oryctolagus_cuniculus	-----MPFETIFSACLMSTA-
>Equus_asinus	-----MPFETVFSSCLMSSAW
>Manis_javanica	-----MPFETVSSCLMSTVW
>Loxodonta_africana	-----MPFEATFSICLMSAAC
>Octodon_degus	-----MPFETVFSSCLMSTA-
>Tupaia_chinensis	-----MPFATIFSSCLMSTV-
>Trichechus_manatus_latirostr	
MRTFYIFFFSLSPPPTRLCKNVPCLIEVISLDFDHNYLFFHVRSWGQLSGEEMPFEATIFSICLMSTAC	

HG0103 ENSGALG00000016558 VEGFD

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>Gallus_gallus
-----MHFKRDASSCMTTTA
>Anser_cygnoides
MTEKLESFLVIGDREMHFKRDASSCVTTTA
>Chaetura_pelagica
-----MHFETDTSSCMTTTA
>Apteryx_australis_mantelli
-----MHFKTATSSCMTTV
>Buceros_rhinoceros_silvestrii
-----MHFETDASIGMTTTA
>Cariama_cristata
-----MHFETDASSCMTTTA
>Charadrius_vociferus
-----MHFETDASSCMTTTA
>Pterocles_gutturalis
-----MHFETDASSCMTTTA
>Colius_striatus
-----MHFKTDVSSCMTTTA
>Columba_livia
-----MHFETDTSSYMTTTA
>Merops_nubicus
-----MHFETDASSCMTTTE
>Alligator_mississippiensis
-----MHFKTDSSSCTIISTA
>Cuculus_canorus
-----MHFETDASSCVMTTA
>Aquila_chrysaetos_canadensis
-----MHFETDASSCMTTTA
>Mesitornis_unicolor
-----MHFKTDASSCMTTTA
>Ornithorhynchus_anatinus
-----MHFERDSSSCTIISTA
>Tauraco_erythrolophus
-----MHFKTDACSCMTTTA
>Opisthocomus_hoazin
-----MHFKTDASSCMTTTA
>Lepidothrix_coronata
-----MHFETDASSCMTTTA
>Egretta_garzetta
-----MHFETDASSCMTTTA
>Melopsittacus_undulatus
-----MHFETDASSCMTTSA
>Aptenodytes_forsteri
-----MHFETDASSCMTTTA
>Struthio_camelus_australis
-----MHFETDASSCMTITA
>Chelonia_mydas
-----MHFETEPSSCMISTA
>Apaloderma_vittatum
-----MHFKTDASSCMTLTA
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>Gallus_gallus	-----MMREAWVRLFPSPCS
>Anas_platyrhynchos	-----MMREAWVRLFPSPCS
>Chaetura_pelagica	-----MREVDRLFPSPCS
>Cariama_cristata	-----MREVVRLFPSPCS
>Charadrius_vociferus	-----MREVVRLFPSPCS
>Colius_striatus	-----MREVVLLFPSPCS
>Columba_livia	-----MREVRVRLFPSPRS
>Merops_nubicus	-----MREVGRLFPSPCS
>Sarcophilus_harrisii	-----MRDFGVLLFPSPCS
>Monodelphis_domestica	-----MGNPR-----PREGKLCVSRLFMMRDFGILLFPSPCS
>Trichosurus_vulpecula	-----MRDFGILLFPSPCS
>Haliaeetus_leucocephalus	-----MREVVRLFPSPCS
>Gavia_stellata	-----MREVVRLFPSPCS
>Balearica_regulorum_gibberic	-----MREVVRLFPSPCS
>Tauraco_erythrolophus	-----MREVWAQLFPSPRS
>Sturnus_vulgaris	-----MREVVRLFPSPCS
MVVPSGKPVVRAGNPVGNHOGVTELVIPGQPTVSSSAMLCVLSPOAPSVSHLSRMREAVRLSPSPCS	
>Phalacrocorax_carbo	-----MREVVRLFPSPCS
>Fulmarus_glacialis	-----MREVVRLFPSPCS
>Melopsittacus_undulatus	-----MREVVRLFPSPCS
>Aptenodytes_forsteri	-----MPAAVRCFLSPQAPSVSHLSRMREVVRLFPSPCS
>Anolis_carolinensis	-----MRQGVVHFFSPCS
>Tyto_alba	-----MREVVVRFSPCS
>Chelonia_mydas	-----MMTEVWALLFPSPCS
>Calypte_anna	-----MREVVVGLSPSPCS
>Apaloderma_vittatum	-----MREVVRLFPSPCS

```
>Homo_sapiens
-----MLVLK-----QKSSLQSLSKNKSRRPFMMRDLTLLSPVCS-
>Leptonychotes_weddellii
-----MMKDFETLLPPLCSW
>Lipotes_vexillifer
-----MMRHLGTLLSPLCS-
>Miniopterus_natalensis
-----MMKEFGMLLYPLCSW
>Condylura_cristata
-----MMKVLGALLSPLCNW
>Oryctolagus_cuniculus
MPSAGSVAPALGAPRRSERRARRSRAAGGGRTGPSRGGRGAGPFMMRDLGAFLLSPLCSR
>Ceratotherium_simum_simum
-----MMKDFGTLLSPPCSW
>Manis_javanica
-----MMKDFGMLLPLLCSW
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>Homo_sapiens	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Anser_cygnoides	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
MWLDLVDPEPKLLFSLGGVCVCRAGVFSRFLSSAAFFNLGFEPEPGKMGNGASDRRGISPSLLLGRVPVVLVF-	
>Chaetura_pelagica	-----MNGASDRRGISPSLLLGRVPVVLVF-----
>Odobenus_rossmarus_divergens	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Lipotes_vexillifer	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Pteropus_alecto	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Dasypus_novemcinctus	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Galeopterus_variegatus	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Monodelphis_domestica	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Aquila_chrysaetos_canadensis	-----MNGDSARRGVSPSLLLGRVPVLGS-----
>Coturnix_japonica	-----MNGASDRRGISPSLLLGRVPVVLVF-----
>Condylura_cristata	-----MNGASDRRGISPSLVSGRVPVVLV-----
>Oryctolagus_cuniculus	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Parus_major	-----MNGASVRRGISPSLLLGRVPVVLVF-----
>Nipponia_nippon	-----MNGASDRRGISPSLLLGRVPVVLVF-----
>Equus_caballus	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Manis_javanica	-----MNGDWDRRGVSPSLLPGRVPALVS-----
>Loxodonta_africana	-----MNGDGDARRGVSPSLLLGRVAVLVS-----
>Ictidomys_tridecemlineatus	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Trichechus_manatus_latirostr	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
>Pygoscelis_adeliae	-----MNGASDRRGISPSLLLGRVPVVLVF-----
>Thamnophis_sirtalis	-----MNGDASARRGMSPCFLGHVLLVVLGSS-----
>Struthio_camelus_australis	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
MWLDLVDPEPKLLFSLGGVYVWRAGVFSRFLSSAAFFNLGFEPEPGKMGNGASDRRGISPSLLSGRVPVVLVF-	
>Chrysemys_picta	-----MNGASDRRGISPSLLLGRVPVVLVF-----
>Calypte_anna	-----MNGDWDRRGVSPSLLLGRVPVLVS-----
MWLDLVDPESKLLFSLGGVCVWRAGVFSRFLSSAFLNLGFEPEPGKMGNGASDRRGISPSLLLGRVPVVLVF-	

>Gallus_gallus
MWLDLADPEPELLFFRGAVGVREACGGYLAFFSLLLPFFFFFLLVGFEPGKMGNGASDRRGISPSLVSGRPVVLEV-
>Anser_cygnoides
MWLDLVDPEPKLFFSLGGVCVCRAG-----VFS--PRFLSSAAFFNLGFEPEPGKMGNGASDRRGISPSLLLGRVPVVLVF-
>Chaetura_pelagica
-----MNGASDRRGISPSLLLGRVPVVLVF-
>Leptonychotes_weddelii
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Orcinus_orca
-----MNGANDRRGVSPSLLLGRVPVLVS--
>Dasypus_novemcinctus
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Galeopterus_variegatus
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Monodelphis_domestica
-----MNGDSARRGVSPSLLLGRVPVLGS--
>Aquila_chrysaetos_canadensis
-----MNGASDRRGISPSLLLGRVPVVLVF-
>Condylura_cristata
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Ochotona_princeps
-----MNGGWERRGISPSLLLGRVPVLVS--
>Lepidothrix_coronata
MWLDLVDPEPKLFFLGGVYVWRAG-----IFS--LRFLSSAAFFNLGFEPEPGKMGNGASVRRGISPSLLLGRVPVVLVF-
>Nipponia_nippon
-----MNGASDRRGISPSLLLGRVPVVLVF-
>Manis_javanica
-----MNGANDRRGVSPSLLPGRVPALVS--
>Microcebus_murinus
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Loxodonta_africana
-----MNGDGARRGVSPSLLLGRVAVLS--
>Ictidomys_tridecemlineatus
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Trichechus_manatus_latirostr
-----MNGDWDRRGVSPSLLLGRVPVLVS--
>Pygoscelis_adeliae
-----MNGASDRRGISPSLLLGRVPVVLVF-
>Thamnophis_sirtalis
-----MNDASARRGMSPCLFLGHVLVVLGSS
>Struthio_camelus_australis
MWLDLVDPEPKLFFLGGVYVWRAG-----VFS--LRFSSAAFFNLGFEPEPGKMGNGASDRRGISPSLLSGRPVVVLVF-
>Pelodiscus_sinensis
-----MNGASDRRGISPSVLGRVPVVLVF-
>Calypte_anna
MWLDLVDPEKLLFFLCGVCVWRAG-----VFS--LRFLSSTAFLNLGFEPEPGKMGNGASDRRGISPSLLLGRVPVVLVF-

>Homo_sapiens	MEQTGPMRERES
>Pseudacris_regilla	MEQTGPMRERES
>Canis_lupus_familiaris	MEQTGPMRERES
>Hynobius_retardatus	MDQTGPMRERES
>Balaenoptera_acutorostrata_s	MEQSEGPMRERES
>Calidris_pugnax	MEQTGPMRRRES
>Miniopterus_natalensis	MEQTGPMRERES
>Latimeria_chalumnae	MEQTGPMRKRES
>Sarcophilus_harrisii	MEQTGPMRERES
>Galeopterus_variegatus	MEQTGPMRERES
>Aegypius_monachus	
MRRGALRAPLGARRKGSHPARRGRRRPRRPLSPLGWVDAAGAVRMEQTGPMRKRES	
>Gallus_gallus	MEQTGPMRKRES
>Condylura_cristata	MEQTGPMRERES
>Oryctolagus_cuniculus	MEQTGPMRERES
>Elephantulus_edwardii	MEQTEVPMREREN
>Ornithorhynchus_anatinus	
MRLRPAPAPS-----PSAPGSSCGPTLLRAPVSLGSHRHGRGVRMEQTGPMRERES	
>Lepidothrix_coronata	MEVTEGPMRKRES
>Geraotherium_simum_simum	MEQTGPMRERES
>Manis_javanica	MEQTGPMRERES
>Ictidomys_tridecemlineatus	MEQTGPMRERES
>Lepisosteus_oculatus	MEHAEGPVRERES
>Trichechus_manatus_latirostr	MEQTGPMREREN
>Takydromus_sexlineatus	MEQTDGPMRKRES
>Chrysemys_picta	MEQTDGPMRERES
>Orycteropus_afer_afer	MEQTGPMREREN

HG0107.1 ENSG00000058668 ATP2B4

>Homo_sapiens
MHILFTPSSGGVGLS
>Chaetura_pelagica
MHILFTPLSGEVGLG
>Ailuropoda_melanoleuca
MHILFTPSSGGVGLS
>Balaenoptera_acutorostrata_s
MHILFTPSSGGVGLS
>Charadrius_vociferus
MHILFTPLSGEVGLG
>Gallorhinchus_millii
MHFLTPSSGGVGLS
>Rhinolophus_ferrumequinum
MHILFTPSSGGVGLS
>Dasypus_novemcinctus
MHILFTLQSGGVGLS
>Latimeria_chalumnae
MHFLFTPLSGEVGLG
>Columba_livia
MHILFTPLSGEVGLG
>Alligator_mississippiensis
MHILFTPLSGEVGLG
>Galeopterus_variegatus
MHILFTPSSGGVGLS
>Aquila_chrysaetos_canadensis
MHILFTPLSGEVGLG
>Gallus_gallus
MHILFTPSSGGLGLG
>Condylura_cristata
MHILFTPSSGGVGLS
>Ornithorhynchus_anatinus
MHILFTPSSREVGLG
>Lepidothrix_coronata
MHILFTPLSGEVGLG
>Equus_asinus
MHILFTPSSGGVGLS
>Nestor_notabilis
MHILFTPLSGEVGLG
>Ictidomys_tridecemlineatus
MHILFTPSSGGVSLN
>Tupaia_chinensis
MFILFTPSSGGVGLS
>Pygoscelis_adeliae
MHILFTPLSGEVGLG
>Gekko_japonicus
MCILFTPSSEEVGLG
>Chrysemys_picta
MHILFTPLSGEVGLS

>Gallus_gallus
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>Anser_cygnoides
MRILFTPSSGGGLG
>Chaetura_pelagica
MHILFTPLSGEVGLG
>Ailuropoda_melanoleuca
MHILFTPPSGQVGLS
>Balaenoptera_acutorostrata_s
MHILFTPPSGQVGLS
>Gallidris_pugnax
MHILFTPLSGEVGLG
>Rhinolophus_ferrumequinum
MHILFTPPSGQVGLS
>Latimeria_chalumnae
MHILFTPLSGEVGLG
>Columba_livia
MHILFTPLSGEVGLG
>Alligator_sinensis
MHILFTPLSGEVGLG
>Galeopterus_variegatus
MHILFTPSSGQVGLS
>Aquila_chrysaetos_canadensis
MHILFTPLSGEVGLG
>Condylura_cristata
MHILFTPPSGQVGLS
>Ornithorhynchus_anatinus
MHILFTPSRREVLG
>Ficedula_albicollis
MHILFTPSSPQLGLG
>Equus_asinus
MHILFTPPSGQVGLS
>Cebus_capucinus_imitator
MHILFTPPSGQVGLS
>Nestor_notabilis
MHILFTPLSGEVGLG
>Ictidomys_tridecemlineatus
MHILFTPPSGQVSLN
>Pygoscelis_adeliae
MHILFTPLSGEVGLG
>Gekko_japonicus
MCILFTPSSEEVGLG
>Chrysemys_picta
MHILFTPLSGEVGLS

>Homo_sapiens	-----MIDMEKLVMGORSRYFSGKCC
>Odobenus_rosmarus_divergens	-----MIDMKKLVMGORSRYFSGKCC-
>Lipotes_vexillifer	-----MTDRKKLVMGORSRYFSGKCC-
>Pteropus_vampyrus	-----MIDMRKLIMGORSRYFSGKCC-
>Dasypus_novemcinctus	
MRREPSPRSRLLSVTGPRPFFSFLSPSENGSCYRARYVHLMIDMKKLVMGORSRHFLGKSCC	
>Galeopterus_variegatus	-----MGORSRYFSGKCCY
>Monodelphis_domestica	-----MGSSRDHLHGKCC-
>Condylura_cristata	-----MIDVKKLVMGORSRYFSGKCC-
>Oryctolagus_cuniculus	-----MIEMKKQVMGORSRYFSGKCC
>Elephantulus_edwardii	-----MIDRKKLVMGORSRYFSGKCC
>Ceratotherium_simum_simum	-----MIDRKKLVMGORSRYFSGKCC-
>Manis_javanica	-----MIDTKKLVMGORSRYFSGKCC-
>Loxodonta_africana	-----MHLMIDMKKLVMGORSRYFSGKCC
>Cavia_porcellus	-----MIDMKKQVMGORSRYFSGKCC
>Tupaia_chinensis	-----MIDMKKLVMGOKSRYFSEKCCY
>Orycteropus_afer_afer	-----MHLMIDMKKLVGHMSRYFSGKCC

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>Gallus_gallus
-----MGRPORYLSKMGLLLG
>Anas_platyrhynchos
-----MGRPORYLSRRGLLLG
>Caprimulgus_carolinensis
-----MGDAERYLSRWGLLLR
>Calidris_pugnax
-----MGQPORYLSRGLLLG
>Colius_striatus
-----MGQPORYLSRRGLLE
>Columba_livia
-----MGQPORYLSRRGLLLG
>Merops_nubicus
-----MGPPORYLSRRGLLLG
>Cuculus_canorus
-----MGQPORYLSRRGLLLG
>Aquila_chrysaetos_canadensis
-----MGQPORYLSRRGLLLG
>Eurypyga_helias
-----MGQPORYLSRRDLLG
>Tauraco_erythrolophus
-----MGQPORYLSRRDLLG
>Opisthocomus_hoazin
-----MGQPORYLSRRGLLLG
>Corvus_brachyrhynchos
-----MGQPORYLSRRGLLLG
>Nipponia_nippon
-----MGQPORYLSRRGLLLG
>Fulmarus_glaucialis
-----MGQPORYLSRRGLLLG
>Nestor_notabilis
-----MGQPORYLSRRGFLG
>Aptenodytes_forsteri
-----MGQPORYLSRGLLLG
>Tyto_alba
-----MGQPORYLSRRGLLLG
>Struthio_camelus_australis
MPFGLGTELTMGQHORYISRWGLLLG
>Tinamus_guttatus
MPFGLGTELTAMGQHORYLSRRGLLLG
>Calypte_anna
-----MGQPERFLSRRGLLLG
>Apaloderma_vittatum
-----MGQPORYLSRRGLLLG

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HG0107.3 ENSDARG00000063433 atp2b2

>Danio_rerio
MGNHVWSDAGLQPIW
>Acipenser_sinensis
MGNCTWSEAGLQP-
>Channa_argus
MGSHTWRSGLQPIW
>Menidia_menidia
MGSHTWSSGSLQPIW
>Porichthys_notatus
MGSHTWMSGSLQPIW
>Oryzias_latipes
MGSHTWSSGSLQPIW
>Micropterus_salmoides
MGNHTWSSGSLQPIW
>Pygocentrus_nattereri
MGNHVWSDAGLQPIW
>Haplochromis_burtoni
MGSHTWSSGSLQPIW
>Austrofundulus_limnaeus
MGSHTWSSGSLQPIW
>Lateolabrax_japonicus
MGSHTWSSGSLQPIW
>Platichthys_stellatus
MGSHTWSSGSLQPIW
>Lepisosteus_oculatus
MGNYTWSGAGLQP-
>Ictalurus_punctatus
MGNVWSDAALQPR

HG0107.3 ENSG00000157087 ATP2B2

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>Homo_sapiens
-----MPVPGSSMGPTWRLLGLQP
>Canis_lupus_familiaris
-----MPAPGSSMGPTWRLLGLQP
>Lipotes_vexillifer
-----MPAPGSSMGPAEWRLGLQP
>Myotis_davidii
-----MPAPGSSMGPTWRLLGLQP
>Dasypus_noveboracensis
-----MSAPGSSMGPAEWRLGLQP
>Condylura_cristata
-----MGPTWRLLGLQP
>Oryctolagus_cuniculus
-----MPALGSSMGPTWRLLGLQP
>Equus_asinus
-----MQAPGSSMGPTWRLLGLQP
>Manis_javanica
MILGATTDPDHVDASGSSMGPTWRLLGLQP
>Nannospalax_galili
-----MPAPGSSMGPTWRLLGLQP
>Tupaia_chinensis
-----MGPTGWRLGLQP
>Trichechus_manatus_latirostris
-----MPALGSSMGATEWRLLGLQP
>Orycteropus afer
-----MPALGNSMGATEWRLLGLQP
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HG0107.4 ENSG00000070961 ATP2B1

>Homo_sapiens
MSVWFKKDFHI
>Mustela_putorius_furo
MSVWFKKDFHI
>Balaenoptera_acutorostrata_s
MSVWFKKDFHI
>Rousettus_aegyptiacus
MSVWFKKDFHI
>Galeopterus_variegatus
MSVWFKKDFHI
>Condylura_cristata
MSVWLKKDFHI
>Ceratotherium_simum_simum
MSVWFKKDFHI
>Loxodonta_africana
MSVWFKEDFHI
>Mus_musculus
MSVWFKEDFHI
>Tupaia_chinensis
MSVWFKKDFHI
>Trichechus_manatus_latirostr
MSVWFKEDFHI


```

>Gallus_gallus
-----MKEETDWDLKAPTSS
>Anas_platyrhynchos
-----MKEEIDWELKARASS
>Apteryx_australis_mantelli
-----MKEEIDWESKARTSS
>Buceros_rhinoceros_silvestri
-----MKEETDWKSKAQTGS
>Cariama_cristata
-----MKEEIVWKLKARTSS
>Calidris_pugnax
-----MKEEIDWELKARTSS
>Colius_striatus
-----MKEEIDWKLKAQTSS
>Columba_livia
-----MKEETDWKLKARTGS
>Merops_nubicus
-----MKEEIDWELKAQTS-
>Alligator_mississippiensis
-----MKAETDWEFKARTRS
>Cuculus_canorus
-----MKEESDWELKARTSS
>Falco_cherrug
-----MKEEIDWELKARTSS
>Gavia_stellata
-----MKEEIDWELKVRTSS
>Eurypyga_helias
-----MKEETDWELKARASS
>Tauraco_erythrolophus
-----MKEEIDWKLKARTSS
>Opisthocomus_hoazin
-----MKEEVDWELKGRSS
>Corvus_cornix_cornix
-----MKEEIGWDLRAQTSS
>Phaethon_lepturus
-----MKEEIDWELKARTSS
>Nestor_notabilis
-----MKEETDWELKAQTS
>Aptenodytes_forsteri
-----MKEEIDWELKARTSS
>Takydromus_sexlineatus
MLIAIVTQILNCLYLTPLSMREETDWLEAGTSS
>Tyto_alba
-----MKEEIGWKLKARTSS
>Pelodiscus_sinensis
-----MREETDWEFKARTRS
>Tinamus_guttatus
-----MKEEVDWESKARTSS

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HG0108.2 ENSG00000135090 TAOK3

>Homo_sapiens
-----MNL SNMEYFVPHTKRY
>Acinonyx_jubatus
MOKTEVLKEDKGFAAKMNL SNTVYFVPFKRY
>Balaenoptera_acutorostrata_s
-----MSL SNTVYFVPYTKRY
>Eptesicus_fuscus
-----MNL SNAVYFVPYTKRY
>Condylura_cristata
-----MNL SNTVHFVPYTKRC
>Oryctolagus_cuniculus
-----MNL SNPVHFLPHTKRY
>Equus_asinus
-----MNL SNTVYFVPYTKRY
>Manis_javanica
-----MNL RNTVYFVPYTKRY
>Marmota_marmota_marmota
-----MNL SNTAHFVPHTKRY
>Tupaia_chinensis
-----MNL SNT-NFVPHTKRY
>Trichechus_manatus_latirostr
-----MNL SNTVYFVPCTKRC

HG0108.3 ENSDARG00000098304 taok1b

>Danio_rerio
MSNQRGLTCRSRTAR
>Pygocentrus_nattereri
MSHQRGLARRSRTAR
>Ictalurus_punctatus
MSHHRGLACRSRTAR

```

>Homo_sapiens
MNGSHRQTSDCSHLQAFKKGEGVLPFGYSGEALQSSHCA
>Anser_cygnoides
-----MLLFDLSQGEELQSSHCA
>Chaetura_pelagica
-----MLLFDLSQGEELQSSHCA
>Ursus_maritimus
-----MLLFDLSQGEALQSSHCAF
>Charadrius_vociferus
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>Myotis_lucifugus
-----MLLFDLSQGEALQSSHCAF
>Columba_livia
-----MLLFDLSQGEELQSSHCA
>Alligator_sinensis
-----MLLFDLSQGEELQSSHCA
>Cuculus_canorus
-----MLLFDLSQGEELQSSHCA
>Galeopterus_variegatus
-----MLLFDLSQGEALQSSHCA
>Aquila_chrysaetos_canadensis
-----MLLFDLFGGEELQSSHCA
>Coturnix_japonica
-----MLLFDLSQGEELQSSHCA
>Condylura_cristata
-----MLLFDLSQGEALQSSHCA
>Lepidothrix_coronata
-----MLLFDLFGGEELQSSHCA
>Nipponia_nippon
-----MLLFDLFGGEELQSSHCA
>Equus_asinus
-----MLLFDLSQGEALQSSHCAF
>Picoides_pubescens
-----MLLFDLSQGEELQSSHCA
>Melopsittacus_undulatus
-----MLLFDLFGGEELQSSHCA
>Marmota_marmota_marmota
-----MLLFDLSQGEALQSSHCA
>Struthio_camelus_australis
-----MLLFDLSQGEELQSSHCA
>Chelonia_mydas
-----MLLFDLSQGEELQSSHCA
>Tinamus_guttatus
-----MLLFDLSQGEELQSSHCA
>Calypte_anna
-----MLLFDLSQGEELQSSHCA
>Orycteropus_afer_afer
-----MLLFDLSQGEALQSSHCA

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>Homo_sapiens
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>Mustela_putorius_furo
-----MIFFILNMICYANAACDSLKSI CYHEAKGRWDFRITGRVREACGFVIRHH--FAHCHTARGSVCALCLLWPPSSLVPSPTPCRHS-----DPLPKWLHNSRSSAV-----
>Hynobius_retardatus
-----MIWYANAACDSLKSI CYQPAKRDHWDYRITGRVREACGFVIRHH--LHTAATCEGLAACLCVCVPE-----
>Tursiops_truncatus
-----MIFFILNMICYANAACDSLKSI CYHDAKGRWDFRITGRVREACGFVIRHH--FAHCHTARGSVCAPCLVWPPSSFPPPPAPPLRP-----A--PKVASQ-----
>Myotis_brandtii
MQHIFIGWGEKNFPQSCYEIQLRFMIFFIILNMICYANAACDSLKSI CYREAGRGRWDFRIMGRVREACGFVIRHR--FAHRHPARGL--SVCAASRLAALVPSPTPCRHS-----DPLPKWLHNSRSSSGVGCAPGPPSS
>Galeopterus_variegatus
-----MIFFILNMICYANAACDSLKSI CYQEAKRGLWDFRITGRVREACGFVIRHY--FAHCHTARGSVCV--CAVSCLAVLLPSPPPPCRHS-----DPLPKWLHNSRSSAV-----
>Oryctolagus_cuniculus
-----MIFFILNMICYANAACDSLKSI CYQEAKGGRWDFRITGRVREACGFVIRHR--FAHRHTARGSVCAPCLVWQPSPPPH--PLPPLRP-----A--PKVASQ-----
>Loxodonta_africana
-----MWLCHSPSFCTLPHCEGL--RVCAVSRLAVLIPSPTLRRHS-----DPLPKWLHNSRSSAV-----
>Ctenomys_sociabilis
-----MTFFILNMICYANAACDSLKSI CYQEAKGRWDFRIAGRVREACGFVIRHH--FAHCHAAARGSVCALCLVRPPSSLPPPPASTPTLSQSGFTVVDPQWWRCLRTRSTLEPN-----
>Trichechus_manatus_latirostr
-----MWLCRSPSFCTLPCEGL--RVCAVSLAVLIPSPTLRRHS-----DPLPKWLHNSRSSAV-----
>Orycteropus_afer_afer
-----MWLCHSPSFCTLPHCEGL--LVRALSRLAVLFPSPTPRRH-----

>Homo_sapiens
-----MYACLDGPEKPNLRNLPMYRTSQLRGSH-----
>Canis_lupus_familiaris
-----MCACLDGPEKPNLRNLPMYRTNQLKGFLLIRRL-----
>Orcinus_orca
-----MCACLDRPEKPSLRELPMYRTNPLKGFLLICRL-----
>Rousettus_aegyptiacus
-----MCACLDGPEKPNLRNLPMYRTNQLKGFLLICRL-----
>Dasypus_novemcinctus
-----MCACSDGPAKPNLRKLPMYRTNQLKGVLLICRL-----
>Galeopterus_variegatus
-----MG-EVRVRLLRGPEQPNLRNLPMHRPNQLKGFPLICRLSVNFVIFQEKRYKAATVTERPPPTISLN
>Monodelphis_domestica
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>Oryctolagus_cuniculus
-----MCACLDGPGKPNLRNLPMHRTSQRKGFSLICRL-----
>Elephantulus_edwardii
-----MYRTNQLKGVSLICRL-----
>Equus_asinus
-----MCSCLDGPEKPNLRNLPMYRTNQLKGSY-----
>Manis_javanica
-----MGEVHMQLLR-PARKAKHRKLPMYRTNQLKGFLLICRL-----
>Cavia_porcellus
-----MFRTNQLKGFSLICRL-----
>Tupaia_chinensis
-----MRCMCACLDGPEKPNLRISAYVONKSAE-GVLINLPSVNFVLFQEKRYKAASVLTEQPPPVSLN
>Trichechus_manatus_latirostr
-----MCACLNRPAPKPNLRNLPMYRTNQLKGVLLFCRL-----
>Orycteropus afer afer
-----MYRTNQLKGVLLICRL-----

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>Homo_sapiens
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>Anas_platyrhynchos
MPPTSCSIIFTQ
>Chaetura_pelagica
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>Canis_lupus_familiaris
MPPTFCFSVFIFTQ
>Orcinus_orca
MPPTFCSSVFIFTQ
>Myotis_brandtii
MPPTFCSSVFIFTQ
>Columba_livia
MPPTSCSIIFTQ
>Cuculus_canorus
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>Falco_cherrug
MPPTSCSIIFTQ
>Gallus_gallus
MPPTSCSIIFTQ
>Condylura_cristata
MPPTFCSSVFIFTQ
>Ochotona_princeps
MPPTFCSSVFIFTQ
>Opisthocomus_hoazin
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>Corvus_cornix_cornix
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>Egretta_garzetta
MPPTSCSIIFTQ
>Ceratotherium_simum_simum
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>Loxodonta_africana
MPPTFCSSVFIFTQ
>Melopsittacus_undulatus
MPPTSCSIIFTQ
>Ictidomys_tridecemlineatus
MPPTFCSSVFIFTQ
>Tupaia_chinensis
MPPTFCSSVFIFTQ
>Aptenodytes_forsteri
MPPTSCSIIFTQ
>Struthio_camelus_australis
MPPTSCSIIFTQ
>Calypte_anna
MPPTSCSIIFTQ

>Danio_rerio
---MRSVLIPAI-FCTKVISRNDKTSFFSLSPPSSN---RSQASVVCSTT---KKQTLL---NALRNTETPRLTSA
>Oryzias_latipes
MKHMRTTELITAI-FQKRLISRNDPKSFFFSITRSHFLFLAR---S---DTRLIGCFASKFLYC---L---
>Odobenus_rosmarus_divergens
MKHMRTTELITAI-FQKRLISRKIQRLFF-LFT-HQLPLPARPLRPLQPP---PPPPPPPPQGRS---RRRRLLLCIPITA---
>Ambystoma_mexicanum
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>Astatyx_mexicanus
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>Neolamprologus_brichardi
---MRTTELITAI-FQKRLISRNDPKSFFFSITRSHFLFLAP---S---NTRLIACFASKFLYC---L---
>Latimeria_chalumnae
MKHMRTTELITAI-FQKRLISRKIQRLFF-LFN-HQISLPLPLSLQ---HRHIACFASKLFVTFSLLLFFANSLPNNNALPILNOTDPKELPSIDL---
>Nothobranchius_furzeri
MKHMRTTELITAI-FQKRLISRNDPKSFFFSITRSHFLFLAP---S---NTRLIACFASKFLYC---L---
>Notothenia_coriiceps
MKHMRTTELITAI-FQKRLISRNDPKSFFFSITRSHFLFLAP---S---NTRLIACFASKFLYC---L---
>Salmo_salar
MKHMRTTELITAI-FQKRLISRNDPKSFF-LFN-HQISLPLPRSL---
>Lepisosteus_oculatus
MKHMRTTELITAI-FQKRLISRNDPKSFFSFQS-PDLTFTSSSLPLTQDT---SPALHP---NYFYIPFTTNTS---FFYTPQQQ---
>Takifugu_rubripes
MKHMRTTELITAI-FQKRLISRNDPKSFFFSITRSHFLFLAR---S---NTRLIACFASKFLYR---L---

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>Gallus_gallus
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>Anser_cygnoides
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>Caprimulgus_carolinensis
MEVISWGGPRALWARVLLSDHWLPPA
>Calidris_pugnax
MEVISWGGPRALWARVLLSDHWLPPA
>Pterocles_gutturalis
MEVISWGGPRALWARVLLSDHWLPPA
>Leptosomus_discolor
MEVISWGGPRALWARVLLSDHWLPPA
>Alligator_sinensis
MEVITGGPRALWAQVLLSDHWLPPA
>Cuculus_canorus
MEVISWGGPRALWAGVLLSDHWLPTA
>Aquila_chrysaetos_canadensis
MEVISWGGPRALWARVLLSDHWLPPA
>Gavia_stellata
MEVISWGGPRALWARVLLSDHWLPPA
>Balearica_regulorum_gibberic
MEVISWGGPRALWARVLLSDHWLPPA
>Tauraco_erythrolophus
MEVISWGGPRALWARVLLSDHWLPPA
>Opisthocomus_hoazin
MEVISWGGPRALWARVLLSDHWLPPA
>Lepidothrix_coronata
MEVISWGGPRALWARVLLSDHWLPPA
>Egretta_garzetta
MEVISWGGPRALWARVLLSDHWLPPA
>Melopsittacus_undulatus
MEVISWGGPRALWARVLLGDHWLPPA
>Aptenodytes_forsteri
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>Protobothrops_mucrosquamatus
-----MGGLRVLIWVRVLLNNHWLIAT
>Struthio_camelus_australis
MEVISWGGPRALWARVLLSDHWLPPA
>Chrysemys_picta
MEVISWGGPRALWARVLLSYHWLPPA
>Tinamus_guttatus
MEGMSWGGPRALWARVLLSDHWLPPA
>Calypte_anna
MEVISWGGPRALWAGVLLSDHWLPPA
>Apaloderma_vittatum
MEVISWGGPRALWARVLLGDHWLPPA

>Homo_sapiens	-----MKRSARGGHWRRSVT
>Anser_cygnoides	-----SARRGHWRKSAT
MC---KDT-ASWLSAKMYMLLVENEERTAKYPMADFRLR-----	
>Xenopus_laevis	-----MEMN-AGFLVPGVISDPSCFNRSDOGGHWRRNAT
>Ailuropoda_melanoleuca	-----M-----PRVGDN-HWIS-LHLSRSARGGHWRRSVT
>Calidris_pugnax	-----M-DFILRSARRGHWRKSAT
>Eptesicus_fuscus	-----MPRLLVETECRAAQPHMADCHQLRAPGHRKRFFPER-----SGVGDNWGFR-LKYLRSARGSHWRRSVT
>Columba_livia	-----M-DFILRSARRGHWRKSAT
>Poecilia_reticulata	-----M-GIHLTSRVEQPLFGHLTFPFRPPLTDRRPSRPPGRTASPCVTE-IRPSNFR-PSLGNTLSCLRFTRGGHWRRGVT
>Esox_lucius	-----MEDKQVVKTAUYETLVAQRHEIYQNKSLPYC-----VHETRFTQGGHWRRGVT
>Otornix_japonica	-----M-DFILRSARGHWRSSAT
>Erinaceus_europaeus	-----M-----CRR-----GS-CGNPRSARGSHWRRSIT
>Scleropages_formosus	-----MRKLHISHE-----LCGMELEHPKHVKRLAGQDFSLNKVITIYDLGEKFPPLRSTRGGHWRRGVT
>Sturnus_vulgaris	-----M-DFILRSARRGHWRKSAT
>Notothenia_coriiceps	-----MEKKQDLDMADGE-----EHEIQPSKFRASHALQDTLNCLRFTRGGHWRRGVT
>Equus_asinus	-----M-EFILRSARGGHWRRSVT
>Cynoglossus_semihaevis	-----MRKYCSV-----LCVRRQRKRFTRGGHWRRGVT
>Chinchilla_lanigera	-----M-EFILRSARGGHWRRSVT
>Salmo_salar	-----MA-----VDEILKRYEFCLNKSHPSYSLHEILPCHRFTRGGHWRRGVT
>Pygoscelis_adeliae	-----M-DFILRSARRGHWRKSAT
>Anolis_carolinensis	-----MCSCKRTQSLGCLMKMYTFWEENPARREKIHMAAGCHPSPVHWKIRFKDS-LSLEII-----LPGVGNARRSTRRGHWRNVIT
>Struthio_camelus_australis	-----MC---KDT-ASWLSAKMYTLVSEIEPRTAKYPMADYHHLREPVRKTPICLADRSLEQFS-----PTL-SDFKRSARRGHWRKSAT
>Takifugu_rubripes	-----MKREADLGMA-----ECTMHIEIQPSKFTPSLGARKTINCLRFTRGGHWRRGVT
>Tinamus_guttatus	-----M-DFILRSARRGHWRKSAT

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>Danio_rerio
-----MGGIAPAVAMVTGLCPGRL
>Acipenser_sinensis
-----MGSDAPCVAMVTGLCPGRL
>Polypedates_megacephalus
-----MVTGLFPGRL
>Porichthys_notatus
-----MERGRSRTAGHPMRVAAACVAMVTGLCPGRL
>Oryzias_latipes
-----MEYDAACVTMVTGLCPGRL
>Canis_lupus_familiaris
-----MVGVAAWVAMGTGLFPGRL
>Orcinus_orca
-----MGTGLFPGRL
>Haplochromis_burtoni
-----MGDDAACVTMVTGLCPGRL
>Dasypus_novemcinctus
-----MGTGLFPGRL
>Alosa_alosa
MSVRGVTKONGRFFCARGPMGAI GPAVTMVTGLCPGRL
>Latimeria_menadoensis
-----MVTGLFPGRL
>Austrofundulus_limnaeus
-----MEDAAACVTMVTGLCPGRL
>Falco_peregrinus
-----MGCVCGSVSMVTGLFPGRL
>Sorex_araneus
-----MGTGLFPGRL
>Ornithorhynchus_anatinus
-----MAGVAAWVAMGTGLFPGRL
>Trematomus_bernacchii
-----MVTGLCPRRRL
>Ceratotherium_simum_simum
-----MGTGLFPGRL
>Platichthys_stellatus
-----MASGRSRPAGHPMGDDAACVAMVTGCPGRL
>Callithrix_jacchus
-----MGTGLFPGRL
>Microtus_ochrogaster
-----MVGVAAWVAMGTGLFPGRL
>Tupaia_chinensis
-----MGTGLFPGRL
>Pelodiscus_sinensis
-----MGCVCGSVSMVTGLFPGRL
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>Gallus_gallus-----MGCVCGGVAMATGLFPGRLL
>Odorrana_margaretae-----MVTGLFPGRLL
>Canis_lupus_familiaris-----MVGVAANVAMGTGLFPGRLL
>Hynobius_retardatus-----MGGPPACAPSNRRRCMRVAMATGLFQGRLL
>Orcinus_orca-----MGTGLFPGRLL
>Pteropus_vampyrus-----MGTGLFPGRLL
>Dasypus_novemcinctus-----MGTGLFPGRLL
>Latimeria_chalumnae-----MVTGLFPGRLL
>Monodelphis_domestica-----MGTGLFPGRLL
>Falco_peregrinus-----MGCVCGSVSMVTGLFPGRLL
>Erinaceus_europaeus-----MEGEACPSRALPGRRRGRLRAGRPVGVAAANVAMGTGLFPGRLL
>Ochotona_princeps-----MGTGLFPGRLL
>Ornithorhynchus_anatinus-----MAGVAANVAMGTGLFPGRLL
>Ceratotherium_simum_simum-----MGTGLFPGRLL
>Cercopithecus_atys-----MGTGLFPGRLL
>Marmota_marmota_marmota-----MGTGLFPGRLL
>Tupaia_chinensis-----MGTGLFPGRLL
>Anolis_carolinensis-----MARVCGGVSMATGLFPGRLL
>Pelodiscus_sinensis-----MGCVCGSVSMVTGLFPGRLL

>Gallus_gallus	-----MKPRRSLLM-LWRSDDCCPL
>Anser_cygnoides	-----MKPRKSFLM-HWSHSDCCPI
>Apteryx_australis_mantelli	-----MLSPACGCSRQGLIVGQT-----GSSDKMKPRRSLLL PWCHSGCCPV
>Cariama_cristata	-----MKPRRSFPT-RWNRSDDCCPI
>Calidris_pugnax	-----MKPRRSFPT-RWNRSDDCCPI
MNRVLWVEKHLQEEECQHSYEVTSLCLPQHLDARIQLRQGLAYCQT-----ASLDKMKPRRSFLM-RWRSDDCCPI	
>Pterocles_gutturalis	-----MKPRRSFLM-RWRSDDCCPI
>Columba_livia	-----MKPRRSFAT-CQSRADRCPI
>Merops_nubicus	-----MKPRRSFPTRRWRSDDCCPI
>Cuculus_canorus	-----MKPRRSFLT-CWSHLDDCCPI
>Haliaeetus_albicilla	-----MKPRRSFPT-RWRSDDCCPV
>Gavia_stellata	-----MKPRRSFPT-RWRSDDCCPI
>Balearica_regulorum_gibberic	-----MKPRRSFPT-RWRSDDCCPI
>Opisthocomus_hoazin	-----MKPRRSFLT-HWSHSDCCPV
>Pseudopodoces_humilis	-----MKPRRSFPP-RWRSDDCCPL
>Nipponia_nippon	-----MKPRRSFPM-RWRSDDCCPI
>Fulmarus_glaucialis	-----MKPRRSFLT-RWRSDDCCPI
>Nestor_notabilis	-----MKPRRSFPT-HWSRSDCCPI
>Aptenodytes_forsteri	-----MKPRRSFPT-RWRSDDCCPI
>Tyto_alba	-----MKPRRSFPM-CWRSDDCCPI
>Chrysemys_picta	-----MYKVFRNL-----YLSTCQTGFCTSDRMNKPKRGFLLYWKNSDCCLV
>Calypte_anna	-----MKPRKSFPV-HWSRSDCCPI
>Apaloderma_vittatum	-----MKPRRSFVT-RQNRSDCCPV

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>Homo_sapiens
MTRMFLNNPRKNPAQK
>Felis_catus
MTRIFLNNQRKTPGAP
>Myotis_davidii
MTRIFLSNPRKNLVEK
>Galeopterus_variegatus
MTRIFLNNPRKNPVQK
>Condylura_cristata
MTRIFLNNQRKNLVQK
>Equus_asinus
MTRIFLNNQRKNLAQK
>Fukomys_damarensis
MTRIFLHNLKKNPVQK

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>Gallus_gallus
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>Anas_platyrhynchos
MESRPTK-LRRCVQDDPARLFTL-----
>Apteryx_australis_mantelli
MESRPTKTWKRCIQDDLGGFLFTL-----
>Buceros_rhinoceros_silvestri
-----MRRCIQDDPARFFTS-----
>Caprimulgus_carolinensis
-----MRRCIQDDPARLFFNS-----
>Cariama_cristata
-----MRRCIQDDPARFFTS-----
>Charadrius_vociferus
-----MRRCIQDDPARFFTS-----
>Colius_striatus
-----MRRCIQDDPDRRLFTSQKFQFV-----
>Columba_livia
-----MRRCIQDDPSRRLFTS-----
>Leptosomus_discolor
-----MRRCIQDDPARFFTS-----
>Alligator_mississippiensis
MGSRLSIIWRECVQDGPSRRFVTL-----
>Aquila_chrysaetos_canadensis
-----MRRCIQDDPARFFTS-----
>Gavia_stellata
-----MRRCIQDDPARFFTSY-----
>Balearica_regulorum_gibberic
-----MRRCIQDDPARFFTSQKSYFQLICNI I
>Tauraco_erythrolophus
-----MRRCIQDDPATRFFTSQKS-----
>Opisthocomus_hoazin
-----MRRCIQDDPARR-----
>Lepidothrix_coronata
-----MRRCIQDDPTRFFTS-----
>Phaethon_lepturus
-----MRRCIQDDPARFFTS-----
>Melopsittacus_undulatus
-----MRRCIQDD-----
>Tyto_alba
-----MRCNQDDPARFFTSQKSYFQLICNI I
>Struthio_camelus_australis
MESRPTKTWKRCIQDDQARGFFTL-----
>Apaloderma_vittatum
-----MRRYIQDDPARFFTS-----

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>Homo_sapiens
MSANRVNRVDITLLKMKNIQY
>Ursus_maritimus
-----MKNIQY
>Pteropus_alecto
-----MKNIQY
>Galeopterus_variegatus
-----MENIKY
>Oryctolagus_cuniculus
-----MKNIQY
>Marmota_marmota_marmota
-----MKIIPY
>Tupaia_chinensis
-----MKDIQY
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HG0116 ENSG0000010270 STAR03NL

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>Homo_sapiens
-----MCLLFRDGEVGRLL
>Ursus_maritimus
MRSPTSFQCLGWDAGTGFRDGEVGRLL
>Myotis_ricketti
-----MRPLLSRDGEVGRLL
>Condylura_cristata
-----MRPFLSRDGEIGKRLL
>Ceratotherium_simum_simum
-----MRSLLSRDGEVGRLL
>Marmota_marmota_marmota
-----MRCLLSRDGEVGRFL
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>Gallus_gallus	MDQHS	SDGETG	KGLL
>Apteryx_australis_mantelli	MDQPS	SDGETG	RRL
>Buceros_rhinoceros_silvestri	MDQPS	SDGETG	RPL
>Caprimulgus_carolinensis	MDQSS	SDGETG	RPL
>Cariama_cristata	MDQPS	SDGETG	RPL
>Calidris_pugnax	MDQPS	SDGETG	RPL
>Pterocles_gutturalis	MDQPS	SDGETG	RPL
>Colius_striatus	MDQPS	SDGETG	RPL
>Columba_livia	MDQPS	SDGETG	RPL
>Leptosomus_discolor	MDQPS	SDGETG	RPL
>Alligator_mississippiensis	MDQPS	SDGEAG	RLL
>Cuculus_canorus	MDQPS	RDGETA	RRL
>Aquila_chrysaetos_canadensis	MDQPS	SDGETG	RPL
>Gavia_stellata	MDQPS	SDGETG	RRL
>Balearica_regulorum_gibberic	MDQPS	SDGETG	RPL
>Opisthocomus_hoazin	MDQPS	SDGETG	RQL
>Lepidothrix_coronata	MDQPS	SDGETG	RPL
>Egretta_garzetta	MDQPS	SDGETG	RPL
>Tyto_alba	MDQHS	SDGETG	RPL
>Struthio_camelus_australis	MDKDDI	AVPSDVPL	TQKIDILL
MGKDDI	AVPSDVPL	TQKIDILL	TSFFFL
LL	LACKL	SPALL	STFFQY
FQKN	I	VEHV	CE
SCVT	VQ	LL	LG
CHES	I	AWG	V
WK	ET	R	K
SS	CM	D	PS
SD	GETG		
RRL	P		
>Chrysemys_picta	MDQPA	SDGEAG	KRL
>Tinamus_guttatus	MDQPS	SDGETG	RRL

>Homo_sapiens
 MLSAAACMNENAAGRF
 >Anser_cygnoides
 MLSAAECMNEKASGTF
 >Ursus_maritimus
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 >Lipotes_vexillifer
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 >Calidris_pugnax
 MLSAAECMNEKASGTF
 >Rhinolophus_ferrumequinum
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 >Dasypus_novemcinctus
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 >Columba_livia
 MLSAAECMNEKASGTF
 >Numida meleagris
 MLSAAECMNEKASGTF
 >Condylura_cristata
 MLSAAACMNENAAGRF
 >Oryctolagus_cuniculus
 MLSAAACMNENAAGRC
 >Sturnus_vulgaris
 MLSAAECMNEKASGTF
 >Ceratotherium_simum_simum
 MLSAAACMNENAAGRF
 >Manis_javanica
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 >Loxodonta_africana
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 >Ctenomys_sociabilis
 MLSAAACMNENAAGRF
 >Tupaia_chinensis
 MLSAAACMNENAAGRF
 >Trichechus_manatus_latirostris
 MLSAAASVNENAAGLF
 >Aptenodytes_forsteri
 MLSAAECMNEKASGTF
 >Anolis_carolinensis
 MLSAAECMNEKASGVF
 >Struthio_camelus_australis
 MLSAAECMNEKASGTF
 >Pelodiscus_sinensis
 MLSAAECMNEKASGTF

HG0117.2 ENSG00000140945 CDH13

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>Homo_sapiens
MPPPRGSLARCSPRICHAKRGSVRKESVL
>Dasypus_novemcinctus
-----MKESVL

>Condylura_cristata
-----MYSPHICHAERGSFMKESVL
>Oryctolagus_cuniculus
-----MKESVL

>Mus_musculus
-----MKESVL
>Tupaia_chinensis
-----MKESVL
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>Homo_sapiens	-----MTRFPPLKPWLLF
>Anas_platyrhynchos	-----MLGDDLKVKMRRFPPLKPWPLF
>Mustela_putorius_furo	-----MTRFLPLKPWLLF
>Hynobius_retardatus	-----MTRFPPLSWLLF
>Lipotes_vexillifer	-----MTRFPALKPWFLF
>Pteropus_vampyrus	-----MTRFPPLKPWLLF
>Monodelphis_domestica	-----MTRFPPLKPWLLF
>Aquila_chrysaetos_canadensis	-----MLGDDLKVKMRRFPPLKPWPLF
>Erinaceus_europaeus	-----MTRFPPLKPWLLF
>Oryctolagus_cuniculus	-----MTRFPPLKPWLLF
>Elephantulus_edwardii	-----MTRFPPLKPWLLF
>Parus_major	-----MLGNDLKVKMRRFPPLKPWPLF
>Equus_asinus	-----MTRFPPLKPWLLF
>Manis_javanica	-----MTRFPPIKPWLLL
>Loxodonta_africana	
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>Fulmarus_glacialis	-----MLGDDLKVKMRRFPPLKPWPLF
>Nannospalax_galili	-----MTRFPPLKPWLLF
>Tupaia_chinensis	-----MTRFPPLKPWLLF
>Trichechus_manatus_latirostr	-----MTRFPPLKPWLLF
>Struthio_camelus_australis	-----MRRFPPLKPWPLF
>Chrysemys_picta	-----MTRFPPLKPWPLF
>Orycteropus afer afer	-----MTRFPPLKPWLLF

>Homo_sapiens
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>Lipotes_vexillifer
MHWSGDGPSLTIN-----
>Pteropus_allecto
MHWSGDGPSLTIN-----
>Condylura_cristata
MHWRGDGPSLTIN-----
>Ochotona_princeps
MHWSGDGPVAQLIP1WRLH1LSPPLQSLQAEVTPGDYLVKVMTRFLLLPWLLF
>Elephantulus_edwardii
MHWSGGAPSLTIN-----
>Tupaia_chinensis
MHWSGNGPSVTIN-----
>Orycteropus afer_afer
MHWSGDGPSLTIN-----

>Gallus_gallus-----MMEFTFSQEELRILDQYR
>Anser_cygnoides-----MMEFRFSQEERRISDQHR
>Chaetura_pelagica-----MMEFTFSEEKLRVVDQYR
>Buceros_rhinoceros_silvestri-----MMEFTFSREKLRLLGQHR
>Caprimulgus_carolinensis-----MMEFTFSQEKLRIILDQYR
>Cariama_cristata-----MMGFTFSPEKLCILDQYR
>Calidris_pugnax-----MMEFTFSQEKLRIILDQDR
>Pterocles_gutturalis-----MMEFTFPREKLRIILDQYH
>Leptosomus_discolor-----MMEFTFSEEKLHISDQYR
>Alligator_mississippiensis-----MMESRFSQDKLHLLDQYR
>Aquila_chrysaetos_canadensisMDNLTVLLNTKYKYGGGGREDYMMMEFTFSQEKLRIILDQYR
>Gavia_stellata-----MEFTFFQEKLRIILDQYR
>Chlamydotis_macqueenii-----MMEFTFSQEKLRIILDQYR
>Tauraco_erythrolophus-----MMEFTFSQEKLRIILDQYR
>Ficedula_albicollis-----MMEFTFSQEKLRIILDQYR
>Pelecanus_crispus-----MMEFTFSQEKLRIILDQYH
>Fulmarus_glacialis-----MMEFTFSQEKLRIILDQYR
>Pygoscelis_adeliae-----MLSCRDSDYMMMEFTFSQEKLRIILDQYR
>Takydromus_sexlineatus-----MMEFKFTQERLHVLDQYC
>Struthio_camelus_australis-----MMELTFFQEKLHILDQYR
>Chrysemys_picta-----MMEFKFSQEKLHILDQYR
>Apaloderma_vittatum-----MMEFTFSQEKLRIKDQYH

>Homo_sapiens
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>Mustela_putorius_furo
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Calidris_pugnax
MKSQPSHPVYPGTYYYCLGKEKAFVV-----
>Rhinolophus_ferrumequinum
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Dasyurus_novemcinctus
MKSPPISHPVCPGTYYYCLGKEKSFVVSLLQIGSWEANLGVKSSAEHAESMMAQTE-
>Galeopterus_variegatus
MKSPPISHPVCPGTYYYCLGREKSFVV-----
>Monodelphis_domestica
MKSLPISHPVYPGTYYYCLGKERSFVYVLQTEYWEEIIV-----
>Macropus_eugenii
MKSLPISHPVYPGTYYYCLGKEKSFVYVLQTEYWEEIIV-----
>Esox_lucius
MKSQPSHPVYPGTYYYCPGKVKLHLAAICVFRV--DFLVTNLLGT-EKSLTPHTNE
>Condylura_cristata
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Ochotona_princeps
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Scleropages_formosus
MKSQPSHPVYSGTHYYCLG-----
>Zonotrichia_albicollis
MKSQPSHPVYPGTYYYCLGKEKAFVV-----
>Ceratotherium_simum_simum
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Manis_javanica
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Cavia_porcellus
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Salmo_salar
MKSQPSHPVYPGTYYYCPGKVKLYLAAISVFTV--DFVVR-----
>Tupaia_chinensis
MKSPPISHPVCPGTYYYCLGKEKSFVV-----
>Lepisosteus_oculatus
MKSQPSHPVYPGTYYYCLGKENLYLAAISVFRV--DFAVRLPIYR-DR-----
>Trichechus_manatus_latirostr
MKSPPISHPVCPGTYYYCLGKEISFVV-----
>Thamnophis_sirtalis
MKSQPSHPVYPGTYYYCLGKVQSFL-----
>Chrysemys_picta
MKSQPSHPVYPGTYYYCLGKEKAFVV-----


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>Homo_sapiens
-----MCSLSMDFWEGPRKGGLEFY---
>Anas_platyrhynchos
-----MYSLSIDFWEGPRKGCSFIE---
>Apteryx_australis_mantelli
-----MYSLSIDFWEGPRKGCSFIE---
>Canis_lupus_familiaris
-----MCSLSTDFWEGPRKGGLEFY---
>Balaenoptera_acutorostrata_s
MPTVNI GDMCSLSMDFWEGLRKGGLEFY---
>Galidris_pugnax
-----MYSLSIDFWEGPRKSCSFIE---
>Dasypus_novemcinctus
-----MCSLSMDFWEGLRKGGLOFY---
>Columba_livia
-----MYSLSIDFWEGPRKSCSFIE---
>Galeopterus_variegatus
-----MCSLSMDFWEGPRKGGLEFY---
>Haliaeetus_leucocephalus
-----MYSLSIDFWEGPRKSCSFIE---
>Coturnix_japonica
-----MYSLSIDFWEGPKGGCSFIE---
>Condylura_cristata
-----MCSLSMGFWEELRKGRAYSLVE
>Oryctolagus_cuniculus
-----MCSLSMDFWEGPRKGGLOFY---
>Corvus_brachyrhynchos
-----MYSLSIDFWEGPRKSCFIE---
>Nipponia_nippon
-----MYSLSIDCWEGPRKSCSFIE---
>Equus_asinus
-----MCSLSMDFWEGLRKGGLEFY---
>Manis_javanica
-----MDFWEGLREGGLEFY---
>Loxodonta_africana
-----MCSLSVDCWERLRKGGLOFIE---
>Nannospalax_galili
-----MCSLSMDFWEGPRKGGLOFY---
>Tupaia_chinensis
-----MCSLSDFWEGPRKGGLEFY---
>Aptenodytes_forsteri
-----MYSLSIDFWEGPRKSCSFIE---
>Struthio_camelus_australis
-----MYSLSIDFWEGPRKGCSFIE---

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>Homo_sapiens
-----MLSCDRPSSCLEEAGLQPGSL-----PLCPD-HPHIPKAVAWLGPEMGRRAFSGSVEAARASPSRCCDRK-
>Felis_catus
-----MGRRASERSTVEARASPSRCCDGQ-
>Balaenoptera_acutorostrata_s
-----MGCRTSAGSTAERASPSRCCRDGQ
>Calidris_pugnax
-----MGQOSRSGSIKEERKSPSRCCDSE
>Pteropus_lecto
-----MGCHASAGSTEERAPPSRCCDGQ-
>Cuculus_canorus
-----MGQOSRSGNIKEERKSPSRCCDSE
>Sarcophilus_harrisii
-----MGQOSYSGSIKKERESPSRCCDSK-
>Galeopterus_variegatus
MQMPRRQTCRAGTTASCLPDWLRASPHSLLPSTPEL-LLLVMIEPRSVPCSRAPAHAVCGSAEVMGAAGVAQLGPEMGGHTSPGSI GAARASPSRCCDRK-
>Monodelphis_domestica
-----MGQOSYSGSIKKERESPSRCCDSK-
>Macropus_eugenii
-----MGQOSYSGSIKKERESPSRCCDSK-
>Balearica_regulorum_gibberic
-----MGQOSHSYSIKEERKSPSRCCCDRE
>Erinaceus_europaeus
-----MGCHAPKSGTEHISTSLSRCCDN-
>Oryctolagus_cuniculus
-----MGRRASLGSDAARAPARRRCCGRK
>Ornithorhynchus_anatinus
-----MGQOSYSGSIKQVKESPSRCCDSE
>Equus_caballus
-----MGRRASRGSTEELRASPSRCCDGQ-
>Manis_javanica
-----MGCHASAGSTEETRASLSRCCDGQ-
>Loxodonta_africana
-----MGCRASGGVEGERAPAGCGCDRK-
>Ictidomys_tridecemlineatus
-----MGQOASSSGTEGAGAFWSCSDGK-
>Tupaia_chinensis
-----MGCRGSPSGIAAARAPASPCRDGK-
>Trichechus_manatus_latirostr
-----MGCRASAGSLEGARASAGRGCDGK-
>Chelonia_mydas
-----MGQOSHSYSIKEDRESPSRCCDSK-
>Orycteropus afer afer
-----MGCRASSGIVEGTWASLGRGCD-E-
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>Homo_sapiens
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>Amia_calva
-----MDGITTATRSTEF-----
>Channa_argus
MTSSLVWDDVKFKMDGTTSAQKSTQH----
>Xenopus_laevis
MTSSVVWDDVKFKMDGTTAAARQLAE----
>Menidia_menidia
-----MDGITTSSQKFTQH-----
>Oryzias_latipes
-----MDGITTKTQKSCTTVNKKV-----
>Hynobius_retardatus
-----MDGTTAAARAGQF-----
>Myotis_lucifugus
MTSSLVWDDVKFKMDGTTAAAAAARASRV-
>Oreochromis_niloticus
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>Pimephales_promelas
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>Fundulus_heteroclitus
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>Galeocharax_variegatus
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>Esox_lucius
-----MDGTTTTTHSTEF-----
>Coturnix_japonica
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>Lateolabrax_japonicus
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>Trematomus_bernacchii
-----MVWDDVKFKMDGTTSAQKSTQHH-----
>Platichthys_stellatus
MTSSLVWDDVKFKMDGTTSAQKAPQO-----
>Heterocephalus_glaber
MTSSLVWDDVKFKMDGTTAAAAAARASRV-
>Salmo_salar
MTSSLE-----
>Thamnophis_sirtalis
MTSSLVWDDVKFKMDGTTAVAAARAGES---
>Chrysemys_picta
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>Takifugu_rubripes
MTSSLVWDDVKFKMDGTTAA-----

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>Danio_rerio
-----MQYSIVPSKLMWLCHRYTVLGCARAARHSANI-NVARAQK-----
>Acipenser_sinensis
MHFDFNVAVCNCVTLAIYLARYCICPNLMLQSGCKYAFGCAIVARHLQKL-HVLRPPWN-----
>Channa_argus
-----MLRLCHQCLSVGCARIARHFTDI-NVLQRP-----
>Porichthys_notatus
---MQQNSLFFILLFLFPPSLPLFSRSLMVRLGHRCSLGCARVARSTHI-NVLQRP-----
>Eptesicus_fuscus
-----MLQPCGAPSTTGCARSARRPAAVLHVGLRPAQPAPR-----
>Oreochromis_niloticus
-----MLRFCHQCSSLGCACIARHFSVI-NVLQRPCKL-----
>Dasypus_novemcinctus
-----MLQPCGAPSTTGCARSARHPTAELHVGLRPAQPAPR-----
>Alosa_alosa
-----MQHYIVASNLMLCFSHOYSAFGCACVARQSTNI-NVVQRA-----
>Esox_lucius
-----MQYTTVNYILMLRVGHKSTTGCACSAARRSQNL-DVVRPP-----
>Apteronotus_leptorhynchus
-----MLHNIIVPSK-LMWFYHQHVLGCAIAQGSANI-NVRSQKLF-----
>Oryctolagus_cuniculus
-----MLQPCGAPSTTGCARSARRSAAELHVGLRPAAPR-----
>Lateolabrax_japonicus
-----MLRLCHQCSSVGCACIARHFTDI-NVLQRP-----
>Notothenia_coriiceps
-----MLRFCHQCSSVGCAGIARHFTDI-NVLQRPCKYL-----
>Equus_asinus
-----MLQPCGAPSTTGCARSARRPAAELHVGLRPA-----
>Cynoglossus_semihaevis
-----MLRLCHQCSSLGCACAAARFTYI-NVLQRR-----
>Callithrix_jacchus
-----MLQPCGAPSTTGCARSARRSAAVLHVGLRPAQPAPR-----
>Microtus_ochrogaster
-----MLQPCGAPSTTGCARSARRPAAELHVGLRPAQPAPR-----
>Oncorhynchus_kisutch
-----MQHTTVNYILMLRVSHKSTTGCACSAARLQNI-NVVRPP-----
>Lepisosteus_oculatus
-----MLQFCCKYTALSCAFIARHLRKM-NVVRPP-----
>Ictalurus_punctatus
MHFVFSVALHFDALYILMLPNNVPFNMLWFCYRPTVLCARAAQRSANL-NVAQAQKQL-----
>Takifugu_rubripes
-----MLRLCHQCSSVSCAW SARHFTHI-NVLQRP-----
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>Danio_rerio
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>Pygocentrus_nattereri
-----MRECVRECDGVYVWDCVRISRRRKRGRETAQGNRRSPLILSAARNERIRRVAGARFTLPVEGSFVRACFFAPLHEASFCAVRADWNVNS
>Latimeria_chalumnae
MMGGSQ-----
>Scleropages_formosus
MMGGSQWLLSYPRG---PRVCVSGGKKRREKR-----GKANPRVLSQI-----
>Salmo_salar
MMGINQWLGSFPGA---P-VCVRASVSEKNSRK-----

>Danio_rerio
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>Channa_argus
MRKKLLKIRKIVESQEKLNKRDVKASGALESGRG
>Xenopus_laevis
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>Menidia_menidia
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>>Oryzias_melastigma
MRKKFVKIRKIVESPEKHSRKDVKATRAFESRQC
>Mustela_putorius_furo
MRKKLLEIPRAV-----
>Pygocentrus_nattereri
MRKKLLKIRRTIVESPEKRPKRDVKAPTGLVSLWC
>Myotis_lucifugus
MRKKLLEIPRAV-----
>Maylandia_zebra
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>Clupea_harengus
MRKKLLKIRKIVETQEKHRRKDVNASADVGSRLC
>Poecilia_reticulata
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>Esox_lucius
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>Lateolabrax_japonicus
MRKKLLKIRKIVESQEKLNKKNVKAPGAPESGQC
>Notothenia_coriiceps
MRKKLLKIRKIVESEEKPNRKNVKATGAPESGRG
>Manis_javanica
MRKKLLEIPRAV-----
>Platichthys_stellatus
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>Rhinopithecus_bieti
MRKKLLEIPRAV-----
>Rattus_norvegicus
MRKKLLEIPRAV-----
>Lepisosteus_oculatus
MRKKLLKIRKILQS-----
>Trichomycterus_areolatus
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>Takifugu_rubripes
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>Homo_sapiens
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>Mustela_putorius_furo
MLKPRDWPWKWEGLDLDFHEESMGLAKIKV
>Lipotes_vexillifer
MLKPRDWPWKWEGLDLDFHEESMGLAKIKV
>Myotis_davidii
MLKPRDWPWKWEGLDLDFHEESVGLAKIKV
>Dasypus_novemcinctus
-----MGLAKIKV
>Galeopterus_variegatus
MLKPRDWPWKWEGLDSTLFHEESMGLAKIKV
>Erinaceus_europaeus
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>Ochotona_princeps
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>Elephantulus_edwardii
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>Equus_caballus
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>Manis_javanica
MLKPRDWPWKWEGLDLDFHEESMGLAKIKV
>Loxodonta_africana
MVKPRDWPWKWEGLDLDFHKEVGLAKIKV
>Jaculus_jaculus
MLKPRDWPWKWEGLDSTLFHEELMGLAKIKV
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Anolis_carolinensis
-----MSVELVKIKT
>Orycteropus afer
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>Gallus_gallus
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>Anser_cygnoides
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>Chaetura_pelagica
-----MFQFIQRIS-----
>Apteryx_australis_mantelli
MNCEKIQANMFQFIORIA-----
>Buceros_rhinoceros_silvestri
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>Caprimulgus_carolinensis
-----MFQFIORIA-----
>Merops_nubicus
-----MFQFIORTA-----
>Cuculus_canorus
MNCEKIQANMFQFIQRIS-----
>Haliaeetus_albicilla
MNCEKIQANMFQFIORIA-----
>Gavia_stellata
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>Chlamydotis_macqueenii
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>Opisthocomus_hoazini
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>Acanthisitta_chloris
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>Phalacrocorax_carbo
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>Picoides_pubescens
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>Fulmarus_glaucialis
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>Nestor_notabilis
MNCEKIQANMFQFIERIA-----
>Aptenodytes_forsteri
MNCEKIQANMFQFIORIA-----
>Tyto_alba
MNCEKIQANMFQFIORIA-----
>Struthio_camelus_australis
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>Chrysemys_picta
MNCVKIQANIFQFIQORVA-----

>Gallus_gallus
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>Anas_platyrhynchos
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>Apteryx_australis_mantelli
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>Buceros_rhinoceros_silvestri
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>Caprimulgus_carolinensis
-----MAGYTTPIQYKAQPSDWY-----
>Cuculus_canorus
MCFPGDLEPRVPGMSGYTMAIQYKAQPSGWY-----
>Haliaeetus_albicilla
-----MAGYTTPIQYKAQPSGWY-----
>Gavia_stellata
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>Opisthocomus_hoazin
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>Corvus_cornix_cornix
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>Phalacrocorax_carbo
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>Fulmarus_glacialis
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>Aptenodytes_forsteri
-----MAGYTTLIQYKAQPSGWY-----
>Tyto_alba
-----MAGCTTPIQYKAQPSGWY-----
>Struthio_camelus_australis
MCFRLDLESRVPGMAGTPL-----
>Tinamus_guttatus
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>Gallus_gallus
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>Anas_platyrhynchos
MQNPSTH-EEKSPLHGNVRGI ALGDNLLHSAAP-----
>Buceros_rhinoceros_silvestri
MQNSSTH-EEKSPL---VVMSEE-----
>Caprimulgus_carolinensis
MQNPST-----
>Cariama_cristata
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>Galidris_pugnax
MQNPSTH-EEKSPL---IVMLEE-----
>Colius_striatus
MQNPSTH-EEKSSL---VVMLEE-----
>Columba_livia
-----MISRGNVRGI AAGDNPLHSAAL-----
>Falco_cherrug
-----MISRGNVRGI AVGDNPLHSATVQDKHR-----
>Gavia_stellata
MQNPSTH-EENSPL---VVMLEE-----
>Eurypyga_helias
MQNPSTH-EEKSPL---VVMLEE-----
>Corvus_brachyrhynchos
-----ME-DFEGERHGNVRGI AVGDNLLHSATL-----
>Pelecanus_crispus
MQNPSTH-EEKSPL---VVMLEE-----
>Picoides_pubescens
MQNPSSH-EEKSPLL---VTLEE-----
>Fulmarus_glacialis
MQNPSTH-EEESPL---VVMLEE-----
>Pygoscelis_adeliae
MQNPSTH-EEKSPL---VVMLEE-----
>Tyto_alba
MQNPSTH-EEKSPL---VVMLEE-----
>Struthio_camelus_australis
MQNLFTQ-EERS-----CLGIATGDNLLHSDPLQEKHH
>Trachemys_scripta
MQNHTVSQEENSPPHYA-----
>Tinamus_guttatus
MQNPSTQ-EEKSPL-----
>Apaloderma_vittatum
MQNPSTH-EEKSPL---VIMLKE-----

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>Homo_sapiens-----MVLPGKRSSVFYEKLDKGFTGGIVLEIGS
>Canis_lupus_familiaris-----MVLPGKRSVVFYEKSDQGFRGI-----
>Myotis_brandtii-----MVLPGKRSALSYEKSDQEFQSGISGL-----
>Dasypus_novemcinctus-----MVLPGKKS AVFYEKSSQEL-----
>Condylura_cristata-----MEPKEMVLPGRRF AVFYEKTDQEL-----
>Oryctolagus_cuniculus-----MVLPGKRSL-YEKSDQEP-----
>Fukomys_damarensis
MKYNLTRNCTIVTLRI FHLLKVEIRHQEPKEMVLPGKRSAVFYEKSDQES-----
>Tupaia_chinensis-----MVLPGKRAAVFSEKSDQEP-----
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>Danio_rerio	-----MRTICSRDLGLGSLGGFS-----
>Anas_platyrhynchos	-----MRTICSRDLROGIS-----
>Apteryx_australis_mantelli	-----MRTICSRDLROGIS-----
>Oryzias_latipes	-----MRTICSRDLGLGGS-----
>Mustela_putorius_furo	-----MRTICSRDLROGIS-----
>Rousettus_aegyptiacus	MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Haplochromis_burtoni	-----MRTICSRDLGLGGS-----
>Austrofundulus_limnaeus	-----MRTICSRDLGLGGS-----
>Monodelphis_domestica	-----MRTICSRDLROGFS-----
>Gallus_gallus	MQESAIGRLDSSVPQCPNRLMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Oryctolagus_cuniculus	MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Corvus_brachyrhynchos	MQESAIGRLDSSVPQCPNRLMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Ceratotherium_simum_simum	-----MRTICSRDLROGIS-----
>Cercopithecus_atys	MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Microtus_ochrogaster	MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGISQEAFFS
>Salmo_salar	-----MRTICSRDLRLGGS-----
>Lepisosteus_oculatus	-----MRTICSRDLROGCS-----
>Pelodiscus_sinensis	-----MSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----

>Homo_sapiens
MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Anas_platyrhynchos
-----MRTICSRDLROGIS-----
>Xenopus_tropicalis
-----MSYCHVKSTSNKTNRFAIVOVERAKFIMRTICSGDPRRGSS-----
>Apteryx_australis_mantelli
-----MRTICSRDLROGIS-----
>Oryzias_latipes
-----MRTICSRDLGLGGS-----
>Mustela_putorius_furo
-----MRTICSRDLROGIS-----
>Hynobius_retardatus
-----MSYCHVKSASPETNRPAIVQVQRAQCTSGAAML-----
>Rousettus_aegyptiacus
MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Haplochromis_burtoni
-----MRTICSRDLGLGGS-----
>Rutilus_rutilus
-----MRTICSRDLGLGSLGGFS-----
>Poecilia_formosa
-----MRTICSRDLGLGGS-----
>Monodelphis_domestica
-----MRTICSRDLROGFS-----
>Meleagris_gallopavo
MQESAIGRLDSSVPQCPNRLMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Apterionotus_leptorhynchus
-----MRTICSRDLGLGSLGGF-----
>Oryctolagus_cuniculus
MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Corvus_brachyrhynchos
MQESAIGRLDSSVPQCPNRLMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----
>Ceratotherium_simum_simum
-----MRTICSRDLROGIS-----
>Microtus_ochrogaster
MQESMIGRLDSSVPQCPNRRMSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGISQEAFS-----
>Salmo_salar
-----MRTICSRDLRLGGS-----
>Lepisosteus_oculatus
-----MRTICSRDLROGCS-----
>Pelodiscus_sinensis
-----MSYCHVKSASNKTNRFAIVOVERAKFIMRTICSRDLROGIS-----

>Danio_rerio-----MPAVFLLRSLVRLFGSRLAASGVQLRRILTTATGHLGTVLRNIWERISSQESKEAILGCVLCILNMHKVDN-----
>Amia_calva-----MHKKVDN-----
>Channa_argus-----MPAVFILLRSLVIRLLSSRLAGSVAQFLRRSLSTGIAHLGTALRHVWDCVRSQESKEAILGCVLCILNMHKVDN-----
>Xenopus_laevis-----MPVPFLLIRTLVRAAGSRLAVSGARQLTKGARWARARLLILLQRLWDRLTSEETROALLSCVLCILNLKHKSNL-----
>Menidia_menidia-----MPAVFILLRSLVIRLLSSRLAGSLAQFLRRSLSTGAAHLGTALRHIWDRVRSQESKEAILGCVLCILNMHKVDN-----
>Porichthys_notatus-----MHKKVDN-----
>Oryzias_melastigma-----MHKKVDN-----
>Ambystoma_mexicanum-----MPLPFLLRLLRTLIRLAGSRLAASGVQFLRRKLAWAGARLAPLLRRVWRRATSEESROAVLGCVLCLNLKRVDGE-----
>Astyanax_mexicanus-----MHKKVDN-----
>Oreochromis_niloticus-----MPAVFILLRSLVIRLLSSRLAGSVAQFLRRILSTGATHLGTALRHIWDRVRSQESKEAILGCVLCILNMHKVDN-----
>Alosa_alosa-----MPAVFLLRSLVIRLLSSKLAGSAAQFLRRSLAAVSHLGTALRHIWDRVRSQESKEAILGCVLCILNMHKVDN-----
>Latimeria_chalumnae-----MPALFLLRLTLFIRLLGSQLAVSAGFLRRSLAAAGRLAALLRRVWDRIRSEESROVALSCVLCILNLHKVDE-----
>Nothobranchius_furzeri-----MPAVFILLRSLVIRLLSSRLAGSLAQFLRRSLTTGAAHLGTALRHIWDRVRSQESKEAVLGCVLCILNMHKVDN-----
>Esox_lucius-----MPAVLVLLRA-----LLSSRLTGSLVQFLRRTLSTTFGHVGAALRYVWDRISSQESKEAILGCVLCILNMHKVDEPEAESR-----
>Apteronotus_leptorhynchus-----MOKKVDN-----
>Lutjanus_erythropterus-----MHKKVDN-----
>Sebastes_caurinus-----MPAVFILLRSLVIRLLSSRLAGSVAQFLRRILSTGAAHLGTALRHVWDRIRSQESKEAVLGCVLCILNMHKVET-----
>Platichthys_stellatus-----MPVFILLRSLVIRLLSSKLAGSLAQFLRRGLSAGAAHLGTALRYVWDRIRSQESKEAVLGCVLCVLMGAKKVEK-----
>Salmo_salar
MGERENPKKRERIPVREREREKSKTRSRQSGGDFIPVLFLSFLSVFLLLSLCSVSGCGSSIMPAVFLFL-----RTLSSRMIGSLLOFLRRTLSTTFSHVGAALRYVWDRISSQESKEAILGCVLCILNMHKVDQPAESH
>Lepisosteus_oculatus-----MPAFFLLRSLILIRLLSSKLAGSAAQFLRRSLSATASHIGSLRHIWDRIRSQESKEAILSCVLCILNMHKVDN-----
>Trachemys_scripta-----MPAPLILLPLLR-----TLARLILLARKRLPLLRRLGARLGSRESREAVLTCLLCILNLRKXADD-----

>Gallus_gallus
MSWIEIRRIFFSLVEEPCPGG-WLH-GL-----F-----WRAKEAGKSQLSRTQR-----ELGHVLSAHL-GNTVCKSRKIIAGIQTAILIFV1FFRRGMHLA-----
>Anas_platyrhynchos
MSWIEIWWIFFSLVEEPCAGG-RLR-AL-----F-----WRAKEGKGSRLSRTER-----ELGHVLSAHL-GNTGCKSERKIFAGIVQTAILIFV1FFRRGMHLA-----
>Panthera_tigris
MSWGARRIGVSFLQEEPGAGGFRWLLPPPL-----GLFPPLVRGGEETGDRGDLRGS-----EASDMCQHIWGAHPSSPRGDLPEQFKLRY-----
>Orcinus_orca
MTSWGARRIGVSFLQEEPRAGGFRWLLPPPL-----VLFPPLV-QGVETGEQDFFGS-----EASDMCQHIWGTHPSSPRGDLLEQFKLRY-----
>Calidris_pugnax
MSWIEIWWIFFSLVEEPCAGS-WLR-GL-----F-----WRAKEGKGSLSRGER-----ELGHVLSAHL-GNTVCKSERKFAGIVQTAILIFV1FFRRGMHLA-----
>Pteropus_alecto
MSWGARRIGVSFLQEEPGAGGFRWLLPPPL-----VLFPPLRG-AETGERGHLRGS-----EASDMCQHIWGAHPSSPRGDLPEQFKLRY-----
>Columba_livia
MSWIEIWWIFFSLVEEPCAGS-WLR-GL-----F-----WRAKEGKGYRLSHAES-----SDMC-----CQHTWIGISAPKGNLLGSFK-----VRY-----
>Aquila_chrysaetos_canadensis
MSWIEIWWIFFSLVEEPCAGG-WLR-GL-----F-----WRVKEGKGSRLSRAER-----ELGHVLSAHL-GNTVCKSERKFAGIVQTAILIFV1FFRRGMHLA-----
>Chlamydotis_macqueenii
MSRWEIWWIFFLLVEEPCAGS-WLR-GV-----F-----WRAKEGKGSRLSRAER-----ELGHVLSAHL-GNTVCKSERKFAGIVQTAILIFV1FFRCGMHLA-----
>Condylura_cristata
MSWGARRIGVSFLQEEPRAGGFRWLLPPPL-----VLFPPVLG-AETGERGDLRSS-----EASDMCQHIWGAHSSPRGDLPEQFKLRY-----
>Oryctolagus_cuniculus
MSWGARRIGVSFLQERAGRWLVAGAAAA-----AARADSAAGPRSDAGAPRRQRGIGHVLSAHL-GRTSVEPEGSFAGTLQTAILILGVTVPGRLSGGSASVRPLESARACVCVCRVGPPLPPPCFPVE
>Elephantulus_edwardii
MSWGARRIGVSFLPEEPSAGGFRWLLPPPL-----LVLPALGRRRAETGERDQGG-----EASDMCQHIWGAQPSPRGDLPEQFKLRY-----
>Lepidothrix_coronata
MSWIEIWWIFFSLVEEPCAGS-WLR-GL-----F-----WRAKEGKGSRLSRAER-----EPGHVLSAHL-GNTVCKSERKFAGIVQTAILIFV1FFRRGMHLA-----
>Ceratotherium_simum_simum
MSWGARRIGVSFLPEEPSAGGFRWLLPPPL-----VLFPPLVG-GETGERGDLRGS-----EASDMCQHIWGAHPSSPRGDLPEQFKLRY-----
>Carlito_syrichtha
MSWGARRIGVSFLQEEPRAGGFRWLLPPPL-----LVLPSPVRGAETRERGDRLGS-----EASDMCQHIWGAHPSSPRGDLPEQFKLRY-----
>Loxodonta_africana
MSWGARRIGVSFLQEEPRAGGFRWLLPPPL-----VLFPPHV-RRATGEWGDLLGS-----EASDMCQHIWGAHLSSPRGDLLEQFKLRY-----
>Microtus_ochrogaster
MSWGARRIGVSFLQEEPRAGGFRWLLPPPPSPQVLPPLVRGAKTOEQGDLRGK-----EASDMCQHIWGAHPKSPRGDLPEQFKLRY-----
>Trichechus_manatus_latirostr
MSWGDRQIGVSFLQEEPIAGGFRWLLPPPL-----VLFPPLV-RRATGERGDVLGS-----EASDMCQHIWGAHPSSPRGDLPEQFKLQY-----
>Chrysemys_picta
MSWIEIWWIFFSLLEEPRAGGCRLL-GL-----L-----WRAKEGKGSRLSRAER-----ELGHVLSAHL-GNTVCKSERRFAGIVQSAIILFV1SFRRGIMHLA-----
>Calypte_anna
MSWIEIWWIFFSLVEEPCAGS-WLR-GL-----F-----WRLKEGKGSRLSRAER-----ELGHVLSAHL-GNTVCKSORKFAGIVQTAILIFV1FFRRGMHLV-----
>Orycteropus_afer_afer
MSWGARRIVSVLKEEASTGSRWLLPPPL-----LVLCSPLVRRRAETGERGDLLGS-----EASDMCQHICGARPSSPRGDLPEQFELRY-----

```
>Gallus_gallus-----MAVNLQRRYR-TWSLKLD---
>Anas_platyrhynchos-----MAVNLQRRYR-TWSLKLD---
>Apteryx_australis_mantelli-----MLYSNAVGSHHOCLEWTIQMAVNIQRRYR-TWSLKLD---
>Buceros_rhinoceros_silvestri-----MAVNLQRRYR-TWSLKLD---
>Charadrius_vociferus-----MAVNLQRRYR-TVCLKLD---
>Colius_striatus-----MAVNLQRRYR-TWSVKLD---
>Columba_livia-----MSEWPRPVCYSMVPTTGALQCCIGILPPVLVDLQMAVNLQRRYRRTWSLKLD---
>Leptosomus_discolor-----MFMSWPRPVCVS-MVPTTGALQCCIGILPPVLVDHPDAVNLQRRYRT-WSLKLD---
>Alligator_mississippiensis-----MAVNLQKRYRTWSQTGLEQSC
>Cuculus_canorus-----MAVNLQRRYR-TWCLKLD---
>Aquila_chrysaetos_canadensis-----MAVNLQRRYR-TWSLKLD---
>Mesitornis_unicolor-----MAVNLQRRYR-T-----
>Tauraco_erythrolophus-----MAVNLQRRYR-TWCLKLD---
>Opisthocomus_hoazin-----MAVNLQRRYR-TWSLKLD---
>Acanthisitta_chloris-----MAVNLQRRYR-TWSLKLD---
>Phaethon_lepturus-----MVPTTGAPROCIGILPPVLVDHPDAVNLQRRYRT-WSLKLD---
>Melopsittacus_undulatus-----MAINLQKRYRT-WCLKLD---
>Pygoscelis_adeliae-----MAVNLQRRYR-TWSLKLD---
>Struthio_camelus_australis-----MSEWPRPIWILPQ---VLYSNAVGSRHQCWWTIQMAVNIQRRYR-TWSLKLD---
>Chelonia_mydas-----MAVNLQKRYRT-WSRKLD---
>Tinamus_guttatus-----MAIQRRYRM-WCLKLD---
```


HG0132 ENSG00000151067 CACNA1C

```
>Homo_sapiens
----MRYSFTRGGSSG-KEQFLGFDAIMGIR
>Anas_platyrhynchos
----MHCNFTKGGSSG-KDQFLVFDAIMGIR
>Xenopus_laevis
----MQSFSAKGGSRG-TDQTRGFDAIMGIR
>Panthera_tigris
----MHYNFTKGGSSG-KEQFLVFDAIMGIR
>Hynobius_retardatus
----MHCYPTTRGDSGEKEQFLGFDSIMGIR
>Tursiops_truncatus
----MHYNFTEGGSSG-KDQFLVFDAIMGIR
>Calidris_pugnax
----MHCNFTKGGSSG-KDQFLVFDAIMGIR
>Pteropus_vampyrus
----MHYNFTQGGSSG-KDQFLVFDAIMGIR
>Dasyopus_novemcinctus
----MHYNFTQGGSSG-KDQFSVFDAIMGIR
>Galeopterus_variegatus
----MHDSLSEGGSSG-RQQFAVFDAIMGIR
>Gallus_gallus
----MHCNFTKGGSSG-KDQFLVFDAIMGIR
>Condylura_cristata
----MHCNLTGGGSG-KAQFLVFDAIMGIR
>Oryctolagus_cuniculus
----MHCKLTRGGSSG-KEQFLVFDAIMGIR
>Scleropages_formosus
MYRGMRCVLLGGSSE--CLFLFFNSIMGIR
>Lepidothrix_coronata
----MHCNFTKGGSSG-KDQFLVFDAIMGIR
>Ceratotherium_simum_simum
----MHYNSTGGSSG-KDQFLVFDAIMGIR
>Manis_javanica
----MYYNFTKGGSSG-KEQFWVFDAIMGIR
>Chinchilla_lanigera
----MHYNLTGGSSG-KEQFLVFDAIMGIR
>Anolis_carolinensis
----MLCNCCTKGGSSG-KDQILGFDAIMGIR
>Struthio_camelus_australis
----MHCNFTKGGSSG-KDQFLVFDAIMGIR
>Tinamus_guttatus
----MHCNLTGGSSG-KEQFLVFDAIMGIR
```

```
>Danio_rerio
-----MESTVDDDDAMEA
>Acipenser_sinensis
-----MESTVDDDDAMEA
>Channa_striata
-----MESTVDDDDAMAA
>Menidia_menidia
-----MESTVDDDDAMEA
>Porichthys_notatus
-----MESTVDDDDAMAA
>Oryzias_melastigma
-----MESTVDDDDAMAA
>Astyanax_mexicanus
-----MESTVDDDDAMEA
>Haplochromis_burtoni
-----MESTVDDDDAMAA
>Alosa_alosa
-----MESTVDDDDAMAA
>Kryptolebias_marmoratus
-----MESTVDDDDAMAA
>Esox_lucius
-----MESTVDDDDAIEA
>Acanthogobius_hasta
-----MESTVDDDDAMAA
>Scleropages_formosus
-----MESTVDDDDAMEA
>Anoplopoma_fimbria
-----MESTVDDDDAMAA
>Platichthys_stellatus
-----MESTVDDDDAMAA
>Salmo_salar
-----MESTVDDDDAMEA
>Lepisosteus_oculatus
-----MESTVDDDDAMEP
>Ictalurus_punctatus
-----MESTVDDDDAMEA
>Squalus_acanthias
MPWIRAMESTVDDDDAMDA
>Takifugu_rubripes
-----MESTVDDDDAMAA
```

HG0133.1 ENSG00000167522 ANKRD11

>Homo_sapiens
MESQTVDDDEAPAV
>Canis_lupus_familiaris
MESQTVDDDEAMAV
>Miniopterus_natalensis
MESQTVDDDEAMAV
>Ceratotherium_simum_simum
MESQTVDDDEAMAV
>Loxodonta_africana
MESQTVDDDEAMAV
>Chinchilla_lanigera
MESQTVDDDEAMAV

HG0133.2 ENSDARG00000051886 ankrd11

>Danio_rerio
MGKTSIGREYQV
>Pygocentrus_nattereri
MGKSSIGREYQA
>Esox_lucius
MGKTSIGGEYQG

```
>Homo_sapiens
-MGSARA-----PPLSRRGAAQPSEHEYIQPCSGTHLHWI-----
>Rousettus_aegyptiacus
MAGPNGEQIVNRTEVEIIYLTKLYSLVSEYTHCSGHTLYWI-----
>Psammomys_obesus
-MGSARA-----PPFFRRGAASPSEHTV-----LLEFIPSPEQH
>Pelodiscus_sinensis
-----MEEEQIHSCFGTHLYWI-----
```

HG0134.1 ENSGALG00000041267 BM11

>Gallus_gallus
MAAWLTFIFC
>Odobenus_rosmarus_divergens
MAAWLTFIFC
>Ambystoma_mexicanum
MAAWLTFIFC
>Lipotes_vexillifer
MAAWLTFIFC
>Astyanax_mexicanus
MAAWVAFIFC
>Galidris_pugnax
MAAWLTFIFC
>Latimeria_chalumnae
MAAWLTFIFC
>Alligator_mississippiensis
MAAWLTFIFC
>Danio_rerio
MAAWLVFIFC
>Sarcophilus_harrisii
MAAWLTFIFC
>Ochotona_princeps
MAAWLAFIFC
>Corvus_brachyrhynchos
MAAWLTFIFC
>Ceratotherium_simum_simum
MAAWLTFIFC
>Manis_javanica
MAAWLTFIFC
>Loxodonta_africana
MAAWLTFIFC
>Chinchilla_lanigera
MAAWLTFIFC
>Pygoscelis_adeliae
MAAWLTFIFC
>Anolis_carolinensis
MAAWLTFIFC
>Chelonia_mydas
MAAWLTFIFC
>Orycteropus_afer_afer
MAAWLTFIFC

>Homo_sapiens
MRGRDRGETMGMWAREPRSGLAAPPSPAE
>Odobenus_rosmarus_divergens
-----MGMLAREPRSGLETPPSPAE
>Orcinus_orca
-----MGMLAREPRSGLETPPSPAE
>Pteropus_vampyrus
-----MGMLAREPRSGLETPPSPAE
>Ochotona_princeps
-----MGMLARAPRSGLETPPGPAAE
>Geraotherium_simum_simum
-----MGLLAREPRSGLETPPSPAE
>Loxodonta_africana
-----MGRLAREPRSGLETPPSPAE
>Dipodomys_ordii
-----MGMWAREPRSGLETPPRPAAE
>Orycteropus_ater_ater
-----MGLLAREPQSGLETPPSPAE

HG0135 ENSDARG00000094132 igf1

>Danio_rerio
MLPQLFPVENVSVM
>Acipenser_sinensis
MFPQLFPVENVCVM
>Amia_calva
MFLQLFPVENVCVM
>Xenopus_laevis
MLPQLFPVYSVCVM
>Menidia_menidia
MLPQLFPVENVCVM
>Oryzias_melastigma
MLPQLFPVENVCVM
>Austrofundulus_limnaeus
MLPQLFPVENVCVM
>Meleagris_gallopavo
MLPQLFPVYSVCVM
>Parus_major
MLPQLFPVYSVCVM
>Mesocricetus_auratus
MLPQLFPVYSVCVL
>Oncorhynchus_kisutch
MLPQLFPVENVCVM
>Lepisosteus_oculatus
MFPQLFPVENVCVM

HG0135 ENSG00000017427 IGF1

>Homo_sapiens
MFPQLFPVYSSCVL
>Acipenser_sinensis
MFPQLFPVENVCVM
>Amia_calva
MFLQLFPVENVCVM
>Xenopus_laevis
MLPQLFPVYSSCVL
>Menidia_menidia
MLPQLFPVENVCVM
>Oryzias_melastigma
MLPQLFPVENVCVM
>Ailuropoda_melanoleuca
MFPQLFPVYSSCVL
>Myotis_brandtii
MFPQLFPVYSSCVL
>Dasyopus_novemcinctus
MFPQLFPVYSSCVL
>Austrofundulus_limnaeus
MLPQLFPVENVCVM
>Monodelphis_domestica
MFPQLFPVYSSCVL
>Meleagris_galllopavo
MLPQLFPVYSSCVL
>Erinaceus_europaeus
MFPQLFPVYSSCVL
>Oryctolagus_cuniculus
MFPQLFPVYSSCVL
>Parus_major
MLPQLFPVYSSCVL
>Equus_caballus
MFPQLFPVYSSCVL
>Nannospalax_galili
MFPQLFPVYSSCVL
>Oncorhynchus_kisutch
MLPQLFPVENVCVM
>Tupaia_chinensis
MFPQLFPVYSSCVL
>Lepisosteus_oculatus
MFPQLFPVENVCVM

```

>Homo_sapiens
-----MVTLFQWTCPRV---LLRRTAVS
>Felis_catus
-----MWRLFQWTCPRV---LLRRSAVS
>Physeter_catodon
-----MWRLFQWTCPRV---LLRRSAVS
>Eptesicus_fuscus
-----MWRLFQWTCPRV---LLRRSAVS
>Dasypus_novemcinctus
-----MRRRSRWTCPRV---LPRRSAAS
>Latimeria_chalumnae
-----MWILFQWTCSSV---LLSQSAAS
>Galeopterus_variegatus
-----MWRLFQWTCPRV---LLRRTAVS
>Monodelphis_domestica
-----MWRLFQWTCPRV---LLSQSAVS
>Condylura_cristata
-----MWRFQWTCPRV---LLRRSAVS
>Oryctolagus_cuniculus
-----MWRLFQWTCPRG---LLRRTAVS
>Ornithorhynchus_anatinus
MRKKTHREGRLPQTAPPPSPSSSRSPSPWSPRPAPDPPAAPVSSARDFSMWRLFRTWCPRV---LLRQSAVS
>Geraotherium_simum_simum
-----MWRLFQWTCPRV---LLRRSAVS
>Manis_javanica
-----MWRLFQWTCPRV---LLRRSAVS
>Loxodonta_africana
-----MWRLFQWTCPRV---LLRRSAVS
>Dipodomys_ordii
-----MWRLFQWTCPRV---LLRRTAVS
>Tupaia_chinensis
-----MWRLFQWTCPRV---LLRRTAVS
>Lepisosteus_oculatus
-----MWKLFQWTCQRV---LLSRSPLS
>Trichechus_manatus_latirostr
-----MWRLFQWTCLRV---LLRRSAVS
>Trachemys_scripta
-----MNSPFQWTCPSAPPLLLRRSAGS
>Orycteropus_afer_afer
-----MWRLFQWTCPRV---LLRRSAVS

```

HG0136.2 ENSG00000125845 BMP2

>Homo_sapiens
MRSTYCRRRSGANDALAEV
>Oryctolagus_cuniculus
MPSTSCRGGSGARDVPAEV
>Ceratotherium_simum_simum
MPITSCRSSGANDAPAEV
>Marmota_monax
MPSTSCRGGSGANDVMVEV

HG0137.1 ENSG00000181722 ZBTB20

```
>Homo_sapiens
-----MNICTRPKPWSNLP EE
>Amia_calva
-----MKICCRPHWTDL PEE
>Anser_cygnoides
-----MNVCTRSKAWSNL PEE
>Panthera_tigris
-----MNICTRPKPWSNLP EE
>Balaenoptera_acutorostrata_s
-----MNICTRPKPWSDL PEE
>Rousettus_aegyptiacus
-----MNICTRPKPWSDL PEE
>Dasypus_novemcinctus
-----MNI FT RPKRWSDL PEE
>Latimeria_menadoensis
-----MKIRVRPKRWTDL PEK
>Gallus_gallus
-----MNVCTKS KAWSNL PEE
>Erinaceus_europaeus
-----MNI STRPKWSDL PEE
>Oryctolagus_cuniculus
-----MNICTRPQPWSDL PEE
>Elephantulus_edwardii
-----MNICTRPKPWSDL PEE
>Lepidothrix_coronata
-----MNVCTRSKAWSNL PEE
>Equus_asinus
-----MNICTRPKPWSDL PEE
>Manis_javanica
-----MNICTRPQPWSDL PEE
>Cavia_porcellus
MSLFLLCRSSLFPA MNICTRPKPWSDL PEE
>Tupaia_chinensis
-----MNICTRPKPWSDL PEE
>Trichechus_manatus_latirostr
-----MNICTRPKPWSDL PEE
>Pelodiscus_sinensis
-----MNICTRAKAWSDL PEE
>Orycteropus afer
-----MNICTRPKPWSNLP EE
```

>Homo_sapiens
-----MSWKCRNLSLPSRKNL-----
>Mustela_putorius_furo
MRSLNSFHLLLTVGSSMSWKCRNLSLPSRKTVAGTFPPPFERKRIGWNKTLPSIWST
>Lipotes_vexillifer
-----MSWKCRNLSLPSRKIP-----
>Rousettus_aegyptiacus
MRSLNSFHLLLTVGSSMSWKCRNLSLPSRKTVTGTFFPPPFERKRIGWNKTLPSIWST
>Erinaceus_europaeus
-----MSWKCRNLSLPSRKIP-----
>Elephantulus_edwardii
-----MSWKCRNLSLPSRQIL-----
>Equus_przewalskii
MRSLNSFHLLLTVGSSMSWKCRNLSLPSRKTVAGTFPPPFERKRIGWNKTLPSIWST
>Cricetulus_griseus
MSSQNSFHLLLTVGSSMSWKCRNLSLPSRKTLWNTVNSTN-----
>Tupaia_chinensis
MRSLSSFHLLLTVGSSMSWKCRNLSLPSRKIL-----

```

>Homo_sapiens
MPRDPCCRASVFPFHLDPVGF
>Anser_cygnoides
MP---EPSCSATFSPFNLDPVGF
>Felis_catus
MPREPRCCRASFFPFHLDPVGF
>Lipotes_vexillifer
MPREPRCCRASFLPFHLDPVGF
>Calidris_pugnax
MP---EPSCSATFSPFNLDPVGF
>Myotis_davidii
MPREPRCCRASFFPFHLDPVGF
>Dasypus_novemcinctus
MPREPRCCRASFFPFHLDPVGF
>Monodelphis_domestica
MQQEPSYCTSFPSFHLDPVGF
>Oryctolagus_cuniculus
MPREPRCYRAGFFPFHLDPVGF
>Corvus_brachyrhynchos
MP---EPSCSATFSPFNLDPVGF
>Equus_asinus
MPREPGCCRASFFPFHLDPVGF
>Loxodonta_africana
MPREPRYCHASFFPFHLDPVGF
>Chinchilla_lanigera
MPREPHCCRASFFPFHLDPVGF
>Tupaia_chinensis
MPREPRSCRASFFPFHLDPVGF
>Trichechus_manatus_latirostr
MPRKPRYCLASFPPFHLDPVGF
>Crotalus_adamanteus
-----MPGLSCFALHLPDPVGF
>Struthio_camelus_australis
MP---EPSCSATFSPFNLDPVGF
>Pelodiscus_sinensis
MQ---EASASASVSPFHLDPVGF
>Tinamus_guttatus
MP---EPSSSAAFSPLNLPDPVGF
>Orycteropus_afer_afer
MPREPRCCRASFFPFHLDPVGF

```

>Homo_sapiens	-----MGRRLGGDP
>Odobenus_rosmarus_divergens	
MFETCRCLRVSHLPLSPQNRNERTETITSVATISAPRRCAASARGASLALGSGCLAAARROHCACRRVHPAPGSGWRFSTMGRRLGGDP	
>Orcinus_orca	-----MGRRLGGDP
>Pteropus_alecto	-----MGRRLGGDP
>Dasypus_novemcinctus	-----MGRRLGGDP
>Oryctolagus_cuniculus	-----MGRRLGGDP
>Equus_asinus	-----MGRRLGGDP
>Loxodonta_africana	-----MGRRLGGDP
>Cricetulus_griseus	-----MGRRLGGDP

HG0139 ENSGALG00000006379 SHH

>Gallus_gallus
MCSVISDLKAAIPAPVLLGIGG-----
>Anas_platyrhynchos
MCSVISDLKPAIPAPVLLGIGG-----
>Apteryx_australis_mantelli
MCSVISDLKAAIPAPVLLGIGG-----
>Charadrius_vociferus
MCSVISDLKPAIPAPVLLGIGG-----
>Myotis_brandtii
MCSVISDQQPAAPAPVWVGIGRESPALVAGRVL
>Latimeria_chalumnae
MCSVINDLKPVISAPTLIGIAG-----
>Columba_livia
MCSVISDLTPAIPAPVLLGIGG-----
>Falco_cherrug
MCSVISDLKPAIPAPVLLGIGG-----
>Oryctolagus_cuniculus
MCSVISDRQPAIPAPVWVGIGGESPAAGKVI
>Opisthocomus_hoazin
MCSVISDLKPAIPAPVLLGIGG-----
>Parus_major
MCSVISDLKPAIPAPVLLGIGG-----
>Nipponia_nippon
MCSVISDLKPAIPAPVLLGIGG-----
>Ceratotherium_simum_simum
MCSVISDQQPAVPAPVWVGISGESPAAGKVI
>Manis_javanica
MCSVISAQQAEPAPVWVGIAQGSPAAAGKV
>Chlorocebus_sabaeus
MCSVISGRQPAIPAPVWVGSGGECPAAGKVI
>Fukomys_damarensis
MCSAISDRQPAIPAPVWAEIGGEYTAAGKVI
>Lepisosteus_oculatus
MYSVINEQKADISAPASVIGG-----
>Pygoscelis_adeliae
MCSVISDLKPAIPAPVLLGIGG-----
>Chrysemys_picta
MCSVISDLKPAIPVLLGIGG-----
>Tinamus_guttatus
MCSVISDLKAAIPAPVLLGIGG-----

HG0140 ENSG00000009307 CSDE1

```
>Homo_sapiens
--MKCNRTDFTT
>Apteryx_australis_mantelli
--MKCNRTDFTT
>Canis_lupus_familiaris
--MKCNRTDFTT
>Physeter_catodon
--MKCNRTDFTT
>Myotis_davidii
--MKCNRTDFTT
>Dasypus_novemcinctus
--MKCNRTDFTT
>Alligator_mississippiensis
--MKCNRTDFTT
>Sarcophilus_harrisii
--MKCNRTDFTT
>Galeopterus_variegatus
--MKCNRTDFTT
>Monodelphis_domestica
--MKCNRTDFTT
>Sorex_araneus
--MKCNRTDFTT
>Oryctolagus_cuniculus
--MKCNRTDFTT
>Ceratotherium_simum_simum
--MKCNRTDFTT
>Manis_javanica
MSMKCNRTDFTT
>Loxodonta_africana
--MKCNRTDFTT
>Jaculus_jaculus
--MKCNRTDFTT
>Trichechus_manatus_latirostr
--MKCNRTDFTT
>Python_bivittatus
--MKCNRTDFTT
>Chrysemys_picta
--MKCNRTDFTT
>Orycteropus_afer_afer
--MKCNRTDFTT
```

>Gallus_gallus
MFVLNTSAEPSTIFLEA-QLRMQPTIK-----
>Anser_cygnoides
MFVLNTSAEPSTIFLEERKLRMQPTIK-----
>Charadrius_vociferus
MFVLNTSAEPSTIFLEV-ELRMQPTIK-----
>Pterocles_gutturalis
MFVLNTSAEPSTIFLE-VQLRMQPTIK-----
>Columba_livia
MFVLNTSAEPSTIFLEG-RLRMQPTIK-----
>Alligator_mississippiensis
-----MQPAIKR-----
>Oculus_canorus
MFVLNTSAEPSTIFLE-VQLRMQPTIK-----
>Aquila_chrysaetos_canadensis
MFVLNTSAEPSTIFP-----
>Eurypyga_helias
MFVLNTSAEPSTIFLE-VKLRMQPKIK-----
>Tauraco_erythrolophus
MFVLNTSAEPSTIFLE-VQLRMQPTIK-----
>Opisthocomus_hoazin
-----MQPTIK-----
>Zonotrichia_albicollis
MFVLNTSAEPSTIFIE-VQLRMQPTK-----
>Egretta_garzetta
MFVLNTSAEPSTIFLE-VQLRMQPTIK-----
>Picoides_pubescens
MFVLNTSAEPSTISPE-VQLRMQPTIK-----
>Python_bivittatus
MFVLNTSAKLSTFFEASQR--MQLTVIEWGPSQFSLW
>Struthio_camelus_australis
MFVLNTSAEPSTLFCRPACL-----
>Chrysemys_picta
MFVLNTSAEPSTIFHEA-----
>Tinamus_guttatus
MFVLNTSAEPSTIFPE-GQLRMQPTIK-----
>Apaloderma_vittatum
-----MQPTIK-----

HG0141.2 ENSG00000152689 RASGRP3

```
>Homo_sapiens
--MIMENVYMLKMSLVF
>Canis_lupus_familiaris
----MEMVYMLKMCLVF
>Balaenoptera_acutorostrata_s
--MIMENVYMLKMPLVF
>Rousettus_aegyptiacus
--MIMEIVCLMLKMSLVF
>Dasypus_novemcinctus
----MKMVYMLKMSLVF
>Erinaceus_europaeus
----MEMVCLMKMSLLF
>Ochotona_princeps
MYMIMENVYMLKMSLVF
>Equus_przewalskii
--MITEMVCLMLKMSLVF
>Loxodonta_africana
--MIMENVYMLKMSIVF
>Tupaia_chinensis
----MEMAYMLKMSLVF
>Orycteropus afer afer
--MIMENVYMLPKMSTVF
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HG0141.3 ENSG00000152689 RASGRP3

>Homo_sapiens
MLMRWLSQLRGYEVVCE---
>Mustela_putorius_furo
--MKWLSQLRGYEA-CELGE
>Equus_asinus
MLTKWLSQLRGYKVKLRE
>Manis_javanica
MLMKWLNQLRG-----
>Tupaia_chinensis
MLMRWLSQLRG-----

>Homo_sapiens
MFSPRPGYFFDIVKLRGK---
>Apteryx_australis_mantelli
MFPPKPVCFDIVKLRGK---
>Odobenus_rossmarus_divergens
MFSPRPGYFFDIVKLRGK---
>Hynobius_retardatus
MFHPKPGCFDIVKLRGK---
>Lipotes_vexillifer
MFSPRPGYFFDIVKLRGK---
>Pteropus_allecto
MFSPRPGYFFDIVKLRGK---
>Monodelphis_domestica
MFPSKSGFFDIVKLRGKSSW
>Aquila_chrysaetos_canadensis
MFPSQPGSFFDIVKLRGK---
>Condylura_cristata
MFSPRPGYFFDIVKLRGK---
>Oryctolagus_cuniculus
MFSPRPGYFFDIVKLRGK---
>Elephantulus_edwardii
MFSPRPGSFFDIVKLRGE---
>Acanthis_flammea
MFPSQPGAFDVVLRGK---
>Loxodonta_africana
MFSLRPGSFFDIVKLRGE---
>Jaculus_jaculus
MFSPRPGYFFDIVKLRGK---
>Trichechus_manatus_latirostr
MFSPRPGYFFDIVKLRGE---
>Pygoscelis_adeliae
MFSPPGGCFDIVKPRRK---
>Struthio_camelus_australis
MFAPTPGCFDIVKLRGK---
>Chelonia_mydas
MFHAKPGCFDIVKLRGK---
>Orycteropus_afer_afer
MFSPRPGYFFHIVKLRGE---

```

>Homo_sapiens
-----MKALQLGPL-ICHLSFQTVL
>Acinonyx_jubatus
-----MKALQLGPL-ICHLSFQTAL
>Lipotes_vexillifer
-----MKALQLGPL-ICHLSFQTAL
>Miniopterus_natalensis
-----MKALQLGPL-ICHLSFQTAL
>Monodelphis_domestica
MKGIFCSGVRALQTGPLSIHLSFQTAL
>Gondylura_olistata
-----MNALQLGPR-ICHLSFQTAL
>Oryctolagus_cuniculus
-----MKALPLRPL-PCHLSFQTAL
>Elephantulus_edwardii
-----MNALQLGLL-ICHLSFQTAL
>Ictidomys_tridecemlineatus
-----MKALQLGPL-ICHLSFQTAL
>Trichechus_manatus_latirostr
-----MKALQLGPL-ICHLSFQTAL
>Orycteropus_afer_afer
-----MKALQLGPL-ICHLSFQTAL

```

HG0143 ENSG00000101958 GLRA2

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>Homo_sapiens
MMPRTGTGFSFFSA-NCTKP-NLFLIFKETRFLPNFESGQ
>Mustela_putorius_furo
MMPRTGTGFOFFSA-NCTNP-NLFLIFKETRFLPDFESGQ
>Orcinus_orca
MMPSTGTGFOFFSA-NCTSP-NLFLIFKETRFLPDFESGQ
>Rousettus_aegyptiacus
-MMPRTGTGFOFFSA-NCTNP-NLFLIFKETRFLPDFEFGQ
>Dasypus_novemcinctus
MMPRTGTGFOFFSA-NCTNP-NLFLIFKEIRFLPDFQSGQ
>Galeopterus_variegatus
MMPRTGTGFOFFSV-NCTNP-NLFLIFKETRFLPDFESGR
>Monodelphis_domestica
MIPRTGTGYFFSP-NYTNP-NLFLIFKAIRLLTDFESGQ
>Sorex_araneus
MMPRTGTGFOFFSA-NCTNP-NLFLIFKETRFLPNFEPGQ
>Oryctolagus_cuniculus
MMPRTGTGFOFFSA-NCSIP-NLFLIFKETRFLPDFESGQ
>Elephantulus_edwardii
MMPRSGTGOFFLV-NCTNP-NLFLVFKETIRFLPDFESGQ
>Equus_caballus
MMPRTGTGFOFFSA-NCANP-NLFLIFKETRLLSDFESGQ
>Manis_javanica
MMPRTGTGFOFFSA-NCTNR-NLFLIFKETRFLTDFESGQ
>Loxodonta_africana
MMPRTGTGFOFFSV-NCTNP-NLFLVFKETIRFLPDFESGQ
>Peromyscus_maniculatus_baird
MMPRTGTGFOFFSA-NCTTP-NLFLIFKETRFLPDFESGQ
>Tupaia_chinensis
MMPKTGTGFOFFSA-N-----
>Trichechus_manatus_latirostr
MMPRTGTGFOFFSV-NCTNP-NLFLVFKETIRFLPDFESGQ
>Anolis_carolinensis
MIPRTGTDFLPSPRHADEGLLFLILKNFKLLLDLGI--
>Chelonia_mydas
MIPRTGTSYFLPP-ICRHPDLLLIFKKIKLLLDLGI--
>Orycteropus_afer_afer
MMPKTGTGOFFLV-NCTNP-NLFLVFKETIRFLPDFGSGQ
```

HG0144 ENSG00000117114 ADGRL2

>Homo_sapiens
MMQTDGFDEAGHL
>Acinonyx_jubatus
MMQTAGFDEAGHL
>Ambystoma_mexicanum
-MQTDGFDEVGNA
>Balaenoptera_acutorostrata_s
MMQTAGFDEAGHL
>Pteropus_alecto
MMQIAGFDEAGHI
>Alligator_mississippiensis
-MQTTGFDDAGHL
>Galeopterus_variegatus
MMQTAGFDEAGHL
>Monodelphis_domestica
MMYTAGFNEAGHL
>Sorex_araneus
MMQTAVFDEAGHL
>Oryctolagus_cuniculus
MMQTAGFDEAGHL
>Elephantulus_edwardii
MMQTAGFDEAGHI
>Equus_caballus
MMQTPGFDEAGHL
>Manis_javanica
MMQTAGFDEAGHL
>Loxodonta_africana
MMQTAGFDEAGHL
>Ictidomys_tridecemlineatus
MMQTAGFDEAGHL
>Tupaia_chinensis
MMQTAGFDEAGHL
>Trichechus_manatus_latirostr
MMQTAGFDEAGHL
>Chrysemys_picta
MIQTTFNDAGHL
>Orycteropus_afer_afer
MMQTAGFNEAGHL

>Homo_sapiens
MIPYGMDRTTCCPTCHCKCFLN
>Canis_lupus_familiaris
MIPYGMDRTTCCPTCHCKCFLN
>Pygocentrus_nattereri
MIPYGMERATCCPTCQCKCFLN
>Charadrius_vociferus
MIPYGMDRATCCPTCQCKCFLN
>Alosa_alosa
MIPYGMERATCCPTCQCKCFLN
>Oculus_canorus
MIPYGMDRATCCPTCQCKCFLN
>Sinocyclocheilus_anshuiensis
MIPYGMERATCCPTCQCKCFLN
>Monodelphis_domestica
MIPYGMDRTTCCPTCHCKCFLN
>Haliaeetus_leucocephalus
MIPYGMDRATCCPTCQCKCFLN
>Aptereronotus_leptorhynchus
MIPYGMERATCCPTCQCKCFLN
>Sturnus_vulgaris
MIPYGMDRATCCPTCQCKCFLN
>Nipponia_nippon
MIPYGMDRATCCPTCQCKCFLN
>Lateolabrax_maculatus
MIPYGME-ATCCPTCQCKCFLN
>Manis_javanica
MIPYGMDRTTCCPTCHCKCFLN
>Melopsittacus_undulatus
MIPYGMDRATCCPTCQCKCFLN
>Mus_musculus
MIPYGMDRTTCCPTCHCKCFLN
>Salmo_salar
MIPYGMERATCCPTCQCKCFLN
>Lepisosteus_oculatus
MIPYGMERATCCPTCQCKCFLN
>Ameiurus_nebulosus
-----MERATCCPTCQCKCFLN

>Homo_sapiens
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCVP--GVFLAEAAARCLSLFFPEKKMD
>Anas_platyrhynchos
-----MTHLLGFETFYPSFKEPLLLFEGIRCLFLFFQRRMD--
>Apteryx_australis_mantelli
-----MTHLVGFKTSYPSFKEPLLLFEGIRCLLLFFQRRMD--
>Panthera_tigris
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSLNCLP--GVFLAGADRCLSLFFPGKRMD
>Calidris_pugnax
-----MTHLLGFKTFYPSFKEPLLLFEGIRCLFLFFQRRMD--
>Pteropus_alecto
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSSNCLP--GVFLAEAVQCLSLFFPRKKMD
>Galeopterus_variegatus
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GVFLAEAA-----
>Haliaeetus_albicilla
-----MTHLLGFKTFYPSFKEPLLLFEGIRCLFLFFQRRMD--
>Meleagris_gallopavo
-----MTHLPGFKTFSPSVEEPFLLSEEIRCLFLFFQRRMD--
>Condylura_cristata
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GLFLAEAVRCLNLFFLGKKMD
>Oryctolagus_cuniculus
MLQ---CCNVSASEGAPRPSHTEPRNRVTHLLGDLPQNCPL--GVFLAEAAARCLSLSFPGKKMD--
>Pseudopodoces_humilis
-----MTHLLGFKTLYPSPGPLLLSEGIRCLFLFFQRRMD--
>Equus_asinus
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GVFLAEAVRCLSLFFPGKRMD
>Manis_javanica
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GVL-AETVRCLSLFFPGKKMD
>Marmota_marmota_marmota
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GVFLAEAAARCLSLFFPGKKMD--
>Tupaia_chinensis
MLQ---CCNVSATKGEKRPQSQTQKHKWVTHLLGYLQSPNCLP--GVFLAEAAARCLSLFFPGKKMD
>Pygoscelis_adeliae
-----MTHLLGFKTFQPSFKEPLLLFEGIRCLFLFFRRRMD--
>Struthio_camelus_australis
MLHRSGFWVLFTEGGKKKAVEIPWKSICMTHLVGFKTS-----

HG0146.2 ENSG00000163681 SLMAP

>Homo_sapiens
MLRQCAVCVNLFKFWG
>Felis_catus
MLRQCAVCFNLFKFWG
>Pteropus_allecto
MLRQCAFCFNLFKFWG
>Galeopterus_variegatus
MLRQCVVCFNLEFWG
>Condylura_cristata
MLRQCAVCFDLKFWG
>Geratherium_simum_simum
MLRQCTVCFNLFKFWG
>Manis_javanica
MLRQCAVCFNLFKFGG
>Marmota_marmota_marmota
MLRQCAVCFNLFKFWG
>Tupaia_chinensis
MLRQCAVCVNLFQFWG

HG0146.3 ENSG00000163681 SLMAP

>Homo_sapiens
MAAGAGKVGKFPASSGAA
>Felis_catus
MAAGAGKVGKFPALSGTA
>Rousettus_aegyptiacus
MAAGAGKVGKFSASSGTA
>Condylura_cristata
MAAGAGKVGKFPASSDMV
>Oryctolagus_cuniculus
MAAGAGKVGKFPASSGTA
>Mus_musculus
MAANAGKVGKFPASSATA

>Homo_sapiens
MKIARLQLASLLQ
>Acinonyx_jubatus
MKIARLQLASLLQ
>Orcinus_orca
MKIARLQLASLLQ
>Eptesicus_fuscus
MKIARLQLASLLQ
>Dasypus_novemcinctus
MKIARLQLASLLQ
>Macropus_eugenii
MKIARLQLESLLQ
>Meleagris_galllopavo
MKIERLOFASLLQ
>Erinaceus_europaeus
MKIARLQLASLLQ
>Oryctolagus_cuniculus
MKIARLQLASLLQ
>Elephantulus_edwardii
MKIARLQLASLLQ
>Equus_asinus
MKIARLQLASLLQ
>Manis_javanica
MKIARLQLASLLQ
>Loxodonta_africana
MKIARLQLASLLQ
>Nannospalax_galili
MKIARLQLASLLQ
>Trichechus_manatus_latirostr
MKIARLQLASLLQ
>Gekko_japonicus
MKIERLOFASLLQ
>Struthio_camelus_australis
MKIERLOFASLLQ
>Pelodiscus_sinensis
MKIGRLQFASLLQ

>Gallus_gallus
MK1ERLQFASLLQ
>Acinonyx_jubatus
MK1ARQLASLLQ
>Orcinus_orca
MK1ARQLASLLQ
>Eptesicus_fuscus
MK1ARQLASLLQ
>Dasypus_novemcinctus
MK1ARQLASLLQ
>Latimeria_chalumnae
MK1TSLHFASLLQ
>Erinaceus_europaeus
MK1ARQLASLLQ
>Ochotona_princeps
MK1ARQLASLLQ
>Elephantulus_edwardii
MK1ARQLASLLQ
>Equus_asinus
MK1ARQLASLLQ
>Manis_javanica
MK1ARQLASLLQ
>Otolemur_garnettii
MK1ARQLASLLQ
>Loxodonta_africana
MK1ARQLASLLQ
>Dipodomys_ordii
MK1ARLQFASLLQ
>Trichechus_manatus_latirostr
MK1ARQLASLLQ
>Gekko_japonicus
MK1ERLQFASLLQ
>Struthio_camelus_australis
MK1ERLQFASLLQ
>Trachemys_scripta
MK1ERLQFASLLQ

HG0148.1 ENSGALG00000011855 RHOJ

>Gallus_gallus
MLEIRWKMEWI
>Apteryx_australis_mantelli
MLEMKWKMEWI
>Caprimulgus_carolinensis
MLEMKWKMEWI
>Charadrius_vociferus
MLEMKWKMEWI
>Columba_livia
MLEMKWKMEWI
>Merops_nubicus
MLEMKWKMEWI
>Oculus_canorus
MLEMKWKMEWI
>Falco_cherrug
MLEMKWKMEWI
>Gavia_stellata
MLEMKWKMEWI
>Eurypyga_helias
MLEMKWKMEWI
>Opisthocomus_hoazin
MLEMKWKMEWI
>Corvus_brachyrhynchos
MLEMKWKMEWI
>Nipponia_nippon
MLEMKWKMEWI
>Picoides_pubescens
MLEMKWKMEWI
>Melopsittacus_undulatus
MLEMKWKMEWI
>Tyto_alba
MLEMKWKMEWI
>Pelodiscus_sinensis
MLEMKWKMEWI
>Calypte_anna
MLEMKWKMEWI

```
>Gallus_gallus
-----MILLWTALVIVRSGCDSLETLV
>Anas_platyrhynchos
-----MILLLTALVIVRSGCDSLETLV
>Apteryx_australis_mantelli
--MYIFNLFTSMILLTALVIVRSGCDSLETLV
>Caprimulgus_carolinensis
-----MILLTDLVIVRSGCDSLETLV
>Cariama_cristata
-----MILLTDLVIVRSGCDSLETLV
>Calidris_pugnax
MIFLSVNLFTSMILLTDLVIVKSGCDSLETLV
>Columba_livia
-----MILLTDLAIVRSGCDSLETLV
>Merops_nubicus
-----MILLTDLVIVRSGCDSLETLV
>Cuculus_canorus
-----MILLTDLVIVRSGCDSLETLV
>Aquila_chrysaetos_canadensis
-----MILLTDLVIVRSGCDSLETLV
>Gavia_stellata
-----MILLTDLVIVRSGCDSLETLV
>Mesitornis_unicolor
-----MILSTDVIVRSGCDSLETLV
>Opisthocomus_hoazin
-----MILLTDLVIVRSGCDSLETLV
>Manacus_vitellinus
-----MILLTDLVIVRSGCDSLETL
>Nipponia_nippon
-----MILLTDLVIVRSGCDSLETLV
>Picoides_pubescens
-----MILLTDLVIVRSGCDSLETLV
>Melopsittacus_undulatus
-----MILFTDLVIVRSGCDSLETLV
>Aptenodytes_forsteri
-----MILLTDLVIVRSGFDSLETLV
>Tyto_alba
-----MILLTDLVIVRSGCDSLETLV
>Struthio_camelus_australis
-----MILLTALVIVRSGCDSLETLV
>Calypte_anna
-----MILWTDLVIVRSGCDSLEALV
```


>Gallus_gallus
MILTIKRVYVQERMGGTVN
>Anas_platyrhynchos
MILTIKRVYVQERMGGTVN
>Calidris_pugnax
-----MQGTVN
>Columba_livia
MILTIKRVYV-ERMGGTVN
>Alligator_mississippiensis
MILRIKKYVQERMGGTVN
>Cuculus_canorus
-----MQGTVN
>Monodelphis_domestica
----MKFLFLQERMGGSVN
>Aquila_chrysaetos_canadensis
MILTIKRVYVQERMGGTVN
>Balearica_regulorum_gibberic
-----MQGTVN
>Ornithorhynchus_anatinus
-----MYVQERMGGSVN
>Lepidothrix_coronata
MILTIKRVYVQERMGGTVN
>Phaethon_lepturus
-----MQGTVN
>Otolemur_garnettii
-----MQGFGN
>Fulmarus_glaucialis
-----MQGTVN
>Aptenodytes_forsteri
MILTIKRVYVQERMGGTVN
>Anolis_carolinensis
MILNKRKGYVQERMGGSVN
>Chrysemys_picta
MILTIKRVYVQERMGGSVN
>Tinamus_guttatus
-----MQGTVN

```

>Homo_sapiens
MWNILKDNISKVNEGRNLGTECKC
>Ursus_maritimus
-----MNECRNLGTEQCKC
>Orcinus_orca
-----MNECRNLGTEQCKC
>Rousettus_aegyptiacus
-----MNECRNLGTEQCKC
>Dasypus_novemcinctus
-----MNECRNLRTLECKC
>Condylura_cristata
-----MNECRNLGTEQCKC
>Ochotona_princeps
-----MNECRNLGTECKC
>Ceratotherium_simum_simum
-----MNECRNLGTECKC
>Manis_javanica
-----MNECRNSGTEQCKC
>Loxodonta_africana
-----MNECRNLGTECKC
>Heterocephalus_glaber
-----MNECRNLGTECKC
>Tupaia_chinensis
-----MNECRNLGTECKC
>Trichechus_manatus_latirostr
-----MNECGNLGTECKC
>Orycteropus afer afer
-----MNECRNLGTECKC

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>Gallus_gallus
-----MAAAAEGGGRGAGRRRRHQOMEHKLT
>Anser_cygnoides
MGRESFGSFVGGALRFNAFLLEKMRRHQOMEHKLT
>Cariama_cristata
-----MEHKLT
>Charadrius_vociferus
-----MEHKLT
>Pterocles_gutturalis
-----MEHKLT
>Merops_nubicus
-----MEHKLT
>Alligator_mississippiensis
-----MEHKLT
>Haliaeetus_leucocephalus
-----MEYKLT
>Gavia_stellata
-----MEHKLT
>Mesitornis_unicolor
-----MEHKLT
>Tauraco_erythrolophus
-----MEHKLT
>Opisthocomus_hoazin
-----MEHKLT
>Parus_major
-----MEHKLT
>Egretta_garzetta
-----MEHKLT
>Fulmarus_glacialis
-----MEHKLT
>Nestor_notabilis
-----MEHKLT
>Aptenodytes_forsteri
-----MEHKLT
>Chelonia_mydas
-----MEHKLT

>Homo_sapiens
MAFWSPLLYLRSKFQLLYISSMLEWQEKGGTDLG-----
>Mustela_putorius_furo
MAFWSPLVCLQSKFRLLYISSMLEWQEKGGTDLG-----
>Orcinus_orca
MAFWSPLVYLQSKFRLLYISSMLEWQEKGGTDLG-----
>Pteropus_allecto
MAFWSPLVCLQSKFHLLYISSMLEWQEKGGTDLG-----
>Dasypus_noveboracensis
MAFWSPLVCLQSKFRLLYISSMLEWQEKGGADLGEKLFGLGITNCKL
>Sarcophilus_harrisii
-----MLEWKEKGGTDLG-----
>Galeopterus_variegatus
MAFWSPLACHQSEFRLLHISSMLQWQEKGT-DLG-----
>Monodelphis_domestica
MAFWSPLMYFQRFQQLLYISSMLEWKEKSGIDLG-----
>Condylura_cristata
MAFWSPLVCLQSKFR-----
>Oryctolagus_cuniculus
-----MLEWQEKGT-DLG-----
>Ornithorhynchus_anatinus
MACWSPLAHRQSGFLILGYSSMLEREERSGTDLG-----
>Equus_asinus
MAFWSPLVCLQSKFLLLYISSMLEWQEKGGTDLG-----
>Manis_javanica
-----MLEWQEKGS-DLG-----
>Loxodonta_africana
MAFWSPLWCLQSKFPLLYISSMVEWQEKGGTDLG-----
>Marmota_marmota_marmota
MAFWSPLVCLQSKFQILLYISSMLEWQEKGGTDLG-----
>Tupaia_chinensis
MAFWSPLVYLQNKFQLLYISSMLEWQEKGITDLG-----

HG0151 ENSG0000006468 ETV1

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>Homo_sapiens
MFLLNLEGSFCSLSPSVAFSPVRCKA--SLVD---R---HC-----
>Acinonyx_jubatus
MFLLNLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Balaenoptera_acutorostrata_s
MFLLKLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Miniopterus_natalensis
MFLLNLEGIFCSSSPSVAFSLKAILFPSRLIEVQIPRKSPAKCSKYKTLs
>Dasypus_novemcinctus
MVLNLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Alligator_mississippiensis
MFLLNLEGIFCSRSPCVTFRL-----LAVQILRKAAQMPRK----
>Galeopterus_variegatus
MFLLNLEGIFCSCSPSVAFSPVRCKA--SLVD---R---HC-----
>Haliaeetus_leucocephalus
MFLLNLEGIFCSRPPRVAFRL-----IGVQIPRKSPDQMPsk----
>Condylura_cristata
MFLLNLEGFFCSRSPSVAFRL-----IDVQIPRKSPA-----
>Pseudopodoces_humilis
MFLLNLEGIFCSRSPRVAFRL-----IGVQIPRKSPDQMPsk----
>Ceratotherium_simum_simum
MFLLNLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Manis_javanica
MFLLNLKGFFCSSSPSVAFSPVRCKA--SLVD---R---HC-----
>Loxodonta_africana
MFLLNLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Chinchilla_lanigera
MFLLNLEGIFCSRSPSVAFSPVRCKA--SLVD---R---HC-----
>Tupaia_chinensis
MFLLNLEGIVCSRSPSVAFSPVRCKA--SLAD---R---HC-----
>Struthio_camelus_australis
MFLLNLEGIFCSRSPGVAFRL-----IGVQIPKKSPODMPsk----
>Chelonia_mydas
MFLLNLEGIFCSRSPCVTFRL-----IGEQIPRKSSGQMPRK----
>Orycteropus afer_afer
MFLPNLEGIFCSSSPTVAF-----RLIEVQIPRKSPAKCSKYKTLs
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>Gallus_gallus
MFLLNLEGNFLQPIAARGLQADWSPDPEEISRSNAH-
>Anas_platyrhynchos
MFLLNLEGIFSQPTAARGLQADWRPDPEEISRSNAQ-
>Rousettus_aegyptiacus
MFLLNLEGIFLQQFA-----
>Mesitornis_unicolor
MFLLNLEGIFLQPIAAPGLQADWSPDPEEISRSNAQ-
>Manacus_vitellinus
MFLLNLEGIFLQPIAARGLQADWSPDPEEISRSNAQ-
>Nomascus_leucogenys
MFLLNLEGSFCSLSPSVAF-----SPVRKASLVDRHC
>Struthio_camelus_australis
MTA-----WSW-LAKTSLWEKADWSPDPEEISRSNAQ-

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>Danio_rerio
-----MLHDGKCFEYLRHGR LH-----
>Megophrys_sangzhiensis
-----MLHDGKCFEYLRHGR LH-----
>Menidia_menidia
-----MLHDGKCFEYLRHGR LH-----
>Felis_catus
-----MLHDGKCFEYLRHGR LH-----
>Pygocentrus_nattereri
-----MLRDGKCFEYLRHGR LH-----
>Miniopterus_natalensis
-----MLHDGKCFEYLRHGR LH-----
>Haplochromis_burtoni
-----MLHDGKCFEYLRHGR LH-----
>Latimeria_chalumnae
-----MLHDGKCFEYLRHGR LH-----
>Fundulus_heteroclitus
-----MLHDGKCFEYLRHGR LH-----
>Equus_asinus
-----MLHDGKCFEYLRHGR LH-----
>Platichthys_stellatus
-----MLHDGKCFEYLRHGR LH-----
>Cebus_capucinus_imitator
-----MLHDGKCFEYLRHGR LH-----
>Peromyscus_maniculatus_baird
-----MLHDGKCFEYLRHGR LH-----
>Salmo_salar
-----MLHDGKCFEYLRHGR LH-----
>Lepisosteus_oculatus
-----MLHDGKCFEYLRHGR LH-----
>Ictalurus_punctatus
MPLATHFLMLHDGKCFEYLRHGR LH-----
>Pelodiscus_sinensis
-----MLHDGKCFEYLRHGR LH-----
>Takifugu_rubripes
-----MLHDGKCFEYLRHGR LH-----
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>Gallus_gallus
MEEVPAGLPLATAPLPQFP-----
>Odobenus_rossmarus_divergens
MEEVKTGLPLATDPLP-----
>Ambystoma_mexicanum
MEEVRAGLPLATAALP-----
>Orcinus_orca
MEEVKTGLPLATDPLP-----
>Rousettus_aegyptiacus
MEEVKTGLPLATDPLP-----
>Galeopterus_variegatus
MEEVKTGLPLATDPLP-----
>Erinaceus_europaeus
MEEVKTGLPLATDPLP-----
>Oryctolagus_cuniculus
MEEVKTGLPLATDPLP-----
>Elephantulus_edwardii
MEEVKTGLPLATDPLP-----
>Ceratotherium_simum_simum
MEEVKTGLPLATDPLP-----
>Manis_javanica
MEEVKTGLPLATEPLP-----
>Macaca_mulatta
MEEVKTGLPLATDPLP-----
>Loxodonta_africana
MEEVKTGLPLATEPLP-----
>Mus_musculus
MEEVKTGLPLATDPLP-----
>Tupaia_chinensis
MEEVKTGLPLATDPLP-----
>Trichechus_manatus_latirostr
MEEVKTGLPLATDPLP-----
>Chrysemys_picta
MEEVKTGLPLATDPLLTVSITNCSAOTHKH
>Orycteropus_afer_afer
MEEVKTGLPLATDPLP-----

>Homo_sapiens
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Leptobrachium_boringii
MPSVWDLISGRCIHSSVNTAVNSYWMVTVTAS---
>Mustela_putorius_furo
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Hynobius_retardatus
MPSVWDVIGGRCIHSSVNTAVNSCLKVALTVS---
>Calidris_pugnax
-----MVALTVS---

>Pteropus_alecto
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Kryptolebias_marmoratus
-----MSLTVSAS

>Galeopterus_variegatus
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Monodelphis_domestica
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Condylura_cristata
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Oryctolagus_cuniculus
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Lepidothrix_coronata
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Mus_musculus
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---
>Salmo_salar
-MGLGREQAEVL SHSSVNTAGNTFLMMSLTVSVS
>Lepisosteus_oculatus
MPSVWDVIGGRC THSSVNTAVNSCLIMALTVS---
>Ictalurus_punctatus
-----MMALTVSVS

>Anolis_carolinensis
MPSVWDVIGGRCRRSVNTAVNSCLMVALTVS---
>Pelodiscus_sinensis
MPSVWDVIGGRC THSSVNTAVNSCLMVALTVS---

HG0155 ENSG00000136535 TBR1

>Homo_sapiens
MAGAVSSAAQAARSKVSFLF
>Anser_cygnoides
MAEAVSSSPQAARSKVSLS
>Canis_lupus_familiaris
MAGAVSSAAQAARSKVSFLF
>Orcinus_orca
MAGAVSSAAQAARSKVSFLF
>Pteropus_vampyrus
MAGAVSSAAQAARSKVSFLF
>Sarcophilus_harrisii
MAGAVSSAAQAARSKVSFLF
>Monodelphis_domestica
MAEAVSSAAQAARSKVSFLF
>Aquila_chrysaetos_canadensis
MAEAVSSSPQAARSKVSLS
>Gallus_gallus
MAGAVSSSPQAARSKVSLS
>Condylura_cristata
MAGAVSSAAQAARSKVSFLF
>Ochotona_princeps
MAGAVSSAAQAVRSKVSFLF
>Elephantulus_edwardii
MAGAVSSAAQAARSKVSFLF
>Ceratotherium_simum_simum
MAGAVSSAAQAARSKVSFLF
>Ictidomys_tridecemlineatus
MAGAVSSAAQAARSKVSFLF
>Trichechus_manatus_latirostris
MAGAVSSAAQAARSKVSFLF
>Struthio_camelus_australis
MAEAVSSSPQAARSKVSLS
>Tinamus_guttatus
MAGAVSSSPQAARSKVSLS
>Orycteropus_ afer_ afer
MARAVSSAAQAARSKVSFLF

HG0156 ENSG00000156113 KCNMA1

>Homo_sapiens
MAVDGCLGWRWRREELPRAPAPAARC
>Apteryx_australis_mantelli
MAGDGGFFGGRWRREELSEAPARPARC
>Odobenus_rossmarus_divergens
MAVDGCGSWWRWRREELPRAPAPAARC
>Orcinus_orca
MAVDGCGSWWRWRREELPRAPAPAARC
>Pteropus_vampyrus
MAVDGCGSWWRWRREELPRAPAPAARC
>Macropus_eugenii
MAVDGCLGWRWRREELPGAPAPPAHC
>Aquila_chrysaetos_canadensis
MAGDGGFFGGRWRREELSEAPARPARC
>Gallus_gallus
MAGDGLFGGRWRREELSAAPARPARC
>Condylura_cristata
MAVDGCGSWWRWRREELPRAPAPAARC
>Zonotrichia_albicollis
MAGDGLFGGRWRREELSEAPARPARC
>Ceratotherium_simum_simum
MAVDGCGSWWRWRREELPRAPAPAARC
>Manis_javanica
MAVDGCGSWWRWRREELPRAPAPAARC
>Loxodonta_africana
MAVDGCGSWWRWRREELPRAPAPAARC
>Melopsittacus_undulatus
MAGDGVFGGRWRREELSEAPARPARC
>Microtus_ochrogaster
MAVDGCGSWWRWRREELPRAPAPAARC
>Trichechus_manatus_latirostr
MAVDGCGSWWRWRREELPRAPAPAARC
>Chrysemys_picta
MAGEGCGGGRWRWELSGAPARPARC
>Orycteropus_afer_afer
MAVDGCGSWWRWRREELPRAPAPAARC

>Homo_sapiens
MCPGPLGREQPPTGGNLALRTAAGTSVCYRDSARTMEILYECGSH
>Phoca_largha
-----MEILYECGSH
>Balaenoptera_acutorostrata_s
-----MEILYECGSH
>Pteropus_alecto
-----MEILYECGSH
>Dasypus_novemcinctus
-----MEILYECGSH
>Galeopterus_variegatus
-----MEILYECGSH
>Condylura_cristata
MCPGALGREQPPVGATWDSVPAGGASVCYLDARRMETL-----
>Oryctolagus_cuniculus
-----MEILHERGSH
>Elephantulus_edwardii
-----MEILYECGSH
>Ceratotherium_simum_simum
-----MEILYECGSH
>Manis_javanica
-----MEILYECGSH
>Loxodonta_africana
-----MAILYECGSH
>Heterocephalus_glaber
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>Tupaia_chinensis
MCPGPLGSEQPPIGATWDSGPAAGASVCDRDTARKMEILYECGSH
>Trichechus_manatus_latirostr
-----MEILYECGSH
>Gekko_japonicus
-----MEILYECGSH
>Pelodiscus_sinensis
-----MEILYECGSH
>Orycteropus_afer_afer
-----MEILYECGSH

[illegible]

>Homo_sapiens
MQENYSPLLARPGEIFSPALSRALCNPKMKDRRGES
>Acinonyx_jubatus
MQENYSPLLARPGEIFSPALSRLLCNPKMKDRRGES
>Balaenoptera_acutorostrata_s
MQENYSPLLARPGEIFSPALSRPLCNPKMKDRRGES
>Pteropus_vampyrus
MQENYSPLLARPGEIFSPALSRPLCNPKMKDRRGES
>Dasypus_novemcinctus
MQENSSPLLARPGEVFSFALSRPLCNPKMKDRRGES
>Sarcophilus_harrisii
-----MKDRRGES
>Galeopterus_variegatus
-----MKDRRGES
>Monodelphis_domestica
-----MKDRRGES
>Condylura_cristata
MQENYSLLVAPGGEIFCPALSRPLCNPKMKDRRGES
>Oryctolagus_cuniculus
-----MKDRRGES
>Ceratotherium_simum_simum
MQENYSPLLARPGEIFSLALSRPLCNPKMKDRRGES
>Manis_javanica
MRGNYSPLLARPGEKIFSPALSRPLCNPKMKDRRGES
>Loxodonta_africana
MQENYCPLLARPGEIFRPALSRPLCNPKMKDRRGES
>Marmota_marmota_marmota
MQENYSPLLARPGEIFSPGLSRALCNPKMKDRRGES
>Trichechus_manatus_latirostr
MQENYQLLARPGEIFRPALSRPLCNPKMKDRRGES
>Takydromus_sexilineatus
-----MKDRRGES
>Chelonia_mydas
-----MKDRRGES

HG0159.2 ENSG00000182197 EXT1

>Homo_sapiens
MQGFVLLRRPSCMKH
>Ailuropoda_melanoleuca
MQGFVLLRRPSCMKH
>Balaenoptera_acutorostrata_s
MQGFVLLRRPSCMKH
>Pteropus_allecto
MQGFVLLRRPSCMKH
>Dasypus_noveboracensis
MQGFVLLRRSGCKMH
>Galeopterus_variegatus
MQGFVLLRRPSCMKH
>Monodelphis_domestica
MQGFVLLRRSGCKMH
>Sorex_araneus
MQGFVLLRRPSCMKH
>Oryctolagus_cuniculus
MQGFVLLRRSGCKMH
>Ceratotherium_simum_simum
MQGFVLLRRPSCMKH
>Manis_javanica
MQGFVLLRRPGCKMH
>Loxodonta_africana
MQGFVLLRRSGCKMH
>Cricetus_griseus
MQGFVLLRRPSCMKH
>Trichechus_manatus_latirostris
MQGFVLLRRSGCKMH
>Takydromus_sexlineatus
MQGFVLLRRSGCKMH
>Pelodiscus_sinensis
MQGFVLLRRSGCKMH

HG0160 ENSDARG0000060089 btaf1

>Danio_rerio
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>Amia_calva
MAPHIKPAWVLSSEQKYPLFLIRMKYLSARSS—GG
>Channa_punctata
MAPHIKTVFWAFNVQGNNSLHLIRLKYLSARTS—EG
>Megophrys_sanghiensis
MAPHIKPGVWLLRCHROISSL—IRFKRLGSCRGPDG
>Menidia_menidia
MAPHIKTVFWVGLVAGQNNLSLILIRLKYLSASS—EG
>Oryzias_melastigma
MAPHIKTVFWIALYVEQKRALLIRLKYLSAKTS—EG
>Micropterus_salmoides
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>Astyanax_mexicanus
MAPRIKPAWVLLFCDDQNYFSLILIRLKYLFGRSA—EG
>Haplochromis_burtoni
MAPHIKTVFWVVLNVQGNNSLNLIRLKYLSAKSS—EG
>Alosa_alosa
MAPHIKPAWVLLFCDDQNYFLLIRLKYLSGRSS—EG
>Latimeria_chalumnae
MAPHIKSGFWVLSNHQIFSLNLLNDQSMFRCCP—EG
>Kryptolebias_marmoratus
MAPHIKTVFWVSPNEGRNKSFLVRLKYLSDSS—EG
>Esox_lucius
MAPHIKSASWVPLGEQQNYSLYLIRLKYLSGSSS—EG
>Notothenia_coriiceps
MAPHIKTVFWVALLGLQNNSLHLIRLKYLSKSS—EG
>Salmo_salar
MAPHIKSASWVPFSEHKNYSLNLIRLKYLSGSSS—EG
>Lepisosteus_oculatus
MAPHIKPDWVLFSEQQNYCLFLIRIKYLSGCSS—AG
>Ictalurus_punctatus
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HG0161 ENSGALG00000017191

>Gallus_gallus
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>Anas_platyrhynchos
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>Caprimulgus_carolinensis
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>Cariama_cristata
MCWLLFVQ-----
>Charadrius_vociferus
MCWLLFVL-----
>Pterocles_gutturalis
MSWLLFVLQTFPNS
>Columba_livia
MCWLLFVL-----
>Leptosomus_discolor
MCWLLFVL-----
>Haliaeetus_leucocephalus
MCWLLFVL-----
>Gavia_stellata
MCWLLFVL-----
>Chlamydotis_macqueenii
MCWLLFVL-----
>Opisthocomus_hoazin
MCWLLFALQTFPNS
>Zonotrichia_albicollis
MCWLLPFVLQTFPNS
>Fulmarus_glacialis
MCWLLFVL-----
>Aptenodytes_forsteri
MCWLLFVL-----
>Tyto_alba
MCWLLFVL-----
>Chrysemys_picta
MCWLLRFVLYTFPNT

>Homo_sapiens
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>Anas_platyrhynchos
----MLRRHVMVYAAQNNLGPAN-----
>Xenopus_laevis
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>Canis_lupus_familiaris
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>Lipotes_vexillifer
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>Eptesicus_fuscus
----MFDRHVMVYTAQNNLGPVS-----
>Gallus_gallus
----MLCRHVMVYAAQNNLGPAN-----
>Erinaceus_europaeus
----MFRRHVMVYTAQNNLGPVS-----
>Oryctolagus_cuniculus
----MFRRHVMVYTAQNNLGPAS-----
>Parus_major
----MLRGHVMVYTAQNNLGPAN-----
>Equus_asinus
----MFRRHVMVYTAQNNLGPAS-----
>Manis_javanica
----MFRRHVMVYTAQNNLGPVS-----
>Loxodonta_africana
----MFRRHVMVYTAQNNLGPVS-----
>Ictidomys_tridecemlineatus
----MFRRHVMVYTAQNNLGPVS-----
>Pygoscelis_adeliae
----MVYAAQNNLGPAN-----
>Anolis_carolinensis
----MFHKHVMVYVSQNNLGPAN-----
>Orycteropus afer
----MFRRHVMVYTAQNNLGPVS-----

>Homo_sapiens
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>Xenopus_tropicalis
MFAAGERSCWRLSVC-----
>Ailuropoda_melanoleuca
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>Hynobius_retardatus
MFAAGESGCGWRLTVC-----
>Orcinus_orca
MFAAGEGGCGWRLTVSY-----
>Rousettus_aegyptiacus
MFAAGEGGCWRLTVSY-----
>Dasypus_novemcinctus
MFAVGEGGCWRTVSS-----
>Gallus_gallus
MFAAGERSCWRLARC-----
>Sorex_araneus
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>Elephantulus_edwardii
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>Corvus_brachyrhynchos
MFAAGELSCWRLTLC-----
>Geraotherium_simum_simum
MFAAGEGGCWRLTVSS-----
>Manis_javanica
MFAAGEGGCCLTVSC-----
>Loxodonta_africana
MFAAGEGGCWRLTVSDSHTSGROVLQYSVCMCRKSSVF-----
>Ictidomys_tridecemlineatus
MFAAGEGGCWRLTVSY-----
>Anolis_carolinensis
MFAAGEGSCWRCIVR-----
>Chrysemys_picta
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>Homo_sapiens
MLTLPITWYSYLVMYLFSQYPVSVCLS
>Xenopus_laevis
-----MFPF SQHP I-----
>Felis_catus
-----MYLFSQYPISVCLS
>Lipotes_vexillifer
MLTLPITWYSYLVMYLFSQYPISVWLS
>Eptesicus_fuscus
MLTLPITWYSYLVMYLFSQYPISVCLS
>Dasypus_novemcinctus
MLTLPITWYSYLVMYLFSQHPISVCLS
>Alligator_sinensis
-----MFPF SHYP I-----
>Galeopterus_variegatus
MLTLPITWCSYLVMYLFSQYPISVCLS
>Erinaceus_europaeus
MLTLPITWYSYLVMYLFSQYPISVCLS
>Oryctolagus_cuniculus
MLTLPITWCSYLVMYLLSQYPISVCWS
>Ceratotherium_simum_simum
MLTLPITWYSYLVMYLFSQYPISVCLS
>Manis_javanica
-----MYLFSQYPISVCLS
>Loxodonta_africana
MLTLRTWYSYLVMYLFSQYPISACL
>Octodon_degus
MLTLPITWYSYLVMYLFSQYPVSVCLS
>Tupaia_chinensis
MLTLPSNHSDLVMYLFPQYLVSVCLS
>Trichechus_manatus_latirostr
MLTLSTWYSYLVMYLFLOYPI SACL
>Orycteropus afer
MLTLSTWYSYLVMYLFSQYPISVCLS

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HG0165 ENSG00000177508 IRX3

>Homo_sapiens
MSIRARSPGNLRQSVRT
>Canis_lupus_familiaris
MSIRARSPGNLRQSVRT
>Orcinus_orca
MSIRARSPGNLRQSVRT
>Pygocentrus_nattereri
MSIRARSPNNLRQSVRT
>Gallorhinchus_millii
MSIRPSTPNNLHESVRT
>Latimeria_chalumnae
MSIRAVSPNNLKQSVRT
>Catostomus_comersonii
MSITKRSSNNLKQSVRT
>Esox_lucius
MSIRARSPNNLRQSVRT
>Gallus_gallus
MSIRARSPNNLRQSVRT
>Erinaceus_europaeus
MSIRAQSPGNRGQSVRT
>Scleropages_formosus
MSIRAKSPNNLRQSLRT
>Parus_major
MSIRAQSPNNLRQSVRT
>Ceratotherium_simum_simum
MSIRARSPGNLRQSVRT
>Heterocephalus_glaber
MSIRARSPGNLRQSVRT
>Lepisosteus_oculatus
MSIRAKSPNNLRQSVRT
>Trichechus_manatus_latirostr
MSIRARSPGNLRQSVRT
>Trachemys_scripta
MSIRTQSPNNLRQSVRT

>Homo_sapiens-----MKLQRRWREGDRI
-----MKMQRSWREGKRI
>Anas_platyrhynchos-----MKMQRSWREGKRI
-----MKLQRRWREGDRI
>Felis_catus-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Rousettus_aegyptiacus-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Dasypus_novemcinctus-----MKLQRRWREGDRI
-----MKMQRSWREGKRI
>Aquila_chrysaetos_canadensis-----MKMQRSWREGKRI
-----MKMQRSWREGKRI
>Gallus_gallus-----MKMQRSWREGKRI
-----MKMQRSWREGKRI
>Condylura_cristata-----MKLQRR-----
-----MKLQRRRREGDRI
>Ochotona_princeps-----MKLQRRRREGDRI
-----MKLQRRWREGDRI
>Corvus_brachyrhynchos-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Equus_przewalskii-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Microtus_ochrogaster-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Trichechus_manatus_latirostr-----MKLQRRWREGDRI
-----MKLQRRWREGDRI
>Struthio_camelus_australis
MDLFLTAGGNLEFFPLPPSLYSIYCEIMKMQRSWREGKRI
>Pelodiscus_sinensis-----MKMQRSWREGKRI
-----MKMQRSWREGKRI
>Orycteropus_afer_afer-----MKLQRRWREGDRI
-----MKLQRRWREGDRI

>Homo_sapiens
MQDAAFSWNRQTWIN-----
>Leptonychotes_weddellii
MRDAALSWNRQTWIN-----
>Balaenoptera_acutorostrata_s
MRDAALSWNRQTWIN-----
>Rousettus_aegyptiacus
MRDAALSWNRQTWIN-----
>Dasypus_novemcinctus
MRDAALSWNRQTWIN-----
>Sorex_araneus
MQDAAPSGERTQWIN-----
>Elephantulus_edwardii
MRDAALSQKRTQWRN-----
>Equus_przewalskii
MQDAALSWNRQTWIN-----
>Microtus_ochrogaster
MRDAALSWSRQTWIN-----
>Trichechus_manatus_latirostr
MRDAALSWNRQTWINCAREKEERSFFL
>Orycteropus afer afer
MRDAAFSWNRQTWINCAREKEGRSFFF

>Homo_sapiens
M I G N E E P R I H K E K S M F I F L Y K G E S E P R R Y F W N E K F G A F L V K-----
>Acinonyx_jubatus
-----M F V F L Y K G E S K P R R Y F W N-----
>Balaenoptera_acutorostrata_s
-----M F I F F C K G E S K P R R Y F W N E K F G A F F S K V K T-----
>Miniopterus_natalensis
M I S N G E P T S H K E K V C S L F F Y T G S Q P R I Y F W N E K F G A F F F F F R R V K D L I-----
>Dasypus_novemcinctus
-----M F V F L Y K G E S K P R R L F Y F F I F G T K S L G L Y-----
>Condylura_cristata
M I G N G E R R I H K E K V C S - F F S K G E S K P R R-----
>Oryctolagus_cuniculus
-----M F V F L C K G E S K P R R Y F W N E K F G A F F R K V K D L R R W C F L F S F E F P T R G E E I N N T S A K K F Q R R K V D R G R M R H-----
>Equus_przewalskii
-----M F I F L S K G E S E P R R Y F C N E K F G A F L G K-----
>Nannospalax_galili
-----M F L F L Y K E E S T P R R Y F W N E K F G A F F R K V K T-----

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>Homo_sapiens
MEGDWGFCRAGSREPGRWR
>Leptonychotes_weddellii
MEGDWGFCRAGNREPGRWR
>Dasypus_novemcinctus
MEGEKGFSAASREPGRWR
>Condylura_cristata
MEGDPGCCRAGSPEPGRWR
>Ochotona_princeps
MEGDWGFCCVASREPGRWR
>Peromyscus_maniculatus_baird
MEGDLGFRGTESREPGLWH
>Trichechus_manatus_latirostr
MEGDWGFCRAGSREPGRWR
>Orycteropus afer afer
MEGDQCFCRAGSREPGRWR

>Danio_rerio-----MPPHRLTGNPVAVKEKG
>Menidia_menidia-----MPPQRLPGTPAVKEKG
>Porichthys_notatus-----MPPQRLPGTPAVKEKG
>Oryzias_latipes-----MPSQRLPGSPAEEKEG
>Micropterus_floridanus-----MPPKRLPGSPTVKEKG
>Pygocentrus_nattereri-----MPPHRLTGNPVAVKEKG
>Haplochromis_burtoni-----MPPQRLPGSPAEEKEG
>Alosa_alosa-----MPPHRLTGSPTVKEKG
>Latimeria_chalumnae-----MPPHRLGRATVKEKG
>Fundulus_heteroclitus-----MPPQRLPGSPVVKEKG
>Apteronotus_leptorhynchus-----MPPHRLTGNPVAVKEKG
>Scleropages_formosus
MQRESRSAGCSELRAQRACAAVMPPHRLTGTPVKGNG
>Platichthys_stellatus-----MPPQGLRGPPAVKEKG
>Salvelinus_alpinus-----MPPHRLPGTPTVKEKG
>Lepisosteus_oculatus-----MPPHSFTGIPVKEKG
>Ictalurus_punctatus-----MQVMPPHRLTGNPVAVKEKG

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>Gallus_gallus
MPAIWIKGDFLSEHEKDC
>Anas_platyrhynchos
MPAIWIKGDFLSEHEKDC
>Hynobius_chinensis
MPE1WSRDWAFLEHEKDC
>Calidris_pugnax
MPAIWIKGDFLSEHEKDC
>Columba_livia
MPAIWIKGDFLSEHEKDC
>Alligator_mississippiensis
MPASRIQGRDFLSEHEKDC
>Oculus_canorus
MPAIWIKEDFLSEHEKDC
>Monodelphis_domestica
MPAIWITEGDLKAEYEKDC
>Haliaeetus_leucocephalus
MPAIWIKGDFLSEHEKDC
>Ornithorhynchus_anatinus
MPAIWIREGDLTAEHEKGC
>Lepidothrix_coronata
MPAIWIKGDFLSEHEKDC
>Picooides_pubescens
MPAICIKGDFLSEHEKDC
>Melopsittacus_undulatus
MPAIWIKGDFLSEHEKDC
>Aptenodytes_forsteri
MPAIWIKGDFLSEHEKDC
>Pelodiscus_sinensis
MPAIWIKERDFLSEHEKDC
>Calypste_anna
MPAIWIKGYFLSEHEKDC

HG0169 ENSG00000114933 IN080D

>Homo_sapiens
MVGKLSFRRAEEQLSGVMSSQCL
>Anas_platyrhynchos
MVGKLLFWRAEEPLSDVMSSRCL
>Chaetura_pelagica
MVGKLLFWRAEEPLSDVMSSQCL
>Hynobius_retardatus
MVGKLLFWRAEELLSGVMSSQCL
>Physeter_catodon
MVGKLSFRRAEELLSGVMSSQCL
>Gallidris_pugnax
MVGKLLFWRAEEPLSDVMSSQCL
>Pteropus_vampyrus
MVGKLSFRRAEERLSGVMSSQCL
>Columba_livia
MVGKLLFWRAEEPLSDVMYSQCL
>Monodelphis_domestica
MVGKLSFRRAEERLSGVMSSQCR
>Aquila_chrysaetos_canadensis
MVGKLLFWRAEEPLSDVMSSQCL
>Gallus_gallus
MVGKLLFWRAEEPLCDVMSSRCL
>Serinus_canaria
MVGKLLFWRAEEPLSDVMSSQCL
>Egretta_garzetta
MVGKLLFWRAEEPLSDVMSSQCL
>Picoides_pubescens
MVGKLLFWRAEDPLSDVMSSQCL
>Melopsittacus_undulatus
MVGKLLFWRAEEPLSDVMSSQCL
>Aptenodytes_forsteri
MVGKLLFWRAEEPLSDVMSSQCL

Homo_sapiens
 MKKLRSAEQIDYSGVPV—LGGTTAVRRTLIFAFNGEQMKK—EKEYI—H—
 >Anas_platyrhynchos
 MKKLLSAEQIDYSGVPV—LGGTTAVKRNKSMLEMEKDEKQTFMKEGEEKYLMHLYRSVF
 >Canis_lupus_familiaris
 MKKLLSAEQIDYSGVPV—LGGTTAVKRTPLAFNKKQMKK—EKQCI—H—
 >Balaenoptera_austrorotrata_s
 MFAFIVEQKVKK—EKQYI—R—
 >Rhinolophus_ferrumequinum
 MKK—EKQDI—H—
 >Dasypus_novemcinctus
 MKK—EKQYI—H—
 >Galeopterus_variegatus
 MKE—EKHYI—H—
 >Oryctolagus_cuniculus
 MKT—AKQYI—H—
 >Equus_asinus
 MTSERLFNPLNLFQKSETQILEELMFAFNGQKMKK—EKRYI—H—
 >Manis_javanica
 MKK—EKQYI—H—
 >Loxodonta_africana
 MKK—EKQYI—H—
 >Ictidomys_tridecemlineatus
 MKM—EKQYI—H—
 >Tupaia_chinensis
 MKK—ENQCI—H—
 >Trichechus_manatus_latirostr
 MKK—EKQYI—H—
 >Anolis_carolinensis
 MKKLLSAEQIDYSGVPV—LGGTTAVKRLALTLTHNLHGE—EKKHI—NCVQSSV
 >Orycteropus_afer_afer
 MKK—VKQYI—H—

>Homo_sapiens	-----MYS-----	KEKRTLAMVOLNODSEADM	QCHLQH
>Acinonyx_jubatus	-----	-----	MQCHLQH
>Balaenoptera_acutorostrata_s	-----	-----	MQCHLQH
>Myotis_davidii	-----	-----	MQCHFQH
>Dasypus_novemcinctus	-----	-----	MQCHLQH
>Columba_livia	-----MM-----	SECHCATVAKKSLRGERRERKKT	RSFASNNMRCAYTLNODSVADTQCHLQH
>Galeopterus_variegatus	-----	-----	MQCHLQH
>Monodelphis_domestica	-----	MYSSLLEFTVLNODSVADM	MQCHFQH
>Condylura_cristata	-----	-----	MQCHLQH
>Corvus_cornix_cornix	-----	-----	MQCHLQH
>Equus_asinus	-----	-----	MQCHLQH
>Manis_javanica	-----	-----	MQCHLQH
MPTRAHRAMMMWGGRWFHHVRLGATVSVRATFISGVLVGERCA	-----	LKRRGLVVVQLNODSEADM	QCHLQH
>Heterocephalus_glaber	-----	-----	MQCHLQH
>Struthio_camelus_australis	-----	-----	MQCHLQH
>Tinamus_guttatus	-----	-----	MQCHLQH

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>Homo_sapiens
MRNFFFQSCFPVDKFSVITVHSSCSAYDFCVYVTIASKTCEQEDREISWSPSLYIKMAECLVMLALH-----
>Felis_catus
-----MAECLVMLALH-----
>Pteropus_vampyrus
-----MAECLVMLALH-----
>Galeopterus_variegatus
-----MAECLVMLALH-----
>Monodelphis_domestica
-----MAECAAMLVRH-----
>Erinaceus_europaeus
-----MAECPVMLALH-----
>Sturnus_vulgaris
-----MAGGTAMLTLL-----
>Equus_asinus
MRNFFFQSCFPVDKFSRDHSTLKLFCVRFVCVVTIASKTCEQEDGEISWSPSLYIKMAECLVMLALH-----
>Manis_javanica
-----MICVCVTIASKTCEQEDGEISWSPSLYIKMAECHASTALSDTYRF-----
>Trichechus_manatus_latiostr
-----MAECLVMLALH-----
>Tinamus_guttatus
-----MAGGTATLTLH-----
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>Homo_sapiens
MLAVLQKAFRAADLDVEEMEDSEPRISK
>Acinonyx_jubatus
-----MEDSEPRISK
>Physeter_catodon
-----MEDSEPRISK
>Myotis_davidii
-----MEDSEPRISK
>Galeopterus_variegatus
-----MEDSEPRISK
>Erinaceus_europaeus
-----MEDSEPRISK
>Equus_asinus
-----MEDSEPRISK
>Manis_javanica
-----MEDSEPRISK
>Heterocephalus_glaber
-----MEDSEPRISK
>Trichechus_manatus_latirostr
-----MEDSEPRISK

>Homo_sapiens
MGDIIRKICGADHKK-----
>Acinonyx_jubatus
MGDIIRKICGADLNKK-----
>Balaenoptera_acutorostrata_s
MGDIIRKICGADLDKK-----
>Rousettus_aegyptiacus
MGDIIRKICGADFNNK-----
>Condylura_cristata
MRDVIIRKICGADLDEK-----
>Equus_asinus
MGDIIRKICGAALNK-----
>Manis_javanica
MGDIIRKICGADLNKK-----
>Heterocephalus_glaber
MSDIIRKICGADLNRVKNPEQESVCDSWAAGVGSVMASEEQLIRIRLS

>Homo_sapiens
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Mustela_putorius_furo
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Balaenoptera_acutorostrata_s
MQLSSQSTLRTRGGINTKTKFFVEGKCNKQACRFPM-RCGVSVCRACPHWRHMLVCVHGVCFSVRREKMLANHRKSPGIY
>Myotis_brandtii
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Dasypus_novemcinctus
MQLNSQSTLRTRGGINTKTKFLWKENAIISK---LAVF-----
>Monodelphis_domestica
MQPRSQSTLRTRGGINTKTKFLWKENAIIRK---LAVF-----
>Gallus_gallus
MOPGSASTLRARRGTSAQTF-----
>Condylura_cristata
MQLSSQSTLRTRGGINTKTKFLWKENAIISR---LAVFRCGVE-----
>Oryctolagus_cuniculus
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVLRCAVE-----
>Ficedula_albicollis
MQLSSQSTLRTRCGINTKTKFFOKENTISK---RLQLSFDAAECE-----
>Ceratotherium_simum_simum
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Manis_javanica
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Mus_musculus
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Tupaia_chinensis
MQLSSQSTLRTRGGINTKTKFLWKENAIISK---LAVFRCGVE-----
>Pelodiscus_sinensis
MQLSSQSTLSTRCGINTKTKFFLEGKYNKAALPVFWCCGV-----

>Homo_sapiens
MDYKKKASKERISP-----
>Mustela_putorius_furo
MDYKKKAGEERISP-----
>Balaenoptera_acutorostrata_s
MDYKKKAGEERIFP-----
>Myotis_brandtii
MDYKKKAGEERISP-----
>Dasypus_novemcinctus
MDYKKKAGEERSTP-----
>Condylura_cristata
MDYKKKAGDERIAP-----
>Oryctolagus_cuniculus
MDYKKKAGEERRSP-----
>Ceratotherium_simum_simum
MDYKKKAGKERISP-----
>Nannospalax_galili
MDYKKKAGEERIAP-----
>Tupaia_chinensis
MDYKKKAGEERLSPGVAIRFAAGSVCCDSFC

>Homo_sapiens	-----MTELACHRRHWYLS
>Anser_cygnoides	-----MTELACHRRHWYLS
>Lipotes_vexillifer	-----MTELACHRRHWYLS
MQERLALTVGRRFRGSGTNPWVHLERKVGPRLRDAVSAMTELACHRRHWYLS	
>Calidris_pugnax	-----MTELACHRRHWYLS
>Pteropus_allecto	-----MTELAFRRHWYLS
>Aquila_chrysaetos_canadensis	-----MTELACHRRHWYLS
>Sorex_araneus	-----MTELACHRYHWYLS
>Oryctolagus_cuniculus	-----MTELVRRRHWYLS
>Elephantulus_edwardii	-----MTELACHRRHWYLS
>Corvus_cornix_cornix	-----MTELACHRRHWYLS
>Loxodonta_africana	-----MTELACHRRHWYLS
>Fukomys_damarensis	-----MTELACHRRHWYLS
>Tupaia_chinensis	-----MTELACHRRHWYLS
>Trichechus_manatus_latirostr	-----MTELACHRRHWYLS
>Chrysemys_picta	-----MTELACHRRHWYLS

>Homo_sapiens	-----MRLTRGRAASPALVQRSPASDQSPVIMQDSGPISSASS
>Anas_platyrhynchos	-----MODGGPISSAVS
>Mustela_putorius_furo	-----MQDSGPISSASS
>Rousettus_aegyptiacus	-----MQGSGPISSASS
>Galeopterus_variegatus	-----MQDSGPISSASS
>Monodelphis_domestica	MITRRGSGTHLSQVLLASLPLVQPSQSTSDQSQAIMQDGGPIRSASS
>Coturnix_japonica	-----MODGEPISAGS
>Ochotona_princeps	-----MODGGPISSASS
>Ornithorhynchus_anatinus	-----MODGGPIRSASS
>Zonotrichia_albicollis	-----MODGGPISSAVS
>Equus_przewalskii	-----MIMQDSGPISSASS
>Loxodonta_africana	-----MQDSGPISSANL
>Octodon_degus	-----MODGGPISSASS
>Tupaia_chinensis	-----MQDSGPISSASS
>Chrysemys_picta	-----MODGGPISSASS

HG0175 ENSG00000151320 AKAP6

>Homo_sapiens
MCKKHQKKT VSGDAVLERSEV---
>Anas_platyrhynchos
MCKKHQKRM I-----
>Felis_catus
MCKKHQKKT VAGDAVLEERSKV---
>Balaenoptera_acutorostrata_s
MCKKHQKKA VAGDAVLEERSKA---
>Calidris_pugnax
MCRKHQKRM I-----
>Rousettus_aegyptiacus
MCKKHQKKT VAGDAVLEERSKV---
>Dasypus_novemcinctus
MCRKHQKRT VAGDAVLEERSKV---
>Monodelphis_domestica
MCRKHQKRMV RAGDALLERSMV---
>Condylura_cristata
MCKKHQKRT V RAGDAVLEERSKI---
>Parus_major
MCRKHQKRM I-----
>Equus_caballus
MCKKHQKKT VGPDAVLEERSKV---
>Manis_javanica
MCKKHQKKT VAGDELPEEGLGHLR
>Fukomys_darlingi
MCKKHQKKT VAGDAVLEERSKV---
>Struthio_camelus_australis
MCRKHQKGT I-----
>Pelodiscus_sinensis
MCRKHQKRM V-----

>Homo_sapiens	MQEVMVGLGD
>Apteryx_australis_mantelli	MQEVMVGLKGE
>Physeter_catodon	MQEVMVGLGD
>Pteropus_alecto	MQEVMVGLGD
>Galeopterus_variegatus	MQEVMVGLGE
>Monodelphis_domestica	MQEVMVGLGD
>Macropus_eugenii	MLGLDQDRHHIWIILQLPLLATGGAVGRKSTCCSSPTGLTNFSMQEVMVGLGD
>Haliaeetus_leucocephalus	MQEVMVQQLGE
>Oryctolagus_cuniculus	MQEVMVGLGD
>Ceratotherium_simum_simum	MQEVMVGLSD
>Loxodonta_africana	MQEVMVGLGD
>Heterocephalus_glaber	MQEVMVGLKSD
>Tupaia_chinensis	MQEVMVGLGD
>Trichechus_manatus_latirostr	MQEVMVGLGD
>Orycteropus_afer_afer	MQEVMVGLGD

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>Homo_sapiens
MLRNHLLYPGAA--AAAAAFAGAEFNKRASEQASAGGKRQRMSAIYPPLLGLSFTAAASS
>Felis_catus
-----MSAIYPPLLGLSFTAAASS
>Orcinus_orca
-----MSAIYPPLLGLSFTAAASS
>Myotis_brandtii
-----MSAIYPPLLGLSFTAAASS
>Dasypus_novemcinctus
-----MSAIYPPLLGLSFTAAASS
>Alligator_mississippiensis
MCRHAHALTAALQALELELELLGAQFNKSERK--RQGEKERKRMSAISPPLLGLPVI AASS
>Galeopterus_variegatus
-----MSAIYPPLLGLSFTAAASS
>Monodelphis_domestica
-----MSAIYPPLLGLSFTSASS
>Condylura_cristata
-----MSAIYPPLLGLSFTAAASS
>Oryctolagus_cuniculus
-----MSAIYPPLPGALSFTAAASS
>Elephantulus_edwardii
-----MSAIYPPLPGALSFTAAASS
>Equus_caballus
MLRNLTLWFWSCCCCCCFWGW-----
>Ictidomys_tridecemlineatus
-----MTAIYPPLGLSFTAAASS
>Pelodiscus_sinensis
-----MSAIYPPLPCAPSVTSASS
>Orycteropus afer afer
-----MSAIYPPLLGLSFTAAP
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>Homo_sapiens-----MGPE-ASSFSTGLALLQVQEGG
>Odobenus_rosmarus_divergens-----MGREAGCSSGLALLQVQEGG
>Balaenoptera_acutorostrata_s-----MGSSEGFSSGLALLQVQEGG
>Pteropus_vampyrus-----MGQAAAFSSGLALFQVQEGG
>Galeopterus_variegatus-----MGLTAATSFNTGLALLQVQEGG
>Monodelphis_domestica-----MGLS-AAWFCTGLALLKVQAGG
>Trichosurus_vulpecula-----MGLS-AAWFSTGLALLKVQAGG
>Oryctolagus_cuniculus-----MGLE-AAGFSTGLALLQVQEGG
>Ceratotherium_simum_simum-----MGRAGGFSSGLALLQVQEGG
>Ctenomys_sociabilis
MFVASIASGSQKDGILTTLDSCWCPGFFPNMGLA-ATGFSTGLALLQVQEGG
>Tupaia_chinensis-----MGFT-AAAFSTGLALLQVQEGG

>Gallus_gallus-----MDLHVQFQITGLALLIKVQEGG

>Anser_cygnoides-----MEVPVFQFITGLALLIKVQEGG

>Apteryx_australis_mantelli-----MDLPVFQFITGLALLIKVQEGG

>Calidris_pugnax-----MDLPVFQFITGLALLIKVQEGG

>Callorhinchus_milii-----MDLPVFQFITGLALLIKVQEGG

>Columba_livia-----MDLPVFQFITGLALLIKVQEGG

>Alligator_mississippiensis-----MDLPVFQFITGLALLIKVQEGG

>Aquila_chrysaetos_canadensis-----MDLPVFQFITGLALLIKVQEGG

>Corvus_brachyrhynchos-----MDLPVFQFITGLALLIKVQEGG

>Egretta_garzetta-----MDLPVFQFITGLALLIKVQEGG

>Fukomys_damarensis-----
MFVSLASGSKDGILRTLSRRGCFPFEMDLAATGFSTGLALQV-QGGG
>Aptenodytes_forsteri-----MDLPVFQFITGLALLIKVQEGG

>Struthio_camelus_australis-----MDLPVFQFITGLALLIKVQEGG

>Chelonia_mydas-----MDLPVFQFITGLALLIKVQEGG

>Gallus_gallus	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLSWGK-----GGGROT-----FSSQQ-----PVLWS-----
>Anser_cygnoides	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLSWGK-----GGGROT-----FSSQQ-----PVLWS-----
LPLAVRRSETDTA-EQ-----IPQD--T-----PNFH--SSLG-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLSGETEREGGKTL-----FLTAV-----SALQS-----
>Apteryx_australis_mantelli	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLSGETEREGGKTL-----FLTAV-----SALQS-----
PPLAALMFREGHSGAN-----SSRDSKLSEFLWDENIR--VEFGLALR--MTILSVCGIF-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPR--SSC-----
>Galidris_pugnax	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPR--SSC-----
-----SSIFREGHGTAN-----SSRYFKLAELLWDASI H--IQLGLALR--E-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GAFSS--Q-QWLFSGPCTRSSD-----LQRGTRQS-----
>Aquila_chrysaetos_canadensis	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GAFSS--Q-QWLFSGPCTRSSD-----LQRGTRQS-----
KLLEILTQCRAPLG-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
>Lepidothrix_coronata	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
SPLEITLQAC-----R--APLG-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
>Microcebus_murinus	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
MSTASLGPVSOHRSLPVSTAMGETAGLPCANDPWLLWDRKVGRGQGRGWPAGPQ--KSP--QAFP IRKHILLVSGCGRAA I CCSWL RPPAHQNSLKNNHFLSAERRGELELEHTHTSLQRALCFPGPA I RCGAPGKGPGSRGAAAKPALLRARPGAGLPRCRLPP	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
ELLSVFCRCRGRGTRSLLGPLLPRTTA-RSRLWIRAGAPVSSPGWASQQLAAQARPCSRCKEDKAGP	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
>Mus_musculus	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
-----MSVLAGIPD-----YSYGTG--RWGGAASGGLEQASEVSPGLSHQEAHPVSVWLCGRAA I CCSWL RPPAHQKQPKQPFPLC-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
>Struthio_camelus_australis	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----
-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----	-----MFDCRGS GSVCCSRLRPEAHQKQPKQPFPLRGEVG--GPFPH--CSGCSPPGTHSSD-----LRRGTRQS-----

```

>Danio_rerio
-----MLSHIERLP-CYNRLR-----DTAVAQYE---REKLEKVAGFPPTGSVVLSEGPCKRGL
>Opsanus_beta
-----MLN-----QSAVMIFTGICGALVVMAMAYYIYWSVLAEGPCKRGL
>Oryzias_latipes
-----MLN-----QSAVMIFTGICGAMVLMAMAYYVYWSVILADGPCKRGL
>Trachinotus_blochii
-----MCMSVVLAEGPCKRGL
>Pygocentrus_nattereri
-----MTAGALQHNGSVVLSEGPCKRGL
>Neolamprologus_brichardi
-----MLN-----QSAVMIFTGICGAMVFMAMAYYVYWSVLAEGPCKRGL
>Clupea_harengus
-----MHT-----Q-SLLHWSKSVS-QIFFKPKKGPVRSVVLSEGPCKRGL
>Fundulus_heteroclitus
-----MLN-----QSAVMIFTGICGAMVFMAMAYYVYWSVLAEGPCKRGL
>Esox_lucius
-----MLS-----QSTVMIFSGICGAFVVLAMGYVYWTIVLSEGPCRRGL
>Scleropages_formosus
-----MLC-----GCYQLRCGVFRGIVAVRWTGS-GLVPGGOVSNKRTRSVILSEGPCKRGL
>Ficedula_albicollis
-----MEDCLLWEG-----LHPGTGTIILSDGPCSRF-
>Salmo_salar
MLKNKYVYGGVQRHQCCFSVELK---TNALDLFGNV-----NRRGDPEIRSVVLADGPCKRGL
>Lepisosteus_oculatus
-----MLANQTSVLIFTGICAALLILAVAYTYVWSVVLSEGPCKRY-
>Pelodiscus_sinensis
-----MRANGKDMETTO-----NSKEHLGSPAVMTVILSEGPCKAY-

```

```

>Homo_sapiens
-----MLRWVSVASPEFLLNEVCRVITWTAVLSEGPCTRS-
>Opsanus_beta
-MLNQSAVMIFTGICGALVVMAMAYYYIYWSVVLAEGPCRRGL
>Canis_lupus_familiaris
-----MSQFSARGRI RTAVLSEGPCTRS-
>Astyanax_mexicanus
-MLNQSAVMIFTGICGALVVMAMAYYYIYWSVVLAEGPCRRGL
>Myotis_lucifugus
-MLASYSTCLFSGVCAALVAVALTYLYWTAVLSEGPCSRY-
>Haplochromis_burtoni
-MLNQSAVMIFTGICGAMVFMAMAYYYIYWSVVLAEGPCRRGL
>Danio_rerio
-MLNQSAVMIFTGICGALVVMAMAYYYIYWSVVLAEGPCRRGL
>Fundulus_heteroclitus
-MLNQSAVMIFTGICGAMVFMAMAYYYIYWSVVLAEGPCRRGL
>Monodelphis_domestica
-MLDSYSTSLFSAVCATL FVMALAYLYWTSVLSVGPCTKS-
>Macropus_eugenii
-MLANYSVCLFSAICANLFV MALAYLYWTSVLSGPCTHY-
>Esox_lucius
-MLSQSTVMIFSGICGAFVVLAMGYYYWTIVLSEGPCRRGL
>Equus_asinus
-----MVGSTSP-----ELWPRTAVLSEGPCTRY-
>Rattus_norvegicus
-MLASSSTCLFSGVCVALLAVALAYFYWTAVLSEGPCRRP-
>Lepisosteus_oculatus
MLANGTSVLIFTGICALLILAVAYTYWSVVLSEGPCRY-

```

HG0180.1 ENSG00000112246 SIM1

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>Homo_sapiens
--MSIFRGPFGAAGSRRK-----WLLRGPTGI
>Anas_platyrhynchos
--MTLFRGAMLSATSRRKGGQKYLWLLRGAASF
>Odobenus_rosmarus_divergens
--MSIFWGPFGFASPNNRRKG-----WLLRGPGAGI
>Orcinus_orca
--MSISREPGFAARNRRKG-----
>Myotis_brandtii
--MSLFGGPGFAARNRRKG-----WLLRGPGAGI
>Monodelphis_domestica
--MSVFRVLVFAAANNRREA-----WFLDGPIDI
>Sorex_araneus
--MSVFRPGGAANNRRKG-----WPRRAPAGL
>Oryctolagus_cuniculus
--MSTFRAPRFAAQNGRKG-----WLLRGPGAGI
>Equus_asinus
MIMSI FRGPFGFAARNRRKG-----WLLGDLAGI
>Manis_javanica
--MMSTFREPGYEAPNNRRKG-----WLLRSPAGI
>Loxodonta_africana
--MSIFRGPFGFAARNRRKG-----WLLWGASGI
>Heterocephalus_glaber
--MSIFOGTGFAAENRRKR-----WLLRGSAGI
>Tupaia_chinensis
--MSIFRGPFGCASPNNRKN-----WLPWGLAGI
>Trichechus_manatus_latirostr
--MSIFRGPFGFAARNRRKV-----WLLRGPGAGI
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HG0180.2 ENSG00000112246 SIM1

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>Homo_sapiens
--MRTVKRWAPPKPLPLVGTEGP
>Mustela_putorius_furo
MVGMSITIKRWAPLHPLPPAGTEVA
>Pteropus_allecto
--MNTIKRRASPHPLPPAGTEGR
>Loxodonta_africana
--MSA1KRWAPPHPLPPVGTEAA
>Tupaia_chinensis
--MIAIRRWAPAHPLPPAGTEVA
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```
>Homo_sapiens
-----MHSVFFLPF-----L-FFFFPGSELLMQIGLYSLMMQPDSPFQDYVARVEF
>Ailuropoda_melanoieuca
-----MRI GPDSLMMQPDSLRDCVARVEF
>Pteropus_vampyrus
-----MQIGLNSLMMQPDSPFQDYVARIEF
>Galeopterus_variegatus
-----MQIGLYSFMQPDSPFQD-----
>Monodelphis_domestica
MHYSSVGGGNLHLGFRLPLVTYFVFLLLFSIHPSKSELLMP SGLYSLMMQPDSPFQDCVA----
>Goturnix_japonica
-----MRPEWGFYTLMMQWDSFQGCVA-----
>Condylura_cristata
-----MHLGLNSLVMQPDSPFQDYVARVEF
>Ochotona_princeps
-----MQMGLYSLMMQPDSPFQDYVARVEF
>Equus_asinus
-----MQIGLNSLMMQPDSPFQDYVARVEF
>Loxodonta_africana
-----MRI GLYSLMMQPASPFQDYVA-----
>Mesocricetus_auratus
-----MPRGLYSLMMQPDSPFQDYVARIEF
>Tupaia_chinensis
-----MQIRLYSLMMQPDSPFQDYVARVEF
>Thamnomphis_sirtalis
-----MEWGLYTLMMQKDSFRDWVS-----
>Chrysemys_picta
-----MQTEWGFYTLMMQWDSFQDYVA-----
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HG0181.2 ENSG00000143776 CDC42BPA

>Homo_sapiens
MYMGEIEDASVK
>Balaenoptera_acutorostrata_s
MYMGEIEDASVK
>Rhinolophus_ferrumequinum
MYMGEIEDASVK
>Erinaceus_europaeus
MYMGEIEDASVK
>Ochotona_princeps
MYMGEIEDASVK
>Geratherium_simum_simum
MYMGEIEDASVK
>Oricetus_griseus
MFMGEIEDASVK
>Tupaia_chinensis
MFMGEIEDASVK
>Trichechus_manatus_latirostr
MYMGEIEDASVK

>Gallus_gallus
MDVNQPKGEHLLALKGPVSH-----
>Ailuropoda_melanoleuca
MEVNPPKGEHLLALKGPVSL-----
>Lipotes_vexillifer
MEVNPPKGEHLLALKGPVSL-----
>Dasypus_novemcinctus
MEVNPPKGEHLLALKGPVFL-----
>Sarcophilus_harrisii
MEVNPPKGEHLLALKGPVSSFSSVQNVERRTRKSNKF-----
>Trichosurus_vulpecula
MEVNPPKGEHLLALKGTVSSFSSVQNVERRTRKSYNYEFKF
>Oryctolagus_cuniculus
MEVNPPKGEHLLALKGPVSL-----
>Sturnus_vulgaris
MDVNQPKGEHLLALKGPVFH-----
>Manis_javanica
MEVNPPKGEHLLALKGPVSL-----
>Papio_anubis
MEVNPPKGEHLLALKGPVSL-----
>Cricetus_griseus
MEVNPPKGEHLLALKGPVSSDLARETVL-----
>Tupaia_chinensis
MEVNPPKGEHLLALKGPVSL-----
>Aptenodytes_forsteri
MDVNQPKGEHLLALKGPVIH-----
>Protobothrops_mucrosquamatus
MDVTQSKGEHLFALKCPVLSYTAHRI RFF-----

>Homo_sapiens	MW	VSAGLCSLRETLFFNCAME
>Leptonychotes_weddellii		
MGRKKADKLSGCNTRDISLPYDLMW	MW	VSAGLCSLRETLFFNCAME
>Lipotes_vexillifer		
	MW	VSAGLCSLRETLFFNCAME
>Rousettus_aegyptiacus		
	MW	VSAG
>Dasypus_novemcinctus		
	MW	VSAGLCSLRETFIF
>Galeopterus_variegatus		
	MW	VSAGLCSLRETLFFNCAME
>Erinaceus_europaeus		
	MW	VSAGLSSLRETVFFLTAMQ
>Elephantulus_edwardii		
	MW	VSAGLCSLRETTTTFVCYGVGVEAGGFQPSDSHRAAPNPLLLSTPANSFAWAEVLV
>Manis_javanica		
	MW	VSAGLCSLRETLFFNCAME
>Loxodonta_africana		
	MW	VSAGLCSLRETLFFNCAME
>Dipodomys_ordii		
	MW	VSAGLCSLRETLFFNCAME
>Protobothrops_mucrosquamatus		
	MMYGGCGQPGVFSLRKTLFFNCAME	
>Pelodiscus_sinensis		
	MW	VSAWIVFIEETLFFNCAVE
>Orycteropus_afer_afer		
	MW	VSAGLCSLRETLFFNCAME

>Homo_sapiens	MLCYEMPRRQRLTSGRN-
>Odobenus_rosmarus_divergens	-MPRRQRLTSSRS-
>Orcinus_orca	MLCCEMPRRQRLTSGRS-
>Pteropus_alecto	MLCCEMPRRQRLTSGRS-
>Dasypus_novemcinctus	MLCCEMPRRQRLTSSRS-
>Monodelphis_domestica	MVCCCEMPRRQRLTSSRS-
>Condylura_cristata	MLCYEMPRROTDKG----
>Oryctolagus_cuniculus	
MRSGLVQLQRADRRERGGEKKHQPPFGLGVGRWTRVHRENTSDRLNYLVAGIACSWNDLRAVFTRVQGPQAEQAPMLYCEMPRRQRLTSSRS-	
>Equus_caballus	MLCYEMPRRQRLTSGRS-
>Manis_javanica	MLCCEMPRRQRLTSGRS-
>Loxodonta_africana	MLCCEMPRRQRLTSSRS-
>Ictidomys_tridecemlineatus	MRCCEMPRRQRLTGGRS-
>Pelodiscus_sinensis	MPCKMPRRQRLTGSR I-
>Orycteropus_afer_afer	MLCCEMPRRQRLTSSRS-

>Homo_sapiens
MHR0SAGNONGEGLY-----
>Canis_lupus_familiaris
MHR0SAGNONGEGL-----
>Lipotes_vexillifer
MHR0SAGNONGEGL-----
>Miniopterus_natalensis
MHR0SAGNONGEGL-----
>Galeopterus_variegatus
MHR0SAGNONGEGL-----
>Erinaceus_europaeus
MHR0SAGNONGEGL-----
>Ochotona_princeps
MHR0SAGNONGEGL-----
>Equus_asinus
MHR0SAGNONGEGL-----
>Loxodonta_africana
MHR0SAGNONGEGLY-----
>Heterocephalus_glaber
MHR0SAGNONGEGL-----
>Tupaia_chinensis
MHR0SAGNONGEGL-----
>Trichomycterus_areolatus
MHR0SAGNONGETKSRK1FV-----GSNNWNS---RLLTCDSFF-----
>Trichechus_manatus_latirostr
MHR0SAGNONGEGLYGSGLCLRLVYERPLYPNPSPQDFGLCVRLGVPGGAGAQ
>Orycteropus_afer_afer
MHR0SAGNONGDGLY-----

>Homo_sapiens	-----MASLGRLGVWVWNRKRPRP1PMVTELYIGSRIRLCAAGSLTSTA-----
>Mustela_utorius_furo	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Orcinus_orca	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Rousettus_aegyptiacus	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Sarcophilus_harrisii	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Sorex_araneus	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Ochotona_princeps	-----MVTELYIGSRIRPCAAGSLTSTA-----
MDARAAGFCSLSLEGCRKYYGYWAGGGGGTHYLIPRLHQSAPSLHGSPGADAGVWVWNRKRPRP1PMATGLYIGSLRRPHRRFSYIDRLRVAL	
>Equus_asinus	-----MSLAP1TTLLSWLLWADRGVWVWNRKRPRP1PMVTELYIGSRIRPCAAGSLTSTA-----
>Manis_javanica	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Loxodonta_africana	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Marmota_marmota_marmota	-----MVTELYIGSRIRLCAAGSLTSTA-----
>Trichechus_manatus_latirostr	-----MSLAP1TTLLSWLLWADRGVWVWNRKRPRP1PMVTELYIGSRIRPCAAGSLTSTA-----
>Python_bivittatus	-----MVTELYIGSRIRPCAAGSLTSTA-----
>Orycteropus_afer_afer	-----MVTELYIGSRIRPCAAGSLTSTA-----

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>Gallus_gallus
MDKMFLPAST-----GQGTAYQKSW
>Anser_cygnoides
MGKMLLPATK-----KLGGAYQESW
>Caprimulgus_carolinensis
MGKMFLPATK-----EQGGSAYQKSW
>Pterocles_gutturalis
---MFLPAT-----EHGGSAYQKSW
>Alligator_mississippiensis
MSKMLLQATKKH---SFKQGSAYQKSW
>Aquila_chrysaetos_canadensis
MGKMFLPTIK-----GQGTAYQKSW
>Gavia_stellata
MGKMFLPAT-----EQ-----
>Lepidothrix_coronata
---MFLPAVK-----GQGRAYQKSW
>Fulmarus_glaucialis
MGKMFLPATK-----EQGSAYQKSW
>Aptenodytes_forsteri
MGKMFLPATK-----EQGSAYQKSW
>Takydromus_sexlineatus
---MFLPAVN-----LRKGSAYQESW
>Struthio_camelus_australis
MGKMFLPAVRKH---SLKQGSAYQKSW
>Chrysemys_picta
---MFLPATKKPICYSCLKQGRAYRKS

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HG0187.2 ENSDARG00000059610 gpr146

>Danio_rerio
MSMEIQQNPMP
>Pygocentrus_nattereri
MSVEIQQNPMP
>Esox_lucius
MSVEVQQNPMP
>Chanos_chanos
MSMEVQQNPMP
>Apteronotus_leptorhynchus
MSMEIKQNPMP
>Oncorhynchus_kisutch
MSVEVQQNPMP
>Trichomycterus_areolatus
MSVEIKQNPMP

>Gallus_gallus
MCMYVVGKSHVNTDSVP-----
>Anas_platyrhynchos
MCMYVVGKSHVNTDSVPRTGLVQPSAGVF-
>Caprimulgus_carolinensis
MCMYVVGKSHVYTEFSATTEGSAAASAVFF
>Pterocles_gutturalis
MRMYVVGKSHVYTEFGATTGGDAASAVFS
>Haliaeetus_leucocephalus
MC1YVVGKSRVYTKFGAATEGSAAASAVFF
>Fulmarus_glacialis
MCMYVVGKSHVYTEFGATTEGSAAASAVLF
>Pygoscelis_adeliae
MCMYVVGKSRVYTEFGATTEASAAASAVFF

```

>Homo_sapiens
-----MTVVLEDHYFWKAG
>Felis_catus
MTLSVLKRTDQKMTAVLEDHYFWKAG
>Lipotes_vexillifer
-----MTAVLEDHYWKTD
>Pteropus_vampyrus
-----MTVVLEDYFWKAG
>Dasypus_noveboracensis
-----MTVVLKDRYFWKAG
>Sarcophilus_harrisii
-----MTETLEHHFYWKAN
>Galeopterus_variegatus
MTLTVLRSTDQKMTVVLEDHYFWKAH
>Erinaceus_europaeus
-----MTVVLEDHYFWKAG
>Oryctolagus_cuniculus
-----MTVVLEVHYFWKAG
>Ceratotherium_simum_simum
-----MTAVLEDHYFWKAG
>Manis_javanica
-----MTAVLEDHYFWKAG
>Loxodonta_africana
-----MTAVFEDHCYWKAS
>Fukomys_darlingi
-----MTVVLEDHYFWKAS
>Tupaia_chinensis
MTWTVLRSTDQKMTVVLEDHYFWKAG
>Trichechus_manatus_latirostris
-----MTAVLEDHCYWKAS

```

>Gallus_gallus
-----MPEASEDHNHWKVC
>Anas_platyrhynchos
-----MPEASEDHNHWKAC
>Pelophylax_nigromaculatus
-----MQEGSEdHNHWRAL
>Apteryx_australis_mantelli
-----MQKMPEASEDHNHWKAY
>Merops_nubicus
-----MPEASEDHNHWKAC
>Alligator_mississippiensis
MVLPPPEP-----SP-PRTKMPEASEDHNHWKAC
>Aquila_chrysaetos_canadensis
-----MPEASEDHNHWKAC
>Gavia_stellata
-----MPEASEDHNHWKAC
>Parus_major
-MQPPPEPQPEPSQPSQSTKMPEASEDHNHWKAC
>Gekko_japonicus
-MLLLE-----PV-PPRATMPEASEDHNHWKAC
>Struthio_camelus_australis
-----MPEASEDHNHWKAY
>Chrysemys_picta
-----MPEASEDHNHWKTY
>Tinamus_guttatus
-----MPEASEDHNHWKAY

```
>Danio_rerio
-----MGIIAFVFQNGALIPYYLKPVHSGAQTIKRREGTEFVH-----
>Amia_calva
-----MGIIIPC-LQNGALIPYYLKPVHFATLTLKNCRWKKDQC-----
>Trachinotus_blochii
-----MGITTAFFLNGALIPYYLKPVHLETQTIKHCS-----
>Micropterus_salmoides
-----MGITTAFFLNGALIPYYLKPVHLETRTIKRCS-----
>Oreochromis_niloticus
-MPPSVVAMGINTASSVKQTLTLHYLKPVHLKTQSIKHCSGDHCSEPGSASLLR
>Latimeria_chalumnae
-----MGYRPTGFRNGALLPYLKPVHLVKVIFTNWAESYF-----
>Esox_lucius
-----MGIKPF-FQNGALIPYYLKPVHFETQTIKNCRLEHQQ-----
>Lutjanus_erythropterus
-----MGISTAFLLKPALIPYYLKPVHLETRTIKHCS-----
>Trematomus_bernacchii
-----MGITTAFFLNGALIPYYLKPVHLETRTIKHCS-----
>Leucoraja_ocellata
-----MGINAADIDDSLLPYLKPVDLVKAAARCLQRWSFLYQ-----
>Salmo_salar
-----MGIIIPF-FQNGALIPYYLKPVHFETQTIKTAG-----
>Lepisosteus_oculatus
MNSHSGIAMGIIIPF-FQNRALIPYYLKPVHFDMTLKDWRWINKYQY-----
>Squalus_acanthias
-----MGINAADIDDSLLPYLKPVDLVKVAARFLQWNRWCO-----
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HG0190 ENSGALG00000006949 CHD2

>Gallus_gallus
MSFFPRTFLY
>Anser_cygnoides
MSFFPRTFLY
>Apteryx_australis_mantelli
MSFFPRTFLY
>Cariama_cristata
MSFFPRTFLY
>Cuculus_canorus
MSFFPRTFLY
>Monodelphis_domestica
MSFFPRTFLY
>Aquila_chrysaetos_canadensis
MSFFPRTFLY
>Gavia_stellata
MSFFPRTFLY
>Chlamydotis_macqueenii
MSFFPRTFLY
>Manacus_vitellinus
MSFFPRTFLY
>Egretta_garzetta
MSFFPRTFLY
>Pygoscelis_adeliae
MSFFPRTFLY
>Struthio_camelus_australis
MSFFPRTFLY

HG0191 ENSGAL00000036097

>Gallus_gallus
MNKRKNPFWTVFLNQASPSISRTF
>Anas_platyrhynchos
MNKQKNPFWTVFLNEASPSISGTY
>Apteryx_australis_mantelli
MNKQKKTFWTVFLNQASPSILGTY
>Calidris_pugnax
MNKQKNPFWTVFLNQASPSVSGTY
>Alligator_mississippiensis
MDRLKKKFWTVFLNQASPSLLETY
>Monodelphis_domestica
MDKLKNSFWIVFPNETSPSSFSAQ
>Aquila_chrysaetos_canadensis
MSKQKNPFWTVFLNQASPSVLGTY
>Ornithorhynchus_anatinus
MDKLKKPLWTVFLPEASLSLGGH
>Lepidothrix_coronata
MNKRKTPITWTVFLNQASPSVSGTY
>Anolis_carolinensis
MDR1KKPFWTVFLNQFFPSMEAC
>Struthio_camelus_australis
MNKQKKTFWTVFLNQASPSILGTY
>Pelodiscus_sinensis
MD1LKKTFWIVFLSQASPSFLGTY
>Tinamus_guttatus
MNKQKKTFWTVFLNQASPSILGTY

>Homo_sapiens	
MQKLPRSCQAISQLSIQKETYHSDLRSCMPGNMGMTKCAMFQNRVRPLVKKN	
>Felis_catus	
	MFQNRV1PLVKKN
>Lipotes_vexillifer	
	MFQNRVRPLVKKN-
>Myotis_brandtii	
	MFQNRVRPLVKKN
>Dasypus_novemcinctus	
	MFQNRVRLLVKKN
>Sarcophilus_harrisii	
	MFQNR1RSLVKKN
>Monodelphis_domestica	
	MFQNR1RSLVKKN
>Condylura_cristata	
	MFQNRVRPLVKKN
>Ceratotherium_simum_simum	
	MFQNRRLPLVKKN
>Loxodonta_africana	
	MFQNRVRPLVKKN
>Ictidomys_tridecemlineatus	
	MFQNRVRPLVKKN
>Trichechus_manatus_latirostr	
	MFQNRVRPLVKKN
>Pelodiscus_sinensis	
	MFQNR1RPLGKKS

>Homo_sapiens
MISFRRMDYNIESITKRGF-----
>Anser_cygnoides
MISFGRMDYNIESITGRGL-----
>Ursus_maritimus
MISFRRMDYNIESITKRGF-----
>Ambystoma_mexicanum
MIRLGRMGYNIESITRAFLGRLOSGN
>Lipotes_vexillifer
MISFRRMDYNIESITKRGF-----
>Myotis_ricketti
MISFRRMDYNIESITKRGF-----
>Dasypus_novemcinctus
MISFRRMDYNIESITKRGF-----
>Monodelphis_domestica
MISF-RIDFNIESITKRGV-----
>Oryctolagus_cuniculus
MISFRRMDYNIESITKRGF-----
>Lepidothrix_coronata
MISFGRMDYNIESITERGL-----
>Equus_asinus
MISFRRMDYNIESITKSGF-----
>Fukomys_damarensis
MISFRRMDYNIESITKSGFCAHYS---
>Pelodiscus_sinensis
MISFGRMDSNIESITRLGL-----

HG0194 ENSG00000143507 DUSP10

```
>Homo_sapiens
-----MCESLAEEERQMVVEEYTYL---
>Ailuropoda_melanoleuca
-----MGESLAEAERQMVVEGYTYL---
>Balaenoptera_acutorostrata_s
-----MCESTAEAEERQMVVEGYTYL---
>Sarcophilus_harrisii
MKLSEWGLDAPSIATVKRQMVVEGYTYL---
>Monodelphis_domestica
MKLSEWGFNVQSIATVKRQMVVEGYTYL---
>Macropus_eugenii
-----MYKSIATVKRQMVVEGYTYL---
>Sorex_araneus
-----MVEGYTY---
>Elephantulus_edwardii
-----MVKGYFIKLF
>Equus_asinus
-----MRESIAEAERQMVVEGYTYL---
>Marmota_marmota_marmota
-----MCQSIAEAEERQMVVEGYTYL---
>Tupaia_chinensis
-----MYETVAQEERQMVVEGSTYL---
>Trichechus_manatus_latirostr
-----MCESLAEEERQMVVEGYTHL---
>Chrysemys_picta
-----MLKGNTYL---
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HG0195 ENSG00000165966 PDZRN4

>Homo_sapiens
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Odobenus_rosmarus_divergens
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Lipotes_vexillifer
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAC
>Pteropus_alecto
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Latimeria_chalumnae
MKNWSQEWRE I PCQCHYLSVLGKLESFALVC--
>Gallus_gallus
MKNSSQVWRV I PCQC I CLSVLGK-----
>Erinaceus_europaeus
MKNSSQVWRV I PFOFTCLSVLGELEDLLSLSAA
>Oryctolagus_cuniculus
MKNSSRDWRV I HFQLPCRSVLGTLEDQLPRSAS
>Elephantulus_edwardii
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Manis_javanica
MKTGGQVWRV I PFRACL PVPGLKEDSRARSAP
>Loxodonta_africana
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Ictidomys_tridecemlineatus
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS
>Trichechus_manatus_latirostr
MKNSSQVWRV I PFOFTCLSVLGKLEDLLSLSAS

HG0196 ENSG00000189403 HMGB1

```
>Homo_sapiens
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPR-----
>Megophrys_sangzhiensis
MLQIGERVKRLRIDPASHSHCSTLSSIDTALET-----
>Odobenus_rosmarus_divergens
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRARRALGDSVPR-----
>Pteropus_vampyrus
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVLAEEK-
>Dasypus_novemcinctus
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGKCEPGRWATRLADEK-
>Galeopterus_variegatus
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPR-----
>Macropus_eugenii
MLQNGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGYSVRR-----
>Condylura_cristata
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPR-----
>Ochotona_princeps
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPRGGK-
>Equus_przewalskii
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPR-----
>Manis_javanica
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRGRAPGDSVPR-----
>Ictidomys_tridecemlineatus
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQVRAGRALGDSVPR-----
>Trichechus_manatus_latirostr
MLQSGESEE-AAGSRSHSHCSTLSSIETAPGQAEPDGTGRLCASRTKNY
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HG0197 ENSG00000196132 MYT1

>Homo_sapiens
MIAFRDVILKEDRQ
>Odobenus_rosmarus_divergens
MIAFRDVILKEDRQ
>Balaenoptera_acutorostrata_s
MIAFRDVILKEDRQ
>Myotis_davidii
MIAFRDVILKEDRQ
>Galeopterus_variegatus
MIAFRDVILKEDRQ
>Monodelphis_domestica
MIAFRDVILKGERQ
>Coturnix_japonica
MIGFRDVILQRGRQ
>Oryctolagus_cuniculus
MIAFRDVILKEDRQ
>Equus_asinus
MIAFRDVILKEDRQ
>Manis_javanica
MIAFRDVILKEDRQ
>Chinchilla_lanigera
MIAFRDVILKEDRQ
>Tupaia_chinensis
MIAFRDVILKEDRQ
>Pelodiscus_sinensis
MIAFRDVMLKRARQ

```

>Danio_rerio-----MCVCVRIRVCAR-VPECRMVARGGKACLHRAERLGNRRAREEVSRLAVCLLQHPAHRERERKSE-----
>Calidris_pugnax-----MLQPC-----C-----ASVARARGEGRKSLFTQTANRLGNNA-GEEVSRLAV-----
>Latimeria_menadoensis-----MCVLYYC-----N-----VEHQWAGREGGRKSLFTQAKCLGNNA-GKEVSRLSV-----
>Fundulus_heteroclitus
MCGGFANEASLKASQSRRCFEKDCRSFRQHVCRQVRGPLLAEEGRKSVFTQTASCLGNRR-GEEVSRLCVCLLQHPALRKKKPRIRFORSTTVQTRSQHGKTGERTGFDVKSFAE
>Monodelphis_domestica-----MCVCVCVCVCVC-VVCV-----VVTVTILLCVCLILQPC-----
>Coturnix_japonica-----MLQPC-----R-----TSVARARGEGRKSLFTQTANRLGNNA-GKEVSRLSV-----
>Ornithorhynchus_anatinus-----MLQPC-----C-----TSAARERAGGRKSLFTQTANRLGNNA-VKEVSRLSV-----
>Manacus_vitellinus-----MLQPC-----C-----TSTARAGAGRKSLFTQTANRPGNSA-GEEVSRAAV-----
>Nannospalax_galili-----MRASEGSRGT-----QPRPRRTARGGKACLHRLHTAWGIMQ-----
>Lepisosteus_oculatus-----MCVIIER-----C-----WTSVGRGRRGEEESLFTQTANRLGNNA-GKEVSRLSV-----
>Ictalurus_punctatus-----MGTDSGYSITVCVRVCVG-----PRWAGREERGGKACLHRPRAWGTE-----
>Python_bivittatus-----MCLMLQQCL-----HISGGRGEKGGKACLHRLQTAWGIMQERK-----

```

HG0198.2 ENSG00000111145 ELK3

>Homo_sapiens
MESRGLSPGSS
>Mustela_putorius_furo
MESRGLSPGSS
>Lipotes_vexillifer
MESRGLSPGSS
>Rousettus_aegyptiacus
MESRGLSPGSS
>Dasypus_novemcinctus
MESRGVSPGSS
>Galeopterus_variegatus
MESRGLSPGSS
>Ochotona_princeps
MESRGLSPGSS
>Elephantulus_edwardii
MESRGVSPGSS
>Ceratotherium_simum_simum
MESRGLSPGSS
>Manis_javanica
MESRGLSPGSS
>Microtus_ochrogaster
MESRGLSPGSS
>Tupaia_chinensis
MESRGLSPGSS
>Trichechus_manatus_latirostr
MESRGVSPGSS

HG0199 ENSGALG0000007989 ADNP

```
>Gallus_gallus
MLRQKGNEQDMTLLCPGFGLTQ
>Anas_platyrhynchos
-----MMLLCPGFGLTQ
>Apteryx_australis_mantelli
MLRQKGKEQDMTLLCPGFGLTQ
>Calidris_pugnax
MLRQKGKEQDMTLLCPGFGLTQ
>Columba_livia
-----MLNQDMTLLCPGFGLTQ
>Alligator_mississippiensis
-----MSLLCPGFGLTQ
>Aquila_chrysaetos_canadensis
MLRQKGKEQDMTLLCPGFGLTQ
>Manacus_vitellinus
MLRQKGKEQDMTLLCPGWGLPQ
>Aptenodytes_forsteri
MLRQKGKEQDMTLLCPGFGLTQ
>Struthio_camelus_australis
-----MTLLCPGFGLTQ
>Chrysemys_picta
-----MSLLCPGFGLTQ
>Tinamus_guttatus
-----MTLLCPGFGLTQ
```

>Gallus_gallus
MHCNGHMNVSGEESAPLRLIVIMAL
>Anser_cygnoides
MYCNGHMNISSGESAPLHLLIIMAL
>Apteryx_australis_mantelli
MHCNGHMNVSGESAPLRLIVTMAL
>Mustela_putorius_furo
MYCNGMNLWGVIFAPSHTLFTMAL
>Hynobius_retardatus
MHCNGHMNVGGAAPAGSCTLFTMSL
>Galidris_pugnax
MHCNGHMNVLGGESAPHLLIIPMAL
>Lepidothrix_coronata
MLCNGHMNVSEGESAPLQLLIIPMAL
>Nannospalax_galili
MYCNGMNLWEVESAPSHALATMAL
>Thamnophis_sirtalis
MNCNGHMNIWRVVFIPSRGLFMAL
>Struthio_camelus_australis
MYCNGHMNVSGESAPLRLIITMAL
>Chrysemys_picta
MHCNGHMNLGVVPAPFFVLSTMAL
>Tinamus_guttatus
MHCNGHMNSSGPIST---HLLVTMAL

>Gallus_gallus-----MVCQKLEDACRAHNNVVMN
>Anser_cygnoides-----MVCQKLEDACRAHNEVVN
>Calidris_pugnax-----MVCQKLEDARRAHNEVVN
>Columba_livia-----MVCQKLEDACRAHNEVVN
>Alligator_mississippiensis-----MVCQKL-----
>Sarcophilus_harrisii
MIRDNIASSTFLIYRASKTDGLSSAVGDACRAHDNEVVN
>Falco_cherrug-----MVCQKLEDACGAHNEVVN
>Pseudopodoces_humilis-----MVCQKLEDACRAHNEVVK
>Aptenodytes_forsteri-----MVCQKLEDAHRAHNEAVN
>Takydromus_sexlineatus-----MVCQKL-----
>Struthio_camelus_australis-----MVCQKL-----
>Trachemys_scripta-----MVCQKL-----

>Homo_sapiens	-----MRSDLELLIARGDYCYIGFQANGKPGGGVWHEEALVTAADWLQPRL-----
>Channa_punctata	-----MRSDTRLLIARADYY-----
>Oryzias_melastigma	-----MRSDTRLLIAHADYYCVSFSTNE-----
>Mustela_putorius_furo	-----MRSDLELLIARGDYCYIGFQANGKAGGGVWHEEALVTAADWPRPRL-----
>Ambystoma_mexicanum	-----MRSDLELLIARGDYCYIGFQANGKPGGGVWHEEALVTAADWPRPRL-----
MLLAGSHPCVCTPPLPPLHPGSGYTAHSPNLEHIIRTPSQINGSLPAPPKRFTLNPKISASPRVPFFFEKFALWLGMRSALEPFIARGDYCYIGCRANGGGGRDRACGNVGY-SD-----	
>Pteropus_vampyrus	-----MRSDLELLIARGDYCYIGFQANGKPRGGVWHEEALVTAADWPRPRL-----
>Pimephales_promelas	-----MRSDPKLLIARADYY-----
>Austrofundulus_limnaeus	-----MRSDTRLLIARADYY-----
>Scleropages_formosus	-----MRSDITLLIARADY-----
>Ceratotherium_simum_simum	-----MRSDMELLIARGDYCYIGFQANGKPGGGVWHEEALVTAADWPRPRL-----
>Cavia_porcellus	-----MRSDLELLIARGDYCYIGFQANRKGGGVWHEEALVTAADWLRPKDKEARGGIGVCSKLOQEKOCVRERGLSHSQVSSSCTLFKSLH-----
>Chrysemys_picta	-----MRSDLELLIARGDYCYIGFQANSSRRGGVWHEALDTASDWPGRGL-----

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>Homo_sapiens
-----MSL-----WHP-FPKFSLGTPRTPAGSHCSRTALVKITQTWISKEYFHCSVONTK
>Xenopus_laevis
-----MSL-----WHP-FPEPRARIPSTPAAHTEYL-----IITG-----
>Ursus_maritimus
-----MSL-----WHP-FPKFRD-SHRTSAGSHHS-----
>Physeter_catodon
-----MSL-----MRLEREAETR-RPRVSKGLHRTSAGSHCS-----
>Rousettus_aegyptiacus
-----MSL-----WHP-FPKFRDSTTPQLDLQALHLH-----
>Dasypus_novemcinctus
-----MSL-----WHP-FPKFSDS---TDPEGSQCSLTAQVTIAQTWISKYIHCFIGHIK
>Condylura_cristata
MVSA-----GMAPCEACEGWI RGRPHSLVMTTCTTSAGSHCS-----
>Oryctolagus_cuniculus
-----MSL-----WHP-FPKLRTSTEPSWVPLFL-----NYVS-----
>Equus_caballus
-----MSL-----WHP-FPKFRE-LHGTSAGSHCSSTALVKLTHTRISKEYFHCSICHTK
>Manis_javanica
MLPRLIGDDQFLLIITWPQSNLR--KIPEMGLHCTSAVSHCS-----
>Marmota_monax
-----MSL-----WHP-FPKFRNSESPSWSLFL-----NCI-----
>Tupaia_chinensis
-----MSL-----WHP-FPKFRDS---TCWVALFL-----SCIS-----
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HG0204 ENSG00000162599 NF1A

>Homo_sapiens
MPLTPAYSRHV
>Felis_catus
MPLTPAYSRHV
>Myotis_lucifugus
MPLTPAYSRHV
>Galeopterus_variegatus
MPLTPAYSRHV
>Condylura_cristata
MPLTPAYSRHV
>Ochotona_princeps
MPLTPAYSRHV
>Elephantulus_edwardii
MPLTPAYSRHV
>Loxodonta_africana
MPLTPAYSRHV
>Nannospalax_galili
MPLTPAYSRHV
>Thamnophis_sirtalis
MPLTPGYSRHV
>Chrysemys_picta
MPLTPGYSRHV
>Orycteropus_afer_afer
MPLTPAYSRHV

HG0205 ENSG00000184611 KCN7

>Homo_sapiens
MGRDFWFKRMLCHKERLARWPGL
>Leptonychotes_weddelii
MGRDFWFKRMLCHKERLARWPGL
>Physeter_catodon
MGRDFWFKRMLCHKERLARWPGL
>Rousettus_aegyptiacus
MGRDFWFKRMLCYKERLARWPGL
>Monodelphis_domestica
-----MICHKEKLAGWSGL
>Erinaceus_europaeus
MGRDFWFKKMLCHKERLARWPGL
>Ochotona_princeps
MGRDFWFKRMLCOPERLARWPGL
>Equus_caballus
MGRDFWFKRMLCHKERLARWPGL
>Loxodonta_africana
MGRDFWFKRMLCHKERLARWPGL
>Marmota_marmota_marmota
MGRDFWFKRMLCHKERLARWPGL
>Trichechus_manatus_latirostr
MGRDFWFKRMLCHKERLARWPGL
>Pelodiscus_sinensis
MGRDAVIGRRMICHKG-----

>Gallus_gallus
MVGAIIPQPRRFWGPVGWQVSSASCANDRPLWDGEIDPEWSGILLOREPHTGGLTWTS
>Anser_cygnoides
MVGAIIPQPRRFWGPVGWQVSSASCANDSPRRDGEVDPEHGGVLLORDAALQH1P---
>Calidris_pugnax
MVGAIIPQPRRFWGPVGWQVSSASCANDRPLRDKEVNPEQSRVLLORDAALQCTP---
>Columba_livia
MVGAIIPQPRRFWGPVGWQVSSASCANDRPLWDRETDPESQSRVLLORDDALQSTL---
>Alligator_mississippiensis
MVGAIIPQPRRFWGPVGWQVSPASCANDRVLRGHGYLARRGGRLRSDAVLQRAP---
>Falco_cherrug
MVGAIIPQPRRFWGPVGWQVSSASCANDRLLRDREVNPEQSGVLLORDAVLHRTL---
>Manacus_vitellinus
MVGAIIPQPRRFWGPVGWQVSSAGCANDRLLWDREVNPEISRVLLORDAVLQTTs---
>Pygoscelis_adeliae
MVGAIIPQPRRFWGPVGWQVSSASCANGRPLRDPEVNPEESGVLLORDAALQCTP---
>Boiga_irregularis
MVGAIIPQPRRFWGPVGWQVSPASFTSHRLLQKEKTPARGROPVQWDAVQPTS---
>Struthio_camelus_australis
MVGAIIPQPRRFWGPVGWQVSSASCANDYPLQDGEPNLEPCGVLLORDAALQRTp---
>Chrysemys_picta
MVGAIIPQPRRFWGPVGWQVSPASCANDRLLLGQESCSARGG-----

>Homo_sapiens	-----MGLVLLSSGAARNGGSHLASAAGMDQTAS
>Canis_lupus_familiaris	-----MDQTAS
>Lipotes_vexillifer	-----MDQTAS
>Myotis_davidii	-----MDQTTS
>Sarcophilus_harrisii	-----MGQTTS
>Galeopterus_variegatus	-----MDQTAS
>Monodelphis_domestica	-----MDQTAS
MEPPAREGED-----TFSTKPYSPRGVLSHMHESLSQGAARDGGSDRASGVGMGTTS	
>Condylura_cristata	-----MDQTAS
>Ochotona_princeps	-----MDQTAS
>Elephantulus_edwardii	-----MDQTAN
>Ceratotherium_simum_simum	-----MDQTAS
MEGVVWGGRRGGRGWGAGAGRRPHQLVGNGLVQLSPGATRNQGGSHLASAAGMDQTAS	
>Manis_javanica	-----MDQTAS
>Marmota_marmota_marmota	-----MDQTAS
>Tupaia_chinensis	-----MDQTAS

>Gallus_gallus-----MSQDDGENPARNRDGLRPEPDQGEIQSTLTAI
>Anser_cygnoides-----MKGENPARNRDGLQPEPDQGEIQSSTLRAI
>Canis_lupus_familiaris-----MOGENPSWINRDGLRTEDEER-----
>Pteropus_vampyrus
MKNEPLPHPCCLSPHAPREEFLRKAAREGFFPSHMIQDAGENPSWINRDGPRTEDEER-----
>Sarcophilus_harrisii-----MEGENPTWINRDGL-----
>Monodelphis_domestica-----MKGENPAWINRDGL-----
>Trichosurus_vulpecula-----MKGENPAWINRDGL-----
>Parus_major-----MKGENPARSRDGLQLEPDRGEPOSSAWRAI
>Ceratotherium_simum_simum-----MIQDAGENPSWINRDGPRTEDEER-----
>Pan_paniscus
MKNEPLPHPCCLSPHAPREEFLRQAAREGFFPSHMIQDAGENPSWINRDGPRTEDEER-----
>Chrysemys_picta-----MKGENPARSGDGLRMRI-----


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>Homo_sapiens
-----MGPELNQMKRDKV-----
>Ailuropoda_melanoieuca
-----MGPEVNQMRDRKVCCGKA I
>Physeter_catodon
-----MGPEPNQMRDRKV-----
>Rousettus_aegyptiacus
MQGRILLGTENGPEPNQMRDRKV-----
>Dasypus_noveboracensis
MQGENPSWNRDGGPEPTQMRDRKV-----
>Galeopterus_variegatus
-----MGPELNQMKTDKV-----
>Sorex_araneus
-----MGPEPNQMRDRKV-----
>Oryctolagus_cuniculus
-----MSPEPSQMKRDKV-----
>Ceratotherium_simum_simum
MQGRILLGTENGPEPNQMRDRKV-----
>Manis_javanica
-----MGPEPNQMRDRKV-----
>Loxodonta_africana
-----MGPEPTQMRDRKV-----
>Marmota_marmota_marmota
-----MGPEPDQMRDRKV-----

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HG0208 ENSGALG00000013272 PRMT8

>Gallus_gallus
MPSWSLHAQVQFSWCFSPV
>Anser_cygnoides
MPSWSLHAQVRFWSWCFSPV
>Chaetura_pelagica
MPSWSLHAQVQFSWCFSPV
>Charadrius_vociferus
MPGWSLHAQVQFSWCFSPV
>Aquila_chrysaetos_canadensis
MPSWSLHAQVQFSWCFSPV
>Mesitornis_unicolor
MPSWSLHAQVQFSWCFSPV
>Zonotrichia_albicollis
MPSWSLHAQVQFSWCFSPV
>Nipponia_nippon
MPSWSLHAQVQFSWCFSPV
>Struthio_camelus_australis
MPSWSLYAQVQFSWCFSPV
>Chrysemys_picta
MPRWSLHAQVQFSWCFSPV
>Calypte_anna
MPSWSLYAQVQFSWCFSPV

>Homo_sapiens
MHPQSPKASLSFSLPNCGKMRRLLEHLLAWLKRK-----
>Canis_lupus_familiaris
-----MRRLLEHLLAWPKRK-----
>Rousettus_aegyptiacus
-----MRRLLEHVG-----
>Dasypus_novemcinctus
MHPQSPKASLSFSLPNCGKMRRLLEHLLAWLKRK-----
>Oryctolagus_cuniculus
-----MRRLLEHLLAWLKRK-----
>Elephantulus_edwardii
MHPQSPKASLSFSLPNCGKMRRLLEHLLAWLKRK-----
>Ceratotherium_simum_simum
-----MRRLLEHLLAWLKRK-----
>Loxodonta_africana
-----MRRLLEHLLAWLKRK-----
>Chinchilla_lanigera
MHPQSPKASLSFSLPNCGKMRRLLEHLLAWLKRK-----
>Trichechus_manatus_latirostris
MHPQSPKASLSFSLPNCGKMRRLLEHLLAAFLPKVFSRLLGAK
>Chrysemys_picta
-----MRWLEQLLG-----

>Homo_sapiens
-----MPCRCCKMCLWPAGGRKRK
>Felis_catus
-----MPCRCCKMCLWPAGGRKRK
>Balaenoptera_acutorostrata_s
-----MPCRCCKMCLWPAGGRKRK
>Rhinolophus_ferrumequinum
-----MPCRSCKTCLWPAGGRKRK
>Dasypus_novemcinctus
-----MPCRCCKMCLWPAGGRKRK
>Condylura_cristata
-----MCLWPAGGRKRK
>Oryctolagus_cuniculus
-----MPCRCCKMCLWPAGGRKRK
>Equus_asinus
-----MPCRCCKMCLWPAGGRKRK
>Manis_javanica
-----MCLWPAGGRKRK
>Nannospalax_galili
-----MPCRCCKMSLRPAGGRKRK
>Anolis_carolinensis
MAEARLLSSVPRREPPCRCKSRLQPAGGRKRK

HG0211 ENSG00000176204 LRRTM4

>Homo_sapiens
MDKPSLHSE
>Mustela_putorius_furo
MDKPSLHSE
>Rousettus_aegyptiacus
MDKPSLHSE
>Condylura_cristata
MDKPSLHSE
>Oryctolagus_cuniculus
MDKPSLHSE
>Lepidothrix_coronata
MDKPSLHSE
>Manis_javanica
MDKPSLHSE
>Loxodonta_africana
MDKPSLHSE
>Heterocephalus_glaber
MDKPSLHSE
>Tupaia_chinensis
MDKPSLHSE
>Trichechus_manatus_latirostr
MDKPSLHSE

```
>Danio_rerio
MLPSILQRRAGPSSSPVSGNTSTV11YAFICLLEPEVDSAVSRSLF-----
>Hynobius_retardatus
-----MV11FSFICLLEQESLARSARFRSVLKLF-----

>Alosa_alosa
MLPSILQ-DAKGPSSTSPVSGNTSMV11FSFICLLEPERLARGRFSSVLKLF-----
>Latimeria_chalumnae
-----MV11FSFICLLEQESLARGRFSSVLKLF-----

>Esox_lucius
MLLSILQ-DAKGPSSTSPVSGNTSMV11FFVYLSGAGAPCQKWSIQQCPEAFML----
>Apteronotus_leptorhynchus
MLPSILQ-DAKGPSSTSPVSGNTSMV11FSFICLLEPERLARGRFSSVLKLF-----
>Lepisosteus_oculatus
MLPSILQ-DAKGPSSTSPVSGNTSMV11FSFICLLEGERLARGRFSSVLKVFDVVVG
>Anolis_carolinensis
-----MV11FSFICLLEQSRPALPEVDSAVS-----

>Pelodiscus_sinensis
-----MV11FSFICLLEQESLARGRFSSVLKLF-----

>Tetronarce_californica
-----MV11FRLVFVWSRRTLSE--VDSAVS-----
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HG0213.1 ENSGALG0000001946 RSP01

>Gallus_gallus
MGLDPSSCAPYGDERTMLPAT
>Anser_cygnoides
MGLDPSSCAPYGDERTMLPAT
>Xenopus_laevis
MGLDPNSCGPYKDESRMLPVT
>Apteryx_australis_mantelli
MGLDPRSCAPYGVDRIMLPAT
>Hynobius_retardatus
MGLHLSTFDYPYGDENRAMLPAT
>Callidris_pugnax
MGLEPSPCAPYGDGRAMLPAT
>Lepidothrix_coronata
MGPRPSSCAPHRDEGRAMLPAT
>Struthio_camelus_australis
MGLDPHSCAPYGVDRIMLPAT
>Pelodiscus_sinensis
MGLDPSSAPYGVGRMLPAT

>Gallus_gallus-----MGMESTALRPGFINVQIALI
>Anser_cygnoides-----MGMESTALRPGFINVQIALI
>Calidris_pugnax-----MGMESTALRPGFINVQIALI
>Lepidothrix_coronata
MQEFALDAFTKLDLTVIIIIKSPDPVDGQGVYGLRPGFINVQIALI
>Struthio_camelus_australis-----MGMESTALKPGFINVQIALI
>Chelonia_mydas-----MGMESAALWAGVINVPITALI

>Gallus_gallus
METNQIESPLGSGCLHAGVKKCCRSSGSPSERRGG
>Anas_platyrhynchos
METNQIESPFGFSSLA-----
>Ambystoma_mexicanum
METNQIESPLGFACLPASVKSDVGRAS-----
>Calidris_pugnax
METNQIESPFGFSSLP-----
>Alligator_sinensis
METNQIESPLGFSSLHARVKSDAGREGAPLRCE---
>Monodelphis_domestica
METNQIESPFGFSPACLS-----
>Acanthis_flammea
METNQIESPFGCSLPA-----
>Struthio_camelus_australis
METNQIESPFGCSSLPA-----
>Chrysemys_picta
METNQIESPLGFSLLHARVKSDAGRERAPLRCE---

>Homo_sapiens	-----MNKTLMKCWKPVETQ-----
>Mustela_putorius_furo	-----MSKTLMRCWKPVETQ-----
>Miniopterus_natalensis	
MLRESWSCIIEVAGGENNAGNTOKRDVVTLSPGLSGLAPTSFIPRLRKKAFGNMSKTLMKCWKPVETQ-----	
>Galeopterus_variegatus	-----MYKTLMRCWKPVEMQ-----
>Monodelphis_domestica	-----MLLPSPGEGSKIGNMNKILINCWKPIGYPTY-----
>Oryctolagus_cuniculus	-----MNKPSMKCWKPVETQ-----
>Equus_caballus	-----MSEALMKCWKPVETQ-----
>Cavia_porcellus	-----MNKALMKCWKPAETQ-----
>Tupaia_chinensis	-----MYKTLRNCWKPVETQ-----

HG0215 ENSDARG0000079280 dhrrsx

>Danio_rerio
MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Channa_argus
MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Pygocentrus_nattereri
MQSLISPVTKAVLVALFIFAILLILYVILWYICRDVDCDHGI
>Maylandia_zebra
MQSFISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Poecilia_latipinna
MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Esox_lucius
MQSFLSPFNKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Platichthys_stellatus
MQSIISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI

HG0215 ENSGALG00000016681 DHRSX

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>Gallus_gallus
-----MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Astyanax_mexicanus
-----MQSLISPVTKAVLVALFIFAILLILYVILWYICRDVDCDHGI
>Maylandia_zebra
-----MQSFISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Sinocyclocheilus_rhinoceros
-----MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Austrofundulus_limnaeus
-----MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Esox_lucius
MSSVMQSFISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Zonotrichia_albicollis
-----MQSLISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Platichthys_stellatus
-----MQSIIISPVTKAILVALFIFAILLILYVILWYICRDVDCDHGI
>Salmo_salar
MSSVMQSFISPVNKAILVALFIFAILLILYVILWYICRDVDCDHGI
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>Gallus_gallus	-----MICGSVQLELSE
>Anas_platyrhynchos	-----MICGSVQLELSE
>Calidris_pugnax	-----MICGIVQLELSE
>Columba_livia	-----MICGIVQLELSE
>Alligator_mississippiensis	-----MICGSVQLELTE
>Zonotrichia_albicollis	-----MICGSVQLELSE
MPGAEILGWFLTKVEGTREPREVDSSQDERASLEMI	CGSVQLELSE
>Aptenodytes_forsteri	-----MICGSVQLELSE
>Takydromus_sexlineatus	-----MVCGSVKLELTK
>Chrysemys_picta	-----MICGSVQLELTE

>Homo_sapiens	-----MICSSARLKLTE
>Canis_lupus_familiaris	-----MICSSARLKLTE
>Orcinus_orca	-----MLCSSARLKLTE
>Eptesicus_fuscus	-----MICSSARLKLSE
>Dasypus_novemcinctus	-----MICSSARLKLTE
>Sarcophilus_harrisii	
MSFYLMFSLILVDFFLFFKKQYVPVSVEMICSSARLELTE	
>Monodelphis_domestica	-----MICSSARLELTE
>Macropus_eugenii	-----MICSSPRLELTE
>Condylura_cristata	-----MICSSARLKLTE
>Elephantulus_edwardii	-----MICSSARLKLTE
>Ceratotherium_simum_simum	-----MICSSARLKLTE
>Manis_javanica	-----MICSSARLKLTE
>Loxodonta_africana	-----MICSSARLKLTE
>Ictidomys_tridecemlineatus	-----MICSSARLKLTE
>Tupaia_chinensis	-----MICSSARLKLTE
>Trichechus_manatus_latirostr	-----MICSSARLKLTE

>Homo_sapiens	-----MNFQVVDLPLRSAQ
>Odobenus_rosmarus_divergens	-----MNFQVVDLPLRSAQ
>Orcinus_orca	-----MNFQVVDLPLRSAQ
>Galeopterus_variegatus	-----MNFQVVDLPLRSAQ
MFLSSASALMLELGPRAARTARKGASSPGGSDGGGALGVLGSEERKVVDP LGRKGSHRASATAKGEGRGRGGGTAYMNFQVVDLPLRSAQ	
>Gallus_gallus	-----MNFQALDLPPRSAQ
>Loxodonta_africana	-----MNFQVVDLPLRSAQ
>Ctenomys_sociabilis	-----MNFQVVDLPLRSAQ
>Trichechus_manatus_latirostr	-----MNFQVVDLPLRSAQ
>Orycteropus_afer_afer	-----MNFQVVDLPLRSAQ

>Gallus_gallus
MRRKSGESQLFTGTGEWLFYLTLSIRV
>Chaetura_pelagica
MKRKSGGSQLFTGTG-----
>Apteryx_australis_mantelli
MKRKSGESQLFTGTG-----
>Buceros_rhinoceros_silvestri
MKRKSGKACQLFTGTG-----
>Calidris_pugnax
MRRKSGESQLFTGTG-----
>Pterocles_gutturalis
MTRRSGESQLFAGTG-----
>Columba_livia
MKRKSAKSLFPGTG-----
>Falco_cherrug
MKRKSGESQLFTGTG-----
>Gavia_stellata
MKRQSGESQLFTGTG-----
>Chlamydotis_macqueenii
MKRKSGESQLFAGTG-----
>Sturnus_vulgaris
MRRKSGAPCLFPATG-----
>Egretta_garzetta
MKRKSGESQLFTGTG-----
>Picoides_pubescens
MKRKSGKSQLFTGTG-----
>Nestor_notabilis
MKRKPGESCVFTGTG-----
>Pygoscelis_adeliae
MKRKSGESQLFAGSG-----
>Struthio_camelus_australis
MKRKSGESQLFTGTG-----
>Tinamus_guttatus
MKRKAGESQLFTGTG-----
>Calypte_anna
MKRKSGESQLFRGTG-----

>Danio_rerio-----MDERSSPADLRERGDYS-----
>Channa_argus-----MRGDGGPKRSPADIRE-----
>Xenopus_laevis
MQL-----QKNGALAESSGCTEW-----STLHTHEGRGRGSPADLRGRADYRG I
>Haplochromis_burtoni-----MREAGQPERSPPADIRE-----
>Cyprinodon_variegatus-----MREDGGPERSPPADIRE-----
>Gadus_morhua
MRIRALDTPVDYGMFLCGYQTGVFFELTHGSMRENGQTERSSPADIRE-----
>Lutjanus_erythropterus-----MREDGGPERSPPADIRE-----
>Notothenia_coriiceps-----MREDGGPERSPPADIRE-----
>Cynoglossus_semi laevis-----MGEDGGPERSPPADI-----

>Danio_rerio
MAHAKAPPSFRLQRLQFN-QQ-----
>Pygocentrus_nattereri
-----MQFN-QQVLL-----
>Clupea_harengus
MAYAKAPPSFRLQRLQFN-QQ-----
>Sarcophilus_harrisii
MALATAPPSFGLRLLLPINQOIYRSALKMSSVSVHLLRQLH-
>Monodelphis_domestica
MALATAPPSFGLRLLLPINQOIYRSALKMSSVSVHLLRQLH-
>Esox_lucius
MAYAKAPPSFRLQRLQFN-QQRAVAGR-KTS-----
>Apteronotus_leptorhynchus
MVHAKAPPSFRLQRLQFN-QQGLAV-----
>Salmo_salar
MAYAKAPPSFRLQRLQFN-QQREKHCQ-SCCGGTQDCYYL-
>Trichomycterus_areolatus
-----MLFN-QQAGLSSDCAKQCDGPTLIGNHR

>Gallus_gallus
-----MLGPAGLGLPT
>Anser_cygnoides
-----MLGPAGLGLPT
>Calidris_pugnax
-----MLGPVGLGLPT
>Aquila_chrysaetos_canadensis
MPSGGVAPVPGSRMLGPAGLGLPT
>Acanthis_flamea
-----MPGPAGLGLPT
>Aptenodytes_forsteri
-----MLGPAGLGLPT
>Struthio_camelus_australis
-----MLGPAGLGLPT
>Pelodiscus_sinensis
-----MMGPAGLDLPT
>Tinamus_guttatus
-----MLGPAGLGLPT

>Gallus_gallus	MPTGNRKLGFEKTRSQ
>Canis_lupus_familiaris	MFDSPGMLLPGLQISELSFVGLLGRWLATLELVQVCPGNGAFPEFRFFVVLSTFTYTIMPTGNRKPVFQKKT
>Calidris_pugnax	MPTGNRKPGFQKKI
>Galeopterus_variegatus	MIMPTGNRKPVFPKKT
>Erinaceus_europaeus	MIMPTGNRKPGFQKKA
>Oryctolagus_cuniculus	MPTGNRKPVFQKKT
>Lepidothrix_coronata	MPTGNRKPGFQKKT
>Homo_sapiens	MIMPTGNRKPVFQKKT
>Struthio_camelus_australis	MPTGNRKLEFQKKS

>Gallus_gallus
MQKPGFLWLLRINSL---
>Anser_cygnoides
MRKSGFLWLLRINSLQHI
>Alligator_sinensis
MQRARFLWMLRIHCL---
>Aquila_chrysaetos_canadensis
MQKPGFLWLL-----
>Corvus_brachyrhynchos
-----MLRTSSL---
>Pygoscelis_adeliae
MQKPGFLWSLRINSL---
>Struthio_camelus_australis
MQKPGFL-----
>Pelodiscus_sinensis
MQWPGFL-----
>Calypte_anna
MQKPGFLWMLRTGSLQHS

>Homo_sapiens	-----MDGRVRERLRLPLPFRVLLRLRLRLGCDWDATVTRASIASIESNAKTOPGSLTGWMK
>Anas_platyrhynchos	-----MDGRGSEKPL---QPCLLLVRLRQRLGCDWDATVTWASIASIESNAKTOPGSLTGWMK
>Monodelphis_domestica	-----MDGRGRERLQMPLPFRLLVRLRQRLGCDWDTTVTWASIASIESNAKTOPGSLTGWMK
>Coturnix_japonica	-----MDGRVRERLRLPLPFRVLLRLRLRLGCDWDATVTRASIASIESNAKTOPGSLTGWMK
MVYFFFFFQLCFSWIFSGSILGSGAGVFKKII CSII FLVWWWMDGRGSEKPL---QPCLLLVRLRQRLGCDWDATVTWASIASIESNAKTOPGSLTGWMK	
>Oryctolagus_cuniculus	-----MDGRVRERLRLPLPFRVLLRLRLRLGCDWDATVTRASIASIESNAKTOPGSLTGWMK
>Ficedula_albicollis	-----MDGRGSEKPL---QPCLLLVRLRQRLGCDWDATVTWASIASIESNAKTOPGSLTGWMK
>Ceratotherium_simum_simum	-----MDGRVRERLRLPLPFLVLLRLRLRLGCDWDTTVTRASIASIESNAKTOPGSLTGWMK
>Rattus_norvegicus	-----MDGVRERLRLPLPFRVLRLRLRLGCDWDATVTQASIASIESNAKTOPGSLTGWMK
>Tinamus_guttatus	-----MDGRGSEKPL---QPCLLLVRLRQRLGCDWDATVTWASIASIESNAKTOPGSLTGWMK

HG0224 ENSG00000118007 STAG1

>Homo_sapiens
MPPDGGGLQLR
>Ailuropoda_melanoleuca
MPPDGGGLQLR
>Lipotes_vexillifer
MPPDGGGLQLR
>Rousettus_aegyptiacus
MPPDGGGLQLR
>Gallus_gallus
MPPDGGGLRLR
>Condylura_cristata
MPPDGGGLQLR
>Ochotona_princeps
MPPDGGGLQLR
>Equus_asinus
MPPDGGGLQLR
>Mus_musculus
MPPDGGGLQLR

>Homo_sapiens
MFAGWDRQSGNMRRPRYSCSRAARAGLGK-----
>Amia_calva
MFAGRAA-----
>Mustela_putorius_furo
MFAGWAGQSRNMRRPRYSCSRAARARLGK-----
>Pteropus_allecto
MFAGWAGQSGNMRRPRYSCSRAARARLGK-----
>Oreochromis_niloticus
MFAVSGCVLGNMSRVRYSESRAARRRPLDKAEETAVRAV
>Poecilia_latipinna
MFAGSASVOGNMSRRRYSESRAAG-----
>Manis_javanica
MFAGWAGQSGNMRRPOHSCSRAARAPPQK-----
>Ictidomys_tridecemlineatus
MFAGWAGQSGNMRRPRYSCSRAARARLGK-----
>Salmo_salar
MFAGWGSVLGNMRRVTYSVRAENRRPLNKAERRPRFVWF

>Homo_sapiens
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Mustela_putorius_furo
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Miniopterus_natalensis
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Coturnix_japonica
-----MLISGRFLGGRGGISFIASPVRSVQSALALGELIDEGVSGRAHFTLSFYL
>Ceratotherium_simum_simum
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Manis_javanica
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Cavia_porcellus
MERFIYRLYYLLWEGRWQYKGMLISGRFWGEGVEY-QFLHHLSGVSNQRWL-----
>Salmo_salar
-----MYLTNGGGGAQGEY-PFLHHLSVASNRIRV-----

HG0226.2 ENSG00000180592

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>Homo_sapiens
MAEQPIESADMVNKF--IKETPWL-----LKNSTLYIWICTSGKAKYPFILLITRMCLFLEEQNT
>Mustela_putorius_furo
-----MCLFLEEQNI
>Manis_javanica
-----MCLFLEEQNM
>Chinchilla_lanigera
-----MSESFFFGRGEYLLVRPEQGVLLNLKKEIIVHFFFL--EGSEISVYSLTTRMCLFLEEQNI
```

>Homo_sapiens-----MRLGGPLL SFGNILDILENDTKICLNLTKKRLNHIDFHPK
>Mustela_putorius_furo
MPGLHLCCSCKHRTVKKILPNFAKEPTSHLGILIMQLGRPLL SFGNILDILENDTKICFNLTKKRLNNIDIHFK
>Chinchilla_lanigera
MPGLHLCCSCKHRTVKKVLPSAKOPTKRLGTLVIQVGRLLLSFGNILDSENDSKLCFNLTKKRLNHTDIDHPK

HG0227.1 ENSGALG00000031929

>Gallus_gallus
-MTALNNWVHFGGYGWSSVY-
>Anser_cygnoides
-MTALNNWVHFGGYHWIPVY-
>Ambystoma_mexicanum
MMTTFNNSWQFGGFHWIRAY-
>Calidris_pugnax
-MTALNNWQFGGFHWISVYS
>Aquila_chrysaetos_canadensis
-MTALNNRWRFGGFRWISVC-
>Lepidothrix_coronata
-MTALNNWQFGGFHWISV--
>Struthio_camelus_australis
-MTALNNWVHFGGFHWIPVY-
>Chrysemys_picta
MMTAFNNWQFGGFHWISVC-

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>Homo_sapiens
-----MGIKVSSEE--PFLP--FVAISTGLQGTSLGFIYVCFTHCLSLCLRHFH-----
>Anser_cygnoides
-----MEKVSNWECSLLPCLSVATISAGLLGVAFLLGFCVCFYCFPLPFQGEFPHYDQAR
>Coturnix_japonica
MRSLQGNCFVTDVSMKVSNWECSLFPCLSVATISAGL-----
>Lepidothrix_coronata
-----MEKVSNWECSLLPCLSVATISAGLLGVAFLLGFCVCFYCFPLPFQGEFPHYDLAK
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>Danio_rerio
MSLTASKEARTCCAARVV-LAIVIVAFONTSLTPQITRIASEVEEKCS
>Astyanax_mexicanus
MSLVASKEARTCSAA-----
>Alosa_alosa
MSPVPSKEARTCFAA-----
>Latimeria_chalumnae
MSLVPSKEARTCCAAGVVLSIVIVGFF-----
>Apteronotus_leptorhynchus
MSLVPSKEARTCFAA-----
>Scleropages_formosus
MSPIGSKETRTRCFGD-----
>Salmo_salar
MSPLHSKEARTCFAD-----
>Lepisosteus_oculatus
MSPIPSKEARTCFAD-----

HG0229 ENSGALG00000005474

>Gallus_gallus
MC1HFWTLPFLGV-----
>Apteryx_australis_mantelli
MCMHFGWTLPFLAV-----
>Calidris_pugnax
MC1HFGWTLPLLCI-----
>Haliaeetus_leucocephalus
MC1HFEWTLPFLGI-----
>Lepidothrix_coronata
MC1RFGWTLPFLGI-----
>Phalacrocorax_carbo
MC1HFGWTLPLLLI-----
>Pygoscelis_adeliae
MC1HFGWTLPLLCI-----
>Pelodiscus_sinensis
MCAHFRWTLPCLGFSDLVLSPEADY

>Gallus_gallus-----MQIMLLECIWVRDEFCITLRSLPIHLLDYLLMTF
>Anser_cygnoides-----MQIMPLECI-----
>Calidris_pugnax
MVAVDLPFLPSSSCWLGAAAGGGGARWAVARPAAGERLRNVHGIGIVPLDCIWVKDESRVSLRSLPTHFLNYLLMVF
>Aquila_chrysaetos_canadensis-----MQIMPLDCIWIKDEFCISFRSLPTHFLNCFLMVF
>Sturnus_vulgaris-----MGEECSIAVKRQQFSPLGSFHGIGIMPLDCIWVKDEFSISLRSLPTHFPDYLLMVF
>Pygoscelis_adeliae-----MQIMPLDCIWVKDEFCVSLRSLPTHFLNYLFMVF
>Anolis_carolinensis-----MLLECIWEHNDFCLPDPRLPVPLMVLSGD-----
>Chrysemys_picta-----MPLECIWVNDSCLSRPCLPIHFLNSLWMVF-----

HG0231 ENSG00000150636

>Homo_sapiens
MQEILLFTHVAATEIL-EQPSKPRGS-----
>Anas_platyrhynchos
MQEILLFTRLCTEKQ-EEPRKPRG-----
>Canis_lupus_familiaris
MQEILLFTHVSVTLSR-----
>Dasypus_novemcinctus
MQEILLFTHVSVTLRR-----
>Monodelphis_domestica
MQEIQLFTHVSVTLRSKSSPASPEGALGRCL
>Pseudopodoces_humilis
MQEILLFTHVSVTLRSKRSPAN-----
>Struthio_camelus_australis
MQEILLFTHVFVTLRSKSSPASPEGVKLD--
>Pelodiscus_sinensis
MQE-ILFTHVSAALSSKNSPASPKGVKSH--

>Homo_sapiens	-----MGVCCSLAAVELKAAAGDOT
>Alligator_mississippiensis	-----MGICSSLAKEELKAAAGYI-
>Monodelphis_domestica	-----MGICCCSPAELNPAEGDOT
>Oryctolagus_cuniculus	-----MGVCWSPPAVELKAAAGDOT
>Equus_caballus	
MGRREESELSPGLLPHLQGCOPGLHTRPALLMGVCWRPAAVQLSAAAGDOT	
>Ictidomys_tridecemlineatus	-----MGFCWSLAAVELKAAAGDOT
>Tupaia_chinensis	-----MGIGWSPAATELQAAAGDOT
>Pelodiscus_sinensis	-----MGICSNLVEAELKAAVG DHT

>Homo_sapiens
MSGGEGSEAGCGMRDAEDLTLLGNSWKWLPQORRRGLR-AWGGRSPPRGC-----
>Mustela_putorius_furo
-----MRAAEDLTLLGNSWKWLPQORRRGLR-TWGGRSPLGC-----
>Balaenoptera_acutorostrata_s
-----MQDAEDLTLLGNSWKWLPQRHRRGLR-IPGGRSPPLGC-----
>Rousettus_aegyptiacus
-----MQDAEDLTLLGNSWKWLPQHRHRRGLR-AWGGRSPPRGC-----
>Monodelphis_domestica
-----MKDGEITLLGNSSPWLLPQAWRRGSENITGATSPAGSPGILSRGEMRDAGRLHLRATVHSG
>Oryctolagus_cuniculus
-----MQDAADLTLLGNSWKWLPPLRRRGLR-ARGGRSPPRGC-----
>Equus_asinus
-----MQDAEDLTLLGNSRWKLPQHQHRRGLR-TRGGRSPPRGC-----
>Chrysemys_picta
-----MKDGEITLLGNSLEWLCGAPRGLTS--SGRSLPLSLLGL-----

HG0234.1 ENSGALG00000011250 ASTC4

>Gallus_gallus
MLTQLELLSIPWILLAHDA
>Calidris_pugnax
MLTQLELLSIPWILLAHDA
>Columba_livia
MLTQLELLSIPWILLAHDA
>Aquila_chrysaetos_canadensis
MLTQLELLSIPWILLAHDA
>Lepidothrix_coronata
MLTQLELLSIPWILLAHDA
>Thamnophis_sirtalis
MLTQLELLSIPWILLAHDA
>Tinamus_guttatus
MLTQLELLSIPWILLAHDA

```
>Homo_sapiens
---MVNMGHYALVNRLRAAQLVLSIFSLALA-FNLVSSGVCRGEDFISIG
>Mustela_putorius_furo
MPGMLHAGHYARVNRLRAAERLV-----
>Monodelphis_domestica
---MLNTGHYALVNRLGAAERLVLSILSCLLLILSLVVCVCGKDFISIG
>Condylura_cristata
---MLNTGHYALVNRLRAAERLVLSIFSLALA-FNLVSSGVCRGEDFISIG
>Rattus_norvegicus
---MLNTGHYALVNRLRAAQLVLSIFSLALA-FNLVSSGVCRGEDFISIG
```

>Gallus_gallus
MLATSESLGNFTVGALRAVLEL-----TAKEARRGOTMGCPVLGLLHEQTPRAPLGCPAKRA
>Anser_cygnoides
MFPTSESPGNFTVEASRCAQSWSSHPKGARKGQOGRTMGYVVLGLLREKPANVPLGFPAKRA
>Calidris_pugnax
-----MGYLVVLGLLRDKPASVPLRFPKRA

>Aquila_chrysaetos_canadensis
MLPTSESPGNFTMEASNCAQSWs-----
>Sturnus_vulgaris
MLPTSESPGNFTMEASHCSQSWs-----
>Struthio_camelus_australis
MLPTSESPGNFKLEVSHCAQSWs-----
>Pelodiscus_sinensis
MFPTSDAPGNFTVETSDCAQFFS-----

```
>Homo_sapiens
MPPAPAAPTRNFAPRSPPPA-----
>Mustela_putorius_furo
MPPAPSPGGNFAPSPPPG-----
>Myotis_lucifugus
---MPATPAGNFAPRSPPPDCLVGLVPP-PPPPPTGPRA
>Ceratotherium_simum_simum
MLPAPAGPATNFARRSPPPD-----
>Ictidomys_tridecemlineatus
MPPARAAPAGNIALRSPPPAAGPRCETPVRPRAAGVSEPR
```

>Gallus_gallus
MVAAGAGGEGPGGARAGGGGGGAEPOR~~TGG~~AGERALLAGGIARLLKWLTKAKNRGHWCVMSSSGGSPRPSPPVRSVMCQYEQ
>Anas_platyrhynchos
-----MSNSGGSLQPALPARSVMCQYEQ
>Calidris_pugnax
-----MSNSGGSLRPPPPACSVMCQYEQ
>Alligator_mississippiensis
-----MSRSGGSLGPPPHYCNVMCQYEQ
>Aquila_chrysaetos_canadensis
-----MSKSGGSLRPPPPACSI~~MCQYEQ~~
>Manacus_vitellinus
-----MKNTSIA~~RHL~~KWLTKPKDLEQWCVMSNSAQSFQPPPPACSVI~~CQYEQ~~
>Struthio_camelus_australis
-----MCQYEH

>Gallus_gallus
-----MCGVISGF-EKR-APARHPFLWLRREEVFCWKMMTEVRLC--
>Cyprinodon_variegatus
MEKTTPTYFLSTQFFLSFSSSL-LLPWLCFPLWLWHRGEVFIWGMTEVGSR--
>Esox_lucius
-----MGLISVFWRPVSPLSPHRFPLWLWREKSLRGADDDRGRLMGK
>Callithrix_jacchus
-----MMTEVRLR--
>Salmo_salar
-----MCRVISRF-EKL-ALALPRFPLCTAE-----
>Lepisosteus_oculatus
-----MMTEVRLC--
>Chrysemys_picta
-----MCGVISGF-EKR-ALAQHPFLWLRREEVFCWKMMTEVRLC--

>Homo_sapiens-----MLGP1GSASRVFTHIRAR-EEK-R---KVSFKPELKFTFMKAHSRSPRA--
>Channa_argus-----MPCWATRAP-----GDAAAYYREPQWRRGGGG-KEKKVSFKPGRETfNMKLH-----
>Latimeria_chalumnae
MKKLWMSLSLQGLHASTPFHIFQALCSNKREVDNSCWSSLSHAMLGORGSGRHVFTHIRVR-EEKKK---KVSFKPEQKTFNMKSHSRSRHRHQ
>Kryptolebias_marmoratus-----MEKRRRG-ERKKVSFKPGRETfNMKPH-----
>Esox_lucius-----MHLPISGLE-ERKKVSFKPGQTSNMKPH-----
>Parus_major-----MLGORGSGRRVFTHIRVR-EERRRKKKKFHLNLNKKTFNMKSHSGNGHGP--
>Lepisosteus_oculatus-----MHLPISGLERKGRKVSFKTWTKTfNMKSHRGSRSQSQ--

HG0239 ENSG00000149256 TENM4

>Homo_sapiens
MEPGRKLPCVQIKIAYFKDYLKDYS
>Mustela_utorius_furo
MEPGRKLPCVQIKIAYLKNYSKDYS
>Physeter_catodon
MEPGRKLPCVQIKIAYFKDYLKDYS
>Pteropus_alecto
MEPGRKLPCVQIKIAYFKDYLKDYS
>Condylura_cristata
MEPGRKLPCVQIKIAYFKDYLKDYS
>Chinchilla_lanigera
MEPGRKLPCVQIKIAYFKDYLKDYS
>Anolis_carolinensis
MESGKLGSAYDQVKTAYFKAHLMDOYS

HG0240 ENSG00000166342 NET01

>Homo_sapiens
MTDPFFLLPSMPQRKIPKGWSEERCRTSSRGGCSDLLRGASETGD
>Calidris_pugnax
MTDPLIPSSMHQ-KKPKGWKSLGS---ESCRKCFHLLLVLYETGD
>Myotis_lucifugus
MTDPFLLPPMPQRKIPQGWTEEGCRSSRRARLPQPAAR---GG-
>Falco_peregrinus
MTDPLIPSSMHQ-KKPKGWKSLGS---ESCRKCFDLLLLVLYETGD
>Pseudopodoces_humilis
MTDPLIPSSMHQ-KKPKGWKSLGS---ESCRKCFDLLLLVLYETGD
>Mesocricetus_auratus
MTDPCLLPMPQKTPKGWREKSCGWTSSRRRCSDLVLLVDETGD
>Chrysemys_picta
MTDPLILPSMHQ-KNPKVWETLGL---KSYRKCFDRLLVLYETGD

>Homo_sapiens	ME	VSGWLCSLLPASSLLWWLGCFFHDFLNLDWAVLCVKPISCDLLLT
>Balaenoptera_acutorostrata_s	MSAP-LK	VSQICSSLLPASSLLWWLGCFSHDILNLDWAVLC
>Coturnix_japonica	MGAVTQP	TACPRAEAV-RSEG-RTGGRPTAAAGPSRRYPACRSHPKYELTACLFALCGESSLPASSLLWWLGYFSHDSLRLDLAVPCLCQSHPSFLL
>Oryctolagus_cuniculus		MIVLNLDWAVLCVKSISYDILT
>Lepidothrix_coronata	MS	A-VGSPGLAAQP-APMGGRLAPKSPSALFPASSLLWWLGCFSHDSLRLDLAVPVPLPIKPELPPLTVKRGAPAPSGSLFLPSP
>Ictidomys_tridecemlineatus		MI FLNLDWAVLCVKTINYDPSLNSVK
>Python_bivittatus		
MIRKDVAEQLGPIWHSPKEKVLFFLSVALFPPRPDSFLNLGGSEANLLPEAAAKGTVRFPERSARG		TKAQAFFLLLPCCWWLGCFSHDFLHLDQAVP

HG0242.1 ENSGALG0000007112 LINS1

>Gallus_gallus
-----MSRGNLEEECLL--ACLFLLLDKNNFKTDLQGSEIIGEDLQRSVIY
>Apteryx_australis_mantelli
-----MDKNNFETNLQ-----
>Columba_livia
-----MLLFLLLDKKNFEADLH-----
>Haliaeetus_albicilla
----MVEEVRSLGNIEEKCLI--VLLFLLLDKNNFKADLQRP-----
>Sturnus_vulgaris
-----MRSLLHLPRLNEEKCPV--VLLFLLLDESWEAALQ-----
>Pelodiscus_sinensis
MSLSSRGFCIIRAILQKECLYRATNPFLLLDRSNFKSDP-----

HG0242.2 ENSG00000140471 LINS1

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>Homo_sapiens
-----MREEVPACTFCELRWPRAGICVPS-----NGGVKRVRLSQ-----IPGFTEETS
>Mustela_putorius_furo
-----MRRKRSACAFPELRWPGG-WCCSF-----NGGVKAGSPNDLRQKLQERRPACVIKQSFPEETS
>Manis_javanica
MWPLRMREEGPTCTFRELRLPGGGSCALEWRFEGRVRFAR-----SLAGK-----
```

```
>Homo_sapiens
---MGSLLSRQLIFQIITYFLHHC
>Physeter_catodon
-----MALSQDTFQIITYFLHHC
>Equus_asinus
MVPRGSVSRQLIFQVITYFLHLC
>Manis_javanica
-----MQLVFQIITYFLHHC
>Chinchilla_lanigera
MVPGGSLFSRQLILQIITYFRHHC
>Struthio_camelus_australis
-----MKRFQIITYFLVHC
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HG0243.2 ENSG00000163697 APBB2

>Homo_sapiens
MLWSDLPsRGtETfAGWkIHKRkLL
>Felis_catus
MLWSDLPsRGtETfAGWkIHKRkLL
>Balaenoptera_acutorostrata_s
MLWSALPsRGtETfAGWkIHKRkLL
>Rousettus_aegyptiacus
MLWSDLPsRGtETfAGWkIHKRkLL
>Dasypus_novemcinctus
MLWLDLPsRGtETfAGWkIHKRkLL
>Galeopterus_variegatus
MLWSDLPsRGtETfAGWkIHKRkLL
>Condylura_cristata
MLGSDLPsGtEAFAGWkIHKRkLL
>Ceratotherium_simum_simum
MLWSDLPsRGtETfAGWkIHKRkLL
>Manis_javanica
MLWSDLPsRGtETfAGWkIHKRkLL
>Loxodonta_africana
MLWSDLPsRGREtFAGWkIHKRkLL
>Fukomys_damarensis
MLWSDLPsRGtETfAGWkIHKRkLL
>Tupaia_chinensis
MLWSDLPsCtETfAGWkIHKRkFL

>Gallus_gallus
MLTGTLSRLKAVVMKQPKYQHFSRIDPSEQMLMVVF-
>Xenopus_tropicalis
MLTGTIRSLNAVVIKHPKITFRKKPYMSDI-----
>Calidris_pugnax
MRTGTLSRLKAVVMKQPKCWCFSRIDPSQQLMIRAVF-
>Columba_livia
-----MIRVVF-
>Tauraco_erythrolophus
-----MMIRVVF-
>Saimiri_boliviensis
-----MKQPKDQLFRSTTDESQAHLRLGSN

>Homo_sapiens-----MQPHTPFYLPYLGYSV--LPRVILCTHYVFLANEEGESNRKRDQRYIGVWHGAHKAH-----
>Mustela_utorius_furo
MRKL--RAG-----TILLAKHSSSYRYLTTPPPFSPDVSSQSPOLLNIAVCRWQHGGPHSPFYLPYLSYRVA--LPRVILCTHYILPANEESESNRKRDQK--
>Pteropus_allecto-----MYTLHGPAKEKSASSSERHKQR-----
>Monodelphis_domestica-----MSSC--LF-PSLQRRLLSSPAVAKYSLAVCGWLHRQPHTFYLPYLGYRID--LPRVIFCTHYIFLENMKSESNRGKR-----
>Rattus_norvegicus
MAVLEGTPIWGIVFFFPGEETEGFLDSKCSSSYTRSL--SARLALDASYLRPLMLNIAVCGWLHMQSYTSPYLPYLSYRYSYCPSRVILCTHHAVPAN-KTESNRKGDKQRQIGAWHRYTGNTSGKKKERKETSLLSLHLLQT
>Thamnomphis_sirtalis-----MKMINKTRSLDKRR-----

>Homo_sapiens
MSKPLGLGVKVSSGLG-L-----SKP---SE-----
>Mustela_putorius_furo
MSKPLGLGVKVSALLGVFI PKCFHNKLF RSGGAGFAL RTP---RPLAGLQAGGTT--R-R-----
>Rousettus_aegyptiacus
MSKPLGLGVKVSA-----
>Ochotona_princeps
MSKPLGLGVKISAGPG-L-----RKL---WP-----
>Parus_major
MSKPLGLGLKVFSAPLGVFIPEEFSTTSYF-----
>Rattus_norvegicus
MSKPLGLGVKVSASLGVFI LKCFHNKLF RGP E AQVSL CGRGGQWP GSSPAAPGFGDSRLRSGSDA CPSRRPGCVAHGQRVQELCELPARSARQLPS I CVLNL

HG0247.1 ENSDARG00000014746 rbfox1

>Danio_rerio
MLALGRCCRDWD-----
>Apteryx_australis_mantelli
MLALGRCCMAWD-----
>Calidris_pugnax
MLALGRCCMAWD-----
>Corvus_brachyrhynchos
MLALGRCCMAWDQSSC
>Chrysemys_picta
MLALGRCCMAWD-----

>Homo_sapiens
MGGSWRKKEGERLPERKKRKKH
>Canis_lupus_familiaris
MGGSWREKEGERLPERKKRKKR
>Orcinus_orca
MGGSWRKKEGERLPERKKRKKH
>Myotis_brandtii
MGGSWRTKEGERLPERKKRKKH
>Dasypus_novemcinctus
MGGSWRKKEGERLPERKKRKKH
>Galeopterus_variegatus
MGGSWRK-EGERLPERKKRKKH
>Macropus_eugenii
MGGSWRKKEGERLPERKKRKKH
>Condylura_cristata
MGGSWRKKEGERLPERKKRKKH
>Ceratotherium_simum_simum
MGGSWRKKEGERLPERKKRKKH
>Manis_javanica
MGGSWRKKEGERLPERKKRKKH
>Cricetulus_griseus
MGGSWRKKEGERLPERKKRKKH
>Tupaia_chinensis
MGGSWRKKEGERLPERKKRKKH

HG0248.1 ENSGALG00000004570 NCOA3

>Gallus_gallus
MVSDSGDPVKSTILCLNAC
>Anser_cygnoides
MTSDSEGPMKNMLCLNVC
>Aquila_chrysaetos_canadensis
MTSDSEGPLKNMLCLNVC
>Manacus_vitellinus
MTSDSEGPLKNRLCLNVC
>Chrysemys_picta
MITGPDGGLKSLLCLNVC

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>Homo_sapiens
-----MAAGGSKYLLDGGLRDQ
>Leptonychotes_weddelii
-----MAAGGSKYLLNSGVTDO
>Orcinus_orca
-----MAAGGSKYLLNSGIRDQ
>Myotis_lucifugus
-----MAAGGSKYLLNSGIRDQ
>Galeopterus_variegatus
MASKSEHADISTAGSKYLLMNSGLRDQ
>Condylura_cristata
-----MAAGGSKYLLNSGVRDQ
>Oryctolagus_cuniculus
-----MAAGGSKYLLNSEHRDQ
>Equus_asinus
-----MAAGGSKYLLNSGVRDQ
>Manis_javanica
-----MAAGGSEYLLNSGVRDQ
>Loxodonta_africana
-----MAAVGSKHLLNSGPRDQ
>Nannospalax_galili
-----MAAGGSKYLLNSGLRDN
```


>Danio_rerio
-----MLCFSHYVLNAHNARKYLRTVIFGRALSVPEPLGLTAVSFYAKRT
>Pygocentrus_nattereri
-----MLRVHNA-----
>Apteronotus_leptorhynchus
MNRFR-HILLCIQHCVLNVHSA-----
>Scleropages_formosus
-----MNVYNVRIY-----
>Gekko_japonicus
MNTWSSRDKGYSIHYVLTVCYRRYLKTIFFPKNLI-PVESVL-----

HG0250 ENSGALG00000014861

>Gallus_gallus
-----MNWKHLDLCRALNQILV-----
>Anser_cygnoides
-----MNWKHLGLFRAVNQLFV-----
>Haliaeetus_leucocephalus
MKENYALKSQLFMNWKHPDLFRVNVQLFV-----
>Manis_javanica
-----MNWKHIDLRRMPCECSPRRSLAQKAAGRHSLG-----
>Aptenodytes_forsteri
-----MNWKRLDLFRAVNQLFV-----

HG0251 ENSG00000185053 SGCZ

>Homo_sapiens
MMLTREAAFFLGMQGFAGF
>Mustela_putorius_furo
MMLSREAAFFLGMQGFAGF
>Rousettus_aegyptiacus
MMLSREAAFFLGMQGFAGF
>Chinchilla_lanigera
MMLSREAAFFLGMQGFAGF
>Chrysemys_picta
-MLSSEAVFLGMQGFAGF

HG0252.1 ENSGALG00000009645 ESRRG

>Gallus_gallus
MSLHGVDFFPSKETGFGFFKIPDDSPD
>Alligator_mississippiensis
MSLHGVDFFPSQETGFGFLQIPDDSPD
>Sturnus_vulgaris
MSLHGVDFFPSKETGFGFFKIPDDSPD
>Microcebus_murinus
MFLHGGVL-----

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>Homo_sapiens
-----MVRVRFVFFVFCQLPVISITVSGSVYRLG--VLCP-----
>Myotis_davidii
-----MVVGIVFFVFCQLPVISITVSDLFIGWEYCVL--SH--KETQVGCQLVLEELSVSSVATGST
>Corvus_brachyrhynchos
MPTGDCGGLLPVHSAELKAQLLPCLRPVYFVFFVFCQLPVISITVLSVYRLGLVLCPSHKEVQVHRCRLVQAEVKDI-----
>Mus_musculus
-----MVVGFFVFLCQLPVISITVSGSVYSLR--VLCP-----
```

HG0252.3 ENSG00000196482 ESRRG

>Homo_sapiens
MCNVPANGFCRLS-----
>Mustela_putorius_furo
MCNVPANGFCRLS-----
>Orcinus_orca
MCNVPANGFCRLSQPKRPASALKSPTHLLNLLQF
>Monodelphis_domestica
MCKVPANGGGVGCRLS-----
>Manis_javanica
MCNVPANGFCRLS-----
>Mus_musculus
MCDVPANGVCRLS-----

HG0253.1 ENSGALG00000015184

>Gallus_gallus
MYQNVNDEALLNLVKGVTSAERAVGAARSGGAGRRAGQGRVGGGPGRAGHGAPSSAAAASRSLDRQRRARKPNTNKAARTVPSSSSLSLFLIF
>Lipotes_vexillifer
MYQNVND-----
>Pteropus_vampyrus
MYQNVND-----
>Anolis_carolinensis
MYQNVNDPPLNLVKGVTSAESVVRVPSGGAVPGLPLLLLLPRG--RD-----

HG0253.2 ENSG00000140332 TLE3

>Homo_sapiens
MSAQSQALTRSTQPREGGRPLPAEP
>Odobenus_rosmarus_divergens
MSAQPRALTRSTQWEGGRPOPAEP
>Orcinus_orca
MSAQPPLALTRSTQREGGRPOPAEP
>Rousettus_aegyptiacus
MSAQSPALTCSTQPREGGRLOPAEP
>Oryctolagus_cuniculus
MSAQPPLALTRSTQPREGGRPKPAEP
>Elephantulus_edwardii
MSSQSPALIRQTQPREGYRPOPADP
>Equus_caballus
MSAQPPLALTRSTQPEGGRPOPAEP
>Manis_javanica
MSARSQALTRTTQPEGGRPOPTP
>Jaculus_jaculus
MSAQPPLALTLSTQWEGGRPOPAEP
>Trichechus_manatus_latirostr
MSAQSPALTRSTQPEGGRPOPAEP
>Orycteropus_ afer_ afer
MSAQSPALTRSTQPEEGGRLOLAEP

HG0253.3 ENSG00000140332 TLE3

>Homo_sapiens
MPGRLICTY
>Odobenus_rosmarus_divergens
MPGRLICTY
>Equus_caballus
MPGRLICTY
>Manis_javanica
MPGRLICTY

>Gallus_gallus
MLDGACGCQTQPEAADGR-R-----DPSCAPPVPPRS-----
>Aquila_chrysaetos_canadensis
MLDGACGCQTQPEAAAAAGYRD1PLRVSRGPFPPAPSASTFAATDWANVSVLRYMKHYCCGEVY
>Pseudopodoces_humilis
MLDGACGCQAQPAAAGHRTGTPR-----PPRARSDEFFSQI-----C-----
>Trachemys_scripta
MLAGACGCQSQPEAAAAAGQPDPR-----APLPAPRRRRQQVMVSCVLHLFL---EERK-----

HG0254.2 ENSG00000072134 EPN2

>Homo_sapiens
MTIQGSYSSLITETEPS
>Galeopterus_variegatus
MTVGGSCSKSITETEPS
>Loxodonta_africana
MIVGGSSRLITETDPS
>Nannospalax_galili
MTIQGSCSIWITETEPS
>Orycteropus_ater_ater
MIVGGSSWMLITETDPS

>Gallus_gallus
-----MSATGSAAVGGAAKPGAGVPAQRRKKVHGKGD~~L~~HRNH
>Alligator_mississippiensis
-----MAASSTA~~A~~AVGGTRESGGAAGGRKKAYGKGD~~P~~HRNY
>Haliaeetus_leucocephalus
MVSRRVGGGEGRLMAATSSAAVAEGTRKSGAGVPAQRRKKVHGKGD~~L~~HRNY
>Trachemys_scripta
-----MAATSTTALVGGTRESGVAAGGRKKAYGKGD~~P~~HRNY

HG0256 ENSGALG00000039901

>Gallus_gallus
MAATTTISLRHSQPCNRFPRDVPELLEFKPPKGRSTQKQCP
>Calidris_pugnax
MAATTTISLRNSQPCNKFTNVPELLEFKPP-----
>Alligator_mississippiensis
MAATTTISLRNSHPCNTFPRMCLNSWSSNRLKGPTTAQTQYS
>Haliaeetus_leucocephalus
MAATTTISLRNSQPCNKFTNVPELLEFKPP-----

>Homo_sapiens-----MLSPVMRRPLVSLRGFWDCSREREGFEISLPKNQGE--LCL-----
>Physeter_catodon-----MLPPVMRGPLMPLRGFWNCSRERWRKAVFN-YRVFP--LCVCFVSEEGYKGRPGSFHCVCVCVCVCV
>Galeopterus_variegatus-----MPLCCPLVSLGACSTEMLPPVMRRLWVSFRGFWNCSEKGGGKHC-----
>Corvus_brachyrhynchos
MGQVRRDHSGSPGPTSLLEQGHGAYSTRLCDSSGMSSLRQTPKPFWAVRSRSLHGFWSCSSSCSGFPLKLSVHQFLPIISCPIVMHHQDEPGTRPLGIHTH-----

HG0258.1 ENSGALG00000016797 FHL2

>Gallus_gallus
MSNCLITKYIVWVIQ-----
>Columba_livia
MPDCLTTKHIVWAIQ-----
>Pelodiscus_sinensis
MPDCLITKYIVWVIQCSNKPLY

HG0258.2 ENSGALG00000016797 FHL2

>Gallus_gallus
MDVTLCPWSRR
>Chaetura_pelagica
MDVTPCPWSRR
>Apteryx_australis_mantelli
MDVTPCPWSRR
>Cariama_cristata
MDVTPCPWSRR
>Calidris_pugnax
MDVTPCPWSRR
>Colinus_striatus
MDVTPCPWSRR
>Columba_livia
MDVTPCPWSRR
>Cuculus_canorus
MDVTPCPWSRR
>Mesitornis_unicolor
MDVTPCPWSRR
>Opisthocomus_hoazin
MDVTPCPWSRR
>Acanthisitta_chloris
MDVTPCPWSRR
>Nipponia_nippon
MDVTPCPWSRR
>Aptenodytes_forsteri
MDVTPCPWSRR
>Struthio_camelus_australis
MDVTPCPWSRR

HG0259 ENSGALG00000009936 AP4S1

>Gallus_gallus
MLKSKMAAPGKGAQFRP-----
>Gekko_japonicus
MLESKMAAPGKAVQPREPRGGCAE
>Pelodiscus_sinensis
-----MAAPGKGAQFGP-----

HG0260.1 ENSGALG00000016890 MBL2

>Gallus_gallus
MLLSMIFFSQKSTSGT
>Anas_platyrhynchos
MLLSMVVFSQKSTSGT
>Apteryx_australis_mantelli
MLLSMVVFSQKSTSGT
>Buceros_rhinoceros_silvestri
MQLSMVFPQKSTTGT
>Calidris_pugnax
MRLSMVFPQKSTSGT
>Columba_livia
MRLSMVFPQKSTSGT
>Merops_rubicus
MRLSMVFPQKSTSGT
>Cuculus_canorus
MQLSMFFFSQKSTSGT
>Aquila_chrysaetos_canadensis
MRLSMFFFSQKSTSGT
>Mesitornis_unicolor
MRLSMVFPQKSTSGT
>Tauraco_erythrolophus
MQLSMVFPQKSASGT
>Opisthocomus_hoazin
MRLSMVFPQKSTSGT
>Taeniopygia_guttata
MRLSMCFPSQKSTSGT
>Egretta_garzetta
MQLSMVFPQKSTSGT
>Fulmarus_glacialis
MQLSMVFPQKSTSGT
>Nestor_notabilis
MRLSMVFPQKSTSGT
>Aptenodytes_forsteri
MRLSMVFPQKSTSGT
>Struthio_camelus_australis
MLLSMVFFSRKSTSGT
>Tinamus_guttatus
MLLSMVFVSQKSTSGT
>Apaloderma_vittatum
MRLSMVFPQKSTSGT

>Homo_sapiens
MSDCLSIHSLIILFLGLDFIKQFITHLQTYMWEFSQQ
>Mustela_putorius_furo
-----MWGFSQQ
>Lipotes_vexillifer
MSDYLPINSLTLFPGLGFFKQFVYLYQTYMWDIFSQQ
>Pteropus_alecto
MSDCLPITII-SSLLGLDFIKQFITYLYQTYMWDIFSQ-
>Dasypus_noveboracensis
MSDCLPINSLI-LFGGLDFIKQFIYLYKTYMWDIFSQQ
>Galeopterus_variegatus
MSDCLPINSLITLLPGLDFIKRFITYLYQTYMWEFSQQ
>Condylura_cristata
MSDRLLINSLTLSPGLDFIKQFITYLYQTYMWDIFPPQ
>Oryctolagus_cuniculus
-----MWEFSSQ
>Elephantulus_edwardii
-----MWDL SQH
>Equus_asinus
MSDCPPINSLTLFPGLDFIKQFITYLYQTYMWDIFSQ-
>Manis_javanica
MSDCLPINSLFTLLPRLNFIKTFIPYLYQTYMWDIFSQQ
>Loxodonta_africana
-----MWDFSQQ
>Chinchilla_lanigera
MSDCLPINSLTLSPGLDFIKQFITYLYQTYMWEFSQQ
>Tupaia_chinensis
MSDCPLINSLITLFPRLDFIKQFITYLYQTYMWEFSQQ
>Trichechus_manatus_latirostr
-----MWDCSQQ

>Homo_sapiens
MTPTMPWALGROWGRL
>Odobenus_rosmarus_divergens
MTPTMPWALGROSGCL
>Lipotes_vexillifer
MTPTMPWALAROSGCL
>Pteropus_alecto
----MPWALGROSGCL
>Condylura_cristata
----MPWAPGROSGCL
>Manis_javanica
----MPWALGROSGRL
>Heterocephalus_glaber
MTPTMPWALGROSGCL
>Tupaia_chinensis
MTPTMPWALGRLSGCL
>Orycteropus_afer_afer
MTPTMPWVLCLQSGCL

HG0260.4 ENSG00000152601 MBL1

>Homo_sapiens
MSCGAHNAPMTRS
>Odobenus_rossmarus_divergens
MSCGAHNAPVTGN
>Lipotes_vexillifer
MSCGAHNAPVTGN
>Pteropus_alecto
MSCGAHNAPVTGN
>Dasypus_noveboracensis
MSCGAHNAPVTRN
>Condylura_cristata
MSCGAHNAPVTRN
>Tupaia_chinensis
MSCGAHNAAVTRN
>Orycteropus_ afer_ afer
MSCGAHNAPVTRN

HG0260.5 ENSG00000152601 MBL1

>Homo_sapiens
MFFPPVSPGSKTVWCILRRQSHQIAGF-----
>Odobenus_rosmarus_divergens
MFFPPVSHPGSKTVWCILKNQPHQILTVFCRSDSHLQPNLAGFLTksPIRRPL
>Pteropus_vampyrus
MFFPPASHPGSKTVWCICKEAAPSDLTVLS-----
>Orycteropus afer afer
MFFPPVLPPGSKTMWCILRRQPHQIPGFYSNLI--LTPS-----

HG0260.6 ENSG00000152601 MBL1

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>Homo_sapiens
--MGLRFICSGDNMAYLPWNIPVFQK-----
>Odobenus_rosmarus_divergens
MIWGCGVFCNNNNMT-----
>Orcinus_orca
-----MTYLPWTITVFKKMILC-----
>Pteropus_vampyrus
-----MTYLPWNSPVFQKMFYFLKRGPLLSINHIMQSWGERGFYISNIIYKLDGKLVCECLCLCDNQFY
```

HG0261.1 ENSGALG00000005867 MARCH8

>Gallus_gallus
MSAAFKPPSCK-
>Anas_platyrhynchos
MSAAFKPPSCK-
>Buceros_rhinoceros_silvestri
MRAAFKPPSCKS
>Charadrius_vociferus
MSAAFKPPSCK-
>Columba_livia
MSAAFKPPSCK-
>Haliaeetus_leucocephalus
MSTAFKPPSCK-
>Eurypyga_helias
MSTAFKPPSCK-
>Corvus_cornix_cornix
MSTAFKPPSCK-
>Nipponia_nippon
MSAAFKPPSCK-
>Picoides_pubescens
MSTAFKPPSCKQ
>Pygoscelis_adeliae
MSAAFKPPSCK-
>Apaloderma_vittatum
MSIAFKPPSCK-

>Gallus_gallus
-----MEYLTQRQEMKPGSNVKGHVKLLHSRNLKDCFT
>Anser_cygnoides
MGFRRCRYFHCRKRNMLPDENCMEIMNPGSNVKGHVKLCHSRNLKDCFA
>Calidris_pugnax
-----MNPGRNVKGHVKLCHSRSLKDCFT
>Zonotrichia_albicollis
-----MNPGSNVKGHVKLCHSRNFLKDCFT
>Struthio_camelus_australis
-----MNPRSRCLKGHVKLCHSRNLKDCFT

>Homo_sapiens
MPAPRDAGRTPGGRLSYFTLRR-----
>Pteropus_allecto
MPAPRDAGYAQPGGCLSDFALRR-----
>Monodelphis_domestica
MPEPRDMGTVTCGRLSDFTLRWKCTQG-----
>Nannospalax_galili
MPAPRDAGCAQPGGRLNHFILPRKCTQEEF-----
>Tupaia_chinensis
MPASGAAGCAQPGGRLSHFTPRGFQQLSESVKSTA

HG0261.4 ENSG00000165406 MARCH8

>Homo_sapiens
MLEAGGGGSAASSEPT
>Ailuropoda_melanoieuca
MLRAGWGGPAASSAPT
>Pteropus_vampyrus
MLQAGGGGLAASSAPT

>Homo_sapiens
MFLLPPGNKALKSAVEKPNVCEIQETMLANHW-----
>Canis_lupus_familiaris
---MPPGNKALKVWSRGPSVGGPDMD-----PREGTHHDLFVGRC-----
>Balaenoptera_acutorostrata_s
MFLLPPGNKALKSAVESPNICGTQEAQLQNTSRKKNHGDLFIGYY-----
>Dasypus_novemcinctus
MFLLPPGNKVLESAVENPNICASQQTMLAKSLVEKHA-VYWLSQLLKYLFTNAR
>Oryctolagus_cuniculus
MFLPPPGHRVLKSAVRKPQHL-----
>Equus_asinus
MFLLPPGNK-LKSAVESANLGTQETMLANHCLNQD-DLFVGHC-----
>Cavia_porcellus
MFLLLPGNQVLKSAPRLQILVEKAL-----

>Homo_sapiens
-----MSLILNLICGNGKVILAGAYC
>Ailuropoda_melanoieuca
MNRGRVTKSSHRSCNCKVTITLNLNVTEGHEGEVILAGTYC
>Balaenoptera_acutorostrata_s
-----MIVAGTYC
>Dasypus_novemcinctus
-----MTVAGAYC
>Cavia_porcellus
-----MILILNLICGSKE-VITMEAYC

HG0262.3 ENSGALG00000017186

>Gallus_gallus
MHSTRKAHNVTVAGKVLFDIPVFVG--VDQLLH-----
>Haliaeetus_albicilla
-----MIQGEVLFDMLSSIVKGRGSFCTESSCVS
>Fulmarus_glaialis
-----MIQGVLFDMMLSSIVKMGWGSFCTESSCVN

HG0262.4 ENSG0000023445 BIRC3

```
>Homo_sapiens
MNTKKIFITMCKIFGGGKEY
>Rousettus_aegyptiacus
-----MCKLFGQ-----
>Equus_asinus
MNTKKVFITMCKVFEG----
```

HG0263.1 ENSG00000169826 CSGALNACT2

>Homo_sapiens
MEILILFLIFDNFLKLV
>Leptonychotes_weddellii
MEILILFLIFDNLLKLV
>Physeter_catodon
MEILILFLFYNLSQKV
>Pteropus_alecto
MEILVLFLIFDNLLKLV
>Equus_asinus
MEILILFLIFDNLLKLV
>Manis_javanica
MEILILFSVFDNLLKLV
>Microtus_ochrogaster
MEILIFFLIFDNFLKLV

>Gallus_gallus
-----MANVGTCDLWLCNDT
>Calidris_pugnax
-----MVMDDIGTSDLCLNDT
>Sturnus_vulgaris
-----MVMDDIGTSDLHLCLNDT
>Struthio_camelus_australis
MSPFPFNGFLSLGWDILNKSFGVNHAYKLMVMDVGTSNLYLCNDT

HG0263.3 ENSGALG00000002543 CSGALNACT2

>Gallus_gallus
MIPGWCLPFCSPSAVFFVWDKKS
>Calidris_pugnax
MTPWWCLPSSSSSAGFFVWGRKS
>Corvus_brachyrhynchos
MIPCWCLPSSSPSAGFSCLG---
>Pygoscelis_adeliae
MTPWWCLPPSPSAGFFVWGRKS

HG0263.4 ENSG00000147408 CSGALNACT1

>Homo_sapiens
MDASSSGGPKRMLPVV
>Balaenoptera_acutorostrata_s
MDESSSGTPGRVLPV1
>Cynopterus_sphinx
MDESSSGGPKRMLPVV
>Ceratotherium_simum_simum
MDESSSRGFRRLPVV

>Homo_sapiens
MELCDSLKFRKSVAEIWNQAFLPQFNN--
>Acinonyx_jubatus
MELCDPSRFRKSIATLWNQAIHFQFNN--
>Lipotes_vexillifer
MEFCDPSRYRKSVGGLEPGSFPSVQQFI
>Rousettus_aegyptiacus
MELCDPSRYRKTVAELWNRAIFYQFNP--
>Dasypus_novemcinctus
MALCDLPKHKRSVTKF-----
>Sarcophilus_harrisii
MELYDLLSHMKSIIIEFWDQTSFHQIINN--
>Galeopterus_variegatus
MQLCDSSRCRKSVAEIWNQAFFFPSVQQLN
>Oryctolagus_cuniculus
MELCDLSSYWKGVTKLWS-----
>Equus_asinus
MELCDPSRYRKRVAKLWNQATFHQFNN--
>Manis_javanica
MELCDPSRYRKSVAKFWNQAIIFYQFNS--
>Loxodonta_africana
MELCDPSRHRKSVTEFWN-----
>Fukomys_darlingi
MELYGPSRYSKSVAEIWNHQSOFHQFNN--
>Trichechus_manatus_latirostris
MELCDPSRHRKSVTELWN-----
>Orycteropus_afer_afer
MKLCDPSKHKKSVTELWNKAFFFPSVKQ--

```

>Homo_sapiens
MYCLISVLETSTIT-----
>Mustela_putorius_furo
MYCLICTLETSTIT-----
>Orcinus_orca
MYCLICILETSTIT-----
>Myotis_lucifugus
MYCLICILEGSTIT-----
>Sarcophilus_harrisii
MYCLISILETSTISINRCSHGVI
>Galeopterus_variegatus
MYCLIIYLEITSTIT-----
>Ceratotherium_simum_simum
MYCLICIFETSTVT-----
>Manis_javanica
MYCLIHILETSTVT-----
>Cavia_porcellus
MYCLIIYVLETSTIT-----
>Tupaia_chinensis
MYCLICILETSTIT-----
>Orycteropus afer afer
MYCLICVLETFTIT-----

```

HG0264.3 ENSGALG00000011831 ANKRD50

>Gallus_gallus
MDSFFWIYIRRD
>Anser_cygnoides
MDSFFWIYIQRD
>Calidris_pugnax
MDSFFWMIYIQRD
>Zonotrichia_albicollis
MDSFFCVYIQRD
>Aptenodytes_forsteri
MDSFFWMIYIQRD

HG0264.4 ENSG00000151458 ANKRD50

>Homo_sapiens
MERPVLMYPDSSK---
>Physeter_catodon
-----MYPDSSKC--
>Manis_javanica
-----MYPDSSKC--
>Trichechus_manatus_latiostr
-----MYPDSSKCRR

HG0265.1 ENSG00000144285 SCN1A

>Homo_sapiens
MELFLQINTSGVMEAGGS
>Mustela_putorius_furo
MELFLQINTSGTMEAGGS
>Rhinolophus_ferrumequinum
MELFLQINTSGAMEAGGS
>Condylura_cristata
MQLFLQINTSGAMEAGGS
>Oryctolagus_cuniculus
MQLFLLINTSGAMEAGGS
>Equus_asinus
MELLLQINTSGAMEAGGS
>Manis_javanica
MELFLQINTSGAMEAGGS
>Heterocephalus_glaber
MELFLQINTSGAMEAGGS

>Homo_sapiens
MAPTAVPPAASSAPLQSGRASRAPR
>Odobenus_rosmarus_divergens
MAPTAVPPAAASAPLQSGRASRAPR
>Orcinus_orca
MAPTAVPPAASSAPQDSGRASRAPR
>Oryctolagus_cuniculus
MAPTAVPPAAASAPLQSGRASRAPR
>Elephantulus_edwardii
MAPTAVPPAAASVPLQSGRASRAPR
>Equus_asinus
MAPTAVPPAAASAPLQSGRASRAPR
>Mus_musculus
MAPTAVPPAAASAPLQSGRASRAPR

>Danio_rerio
MATSAVSPGSKHP-----
>Astyanax_mexicanus
MATSAVSPGSLRHP-----
>Austrofundulus_limnaeus
MATAAVTPDSFLHPQFTDSCRDAC
>Apteronotus_leptorhynchus
MATSAVSPGSRHP-----
>Salmo_salar
MATTAVSPESFRHLQSNNAFLGSL
>Lepisosteus_oculatus
MATTAVSPESFRHLQSSDAVLDFC

```
>Homo_sapiens
-----MAATTNSALKTVPCPLSTIT-
>Odobenus_rosmarus_divergens
-----MELICAPSOGLLATDSSPAGVWEMAAAADTALKTATCPLSTVT-
>Orcinus_orca
-----MAASASAALKTVTCLVSTVT-
>Rhinolophus_ferrumequinum
MQPARRRPWPGTAARSSDAERAAPGGLTEGLLATDLSPIGAWEMAAATNAALKTVTCPLSTVT-
>Galeopterus_variegatus
-----MAAAANSALKTVTCPLSTIT-
>Oryctolagus_cuniculus
-----MIGSSPADAWEMAVTAHSALKTVKCSLSTIT-
>Equus_przewalskii
-----MAATANAALKTATCPLSLLRR
>Fukomys_damarensis
-----MAAAANSALKTVTCPLSTIT-
>Tupaia_chinensis
-----MAAAANSALKTVTCLLSTVT-
```

>Homo_sapiens	-----MAATTNSALKTVPCLLSTIT
>Canis_lupus_familiaris	-----
MWQPRAPTPLPGRTVPRAPGRHLVIFRGLNSHHGLLWPSRGGAGGSIGRGVORPGFLCPSCHSLQCSFVTLGKSLLCSEPLFPCRVELILPTSQGLLVTDSSPAGVQEMEAAADTALKTATCLLSTVT	
>Orcinus_orca	-----MAASASAALKTVTCLVSTVT
>Rhinolophus_ferrumequinum	-----
MQPARRRPWPGTAARSS-----E-----DAERAAPGGLTEGLLATDLSPIGAWEMAAATNAALKTVTCPLSTVT	
>Galeopterus_variegatus	-----MAAANSALKTVTCPLSTIT
>Condylura_cristata	-----
MRPARRRPWPGTAAR-----SSEDAECAAPGALTEGLPVTSSFAAGTWEMAASASAALKTAACLLSTVT	
>Oryctolagus_cuniculus	-----MIGSSPADAWEMAVTAHSALKTVKCSLSTIT
>Fukomys_damarensis	-----MAAANSALKTVTCPLSTIT
>Tupaia_chinensis	-----MAAANSALKTVTCLLSTVT

HG0266.2 ENSGALG0000001181 KCNJ5

>Gallus_gallus
MFCHAGQREGRRRRPRDQKTTTACW
>Calidris_pugnax
MFSPNRQREEGRGQPRDPKTSALW
>Aquila_chrysaetos_canadensis
MFSNNRQREEGRGQPRDQKTTPAIW
>Parus_major
MFAASRQREGRRRQPGAPRTTPAPW
>Struthio_camelus_australis
MFCNNRQEEGEREPRDKKTTPALW

HG0267 ENSDARG00000028173 slc4a2a

>Danio_rerio
MLPESSQLSLSKREKG
>Pygocentrus_nattereri
MLPESSQLSLSEREKG
>Apteronotus_leptorhynchus
MLPKNCQLSLSEKEKG
>Scleropages_formosus
MLPKSTPLSLSEKEKG
>Lepisosteus_oculatus
MLPKSSPLSLSEKEKG
>Trichomycterus_areolatus
MLPRTTQLSLSKREKG

>Danio_rerio
MLPVNSCLSLSEKEKG
>Trachinotus_blochii
MLP-KSCLSPSEKEKG
>Pygocentrus_nattereri
MLPESSQLSLSEREGK
>Pundamilia_nyererei
MLP-KSCLSPSEKEKG
>Alosa_alosa
MLPISSGLSPSEKEKG
>Kryptolebias_marmoratus
MLP-KSCLSPSEKEKG
>Apteronotus_leptorhynchus
MLPKNCQLSLSEKEKG
>Plecoglossus_altivelis
MLPKRSCLSPSEKEKG
>Scleropages_formosus
MLPKSTPLSLSEKEKG
>Sebastes_caurinus
MLP-KSCLSPSEKEKG
>Platichthys_stellatus
MLP-KSCLSPSEKEKG
>Lepisosteus_oculatus
MLPKSSPLSLSEKEKG

>Homo_sapiens-----MPPPRCPESRSDSEKG
>Panthera_tigris-----MPPPCCPESRSDSEKG
>Balaenoptera_acutorostrata_s-----MPPPCCPESRSYSEKG
>Myotis_brandtii-----MPPPCCPESRSDSEKG
MVSRSQRPGRHLC TGS HFS PGHL VMPPCCPESRSDSEKG
>Galeopterus_variegatus-----MPPPCCPESRSDSEKG
>Oryctolagus_cuniculus-----MPPPCCPESRSDSEKG
>Equus_asinus-----MPPPCCPESRSDSEKG
>Manis_javanica-----MPPPCCPESRSDSEKG
>Loxodonta_africana-----MPPPCCPESRSDSEKG
>Mus_musculus-----MPPPCCPESRSDSEKG
>Trichechus_manatus_latirostr-----MPPPCCPESRSDSEKG
>Orycteropus_afer_afer-----MPPPCCPESLSDSEKG

HG0268.1 ENSDARG00000011703 clocka

>Danio_rerio
MSTSRLKVLSQLRP
>Pygocentrus_nattereri
MSTSRLKLLSLPLQP
>Clupea_harengus
MSTSRLKVVSLPLRP
>Lepisosteus_oculatus
MSTSRLKQDSLRLRP
>Trichomycterus_areolatus
MSTSRLKLLSVPLQP
>Takifugu_rubripes
MSTSRLKVLSPPLRP

```
>Homo_sapiens
-----MVGHIIEEYLEPIVS
>Panthera_tigris
-----MVSHIEEYIEPIVF
>Myotis_lucifugus
-----MP-PYVTLSDRILRLMVSHIEEYIEPIVF
>Galeopterus_variegatus
-----MIGHTEEYLEPIVF
>Equus_asinus
MNPQASFMPPNSHHILRRILRLMVSHIEEYIEPVVF
>Heterocephalus_glaber
-----MVGHIEEAELEPIVF
```

>Homo_sapiens
-----MITRRQLVLRRTNVYYKTKT
>Physeter_catodon
-----MRRSTNVYYKTKT
>Pteropus_alecto
-----MLIPQIKRRSTNVYHKTKT
>Loxodonta_africana
-----MKETFDV-RDKDQTKRENTKCGKWRPYRRSTNVYHKTKT
>Heterocephalus_glaber
MTRTAEFVSGKPAASF SRKINSMQSSPILPLCRPATILRRSTNVYHKTKT

HG0269.1 ENSGALG00000028685 SEMA5A

>Gallus_gallus
MVTIERCFSPMSARRVSS
>Anser_cygnoides
MVTKRCSHMSARRVAG
>Columba_livia
MVTKRCSHMSARRVAS
>Corvus_brachyrhynchos
MVTKRCSHMSARRVDS
>Aptenodytes_forsteri
MVTKRCSHMSARRVVS
>Struthio_camelus_australis
MVTKRCSHMSARRTAS

HG0269.2 ENSDARG00000061471 sema5ba

```
>Danio_rerio
MLVMPLCIPEAHLGS
>Salmo_salar
--MTSCCIPEAHLGS
>Ictalurus_punctatus
-MSLWKCIPAEHLGS
```

HG0269.3 ENSGALG00000011686 SEMA5B

```
>Gallus_gallus
MPLTQTEITKDFPWCLTSNMTLQ
>Lepidothrix_coronata
-----MTLNMTLQ
>Aptenodytes_forsteri
-----MTSNMTLQ
```

>Gallus_gallus
MVNVTVMFHKCRSRITIFPCFLFFFFSFLFFFFFIS--SLARMSE---LD-----
>Calidris_pugnax
MVNLTGKMFCKCRSRITIFPCF-LFFFF----FFFSIS--SLARMSE---LD-----
>Pterocles_gutturalis
MVNLTGKMFVKYRSRITIFPCF-LFLFF----FFLIS--SLARMSE---LD-----
>Columba_livia
MVNLTGKTFHKCRSRITIFSCFLFFFF-----LFVFSFHHWQESVNWIDMEVIEEEK
>Aquila_chrysaetos_canadensis
MVNLTGKMFCKCRSRITIFPHF-LFFFLS-FFFFFFFIS--SLARMSE---LD-----
>Gavia_stellata
MVNLTGKMFVKCRSRITIFPCF-LFFFF-FFFFFLIS--SLGRMSE---LD-----
>Chlamydotis_macqueenii
MVNLTGKMFVKRSRITIFPCFLFFFF-----FFFSFHHWQE-----
>Opisthocomus_hoazin
MINLTGKMPHKCRSRITNFPCLFLFLF-SFFHFIIIGKN-----E-----
>Manacus_vitellinus
MVNLTGKMYRKCRSGITIFPCFLFFPF-FFFHFIIIGKN-----E-----
>Phaethon_lepturus
MVNLTGKMFVKCRSRITIFPCF-LFFFF----FFFS--SLARMSE---LD-----
>Melopsittacus_undulatus
MVIITGKMFCKCRSRITILPSLFLFLFLCLW-----
>Aptenodytes_forsteri
MVNLTGKMFVKCRFKITIFLCFLFFFF----FIFFSFHHWQE-----
>Tyto_alba
MVNLTGKMFHKCRSRITIFPCFLFFFF-SLFFFFFFFFFFFFHHWQE-----
>Apaloderma_vittatum
MVNLTGKMFCKCRSRITIFPFS-F-----FFFFFFIS--SLARMSE---LD-----

>Gallus_gallus
MISFLFLALPPPSLSLISLT
>Calidris_pugnax
MISFLFLALPPPSLSH----
>Pterocles_gutturalis
MISFLFLALPPPSLSH----
>Columba_livia
MISFLSLALPPPSLSH----
>Falco_cherrug
MISFLFLALPPPSLSLISLT
>Gavia_stellata
MISFLFLALPPPSLSH----
>Chlamydotis_macqueenii
MISFLFLALLPPPSLSH----
>Opisthocomus_hoazin
MISFLFLALPPP-LSLISLT
>Lepidothrix_coronata
MISFLFLALPPPSLSLV---
>Nipponia_nippon
MISFLFLALPPPSLSH----
>Fulmarus_glaucialis
MISFLFLALPPPSLSH----
>Aptenodytes_forsteri
MISFLFLAVPPPSLSLISLT
>Tyto_alba
MMSFLFLALPPPSLSH----


```

>Homo_sapiens
MEAPGVLRMDQPPAPRPSRPIRRAPA
>Leptonychotes_weddellii
-----MDQPPAPRPSRPIRKAPA
>Lipotes_vexillifer
-----MDQPPAPRPSRPIRRAPA
>Eptesicus_fuscus
-----MDQPPRPGPHVQ-----
>Dasypus_novemcinctus
-----MDQPPAPRPSRPIRRAPA
>Monodelphis_domestica
-----MDQPPLPLPSCPIRRDP
>Macropus_eugenii
-----MDQPPLPLPSCPIRRDP
>Condylura_cristata
-----MDQPPAPRASRPIRRAPA
>Elephantulus_edwardii
-----MDQPPTPRPSRPIRRAPA
>Ceratotherium_simum_simum
-----MDQPPAPRPSRPIRRAPA
>Ictidomys_tridecemlineatus
-----MDQPPAPRPSRPIRRVP

```

HG0271.1 ENSGALG0000004064 GPER1

>Gallus_gallus
MELELCHLPTCTKENQ-
>Caprimulgus_carolinensis
MELKFCYLPACMKKLC-
>Cariama_cristata
MELKFYYLPTCTKKHC-
>Calidris_pugnax
MELKFCRLPTOPEKRCR
>Pterocles_gutturalis
MELKFYYLPTCMKKHC-
>Merops_nubicus
MELKFYYLPPCTKKHC-
>Haliaeetus_albicilla
MELKFYHLPTCVKKHC-
>Gavia_stellata
MELKFYYLPTCMKKHC-
>Eurypyga_helias
MELKFYYLPTCMKKHC-
>Pelecanus_crispus
MELKFYYLPTCMKKHC-
>Fulmarus_glaucialis
MELKFYYLPTCMKKHC-
>Apaloderma_vittatum
MELKFYYLPTCMKKHC-

HG0271.2 ENSG00000164850 GPER1

>Homo_sapiens
MPGSLQGESRFFLKMDSPFKTELWEPFGKS
>Orcinus_orca
MPGSLPRASPFLKKRDFLLKNGFWEPGGS
>Equus_asinus
MSGSLQRAAPFFLKMDLLFKTDFCGPWGKS
>Mesocricetus_auratus
MPGSLPRESPPFFVKMOLLKTDFCDFPFSKS
>Tupaia_chinensis
MLDSLQRESPPFLTMDSWFKTDFCDFFGNS

HG0271.3 ENSDARG00000074661 gper1

```
>Danio_rerio
MLMDWRKQDCAGLNTCEKQSVQKKKKKQDP
>Pygocentrus_nattereri
MPVDWRRQGSAGIKTCEEQSVQKNQERHNP
>Salmo_salar
MHMDWMRQASTGIRTCQKTAQKKRKKQSP
>Ictalurus_punctatus
MLLDWRRQSSGIKMKQKQTVQKKHSL---
```

>Drosophila_melanogaster
-----MSDTRKDPCKPNACRIQACLTKNHQYQEDKCLDVLEAMRQCCLKWHKES---LCCSGIDLEKTYLPDASKEKNATGKSNK-----
>Boeckxelia_potanini
MDREYNSVLKPRDPCKPKACAIQRCLERTHYNVVLCPFYEQLTECCRQFAARS---DACGSEEOPPASALDREPVA-----
>Parasteatoda_tepidariorum
-----MKQKEPCQKYACELQKCLKENNFQGEHCLSVIKSLLOCCEKNWFKS---KCCGFI ESSDMVPDL-----
>Meinertellus_cundinamarensis
-----MKKDPCKIFACEIQKCLQENKFQESACQAAIINALKKCCCKWRKES---LVCSGIKIDDELNKDIPQK-----
>Mastotermes_darwiniensis
-----MKKDPCKPHACSIQKCLKENNYQESACQEFIELLKECCRKWSSAS---ISCSGIDTQEPSQTPEDKKQ-----
>Carabus_granulatus
-----MPVTKDPCKATACKIQKCLKENNYQESACADVLEEMKECCRKWAKVS---LCCSGIKIEDKAGSSSFNQSVK-----
>Carcinus_maenas
-----MKKDPQORQACDIQDCLQRNKYQEAACEIQIINALQECCKWHKES---GCCAGVCLKGTVSDAALKTKPSSQKSNVK-----
>Forficula_auricularia
-----MPRIDPKNPCMHSYCDYNKCLTETNYKEDCKYYLDQLRNCCKFAHLNS---LSCGIGKFDPPKENDHTETVTK-----
>Occas_japyx_japonicus
-----MPAKPNDPCKPLACIQKCLVANDFLESKEEEVKRMLACDILWGSETSGGRSCSGFWINRPGEAPRKRGKAKK-----
>Aposthonia_japonica
-----MPKDPCEPHACKIQKCLTENNFQGECKAVIDDMINCCCKWGGES---LCCSGFLSGNKTDSSKEGSSAVTNEGKPSSET-----
>Eurylophella_sp._AD-2013
-----MKGDPCQLQACAIQKCLQVNNYQEAACPKFEEMRKCCCKWGLS---GCCSGFKDPELISSENROGDKVASK-----
>Galioisiana_yuasai
-----MKDPCKPYACKIQKCLKEHNYQESACKDVIEEMVICCRKWGDIS---LCCSGIDTGKTNGSSGSKTVSGKT-----
>Pachypsilla_venusta
-----MSKKKDPCKVHACIQKCLKENDFQESCKLOFYEYMRQCCVKFHADS---ICCSGIDINKSYLKDNEKSSPSKTDHIERSTLVAKISSYSSRSNNILFERFFQ-----
>Brachyistis_timberlakei
-----MTTDPCKPYACKLQKCLKDNVYQPSCEEVIEEIROCCIKHSKAS---IVCGIDTSGQYEHNTVDYKATK-----
>Ixodes_persulcatus
-----MKAVDPCKEACAIQKCLQEHNYQESADACVIEIKEMLKCCCKWREMS---GCCSGFLKDEASKKAKGELKSKT-----
>Antheraea_yamamai
-----MSKDPCKRFACDIQKCLVNNYQEVRCASFVEMRRCCCLKFKPSS---LVCEGYDLEPKFAPVTDRAKK-----
>Mantis religiosa
-----MKKDPCKPYACEIQKCLKEHNYQIEPCQKFVEYLDDCCRKWGDVS---ISCSGIDTRTSPMKASDKE-----
>Panorpa_vulgaris
-----MSNVKDPCKPSACKIQKCLQEHNFQEGSCIDVIEQMLCCVKWEGKS---FVCGINTAEPADLAISPKHTKHS---RY-----
>Dermatysus_gallinae
-----MPKGDPCQKQACDIQKCLQANNYQEALCVEAFRAMDLCCCKWGLS---GCCGTGIEQQLKKKI ANESTKTPISFN-----
>Pseudomallada_prasinus
-----MPKPYIDPCKEFACRIQKCLRENNFQEHRCQVIEELRQCCVKWSES---ISCSGIDINSKPEEQ-----
>Triops_newberryi
-----MKECCKWQERS---QSCAGFLVPEIEKKKNEPLS-----
>Calopteryx_splendens
-----MKQCCDKWFDES---LCCSGFKKPSSES-----
>Stenobothrus_lineatus
-----MRKDPCKPIACKIQKCLTENRFQEPACQRLVLEEMKECCRKWAHIS---LCCSGIDTSDKPKD-----
>Extatosoma_tiaratum
-----MKDPCPKQACKIQKCLTENNYQEAACKDVIEKMEVCCCKWADVS---LCCSGINTKETTANSPEEI-----
>Menopon_gallinae
-----MTKDPCKSLACALQKCLKENDFQEEERCKKVLDDIRTCCKKFEIS---VVCSGIDVSEKIK-----
>Cosmioperla_kuna
-----MKKRDPCKAHACRIQKCLAEKNFQESACQAVLEDMRSCCRKFKMVS---LCCSGIDIGDTPTLETASEPKK-----
>Ecotopsocus_briggsi
-----MPKKVPEPCPLACALQKCLTENNYQEAACKEAISALKDCCAKWGETSP---VVCSGFNK-----
>Xanthostigma_xanthostigma
-----MKDPCKLTACKIQKCLQEHNFQEDACADVLEEMRQCCLKWYKES---LCCSGIRLDEPKIKEKKSINQSKTN-----
>Ctenocephalides_felis
-----MRSKDPCKANACMIQKCLSENNFQESACTDVI ELMRLCCVKWGTKS---FVCGIKTEKETSSSTSVENN---KIPYKLDHKS-----
>Thrips_palmi
-----MSKRSKDPCKPFACAIQDCLNAKNFQESACVDVIEENLNECCRHWHKHS---LVCSGMLIGPAEVEKSDVKSDGTSGVEVRKA-----
>Hydroptila_sp._AD-2013
-----MKQKDPCKATACKIQKCLRERGFQEEERCADVLEEMRQCCLKWHKVS---LCCSGIKLDPPKIEKETK-----
>Zorotypus_caudeilli
-----MKKKKDPCELYACMLQKCLTENNFRESCCI AVLQELRECCRIWGNAS---ICCSGFDNSPKAEKEPENKEPSSAKK-----
>Thermobia_domestica
-----MKGGDPCKQACDIQKCLKIHNYYQVSACKDFFEAMKKCCCKWGLS---GCCSGFKKERELEEAGTK-----

>Drosophila_melanogaster
---MESVRKANQRIRNYPVLLSKCADKATAYAVCVSRD-----LNQHKICDTEFKEFLSCIRKTALEMKTKL
>Oxyacanthus_curtus
---MESVRKARERMKRFPMILLKECHDPATSYARCVALK-----ENVLKDDCSQEFQMFKNCLASAAKMGTKM
>Machilis_hrabei
---MESVRKAKVRLQMYPKLLAQCGREGSAYAOQCVITI-----ENLKKGDCSKEFQDFRVCIQKAACKLNTRL
>Argulus_siamensis
---MDSVKNQQLSKSYTOSIVKCNQEASMYAOQVLVQ-----DDLKKHACSEEFKLVICINKVIQKK-----
>Periplaneta_americana
---MESVLKAKQRLRRYPPELLVQCTGPATAYAMCVLAK-----ESVRHAECDFEQFQLQLQKAARHLGTRL
>Euwallacea_fornicatus
---MESVSKAQRFROYYPVIFAKCSREASVYATCVLKQ-----DNIKKNDCAEFSGFRTQLRKAASVSLKTKI
>Farfantepenaeus_aztecus
---MESVKKQNLRLNYPKLVANCAPVATEYARCVALK-----GNVLKGDCAQEFQAFKRCILESAAKMKTKI
>Ocas_japyx_japonicus
---MESVKKARSFQMYPKLLAECGGPAAAYAKCVATH-----EDLPKGACEKEFQGLKECLQAAAKMGTRL
>Aposthonia_japonica
---MESVRKAKVRMRYPPELLKTCSPAAAYAKCVAKS-----GNIRHCEELFIKFMSCMTAAKNLGSRL
>Eurylophella_sp._AD-2013
---MESVSRARLRWFPRFLAECAAEGTSYAQCVAQQ-----DNPORGACAEFEQFSRCVRGAQKHGTRI
>Meganyctiphanes_norvegica
---MESVKKARNRLKAYPKLAAQCTGVATEYARCVALK-----ENVMKGDCNAEFEAFKKLMDSAKRMNTRL
>Grylloblatta_bifratrilecta
---MDSVKNQGRRLQRYPLLVNCPAITYATCVVSK-----DNVKKACEKEFKLLLEGLHKAARKRGTRL
>Kerria_lacca
---MDSVSKAKNRHKKYPLVFIECRNEGLYAACVASK-----QDIQFQCNVEFNFKNKLMSKAIKLGTKL
>Pseudomasaris_vespoidea
---MEAVKNAKDRLRKYPLLLAECDDAATKYAVCVLAK-----KNLQKNDCEAEFHEFKIQLTKAAKHRTKL
>Metaphatus_ochraceus
---MESVQKARDRLAKYPLIFGKCGQATLYARCVCLK-----DNVKKDDCAPEFKEFMSCLKTTAKDMKVRF
>Mantis religiosa
---MESVRKAKQRLRHYPKLLAECGPATAYASCVLAK-----ENVKRGDCQEFQALRKQLHQAQKHIGSRL
>Boreus_hymalis
MQVMDSVRSARQLSQYPKFLAECTQSATQYAMCVCRD-----TNVQKQDCINEFNAFKQCFQKAAKAKVKL
>Chrysopa_pallens
---MESVKKAKHFRNYPVLLTECRNEASEYAAQVLNS-----GGIKYKECAKEFTNFKNCIQKAAVKHKTCL
>Triops_newberryi
---MEPLRKARTLRHNYPLVIAECGPQATSYGRCIALKL-----DDLKDDTCVKEFEAFKGLQQAASKKLKTKL
>Epiophlebia_superstes
---MEAVNRAGRMRRFPRLLSLCTAEGNAYAVCI1AAHESGGPRGTGLTKGQCDAEFQALKLCVSEAAKAGTRI
>Stenobothrus_lineatus
---MEAVQAAARSRLRKYPLLLSKCSTEASLYATCVLSR-----DNIKHSECEQEFKRLTTQLQKAAQKAGTRL
>Medauroidea_extradentata
---MDSVRKHSRLQRYPELLRRCSEATAYAGCVIGK-----ENVKRWDCDEEFKQLMSCLRSAAKYAKIRL
>Menopon_gallinae
MGKVEVLKMAKTRLRKYPDLFAECRTGGAAYAACVVKQ-----ENVTRNSCAAEFQNFKNCAKMSAARLSTRL
>Cosmioperla_kuna
---MESVRRARLRRYPELFAVCHAPATKYAACVVNK-----DNIKHNECGKEFLFKQLLEQAQKCGTRL
>Ectopsocus_briggsi
---MEAVQRSARLRLARYPFHLTAC1EGGAYATCVLEK-----ENLTKDACVKEFRALVKMKVSAAKSGSRL
>Xanthostigma_xanthostigma
---MESVKLARTFRKYPPLLLTECHNFAAYASCVLVK-----ENIQNDCAKEFEAFKNQLKKTALKHKTRL
>Oropsylla_silantiewi
---MDSVRKARARFSDYPSLLGECATQATTYASCVCRD-----LNVEKDRCLKEFTELQKCVKKAASKAKVRI
>Gynaikothrips_ficorum
---MESVRKAKRLRLSRYPALLAECREPAKQYAAQVSRQ-----DNVVKGSQTEFVRFKGQLLKASAKMATRM
>Annulipalpia_sp._AD-2013
---MESVKKAHTRLROYYPVLLACGESASAYAKVIRL-----DTVKNDCSKEFNFSKQLMKAADKMKTKM
>Zorotypus_caudelli
---MDALTKARNRLKKYPQHLKECTEPAAYASCVIRK-----DNLKKGDCKEFKELKGLLLVAEKRKTKL
>Atelura_formicaria
---MESVKKARGRLRKYPQLLAGCAKEGTYAKCVMDN-----ANVKGCGCTKEFEELKTKLIKAAKKQGTRI

HG0272.3 ENSG00000143315 P1GM

```
>Homo_sapiens
MPDVIVCSRFGWQPGGWEMRRPPAAKNRREG
>Rhinolophus_ferrumequinum
-----MRROPEGRSRS-----
>Ceratotherium_simum_simum
-----MRPPEARNRRED-----
>Manis_javanica
-----MRGPPEARNAS-----
```

>Gallus_gallus
MSLFIRLYLKRP
>Anas_platyrhynchos
MSLFIRLYLKRP
>Chaetura_pelagica
MSLFIRLYLKRP
>Apteryx_australis_mantelli
MSLFIRLYLKRP
>Cariama_cristata
MSLFIRLYLKRP
>Galidris_pugnax
MSLFIRLYLKRP
>Merops_nubicus
MSLFIRLYLKRP
>Cuculus_canorus
MSLFIRLYLKRP
>Aquila_chrysaetos_canadensis
MSLFIRLYLKRP
>Gavia_stellata
MSLFIRLYLKRP
>Eurypyga_helias
MSLFIRLYLKRP
>Opisthocomus_hoazin
MSLFIRLYLKRP
>Nipponia_nippon
MSLFIRLYLKRP
>Fulmarus_glacialis
MSLFIRLYLKRP
>Aptenodytes_forsteri
MSLFIRLYLKRP
>Struthio_camelus_australis
MSLFIRLYLKRP
>Tinamus_guttatus
MSLFIRLYLKRP

HG0273.2 ENSG00000140943 MBTPS1

```
>Homo_sapiens
MECPGVFAAEAPLSRARRP--
>Felis_catus
METRGVFAAEAPLSRARGTRA
>Lipotes_vexillifer
MEILGVFAAEAPLSRAGRTRA
>Rhinolophus_ferrumequinum
METRGVFAAEAPLSRAHRTA
>Condylura_cristata
MESRGVFAAETPLS-----
>Equus_asinus
MESRGVFAAEAPLSRARRTRA
>Manis_javanica
MEARGVLAEEAPLSPARRN--
>Psammomys_obesus
METRGVFAAEAPFSRARQLRA
>Trichechus_manatus_latirostr
METRGVLSVEARLSRARRTGA
```

HG0273.3 ENSG00000140943 MBTPS1

>Homo_sapiens
MLQLLAETKIHf
>Chinchilla_lanigera
MLQLLAETKIHf
>Tupaia_chinensis
MLQLLAETKIHf

>Homo_sapiens
MTGPSGGQYRPPRSPWSSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Ailuropoda_melanoieuca
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Orcinus_orca
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Myotis_davidii
MTVPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Dasypus_novemcinctus
MTGPGGGQY-----MEAAAP
>Galeopterus_variegatus
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Condylura_cristata
-----MEAAAP
>Orctolagus_cuniculus
MTGPGGGQYRPPRSPRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Elephantulus_edwardii
MTRPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Equus_caballus
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Manis_javanica
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Loxodonta_africana
MTDTGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Trichechus_manatus_latirostr
MTGPGGGQYRPHRSPRRSPFGPAQSSESVHPLYSALKRISKMEAAAP
>Orycteropus_afer_afer
MTGPGGGQYRPHRSPRRSPFLGPAQSSESVHPLYSALKRISKMEAAAP

>Danio_rerio-----MLLRNKSYPKICKDNATGAARSESNKVOHHLRLAHSRDRSSRV
>Astyanax_mexicanus-----MLLRNKSDDPKICEENAAGAARTESNKTC-----
>Ictalurus_punctatus
MGGQTHTHTHTHHTQTTESSQPCIMPLRCNKKLPENLHGNAATGAAWSESNKVVLTLY-----

>Homo_sapiens	-----MKKIFLKLHILQEKNHKCFSVLPEYMI-----
>Canis_lupus_familiaris	-----MKKSFLKLHIVQKNPKCFHILFELRIKKFP-----
>Balaenoptera_acutorostrata_s	-----MKKFFFLKLHILQEKIPNVFIFQLNTKFKQGVSTEVRRLRKCASPCSGLLTG-----
>Rousettus_aegyptiacus	
MCVRSAAGRPGFASASALAATRASQEPPRRPARGAGEEIIINLLNEKSFLKVAYTPRKNPKCFHILPEYKI-----	
>Ceratotherium_simum_simum	-----MKKFFFLKLHVLQEKNRSFLNILLPEFKI-----
>Manis_javanica	
MCVRPTPGRPGFASASVLASTRASEEPPQRPARGAGEEIIINLLNEKIILKVTYSRKNPKCFYILPENKI-----	
>Cavia_porcellus	-----MKKRILKVGYTPRKKPKCFSVLPDYKI-----

HG0275.2 ENSDARG00000045540 ppp6r2a

```
>Danio_rerio
MLGHSVPSPAFCHSNACRPVEEV
>Pygocentrus_nattereri
MPGRSVLSAFCHSNACLLVEEV
>Ictalurus_punctatus
-----MPSAVCHSNACLLVEKV
```

HG0276.1 ENSGALG00000008912

>Gallus_gallus
MDSSSSITVTWNIQHMM
>Anas_platyrhynchos
MDLSL SVTVTWNIQHCL
>Callidris_pugnax
MDSSLHVTATWSIQHHL
>Manacus_vitellinus
MDSSL SVTVTWSIQOHL
>Pygoscelis_adeliae
MDSSL SVTVTWSTQHHL

HG0276.2 ENSG00000073734 ABCB11

```
>Homo_sapiens
MMKTEVGKGCETF
>Equus_asinus
-MKTEVGKGCKTL
>Trichechus_manatus_latirostr
MMKTEVGKGCKTL
```


HG0277.1 ENSG00000102531 FNDG3A

>Homo_sapiens
MAAAAFVVPVKQKAGATRRGSEERG
>Felis_catus
MAAAAFVVPVKQKAGATRRGSEERG
>Orcinus_orca
MAAAAFVVPVKQKAGATRRGSEERG
>Pteropus_vampyrus
MAAAAFVVPVKQKAGATRRGSEERG
>Monodelphis_domestica
MAAVGVVISRVKQKEGATGRLGEERG
>Condylura_cristata
MAAAAFVVPVKQKAGAARRGSEERG
>Ochotona_princeps
MAAAAFVVPVKQKAGATRRGSEERG
>Elephantulus_edwardii
MAAAAFVVPVKQKAGATRRGSEERG
>Ceratotherium_simum_simum
MAAAAFVVPVKQKAGATRRGSEERG
>Octodon_degus
MAAAAFVVPVKQKAGATRRGSEERG
>Trichechus_manatus_latirostris
MAAAAFVVPVKQKAGATRRGSEERG
>Orycteropus afer afer
MAAAAFVVPVKQKAGATRRGSEERG

HG0277.2 ENSGALG00000004169

>Gallus_gallus
MAERSVGGRRRG
>Calidris_pugnax
MAERSVGGRRRG
>Haliaeetus_leucocephalus
MAERSVGGRRRG

```
>Homo_sapiens
-----MPGHLQPPAGTSCPGGV-----
>Myotis_lucifugus
MGNFPGQWGRRGAGRELLPGRSSLRCCLLLKQEALLQAKLSLGCSSDIPECVRVMHRAVMRGHFQPPAGTSCPDVRVTPTASSPRAQGACTW
>Dasypus_novemcinctus
-----MLCAVMRGHLQPSSTSCPG-----
>Condylura_cristata
-----MRGHLWPPAGTTCGGRV-----
>Oryctolagus_cuniculus
-----MRGHLQPPAPTPCGRVCAPTASSPRAQGARTW-----
>Equus_caballus
-----MLQGKLSPDGNSDTTKCVVMQSAVMRGHLQPPAKTSCPGRV-----
```

```
>Danio_rerio
-----MHKSRRAAEMKP---DWL
>Channa_argus
MYIKKSRVESCRSFYMRCTCFG1SFVEEAADAPPTSQRREFPVGRRGRSSRGHGRHELARKPALASRQCRTSRGNEQVPMHKSROPSEAEMKADSDWL
>Alosa_alosa
-----MHKLKRRTAEMKADSDWL
>Lateolabrax_japonicus
-----MHKSROPSEAEMKADSDWL
```

HG0279.1 ENSG00000175928 LRRN1

>Homo_sapiens
MFTFSARCPYHNIVFTFC
>Leptonychotes_weddellii
MFTFSACCPYHYLVFNFC
>Balaenoptera_acutorostrata_s
MFTFSARCPSYHYTVFTFC
>Rhinolophus_ferrumequinum
MFTFSARCP-----
>Galeopterus_variegatus
MFTFSACCPCHRTVVFTFC
>Geratherium_simum_simum
MFTFSACCATYHYIVFTGC
>Manis_javanica
MFTFLVCCPTYHOTVSAFC
>Nannospalax_galili
MFTFSACGST-----
>Orycteropus afer afer
MLAFPACCPTHHYIGFTFC

HG0279.2 ENSGALG00000035099 Lrrn1

>Gallus_gallus
MSAPPLRGGEERLG-QRPPGCRNVFRHGFVEDPGTORSS
>Anas_platyrhynchos
-----MTRLRTKANGTIYRNIFRHRFAEDPGTORSG
>Callidris_pugnax
-----MLSGTP-----NSRLCSRAVRNLFRRHFAEDSGTORNS

HG0280.1 ENSG00000156299 TIAM1

```
>Homo_sapiens
-----MAHLEILTKPLLFPMGFLAHSHRLR
>Acinonyx_jubatus
-----MGFLAPPHRLR
>Oryctolagus_cuniculus
MLCILVPQLGPEQPAMMAPLEILTKLLFCMGFSAHYPR--
>Equus_caballus
-----MGFLAHYHRFR
>Ictidomys_tridecemlineatus
-----MAPLEILTKPLLFGMGFLAHSSRLR
>Tupaia_chinensis
-----MAYLKILTQLLLSEMGILAHSHRLR
```

>Drosophila_melanogaster
MGAKESVEAAAKMNADGWHVERSSRYHNHRH-NQRSQSLNRGQALSQ-----ADVSGMW
>Rhynchophorus_ferrugineus
MGAKGSVEAA-KINAQNNNSFEHNHSKQFVGH-HQRSQSLNRGVREQWSGRGADLGGSDMW
>Trichoplusia_ni
MGAKESVEAA-KFSAQNNNNFEHAAVKHPYRHGTQRSQSLNRGHSLSR-----TD---GTW
>Chrysopa_pallens
MGAKGSVEAA-KYNAQOWNSMEGSRHRH-----SQRSHSLNRGHSLSR-----AP---DMW
>Oropsylla_silantiewi
MGAKGSVEAA-----KENWEHIERGR---HHRL-HQRSQSLNRGHSLSR-----ADTAGMW

>Gallus_gallus
MGRMSSTVFTRNS
>Anas_platyrhynchos
---MSSTVFTQSS
>Apteryx_australis_mantelli
---MSSTVFAQSS
>Buceros_rhinoceros_silvestri
---MTSTVFTQSS
>Calidris_pugnax
MCTMSSTVFTQSS
>Colinus_striatus
---MSSTVFAQSS
>Aquila_chrysaetos_canadensis
---MSSTVFTQSS
>Chlamydotis_macqueenii
MCKMSSTVFTQGS
>Pelecanus_crispus
---MSSTVFTQSS
>Picoides_pubescens
---MSSNVFTQSS
>Fulmarus_glacialis
---MSSTVFTQSS
>Melopsittacus_undulatus
---MSSTVFTQSS
>Calypte_anna
---MSSTIFTQSS

HG0281.2 ENSG00000100150 DEPC5

>Homo_sapiens
MTSLPQAWNS
>Leptonychotes_weddellii
MTSLPQAWNS
>Balaenoptera_acutorostrata_s
MTSLPQAWNS
>Miniopterus_natalensis
MTSLPQAWNS
>Dasypus_novemcinctus
MTSLPLAWNS
>Galeopterus_variegatus
MTSLPQAWNS
>Condylura_cristata
MTSLPQAWNS
>Oryctolagus_cuniculus
MTSLPQAWNS
>Equus_przewalskii
MTSLPQAWNS
>Manis_javanica
MTSHPQAWNS

>Danio_rerio-----MEGPVRICHRENVFRC
>Channa_argus-----MFFPSARTSSPCLMEGPVRICHQKNAFCC
>Trachinotus_blochii-----MEGPVRICHQKNASCC
>Micropterus_floridanus-----MEGPVRICLQKNAFCC
>Pygocentrus_nattereri-----MEGPVRICQKNAFCC
>Neolamprologus_brichardi-----MSLKPSRTLSPFLMEGPVRICQKNAFCC
>Esox_lucius-----MEGPVRICHQKNELFF
>Lateolabrax_maculatus
MWVEWNSSLTPPPPPPAVFMLPSSRTLSPCLMEGPVRICLQKNAFCC
>Sebastes_caurinus-----MLLPSSRKHSPCLMEGPVRICLQKNAFCC
>Cynoglossus_semi laevis-----MSRPLSYTFCPLMEGPVRICHQKNASCC
>Oncorhynchus_kisutch-----MEGPVRICHQKNELFC
>Trichomycterus_areolatus-----MEGPVRICCYRNAFCC

HG0282.2 ENSG00000144857 B0C

```
>Homo_sapiens
MKSCRHL YRLRVAARK
>Condylura_cristata
MKSCQHSRLRVAARK
>Loxodonta_africana
MKSCQHSRRRVAATK
```

HG0283.1 ENSGALG00000010270 AREL1

>Gallus_gallus
MQVPGVPF SVTAFSMA SL C
>Anser_cygnoides
MQIPGVSF SVI IFSMA SSC
>Apteryx_australis_mantelli
MQVPGVSL SVMNFS L A SSC
>Charadrius_vociferus
MQVPGVSL SVI IFSMD SSC
>Colius_striatus
MQVPGN-----
>Leptosomus_discolor
MHVPGI SL SVI IFSMA SSC
>Haliaeetus_leucocephalus
MQVPGVSP SVI IFSMA SSC
>Mesitornis_unicolor
MQVPRVSL SVI IFSMA SSC
>Opisthocomus_hoazin
MQAPGVSP SVI IFSMA SSC
>Phaethon_lepturus
MQVPGVSL SVI IFSMA SSC
>Picoides_pubescens
MQVPGVSL SVI IFSMT SSC
>Fulmarus_glacialis
MQVPGVSL SVT IFSMA SSC
>Struthio_camelus_australis
MRVPGVSL SVMNFSMA SSC
>Apaloderma_vittatum
MQIPGVSL SVI IFSMA SSC

HG0283.2 ENSG00000119682 AREL1

>Homo_sapiens
MDRPFLLTLWRFSMWKLEDKVKGAKSYLLW-
>Panthera_tigris
MDRHFPLTLQQFSFLWKLEDKVNGARSYLLW-
>Balaenoptera_acutorostrata_s
MDRHFLLTLQLFSFMWKLEDKVKVAKSYLLW-
>Pteropus_alecto
MDRHFLLTLQLFSLMWKLKTR-----
>Dasypus_novemcinctus
MDRPFLLTLWLFSSMWKLEDKVGGKSYLFW-
>Galeopterus_variegatus
MDRPFLLTLRLFSFMWKLEDKAKGAKSYLLW-
>Condylura_cristata
MDRHFLLTLQLFSFMWNLKDKVTATKSTCSGE
>Oryctolagus_cuniculus
MDNDLPMTLWLFSSFMWKLEDKVKEARDYLLW-
>Equus_asinus
MDRHFLLTLWLFSLWKLEDNVKGAKNYPLW-
>Manis_javanica
MDRCFPSTLQLFSMWKLEDKVKGAPYLLC-
>Dipodomys_ordii
MDRPFVTLWLFFFMMWKLEDKVKGAKSYLLR-
>Tupaia_chinensis
MDRGFLLTLQLFSFMQTRWKTR-----
>Trichechus_manatus_latirostr
MDRPFLLTLQLFSFMWKLEDRVKGAEVLCFGE
>Orycteropus_afer
MDRPFLLTLQLFSMWKLEDKVEGARSDLLW-

>Homo_sapiens	-----MGVKDGRGPAAAVQRSGGMNLT
>Leptonychotes_weddelii	-----MGVKDGRGPAAAVQRSGGMNPT
>Physeter_catodon	-----MGVKDGRGPAAAVQRSGGMNLT
>Miniopterus_natalensis	-----MGVKDGRGPAAAVQRSGGMNLT
>Galeopterus_variegatus	-----MGVKDGRGPAAAVQRSGGMNLT
>Erinaceus_europaeus	-----MGVKDGRGPAAAVQRSGGMNLAC
>Ochotona_princeps	-----MGVKDGRGPAAAVQRSGGMNLT
>Ceratotherium_simum_simum	-----MGVKDGRGPAESAVQRSGGMNLT
>Mesocricetus_auratus	-----MGVKDGRGPAAAVQRSGGMNLT
MPCFLSLLSGNSDAWLFVFMVMTFTLSLSLTPSLPPSLPPSFLPSLSPLSRRMGVK	-----MGVKDGRGPAAAVQRSGGMNLT
>Tupaia_chinensis	-----MGVKDGRGPAAAGQRSGGMNLT
>Trichechus_manatus_latirostr	-----MGVKDGRGPAAAVQRSGGMNLT
>Orycteropus_afer_afer	-----MGVKDGRGPAAAVQRSGGMNLT

>Gallus_gallus
MPPGFSVGFP IWRNICALSHCGKLNCGS
>Anser_cygnoides
MPLGFPIGFHIWRNISDLSHSVAD----
>Haliaeetus_albicilla
MPPDFLLDFTCGKIL-----
>Melopsittacus_undulatus
MPPDFLSGFTSGKLL-----

HG0285.1 ENSGALG00000012156 DPP10

>Gallus_gallus	
MLRGRPRAAQEEHGGADTGLGFPPAGAVAPRLPPAFFLYFSSSSAAAPLRGEVGMRLAPREGCGPQORQ	
>Calidris_pugnax	
	-----MRLAPREGCGPQORQ
>Acanthis_flammea	
	-----MRLAPREGCGPQORQ

```
>Homo_sapiens
-----MNOVNALFRAK
>Loxodonta_africana
MELSLAFCYISPRALRMMNOVNALFRAK
>Ctenomys_sociabilis
-----MNOVNALFRAK
```

>Homo_sapiens
MSLSAQYLR-----
>Leptonychotes_weddellii
MSLSAQYLR-----
>Lipotes_vexillifer
MSLSAQYLR-----
>Eptesicus_fuscus
MSLSAQYLR-----
>Erinaceus_europaeus
MSLSAQYLR-----
>Elephantulus_edwardii
MSLSAQYLR-----
>Heterocephalus_glaber
MSLSAQYLRFMDSKWKAMGFYMLD
>Trichechus_manatus_latirostr
MSLSAQYLR-----
>Orycteropus afer afer
MSLSAQYLR-----

HG0286.2 ENSDARG00000060767 smg7

```
>Danio_rerio
-MDNMAPGVDLACESVVV
>Pygocentrus_nattereri
MMDNMAPGVDLASGSVVV
>Apteronotus_leptorhynchus
----MAPGVDLASGPVVV
>Trichomycterus_areolatus
-MDNMAPGIDLAPEPAVV
```

```
>Homo_sapiens
MLQTDLSVLHEHTCGRQMTVLYPVLL
>Acinonyx_jubatus
-----MTVPHPVLF
>Balaenoptera_acutorostrata_s
-----MTVLHPPELL
>Rousettus_aegyptiacus
-----MTVLHPMLL
>Oryctolagus_cuniculus
-----MTALSPVLL
>Equus_asinus
-----MTVLHPLLP
>Loxodonta_africana
-----MSVVCP---
>Heterocephalus_glaber
MLQTDPSVFHAHACAGQMTVPHPVLL
>Tupaia_chinensis
-MLRSPSVLHEHVCGGQMTALLPVLL
```

>Danio_rerio
MQGSLLCSYHSEGRPTSTFS-----
>Amia_calva
MQCGHLCYHSEVRPTWPFPLKTIISPPISEPKPSRRRG-----
>Channa_punctata
MQCGHLCYHSEVRTTCTFSRKCKKTRLCFVIF----FVRQLLLVLLLI
>Oryzias_latipes
MQCSRLCSYHSEVRTACTFFAKCKITQNSRATSSTTLVQTIIIFS-----
>Pygocentrus_nattereri
MQCGHLCYHSEVRPTSTILLK-----
>Plecoglossus_altivelis
MQRSLLCYHSEELCDNKVTGGEESS-----
>Cynoglossus_semi-laevis
MQRDHLCSYHSEVRTTYRESAGDSCY-----

HG0288.1 ENSGALG00000006655 MAP3K13

>Gallus_gallus
MIRYWLPASRLNCPVL--
>Apteryx_australis_mantelli
MIRYWVHMLHLNCGVVLIL
>Calidris_pugnax
MIRYWVRVSHLNCVVLIL
>Falco_cherrug
MIRYWLHVSHLNCVVLIL
>Aptenodytes_forsteri
MIRYWVCVSHLNCVVLIL

```
>Homo_sapiens
-----MYCGIQI--LALWERFWSPLLSONSVPKIF
>Mustela_putorius_furo
MERAKDRAELVGLPVFLVSTYQLLRCAVAVRGRTHTRFWSPLLHPNSVPLIL
>Rhinolophus_ferrumequinum
-----MCRNSSLLFWSPLLRQNSIRVIL
>Mus_musculus
-----MPFWSPLLHOTSVAALF
>Tupaia_chinensis
-----MHQNSLPATL
```


HG0289 ENSG00000072415 MPP5

>Homo_sapiens
MDFILQNGENWLGKIDL
>Odobenus_rosmarus_divergens
MDFILQNGEIGFIDGEIDL
>Balaenoptera_acutorostrata_s
MDFILQNGEIGFIDGEIL
>Miniopterus_natalensis
MDFILQNGEIGFIDGEIDL
>Dasypus_noveboracensis
MDFILQNGENWLYRKFI--
>Galeopterus_variegatus
MDSILQNGENWLYRKNFI--
>Condylura_cristata
MDFILQNGEIGFIDGEIL
>Ceratotherium_simum_simum
MDFILQNGEIGFIDGEIDL
>Manis_javanica
MDFMLQNGEIGFIDGEIDL
>Loxodonta_africana
MDFILQNGENWLYRKNFI--
>Nannospalax_galili
MDFILQNGENWLYRKFI--
>Tupaia_chinensis
MDFILQNGENWLYRKNFI--
>Trichechus_manatus_latirostr
MDFILQNGENWLYRKNFI--
>Orycteropus afer afer
MDFILQNGENWLYRKIDL

>Gallus_gallus
-----MDFTQQRNENWPNISISI-----
>Anser_cygnoides
-----MDFTQHHNKNWPNSISV-----
>Chaetura_pelagica
-----MDFTQHHNENWPHSSISV-----
>Apteryx_australis_mantelli
-----MDFTPHHNKNWPYSSICV-----
>Buceros_rhinoceros_silvestri
-----MDFTQHHNENWPNSSISVCGE-----
>Caprimulgus_carolinensis
-----MDFTQHHNENWPNRSISV-----
>Cariama_cristata
-----MDFTQHRNKNWPNSSISV-----
>Calidris_pugnax
-----MDFTQHHNENWPNISISV-----
>Pterocles_gutturalis
-----MDFTQHHNENWPSSISV-----
>Colius_striatus
-----MDSTQHHNKNCPNSSISV-----
>Columba_livia
-----MDFTQHRNKNWPSSISV-----
>Leptosomus_discolor
-----MDFMQRHNENWPSSISV-----
>Cuculus_canorus
-----MDFTQHHNENWPNSSISV-----
>Aquila_chrysaetos_canadensis
-----MDFTQHHNENWPNSSISV-----
>Gavia_stellata
-----MDFTQHHNKNWPSSISV-----
>Mesitornis_unicolor
-----MDFMQRHNENWPNSSISV-----
>Tauraco_erythrolophus
-----MDFTQHHNENCPNSSISV-----
>Opisthocomus_hoazin
-----MDSTQHHNKNWPNSTISV-----
>Lepidothrix_coronata
-----MDFTQHHNKNWPNSSICV-----
>Phalacrocorax_carbo
-----MDFTQHRNENWPNSSISV-----
>Plcoides_pubescens
-----MDFTHHNENWLNSSIFA-----
>Fulmarus_glacialis
-----MDSTQHHNKNWPNSSISV-----
>Melopsittacus_undulatus
-----MDFTQCHSENWPNNISI-----
>Aptenodytes_forsteri
-----MDFTQHHNKNWPNSSISV-----
>Tyto_alba
-----MDFTQHHNENWPNSSISD-----
>Struthio_camelus_australis
-----MDFMPPHNENWPYSSICV-----
>Tinamus_guttatus
-----MDFTPHHNENWPFSTICV-----
>Calypte_anna
MGNIFQVMDFRQHNSWPSSISA-----
>Apaloderma_vittatum
-----MDFTQHPNENWPNSSFSV-----

HG0290.1 ENSG00000116539 ASH1L

>Homo_sapiens
MLVSSFGDPCFLWNTVL
>Acinonyx_jubatus
MLVASFGDPCFLWNTVL
>Balaenoptera_acutorostrata_s
MLVASFGDPCFLWNTVL
>Rhinolophus_ferrumequinum
MLVAHFGDPCFLWNTVL
>Dasypus_novemcinctus
MLVASFGDPCFLWNTVL
>Sarcophilus_harrisii
MLVASFGEOPFLNITF
>Monodelphis_domestica
MLVASFGEOPFLKTVL
>Sorex_araneus
MLVASFGDPCFLWNRVL
>Ochotona_princeps
MLVPSFGDPCFLWNTIL
>Ceratotherium_simum_simum
MLVASFGDPCFLWNTVL
>Manis_javanica
MLVASFGDPCFLWNTVL
>Loxodonta_africana
MLVASLGDLCLWNTIVL
>Dipodomys_ordii
MLVASFGKSCFLWNTVL
>Tupaia_chinensis
MLVSSFGDPCFLWNTVL
>Trichechus_manatus_latirostr
MLVASLGGDLCLWNVVL
>Orycteropus_afer_afer
MLVASLGDLCLWNTIVL

HG0290.2 ENSDARG00000070981 ash11

>Danio_rerio
MEARLTREARSDEPELH
>Astyanax_mexicanus
MEARLTPOARSDSPELD
>Haplochromis_burtoni
MEARLTREARADTSRPS
>Austrofundulus_limnaeus
MEARLTREARADTSRPS
>Notothenia_coriiceps
MEARLTREARADTSRPS
>Cynoglossus_semihaevis
MEARLTREARADTSRPS

>Gallus_gallus
-----MDRNLES~~L~~HGGFGISTC
>Anser_cygnoides
-----MDVNL~~E~~SLDLGGFGISTR
>Apteryx_australis_mantelli
-----MDLN~~E~~SLDLGGGISTC
>Buceros_rhinoceros_silvestri
-----MDVN~~E~~SLDLGGFGISTC
>Calidris_pugnax
-----MDLN~~E~~SLDLGGFGTSTC
>Pterocles_gutturalis
-----MDLN~~E~~SLDLGGFGISTC
>Colius_striatus
MFFPF~~S~~FFFFSPVNSMDLN~~E~~SLDLGGFGISTC
>Leptosomus_discolor
-----MDLN~~E~~SLDLGGFGISTC
>Cuculus_canorus
-----MDLN~~E~~SLDLGGFGISTC
>Balearica_regulorum_gibberic
-----MDLN~~E~~SLDLGGFGISTC
>Opisthocomus_hoazin
-----MDLN~~E~~PSDLGGFGISTC
>Lepidothrix_coronata
-----MDVN~~E~~LEPLDLGGFGISTC
>Pelecanus_crispus
-----MDLN~~E~~SLDLGGFGISTC
>Calypte_anna
-----MDRN~~E~~SSNVGGSRISTC
>Apaloderma_vittatum
-----MDVN~~E~~SLDLDSFGISTC

HG0291.2 ENSG00000151892 GFRA1

>Homo_sapiens
MELNFGRPQHQSCPG1AAR
>Mustela_putorius_furo
MELNFGRPQRGCPG1AVC
>Lipotes_vexillifer
MELNFGRPQGRPG1AAR
>Galeopterus_variegatus
MELNFGRPEERSRPG1AAC
>Condylura_cristata
MELNFGRPQRGCPG1AAC
>Ochotona_princeps
MELNFGRPEEHDLPG1AAC
>Equus_przewalskii
MELNFGRPQRGSPG1AAC
>Rattus_norvegicus
MELNFWPEERSRPG1AAR
>Trichechus_manatus_latirostr
MELNFGRPQGRPSFAAC
>Orycteropus afer afer
MELNFGRREGRPS1AAC

HG0292.1 ENSGALG00000006502 PCGF5

>Gallus_gallus
MPGKVPLRRAAPQLS
>Chaetura_pelagica
MPGKVELHRAAPQLL
>Buceros_rhinoceros_silvestri
MPGEVHLHRAAPQLL
>Caprimulgus_carolinensis
MPGEVQLHRAAPQLL
>Cariama_cristata
MPGEVQLHRAAPQL-
>Gallidris_pugnax
MPGEVQPRRAAPQLS
>Leptosomus_discolor
MPGEVQLPRAAPQLS
>Falco_cherrug
MPGEVQLHRAAPQLP
>Balearica_regulorum_gibberic
MPGEVQLHRAAPQLL
>Ficedula_albicollis
MPGEVQLHRAAPQLL
>Nipponia_nippon
MPGEVQLHRAAPQLL
>Aptenodytes_forsteri
MPGEVQLRRAAPQLL

HG0292.2 ENSG00000180628 PCGF5

>Homo_sapiens
MALSP~~LR~~RRWDRLGEDAAEETNSQDMGKRNHQKE
>Felis_catus
-----MVSDMGKONHQKE
>Lipotes_vexillifer
-----MGKONHQKE
>Pteropus_vampyrus
-----MGKRNHQKE
>Dasypus_novemcinctus
-----MGKONHQKE

HG0293 ENSG00000152127 MGAT5

```
>Homo_sapiens
----MEVRKGNQLTQEPE
>Acinonyx_jubatus
----MEMRKGNQLTQEPE
>Orcinus_orca
----METRKGNRLTQEPE
>Pteropus_allecto
----MEARKGNWLTQEPE
>Sarcophilus_harrisii
----MELKEGNRLTQEPE
>Galeopterus_variegatus
----MGVKKGNRLTQEPE
>Monodelphis_domestica
----MEMKEGNWLTQEPE
>Condylura_cristata
----MEARKGNRLTQEPE
>Ochotona_princeps
----MEVRKGSLLTQEPE
>Ceratotherium_simum_simum
----MEVSKGNRLTQEPE
>Loxodonta_africana
----MELRKGHRLTQEPE
>Chinchilla_lanigera
MKGRMEARKGNQLTQEPE
>Tupaia_chinensis
----MDVRKGNWLTQEPE
>Orycteropus afer_afer
----MELRKGHQLTQEPE
```

```
>Gallus_gallus
MLRKAHWPTNRMELKYGYMLTKESE
>Anser_cygnoides
-----MELRYRYTLTKESE
>Chaetura_pelagica
-----MELKYGYTLTKELE
>Buceros_rhinoceros_silvestri
-----MELKYGYTLTKELE
>Caprimulgus_carolinensis
-----MELKYRYVLTKELE
>Cariama_cristata
-----MELKYGYTLTKELE
>Calidris_pugnax
-----MELKYGHTLTKELE
>Haliaeetus_albicilla
-----MELKYGYTLTKELE
>Gavia_stellata
-----MELKYGYTLTKELE
>Eurypyga_helias
-----MELKYGYMLTKELE
>Sturnus_vulgaris
-----MELKYGYVLTKEWE
>Pelecanus_crispus
-----MELKYGYMLTKELE
>Fulmarus_glacialis
-----MDLKYGYTLTKELE
>Nestor_notabilis
-----MELKHGYMLTKELE
>Tinamus_guttatus
-----MEVKYNYMLTOESD
>Calypte_anna
-----MELKHGYTLTKELE
>Apaloderma_vittatum
-----MELKYGYLTTEELE
```

```
>Gallus_gallus
-----MMGRNILLAFRIRASPSVRICQG
>Anser_cygnoides
-----MMGGNIPLAVRIRASPSARICQG
>Apteryx_australis_mantelli
-----MMGENIIMAVRIQASPRARIYQG
>Calidris_pugnax
-----MMGGNIPPAVRIQASPSARICQG
>Columba_livia
-----MMGGNIPPAVRIRASPSVRICQG
>Aquila_chrysaetos_canadensis
MGQKRIFDFMMGGNIPLAVRIRASPSARICQG
>Zonotrichia_albicollis
-----MMGGNIPLALRIRASPSVRICQG
>Struthio_camelus_australis
-----MMGENIFMAVRIQASPGARIYQG
>Tinamus_guttatus
-----MMGENISMAVKIRVSPGARIYQG
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HG0294.2 ENSG00000183722 LHFP

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>Homo_sapiens
MFPPEKDSKLCVRPGRGREGGRRPPAMDHHL-----
>Myotis_ricketti
MFRPGKTASCVCAPARG-EGGRRPPAMDHHPYYGGPEVEAQ
>Galeopterus_variegatus
MFPAPRESKLCVRPGPGREGGRRPPAMDHRSYRGWEVDAQ
>Oryctolagus_cuniculus
-----MFRQVVCAPGTHREGGRRPPTMDHRSYHREWEVDAQ
>Dipodomys_ordii
MCVSGKDLKLCARPGPGRKGGCRPPAPRPHPTTLSHG-----
>Tupaia_chinensis
MFPPGNSKLCARSGPGREGGRRPPAMDHHPYYREWEVDIQ
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HG0295.1 ENSG00000166888 STAT6

>Homo_sapiens
MYVVCALSYFSFWWWWKGGGASRASLELAGGSYRPMGPGSAR
>Ailuropoda_melanoleuca
-----MGPGSAR
>Balaenoptera_acutorostrata_s
-----MGPGSAR
>Pteropus_allecto
-----MGPRSAR
>Sarcophilus_harrisii
-----MGPGSVH
>Galeopterus_variegatus
MQVSPELAGGSYRPMGPGSAH
>Monodelphis_domestica
-----MGPGSVH
>Erinaceus_europaeus
-----MGPGSAH
>Ceratotherium_simum_simum
-----MGPGSAR
>Manis_javanica
-----MGPGSAC
>Loxodonta_africana
-----MGPGSAR
>Nannospalax_galili
-----MGPGSAR
>Tupaia_chinensis
-----MGPGSAR
>Trichechus_manatus_latirostr
-----MGPGSAR
>Orycteropus afer afer
-----MGPGSAC

>Gallus_gallus	-----MRAGVPSLCP-----QLRCAGGGRKQPEHSAARLRRLTFWKEIAALSSFL
>Odobenus_rossmarus_divergens	-----MVYRRLTFEEEIAVLCsFL
>Orcinus_orca	-----MVYQRRLTFEEEIAALGSFL
>Pteropus_alecto	-----MVYQRRLTFEEEIAALCSFL
>Elephantulus_edwardii	-----MVYRRLTFEEEIAALCSFL
>Ceratotherium_simum_simum	
MRKLRPWFGISRARDFPALPPSSGHSCA--S-----GPPQSRAAAGRWDSRGSPPSGQSPRPAPPSLATPGPAAAAAAHSPGSQRPRAEAGRERQRLGGVLAKARALCMVYRRLTFEEEIAALCSFL	
>Chlorocebus_sabaeus	
MRKLRPRFGISRARDFPAPPTNHIPAIL--TRPGSGTLPRSRSRGPAGTPGGPRRRGSPHARRRPALPPAGTAAVAHSGSGRRPRAEAGRERAGLGGVLARARALCMVYRRLTFEEEIAALRSFL	
>Cricetulus_griseus	-----MVYRRLTFEEEIAALCSFL
>Trichechus_manatus_latirostr	
MRKLRPWFGISRARGFPTLPLSPQRLQRLPATISGRFRGAAGKGWILGLPGDPAVGAAPRAAPPRLAARGPATAAAHGSPGSQQPRAEAGRELGSREGELGRARALCMVYRRLTFEEEIAALRSFL	

>Gallus_gallus
MQIARGRRWRRRVLGKTGTRISFSLQGESSEFRCKRKETWRNCCISLPYKHISHLD
>Mustela_putorius_furo
MQITG-GGW---CLGKNRRNQNFLIAG-----
>Rousettus_aegyptiacus
MQINR-GGW---CLGKNRRNQNFLIAG-----
>Monodelphis_domestica
MQITG-GGW---CLEKTGTRISFSLQGERSEFR-----
>Papio_anubis
MQITG-GGW---CLGKNRRNQNFLIAGRTL-----
>Mesocricetus_auratus
MQITG-GGW---CLGKNRRNQNFLIAG-----

HG0297 ENSGALG00000031684

>Gallus_gallus
MCFCFVLQRFFWRLIFTF
>Lipotes_vexillifer
MCFCFVL-----
>Rousettus_aegyptiacus
MCFCFVL-----
>Oryctolagus_cuniculus
MCFCFVL-----
>Elephantulus_edwardii
MCFCFVL-----
>Cebus_capucinus_imitator
MCFCFVL-----
>Jaculus_jaculus
MCFCFVL-----

HG0298 ENSGALG00000042308

>Gallus_gallus
MES1VWECG
>Acinonyx_jubatus
MES1VWECG
>Myotis_davidii
MESVWECG
>Cerocebus_atys
MESVWECG

>Gallus_gallus-----MLGKEKEKNVIRRGVTROSVPRFVFPGVAERDQS-----
>Notothenia_coriiceps
MLTFGSP-----QLSPPVKIGGVRFR--GLLLCVTRQRKGGGKKKNVIRRGVTROSLPRFVSWSGCKTSVNNLP
>Platichthys_stellatus
MLTFGSP-----QLSPPVKIGGVRFR--GLLLCVTWRKGGGKKKNVIRRGVTROSLPRFVSWSGCKTSVNNLP
>Takifugu_rubripes
MFNPEDAHVWLSIIPSRDRWRAFQASPPLCST-AKKRRWKEKNVIRRGVTROSLPRFVSWSGCKTSVNNLP

>Drosophila_melanogaster-----MVNVMMKGVLECDPAMKQFLLHDEKLALGRKFIIQDLDENHLFISTDIVEVLQARVDDLMQISFPLHDKDA-----
>Eulimnogammarus_cruentus-----MVNVYIKGILIKCDPVMKQFLLHLDLALGSKFVLANLDDCHLFVAGDVYEQLKVRVDELYEKVYNNYSASNPKSFE-----
>Latrodectus_tredecimguttatus-----MVVYMKGILVECDPAMKQFLLHLDLALGSKFIIEDLDETHLFIAPDMLIILQTRIDDLMDQISFPLAEK-----
>Machilis_hrabei-----MVNVKKGILVECDQAMKQFLLHLDLGLGKFIIVQDLDETHVFIAPETILETLQSRIDDLMDQISFPLADKGM-----
>Argulus_siamensis-----MVNFKGILVECDPAMKQFLLHLDLTFALGKFIIVQDLDNHLFISSDIETLKARIDDLMDQISFPLAEKGA-----
>Mastotermes_darwiniensis-----MKYIQYLRRKSTIEMVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADILETLQSRVDDLMQISFPLADRL-----
>Sitophilus_oryzae-----MVNVMMKGVLRCDNAMKQFLLHLDLALGSKFIIQDLDENHLFIADILDTLQAKIDDLMDQISFPLADKGN-----
>Eriocheir_sinensis-----MVNVMMKGVLIKCDPVMKQFLLHLDLTMKLGSKFVLVDLDECHLFVQPEVYNSLKNLIDEQYKVVYNNQSSLE-----
>Forficula_auricularia-----MVNVMMKGVLECDHAMKQFLLHLDLALGSKFIIQDLDETHLFISSDIETLQARVDDLMQISFPLADRL-----
>Daphnia_magna-----MKQLLLHLDLDETHALGNKFIIVQDLDETHLFIAPLEYLQTRIDDLMDRISFPLAERETD-----
>Occasjapyx_japonicus-----MVNVMMKGVLECDPAMKQFLLHLDLALGSKFIIQDLDETHIFISADILEVLQTRIDDLMDQISFPLADKNN-----
>Haploembia_palaui-----MVHYTKGILIECDHAMKQFLLHLDLALGKFIIVQDLDETHLFIADILTLQARIDDLMDQISFPLADKGF-----
>Eurylophella_sp._AD-2013-----MVNVTKGSLITCDPAMKQFLLHLDLALGKFIIVQDLDETHLFVSSDIVEILRNRVDDLMQISFPTDKQQ-----
>Meganyctiphanes_norvegica-----MVNVMMKGVLIKCDPVMKQFLLHLDLALGSKFVLVDLDECHLFVQPEVYKLTTRIDELYEKVVYNNQSSDSWQASRYE-----
>Grylloblatta_bifratrilecta-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADILETLQARVDDLMQISFPLADKGL-----
>Cuerna_arida-----MVNVMMKGVLECDHAMKQFLLHLDLALGSKFIIQDLDETHLFIADILDVLQARVDDLMQISFPLAEKGL-----
>Copidosoma_floridanum-----MVNVMMKGVLECDPAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQGRVDDLMQISFPLADKGL-----
>Asellus_aquaticus-----MVQVQKGVLIKCDPVMKQFLLHLDLALGSKFVLVDLDDCHLFVQSDIYNLSKVRIDELYEKVVYNNISGSNQGNFE-----
>Antheraea_assama-----MVNVMMKGVLECDPAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQARVDDLMQISFPLADKGL-----
>Mantis_religiosa-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDDTHLFIADILDALQARVDDLMQISFPLADKGF-----
>Tanzaniophasma_sp._AD-2013-----MKQFLLHLDLDTTALGSKFIIQDLDETHLFIADILETLQARVDDLMQISFPLADKGL-----
>Boreus_hyemalis-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHVFISSDIETLQARVDDLMQISFPLHDKGL-----
>Corydalinae_sp._KMRSPBM-2012-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGN-----
>Cyprinidinae_sp._BMR-2011-----MVNALKGILVECDPAMKQFLLHLDLALGSKFIIQDLDETHLFISSDILDTLQAKIDDLMDKISFPIETET-----
>Osmylus_fulvicephalus-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLSEKGY-----
>Triops_newberryi-----MVNVVKGILVECDPAMKQFLLHLDLALGSKFIIQDLDDTHVFIADILEVLQARIDDLMDQISFPLHEKDP-----
>Epiophlebia_superstes-----MVNVMMKGVLECDHAMKQFLLHLDLALGSKFIIQDLDETHLFIADILGLRARIDDLMDQISFPLADKGY-----
>Platynocheilus_peltifer-----MKQFLLHLDLALGSKFIIQDLDETHLFIADILETLQAKIDDLMDQISFPLADKGL-----
>Proasarthria_tetralix-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQARVDDLMQISFPLADKGL-----
>Timema cristinae-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQARVDDLMQISFPLADKGL-----
>Menopon_gallinae-----MKGILVECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Leuctra_sp._AD-2013-----MVNVKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADILGLQAKIDDLMDQISFPLADKGL-----
>Polydesmus_angustus-----MVNVMMKGVLECDPAMKQFLLHLDLALGSKFIIQDLDDTHLFIADIVETLQAKIDDLMDQISFPLAEK-----
>Acerentomon_sp._AD-2013-----MVNVVKGVLVECDPAMKQFLLHLDLALGSKFIIQDLDETHLFISSDILETLQAKIDDLMDQISFPLSEK-----
>Liposcelis_bostrychophila-----MVNVTKGILVECDPAMKQFLLHLDLALGSKFIIQDLDDTHLFIADILETLQAKIDDLMDQISFPLADKGL-----
>Inocellia_crassicornis-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDDTHLFIADIVETLQAKIDDLMDQISFPLAEK-----
>Ceratophyllus_gallinae-----MVNLKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Archispirostreptus_gigas-----MVNVMMKGVLECDPAMKQFLLHLDLALGSKFIIQDLDDTHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Stylops_melittae-----MSLKLKVRQKFFDNRPHRILLYNVVKGVLIKCDPAIKQFLIVLDETLKGRFIIQDLDETHLFISSDILETLQAKIDDLMDQISFPLADKGL-----
>Thrips_palmi-----MVNVVKGVLVECDQAMKQFLLHLDLALGSKFIIQDLDDTHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Platycentropus_radiatus-----MVNVMMKGVLECDQAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Zorotypus_gurneyi-----MVNVMMKGVLECDHAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGL-----
>Atelura_formicaria-----MVNVTKGVLECDHAMKQFLLHLDLALGSKFIIQDLDETHLFIADIVETLQAKIDDLMDQISFPLADKGL-----

>Drosophila_melanogaster
-----MAFP-----TTSAQQA-ETNRKILEEIQTKKQLLAGGIINLGLSPNQMPA--PQLLGGPTTVNPDFQAGV-----GIATNATSTARSAFNPTSSTLGGFFIQDQSYFGNSFIPVLPRLLEPLSPATTPTPNAP
PSHSISK
>Machilis_hrabei
-----MTLDFDMAFO--PANNKQEM-Q-NRKILEELQLKKQLLKEGAPTSPL--STP--PLS--PN-----POGFPLLP-----SEAHMLPSSORTALQCAHSQSFGYFITQDSSFGNIIIPVLPFRFEQNSK-----

>Periplaneta_americana
-----MAFO--PPSARQEL-A-NRKILEEIQLKQKQIILKQGVAPLSNPTL-TP--SLSAVGG--VNLVPSMS--PEAHMSSSORAALQHAHSQSFGYFVTQDSSFGNIIIPVLPFRFDIK-----

>Pogonus_chalceus
-----MAFT--QTNAQREI-T-SRKILEELHLKKQMLLKQGAVTSLNTPAP-----ILPLVSPQTGTIPFTGAPAAALLGEAQTTSAORTALHSAHSQSFGEFITQDSSFGNIIIPVLPFRFDNK-----

>Procambarus_clarkii
-----MTLKQGVSQLNAPATSQ--PT-G-----WSSGTDGHIAGNSQRSNLLQANSQSFGYFITQDSSFGNIIIPVLPRLPEK-----

>Apachys_charteceus
-----MAFO--PPSARQEI-A-NRKILEELQLKKQIILKQGAATSLNTQLTPNV--PVSGTTPSFVSGLNRGLVSASSPMSSEPYMTAORTA----LQSYGYFVTQDQSLYGNIIIPVLPFRFESK-----

>Campodea_augens
-----MAFO--PVNNRQDL-Q-NRKILEELQMKQMLKQGAAPVSLNSTTSPSG--M-----GTVTAANSASFHL-----PPMQMLQHNORNALQLANSQSFGHFVTQDQSAFGNTLIPVLPRLPTPKP-----

>Haploembia_palau
-----MAYO--PPTARQDV-ATSRKILEELQLKKQLLLKQGVQSTLTSTLSSL--SMPAT-----DTAN-----ITANMMSSAQRALNHAHSTSGFYFITQDSSFGNIIIPVLPRLHESK-----

>Isonymchia_bicolor
-----MAFO--PPSNRQEL-Q-NRKILEELHLKKQLLLKQGAVTALNSNFGS-----S-----PSVPTYGS-----SDTHMMSNORTQLQIANTQSYGYFVPQESSFGNFIIPVLPFRFDTPPSK-----

>Meganyctiphanes_norvegica
-----MASQ--APGRGAADS-NTORKILEDLQKKQMLLKQGAQALNAPAQGT--AT-G-----WSSGTDGHIAGNSQROV-QOTTNQSFYFVTQDSSFGNFIIPVLPRLPETK-----

>Galioisiana_yuasai
-----MALQ--PTNVROEL-A-NRKILEELQLKKQLLLKQGAAPSLINTPTITT--SLSMT--A-----GTGPLSMS-----PEAHMLSSNQRALQHAHAQSFGEFVTQDSSFGNIIIPVLPFRFDVAK-----

>Tigriopus_californicus
MAANPSIHPTNSTSGGASGPAVSAGTAAATGGSLAFG--NPSSGKI-DQORKILEELERQKKQLAKGNLGPAAASAPAPNHTPNSSG-----PASGTLKAMEQGDVPSIILQAQAAAMELANKSQSFGYFITQDQSAFGNIIIPVLPRLQPK-----

>Clastoptera_arizonana
-----MDFR--QSQSAREL-A-NRKILEELALKQMLLKQGAQPLGST-----P--ISMPMV-----TPATNIPANIAPDVHVMSSTTARAALHANSQSFGEFVTQDSSFGNIIIPVLPRLLEK-----

>Leptopilina_clavipes
-----MAFS--QTN-SREL-Q-NRKILEELQLKKQMLLKQGVTTNLGSSLTSTAGS-----ATTVPATQTSQDGTISASQRAALHNAHSNSGYFVTQDSSFGNIIIPVLPFRFDNK-----

>Bombyx_mori
-----MAFP--QPNAQREL-T-NRKILEELQLKKQMLLKQGAAPLTA--LSQPNP--VSQLPWCSIPPV-SATAGFPQLPEANVINTSHRAALQHANATSGFYFVTQDSSFGNIIIPVLPFRFENK-----

>Mantis religiosa
-----MAFO--PPSARQEI-A-NRKILEEIQLKQKQLKQGVQTNLS--TP--IAPLVGAG--VNVPMTVS--PEAHMLSSQRAAFQHALLOSGFYFITQDSSFGNIIIPVLPFRFDK-----

>Tanzaniophasma_sp._AD-2013
-----MAFO--P-ASRQEI-A-NRKILEELQLKKQLLLKQGVPTLNTPAL-SQ--SIPGVSPS--PILPTSLP--SDAHMTSSQORVALQHAHQMSFGYFVTQDSSFGNIIIPVLPFRFDTK-----

>Nannochorista_philpotti
-----MAFP--Q-TNTQD--HRKILEELQAKKQMLLKGAATLTTPQLPN-----ILTTPVANQITDTHAINSTQRNALNANSTSGFYFVTQDSSFGNIIIPVLPFRFDKPV-----

>Corydalus_cornutus
-----MAFP--QPNAQRDL-A-ARKILEELQLKKQLLLKQGVQATTANSVTT--N--LSTLPTTTGAPNSTGGP--LSTDHSMSSAQRALHAAHTQSFYFVTQDSSFGNIIIPVLPFRYDTK-----

>Euroleon_nostras
-----MAFP--QPN-QREL-A-NRKILEELQLKKQIILKQGVQATANTNMLTT--P--LGPVITSIGTVINOTGP--GTPQEHNLTSQAARALHSAHTQSFGYFITQDQSAFGNIIIPVLPFRFDVK-----

>Triops_newberryi
-----MSFO--PAPGQEL-A-SRKILEEIQMKKLLKQGGPLPTTTPNVN-VP--LASQ-----TGQVSAPTANPELQSLNPTQRAALQHAHAHSFGYFVTQESAYGNIIIPVLPRLLEVAPSK-----

>Calopteryx_splendens
-----MAFO--PPSSRQEI-Q-NRKILEELQLKKQLLLKQGAASALNTPIPPP--PMPV--G-----NTMPL-PT-----GEQHLVSSSTORSALQFAHTHSFGYFVTQDQSLFGNIIIPVLPFRFDMK-----

>Ceuthophilus_sp._AD-2013
-----MAFO--PPSARQEL-Q-NRKILEELQLKKQIILKQGVAPTLSI--SP--SLSV--G-----GSNAVAMT--PEAHMSSSORAALQHAHTQSFGEFVTQDSSFGNIIIPVLPFRFDK-----

>Peruphasma_schultei
-----MAYO--PPSVRQEM-A-TRKILEELQLKKQMLLKQGVAPTSSQNL-SA-----IPMSGGLT--PDAHMMSSAORTALQANSQSGFYFITQDSSFGNIIIPVLPFRFDSK-----

>Menopon_gallinae
-----MAFO--PSTRPDIGNPKKILEELNLRKQLLKIG-TAQTLNPSALNTP--I-----GVPLINSNPVSTDNQMSTTARAALQHANSTSGFYFVPQESSFGNIIIPVLPFRFIESK-----

>Perla_marginata
-----MAFO--APNLQREL-A-NRKILEELQLKKQMLLKQGVQATLNTSIPSS--IPIG--M-----PASGLGVP--AELHLVSPAQRALQANSQSFGEFVTQDSSFGNIIIPVLPFRFEVKPSL-----

>Acerentomon_sp._AD-2013
-----MAFOQTTPNSRPDL-QQSKKILEELQMKKQMLLKGVNSTNQSSCP--PA-----STAPISG--TPDVHMMSPQSORSALQANATSGFYFITQDSSFGNIIIPVLPFRYDNK-----

>Ectopsocus_briggsi
-----MAFO--SNSAGDFPNPORKILEELNLKKQLLKSG-TAQTLNPSALNAP--I-----GLPSLNP-PVAPENQMSNIARSALNSANTTSFGYFVAQESSFGNIIIPVLPFRFPEAK-----

>Xanthostigma_xanthostigma
-----MAFP--QPNAQREL-A-NRKILEELQLKKQLLLKQGVQASTTIVASNIS--P--IGASTLPAGPPTVQSGA--PSMDTHNLSSAQRALHSAHTQSFGEFITQDSSFGNIIIPVLPFRFDTK-----

>Ceratophyllus_gallinae
-----MALP--PTNAQOD--HRKILEELQKKQMLLKGAAPTLLNTLPTS--I-----IPNPGIIPGNDMHMINSTQRIALRNANSTSGFYFVTQDSSFGNIIIPVLPFRIDAE-----

>Gynaikothrips_ficorum
-----MSFO--PTN-SRKD-P-NRKILEELQKKQMLLKSGAGVSPSPVP-----NLASEPOANKVQCMVMGAAIAQSFAYYIPQESNFGNIIIPVLPFRFDKN-----

>Annulipalpia_sp._AD-2013
-----MAFN--QPNAQREL-T-NRKILEELQLKKQIILKQGPAPNLTGSSVSLTSAPT--PAQLPVSTIPPI-SATTILPQISDTHLINTSHRAALNANATSGGFVPQDSSFGNIIIPVLPFRFDSK-----

>Zorotypus_gurneyi
-----MAFO--PPSSRQEQ-A-NRKILEELQMKKQLLLKQGVSQLTVPSITP-----LSVS-----TPVISGLT-----PEAHMSSPAQRVALQHAHSQSFGYFITQDSSFGNIIIPVLPFRFDSK-----

>Thermobia_domestica
MFRLLNHLRIERW-NG-----KENLGIIRVCMMAFO--APNARGEI-Q-NRKILEEIQMKKQLLLKQGAAPNLNSPNTLTP--TN--IPVT-----GPMPMYMS-----PEAHMSSSORTALQHAQCSFGFYFITQDSSFGNIIIPVLPFRFDNK-----

>Drosophila_melanogaster
 -----MDSDSTVTSLEENTDFC-----TNPTRDTLAEGITNLFKPTIERLDERVASTIQLAELRGQLDALAAQLDIEKAQ-SQIPEFADKVKELLNKHKVTVISNVLTSQERLTGLHKLIEKEQRRRQALLDSALSTNIS-----

>Oxyacanthus_flavus
 -----MADSDSVSTSVGQDTEDLV-----SP-----TRDALVDGIMGLMKPLDQLDDRVRTRASQSELQQGLEGLQQQLTSVQOKT-QCPLDLDDYIKKLNQAKRRVVVNNILQTTQERLNKLNQMIKENTRQALLDPSMTAS-----

>Machilis_hrabei
 -----MEVDTESTNTSLDDKTEDFG-----ENPTRDTLAEGITMVKIPTIDQLDERVKVTRI SQVELKQOIEALAEELKKIADAQ-QCPLDLDDYIYKKLLNKKRRVTVSVNVLQNAQDRLNKIHQLVAREGSRRRALLEPSPVTPGSGP-GT-----SROVNP1

>Cryptocercus_wrighti
 -----MDLDTSTTTSIDDKTEDFC-----ENPTRDTLAEGLMCLLKPTIDQLDERVRATRI SQVELKQOIEGLAEELKKISESQ-QCPLDLDDYIYKKLLINAKLKVVTVSNILQTAQDRLNKVHQIAREQSRRRALLEPSPITTPLEAT-NA-----SIQ----

>Pogonus_chaleous
 -----MDVDSSTATSIDENTENFC-----DNPTRDTLAEGLMGLIKPTVDQLDERVRATRI SQVELKQOIESLSEELKKVSETQ-QTVVDLDAYYKKLLINAKHRVTVLSNVLQNAQDRLNKVHQSIERETIKRKAFLESTPGEATTSTTSSVI-----

>Astacus_astacus
 -----MADTESSTCTSVDDRTDVL-----SP-----TRDALVDGIVGLLKPCLDQLDDRVRATRVSQSELHQQLEGLAEELSRVQEQ-RCPLQLDAYIKKLNQAKRRVVVNNILQNTQDRLNKLSQVKNENARRALLETTSPLPITPSTSLHA-P-----

>Occasjapyx_japonicus
 -----MEVDTASTTTSLEDKTEDFGFGDGNPTRDLSLAEGLVALLKPTLQQLDERVKNTKISQVELRQOIEALTEELRGIAEQ-QCPIDLDDHYKKLLINARRRVTVSVLTQTTQERLNKHLVQRETGRRRALLEPSPGAPPSASALPFQ-P-----

>Baetis_sp._AD-2013
 -----MCLLKPTIDSLDERVRATRI SQVELRQOIDGLADEIKKISDEQ-QCPLDLESYVKKLLNKKRRVTVSVNQLQVAGERLNKVHQLVERESARRKALLEPSPVSPSAHP-IE-----TNPSIQ----

>Meganyctiphanes_norvegica
 -----MIGSFNMADTESTCTSVDDRTEDLV-----SP-----TRDALVDGIVSLLKPCLDQLDERVTRTL SQSELHQQLEGLAEELSRVKDQV-ECPLQDLSYIKKLNQAKRRVVVNNILQNTQDRLNKLSQVKNETTRRRALLETTST-ASTPSTSLHA-P-----

>Galloisiana_yuasai
 -----MDLDTSTTTSIDDKTEDFG-----ENPTRDTLAEGLICLLKPTIDQLDERVRATRI SQVELKQOIEGLSDELKKISGEQ-QCPLDLDDYIYKKLANAKQKVTVSVNVLQAVQERLNKVLIQIDKDEARRRALLEPSPVISPDLVE-ST-----STQ----

>Clastoptera_arizonana
 -----MDVETGSTMSTSLDDKTEDFC-----ENPTRDTLAEGLMGLMKPTIDQLDERVKVTRI SQVELKQOIEGLSEELKKISAEQ-SSPLDWEAYANKLTNAKHKITVSVNQLQAAQERLYKVSQINKETARRQALLKQSSPTSTSDSKPLS-----SVQ----

>Ganaspis_sp._G1
 -----MDLDTASDNTSLDDKTEDFC-----DNPTRDALTEGLMGLLKPTVDQLDERIRSTRI SQIELKQOIDSLEELVKISESL-QQPLEDLSYKKLLVNAKQKVTVSVNQLQTTQDRLNKHQAIERESAKRRALLDHSSSYNDETQKSAAK-ERETGHSSVDVQQ-----

>Aseillus_aquaticus
 -----MADSDSTCTSVNDRTEDLI-----SPKPTRDALVDGIVGLLKPCLDQLDEKVRTRL SQSELQQQLTELSTQLNRVQDQV-QCPLQDLSYIKKLNQAKRRVTVNNVLQSTQDRLNKLGQVQGETSRRKALLESQSSSTALI-----

>Triodia_sylvina
 -----MDADTESTTTSIAEANTGLC-----DNPTRDTLAEGLIGLLKPTVDQLDERVRATRI SQVELKQOIDLTEELKKINQAL-SNHPDIESYVKKLITCKHKVTVLVNVLQSTQERLNKIRRMISLEEGVRRAVPALEAQSEPESTSATLISPEGs-IN-----

>Mantis_religiosa
 -----MCLLKPTIDQLDERVRATRI SQVELRQOIEGLAEELKKISEAQ-QCPLDLDYVYKKLLINAKLKVVTVSNILQTAQERLNKHQIARETSRRKALMEPSPITTPLEAG-NP-----SIQ----

>Tanzaniphasma_sp._AD-2013
 -----MCLLKPTIDQLDERVRATRI SQVELKQOIEGLSEELKKISDGO-QCPLDLDYVYKKLLNKKRRVTVSVNQLQTAQERLNKHVHIQIAKETARRRALLEPSPITPLEVS-NT-----TVQ----

>Nannochorista_philpotti
 -----MDADSESTATSIDENTENFC-----DNPTRDTLSEGLMGLIKPTIDQLDERVRATRVSQLELKQOIDRVSEDVRIKIDNK-KPPAELDDYVYKKLVNTLKVVTVITNILQSVQERLNKIHQOIRETARREAGLSSQTEPYDSEVASGSN-Q-----LQNNLN

>Corydalus_cornutus
 -----MDDTTESTATSIDENTENFC-----ENPTRDTLAEGLMGLLKPTIDQLDERVRAMRI SQSELKQOIEILHEELRKIAELQ-QYDLDDYVYKKLVTAHKVTVI LVNQLQCAQDRLNKHAGIEKETIRRKALLEKLPVPQSPPPVPTSSDGLGH-FGG----

>Chrysopa_pallens
 -----MEDTESTATSIDENTENSC-----DNPIRDTLAEGLMGLLKPTIVQLNERANAVRI SQSELKQOIEITLOEEIKKISELQ-QSDVDIDSYVYKKLMTAKHKVAVSTVLQNAQDRLNKIHSGIEKETNRKKIVLEKSNITLQEPSSSSIS-----

>Triops_newberryi
 -----MDSEVISNDTSLDDKIEDFG-----DYPTRDILAEGIVNLLRPTVEGLDQSIDRTQSQAEELRTQIEALTSALNVVAENH-SCPIDLEPYIKKLLDSKRRITVIVSSVLQTSQDRLVKVHHLAQKDIAARRKSSLDTOASVPAP-----

>Calopteryx_splendens
 -----MEQDNDNKVSASVSKTNSFG-----ENPTGDALAEGLICLFKPTIDLLDERITATRNSQLELKDKIEILAEELRKISELH-KCPLDLELYVYKKLAGAKRKVTVSVNVLQNTQERLSKVQVOVAREAQRRRALLEPSPAMPSPVSVESNA-----SLQ----

>Prosarthria_teretirostris
 -----MELDTSTTTSIDDKTEDFC-----ENPTRDTLAEGLMCLLKPTVDQLDERVRATRIQVELKQOIEGLAEELRKISATQ-QCPLDLDDYIYKKLMNAKQKVTVSVNQLQTAQDRLNKHVHLIEKESRRRTLLEPSPSTTPLEAT-NP-----SIQ----

>Medauroidea_extradentata
 -----MCLLKPTIDQLDDRVAVRISQVELKQOIDGLSEELKKIAESQ-SCPLELDAYYVKKLMNAKLKVTVSVNQLQTAQERLNKVHANIKEAAKRKALLEPSPQKTPPLEVS-QP-----SIQ----

>Menopon_gallinae
 -----MEVDTESTNTSVEDKTEDFC-----DNPTRDALTEGLMRLFKPTIDQLDEKVRTIRISQVELKQOIESLSDELKKINESSTDEIDLDVYVYKKLMTVKHKVTVSVNQLQNSEERLLKQQISKDSSTRKALLESTSVTQVSVTEPDD-----SSVQ----

>Leuctra_sp._AD-2013
 -----MDLDDASTTTSIDDKTEDFC-----ENPIRDTLTEGLMCLLKPTIDQLDERVRATRI SQVELKQOIEGLSDELKKISDAQ-QCPLNLDLYVYKKLTNAKLKVTVSVNQLQTAQERLNKVHQMIAREAARSRALLEPSPISPLETV-NP-----SIQ----

>Acerentomon_sp._AD-2013
 -----MEIDTDSRNTSLDDKTEDYD-----DNPTRDALVDGIMISLLKPAIDQIDERVKATRLSQLELGEQIGSLAEIEKRVSEEQ-NCPLDLDYVYQKLNQAKKRITVSVNVLQSVQDRLNQLHNIATQELTROQSLTEVEAPQGSSEDQ-----

>Liposcelis_bostrychophila
 -----MRLFKPTIDQLDDKVRTIRISQVELKQOIESLSEELKKISESNVQKELDLDVYVYKKLMNVKHKVTVSVNQLQNSEERLLKQQISKDSSTSHKALLETTETTSQATQAEPS-----SAIQ----

>Inocellia_crassicornis
 -----MDDTTESTATSIDENTENFC-----DNPTRDTLAEGLMGLLKPTVDQLDERVRATRI SQVELKQOIEGLSEELKKISEAQ-QTNLELDAYYKKLINSKQKVILVSNQLQAAQDRLNKIHIAIDKESAKRKALLEKTPAGSTSTLETSTQNR-----

>Oropsylla_silantiewi
 -----MEPDSESTNTSLDENTENFC-----DYPTRDTLSEGLMGLIKPTVDQLDEERVQATKASQIALKSQIDEVSENEISKISNR-KPPELDELYKKLVNTKKNKITVVTNQLQATQERLNRIHISIEKETORRESLATNISLPS-----TSGSQ-----INL----

>Gynaikothrips_ficorum
 -----MEGDASTNTSNDKTDYYC-----DNPTRDTLADGLMCLLKPTVDQLDERVRATRI SQNEVKGHLNLSLSEELKKISDAQ-QCPIDLDDYVYKKLMNAKQKITIVSTFLNSAQDRLLSKLSQOISREQSRRKALLEPSPQSTLFDASS-GS-----VI-----

>Platycentropus_radiatus
 -----MDGDTSTATSVEENTENFC-----DNPTRDTLVEGLMGLLKPTVDKLDSEVRATRI SQVELKQOIDGLADELKKISDSQ-SNFLDLEEVYKKLMNSKRKITAISTILQSTQERLDKVHVLVSREAAKQALLESSEQSASTSGFNDY-SQ-EQN-IN-----

>Atelura_formicaria
 -----MDVDTESTNTSIDDKTEDFG-----ENPTRDTLAEGLMCLLKPTIDQLDERVRATRI SQVELRQOIDGLAEELKKISEAQ-HCPLDLDYVYKKLLDAKRRVTVSVNQLQNAQDRLNKVHQLVARESVRRRALLEPSPVTPPSTAL-PE-----AKSSQQ-----

>Drosophila_melanogaster
MHTDL-SHLHTPA CNKLIELLQACHEN-NAFAKFVGV CNSIDDKVVKCLKGERIARSAANRAKAREOAKYKEKLLQGESN-----
>Hyalellopsis_costata
MHPDL-SPHLHTEPCNEIIQKLFNCHKE-HSLLKFLGT CNDLDOHVWTCLKAERVERRALNRFKAEQRYQQLKEHMKSS-----
>Machilis_hrabei
MHPDL-STHLHTEDCNQLIQLLKDCHDR-NIFNKFVGVCNEDNAVVKCLRKEREENRRKANLEKSREKQKRI SQARAAQ-----
>Mastotermes_darwiniensis
MHTDL-STHLHTEECNKLIELLKDCHKE-HSFGKFLGYCNDADREVIKCLRKEREQNRKANQQAQLMDQKVRTSYPE-----
>Gyrinus_marinus
MHTDL-SPHLHSEKCNELIKQLQTCHTE-FPIGKFFGYCNSVDAAMVRCLKAERIERSKLNREKAREQEQIKRIL-----
>Astacus_leptodactylus
MHPDL-SPHLHSDCNELISKLHACHKE-NKFLKFVGICNDIDSAVWVKCMKAERLQRRKANRLGEEQRKKVFAKLDEGYSWKMM-----
>Forficula_auricularia
MHPDL-SPHLHGETCLKIIEAYKTCLIE-HPFGKFINYCGKDAELNRCLKEERETRRRQNF EKSSYYKMDLKKGDQEK-----
>Daphnia_pulex
MHSNL-SPHLHTECNQLIQLLLACHKE-NPVGRFVGFCNKQDTLMVACLRKEREANRSVNAEKSIIKQEEIRRLKEQESI-----
>Occas_japyx_japonicus
MHPDL-SAHLHTEPCNVLI EALKACHSE-HKFAGFVGVCNEADSAVLRCLRDREENRRKANFEKSAEKRRRLRNAADQARSE-----
>Isonymchia_bicolor
MHPDL-SSHLHTECNLLITDLKACHSQ-NKFGRFGLGCNDLDKELVKCLREEREQNRKNFDSRAKQKAVLERL-----
>Meganyctiphanes_norvegica
MHPDL-SPHLHLECNLITAKLKDCHNE-NKFAKFMGACNDIDKAVNCKLKKEREIKRANRAAGKEKREATLKKIEEGHSWKEL-----
>Galioisiana_yuasai
MHPDL-SAHLHTECNLITKLKECHEE-NKFRKFLGICNDIDTKLAACLROERADNRKANQEKARQTQE-----KLKRVALKAKSONL-----
>Ceroopis_vulnerata
MHPDL-SSHLHTEPCNELITQLLECHKN-HNFLRYFGHCTHLDNVMLKCLRKERLTRAANAAKAVEKNQOVREMRRELYN-----
>Fopius_arisanus
MSDYSRLPLHOGACNELYYOVQCEKSHHASKIIFGKSDVHVALTCKLONKLNLAANREOSRIRQENARKKLKAEKNSMKQ-----
>Biston_suppressaria
MHTDL-SAHLHTECNVLIKKLQDCHSE-HSFLKFVGVCNDFYEMRKCLKGERLRKANLDESRRKHAEIRARIVAQEQAKH-----
>Mantis religiosa
MHPDL-SPHLHTECNQLINKFHECHKN-YPYKFLGV CNLDKAVNCKLKNERIERRRLNQLKARELQEKAKSKPSA-----
>Tanzaniophasma_sp._AD-2013
MHPDL-SPHLHSAECNLI VTKLRECHQE-HKFGRFLGLCNDADLELVCLRKEREANRLNPNWNSRERQKNI CESKASN-----
>Nannochorista_philpotti
MHPDL-SPHLHTECNLI VQQLKECHNE-HQFRKFVGVCNSIDSKLIKCFKAERENWRRNKELADTRRETTYRLMEAAKE-----
>Corydalus_cornutus
MHTDL-SPHLHTEECNYIINLLKACHTD-NPFKRFLGV CNIDRDLIKCLRKEREQNRKLNFEKSREKQERLKQTOKLT-----
>Euroleon_nostras
MHPDL-SPHLHTEPCNELIQQLHECHRD-HPLRFKVGVCNDIDRVLLKCLRKEREQERSRLNRQKAFEKQERIKRLLSEQEQKS-----
>Triops_newberryi
MHSDL-SAHLHSEPCNALIELLLKCHKE-NPVRKFTGYCNSQDTAVTVCLKKEREQNRKLNADKSAQRQKAIQERLRQAQQEKAGS-----
>Cordulegaster_boltonii
MHPDL-SPHLHTECNLITKLKTHSE-NRFKFMGICNDIDRELLDCLRKERNRRKANFEKSREKRQIVQEKLKQEKVK-----
>Ceuthophilus_sp._AD-2013
MHPDL-SPHLHTECNVIRKLHECHRV-NNIGKFFGYCNDVDNELVKCLRKERDIRRKSNL ENSRAQEKYKIDILKVQKEGQS-----
>Peruphasma_schultzei
MSKNV-LKHNYSGMCTGLLEKLT ECRD-NKYTKFFGV CNDAFKELDKCLQKEYEDRRTENHAKARALQERKLGKQSQOQT-----
>Perla_marginata
MHPDL-SPHLHTEECNVLIKKLKDCHEQ-NTFGKFLGF CNSADNELLKCLRREREIRRKANFDKAKEFOAKIROPIQV-----
>Acerentomon_sp._AD-2013
MHTNL-APHLHTECNELIQKLFQCRLD-HPVLRFVGVCNDLDILMTKCLKRERLERRRISIEQSTKSRLERLELRQERQKETESANQQA-----
>Inocellia_crassicornis
MHSDL-SPHLHSEDONKVI AELHKHAD-HPFKKFIGHCNDIDRALVKCLKKERLERTRINYEKSI IROKEIRERMKNMS-----
>Ceratophyllus_gallinae
MHSDL-STHLHSEECNAIVORLTACRQE-NSFKKFLGACNDIDRELVKCFRKDREARRKKNKEASDLRYNKKLNI-----
>Rhyacophila_fasciata
MHTDL-SPOLHTECNKIIITALKTCHQE-HAFRKFIFGCNSIDDMIKCLKEERLRRRAANIKASAEKHAAILKRIEQNTNA-----
>Zorotypus_gurneyi
MHTDL-SRHLHTEECNLIQKLQECHTG-HPFAKFIFGCNDFDSEMRCLKKERLERKRINLEQAVARRERMNKAIHADVNNK-----
>Tricholepidion_gertschi
MHPDL-SAHLHTECNLITSKLKECHKE-YKFRRFVGACNDIDHCLTKCLAEAREANRKVNLERARRQQEVVRQKMRV-----

>Drosophila_melanogaster
-----MKIMISQVGRELYKVLRLDHRVFNNGEIEAFLENFVRRNDSEVEKLFQVTEIVGSLKYDLSRCSATGRGSGAE-NLAQLDTEVSHLLDGVNALLAKA-KV-ERTASTQLEARLAREQRRAEFLTNLEHGYYRIENSFEEKEEEEIAELYSOL
QLKLNIAK-----
>Hyalella_azteca
-----MAITSEVEEVFSRLFDHRPFLKGEIYFFKREFEЕКRGDREVEELFRALELTTEIKQAQVEK----VVEASDA-NLPRTIADIQVALRMCHTSLDSD--SRTSRLSSEIERQREDRQQLAVAKAEVAKLASINAAAYDLKEKELREKFAKL
DSSNTQDS-----
>Machilis_hrabei
-----MGNRIAEKE---D-SRRSVDTLEENRVSRHEWETFTVDMAEKCSKIDQTFKNGDEMKEYYSOL
EKKLHLDQ-----
>Mastotermes_darwiniensis
-----MAAVKDVGIEWTRLFDHRPFLSGEIKFFLKEFEЕКRSDEVERLFQILERATEIKETQLDR----VKLASDV-HLPTLNANLEAVAVGMGNRIEKE---E-EHQSDTALTARREIRKAEWESFIEDMTQKCSKVDAFTQOEKEELKEFYSDL
EKKLHIGK-----
>Calanus_firmarcticus
-----MSAINRSGFEDITVHSRLFNHRPFLQGEVKhFVREFEЕКRGDREVENIFSQLERVSELRLGLPG----LLSSAGNSSTSLVANLEVAESMLGRILEQG--E-TGEVEKTLVASREAREKENTFLKEVQIRCKKVDQSGFEQEDSIRKKYYQDL
ESGS-----
>Pogonus_chalceus
-----MSQLSKDITGEIWNRLFDHRAFLNGEINFLVKEFEQKRLDKEVEYLFRLLEQITDIDKDTQIVR----LRQVGN-SLPSINKNLFALNACKRIEDIE--L-KYKEDTSLALAEERKLRWKFDVDMHSCSRVDNTFQEKEEELHEFYTDL
ERKLQIAK-----
>Euyclops_serrulatus
-----MVSKDVGVSYSRLFNHRPFLQGEARHFVKEFEЕКRNDREVENIFNTLETVTLEKDCQIDK----VKGQCEL-NLTTLSANLLVANSMSCKILDQE--R-TSDFDQALESSROVREKESQFSDIWNKCEKIDDAYKQKEKDLRLHYQKL
ENFVLQD-----
>Farfantepenaeus_aztecus
-----MASAASDVNEVFSRLFDHRPFLKGEIYFFKREFEЕКRGDREVEQLFRSLELTIEIKEQDIEK----IVNSSDD-NLPRTIADIQVALHMLDITDE--KKFNS-EELLAKKRAEKRSKLTATQAVEQEKLNFLNNYLEKEQALRAQFSL
EKSAGF-----
>Forficula_auricularia
-----MCNRIEKE---Q-LTRKAITLQKHRESRAEWEKFIGDMTTTCKSVDTFLEKEDELRHFYSOL
EDKLHIAN-----
>Occasjapyx_japonicus
-----MATRISACD--T-QFDSSEILCERRVAREQEWERFLQDTSEKSVRVDNFADKDELQLRGYSSL
EDKMRP-----
>Baetis_sp._AD-2013
-----MSSI PKDVGIEWSRLFDHKPFVQGEVKhFLKEFEЕКRREDREVEKVFQLLEQVADIKDVQIEK----TIKSCGN-QLSILNSNLEAVATGMCDISLRE--E-ENSVDVALMVKRESRKAWEAFIRDGMCEKARVDKTFKEREEREDYQEL
ERKLHLDKTP-----
>Meganyctiphanes_norvegica
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>Gallioisiana_yuasai
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>Graphocephala_atropunctata
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>Solenopsis_invicta
-----MASITKDTGIEWSRLFDHRPFVQGEITFFLREFQEKRADREVERLFKILEYSTELKESQLDR----TEQLGDG-HLPSLKANVDVALSMCNVLQKE--E-NFDSDSVLNENRLARREWEKFIINDMSDKCORVDQTFQEKENEIOEFYVDL
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>Eogystia_hippophaecolus
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>Tanzaniophasma_sp._AD-2013
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>Panorpa_vulgaris
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ERKLHIHK-----
>Corydalus_cornutus
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>Osmylus_fulvicoephalus
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>Triops_newberryi
-----MSALDNLIEKELSYRQYASL
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>Epiophlebia_superstes
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>Stenobothrus_lineatus
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>Ramulus_artemis
-----MSCRILDKE--Q-QHLADNSLEARRELKKAENHDFITDMTDKCFKVDRTFEEKERELSDFYVDL
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>Cosmioperla_kuna
-----MCNRIEND--E-RHRSDDTLVAKRELKKEWEKFIEDMTQKCSRVDTFEEKEEELKEFYADL
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>Inocellia_crassicornis
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>Ctenocephalides_felis
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>Lepeophtheirus_salmonis
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EESI EKKN-----
>Frankliniella_cephalica
-----MCNRMIKSE--E-EHLADNSLEAKRALRKADWENFISDMAGRCSRVDSFTQEKEEELREFYDL
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>Rhyacophila_fasciata
-----MSDLTKDCGKIWNRLFDHRPFLNGEIKFMLREFEЕКRSDEVTNLSALENATEIKONQOVR--MKESAA-LQPELATHLVKALSAYEDIEGYK--T-ELSEDTTLEKRREIRKKEWARFTSEMSDYTRIIDNAFEKKEELKDFYADL
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>Atelura_formicaria
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>Drosophila_melanogaster
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>Asprogamarus_rhodophthalmus
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>Meinertellus_cundinamarensis
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>Prorhinotermes simplex
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>Dastarcus_helophoroides
MSAATFSQGRFVPTPPEKGSFPLDHEGLCKKFVVKYMGCLRSNNNNNSACREEARAYLACRIDNNLMTKEEWSKLGFDSEPEKQH-----
>Astacus_leptodactylus
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>Forficula_auricularia
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>Daphnia_pulex
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>Occasjapyx_japonicus
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>Aposthonia_japonica
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>Meganyctiphanes_norvegica
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>Halymorpha_halys
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>Psytallia_concolor
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>Armadillidium_vulgare
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>Metalliticus_splendius
MSSMTFGQKQFAPVPPKGSFPLDHEGQCKKAMLYMITCLNANSNDNSCRAEAKYVLCRMDNNLMAKEEWSKLGFDVEAKLQKE-----
>Boreus_hyemalis
MSSMTFGQKFTPTPADKGSFPLDHEGLCKKMLKYMHCLRMSKNDSLCROEAKYVLCRMDNNLMAKEDWSKLGFKESDVVK-----
>Chrysopa_pallens
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>Grylotalpa_sp._AD-2013
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>Medauroidea_extradentata
MSSVTFGQKSFTPTPPDKGSFPLDHEGQCKREMLKYLLCLRANNNDNSACRREAKTYLDCRMDNNLMAKEEWSKLGFDLNLDSKGSKSL-----
>Menopon_gallinae
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>Cosmioperla_kuna
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>Acerentomon_sp._AD-2013
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>Ectopsocus_briggsi
MSSMTFNQKFTPTPADKGSFPLDHENLCKQQMMKYMQCLRVSKADNSKCRLESKYLACRMEHQLMTKEPWSKLGLEDLQKTVQ-----
>Inocellia_crassicornis
MSAMNF-QRTFPTPPDKGSFPLDHEGLCKDQWIRYMTCLRQNRDNSCCRILEAKDYLCRMDNNLMLKEDWSKLGYSQDNKNVKKD-----
>Ceratophyllus_gallinae
MSSMTFSQKSFPTPADKGSFPLDHEGQCKKFWIKYMSCLRQHKNDNSCRNEAQAYLDCRMDNNLMAKEDFSKLGFDNSNEINK-----
>Caligus_rogercresseyi
MASNVFGAKNFKVPAPEKGSFPLDYEKGCKKEYLKFMI CLKDNKYVVENCREEKSNYLVCRMDHGLMAKETLPNLGFKEEENKKAOK-----
>Mengenilla_moldrzyki
MSNPLLRQKYSKPTPPKGSFPLDHNAICKKEMLYIICLRNNENGSGNCRELAKSYLCRMDNNLMASEEWSHLGF-----
>Frankliniella_cephalica
-----MAQFAKSRFVPTPPEKGSFPLDHGVCCKDLMRKYMTCLSSNKQDNTKCRKEIKTYLDCRMDNNLMAREEWKLLGLQEDVGAKSEVVK-----
>Zorotypus_gurneyi
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>Drosophila_melanogaster
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>Micruropus_glaber
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SESASATAQTAKPEAVASETSK
>Machilis_hrabei
-----MAIK-----YSGG-----RVSPHLPK-----RTLMOQYPRIIISGLLITTGLLVFFSKPLYDAFCGDTVTVETLRARAAKSQSQ-----

>Reticulitermes_flavipes
-----MK-----QQPPFVRQKVLKD-----RWNIGQRNPRTFVGLFTASSLLVLFSRPLYDIFVREYPPVPVDPQLPK-----

>Calanus_finmarchicus
MADRGWHSFGHPS-----YKKDRVGQTDPS-----RGTSLDE-----IKRRSKQKNADKRFNSPFAFHEPKYNK-----VNLINRYRPLRFGVAFTTVCVLLIYFSKPIYDATLREPTQVELDRANFLKRRME-----VGGWWDNPFWKR-----SSDKPE-----K-----

>Carabus_granulatus
-----MNDNR-----RTVIRK-----RSWLQRHPKIFFWGTVSSSLIFFSRPIYDIFIRTDIFPPPTPEKESKQ-----

>Farfantepenaeus_aztecus
-----MSKVPKSPYPRAKIDLPQSYRSGPTGSORPGRETEGSNSRLLQQQDP SHYR-----YNPESVKS-----NKPEVSRF-----RRIWIYRNPFRFQIIIGLGIGLTIFFSRPLYDIFLREHIEGPLPVKQK-----

>Occasjapyx_japonicus
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>Eurylophella_sp._AD-2013
-----MNRPKPP-----KK-----P-----HYLNQIGK-----RSWVQRNPRAFVIIFTTCLTIYFSRPLYDIFFREYPEGH1PKNYIFQKKEE-----

>Grylloblatta_bifratrilecta
-----MK-----QQPIVRRKILKD-----SPWYQRNPRLFVGLFTTGCLLVLFSRPLYDVFLRAPTPGAPHPKSR-----

>Meccus_pallidipennis
-----MWKE-----KVETPKFRKTSKD-----LPWVNRNPRIIFIILTTAFALSIFFSKPAYDLMYAERVPHPSLSRSLDAGKGQ-----

>Chyphotes_mellipes
-----MTALDPCKK-----FACKLQOCLKDNVYQP-----SRCEGVIEE-----LRQCCIKNSTHSVCEGIDISKPYDHKTVDYKTAIR-----

>Palaephatus_luteolus
-----MDQRRRSKVLGK-----RSWMYRYPKQITFTTLGLGIFFSKPIYDIFIRKYEDFDYTEPPTTLGQRN-----

>Mantis_religiosa
-----MN-----PKP-FIRRKVLKD-----RSWIYRNPRAFVGITTAASMLIFFSRPLYDAFVRDLPEAPPEPRVRLKPSHF-----

>Tanzaniophasma_sp._AD-2013
-----MK-----EQPIVRRK-VLKD-----SPWYIRNPRTFVGIFTTCLLVLFSRPLYDAFLRDYTSPPPAAPRSLK-----

>Boreus_hymalis
-----MSVRGPTMIH-----RTWIQRNPRLFSGVFITGSLLIFFSRPIYDMFRTDFAPPROSLYKK-----

>Corydalus_cornutus
-----MSNRK-----NPVMVK-----HSWARRNPKLFSAFVTTSLLIFFWSRPIYDIFFRPVNEMAPPRKVKFD-----

>Chrysopa_pallens
-----MKE-----RTVLKK-----RSWAQRNPRAFFAIFATTSLLIYFSRPIYDIFREDYDTYKKRMEKERSQ-----AAE-----

>Triops_newberryi
-----MDPSN-----RKVVNSRFGEKVK-----LPWYRRKPIILFQKIFISVSLIIFFSRPLYDIFLRSYIEGPNIPDPYSINER-----LGSRVVLK-----PKTPE-----EKS
E-----
>Cordulegaster_boltonii
-----MNEFKPW-----KEKFPP-----PSRKLLKE-----HSWIQRNPGLFSSVFTLGCLMIFFSRPLYDAFLRDSVEGROVLPSNSK-----

>Schistocerca_gregaria
-----MKES-----K-ESPVRKVLKD-----QPWIKRNPRAFAGLLTASFLLAFFSRPLYDIFLRKDNVVPLESPRIAK-----

>Timema_cristinae
-----MKEKLVRROVLKD-----RPFYQRNPRLFGGVFTTVCLLIYFSRPIYDIFFRPDFAPAPIDQIRAIRKKVSD-----

>Leuctra_sp._AD-2013
-----MDRK-----PS-PVVRROVLKD-----LPWTRRNPRLFAGIFLTGSMILLFSRPIYDIFIRDNPEQTPLSAN-----

>Raphidia_ariadne
-----MOKRNTILHK-----PTFLQRNPRIIGFSLITLSMLMLFSKPIYDTFFAPNYKFPKPKN-----

>Oropsylla_silantiewi
-----MNGGPRRAIRKD-----LPWAYRNPRAANIIVIGSLTIFSKPIYDIFLQEPIDYTVKIWQKIKANIESKKGSE-----

>Annulipalpia_sp._AD-2013
-----MSYPY-----GKPPK-----P-----VDPPI-----K-----RDPLKQRRPVLKN-----QSFVYRYPGTGTGVMTLGLA1FFSRPIYDVFFSEMFPDLADPILCDHP-TRGVKGKRYVAP-----EQQ-----Q-----

>Zorotypus_caudelli
-----MN-----SEGPKIRKAVLKD-----RSWIYRHPQLFIYSCATIGFLIIFHRPIYEMFNLPPIKTO-LDEAKSKKNSVKISE-----

>Atelura_formicaria
-----MQ-----PRQKPLKD-----RSWVQRNPRTFTVTLTSTCLLIFFSRPLYDAFLRPAEPPSPVPMKK-----

>Drosophila_melanogaster
-MSAQYQRFKVLKEWPAEKSQV---GRDLGEQIRKQVTKLSLEG---GATDKELDRQINSLERLSNNVYAKKYPRTFE-STATGLTAAQCQVLSSEFLQVYNEDSKKKK-----
>Hyalella_azteca
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>Machilis_hrabei
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>Argulus_siamensis
-----MLKQSDALSKMLNNSYKMYPRKF-K-STALGLDYETCKVANSNEFLKSMK-----
>Cryptocercus_wrighti
-MARSYRNFLQLLELWPDSTKV---GRDLGOHIRQOVKVAFTGEVF--PGDETECNRIYASLKRADNRVGGMYPREST--TCASGLLADQCQAILSHQFLEELRESEK--GFFSKLFHRKS-----
>Carabus_granulatus
-MAASYKMLKLLKEWPDKNKR---GQDLGEHLRKQVQAFAARQF---DTNQECCDRKYSLKRIAEDHHLKTHPRTLK--SSATGLTAEQCQILSPEFLEALERDQ--SVFRRIFSF-----GSKK---
>Litopenaeus_vannamei
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>Forficula_auricularia
-MAHSYKIALQILEKWPICSSKK---GRDLGEFIRNQFNIGFKDQOIL--FGSEVECNRLSEIKRISENYHANKYKRTLN--SSSTGLTAECEKSLSNEFLKHLNK-----
>Occas_japxy_japonicus
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>Eurylophella_sp._AD-2013
-MAQHYKNFLRLLEKWPDSKK---ERDLGLIVRQVKQAFPSGEST--PVNIDECXYGILKRLVDNHLNLHKKLE--SSSTGLSAEECQVLSSTEFLLKELEKQDR--SLWSRLFNRNKE-----
>Meganyctiphanes_norvegica
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>Gallioisiana_yuasai
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>Clastoptera_arizonana
-MANHYRNFLRLLEKWPVDSKSK---SRDLGFFIREQLKVNFPQGEIARNIDEEKCNEAYNSLNRLDANNYYFDKYQRKFH--SSATGLDAEQCTVLSDEFLEYLKEENNOTIVSKVFGNKNKEQ-----
>Argochrysis_armilla
-MAGNYKNYLLLELWPLDKSKA---GRDLGOHIRDQVKVAFSGDVGNDINRQECNRYQSLQRIVGNHYGKYPTRTLS--SSASGLTKECQNEILSPEFNEYLYYDQ--SFFEKVRLSLALIFTRSNKAKKS-----
>Danaus_plexippus
-MTSQYKFKTKLIAKWPIDNNKA---ERDLGKFIKDKVKAFFEGGNSK--NLDSELCRQLYSLNKIADNHYRNKYKRIHD--SSATGLSSEENLVLSSSEVLQYKLENK--GFFKNIFKKD-----
>Boreus_hymalis
-MAASYKYLLLEKWPIDKTKN---ARDLGLYLROQVKLTFGGGVVS--RAEEKCECERQLHALNRLADNTYKLFRTST--STATGLSADQCQILSTDFLELLQEEDK--GMMSKIMSKAKPKT-----
>Euroleon_nostras
-MSNSYRFLNLLKDWPLDITTK--NRDLGQHLRDRIKVAFATGEQF--QGDQKCDLEYLALRLADNYAKKYPRTLQ--SSATGLSLKECKDIIISNEFLESVKEDEK--SVLQKLFSSKSRVVAN-----
>Calopteryx_splendens
-MAGRYKFLRLLESWPVDNSKK---GRDLGYHIRKKLLEAFPMGETS--SFNAEECEKYVLSKKINDNYGDKYKRHTN--VTSTGLTYEQCAGVSTEFLETVSAGR-----LFKLSQKR-----
>Stenobothrus_lineatus
-MANNYRKFVLLLESWPVDSKTK---ERDIGFYLRERVKKAFTAGELF--EGDQEKAREHASLKRADNVYGKLYKRITS--SSATGLTAECCNVLASEFLTLQKENR--SIFSRFLFRGK-----
>Clitarchus_hookeri
-MANHYRNFLKLEGWPIDASKK---GRDLGEHLRDQVKTAFNAGEVS--RIDKAKCEKIYMSLKKLADNHYGNLYHRTSS--SSAMGLTAEQCQVMSTEFLLKSEEEK--GFFKRIFKRD-----
>Leuctra_sp._AD-2013
-MAGIYRDFRLILEKWPVDTTKK---GRDIGEYIRQOVKVAFPAGEVF--KGDEEHCKRQASLKRLSENHYGELYKRTSQ--SSATGLTAEQCQVLSSEFMMEMVEESNK--SFLSKLFGRNKDS-----
>Acerentomon_sp._AD-2013
MSAPLYHYMKLLERWPVDSKK---GRDLGEFLRTKIFSEFKYGETS--NVDVLCERKFALNRLSADHYMTKYPRLYT--STSSGIVSVEQCKVLSTETLKQLEYEDT--GVLKRTFWNLTSYKNKYVDSKK-----
>Xanthostigma_xanthostigma
-MASNYRFLLELLKDWPLDKTE---GRDLGQHIRDKVKVAFAGDIS--QTNQEECDKYNSLKRLSSEYANTYPRKVS--SSSTGLKSDQCTOILSNEFLELLEQEDR--SPVSKLFNRSKK-----
>Oropsylla_silantiewi
-MASSYKTFMKILKWPIDKTKK---DRDLGRYLRDSIKTVFTKGEVS--TVDEVKCSKQLEALDRIANNTNFVKYKREFA--SSATGLTSEQCNTVLSTDFLEYLEYENK--GIVTKLVTKPPAVES-----
>Caligus_rogercresseyi
-MSASSRWLKLLOSWPSEPSSK---SRDLSQLLLKRKSPSS-----EAEVRALETLLSNKLALKYSRVYSEATATALGREDLKTLTSTDFLESSTAYANLSFWERIKLKFFSK-----
>Thrips_palmi
-MAQLYERFLKVLQKWLNADYPPPLRSLPAHLRDQGAFAFARGEF--SGDTLQCEKRLSSLERLTTNQIARAYPRTOQ--TGALGLTSDQCQVFLSDSYOKSLETSATTSLFQRIVSSFRQSGKEKA-----
>Platycentropus_radiatus
-MTSQYRNFLKLLKWPDPSSK---GRDLGDIRVCIKAAFNTEQGF--TGDLKECQKYESLNRILISNOHGMLFKRTKA--HSSTGLTAEQCNLVLSSDFLEYLQGEER--SIFANILPKQD-----

>Drosophila_melanogaster
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>Meinertellus_cundinamarcensi
MPYAIIVGNLKQSEGAGRPWQVSAGLKDKEIQLNRFQCLT--KDKYTVVFYQHPCIILTALEVIgyrvvsscpagE--NENRSDEYVWTVRKDFSEPEPSDAEEENG1-----
>Coptotermes_gestroii
MPYILVRGNLSSYG--KDYPRWVLVSLKACDIEQLKRFASGG--YCDSTIVYLQHPCVILTALEVLGYQVVASSTSIK-----QDYNEYMWTMRKEFSEPEPMVKPTLKQ-----
>Lepicerus_sp._AD-2013
MPYILVRGNLASYG--HKYFPRVLVSLKAGDIDQLNRFASGG--YSDDYTIVYLQHPCVILTALEVLGYRVVASSTSVK-----QDYNEHMWTMRKEFAEPEPDADTETDV-TTLC-E-----
>Apachyus_charteceus
MPYILVRGNLASYG--HKHPWRVLVSLKASDIEQLKRFASGG--YTDESTIVYLQHPCVILTALEVLGYRVVASSTSVK-----QDYNEYMWTMRKEFSEAPLLTCKPTN-----
>Aposthonia_japonica
-----MWTMRREFTEPDTSKPGF-----
>Ephemera_danica
MPYILVRGTVTQHP-----CAHVSGLKASDIEQLKHFGSARKAVPADDLTVSYALHPCVILTALEVLGYSVVSCTAGPTG--PGGETQYLWTLHKDFEPEPDSLYNHH-----
>Grylloblatta_bifratrilecta
MPYILVRGNLASYG--HRNPWRVLVSLKAGDLEQLKGFSSGG--YSDSTIVYCHHPCVILTALEVLGYKVIASSSTSVK-----QDYNEYMWTMRKEFPEPEPSQTKQPVLT--CN-----
>Lygus_lineolaris
MPYILVRGNLASYG--NRYPRWVLVSLKAGDLEQLQRFNCGG--YCDNSTIVYLHPCVILSALEVLGYQVVASSTAVK-----QDYNEYMWTMRKEFAEPEPTKEKEKTN-----
>Bombus_terrestris
MPYILVRGNLASYG--HRYPRWVLVSLKASDIEQLSRFASGG--YCDSTIVYLQHPCVILTALEVLGYKVASSTSVK-----QDYNEYMWTMRKDFSEPEPEPVIKTGKLP-RR-----
>Zygaena_fausta
MPYILIRGNLASYG--HKHPWRVLVSLKAADIEQLKRFACGG--YSDSTIVYLQHPCVILSALEVLGYKVASSTAVK-----QDYNEYMWTMRKEFSEPEPSIIVEQDNIN-NYSK-EAMHLGNQKDDV-----
>Mantis religiosa
-----MWTMRKDFASPEPQLAKPTLKQ-----
>Tanzaniophasma_sp._AD-2013
MPYILVRGNLASYG--DRNPWRVLVSLKAAEIEQLKGFASGG--YCDNSTIVYLQHPCVILTALEVLGYKVASSTSIK-----QDYNEYMWTMRKEFSEPNQTKL-----
>Boreus_hyemalis
MPYILIRGNLASYS--HKYPWRVLVSLKATDIEQLKRFACGG--YCDSTIVYLQHPCVILTALEVLGYKVASSTSVK-----QDYNEYMWTMRKEVFETPCIAPSTVTII-SPSVDERDNIANISKEALTITPNKIDE-----
>Corydalus_cornutus
MPYILVRGHLTSYG--HRYTPRVLVSLKANDIEQLSRFPSSG--YSDDLTIVYLHPCVILTALEVLGYKVIASSSTSVK-----QDYNEYMWTMRKDFTEPEPVNVKEVAHDA-----
>Chrysopa_pallens
MPYILVRGHLTSYG--HKYTPRVLVSLKAPDIEQLSRFPSSG--YADDLTIVYHPCVILTALEVLGYKVIASSSTSVK-----QDYNEYMWTMRKFAEPEPDPLSK-----
>Triops_newberryi
MPYIVVSGNLTYPK--SGTPWKVGIISGLKGIELQELDRFILEG--QADPHTVFVKHPIVLLNMLEVLGYRVISSYSTDKPTINISQEPVPISVWMTMRREFPEPEPSDDSDSNHPTDASL-----
>Epiophlebia_superstes
MPYIIRGNLASYS--NRNPWRVLVSLKAGDITQLKRFPSGG--YCDSTIVYMQHPCVILTALEVIgyrvvssstsvK-----QDYNEYMWTMRKEFTEPEPSVTSFDSGITT-EPLP-----
>Geuthophilus_sp._AD-2013
MPYILVRGNLASYG--HRHPWRVLVSLKATDIEQLKRFASGG--YSDSTIVYLQHPCVILTALEVLGYKVASSTAVK-----QDYNEYMWTMRGEFAEPEPLLSKPTSPTS-----
>Peruphasma_schultzei
MPYILVRGNLASYG--HKHPWRVLVSLKASDIDQLKGFASGG--YCDSTIVYLQHPCVILTALEVLGYRVVASSTSVK-----QDYNEYMWTMRKEFSEPEPHAAPGY-----
>Leuctra_sp._AD-2013
MPYILVRGNLASYG--HKNPWRVLVSLKAAIDIEQLKRFASGG--YCDNSTIVYLQHPCVILTALEVLGYKVASSTVIK-----QDYNEYMWTMRKDFAEPEPQTVSNPE-----
>Ectopsocus_briggsi
MPYILVRGNLASYG--HRDPFRVLVSLKAGDIEQLKQYPCGG--YTDEVTIVYLAHPCIIILNLEVLGYRVIASSTTGVK-----QDYNEYMWTMRKEFHEPEPLERN-----
>Ctenocephalides_felis
-----MWTMTKEFSEPDTKCGESKHE-----
>Thrips_palmi
MPYIIVRGNLASYG--NRYPRWVLVSLKAGDIEQLSRFASGG--YCDSTIVYLQHPCVILSALEVLGYHVVASSTSVK-----QDYNEYMWTMRKDFSEPEPVAPITAKPS-A-----
>Annulipalpia_sp._AD-2013
MPYILIRGNLASYG--HKNPWRVLVSLQAADIEQLKKFACGG--FCDTSTIVYLQHPCVILSALEVLGFRVVASSTAVK-----QDYNEYMWTMRFEPEPEPSVFMERDNIT-NIT-KEAMNIADIGNIKANDL-----
>Thermobia_domestica
MPYIVVRGNLTALGNNHSQPRWVLVSLKAGDILNLKRFQCGD--YPDDFTIAFLQHPCVILTALEVLGYRVVSSSSS-----NNEYMWTMRKEFSEPEPIQNSESFD-----

>Drosophila_melanogaster
-----MSVVEAEVLQKIDLIEP-TTGKLFHE--HKTELLFCRPHLMPLKTAALERLEEMHRDTARQLQKKR-----QQKKKSTEPTGSL-----
>Talitrus_saltator
-----MSGLEKVLPR-RKGLLYQE--ESYQALACRPKLMPLKSIITLEKLEAMQOQLQERSKEQL-----QQQELSTQQQ-----
>Argulus_siamensis
-----MSEEDKLKLLKEVIP-YQGVVFQE--DVPNFI LCKPKLMPKSVTLEKLEKMQKEAQERVKVQQ-----NEVDONADISS-----
>Cryptocercus_wrighti
-----MSEERKIPALKEVIP-YKGLLHHE--EIPFEL LCKPKLMPLKSVTLEKLEKMQKEAEELKKQQ-----MNEQRS-----
>Oxysternon_conspicillatum
-----MSEGEIKPIVP-KTGQLLIE--NPEELILCKPRLIPLKSVTLEKLEKMQEEAIKTLRESR-----EKTEG-----
>Eucyclops_serrulatus
-----MPKG-EVKVTVGSEPFREVLP-KRGLIFQE--SSPQLVLCKPKLLPLKSVTLEKLEKMQKEATEKAREQM-----IEQQKQEDERLFGSVSENAETHAPESVSFE-----
>Farfantepenaeus_aztecus
-----MPGSEAGQVLKEVLP-RKGLLYQE--DSSPLALCRPKLMPLKSVTLEKLEKMQKAAQEKGRQQQ-----EEQ-LERQATAPA-----NGSRI-----F-----
>Occasjapix_japonicus
-----MSEGSKTTAAPQOLFKEILP-RKGLLHQE--DIPTYALCKPKLMPLKSVTLEKLERVOREAQEKVLDRS-----NOPEQN-----
>Eurylophella_sp._AD-2013
-----MGSDKDSVKEILP-KKGLLFSE--DIASLILCKPKLMPLKTLTLEKLEKMQKEAEVRGEEH-----EKEANESF-----
>Tigriopus_californicus
-----MVLCKPKLLPLKSFTLQKLEAMQSEAKIKAAQAL-----RPNEDLEHNDEDE-QRLAADGAAFISESVSFE-----
>Nilaparvata_lugens
-----M-ANLEGSSDSNIOEYLP-TTGLVHNE--EIKELIFCKPKLMPLKSVTLEKLEKMQKEADQKLKEQQ-----RLPTAAPLPTFQS-----
>Argochrysis_armilla
-----M-SQAADNISEEIDIVLP-KOGLLYKE--ESLDYILCKPKLMPLKSVTLEKLEKMQDAEQKLKOTE-----VTTNGYKENK-----
>Metaphatus_ochraceus
-----MRFERMQGEASRWKKEKL-----KSAKKN-----
>Boreus_hymalis
MSINDLNKNITLDSKTVPQYVLP-PYGEICLK--YESKCLKSHPHIMPLKSVTLEKLEKMQGEAFKQVQENA-----KLKEDY-----
>Corydalus_cornutus
-----MSNTLNEKNVKYVIPSNITGQLFFE--DTRQLVLCKPRLMALKSLTLEKLEKMQIDAEEKMLHK-----SNYS-----
>Osmylus_fulvicephalus
-----MSGSSSTTPMRPVLINTGQLFFE--DTKELILCKPRLMPLKSVTLEKLEKMQKLAEEVRAHR-----NSTVEEHK-----
>Triops_newberryi
-----MEESKNTPEVPQRIIP-EHGLIHLE--CNSSWSLCKPKLMPLKSVTLDKLELMQKAAQEKMQMK-----DSSSQS-----
>Cordulegaster_boltonii
-----MSDGFKIDR--ENFSVPRGLIQYQ--DFPHFVLCKPKLMPLKPVNLRKLEEMQREILKKVKSQE-----NAQHE-----
>Teleogryllus_commodus
-----MSKDQTPVLKDFIP-NSGMIYHE--DLPOYILCKPKLMPLKSVTLEKLEKMQDAEDKKQQR-----LEQINEGNVNVNP-----
>Sipylodea_sipylus
-----MSSHNPALKKEFIP-RKGFVVPE--DETQYILCKPKLMPLKSVTLMKLEKMQORDANEKLLKQK-----AEPQNDTC-----
>Menopon_gallinae
-----MSSSHNDTDLKYTLP-TTGYIFEE--DVNRYVLCKPKLMPKMSITLEKLEKMQKEAEDKFKSHM-----NSKCEE-----
>Liposcelis_bostrychophila
-----MSTVNNENLKFTLP-TTGFYEE--DISQYILCKPKLMPLKSIITLEKLEKMQKEAEELKKSQQ-----AYTKKE-----
>Caligus_rogercresseyi
-----MQEESQARAALVLRREGQHLLRSTGPQGIP-----PQHDAEILSMTTOTHNGNKDEEE-----
>Frankliniella_cephalica
-----MSEPANVHVHIL-STGVIOQGEKDFQPTLCKPKLMPLKSVTLQRLQEDMQKLAEEKLQQQ-----INSSTGESTOL-----

>Drosophila_melanogaster
-MNDIKRLKDDQREKHPGFDGYMDCMTRSLFTGLATFCLSFSGTYFAQKIVQ-SK1R---YPIKYNIILSSLVATGVSYQITSTRTKACQAAWMAFEDKHSLVLEKETF-----
>Poekilogammarus_pictoides
MSDRKSRMVNQFGEEHPAIGSYLECVSRAYLTGLAGFSLSFACYSVQRLTA-HRLP---YTANGDLLAAIVASAVAYKVTANHVOHCNFWMAAEDKHTYLNPIQDKGDTQQL---
>Machilis_hrabei
-MNDLNLKEEYGDQYPAFGSYTECMRALLTGLSSFVIFSFGVYIFQTLMK-KHLP---YGSKANVLSSGVASIVSYIITAKRTQACQAAWMAAEDKHTYLNPISEKGNKKDT---
>Argulus_siamensis
-----MKTNYFYGGFYVIGLGAEEVIQKVVG-AEKY---YGKSIKIGTSLMAAVLVAFKFTLNGAKESAILKDRSH-----
>Prorhinotermes simplex
-MENINELKKQQRDIHPFGSYLECMTRSLFTGLAAFTLAFSGSFIGQSLLK-KHIP---YGNNTYILLSALLATGISYQVTTQRTKACQAAWMAAEDKHTYFKRGSQAE-----
>Eucyclops_serrulatus
MLLAQEASSETKKDS--IPASQVEQOTRSVMYGVATGTISFVGYYFAQRFLTRHYKG---ASVSLFATLSFFGGFSGYMMVTDAKLKDCAKSKKFKFESSN-----PNK-----
>Farfantepenaeus_aztecus
-MNNINTELINOYKDAFPFAGGYMECMRSLTGLSSFCLAFGGTYITQHLTN-KYLP---YGRKNHIIVSSLIACAVAYKVTISIRAEACQAGWMAAEDKHTYLNPISEKRTVDVEEE
>Occas_japox_japonicus
-MNNMNEVVKKEEKYPFGSYTECMRALLSGMSAFALAFSGTYLLQTALS-RHLP---YGGKGFVLVSSFVAVGASVRTTTTRACQCRANVRADGIKDDF-----
>Isonychia_bicolor
-MNNVQLKKEQYSGEHRGFGIYLECMRALLMGLSSFCLAFATSYIPQSLLK-KOLPTSYGVGGRIILTSSVLAAGVSYIITSORTKQAAWMAVEEKYTYLTPISVIENIESK---
>Meganyctiphanes_norvegica
-MONTSDTIKQYKGAFFAFGSGYMECMRSLTGLSAFSLFGGTYVAQHLTA-KHLP---YDRKLHILFSSIIVAVSYKVTSVRTNACQAAWMAAEDKHTYLNPISERPKTVDEEE-
>Cuerna_arida
MSRGKERLLELYGDDHPGFGSYLECMTRANFTGLATFTIAFSSTYIAQSILK-NKLP---YSSKFFILSSTAIAAFYSYKVKSKARSOVCQAAWLAEDKSTYFTELEKTSPTPVS---
>Tentredo_koehlerii
-MNSNDNSDTIISAKFPGYSGYLECMTRSLFTGLSTFAIVFSGAFFGQRFMH-KSTP---YSKKSTILISTSLAALASYIITSSYTVACKSWARANGN-----
>Mantis religiosa
-MENINELKROQSEKHPGFGSYLECMRSLTGLASFTLAFSGSFIGQSLLK-NKLP---YGNKSGILISSLLAVGVSYQVTSORTKACQAAWMAAEDKHTYLNKDIPIAST-----
>Boreus_hymalialis
-MNDIKKLKQKDAHPGFGSYLECMTRALFTGLATFSITFSGIYFIQKSQS-KRLP---YTSNGCILLVSGFAVLASYIITASKTKICQAAWMAAEDKHTYLNKELDKVS-----
>Triops_newberryi
-MNNIGELKERYTQIYPAFGSYTECMRALLTGLSASIFGFSASYFAQYLLK-NRIP---YGLKGQVLTSSAIAILVSYKVTSDRSKACQAAWMAAEDKHTYLQDVEKPRSS-----
>Calopteryx_splendens
-MNNINALKEQYKEVHPGFGSYLECMRSLTGLASFTLAFAGTYIGQSLLK-KSLP---YKKKSFVILSSLVAVAVSYRVTSVRKACQAGWLAEEKHTFFSENPTSDK-----
>Ceuthophilus_sp._AD-2013
-----MVFASTYLSQKLLQ-KKLP---YGGNMFVLVSSLLAVGVSYQVTAHRTNCOQSGWMAAEDKCTYFTQNMPE-----
>Extatosoma_tiaratum
-MNDINQLKREQSEKHPGFGSYLECSSRGLLTGLASFTLAFSATYISQTLLO-NRLP---YSRNSIILCSACAAIAVSYHVTSSRMQACQAAWLAEDKHTYLSGIGEAD-----
>Leuctra_sp._AD-2013
-MNDIKKLKEQHSEAHPPGFGSYLECMRSLFTGLAAFTLAFSGSFLAQSLLK-KHLP---YRMNGYILVSSGLAVATSYHITAKRTSACQAAWMAAEDKHTYLTDOPEQKN-----
>Inocellia_crassicornis
-MNDIKILKEQORESHPAFGSYLECMTRALFTGLASFTIVFSSTFTQKLLVKNKIFP---YRLPRAILISSACAVLSSYQITATRTKSCQAAWMAAEDKHTYLTETK-----
>Thermobia_domestica
-MSS-SNQRKGLSONHHAHGSYLECMTRALTGLSSFTIAFSAAYLSQYTFR-HRLPF--SSRRGPICSLVVASAFTYTTSTRLKECELASVPSEKTTSFRIIQEKQ-----

>Drosophila_melanogaster
-----MSLQTLGAFIFTILASVSIVAAIILLGWFLIWKAFLSKFRLVRELLGGEEPEDQQPLAWDHONQOPHHHGRARKARRD-----
>Cryptocercus_wrighti
-----MKELLAVFSIISSFLVLVLVCLGWYLVWKFLLSRFRVRELLGGMTSTSVS-----DLKNGRSRIKKTRRE-----
>Aleochara_curtula
-----MKDIIILAITTVISSLAIVFLILLGWYIVWKFLSRFRVRELLGGSPAGETP-----E-----NKNRSKRSRRD-----
>Forficula_auricularia
MS-----IDLVPNEGNSVFTPDMSIQILAIAYSIVSIIIVLAI VAFVWYLLWKFFLSKFRFVREFVGAITYETPTEN-----E-NTKSTKRSRTRRLD
>Aposthonia_japonica
-----MKEFLLAVFSISSLVLLVGLVGFVWYLVWKFLLSRFRVRELLGGSSSESSVN-----DLKNGRSRIKKTRKD-----
>Graminella_nigrifrons
-----MEFVLAI FSLSSFVVVIAIVCLGWYLVWKVFLSNFRVRELLGGMSDTPPVE-----G-ETRKARIKKARRE-----
>Pseudomasaris_vespoidea
-----MQEIVLAAFSVISSLLIVFGLVLLGWYLVWKFLLSRFRVRELLGGMSESSVN-----DLKNGRSRIKKVRRD-----
>Tischeria_quercitella
-----MKQTLAIVALLSSVALVCLFVLICWFILWKCCLSKFRFVRELLGGMSESPAS-----EVRO-PTRAKKLRKE-----
>Mantis_religiosa
-----MKEFFLAIFSIISSVFLVLFVCLGWYFVWKFLLSRFRVRELLGGMSESNAS-----DLKNGRSRMKKMRD-----
>Bittacus_pilicornis
-----MTSESSVN-----DLKNGRNR IKKVRD-----
>Sialis_lutaria
-----MSETSSQT-----NLKNEKGRVKVVRRE-----
>Osmylus_fulvicephalus
-----MSKNIMNVENIMLMLVTIFVTFTVIVFIFLWGFIVWKCCLSRFRVKELLSEKQEEVPV-----RKSSRSRRVHRE-----
>Laupala_kohalensis
-----MMELFLAVFSIISSVLLVFLVFLGWYLVWKFLLSRFRVRELLGGMSESASVN-----DLKNGRSRMKKTRD-----
>Medauroidea_extradentata
-----MKDFLLAVSTVSVAVITVTLVIFGWYLVWKFLLSRFRVRELLGGANDTPPGS-----E-----GKRKKVRRD-----
>Leuctra_sp._AD-2013
-----MEILLTIFSVLFSALVVSAGLWYLVWKFLLSRFRVRELLGGMSESQSA-----DLKSGRSRIKKTRLD-----
>Ectopsocus_briggsi
-----MISAI FIFSFLIAFVVVIGLVTFGWFLWKYLLSRFRVRELLGGSDRSTSDS-----P-ESTRPRTRPNRKARID
>Xanthostigma_xanthostigma
-----MNGNEHPP-----NORKSSRSKKVRRD-----
>Ctenocephalides_felis
-----MKDFLLACVSISSVLIVLILVSAGYIVWKFLSRFRVRELLGGMSESTVV-----DLKNSRNK IKKVRRD-----
>Frankliniella_cephalica
-----MKEILLAVFSLFSSLTLVLALVALGWFLVWKFLLSRFRVRELLGGSRSESRIVA-----ELKTGSRRAKSSRE-----
>Annulipalpia_sp._AD-2013
MCFTHSQKLGKCRNHFRPMFE-----GSSSTSSLVMAALSAGLPILLVLLIATGWFLVWKCFLSKFRFVRELLGGNADQPSA-----EPKDNRNRSKKVVRRE-----
>Zorotypus_caudelli
-----MNEFLAASFIISSFILVLIVSVGWYLVWILFSLSRFRVRELLGNNSENOVSS-----K-----KSRL-----

>Drosophila_melanogaster
-----MCGLHFRTRNSPSQKTSLRWGDCCLA-----
>Hyalella_azteca
-----MCGLGFRLLKNTPSKTSLRWGDCGCGY-----
>Parasteatoda_tepidariorum
-----MVSLRTRLRNFPSKTSLRWGDCVRFFP-FSLTFQ-----
>Argulus_siamensis
-----MTCNLGFRTRKNTPCQKTSLRWGDCY-----
>Prorhinotermes_simplex
-----MCGLAFRTRNSPSQKTSLRWGDCCTNYSFSHNYPLH-HRQLHSLQSVQKLKTSAMRVFTAFALHQRFHHSVSLK1
>Calanus_finnmarchicus
-----MAVCSLGYQTENTPSKTSLRWGDCRVYAVFSLHACK-QDR-----
>Nicrophorus_vespilloides
-----MCALGFRTRNSPSQKTSLRWGDCCLAS-----
>Homarus_americanus
-----MCGLGFRLLKNTPSKTSLRWGDCGGRGVVKRSCSSRR-QEG1-----
>Tigriopus_californicus
-----MTTATLGFTTENSPSKRTSLRWGDDCLQIKQTHLDRSC-----
>Aphis_glycines
-----MCSLGFKTRNSPSQKTSLRWGDCCLF-----
>Polistes_dominula
-----MGGLAFRTRNSPSQKTSLRWGDCPPNPNPPSSSALWKNRQDMPPVPV-----
>Ornithodoros_turicata
-----MVSPRYRLRNFPSKRTSLRWGDCSTRGLHRHLLSAQ-----
>Tischeria_quercitella
-----MCGLRFRTRNSPSQKTSLRWGDC-----
>Varroa_jacobsoni
MPYMSPGKSNGNLVRHRNFPSKRTSLRWGDCSPAYQLPPLHCAASL-LGPF-----H-----
>Triops_newberryi
-----MCGLGFRTRNSPSQKTSLRWGDCCFSRNSTFVSF-----
>Nothrus_palustris
-----MFRLIRLRLRNFPSKTSLRWGDCGQNVQLKNY-----
>Locusta_migratoria
-----MSSCGPAFRTRNSPSQKTSLRWGDCAAAAHL-----
>Liposcelis_bostrychophila
-----MCGLGFKTRNSPSQKTSLRWGDCCFNYNY-----
>Oropsylla_silantiewi
-----MCGLGFRTRNSPSQKTSLRWGDC-----
>Caligus_rogercresseyi
-----MSVGYGTENSPSKRTSLRWGDCCLLAINSED-----

>Drosophila_melanogaster
-----MSDTRKDPCKPNACRIQACLTSKHRR-----
>Gmelinoides_fasciatus
MDREYNSVLKPKDPCKPKACAIQRCLERTRYNVVLQOPYYEKLTECCRQFAARSDA---CGSEEQPPAS-A-----
>Meinertellus_cundinamarensis
-----MKKDPCKIFACEIQRCLQENKFQESACQAAINALKKCCKKWREDSLV---CSG1KIDDELNKDIPQK-----
>Reticulitermes_flavipes
-----MKKDPCKHACAIQKCLKENSYQEQSCQQTIELLRECCCKWGNASVS---CSG1DTRKTP-SQTVRSLACLA-----
>Lepicerus_sp._AD-2013
-----MSSRDPCPKPFACAIQKCLKGKEIKRIICFITLFI---IVYLRKKLPRAGL---SKGNNTNDKM-L-----
>Occasjapyx_japonicus
-----MPAKPNDPCKPLACAIQRCLVANDFLESKEEEVKRMLACCDLWGSETSGGRSCSGFWINRPGEAPRKRQEAKK-----
>Clasoptera_arizonana
-----MKKDPCKKFACEIQKCLKENEFQEDKCKQYIEYLRNCCKTFGPQSTS---CSG1KTSPPKVD-----
>Lasius_neglectus
-----MTTVDPCKQFACKLQKCLTDNVYQPSRCQEIIEELRKCCIKHSSISTV---CDGINTSKRYEHNTVDYRKVLK-----
>Papilio_xuthus
-----MEFLYMPADPKKFACEIQRCLSENKFQEVRCARVFESMRQCCLKFKHISLV---CEGYRLPREFAPVTDROPKKN-----
>Tanzaniophasma_sp._AD-2013
-----MKDPCKPFACAIQKCLFVYTCHC-----
>Nannochorista_philpotti
-----MPLPSKDPCKLNACKIQKCLKEHNYQEDACLDIIEQMRLCCVKWGNKSYV---CNGIKTESKQPKYETSNEVKI-----
>Cordulegaster_boltonii
-----MKRTKKDPCKVHACRIQQCLKENKFQEDNCKDIINEMQKCCDKWIFYESLC---CSGFKKPLQS-----
>Tetrix_subulata
-----MKKKDPCKPIACKIQKCLVV-----
>Ramulus_artemis
-----MKKDPCKVQACKIQKCLAENNYQESACKEVIKEMVECCRKWSVSLC---CSGINTKVST-ASSAEV-----
>Cosmioperla_kuna
-----MKKRDPCKAHACRIQKCLAENNFQESACQAVLEDMRSCCRKFKNVSLC---CSG1DIGDTP-TLETASEPKK-----
>Inocellia_crassicornis
-----MKDPCKLTACKIQKCLKENRYQEDACAEVLEEMROCCLKWHOVSLC---CSG1RLDEPKIKD-KKLSSKDDNN-----
>Oropsylla_silantiewi
-----MRPKDPCKANACMIQKCLNENNFQESACGEVLEMLRLCCVKWGDKSFV---CNGINLEKAENSTDNTKSTKLKPQOKS-----
>Rhyacophila_fasciata
-----MKDPCKASACKIQTCLKENGYESRCADVLEAMQCCLKWHKESLC---CSG1RLEPRPVLOTRQAEHSENTDKN-----

>Drosophila_melanogaster-----MSGYQYLDVKIKLRDPDSVLTLPVFFGCGIHSSLASIFGEIGGQITILEIVKSSSQKRSILRVPENVLDRVRVAIALIGYYQEVPC-HFQVLSTSRKPLDFEESPEEFVAFN-
 >Blattella_germanica-----MSGYYYLDVSLFEFEGGSRPENAVYLYKNHILQALNTLFGVEGASTRVDILKYNPNTQRAVLRCPASYYVKLRSSLGCGYNAVAC-VYRIHNTSSCLLSLLGTSTRYKH-
 >Anoplophora_glabripennis-----MSKYYYLDVSLQLAKTSENTITATYFKNNIVNAVNQLFGEVATAVNIDILKYNSNQRAILRPVKTHYIKLRSSLTCGYEGEPC-AYRIHKASPLLLAQGDSRDYQH-
 >Aposthonia_japonica-----MLSMKTLFGETGTCTDVIDIKYNEKSRRRAVIRCPSSSYIKLRSALTLGNGYSDIPC-VYRVHNASSPPLSLLGNSRNYKH-
 >Xenophysella_greenladeae-----MQALKSLFGEAGGSTCVDILKYDPCHKRAILRCPSYAYVKLRSALTLGNGCSGEEC-AFRIHCCSPSLLALTANSRTYSHR-
 >Psytalia_concolor-----MQYLDVSLDPSNPSREISPVFLKSHVTQSLKQLFGEKGADCSIDILKYNSTTRRFILRCSSQDYVRLRASLTASTYEEDNC-IYTVNRSSASPFGLLANGRDYNH-
 >Nemophora_degeerella-----MTDYFYLDVSLDLTSDNVEISALYKKHIDLSLNTLFGVEGASIPVDILKYEPTKRSILRVPEEFYVKLYSSLTCGKYQNILC-AYRVHKTTPSLLSLLGDSRTHKF-
 >Mantis religiosa-----MSDYYYLDVSLFIAGKEQEVAVYFKNHVMQSLRTLFGVEVGCCIIVDVLKYNPEEQRAVLRVPASSYVKLRSSLTCGEYENTVC-AYRVHNTSPCLLSFLGNSRNYHH-
 >Panorpa_vulgaris-----MSNYYYLDVSLLESA-KSKVSAVLFKKHVIESLQSLFGSISATQIDILRYNREQIRAIIRVPEKYVKLRSALTLGGYEKFC-AYTIHSSSPCLLSILADSRSYEH-
 >Chrysopa_pallens-----MSNYHYLDLTLELPKGLKREISAIFFKKHVMQALNALFGEVGASTVDLLKYESIPHRAIRVPSVYYVKLRSSLTAGDYEGIPC-AYRIHKSSTYLLNLLGDSRNYNHE-
 >Prosarthria_teretirostris-----MSDYYYMDISLIGSSPTEEKVSAYFKDHVMQSLRTLFGVEGSSINVDVLKYDIEKQRAVLRCPASYYVKLRSSLTLGDIYCGSPC-VYKVHQSAYLLSLLGNSRNYKH-
 >Menopon_gallinae-----MKGYYYLDVLIKFEQG-KISLDENLKTIIIVYSLNTLFGEGGSAIEVDVLKYTOTDQRAILRCLADKYVKVRASLLNEAYGVQL-QLQVVKASALLSLQNSRNYKFA-
 >Liposcelis_bostrychophila-----MSSYYYLDVQTKFHOGETIQLTPSEAKETIRKNLKELFGEQGLQSVELKSYLKEGRFILRCSCSFYVKLRSSLIVCSSLG-N-NFKIIKTSPSLLSLLKSPWETDF-
 >Raphidia_ariadne-----MNIFCNYFDIFVILLNVYK-YKEFEKGINKEVTVAFFKKHVLNALNLHGEVGASTTVDILKYDSTRRAVLRIPISNYIQLRNALTLVGDIYEGIPC-AYRIHNCAYLLNLLIGDSSLYIH-
 >Stylops_melittae-----MSNYFYFDISLELEANSTFKPSINNIINSHIQQSILKLFGEGLPHEFHILKYNAENRFIIRIPKDDFIKFHTALTLSDTFNHVPITTYRIHKITPFL-FLNSRSTFEY-
 >Megalurothrips_sjostedti-----MSKFFYLDVSLFEFDQKQSOVDAVAFKNYIWTAIRTLFGDFGASINVDLLKYNEKDRGIRCPAREYVKVRGSLTFCGKIQGTTC-RFLVHQSSSLTLGCGNSRNYKHC-
 >Hydroptila_sp._AD-2013-----MTYHYLDVTLDVNIQSAFNITPSSFMKNWMTNSVEELFGEIGGAIDIKLLKYNQEDKRAILRVQSNSEKLYAALTGKGYESFEC-AYRIHKTSQSLALTSSSLTYTH-
 >Zorotypus_gurneyi-----MNDYSYFDVSLLEVADE-NISISKNSFKRHVLSLNTLFGVEGESVDLKILKYNVQLHRGIIKCPAESAVKLHSALTLGKFDKYYS-VYKVHKSSTSLLSLAANSRTYNHVVK

>Drosophila_melanogaster
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>Leptinotarsa_decemlineata
MI-----KSRQLKRTKNS-----LNKPIKDREKKSEADRIDSDDEOGFSKWIRSEEGLDNLKLFVLGNTLIMFIAISWPQIKEVLDSAYLYVEFTERR--
>Aposthonia_japonica
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>Acanthocasuaria_muelleriana
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>Polistes_canadensis
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>Euroleon_nostras
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>Prosarthria_tetretirostris
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>Zorotypus_gurneyi
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>Drosophila_melanogaster
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>Homarus_americanus
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>Teleogryllus_commodus
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>Thrips_palmi
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>Hydroptila_sp._AD-2013
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>Atelura_formicaria
-----MMA-----FSRFLF-----EHTVDHSHAFVQR
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>Drosophila_melanogaster
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>Microphorus_vespilloides
-----MD-ILCNH-----LOVKM--IKIDNTF--LQNHQRETTGIKKLYNSFFVMF
>Trachymyrmex_zeteki
-----MRCSGVAMIFEDAFVVS-----RFLSL--KSRGCTL--LETHRQRETTGIKKLYNSFFVMF
>Papilio_polytes
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>>Osmylus_fulvicephalus
-----MDSGI-R-CHYCL-----VQIKM--NRIENSL--LQSHRQRETTGIKKLYNSFFVLF
>Xanthostigma_xanthostigma
-----MDTR--Y-FAFYF-----IQDKM--NTIENVL--LQSHRQRETTGIKKLYNSFFVLF
>Ceratophyllus_gallinae
-----MELKLLQDF-----S-STRIF-----VNKML--LKIENTL--LQSHRQRETTGIKKLYNSFFVLF
>Stylops_melittae
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HG0318 FBgn0035293 C65687

>Drosophila_melanogaster
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>Tribolium_castaneum
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>Copidosoma_floridanum
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>Boreus_hymalia
MKYRN-KSGDILQIQFRTFLIVESGKRS-----
>Corydalus_cornutus
MKYNC-SNRQIIQIQFRTFLDKRIIDNRILIR
>Osmylus_fulvicephalus
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>Oropsylla_silantiewi
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>Drosophila_melanogaster
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>Polymmatius_icarus
-----MRNSTTKQLSDQDLITLHSVFGPV-LORALEILEKQPLLEVYTT-ANKSRTLLEVKGKDLRYRIFPMVNFPCQAFKHQVLE-----KRIQLTCKHILAGKIALI---LGKTKEHEVT
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>Panorpa_vulgaris
-----MSKEKSTFLPHT---LVELIAKVKKSYSANKSFSEEDFLSLHSIFGTV-LEKALEILDRYN-ITVYRT-SS-SRGLIQVASH-DTYKLFQDVNYCQCAFQVQLG-----TQKQYTCKHVLAAILADI---TGKIIITEQIS
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>Annulipalpia_sp._AD-2013
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>Drosophila_melanogaster
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>Frankliniella_cephalica
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>Anguilla_japonica
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>Basilichthys_microlepidotus
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>Oryzias_melastigma
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>Tripterygion_delaiei
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>Seriola_quinqueradiata
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>Micropterus_salmoides
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>Pygocentrus_nattereri
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>Clupea_harengus
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>Apteronotus_leptorhynchus
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>Lutjanus_erythropterus
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>Plecoglossus_altivelis
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>Scleropages_formosus
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>Lateolabrax_maculatus
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>Gasterosteus_aculeatus
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>Solea_solea
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>Oncorhynchus_nerka
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>Ictalurus_punctatus
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>Pagrus_major
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>Takifugu_rubripes
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>Danio_rerio
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>Channa_punctata
-----MCTQDDSPFPFPPRRSKIK
>Anguilla_anguilla
-----MCARNYENPFPPVRRSKIK
>Menidia_menidia
-----MCTQDDNPFPHRRSKIK
>Opsanus_beta
-----MCTQDDNPFPPRRSKIK
>Oryzias_latipes
-----MCTQDDNPFPPRRSKIK
>Tripterygion_delaissi
-----MCTQDDNPFPTRRSKIK
>Micropterus_salmoides
-----MCTQDDNPFPPRRSKIK
>Pygocentrus_nattereri
--MSLDMRKDEENPFPPRRSKIK
>Haplochromis_burtoni
-----MCTQDDNPFPPRRSKIK
>Austrofundulus_limnaeus
-----MCLQDDNPFPLRRSKIK
>Esox_lucius
-----MCTRDDNPFPPRRSKIK
>Gadus_morhua
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>Apteronotus_leptorhynchus
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>Scleropages_formosus
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>Lateolabrax_japonicus
-----MCTQDDNPFPPRRSKIK
>Sebastes_caurinus
-----MCTQDDNPFPPRRSKIK
>Cynoglossus_semilaevis
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-----MCTRDDNPFPPRRSKIK
>Ictalurus_punctatus
--MVLDMHERDEEKSFARRSKIK
>Takifugu_rubripes
-----MCTQDDNPFPPRRSKIK
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>Danio_rerio
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>Channa_punctata
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>Menidia_menidia
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>Porichthys_notatus
---MFSPVKSSYFRV-SPAIVNRELGKTKMR
>Oryzias_latipes
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>Trachinotus_blochii
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>Micropterus_floridanus
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>Haplochromis_burtoni
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>Clupea_harengus
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>Poecilia_mexicana
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>Esox_lucius
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>Acanthogobius_hasta
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>Apteronotus_leptorhynchus
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>Lutjanus_erythropterus
---MFSPVKSSYFRV-SPAIVNRELGKTKMR
>Plecoglossus_altivelis
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>Scleropages_formosus
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>Lateolabrax_japonicus
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>Notothenia_coriiceps
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>Hippoglossus_hippoglossus
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>Salmo_salar
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>Takifugu_rubripes
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>Danio_rerio
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>Channa_punctata
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>Clupea_harengus
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>Acanthogobius_hasta
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>Lutjanus_erythropterus
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>Scleropages_formosus
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>Lateolabrax_japonicus
MSEVFVFLFLIFLAYLDT
>Sebastes_caurinus
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>Cynoglossus_semihaevis
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>Oncorhynchus_mykiss
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>Lepisosteus_oculatus
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>Danio_rerio
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>Channa_argus
-----MYLIQVKNHDCCH
>Menidia_menidia
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>Porichthys_notatus
-----MYLIQVKNHDCCH
>Oryzias_melastigma
-----MYLIQVKNHDCCH
>Micropterus_salmoides
-----MYLIQVKNHDCCH
>Pygocentrus_nattereri
-----MYLIQVKNHDCCH
>Haplochromis_burtoni
-----MYLIQVKNHDCCH
>Alosa_alosa
-----MYLIQVKNHDCCH
>Austrofundulus_limnaeus
-----MYLIQVKNHDCCH
>Esox_lucius
-----MYLIQVKNHDCCH
>Apteronotus_leptorhynchus
-----MYLIQVKNHDCCH
>Scleropages_formosus
-----MYLIQVKNHDCCH
>Lateolabrax_japonicus
-----MYLIQVKNHDCCH
>Sebastes_caurinus
-----MYLIQVKNHDCCH
>Cynoglossus_semi-laevis
-MLVYKPDFHFFPQLVMYLIQVKNHDCCH
>Salmo_salar
MLVYNPDFHFFPQLVMYLIQVKNHDCCH
>Ictalurus_punctatus
-----MYLIQAKRNHDCCH
>Takifugu_rubripes
-----MYLIQVKNHDCCH

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>Danio_rerio
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>Channa_argus
-----MSDGECDFFCFFRCC
>Menidia_menidia
-----MSDGECDFFCFFRCC
>Oryzias_latipes
-----MSDGECDFFCFFRCC
>Tripterygion_delaissi
-----MSDGECDFFCFFRCC
>Micropterus_salmoides
-----MSDGECDFFCFFRCC
>Pygocentrus_nattereri
-----MSDGECDFFCFFRCC
>Oreochromis_niloticus
-----MSDGECDFFCFFRCC
>Austrofundulus_limnaeus
-----MSDGECDFFCFFRCC
>Acanthogobius_hasta
-----MSDGECDFFCFFRCC
>Apteronotus_leptorhynchus
-----MSDGECDFFCFFRCC
>Plecoglossus_altivelis
-----MSDGECDFFCFFRCC
>Scleropages_formosus
-----MSDGECDFFCFFRCC
>Lateolabrax_japonicus
-----MSDGECDFFCFFRCC
>Anoplopoma_fimbria
-----MSDGECDFFCFFRCC
>Cynoglossus_semihaevis
-----MSDGECDFFCFFRCC
>Ictalurus_punctatus
-----MSDGECDFFCFFRCC
>Takifugu_rubripes
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>Danio_rerio
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>Amia_calva
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>Channa_punctata
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>Menidia_menidia
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>Porichthys_notatus
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>Oryzias_latipes
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>Tripterygion_delaiei
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>Pygocentrus_nattereri
-----MSFNFTGLQNK-----RGKGTLCVKEKQKEKRTGKOD-----
>Oreochromis_niloticus
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>Esox_lucius
-----MSFNFTGLQNK-----RGKGTSTVKENSKRGTFK-----
>Apteronotus_leptorhynchus
-----MSFNFTGLQNK-----RGKGTLSVVENRKKRTIKDII-SPKIFKQATKKRNILQIMRFHKLAI AFL-----
>Scleropages_formosus
-----MAFNFTGLQNK-----RGERGPCAALKKTERNGHKH-----
>Cynoglossus_semihaevis
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>Salmo_salar
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>Lepisosteus_oculatus
-----MSFNFTGLQNKD-----GKGDTLR-----
>Ictalurus_punctatus
-----MSFNFTGLQNK-----KKGDTVPAKTRKKDGGRRKKKRSRCNLTRKGRRTSRRLGFCOEVSVALF-----
>Takifugu_rubripes
MLLLSWAGISRRRMSFNFTGLQNK-----RGKGTPORVKGEKQE-----

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>Menidia_menidia
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>Oryzias_latipes
-----MMTEVVKMSTRRMKSSQL
>Tripterygion_dalaisi
-----MMTEVVKMSTRRMKSSQL
>Astyanax_mexicanus
-----MMMEVVKMSTRRMNSQL
>Neolamprologus_brichardi
-----MMTEVVKMSTRRMKSSQL
>Alosa_alosa
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>Kryptolebias_marmoratus
-----MMTEVVKMSTRRMKSSQL
>Esox_lucius
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>Gadus_morhua
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>Apteronotus_leptorhynchus
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>Plecoglossus_altivelis
-----MCSEVVKMSRRMKSAQL
>Scleropages_formosus
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>Lateolabrax_japonicus
-----MMTEVVKMSTRRMKSSQL
>Notothenia_coriiceps
-----MMTEVVKMSTRRMKSSQL
>Cynoglossus_semi-laevis
-----MMTEVVKMSTRRMKSSQL
>Oncorhynchus_mykiss
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>Takifugu_rubripes
-----MMTEVVKMSTRRMKSSQL
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>Danio_rerio
MRMVRREDSIQLIWKRCSTAAALHIARGNR-LESR-----
>Channa_argus
-----MNRNQTKWKRCSVAAAFHIARTNARVETR-----
>Menidia_menidia
MRMVRGDRNQTKWKRCSVAAAFHIARTNVRVESR-----
>Oryzias_melastigma
MRMVRRYRSQTKWKRCSVAAAFHIARTNDRLESR-----
>Tripterygion_delaissi
MRMVRRSRNQTKWKPCSGAAASPIARTRVGTR-----
>Micropterus_floridanus
MRMVRRYRNQTKWKRCSVAAAFHIARTNVRVENR-----
>Pygocentrus_nattereri
MQMVRREERSQPEWKRCSTAAALHIARRNR-VENR-----
>Maylandia_zebra
MRMVRRYRNQTKWKRCSVAAAFHIARTNVRVENR-----
>Alosa_alosa
MRMVRGERLPRKWKQCSNTATFHVARTNWIENR-----
>Austrofundulus_limnaeus
MRMVRRYRNQTKWKRCSVAPAFHIARXNVRVENR-----
>Esox_lucius
MRMVRDRDIQTKWKQCSIAAFHIARTSRVENR-----
>Gadus_morhua
MRMVRRARNQTKWKRCSLDAVPHIARRHVRVETR-----
>Apteronotus_leptorhynchus
MRMIREQRSETKWKQCSFTAAAFHIDWKHR-LGNR-----
>Plecoglossus_altivelis
MRMVRRERIQTKWKQCSIAAFHIARTRV--GNR-----
>Notothenia_coriiceps
MRMVRRYRNQTKWKRCSDAAAFHIARTNVRVENR-----
>Salmo_salar
MRMVRDRDIQTKWKQCSIAAFHIAISTTRVENRELVNKYGNVTYLSEKLQGSIVNWFK
>Takifugu_rubripes
MRMVRPSRNRAGWEACSVAVAFHIARYSARVESR-----

>Danio_rerio
MDEVDLTVFVCH--HQCLPLSNCVLFFVYVKRTPPLLGSGPL-HCKSNC-----
>Acipenser_sinensis
MDGVVWTVLVSQ--CLRLLFCDCILFFSNYKRTPPVQGPDP--HCNCIHCPY-
>Amia_calva
MDGVDLMVLVCO--HPCLIFCDSVLFFSIYKRTPLQGPDPV-RCKILNFLC-
>Menidia_menidia
MDGVDLKRLEYQ--QQHPAFSCSVLSLIFKRTPPLHHQSPNYICKDIL---
>Pygocentrus_nattereri
MDGVDLTVLVCH--HQRLLLCDCVLFFIYKRTPPLSSDHK-YCNSNCL---
>Clupea_harengus
MDGVDTVVLQCP--LQCLPVDCVLFFSIYKTRPIQGFQPV-CCLYSRNCSC
>Kryptolebias_marmoratus
MDGVNLKILLYR--HQCSAFCCSVRSFSTYKRTPPIIHPQSLRYIYKDSL---
>Esox_lucius
MDGVDLTVLVCH--HORLLLCDCFLFFSIYKRTPPLGPTTPPERCKSNRDCCC
>Acanthogobius_hasta
MEENYLK---SP--PRHCGLYNSDQSFSNYKRTPPLHIVNL-HCKSRNYKQ-
>Apteronotus_leptorhynchus
MDGVDLTVLVCR--HQCLLLCDCILFFVYKRTPPLGLQPT-YCISNCL---
>Plecoglossus_altivelis
MDEVDLKSIVCL--HPCPPFCDCVL-FSIYKRTPPVLHLHRE-PCLHSNWL---
>Scleropages_formosus
MGCVDLMVLVCGQHQCLLFCDGVLFFSTYKRTPPLVGPDPV-WCKSIRYFC-
>Lateolabrax_japonicus
MDGVDLKRIVYQ--QQHSEFCGVSQFTIYKRTPPLHLQSLHYIYKDRL---
>Trematodus_bernacchii
MDGVDLKRIVYQ--HQHSVFFCGVSQFTIYKRTPPLYPQSLHYIYKDRQ---
>Oncorhynchus_mykiss
MDGVDLTVLVCH--HORLLLCDCFLFFSIYKRTPPLGPTTPPERCKSYSNYCC
>Lepisosteus_oculatus
MDCVNLMLIVCL--HQHLIFCDILFFFIYKRTPPLQGPDP--HCKILSFHC-
>Trichomycterus_oreolatus
MDGVDLTLLIYH--RQRLCLSDCILFYAYKRTPPLG-----

```
>Danio_rerio
MYATLSVSSIMAEDPGGAFFNFTLLITDFSLPLL---ERWQG---
>Channa_punctata
-----MAEDPGGTFNFSSIFLFFSLPQLAETWQDRKPR
>Oryzias_melastigma
-----MAEDSGGTFNFYLIFLPFVPKLVETWLDL---
>Micropterus_floridanus
-----MAEDPGGTFNFSLIFFSFSLPPLAETWQDSQAR
>Pygocentrus_nattereri
-----MAEDPGGAYRIFSFIFLRFSPLL---QTWQGAQSR
>Neolamprologus_brichardi
-----MAEDPGGTFNFSVIFLSFSLPQLAETWQDSQSR
>Cyprinodon_variegatus
-----MAEDPGGTFNLSVIFLSFSLPRLAETWQDSQAR
>Esox_lucius
-----MAEDPGGTLNFSPTFFSLLLVETWQDTQP-
>Gadus_morhua
-----MAEDPGGTLKFTOFFISFYLGLLVETWQHTQSR
>Scleropages_formosus
-----MAEDPGGPYFNLSFIFLSFSLLVVPTWQEPQLR
>Lateolabrax_maculatus
-----MAEDPGGTLFKFSLIFLSFSLPLP-----
>Sebastes_caurinus
-----MAEDPGGTFNLSSFIFLSFSLPPLAETWQDPQAR
>Scophthalmus_maximus
-----MAEDPGGALFNFSTIIFLSFSLPRLAETWQDSHPR
>Salmo_salar
-----MAEDPGGTIFNFSPTFFLFSLPLLVETWQDTQPR
>Lepisosteus_oculatus
-----MAEDPGGVDFNFSFISFRFSLLVVATWQEPQSR
>Ictalurus_punctatus
-----MAEDPGGAYFNFSLNFOLLPL---ETWGTQSR
>Takifugu_rubripes
-----MAEDPGGTISNFSLFFLFALPPLAETWQDSQVC
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>Danio_rerio
MKRNSVYRFLSVFSCLLVCVFLF-FWGFAFYSMVLAP--
>Amia_calva
MKRNGVYQFFSVFSCLVVFLFLFWFFVFYTMVMT--
>Channa_argus
MKRNGAYRFLSVFSQFVCAFLFLFWFFIFYSVLAP--
>Menidia_menidia
MKRNGAYRFLSVFSQFIVCVFLFLFWFFVFYSMMHAP--
>Porichthys_notatus
MKRNGAYRFLSVFSQFVVCVFLFLFWFFVFYSVLAP--
>Oryzias_melastigma
MKRNGAYRFLSVFSQFIVCAFLFLWFSVFYSMLRAP--
>Pygocentrus_nattereri
MKRTGAYRFLSVFSCLLVCVFLFLFWFFVFYSMVLAP--
>Haplochromis_burtoni
MKRNGAYRFLSVFSQFIVCAFLFMFWFFVFYSMVLAP--
>Poecilia_formosa
MKRNGAYRFLSVFSQFVVCVFLFLFWFFVFYSMVLAP--
>Esox_lucius
-MRSGAYKFLTVFSCLIVCGFMFMFWFFVFYSFAP----
>Apteronotus_leptorhynchus
MKRDGAYRLLSVFSCLVIFVFLFFWVFVYSMVLAP--
>Plecoglossus_altivelis
-MKRNGAYKFLSVFSQFVVCVCAFLFLFWLFFIFYSMMLAP--
>Scleropages_formosus
MKK1CAYRLLSVLSCVGI CLFLFLFWFFVFYTLVMAP--
>Lateolabrax_japonicus
MKRNGAYKFLSVFSQFIVCAFLLLFWFFIFYSMVLAP--
>Platichthys_stellatus
MKRSGAYRFLSVLSFFAVCASLLLFWF11FYTMHVT--
>Trichomycterus_areolatus
MKRNGAYRFLSVFSQFAVCAFI1FWFFVFYSMFLAPEN
>Takifugu_rubripes
MKRNGAYKFLSVFSQFIVCAFLFI1FWFFIFYSMVHAP--

>Danio_rerio
MQEIAAIL-----SAAODGRFLLSCEQCCRFIFCHE
>Porichthys_notatus
MRE---ATADTRSSLQDGRFLLSFVKARFLLLP-
>Astyanax_mexicanus
MQETAAIL-----SAAODGRFLLSSELKYLFIKCHE
>Oreochromis_niloticus
MQETAS-----TLSSAFODGRFLLSFEQKYRFIFCHE
>Kryptolebias_marmoratus
MQETAATLSSPSSLFQDGRFLLSFQKARFIFCHE
>Esox_lucius
MQETATL-----SVAODGRFLLSSEQKSRFIFCNE
>Acanthogobius_hasta
MQEIAATLSSP---VSODGRFLLSFERKSRCTPLP-
>Plecoglossus_altivelis
MQETATL-----TVAODGRFLLSSEISLYFLP---
>Scleropages_formosus
MQEEPLL-----SADODGRFLLSSELRSPPTIYLP-
>Notothenia_coriiceps
MQETAA-----TLSSLFODGRFLLSFEQKSRFIVLP-
>Cynoglossus_semiarctus
MQENTATL-----SSODGRFLLSFEONRRFIFCHV
>Oncorhynchus_kisutch
MQETATL-----SGAODGRFLLSSEQISRFIFCHE
>Lepisosteus_oculatus
MQETATL-----TVAODGRFLLSSKLSRFIFLP-
>Trichomycterus_areolatus
MR-----DQDRIVSAAODGRFLLSSGLKDLLTVLQ-
>Takifugu_rubripes
-MNWASNAATLSSALQDGRFLLSSEKKPLFIFLP-

>Danio_rerio	-----MTSLCGYHRNQGSTADG-----
>Anguilla_japonica	-----MTSLHGYHRNQGSPSANG-----
>Trachinotus_blochii	-----MTSLLGFNKSQSSTADG-----
>Micropterus_floridanus	
MRVKLFROEKQHGLLCFGSFLLCDMTSVLGYNRSQSSTAAGGRHLVRCVFLQCKALPRQSPQ	
>Astyanax_mexicanus	-----MTSPSGYHRNRRSTADS-----
>Maylandia_zebra	-----MTSRLGYKRSSSTADG-----
>Alosa_alosa	-----MTSPCGCHRNQGC PADG-----
>Esox_lucius	-----MRS LHGYHRNQGSTVDG-----
>Acanthogobius_hasta	-----MTSLIEYTRNQGSSSDG-----
>Apteronotus_leptorhynchus	-----MTSPSSCHRNQGSTADS-----
>Plecoglossus_altivelis	-----MTSLHGYHRNQGSTAHG-----
>Lateolabrax_japonicus	-----MTSLLGSNKSQSSTADG-----
>Anoplopoma_fimbria	-----MTSLFGYNKSQSSTADG-----
>Oncorhynchus_mykiss	-----MTSLSGYHRNQGSTAEG-----
>Ictalurus_furcatus	-----MTSSSGCHRNQGSTADS-----

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>Danio_rerio
MWIVIALEEKFDLLNNVVRGPASWILVFLDILKIIGNS
>Channa_striata
MWIATPLQDDKSLLRNNVRRCASWILVFLDILKIIGNS
>Porichthys_notatus
MWIATALKENKOLLRNNVTRRTSWILVFLDILKVVGNS
>Oryzias_latipes
MWIATP-QESODLPNDVRRCASWILVFLDILKIIGNS
>Pygocentrus_nattereri
MWIVIPFEEILDLLQNNVRRGFASWILVFLDILKTVSNG
>Ophthalmodon_ventralis
MWIATPLQENKOLLRNNVRRCASWILVFLDILKIIGNS
>Poecilia_latipinna
-----MWRENKOLLRNDVRRCASWILVFLDILKIIGNS
>Gadus_morhua
MWIATPLQENDSLLQNNVKRYASWILVFLDILKNIIGNS
>Apteronotus_leptorhynchus
MWIVILFEENISLPENNVRRGFATWILVFLDILKIIGNS
>Notothenia_coriiceps
MWIATPLQEDKGLLRNNVRRFASWILVFLDILKIIGNS
>Scophthalmus_maximus
MWIATALQENTGPLRNNVRRYASWIFVFLDILKSIIGNS
>Oncorhynchus_mykiss
MWIATSFENKGLLQNNVKRYASWILVFLDILKIIGNS
>Ictalurus_punctatus
MWIVRAFEOKLSLRDHVSGFASWILVFLDILKIIGNS
>Takifugu_rubripes
MRILISLQENKGLRKNVTSASWILVFLDILKIIGNS

>Danio_rerio-----MRV1YVQAGVVAASFPEIFCGRLK-----QRNNGEIMTERATGKTRHNGVGYIME
>Channa_argus-----MRSCTWAVDKMRVIFIQNAGFVAAFSPRRCESVMLAAFRITTDNVNEAAELTTARSCQS-----SEE
>Menidia_menidia-----MRSRTWAADKMRVIFIQNAGFVAAFSPFS-----
>Oryzias_latipes-----MRCSTWAVDKMRVIFIQNAGFVAAFSPFS-----
>Pundamilia_nyererei-----MRSFTWAVDKMRVIFIQNAGFVAAFSPFS-----
>Clupea_harengus-----MRV1YIQNAGFVAAFSGGNDG-----
>Kryptolebias_marmoratus-----MRVLFTQNAGFVAAFSPLL-----
>Esox_lucius-----MRV1FIQNAGFVAAFSGGNDAEGFAC-----
>Apteronotus_leptorhynchus-----MRV1YIQNAGCVAAFSGSNDG-----
>Notothenia_coriiceps-----MRSCTWAVDKMRVIFIQNAGFVAAFSPRRCESVMLAAFRITTDKVNPELTTARSCKS-----TEE
>Cynoglossus_semilaevis-----MRVYTWAKDKMRVIFIQNAGFVAAFSPRRCESVTLAAFRVTNTA-EEPELNTNKSCQS-----AE-
>Salmo_salarMA1FKTSELD1SDHSASLKSTWAWSTCAIHRVQGLNDVAPEDKMRVIFIQNAGFVAAFSGGNDAEGFAC-----
>Takifugu_rubripes-----MNGOPHLDKMRVIFIQNAGFVAAFSPRRRESVMSAAFRITTDKVTDLQ-SASAGSCQA-----IKE

>Danio_rerio-----MFLHRADLSLRPRTKYRDS-----
>Channa_argus-----MFLHRADLNLSPRTKRFPLVRLRVGFLLPERSWRQTGGV-----
>Micropterus_salmoides-----MFLHRADLNLSPRTKRFPLR-----
>Oreochromis_niloticus-----MCLHRAHLNLSPRTKRAPLR-----
>Alosa_alosa-----MCLHRLDSNLRPRTKYRGLH-----
>Esox_lucius-----MFYHRADLSLRPRTKYRDFH-----
>Lutjanus_erythropterus-----MCLHRADLNLSPPTKRFPLR-----
>Plecoglossus_altivelis-----MFLHRTDLSLRPRTKYRDFH-----
>Lateolabrax_maculatus-----MFLHRADLNLSLRTKRAPLI-----
>Salmo_salar-----MFHYRADLSLRPRTKYRDFH-----
>Ictalurus_punctatus-----MIAGARSLGGSGGRSCSMFHHRANLSLRPRTKYRAFD-----
>Sparus_aurata-----MFLHRADLSFSRPTKRVPLK-----

>Danio_rerio
MLTCRGSSPPQSAVIGCWME
>Channa_argus
-----MIGCWME
>Pygocentrus_nattereri
-----MIGCWME
>Neolamprologus_brichardi
-----MIGCWME
>Alosa_alosa
-----MIGCWME
>Poecilia_reticulata
-----MIGCWME
>Esox_lucius
-----MIGCWME
>Lateolabrax_japonicus
-----MIGCWME
>Trematomus_bernacchii
-----MIGCWME
>Salmo_salar
-----MIGCWME
>Ictalurus_punctatus
-----MIGCWME

>Danio_rerio
MNPDLFMPVQWAGPCCPVRTGPKPPFVLFCWVNLNPEQRHSRKRVOHT---
>Menidia_menidia
MNPDI FMSVLRAEPRCPARTGPKPSFVLFCWAKLNSEQRHSREGIVRTQTR
>Oryzias_latipes
MNPDI FMSALWAEPRCPARTGPKPSFVLFCWAKLNSEQRHSRDGVST----
>Pygocentrus_nattereri
MNPTSFMSVQWAGSRCPARTGPKPPFVLFCWAE LNPEQRHSRKRVOHT---
>Oreochromis_niloticus
MNPDSFMSVLWAEPRCPARTGPKPSFVLFCWAKLNSEQRHSREGIKRT---
>Alosa_alosa
MNL SQFMGFLWTEPCSPARDGPKPTFVLFCWAE LSPEQRHLCKGATHT---
>Kryptolebias_marmoratus
MNPDI FMSLLWAEPRCPARTGPKPSFVLFCWAKLNSEQRHSREGIERT---
>Esox_lucius
MNPDI FMSVLWAEPRCPARTGPKPTIVLFCWAE LNSEQRHSRKGIKHT---
>Lateolabrax_japonicus
MNPDI FMSVLWAEPRCPARTGPKPSFVLFCWAKLNSEQRHSHKGIERT---
>Platichthys_stellatus
MNPDI FMSVLWAEPRCPARTGPKPSFVLFCWAKLNSEQRHSHKGIERTFL-
>Salmo_salar
MNPDI FMSVLWAEPRCPARTGPKPTFVLFCWAE LNSEQRHSRKGIKRT---

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```
>Danio_rerio
--MQRLGTYKLHEKPPNKGR--
>Channa_punctata
--MPRSGLHKLHAKPPNLRVYQ
>Menidia_menidia
--MPRFGHLHKLHAKPPNIRD--
>Neolamprologus_brichardi
--MPRFGIHLHKLHAKPPNLR--
>Poecilia_reticulata
--MRRFGLQKLHAKPPNLRDY-
>Esox_lucius
--MQTFGPYKLHEKPPNPRR--
>Anoplopoma_fimbria
--MPRFGHLHKLHAKPPNIRD--
>Oncorhynchus_masou
--MQTFVPYKLHEKPPNPRR--
>Ictalurus_furcatus
MYMYKLGTYKLHEKPPNHGR--
```

>Danio_rerio-----MMTRIWSYFVPWKRGR
>Amia_calva-----MMFIWYFVPWKRGR
>Anguilla_japonica-----MMFIWYFVPWKRGR
MSLLFFNYIQKDVHLMMLVWYFVPWKRGR
>Alosa_alosa-----MMILWAHFVPWKRGR
>Esox_lucius-----MMFIWYFVPWKRGR
>Apteronotus_leptorhynchus-----MDFYPMIYYAYFLPWKREKR
>Plecoglossus_altivelis-----MMLIWAYFVPWKRGR
>Salmo_salar-----MMFIWYFVPWKRGR
>Lepisosteus_oculatus-----MLIWAYFVPWKRGR

```
>Danio_rerio-----MYDRLDPRVERRLLSKRQTGSAA
>Amia_calva
MQSETSLLDGGRKRSRDRPGLFLLYITGLVEVFLKMYDRLDPRGELEGLSODKVGSAV-
>Alosa_alosa-----MYDRLDPRVDRGRLESHKMGSAV-
>Esox_lucius-----MYDRLDPRRERRHVSKGIIGTVV-
>Apteronotus_leptorhynchus-----MYDRLDPRVERRRLLSRHKMGSAV-
>Scleropages_formosus-----MYDRLDPRQEAEGSSEHTSGCAAV
>Salmo_salar-----MYDRLDPRRPRRVSKGIIGSVV-
>Lepisosteus_oculatus-----MYDRLDPRGEREGLSODKVGSAV-
>Trichomycterus_areolatus-----MYDRLDPRVERRRLLSEHIMGSAV
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>Danio_rerio
-----MDYSRTDANLGFPTLLP-----
>Menidia_menidia
-----MPVMDYGRTSANLGIWHS-----
>Porichthys_notatus
-----MSVMDYSRTDANLSRHSQSSIRLH
>Trachinotus_blochii
-----MPVMDYSRTDANLSIWSQNSIPPY
>Micropterus_floridanus
-----MQVMDYSRTDANLSIWSQNSIPPY
>Pygocentrus_nattereri
-----MDYSRTYANLGFPAKLSP-----
>Alosa_alosa
MKRVGYCKVPVQAQAMDYSRTDANLGFPAKLSS-----
>Notothenia_coriiceps
-----MLVMDYSRTDANLSIWSQNSIPPY
>Ictalurus_punctatus
-----MPVMDYRRTDANLAFSAEVSP-----

>Danio_rerio
MAEDYWERAALGYYYCC
>Acipenser_sinensis
MAEDYWESTAALGKH---
>Amia_calva
MAEDYWETAAPGHY---
>Astyanax_mexicanus
MAEDYWEHTAALGHC---
>Clupea_harengus
MAEDYWESTVALGYC--
>Esox_lucius
MAEDYWESTVALGYC---
>Salmo_salar
MAEDYWESTLALGYFC--
>Lepisosteus_oculatus
MAEDYWELPAARGHY---

HG0345 ENSDARG00000035910 znf281b

>Danio_rerio
MEEANSCKGTLFWL
>Channa_punctata
MEEPSSCKRTMFWL
>Trachinotus_blochii
MEEPSSCGKTMFWL
>Micropterus_salmoides
MEEPSSCGRTMFWL
>Astyanax_mexicanus
MEEGNSCERTMFWH
>Maylandia_zebra
MEEPSSCGRTMFWL
>Notothenia_coriiceps
MEEPSSCGRTMFWL
>Ictalurus_punctatus
MEEGNSCRRTMFWQ

>Danio_rerio-----MFVCTVAASASAGKQMDSSAQVPNIIDLLLWNNMKGVVMDSCPAHG-----
>Channa_punctata-----MQMDRSRQVPNIELPVWYSY-----
>Oryzias_melastigma-----MDRSQVSSIGLPVWSST-----
>Pygocentrus_nattereri-----MDSRQPPNIIDLLLWNYLK-----
>Apteronotus_leptorhynchus-----MDRSRQAPHIGLLLWN-----
>Lateolabrax_maculatus-----MQMDRSRQVSNIELPVWYSY-----
>Notothenia_coriiceps-----MQMDRSRQVSNIELPVWYSY-----
>Lepisosteus_oculatus
MRKILKRKGEEGSELTAELQRRVLLSVSSVGNASDNEDQNGTQMDSSRQTSSIDLLFWNYLKSFN-----

>Danio_rerio-----MADLSKSKPGLK---

>Pygocentrus_nattereri-----MADLSKSNPGLK---

>Oreochromis_niloticus-----MADLSKSNPGLK---

>Poecilia_formosa
MGEEYEMDSVQRANRVDDVKMADLSKSNPGLK---
>Apteronotus_leptorhynchus-----MADLSKSNPGLK---

>Cynoglossus_semi laevis-----MADLSKSNPGLK---

>Salmo_salar-----MADLSKSNPGLK1ET

>Lepisosteus_oculatus-----MADLSKSNPGLK---

HG0348 ENSDARG00000036139 lctla

>Danio_rerio
MSFLLAALDKLAYLLSLVAFCVSLSYSWLK
>Opsanus_beta
MSLILTVLDKLAYFLSLVAFCVSLSSWMK
>Pygocentrus_nattereri
MSFLLAALDKLTYFLSLIAFCVSVSYSWLK
>Oreochromis_niloticus
MSLILTVLDKLAYFLSLIAFCVSVSYSWLK
>Fundulus_heteroclitus
MSLILTVLDKLSYFLSLVAFCVSASHGWLK
>Esox_lucius
MSLLLTVLDKLTYYLLSLIAICVSASNSWLK
>Salmo_salar
MSLILTVLDKLTYYFLSLIAFCVSVSYGWLK

>Danio_rerio-----MHQSWLTLVAACLVKQVAVQ
>Channa_punctata-----MVFVSFFVFIIF-LYFGREHLLTAQRNHIMHQSWMKLVAACL-----
>Micropterus_dolomieu-----MLQSWIKPVAACL-----
>Alosa_alosa-----MHQSWMLVPACL-----
>Apteronotus_leptorhynchus-----MQESWFMPPVAACL-----
>Notothenia_coriiceps
MFVCRKLCFSLAAQTITQPLTAEHRNHIMFQSWIKPVAACL-----

```
>Danio_rerio-----MQVDIISHTCPCHSGSPCSRLKPRYLLPSRNGKKIFP-----
>Lipochromis_sp._matumbi_hunt-----MGGNNMVTWRSGERRSWIDSAQATAEMNSEWCS-----VCMPLDLISPTCPCHSDSQAR-----
>Poecilia_reticulata-----
MLLFGRGKISASPGINTLADISRFCELRVLVGHIIHMDAPVRENRRGGKAVTWRCGERRSWMGRAQATAEMSRRERWS-----VCKPLDLISPTCPCHSDSQPR-----
>Esox_lucius-----MALDLISPTCPCHSDTPRS-----
>Apteronotus_leptorhynchus-----MSSLMTGQKEGGFCVTSQCRERLSWTAKEQGTAEMKSERCALCENVCMQVDIISPTCPCHSGFIAARGMKLR-----
>Platichthys_stellatus-----MINTERCG-----VCMPLDLISPTCPCHSDSQQR-----
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>Danio_rerio
MRTKPCFLWLNSQTSLSCTLSSGI--
>Pygocentrus_nattereri
MLTOPCFLWLNSQTTISCTINSVAV--
>Esox_lucius
MLTOPCSLWLNSQTPPTHIVPSDYSD
>Apteronotus_leptorhynchus
MLTOPFLLWLNSQTTTRSCTVNSAV--
>Salmo_salar
MLTOPCSLWLNSQTPPTHILRSD---
>Ictalurus_punctatus
MHTQPCFLWLNSLTTLTCITSSDS--

>Danio_rerio
MGNIIQVLPKFRQDLTQAWRRGTHLPLFLDL-----
>Astyanax_mexicanus
MGNIIQMLPKFRQDLKQARRGVMHLPLLLNL-----
>Alosa_alosa
MGSIIQMLPKYRQDLSRAWSTGMHLPFLSDL-----
>Esox_lucius
MENILELLPKHRQGLTCANGRAATHTCRGRTCSLVAPSNLFFITT
>Salmo_salar
MENILELLPKHRQEGTHANGRAATHTCRRKSSLVAPLNRRFFITT
>Ictalurus_punctatus
MGNIIQMLPKFRQDLMQSLERAKAPASFTQPVREL-----

>Danio_rerio-----MANMHTRLGWKKHADVNPMSLEECEP
>Astyanax_mexicanus-----MQTMPEWNGPTSVTPFMSWEEGEDP
>Alosa_alosa-----MAKMCTRLAWSKAVLLTPHKTWDEGERDP
>Esox_lucius-----MAQMGARMVWGKGLVTPHMTWNKEECDP
>Salmo_salar-----MAQMGARTVWGKGLVTPHMTWNKEECDP
>Trichomycterus_areolatus
MSFFKTTTRVKQSI NELSDGKVSSVTLLTTVRNISLMAMMQTRLEWNGPTCMNPFMSAKEGKCDP

HG0354 ENSDARG00000019897 gpat4

>Danio_rerio
MIIIFPYMPKSMFQRRLOKL R HSRGVQGSVFR
>Astyanax_mexicanus
-----MKALFORRLQKLRL-----
>Esox_lucius
-----MKALFORRLQKLRLYMD-----
>Apteronotus_leptorhynchus
-----MKTLFORRLQKLRL-----
>Ictalurus_punctatus
-----MKALFORRLQKLRL-----

HG0355 ENSDARG00000019930 ta11

>Danio_rerio
MDDPPQNGSMHTLTSTARRR---
>Acipenser_sinensis
MDGPTQNGSTQFLTSTKYKR---
>Amia_calva
MDGPPQNGSTHGIIISTHNR---
>Osmerus_mordax
MDDHRQNGSTHTPSTTFKQRLRT
>Salmo_salar
MDDPRQNGSTHTLSTTLRLW---

HG0356 ENSDARG00000020475 znrf1

>Danio_rerio
MIRPGKWAVASARHSCFSQT
>Alosa_alosa
MFRPGERAVASHRHWSQT
>Esox_lucius
MFRSGKWAVASVRHSCFSQT
>Salmo_salar
MFLSGKWAVASVIHSCFSQT
>Ictalurus_punctatus
MIRPRKRALASPGHSCFSQT

>Danio_rerio
MSAGHAHHLSIRVPLLNL-----
>Oreochromis_niloticus
MSAGHAYRLSIHVLLTTSGVGL-----
>Cyprinodon_variegatus
MSAGHT-----
>Esox_lucius
MSAGHAQPLSIHVPLLTTIRVSIQMORDRYSAPRRQHPGLYDKAKKRL
>Salmo_salar
MSAGHAQPLSINVPLLTTSRVGI-----

>Danio_rerio
MAALTVSCRVYAFFR-----
>Pygocentrus_nattereri
MAALTVSCGVYAFRL-----
>Alosa_alosa
MAALTLSCRVYYFLR-----
>Plecoglossus_altivelis
MAALSVSCFFVFFNIADKSEIHSFTLESKKLK
>Ictalurus_punctatus
MAALTVPCRACAFRL-----

```
>Danio_rerio
-----MSASYCPYPLRHKGDCFESKEKQDK
>Astyanax_mexicanus
-----MSASYCPNPLRRKRDCFKT-----
>Alosa_alosa
-----MLLIF-----LPPQKMSASYCPYPSRKKRNCKTKE-----
>Apteronotus_leptorhynchus
-----MSASYCPYPLRHKRDCLKT-----
>Ictalurus_punctatus
MTGRLESIIIMLPIFSLLPPTSQKMSASYCPYPFRRKRACFKT-----
```

>Danio_rerio
MCP1WKDELNFILQRDPKLIYICH-
>Pygocentrus_nattereri
MPP1WKDELQFVLK-----
>Clupea_harengus
MST1WKDDLNCVFTFKLKKLYICQL
>Cyprinodon_variegatus
MCPVWKDELNCTRR-----
>Anoplopoma_fimbria
MCT1WKDELNRA-----

HG0361 ENSDARG0000077581 zzz3

```
>Danio_rerio
MCSKRFAEVRCPHTAAEERAPR---
>Oryzias_latipes
--MFIIIGQTRCPHSAAEERAPG---
>Haplochromis_burtoni
----MSPAGRCPHLAAEERAPR---
>Apteronotus_leptorhynchus
MCSRRF AEVRWPHSAAEESTIMRSQ
>Ictalurus_punctatus
-----MRCPYSAEESTIMRSQ
```


>Danio_rerio
MSF1SHRNCRTEENLRNVFNLF-----
>Esox_lucius
MSF1LQRNCRTEENHRTQFPISLTTVSGELTTM-----
>Apteronotus_leptorhynchus
MSF1SHRNCKDGENFRNVSACFSKLLMGINCYELKFLKPIK
>Scleropages_formosus
MSF1LQRSCRTENLRTHFNLSLFKQMGN-----
>Salmo_salar
MSF1LQRNCRTEENLRTHQFPISLTTVSGELTTM-----

>Danio_rerio
MRYNLPALKKFLQKGGDQQTYS
>Alosa_alosa
MRHNLPAKKFLRKGGGLHQTYS
>Esox_lucius
MRYNLPARKK-----
>Notothenia_coriiceps
MRYNLPARKKRL-----
>Cynoglossus_semi laevis
MRYNLPARNR-----

HG0364 ENSDARG0000004988 ppp3ca

>Danio_rerio
MPLHQPHLVTANTRRE
>Alosa_alosa
MPLHQPHLAPAKTYRE
>Esox_lucius
MPLHQPHLATAKTHRE
>Salmo_salar
MPLHQPHLATAKTHRE

HG0365 ENSDARG00000016132 keap1a

```
>Danio_rerio
-----MPTWLETESCYSGLLTRQKKHGSLSLNDNQLCLYFFMARGWV
>Pygocentrus_nattereri
MYHSVMPLWSEMDHCHDGLRTRQKKHGSLSPSDHQLCLYFFMTRGWV
>Apteronotus_leptorhynchus
-----MPIRSETVPCHHGLQTRONKRSSLSPSDHQLCLYFLMTRGWV
>Trichomycterus_areolatus
-----MPIWSAQDP SHDGLRLRLKKPGSLSPSDHQLCLYFFMARGWI
```

HG0366 ENSDARG00000017803 gsk3b

>Danio_rerio
MELSGSERP-RISVLKLGNNKILIRIAG
>Pygocentrus_nattereri
MELAGAERP-RVSVSKPGNNKTLRLILG
>Apteronotus_leptorhynchus
MELRGTERP-WISVFKLGNNKILIRIVG
>Ictalurus_punctatus
MELRGAEVQWWISVFKSGDW-----

```
>Danio_rerio
-----MFTVLPRTDFKETMRSTRGRSLVGFH-----
>Astyanax_mexicanus
MKNVCLFAPFPKTDLEETMRSLRGRFAVAFWIQ-----
>Esox_lucius
-----MSAVLPKTDQKEAMRGGGSCQAVLWIQLLGF-----
>Ictalurus_punctatus
-----MRSPTGRSALADQIQYEACVCACICERVSECACMRAHAITSCLMHAVMCSTPQKEEP-----
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HG0368 ENSDARG00000058606 sik1

>Danio_rerio
MTCKCKCKNHLCGGRRWKLFAS
>Clupea_harengus
MTCKSAVNLFDGGRRWLFVC
>Chanos_chanos
MTCKFVSKSDFSCGGRRWLFVY
>Apteronotus_leptorhynchus
MTYKYASENHFGCERRWLLVL

HG0369 ENSDARG00000059276 hoxd4a

```
>Danio_rerio
-----MKSLHLDWPSWSHGRLTLFS
>Pygocentrus_nattereri
MASSALIGFLHLDWPSWSHGCPILFS
>Lateolabrax_japonicus
-----MDQHLLYWPISRSHGSLTLFS
>Sebastes_caurinus
-----MNQHLLHWPISRSHGSLTLFS
```


HG0370 ENSDARG00000062693 nr_xn3b

>Danio_rerio
-----MWNQNNRIRSNMENLFCNPERRLKGTSVVKHF--
>Pygocentrus_nattereri
MLSFTMQRYCRVKSNMEDLCYKPGSRFKRMSSGKQIGH
>Esox_lucius
-----MGHGCGSEAKMATVCFNPCSRLKGNSSNGSLYH
>Salmo_salar
-----MVAVCFNPCSRLKGKSSDGPLYH

HG0371 ENSDARG0000062765 whsc111

>Danio_rerio
-----MEHAEAGPVRKRET
>Pygocentrus_nattereri
-----MEH-AEGPVRKRET
>Alosa_alosa
MIVHLCEQKQGSNIWHLFRMEH-AEGPVRKRET
>Scleropages_formosus
-----MEH-AEGPVRERET

HG0372 ENSDARG0000069467 igsf9bb

```
>Danio_rerio
MQGMSKRVSAAADSASNDQGLG-
>Apteronotus_leptorhynchus
---MSKRISADDASNVLGARL
>Lepisosteus_oculatus
---MSKRVLAGDCANTVQGARR
>Ameiurus_nebulosus
---MSERTPAAASASSIPGARL
```

```
>Danio_rerio
MTVALRSAEAVINALGFLFEVFLFFITLSSRLRMCLLCLSF TALHGCFR-----
>Pygocentrus_nattereri
-----MRLCLSF TALHCPVPDRKCAVGRH
>Apteronotus_leptorhynchus
-----MIALKMCLLCLSF TAPHCPVPGGTSAEGRH
>Trichomycterus_areolatus
-----MCLLCFSCTALHCPVAGRKCAVGRH
```

>Danio_rerio
MISWKIELRVFVAAFRCTSLCRLQSRQGGKMPSRQT-----
>Pygocentrus_nattereri
MISWKTAFRVFVAVVRSRSFFSL-----
>Esox_lucius
MISWKTLFRVSLA-ARWPGLCRLHTKRRKDASARTLTPFFLLPPPLP
>Apteronotus_leptorhynchus
MISWKVASHISVA-VRFWSFQRL-----

>Danio_rerio
MGKDLFSSYP-----
>Porichthys_notatus
MGKNLFSSYPQTRTRM
>Plecoglossus_altivelis
MGKNLFSSYP-----
>Oncorhynchus_kisutch
MGKNLFSSYP-----

HG0376 ENSDARG00000077229 ano8b

>Danio_rerio
MTHNNLHFTLTFI
>Alosa_alosa
MSHNNLHFTTTFI
>Apteronotus_leptorhynchus
MTHNNLHFTTTFI
>Lepisosteus_oculatus
MSHGNNLHFTTTFI

```
>Danio_rerio
MQPRFSGIGVMHIFSSHLSPPNLSGYEGRPMAKTGHS-----
>Astyanax_mexicanus
-----MHIFNSHPSQLEHFGHGQEPATKELCVFLMEKAFLRNISLSCSFFSFALRSPEPGIVLHEW
>Alosa_alosa
-----MHIFNSHFS-----
>Ictalurus_punctatus
-----MSIFISHLSQWDHFGYGGRPVAKNLCVHTYGKFSLRNISLSCFFSLTFLEKP-----
```


HG0378 ENSDARG00000080009 bahcc1b

>Danio_rerio
MIGTYFFGRQSONCAECKT-----
>Apteronotus_leptorhynchus
MTGTYFFGRQIKNCAECETWAKLVTGL
>Scleropages_formosus
MIGSYFSGWGSDQYRECNT-----
>Trichomycterus_areolatus
MTGTYFFGRHTQNGAECKT-----

HG0379 ENSDARG00000104372 gnb1b

>Danio_rerio
MRGFDSTIIVFFGQCHINKGHLRLRTDQNVSRQ-----
>Esox_lucius
MRGLEGYTVTFSSQCKTQSLRQLRKGSVPAAGERQKY
>Apteronotus_leptorhynchus
MRGFDSTIIVFFGQCHIKGQLRLSTDQCVSRQDE-----
>Ameiurus_nebulosus
MRGFDSTVFSFGQCHIKHQLRLNTDPCVSRQ-----

HG0380 ENSDARG00000005350 dip2ba

>Danio_rerio
-----MAEGVVL~~R~~MDCYSPFNSRFMP
>Plecoglossus_altivelis
-----MAEGPIVRMDCLPDLNACSMS
>Trichomycterus_areolatus
MGSRDQRSASHTMAEGAAVRMDCSSHFNTRFES

>Danio_rerio
-----MACSSDRMNGG
>Astyanax_mexicanus
MGLEGLCLGCDEKPKMACSLDRMNGG
>Clupea_harengus
-----MACSTD RMNGG

HG0382 ENSDARG00000017242

```
>Danio_rerio
MTEPFFTADACGGGLTCRC
>Alosa_alosa
MQEPFFRTNECGGG-----
>Apteronotus_leptorhynchus
MKQPLFTADECGGGLTCLC
```

HG0383 ENSDARG00000036501 rab39bb

>Danio_rerio
-----MMLLLSLPFHLHKTSKHFSIFQTWIKT-----
>Alosa_alosa
MRDESGYMMLLMLLPFHQ-QNSKHFFIFKTSWSENNTSQYHN
>Platichthys_stellatus
MRDESGDMMLLLALPFHQ-QTSKHTQPAPT-----

HG0384 ENSDARG00000054748 cuedc1b

>Danio_rerio
MQLNKQKKRRKGFLSLQWTRFFIV
>Pygocentrus_nattereri
MQLNKQKKRKKAFSFLSGLT----
>Apteronotus_leptorhynchus
MQLKKQKKRRKGLLLPPWTP TTLH

HG0385 ENSDARG00000059549 akap10

>Danio_rerio
MNEGNGRESSGCCL
>Salmo_salar
MNEGTRESTGCCH
>Ictalurus_punctatus
MNEGTRESTRICCH

HG0386 ENSDARG0000062084 c1cn1a

>Danio_rerio
MCEEETERLSVCVCMCPCHPRVGMLRQTGSLFLGQ
>Alosa_alosa
-----MLRQTSGLFLGQ
>Salmo_salar
-----MLRQTAGLFLGQ

HG0387 ENSDARG00000071150 cica

>Danio_rerio
MQERNRVEDIDRLGLTGNQED
>Astyanax_mexicanus
MREGNRVEDIDRLRLTENLED
>Apteronotus_leptorhynchus
MRVGNRVEVLDRLGHTGNLED

HG0388 ENSDARG00000077228 ntrk3a

>Danio_rerio
MQPVEEDSLGALIFEPFLH
>Alosa_alosa
MQPGDEDSIGVSIFFQPFHL
>Salmo_salar
MQPREEDKPGVVIFFEPFLI

HG0389 ENSDARG0000077361 bptf

>Danio_rerio
MAAASDLKRGAGRSF
>Alosa_alosa
MAAMSDPKRDAGRSF
>Apteronotus_leptorhynchus
MAAASDSKRDAGHSF

HG0390 ENSDARG00000090035 rtn4r

>Danio_rerio
MTERGT-TGRRRCSPSRARTATVG
>Esox_lucius
MTERGS-TRRRRCSPTRFSRKTSG
>Apteronotus_leptorhynchus
MTERGRINGRLCSPSRAFKATVG

HG0391 ENSDARG00000099634 elna

>Danio_rerio
MIHRTKGFALS
>Pygocentrus_nattereri
MIHRTGAFALS
>Trichomycterus_areolatus
MIHRTGFAFS

HG0392 ENSDARG00000100003 glulb

>Danio_rerio
MRMRDKQGLPYKTLWKYSHSYSDLYFLIGLI
>Astyanax_mexicanus
--MREKQARKSSRSWTHSQSGIDYLFLLKGFL
>Ictalurus_punctatus
--MREKEFVLSY-----

>Gallus_gallus
MELKGPOMKELEHVSDSLRCV--
>Anser_cygnoides
MELKGPOMQELHVSESVRCVWQ
>Chaetura_pelagica
-----MKELEHVSEGLRCV--
>Apteryx_australis_mantelli
MELKGPOMQELERVSESLRCV--
>Buceros_rhinoceros_silvestri
MELKGPOMKEREHVSEGLRCVWQ
>Caprimulgus_carolinensis
MELKGPOMKEREHISEGLRCV--
>Cariama_cristata
MELKGPOMKELEHVSEGLRCV--
>Calidris_pugnax
MELKGPOMKELEHVSEGLRCV--
>Pterocles_gutturalis
MELKGPOMKELEHVSEALR----
>Colius_striatus
MELKGPOMKELEHVSEGLRCV--
>Columba_livia
-----MKELEHVSEGFRCV--
>Leptosomus_discolor
MELKGPOMKELEHVSEGLRRV--
>Oculus_canorus
MELKGPOMKELEHVSEGFRCV--
>Aquila_chrysaetos_canadensis
MELKGPOMKELEHVSEGLRCV--
>Gavia_stellata
MELKGPOMKELEHISEGLRCV--
>Mesitornis_unicolor
MEPKGPOMKELEHVTEGLRCV--
>Tauraco_erythrolophus
MELKGPOMKELEHVSEGLRCV--
>Opisthocomus_hoazin
MELKGPEMKKEHVSEGV-----
>Ficedula_albicollis
MELKGPOMKERTRTSLTV-----
>Phaethon_lepturus
MELKGPOMKELEHVSEGLRCV--
>Ploides_pubescens
MDLKGPMKELEHVAEGLRCV--
>Fulmarus_glacialis
MELKGPOMKELEHVSEGLRCV--
>Nestor_notabilis
MELKGPOMKELEHVSEGLRCV--
>Aptenodytes_forsteri
MELKGPOMKELGTPF-----
>Tyto_alba
MELKGPOMKELEHVTEGLRCV--
>Struthio_camelus_australis
MELKGPOMQELHVSESLRCV--
>Tinamus_guttatus
MELKGPOMQELHGAELRCI--
>Calypte_anna
MEIRGPEMKEQEHISEDLRCV--
>Apaloderma_vittatum
-----MKELEHVSEGL-----

>Gallus_gallus
MRSPCMHTQIQAHADFTD-----
>Anser_cygnoides
MHTPCVHAQIQAHAEFTR-----
>Chaetura_pelagica
MHSPCMCTOMQAHADFTH-----
>Apteryx_australis_mantelli
MHTPCHTHTQIQAHADFTH-----
>Caprimulgus_carolinensis
MHTPCMRTOMQAHADFTH-----
>Gariama_cristata
MHAPCMRTOMQAHAEFTH-----
>Charadrius_vociferus
MHTPCMRTOMQARADFTY-----
>Pterocles_gutturalis
MHTPCMRTOMQAHADFTH-----
>Colius_striatus
MHTPCMHAOMQAHAGFTH-----
>Columba_livia
MHTPCMCTOMQAHADFTH-----
>Merops_nubicus
-----MQAHAEFTHSNLS
>Aquila_chrysaetos_canadensis
MHAPCMHTOMQAHADFTH-----
>Gavia_stellata
MHTACMRTOMQAHADFTH-----
>Chlamydotis_macqueenii
MHAPCMRTOMQAHADFTR-----
>Tauraco_erythrolophus
MHTPCMCTRMQAHADFTH-----
>Manacus_vitellinus
MRSPCVHAOMQAYAAFTH-----
>Egretta_garzetta
MHTPCMCTOMQAHADFTH-----
>Fulmarus_glacialis
MHTPCMRTOMQAHADFTH-----
>Nestor_notabilis
MHTPCMCTOMQAHAVFTH-----
>Pygoscelis_adeliae
MHTPCMRTOMQAHADFTH-----
>Tyto_alba
MHTPCMRTOMQAHADFTH-----
>Struthio_camelus_australis
MHAPCTHT-----
>Tinamus_guttatus
MHTACTHSOLQARADFTH-----
>Calypte_anna
MHAPCMCTOMKAHADFTH-----
>Apaloderma_vittatum
MHTPCVCTOMQTHADFTH-----

>Gallus_gallus
MLLAHRDKLLWPKHRLPLVKT
>Anser_cygnoides
MLLAHLDKSLWPEHRLPLVKT
>Apteryx_australis_mantelli
MLLAHLDKLLWPKHRLPLVKT
>Buceros_rhinoceros_silvestri
MLLAHLDKLLWQHPLHLVKT
>Caprimulgus_carolinensis
MLLAHLDKLLWPKHRLPLVKT
>Cariama_cristata
MLLAHLDKLLWPKHRLPLVKT
>Calidris_pugnax
MLLAHLDKLLWPKHRLPLVKT
>Colius_striatus
MLLAHLAKLLWPKHRLPFVKT
>Columba_livia
MLLAHLDKLLWPKHRLPLVKT
>Merops_nubicus
MLLAHLDKLLWPKHRLPLVKT
>Aegypius_monachus
MLLAHLDKLLWPKHRLPLVKT
>Gavia_stellata
MLLAHLNKLWPKHRLPLVKT
>Chlamydotis_macqueenii
MLLAHLDKLRWPKHRLPLVKT
>Tauraco_erythrolophus
MLLAHLDKLLWPKHRLPLVKT
>Opisthocomus_hoazin
MPLAHLDKLLWPKHRLPLVKT
>Geospiza_fortis
MLLSHVOKLLWPKHRLPLVKT
>Egretta_garzetta
MLLAHLDKLLWPKHRLPLVKT
>Fulmarus_glacialis
MLLAHLDKLLWPKHRLPLVKT
>Nestor_notabilis
MLLAHLDKLLWPKHRLPLVET
>Pygoscelis_adeliae
MLLAHLDKLLWPKHRLPLVKT
>Tyto_alba
MLLARLDKLLWPKHRLPLVKS
>Struthio_camelus_australis
MLLAHLDKLLWPKHRLPLVKT
>Tinamus_guttatus
MLLAHLDKLLWPKHRLPLVET

>Gallus_gallus
 -----MKDHCKEPWTFFVSYNTVIQRV

>Chaetura_pelagica
 MQIKQRKKECQEWPSLISAKDHCVRPWILAVSYNVLIQRV

>Caprimulgus_carolinensis
 -----MKDHCREPWILVYKCT-----

>Cariama_cristata
 -----MKDHYREPWILVVSYNILIQRV

>Charadrius_vociferus
 -----MKDHFREPWILVVSYNILIQRV

>Pterocles_gutturalis
 -----MKDHSREPWILGVSYNILIQRV

>Colius_striatus
 -----MKDHCREPWILVVSYNILIQRV

>Merops_nubicus
 -----MKDHCKEPWLLVVSYNVLIQRV

>Gavia_stellata
 -----MKDHCREPWILVVSYNILIQRV

>Balearica_regulorum_gibberic
 -----MKDHCREPWMLVSCNILIQRV

>Tauraco_erythrolophus
 -----MKDHCREPWILVVSFNILIQRI

>Opisthocomus_hoazin
 -----MKDHCREPWILVYKCT-----

>Pelecanus_crispus
 -----MKDHCREPWILVVSYNILIQRV

>Picoides_pubescens
 -----MKGHCREPWILVVS-----

>Fulmarus_glacialis
 -----MKDHCREPWILVVSYNILIQRV

>Nestor_notabilis
 -----MKDHCREPWILLVSCNILIQKV

>Aptenodytes_forsteri
 -----MKDHCREPWILVVSYNILIQRV

>Tyto_alba
 -----MKDQCRKSWILAVSYNILIQRV

>Struthio_camelus_australis
 -----MKDHCEEPWTFVYKCT-----

>Tinamus_guttatus
 -----MVSMKDHCEELWTFVYKCT-----

>Calypte_anna
 -----MKDCYREPWILVVSYNILIQSV

>Apaloderma_vittatum
 -----MKDHCREPWILVVSYNVLIQRV

>Gallus_gallus
-----MQKKTNKGRKDVKHDLP

>Anas_platyrhynchos
MKTNLSWLLQLHQLSATSSERPAQTPQVVDQSSFSSSSHLGAQSFYVVLGLNTRLLKLFVLMRKWISQLSTNKTNGKKDVKHGLP
>Calidris_pugnax
-----MWKWI SQLNANQTNGKKDVKRGLP

>Pterocles_gutturalis
-----MWKWI SQLNANQTNGKKDVEHGLP

>Columba_livia
-----MWKRILQLNANQTNGKKDVKRGLP

>Gavia_stellata
-----MWKWI SQLNANQTNGKKDVKRGLP

>Nipponia_nippon
-----MWKWI SQLNANQTNGKKDVKRGLP

>Fulmarus_glacialis
-----MWKWI SQLNANQTNGKKDVKCGLP

>Pygoscelis_adeliae
MKTNP SWLLQLHQLSAT-----RFVLMWKWI SQLNANQTNGKKDVKRGLP

>Gallus_gallus
MAESPSWDLGVCTG
>Apteryx_australis_mantelli
MAEGLSWDLGVCTG
>Buceros_rhinoceros_silvestri
MAESPSWELGVCTG
>Cariama_cristata
MAESLSWELGVCTG
>Colius_striatus
MAESLCWELGVCTG
>Leptosomus_discolor
MAESLSWELGVCTG
>Cuculus_canorus
MAESLCWELGVCTG
>Falco_cherrug
MAESLSWELGVCTG
>Gavia_stellata
MAESLSWELGVCTG
>Eurypyga_helias
MAESLSWELGVCTG
>Tauraco_erythrolophus
MAESLSWELGVCTG
>Opisthocomus_hoazin
MAESLSWELGVCTS
>Corvus_cornix_cornix
MAESLSWELGVCTG
>Egretta_garzetta
MAESLSWELGVCTG
>Fulmarus_glacialis
MAESLSWELGVCTG
>Aptenodytes_forsteri
MAESLSWELGVCTG
>Tyto_alba
MAERLSWELGVCTG
>Struthio_camelus_australis
MAGGLSWDLGVCTG
>Apaloderma_vittatum
MAESRSWELGVCTG

>Gallus_gallus
-----MMEEKVRLARAALNY
>Chaetura_pelagica
-----MMEEKVRLADGAVNY
>Buceros_rhinoceros_silvestri
-----MMEEKVRLADGAVNY
>Caprimulgus_carolinensis
-----MMEEKVRLADGAVNY
>Cariama_cristata
-----MMEEKVRLADGAVNY
>Charadrius_vociferus
-----MMEEKVRLADGALNY
>Pterocles_gutturalis
-----MMEEKVRLADGGMNY
>Colius_striatus
-----MMEEKVRLADGAVNY
>Leptosomus_discolor
-----MMEEKVRLADGAVNY
>Aquila_chrysaetos_canadensis
-----MMEEKVRLADGAVNY
>Chlamydotis_macqueenii
-----MMEEKVRLADGAVNY
>Tauraco_erythrolophus
-----MMEEKVRLAGGAVNY
>Opisthocomus_hoazin
-----MMEEKVRLADGALNY
>Corvus_brachyrhynchos
-----MMEEKVRLADGAVKY
>Egretta_garzetta
-----MMEEKVRLADGAVNY
>Nestor_notabilis
-----MMEEKVRLADGAVNY
>Struthio_camelus_australis
MYSYNPLSLEKMMEEKVRLADVAVNY
>Calypte_anna
-----MMEEKVRLADGAVNY

>Gallus_gallus
-----MTNHFCVCTTRIQNS-----
>Anser_cygnoides
-----MTNHICLCTTRIQNS-----
>Chaetura_pelagica
-----MTNNICLCTTRIQEFLNRRLV
>Caprimulgus_carolinensis
MIFKCIFMTNHICLCTTRIQNS-----
>Cariama_cristata
-----MTNHTCLCTTQIRNS-----
>Charadrius_vociferus
-----MTNHIC-----
>Pterocles_gutturalis
----MHFMTNHICLCTTQIQNS-----
>Columba_livia
-----MTDHICLCTTREQNS-----
>Leptosomus_discolor
MIFKCIFMTNHICLCTTRIQNS-----
>Falco_cherrug
-----MTNHICLCTTQIQN-----
>Gavia_stellata
-----MTNHICLCTTRIQNS-----
>Mesitornis_unicolor
-----MTNHICLCTTRIQNS-----
>Tauraco_erythrolophus
-----MPNHICLCTTRIQNS-----
>Taeniopygia_guttata
-----MTNYICLCTTRIQNS-----
>Pelecanus_crispus
-----MTNHICLCTTRIQNS-----
>Fulmarus_glacialis
-----MTNHICLCTTRIQNS-----
>Aptenodytes_forsteri
-----MTNHICLCTTRIQNS-----
>Apaloderma_vittatum
-----MTNRICLCTTRIQNS-----

>Gallus_gallus
MISLAVQHEISYFSV
>Anser_cygnoides
MISLAVQDEISYFNV
>Apteryx_australis_mantelli
MISLAVQDEI-----
>Caprimulgus_carolinensis
MTSLAVQDEISYFNV
>Calidris_pugnax
MISLAVQDEISYFNV
>Columba_livia
MISLAVQDEISYFNV
>Cuculus_canorus
MISLAVQDEISYFNV
>Aquila_chrysaetos_canadensis
MISLAVQDEISYFNV
>Balearica_regulorum_gibberic
MISLAVQDEISYFNV
>Geospiza_fortis
MISLAVQDEISYFNV
>Egretta_garzetta
MISLAVQDEISYFNV
>Picoides_pubescens
MISLAAQDEISYFNV
>Fulmarus_glacialis
MISLAVQDQISYFNV
>Aptenodytes_forsteri
MISLAVQDEISYFNV
>Tyto_alba
MISLAVQDEISYFNV
>Struthio_camelus_australis
MISLAVQDEISYFNV
>Tinamus_guttatus
MISLALRDEISYFNV

>Gallus_gallus
--MILLQNLFLNGSMLFASRRRC
>Anas_platyrhynchos
MQMIPLQNLFLNGSMLFSNRRW
>Apteryx_australis_mantelli
--MIPLQSLFLNGSMLFSSRRW
>Charadrius_vociferus
--MIPLQGLFLNGRMLFSSRRW
>Leptosomus_discolor
--MIPLQSLFLNGSMPFSSRRW
>Falco_cherrug
--MILLQSLFLNGKVLFSRRW
>Gavia_stellata
--MIPLQSLFLDGRMLFSSRRW
>Balearica_regulorum_gibberic
--MIPLQSLFLNGRMLFSSRRW
>Sturnus_vulgaris
--MISLQSLFLNGSVLLPSRRW
>Egretta_garzetta
--MIPLQSLFLNGRMLFSSRRW
>Fulmarus_glacialis
--MIPLQSLFLNGRMLFSSRRW
>Nestor_notabilis
--MILLQSLFLNGRVLFSSRRW
>Pygoscelis_adeliae
--MIPLQSLFLNGRMLFSSRRW
>Tyto_alba
--MIPLLSLFLNGRMLFSSRRW
>Struthio_camelus_australis
--MIPLQSLLLNGSMIFSSRRW
>Tinamus_guttatus
--MIPLQRLFLNGSMFFSSRRW
>Apaloderma_vittatum
--MIPLQSLFLNGRMLFSSRRW

>Gallus_gallus
MARCWKGREQPMLLI
>Anas_platyrhynchos
MARCWKGRERPMLLL
>Chaetura_pelagica
MAQCWKGREQPMLLF
>Calidris_pugnax
MARCWKGREQPMLLF
>Pterocles_gutturalis
MARCWKGREQPMLLF
>Columba_livia
MARCWKGREQPMLLF
>Leptosomus_discolor
MALCWKGREQPMLLF
>Falco_cherrug
MARCWKGREQPMLLF
>Chlamydotis_macqueenii
MARCWKGREQPMLLF
>Tauraco_erythrolophus
MARCWKGREQPMLLF
>Taeniopygia_guttata
MARCWKGREQPMLLF
>Pelecanus_crispus
MARCWKGREQPMLLF
>Fulmarus_glacialis
MARCWKGREQPMLLF
>Aptenodytes_forsteri
MARCWKGREQPMLLF
>Tyto_alba
MAQCWKGREQPMLLF
>Struthio_camelus_australis
MARCWKGREQPMLLF
>Calypte_anna
MARCWKGREQPMLLF

>Gallus_gallus
 MNPPPTNPFSRMLSGKEAFQHEIQSIPITCMPN-----
 >Anser_cygnoides
 -----MLSAEEAFFQHVIQCIPVRIMR-----
 >Chaetura_pelagica
 -----MLSGKEEFFQHEIQCLPTI-----
 >Cariama_cristata
 MNLPPNIQLLSGMLSGKEAFFQHEIQCIPII-----
 >Charadrius_vociferus
 -----MLSGKEAFFQHEIQCIPII-----
 >Pterocles_gutturalis
 -----MLSGKEAFFHPEIQCIQII-----
 >Columba_livia
 -----MLSGKEAFFQHGIQCIPII-----
 >Merops_nubicus
 -----MLSGKEEFFQHEIQCIPII-----
 >Aquila_chrysaetos_canadensis
 -----MLSGKEAFFQREIQCLPII-----
 >Gavia_stellata
 -----MLSGKEAFFQHEIQCIPII-----
 >Balearica_regulorum_gibberic
 -----MLSGKEAFFQHEIQCIPII-----
 >Tauraco_erythrolophus
 -----MLSGKKAFFQHEIQCIPII-----
 >Lepidothrix_coronata
 -----MLSGKEAFFQHEIQCIPIISMFN-----
 >Fulmarus_glacialis
 -----MLSGKEAFFQHEIQCIPIV-----
 >Tyto_alba
 -----MLSGKEAFFQNEIQCIPII-----
 >Tinamus_guttatus
 -----MLSGKKAFFQHVIQCIPVCLGSSTSKASRKRPHAVATGFRTSVLSCF

>Gallus_gallus
MLSIAGN-----QVLMFNPFLYEISTQATE
>Anas_platyrhynchos
MLSIAGSQMKP-----
>Apteryx_australis_mantelli
MLSIAGSQMKP-----
>Calidris_pugnax
MLSIAGSQMNSQMKTVMLMFNPFHLRQISPQATE
>Struthio_camelus_australis
MLSIAGSQMKP-----

>Gallus_gallus
MEHSTRKDKTVLTR---
>Apteryx_australis_mantelli
MEHSTGKNKTVLTW---
>Buceros_rhinoceros_silvestri
MEHSARKNKSVLTG---
>Caprimulgus_carolinensis
MEHSTRKNKTVLT----
>Charadrius_vociferus
MEHSTRKNKTVLTR---
>Colius_striatus
MEHSTRKNKTVLTR---
>Leptosomus_discolor
MEHSTRKNKIVLTR---
>Haliaeetus_leucocephalus
MEHSIRKNKTVLTR---
>Gavia_stellata
MEHSPRKDKTVLTR---
>Chlamydotis_macqueenii
MEHSTRKNKTVLTRQFA
>Tauraco_erythrolophus
MEHSTRRSKTVLTR---
>Ficedula_albicollis
MEHSTRKDKTVLTR---
>Fulmarus_glacialis
MEHSARKNKTVLTR---
>Nestor_notabilis
MEHSTTKTKTVLTR---
>Aptenodytes_forsteri
MEHSTRKNNTVLTR---
>Tyto_alba
MEHSTRKNKTVITR---

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>Gallus_gallus
-----MLLSSLWAFDLRFFS

>Anser_cygnoides
-----MW-----NTLL-AYLRVRE--AVQEVLCRLYKYSVRQ-----AVISLSLLQISAACLGHMLLSRLRAFLDLRFFS

>Cariama_cristata
-----MLLISLRAFLDLRFFS

>Charadrius_vociferus
MKERLARVGD LKSFSPSPLTHSQTEELHRHQEITLHQDARSR-YFLPCTQQVTSFEILFSPLKQISAACLG YMLLISLRAFLDLRFFS

>Pterocles_gutturalis
-----MLLSSLQAFDLRCFS

>Colius_striatus
-----MLLIGLRAFLDLRFFS

>Leptosomus_discolor
-----MLLISLRAFLDLRFFS

>Aquila_chrysaetos_canadensis
-----MDNHGKISTACLG YMLLISLRAFLDLRFFS

>Gavia_stellata
-----MSTACLG YMLLISLRAFLDLRFFS

>Chlamydotis_macqueenii
-----MLLISLQAFDLGFFS

>Opisthocomus_hoazin
-----MSTACLGCM L L I S L R A F L D L R F S S

>Acanthisitta_chloris
-----MLLISLLASDLRFFS

>Phalacrocorax_carbo
-----MSTACLG YMLLISLQAFDLRFFS

>Struthio_camelus_australis
-----MLLSSLRAFLDLRFFS

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>Gallus_gallus
-----MPHPDIFSPELSKLPVL-----
>Charadrius_vociferus
-----MPDPGIFSPVLSKLPVSRSCSVL
>Pterocles_gutturalis
-----MPHPGILCPVLSKLPVLRSCSVL
>Colius_striatus
-----MPNPGIFFPVLSKLAVLRSCGGL
>Leptosomus_discolor
-----MPDPGIFSPVLSKLPFLRSCSVL
>Haliaeetus_albicilla
MKERLARAGELKSFSPSPLVSQCKDRRTTETSEISTLAFLRMPDPGIFSPALSKLPVSRSCSVL
>Chlamydotis_macqueenii
-----MPDPDIFYPVLSKLPVLRSCSVL
>Phalacrocorax_carbo
-----MPDPGIFSPILSKLPVLRSGSVL
>Picoides_pubescens
-----MLDPGIFSPVLSKLPVLRSCSVL
>Fulmarus_glacialis
-----MPDPGIFSPVLSKLPVLRSCSVL
>Nestor_notabilis
-----MPDPGIFSTVLSKLPVSRSCSVL
>Pygoscelis_adeliae
-----MPDPGIFSPVLSKLPVLRSCSVL

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>Gallus_gallus
MKAAAMLGASGRFWCGVC
>Chaetura_pelagica
-----MLGASGRFRCGVC
>Apteryx_australis_mantelli
MKAAAMLGASGCFWCCLC
>Calidris_pugnax
MKAAAMLGASGRFWCGLC
>Columba_livia
MKAAAMLGASGRFWCGVC
>Leptosomus_discolor
MKAAAMLGASGRFWCGVC
>Aquila_chrysaetos_canadensis
MKAAAMLGASGCFWCGVC
>Tauraco_erythrolophus
MKPSSMWRASGRFRCGVC
>Pseudopodoces_humilis
MKAAAMLGAAGRGPC---
>Nipponia_nippon
MKAAAMFGASGRFWCGVC
>Picoides_pubescens
MKAAAMLGGSGRFWCGVC
>Melopsittacus_undulatus
MTAAAMLGASGSFWCGVC
>Pygoscelis_adeliae
MKAAAMFGASGWFWCGVC
>Calypte_anna
MKAAAMLGASGRFRCGVC

>Gallus_gallus
MERARVLRGSRQLALLRRAPAGYIMFYHCLCACFI
>Anas_platyrhynchos
-----MFYHSLCACFV
>Chaetura_pelagica
-----MFHHCLCTCFL
>Buceros_rhinoceros_silvestri
-----MFHHCLCACFV
>Cariama_cristata
-----MFQHCLCACFV
>Calidris_pugnax
-----MFHHCLCACFA
>Columba_livia
-----MFHHCLCACFV
>Cuculus_canorus
-----MFHHCLCACIV
>Aquila_chrysaetos_canadensis
-----MMFHHCLCACFV
>Eurypyga_helias
-----MFHHCLCACFA
>Tauraco_erythrolophus
-----MFHHCVCAFV
>Lepidothrix_coronata
MGRERA--DAACAPGCTASAAGYIMSHHCLCACFV
>Egretta_garzetta
-----MFYHCLCACFV
>Nestor_notabilis
-----MFHHCSCAFV

>Gallus_gallus
MTGRSPEAAAAARTA-AAAHTLPREQH
>Anas_platyrhynchos
MTGRSPEAAAAARAA-AAAHTLHREQH
>Chaetura_pelagica
MTGRSPEAAAAARAA-AAAHTLHREQH
>Apteryx_australis_mantelli
MTGRSPEAAAAARAA-AAAHTLHREQH
>Charadrius_vociferus
MTGRSPEAAAAARAA-AAAHTLHREQH
>Columba_livia
MTGRSPEAAAAARTA-AAAHTLPREQH
>Cuculus_canorus
MTGRSPEAAAAARAAAAAHTLHREQH
>Aquila_chrysaetos_canadensis
MTGRSPEAAAAARAA-AAAHTLHREQH
>Lepidothrix_coronata
MTGRSPEAAAAARAA-APAHTLHREQH
>Nipponia_nippon
MTGRSPEAAAAARAA-AAAHTLHREQH
>Melopsittacus_undulatus
MTGRSPEAAAAARAA-AAAHTLHREQH
>Aptenodytes_forsteri
MTGRSPEAAAAARAA-AAAHTLHREQH
>Struthio_camelus_australis
MTGRSPEAAAAARAA-AAAHTLHREQH
>Calypste_anna
MTGRSPEAAAAARAA-AAAHTLHREQH

>Gallus_gallus
MVSTPCEPPLQK-----
>Anser_cygnoides
MDSTSCEPPLQK-----
>Apteryx_australis_mantelli
MNSTSCEPPLQKATLAQKWNL
>Cariama_cristata
MDSTSCEPPLQK-----
>Pterocles_gutturalis
MNSTSCEPPLQK-----
>Columba_livia
MDSTSCEPPLQK-----
>Chlamydotis_macqueenii
MDSTSCEPPLQK-----
>Opisthocomus_hoazin
MDSTSCEPPLQK-----
>Zonotrichia_albicollis
MDSTSCEPPLQK-----
>Phalacrocorax_carbo
MDSTSCEPPLQK-----
>Fulmarus_glacialis
MDSTSCEPPLQK-----
>Melopsittacus_undulatus
MDSTSCEPPLQK-----
>Pygoscelis_adeliae
MDSTSCEPPLQK-----

>Gallus_gallus
MGASTEWWFGSQKPCSLICV
>Anas_platyrhynchos
MGASTKSFFRGSQKPWRLIPV
>Cariama_cristata
MGASTKCFFRGSEKPCSLIPK
>Calidris_pugnax
MGASTECCFFRGSQKPCRLIPV
>Columba_livia
MEASTKCFFRGFQKPCSLIPV
>Leptosomus_discolor
MGASTKCFFRGSQKPCSFIPV
>Aquila_chrysaetos_canadensis
MGASTKCFFRGSQKPCSLIPV
>Eurypyga_helias
MGSSTECFFRGSQKPHILIPD
>Parus_major
MGASIERFFRGSQKPCSHIPV
>Phaethon_lepturus
MGASTGCFFRGSQKPCRLIPV
>Fulmarus_glacialis
MGASTECCFFRGSQKPCSLISV
>Melopsittacus_undulatus
MGASTKCFFRGSQKPCTLIPV
>Aptenodytes_forsteri
MGASTECCFFRGSQKPCSLIPV

>Gallus_gallus
-----MAIPTLTLLKWRLSSL
>Anser_cygnoides
MAEKWFYKMTPTLTLLKWRLSSL
>Cariama_cristata
-----MTAPTLTLLKWRLSSL
>Calidris_pugnax
-----MTAPNLTQLKWRLSSL
>Aquila_chrysaetos_canadensis
-----MTAPTLTLLKWRLSSL
>Gavia_stellata
-----MTAPTLTLLKWRLSSL
>Eurypyga_helias
-----MTAPTLTLLKWRLSSL
>Tauraco_erythrolophus
-----MTASTLTLLKWRLSSL
>Sturnus_vulgaris
-----MTVPTLRLLLEWRLSSL
>Nipponia_nippon
-----MTPPTLRLLKWRLSSL
>Picoides_pubescens
-----MTAPTVILLKWRLSSL
>Fulmarus_glacialis
-----MTAPTLTSLKWRLSSL
>Aptenodytes_forsteri
-----MTAPTLTLLKWRLSSL

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>Gallus_gallus
-----MNERNKIFLCTHESFREPLM
>Chaetura_pelagica
-----MKERNKNLPCTHESFSEHLI
>Caprimulgus_carolinensis
-----MKERNKNLPCTHESFSEPLI
>Cariama_cristata
-----MKERNRNLPCTHQSFCPLI
>Calidris_pugnax
-----MKERNKNLHRTHESEPLI
>Pterocles_gutturalis
-----MKERNKNLPRTHESFSEPLI
>Colius_striatus
-----MKERNKNLPCTHESFSEPLI
>Columba_livia
-----MKERNKNLPCTHETFEPLI
>Haliaeetus_leucocephalus
-----MKEKNKNLPCTHESFSEPLI
>Chlamydotis_macqueenii
MTENLQGVSPMAAWDEDGGYIRSSTDLTFMKRKNLHNTHESFREPLI
>Lepidothrix_coronata
-----MKERNKKLPYIHESFSEPLI
>Nipponia_nippon
-----MKEKNKNLPHTHESFSEPLI
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HG0413 ENSGALG00000005475

>Gallus_gallus

MRSCCWLLDFVSG

>Anser_cygnoides

MQSCCWLLDFVSG

>Charadrius_vociferus

MQSCCQLLEFVSG

>Colius_striatus

MQSCCQLLGFVSG

>Falco_cherrug

MQSCCQLMDFVSG

>Gavia_stellata

MQSCCQLLDFVSG

>Balearica_regulorum_gibberic

MQSCCQLLDFVSG

>Opisthocomus_hoazin

MQSCCQCLDFVFG

>Egretta_garzetta

MQSCCQLLDFVSG

>Melopsittacus_undulatus

MQSCCQLLDSVSG

>Struthio_camelus_australis

MQSCCQFLDFFSG

>Tinamus_guttatus

MQSCCQFLLVFLSG

HG0414 ENSGALG00000032599

>Gallus_gallus

MMKALQWERAVVQG

>Anser_cygnoides

MMKAPQWEHAVVQG

>Chaetura_pelagica

MMKALQWDRAVVQG

>Buceros_rhinoceros_silvestri

MMKALQWERAVVQG

>Charadrius_vociferus

MMKALQWERAVVQG

>Columba_livia

MMKALQWERAVVQG

>Cuculus_canorus

MMKAPQWERAVVQG

>Aquila_chrysaetos_canadensis

MMKALQWERAVVQG

>Sturnus_vulgaris

MMKALQWERAVVQG

>Phaethon_lepturus

MMKALQWEHAVVQG

>Pygoscelis_adeliae

MMKALQWERAVVQG

>Calypte_anna

MMKALQWDRAVVQG

HG0415 ENSGALG00000034970

>Gallus_gallus
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>Anas_platyrhynchos
MLSATVMTREASPAKD
>Chaetura_pelagica
MLSTTVMKREAPLARD
>Cariama_cristata
MLSATVMKESPLARD
>Charadrius_vociferus
MLSATVMKREAPLARD
>Pterocles_gutturalis
MLSTTVMKREAPLARD
>Leptosomus_discolor
MLSTTVMKREAPLARD
>Cuculus_canorus
MLSRTVMKIEALLAKD
>Gavia_stellata
MLSTTVMKREATLDRD
>Balearica_regulorum_gibberic
MLSTTVMKREAAALARD
>Pelecanus_crispus
MLSTTVMKREASLARD
>Fulmarus_glacialis
MLSTTVMKREAPLARD

>Gallus_gallus
MKDYISRCWILGII
>Anas_platyrhynchos
MESYISCLCWILGII
>Charadrius_vociferus
MESYISCLCWILEII
>Leptosomus_discolor
MESYVSCLCWILGII
>Gavia_stellata
MESYISCLCWILGII
>Eurypyga_helias
MENYLSCLCWILRII
>Egretta_garzetta
MENYISCLCWILGII
>Fulmarus_glacialis
MESYISCLCWILGII
>Tyto_alba
MESYVSCLCWILGII
>Struthio_camelus_australis
MENYVSCLCWISGNI

>Gallus_gallus

-----MDFSALTIPDGGKHVVGELGE

>Anas_platyrhynchos

-----MDFSGLTIPDGGMHIVGGELGE

>Apteryx_australis_mantelli

MAVVIHLQGLPIVVGTMDFSGVTIPDGGVHIVGGELGE

>Calidris_pugnax

-----MDLSGLSIPDGGVQIVGGELGE

>Columba_livia

MAVVIHLRGLPGVVGTMDFSGLTIPAGGVHVVGELGE

>Haliaeetus_albicilla

MAVFIHLQGLPIVVGTMDFSGLTIPDGGVHIVGGELGE

>Parus_major

MAVVIHLQGVPIAVGTMDFSGLTIPDGGVHIVGGELGE

>Pygoscelis_adeliae

MAVVIHLQGLLIVVGTMDFSGLTIPDGGMHIVGGELGE

>Struthio_camelus_australis

MAVVIHLQGLPIVVGTMDFSGLTIPDGGVHIVGGELGE

>Gallus_gallus

-----MKNCIFSSTFCTSLLPDFSRA-----

>Anser_cygnoides

-----MKNCIFSSTFGTSLLPDFSRACVVLVIGDA--

>Caprimulgus_carolinensis

-----MKNCIFFSTFSTSLLPDFS-----

>Calidris_pugnax

-----MKNCIFFSTFDASLLPDFSRA-----

>Haliaeetus_albicilla

-----MKNCIFFSTFDTSLLPEFSRA-----

>Eurypyga_helias

MACYYLNSLNYPFSAERIMKNCFLFSTFATSLLPDFSRAVVLVIKGTFT

>Tauraco_erythrolophus

-----MRNCIFSATFDTSLLPDFSRA-----

>Phaethon_lepturus

-----MKNCIFFSIFDTSLLPDFSRA-----

>Tyto_alba

-----MKNCIFFSTFGTSLLPDFLRA-----

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>Gallus_gallus

MGGRPLEPCSPSQSC

>Anas_platyrhynchos

MGGRPLEPCGSHSC

>Apteryx_australis_mantelli

MGDRPLQSCSPSQSC

>Calidris_pugnax

MGEHPLKPCSPSQSS

>Columba_livia

MGECPLEPCGPSQSC

>Haliaeetus_albicilla

MGERPLEPCGPSQSC

>Corvus_brachyrhynchos

MGERPLEPCGPSQSC

>Aptenodytes_forsteri

MGERPLEPCGPSQSC

>Tinamus_guttatus

MGDSPLHICSPSQSC

>Gallus_gallus

MPKIIHLNRQGLITRAANSLISLF

>Anser_cygnoides

MPKIIHPKQQGLITRAVNSLISLF

>Apteryx_australis_mantelli

MPKIIHPKQRGLITRAGNSLIGLF

>Calidris_pugnax

MPKIIHPKQQGLITRAVNSLISLF

>Aquila_chrysaetos_canadensis

MPKIIHPKQQGLITRAVNSLISLF

>Corvus_brachyrhynchos

MPKIIHLKQQGLITRAVNSLISLF

>Nipponia_nippon

MPKIIHPKQQGLITRAVNSLISLF

>Calypste_anna

MPKIIHPKQQGLITRAVNSLISLF

>Gallus_gallus

-----MEANLKRAKKGDLKVSVHRMEIERIRYVLSSYLRCRLAKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVALLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Anser_cygnoides

-----MESNLKRAKAGDLKVSVHRMEIERIRYVLSSYLRCRLVKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Apteryx_australis_mantelli

-----MEIERIRYVLSSYLRCRLVKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Charadrius_vociferus

-----MEANLKRAKRGDLKVSVHRMEIERIRYVLSSYLRCRLVKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Falco_cherrug

-----MEANLKRAKRGDLKVSIRHMEIERIRYVLSSYLRCRLVKIEKFFP
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>Geospiza_fortis

MAGAMAAAAGGSDGSEELVLTPAQLIHSLEQAWLNEKFAPELLESKPEIECVVEQLDHMEANLKRAKKGDLKVSVHMEIERIRFVLSSYLRCRLVKIEKFFP
HILEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYRTV
APLVASGAVQLI

>Nipponia_nippon

MAAASGEGTAADSDGSEELVLTPAQLIRSLEQAWLNEKFAPELLESKPEIECVVEQLDHMEANLKRAKRGDLKVSVHRMEIERIRYVLSSYLRCRLVKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Struthio_camelus_australis

-----MNEANLKRAKKGDLKVSIIHMEIERIRYVLSSYLRCRLVKIEKFFP
HVLEKEKSRAEGEPSILSPEEFADFAKEYMANTETYLKNVALKHMPPNLQKVSLLKSVKPNLDSFVFLRVLRQENILVEPETDEGREYIDLEEGSQHLIRYKTI
APLVASGAVQLI

>Gallus_gallus
-----MKGKMKNRLWESSWEL
>Anas_platyrhynchos
-----MKDRLFENSCWKL
>Leptosomus_discolor
MLIDAASPKKHESNPKKKSLRGGKCNMKGKMKNWPFENSCWEM
>Aquila_chrysaetos_canadensis
-----MKGKMKNWPFENSCWEL
>Gavia_stellata
-----MRGKMKNWPFENSCWEL
>Balearica_regulorum_gibberic
-----MRGKMKNWPFECCWEL
>Fulmarus_glacialis
-----MRGKMKNWSFECCWDL
>Aptenodytes_forsteri
-----MRGKMKNWPFENSCWEL

HG0423 ENSGALG00000006329

>Gallus_gallus

MLSKLVGKKGHLSVL

>Leptosomus_discolor

MLSKLVGKNSGHLVSVL

>Aquila_chrysaetos_canadensis

MLSKLVGKNSGHLVSVL

>Gavia_stellata

MLSKLVGKNSGHLVSVL

>Balearica_regulorum_gibberica

MLSKLVGKNSGHLVSVL

>Phaethon_lepturus

MLSKLVGKNSGHLVSVL

>Tyto_alba

MLSKLVGKNSGHLVSVL

>Tinamus_guttatus

MLSKLVGRNSGHLVSVL

HG0424 ENSGALG00000039553

>Gallus_gallus

MTIYLSCIRQRCCCLQ

>Anser_cygnoides

MTIYLSCIRKRFCLQ

>Calidris_pugnax

MTIFLSCIRKRFCL-

>Cuculus_canorus

MTIFLSCIRKRF--

>Haliaeetus_leucocephalus

MTIFLSCIRKRFCL-

>Acanthisitta_chloris

MTIFLSCIRKRFCL-

>Phalacrocorax_carbo

MTIFLSCIRRRFCL-

>Aptenodytes_forsteri

MTIFLSCIRKRVCL-

HG0425 ENSGALG00000043044

>Gallus_gallus

MIQKTVRSCDCKMSSFYMLKGGKLLQEL

>Caprimulgus_carolinensis

-----MSSFHMLKGGKLELQE-

>Falco_cherrug

-----MSSFHSLLKGGKLLQE-

>Meditornis_unicolor

-----MSSFHMLKGGKLLHQE-

>Tauraco_erythrolophus

-----MLKEGKRLLQE-

>Opisthocomus_hoazin

-----MSSFQLMPKGGKLLQE-

>Ficedula_albicollis

-----MDCEMNSFHLILKEGKLLQK-

>Tyto_alba

-----MSSFHMLKGGKLLQE-

>Gallus_gallus
-----MLLRKDTPDFQK

>Anser_cygnoides
-----MLLHKDTPDFQK

>Calidris_pugnax
-----MLFHKDTPDFQK

>Columba_livia
-----MLFHKDTPDFQK

>Falco_cherrug
-----MLFHKDTPDFQK

>Ficedula_albicollis
MPVELRAGHSSLTSGWRWRKKVLAAVAAGLVKRSLVPLMYRMKAEISGCPQRTNPFNQTNQRERHMLFHKDTPDFQK

>Aptenodytes_forsteri
-----MLFHKDTPDFQK

HG0427 ENSGALG00000005550 ST6GAL1

>Gallus_gallus

MKVFLLELFSASRGCCVWGYPALNPGQKSANSQK

>Anser_cygnoides

MKVFLLELFRVSHNRCVLVYPALTPGRKSANSQK

>Calidris_pugnax

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>Columba_livia

MKLFLLELFSASQNCCVLRCPA-----

>Aquila_chrysaetos_canadensis

MKVFLLELFSASQNCCVLRYP A-----

>Ficedula_albicollis

MKVFLLELFNTRSCCVLGYP A-----

>Aptenodytes_forsteri

MKVFLLELFSASQNCCVLGYPA-----

HG0428 ENSGALG00000005976 TCEA2

>Gallus_gallus

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>Charadrius_vociferus

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>Leptosomus_discolor

MSVPVDGRFSAPLLK

>Haliaeetus_albicilla

MSVPVDGRFSTPLLK

>Gavia_stellata

MSVPVDGRFSTPLLK

>Pelecanus_crispus

MSVPVDGRFSTPLLK

>Fulmarus_glacialis

MSVPVDGRFSTPLLK

HG0429 ENSGALG00000006626 PDE6C

>Gallus_gallus

----MPLYSMYKVPFSY

>Anser_cygnoides

-----MYKVPFSY

>Columba_livia

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>Gavia_stellata

MYYACELYNMYKVPFSY

>Opisthocomus_hoazin

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>Pelecanus_crispus

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>Tinamus_guttatus

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>Gallus_gallus

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>Anser_cygnoides

-----MLSTGTSASDARTLLKTYFVVLKGR

>Apteryx_australis_mantelli

MKVYVLKELTCLRRSQWYQGNGAQKQEGSPKTTNLAVLGHRCKMLSMGTFASDAR-ILKIYFFAWLTGR

>Calidris_pugnax

-----MGIAPYF-----FLVNAVNRLLQRSKMLSVGTSASDARTLQKAYFVAWLKGR

>Columba_livia

-----MLSLETSAYDAGTLLKTYFVAQLKGR

>Haliaeetus_albicilla

-----MKIFSLIRSKMLSMETSASDARTLLKTYFVAWLKGR

>Zonotrichia_albicollis

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>Aquila_chrysaetos_canadensis

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>Manacus_vitellinus

-----MSAFDLCLANPKDWSRLKIM

>Melopsittacus_undulatus

-----MQEVVMFAFDLCLTNPKDWS-----

>Aptenodytes_forsteri

-----MFAFDLCLTNPKDWSRLKIM

>Struthio_camelus_australis

-----MPAFDALCLINPKHWSPLKVM

>Tinamus_guttatus

-----MVMFAFDLCLVNPKHWSPLKIM

HG0432 ENSGALG00000040546

>Gallus_gallus

MLENFTSVLIVISEHPPKN----

>Anser_cygnoides

MLENFTSVLIVISEHPPKN----

>Calidris_pugnax

MLEYFTSVLIVISEHPQRTETLH

>Columba_livia

MLENFTSVLIVISEHPQRTETLH

>Haliaeetus_albicilla

MLENFTSVLIVISEHPQRTETLH

>Corvus_cornix_cornix

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>Aptenodytes_forsteri

MLENFTSVLIVISEHPQRTETLH

HG0433 ENSGALG00000002952 NRG4

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>Calidris_pugnax

MQMRDYVDSADCPVRV

>Columba_livia

MQIRDYVDSADCPVHV

>Aquila_chrysaetos_canadensis

MQIRDYVDSADCPVHV

>Zonotrichia_albicollis

MRIRDYVDSADCPVHV

>Aptenodytes_forsteri

MQIRDYVDSADCPVHV

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>Calidris_pugnax

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>Aquila_chrysaetos_canadensis

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>Pygoscelis_adeliae

MSTHTFIFLCLETPDGRLSGESF

>Struthio_camelus_australis

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HG0435 ENSGALG00000010778 CHRM3

>Gallus_gallus

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>Anser_cygnoides

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>Egretta_garzetta

MVMAKSFISVWYNGLPVG

>Aptenodytes_forsteri

MVMAKSFISVWYNGLPVG

>Gallus_gallus
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>Anser_cygnoides
-----MESIFKTVNLGRSIHCSICIS-----
>Apteryx_australis_mantelli
-----MESTFKTVNL-----
>Calidris_pugnax
-----MESTFKTVKL-----
>Columba_livia
-----MESTFKTVKL RMSIHFNNS-----
>Pygoscelis_adeliae
-----MESTFKTVKL-----

>Gallus_gallus
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>Haliaeetus_leucocephalus
-----MCPTLDIPALNV
>Parus_major
-----MCPTLDIPALNV
>Melopsittacus_undulatus
-----MCPTLDIPALNV
>Aptenodytes_forsteri
-----MCPTLDIPALNV

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>Gallus_gallus

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>Anser_cygnoides

MWYTAWC-----

>Falco_cherrug

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>Corvus_brachyrhynchos

MWFAGRCCLTCKERWFCV

>Aptenodytes_forsteri

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>Gallus_gallus

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>Calidris_pugnax

MQKTIPCLFVHE

>Aquila_chrysaetos_canadensis

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>Taeniopygia_guttata

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>Pygoscelis_adeliae

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>Anas_platyrhynchos

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>Calidris_pugnax

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>Corvus_cornix_cornix

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>Aptenodytes_forsteri

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>Gallus_gallus

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>Apteryx_australis_mantelli

MNCKTRGSVAAIPTSGFPSLL

>Corvus_brachyrhynchos

MNFKTAGSVAALPTSSFPSLL

>Struthio_camelus_australis

MNCKTRGSVAAVPTSGFPSLL

>Tinamus_guttatus

MNCKTRGSVAAVPTSAFPSLL

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>Gallus_gallus

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>Calidris_pugnax

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>Aquila_chrysaetos_canadensis

MAVMKYFLVLD**M**TFTTT**M**N-**Q**EKPIKSS

>Corvus_brachyrhynchos

-----MTFST**M**N-**Q**EPVKSS

>Struthio_camelus_australis

-----MTFTIR**M**N-**Q**EKPAKSS

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>Gallus_gallus
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>Anas_platyrhynchos
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>Calidris_pugnax
MGWVSNHVS-----
>Struthio_camelus_australis
MGWVSNHVS-----
>Tinamus_guttatus
MGWVSNHVS-----

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>Gallus_gallus

-----MLYLPKEKILHPAFELRESRNKTTQNNPPR-----RKRPTVLLPDH

>Aquila_chrysaetos_canadensis

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>Lepidothrix_coronata

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>Struthio_camelus_australis

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>Gallus_gallus

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>Anas_platyrhynchos

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>Pygoscelis_adeliae

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>Anser_cygnoides
-----MATWALEVEI
>Calidris_pugnax
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>Parus_major
-----MISTATWAFKAGV

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>Gallus_gallus

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>Anser_cygnoides

MKLILK-----

>Calidris_pugnax

MKLILKECFQKEN

>Corvus_cornix_cornix

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HG0448 ENSGALG00000011762 UBA6

>Gallus_gallus

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>Aquila_chrysaetos_canadensis

MNPGLPAIPAC

>Lepidothrix_coronata

MSPGLPAIPAC

>Aptenodytes_forsteri

MNPGLPAIPAC

HG0449 ENSGALG00000014106 PPF1BP1

>Gallus_gallus

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>Apteryx_australis_mantelli

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>Aquila_chrysaetos_canadensis

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>Pseudopodoces_humilis

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>Gallus_gallus

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>Anas_platyrhynchos

MGMNGKRKDMRNS--THNGRDL CERFY

>Calidris_pugnax

-----MRDR--SHDGRDLCERFC

>Aptenodytes_forsteri

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>Gallus_gallus

MGL-----CTD---FR---LYRSESGQVTEEDAGTVRTSEK

>Apteryx_australis_mantelli

-----MLKTCEK

>Aquila_chrysaetos_canadensis

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>Lepidothrix_coronata

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>Chaetura_pelagica

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>Apteryx_australis_mantelli

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HG0453 ENSGALG0000005995 SLC13A5

>Gallus_gallus

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>Calidris_pugnax

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>Manacus_vitellinus

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HG0454 ENSGALG00000007186 TMEM268

>Gallus_gallus

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>Anas_platyrhynchos

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>Falco_cherrug

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>Gallus_gallus

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>Anas_platyrhynchos

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>Columba_livia

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>Pseudopodoces_humilis

MHYSKFLVSSSG

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>Gallus_gallus

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>Apteryx_australis_mantelli

MEQLGQIGSLHFMLLAYRTQIYL--

>Gavia_stellata

MEQLGQIGSLHFMLSAYHGTQTTLCL

HG0458 ENSG00000060339 CCAR1

>Homo_sapiens

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>Acinonyx_jubatus

MRRRGEAWRKRGKLAHAPKADGFEMASVLAGTRFRSLL-----

>Balaenoptera_acutorostrata_s

-----MASVLAGTGFRSLLLKTNK

>Miniopterus_natalensis

-----MASVLAGTRFRSLL-----

>Dasypus_novemcinctus

MGRKGEAWRKREKLAHAPKADGFEMASVLAGSRLRLF-----

>Sarcophilus_harrisii

-----MASALAATRLRSPL-----

>Galeopterus_variegatus

-----MASVLTGTRLR-----

>Monodelphis_domestica

-----MASALAATRLRSFL-----

>Trichosurus_vulpecula

-----MASALAATRLRSLL-----

>Sorex_araneus

-----MASLLAGTRFRSLP-----

>Oryctolagus_cuniculus

-----MASVLAGTRLRTLL-----

>Elephantulus_edwardii

-----MASVLTGFRLRSLL-----

>Equus_caballus

-----MASVLAGTRFRSLL-----

>Manis_javanica

-----MASVLAGTRFRSLL-----

>Loxodonta_africana

-----MASLLTRSRLRSLL-----

>Fukomys_damarensis

-----MASVLAGTRFRSLL-----

>Tupaia_chinensis

-----MASALAGTRLR-----

>Trichechus_manatus_latirostr

-----MASVLTGIRFRSLL-----

>Orycteropus_afer_afer

-----MASVLAGTRLRSLL-----

>Homo_sapiens
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>Canis_lupus_familiaris
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>Lipotes_vexillifer
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>Eptesicus_fuscus
MKGRNSTMISFSTVQNSFP
>Dasypus_novemcinctus
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>Sarcophilus_harrisii
-----MISFSTLQHPLP
>Galeopterus_variegatus
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>Monodelphis_domestica
-----MISFSTLQHPLP
>Condylura_cristata
-----MISFSTLQHSLP
>Oryctolagus_cuniculus
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>Manis_javanica
-----MISFSTVQHCLP
>Loxodonta_africana
-----MISFSTLQHFLP
>Marmota_marmota_marmota
-----MISFSTLQHSLP
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
-----MISFSTLQHSLP

>Homo_sapiens
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>Orcinus_orca
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>Myotis_brandtii
MGICLTYFIEESDGISGLRWY
>Dasypus_novemcinctus
MGICLTYFIEELECISD----
>Galeopterus_variegatus
MGICLTYFIEELNGISD----
>Erinaceus_europaeus
MGICLTYLTEELDGIND----
>Oryctolagus_cuniculus
MGICLVDLIEELDGVSD----
>Ceratotherium_simum_simum
MGICLTYFIEELDGVSD----
>Jaculus_jaculus
MGICLTYFIEEFDGISD----
>Tupaia_chinensis
MGICSTYFIEELDGISD----
>Trichechus_manatus_latirostr
MGICLLYFIEELDDISD----
>Orycteropus_afer_afer
MGICLTYFIEELDGISD----

>Homo_sapiens
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>Lipotes_vexillifer
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>Rousettus_aegyptiacus
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>Galeopterus_variegatus
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>Trichechus_manatus_latirostr
MSASLLLWEEEEKEE---EEEEEEEEKAGAGGAVAEAAATAKVLPPPPFPSSPGPSEGWSCRRLQSVTARLGARPRIKGGIGCSLEIQPSDLAGWAFACYTL
>Orycteropus_afer_afer
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>Homo_sapiens

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>Eptesicus_fuscus

MAMV----MAAVTRTAPIKLRSEYIQKVPRRNFLPEKLKKQYL

>Dasypus_novemcinctus

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>Sarcophilus_harrisii

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>Macropus_eugenii

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>Condylura_cristata

-----MAAVTPTAPVKLRSGRYIQKVPRRTFLLEKMKKQYL

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>Ceratotherium_simum_simum

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>Manis_javanica

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>Loxodonta_africana

-----MRYMQKVPRRNFLPEKLKKQYL

>Nannospalax_galili

MEAV----MAAAPRTAPVKLHSGRFIQKVPRRNFLSEKLKKQYL

>Tupaia_chinensis

MAMV----MAAVTRTAPVKLRSGRYIQKVPRRNFLPEKLEKQYL

>Trichechus_manatus_latirostr

MAVV----MAAVRTAIVELRSKRYIQKVPRRNFLPEKLKKQYL

>Orycteropus_afer_afer

MAMV----MAAVTQRAPVKLRSGRYIQKVPGRNYLPEKLKKQYL

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>Lipotes_vexillifer

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>Miniopterus_natalensis

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>Dasypus_novemcinctus

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>Sarcophilus_harrisii

MAPARERPWPQR

>Galeopterus_variegatus

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>Monodelphis_domestica

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>Erinaceus_europaeus

MAPVRERPWPTQ

>Oryctolagus_cuniculus

MAPVRERPWPQR

>Elephantulus_edwardii

MAPARERLWPQR

>Equus_asinus

MAPVRERPWPTQ

>Manis_javanica

MAPVWERPWPTQ

>Loxodonta_africana

MAPVRERSWPQR

>Dipodomys_ordii

MAPVRERPWPSQ

>Tupaia_chinensis

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>Trichechus_manatus_latirostr

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>Homo_sapiens
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>Acinonyx_jubatus
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>Orcinus_orca
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>Pteropus_allecto
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>Dasypus_novemcinctus
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>Loxodonta_africana
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>Trichechus_manatus_latirostris
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>Orycteropus_afer_afer
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>Ailuropoda_melanoleuca
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>Balaenoptera_acutorostrata_s
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>Eptesicus_fuscus
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>Dasypus_novemcinctus
-----MKGPSWGLLATGAGS
>Sarcophilus_harrisii
-----MKGLSWGLPATSAVS
>Galeopterus_variegatus
-----MKGPSWGLLATSAVS
>Monodelphis_domestica
-----MKGLSWGLPATSAVS
>Erinaceus_europaeus
-----MKGPSWGLLATSAVS
>Oryctolagus_cuniculus
-----MKGPSWGLLATGAGS
>Elephantulus_edwardii
-----MKGPSWGLLATSAVS
>Ceratotherium_simum_simum
-----MKGPSWGLLATSAVS
>Manis_javanica
-----MKGPSWGLFATSAGS
>Loxodonta_africana
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>Dipodomys_ordii
-----MKGPSWGLLATSAVS
>Trichechus_manatus_latirostr
-----MKGPSWRLFATSAGS
>Orycteropus_afer_afer
-----MKGPSWGLLATSAVS
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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Physeter_catodon
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>Pteropus_alecto
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>Dasypus_novemcinctus
-----MLRHMGGQQGGHPVQRGPL

>Sarcophilus_harrisii
-----MLRHAGQHQRGCP IRRGPL

>Galeopterus_variegatus
-----MLRYMGWQRGHP IQRGPL

>Monodelphis_domestica
-----MLRHAGHHQRGCP IRRGPL

>Macropus_eugenii
-----MLRHAGQHQRGCP IRRRPL

>Condylura_cristata
-----MVGDLDPGRRRFQSGFD-----WRNLWSSCWLT PLADGMLRHMGRQKGRPIQGGPL

>Oryctolagus_cuniculus
-----MVGGLDPPGRRRFQKGF-----WRNLWSSCWLV PLADGMLKYMGRQRGHPFQRGPL

>Ceratotherium_simum_simum
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>Manis_javanica
-----MCVQGGGRQKQLELR LKEESWRLIS-----VQRKLSRATVFDLSGWL APLADGMLRHKGWQRGHP IQRGPL

>Loxodonta_africana
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>Chinchilla_lanigera
-----MLRYMGWQRGHP IQRGPL

>Tupaia_chinensis
-----MSHEGGWLA PLADGMLTYMGWQQGHL IQRGPL

>Trichechus_manatus_latirostr
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>Homo_sapiens

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>Orcinus_orca

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>Rousettus_aegyptiacus

-----MRNSKERIQLQFKSLQNLRLSLLL-----
>Dasypus_novemcinctus

-----MRNSKERIQLQLKAYKI-----
>Sarcophilus_harrisii

-----MKNRTERIYFPFKSRRNLRFSLLL-----
>Galeopterus_variegatus

-----MRNSKDRIQLQFKSLQNLRLSLLS-----
>Condylura_cristata

-----MRNSKETIQLQFKSLQNLRPSLLL-----
>Elephantulus_edwardii

-----MRNSKERIQLQFKSLQNLRLSLLL-----
>Equus_caballus

-----MRNSKERIQLQFRSLQDLRLSLLS-----
>Manis_javanica

-----MRRSKERIQLQLKSLHDLGVSLLL-----
>Loxodonta_africana

-----MRNSKERIQLQFRSLQNLKLSLLL-----
>Rattus_norvegicus

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>Tupaia_chinensis

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>Trichechus_manatus_latirostr

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>Orycteropus_afer_afer

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>Lipotes_vexillifer
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>Miniopterus_natalensis
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>Dasypus_noveboracensis
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>Sarcophilus_harrisii
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>Galeopterus_variegatus
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>Macropus_eugenii
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>Oryctolagus_cuniculus
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>Equus_przewalskii
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>Manis_javanica
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>Loxodonta_africana
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>Marmota_marmota_marmota
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>Orycteropus_afer_afer
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>Homo_sapiens
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>Mustela_putorius_furo
-----MTSRHRRENRVQAQKLFPHHHLLKN
>Tursiops_truncatus
-----MTSQHLRENRVQAQKLFPHHHLLKN
>Pteropus_vampyrus
-----MTSRHRRENRVQAQKLFPHHHLLKN
>Dasypus_novemcinctus
-----MTFRHRRENRVQAQKLFPHHHLLKN
>Sarcophilus_harrisii
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>Galeopterus_variegatus
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>Monodelphis_domestica
-----MTARYASENRVQAQKPFLYHHLLRN
>Condylura_cristata
-----MISRHRRENRVQAQKLFPHHHLLKN
>Oryctolagus_cuniculus
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>Equus_asinus
-----MTSWHRRENRVQAQKLFPHHHLLKN
>Manis_javanica
-----MTSWHRRENRVQAQKFLHHHHLLKN
>Loxodonta_africana
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>Nannospalax_galili
-----MTSRHRRENRVQAQKLFPHHHLLKN
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Homo_sapiens

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>Orcinus_orca

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>Miniopterus_natalensis

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>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

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>Marmota_marmota_marmota

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>Tupaia_chinensis

-MLWFCAGDPSLLSIQTKKTGI

>Homo_sapiens	MLLPRLVLETDLDRSPTLGVHSEWENEGRRVRISQPLSSPGQNPWMSLWDRSS-----
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>Orcinus_orca	-----MNLWDSS-F-----
>Myotis_brandtii	-----MSLWDPSS-----
>Dasypus_novemcinctus	-----MSPWDVSF-----
>Galeopterus_variegatus	-----MSLWDPSS-----
>Macropus_eugenii	-----MNLWDSS-YPFGLALRDW--
>Erinaceus_europaeus	-----MSLWDPSS-----
>Oryctolagus_cuniculus	-----MSLWDPSSWPRGLKPVALGL
>Equus_asinus	-----MSLWDPSS-----
>Manis_javanica	-----MSLWEPSS-----
>Loxodonta_africana	-----MSLWDPSSWPCGLEPVALGL
>Ictidomys_tridecemlineatus	-----MRLWDPSS-----
>Tupaia_chinensis	-----MSLWDPSF-----
>Trichechus_manatus_latirostr	-----MSLWDPSSWPCGLEPVALGL
>Orycteropus_afer_afer	-----MSLCDPSF-----

>Homo_sapiens
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>Physeter_catodon
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>Eptesicus_fuscus
MKGAKLPAAGQASR
>Dasypus_novemcinctus
MKGAKLPAAGQASR
>Sarcophilus_harrisii
MKGTELPAAGHSSR
>Monodelphis_domestica
MKGTELPAAGHSSR
>Condylura_cristata
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>Oryctolagus_cuniculus
MKGAKLPAAGQASR
>Ornithorhynchus_anatinus
MKGTKLPAAGHSSR
>Ceratotherium_simum_simum
MKGAKLPAAGQASR
>Manis_javanica
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>Loxodonta_africana
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>Cavia_porcellus
MKGAKLPAAGQASR
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Panthera_tigris
----MWAPQPAERGAEPQRSPF
>Balaenoptera_acutorostrata_s
----MWAPQPAERGAEPQRSPF
>Rousettus_aegyptiacus
----MWAPQPSAERGAEPQRSPF
>Dasypus_novemcinctus
----MWPPQPAERGAGKPQRSCF
>Sarcophilus_harrisii
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>Galeopterus_variegatus
----MWAPQPAERGAGKPQRSPF
>Condylura_cristata
----MWAPQPAERGAEPQRSPF
>Ochotona_princeps
----MWAPQPAERGAGKPQRSPF
>Elephantulus_edwardii
----MWAPRPTAARGAGKPQRSPF
>Equus_przewalskii
----MWAPQPAERGAEPQRSPF
>Manis_javanica
----MWAPQPAERGAEPQRSPF
>Loxodonta_africana
----MWAPQPAERGAGKPQRSPF
>Heterocephalus_glaber
----MWAPQPTAERGAGKPQRSPF
>Trichechus_manatus_latirostr
----MWAPQPATERGAGKPQRSPF
>Orycteropus_afer_afer
----MWAPQPAERVAGKPQRSPF

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>Homo_sapiens
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-----MTIKEHTWTCGTWKCVRKRKSIIF--
>Balaenoptera_acutorostrata_s
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>Pteropus_alecto
-----MSIKEHTWTCGTWKCVRKRKAVIL--
>Dasypus_novemcinctus
-----MTVKGDTWTHGTWKCVRQRKSIIL--
>Galeopterus_variegatus
-----MTIKEHTWTCGTWKCVRKRKSVL--
>Macropus_eugenii
-----MSINEDTWTFTWKCVRKQGLQGF--
>Condylura_cristata
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Ceratotherium_simum_simum
-----MTVKEHTWTCGTWKCVRKRKSIIL--
>Loxodonta_africana
-----MTIKEEDTWCATWKCVRKRKTSINL--
>Chinchilla_lanigera
-----MTIKEHTWTCGTWKCVRKRKSIIL--
>Trichechus_manatus_latirostr
-----MTVKEDTWTGTCWKCVRKRKSIISL--
>Orycteropus_afer_afer
-----MTVQEDKWTWGTWKCVRKRKPVIL--

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>Tursiops_truncatus
-----MEEVRKLARSPRASQDPVTQ
>Rousettus_aegyptiacus
-----MEEVRKLARSPRASQDQVTQ
>Monodelphis_domestica
-----MEEVRKLARSPRARQDPVTQ
>Condylura_cristata
-----MEEVRKLARSSRASQDQVTQ
>Oryctolagus_cuniculus
-----MEEVRKLARSPRASQDPVTQ
>Elephantulus_edwardii
-----MEEVRKLARSSRASQQPATQ
>Equus_przewalskii
-----MEEVRKLARSPRASQDPVTQ
>Manis_javanica
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>Loxodonta_africana
-----MEEVRKLARSPRASQDPVTQ
>Peromyscus_maniculatus_baird
-----MEEVRKLARSPRASQDPVTQ
>Tupaia_chinensis
-----MEEVRKLAQSPRASQDPVTQ
>Trichechus_manatus_latirostr
-----MEEVRKLARSRRASQDPVTQ
>Orycteropus_afer_afer
-----MEEVRKLARSPRASQDPVTQ
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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Lipotes_vexillifer
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>Pteropus_alecto
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>Dasypus_novemcinctus
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>Galeopterus_variegatus
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>Monodelphis_domestica
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>Condylura_cristata
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>Ochotona_princeps
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>Equus_asinus
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>Manis_javanica
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>Loxodonta_africana
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>Marmota_marmota_marmota
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>Tupaia_chinensis
MRKGDACHPSCAKIEK-----
>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Leptonychotes_weddellii
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>Orcinus_orca
MSDSEPSARALTR
>Myotis_davidii
MSDSAPSAQALTR
>Dasypus_novemcinctus
MSDSAPSAQALTR
>Erinaceus_europaeus
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>Oryctolagus_cuniculus
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>Equus_przewalskii
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>Manis_javanica
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>Loxodonta_africana
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>Mus_musculus
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>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Pteropus_alecto
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>Monodelphis_domestica
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>Oryctolagus_cuniculus
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>Equus_przewalskii
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>Loxodonta_africana
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>Octodon_degus
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>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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>Homo_sapiens
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>Canis_lupus_familiaris
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>Orcinus_orca
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>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
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>Sarcophilus_harrisii
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>Galeopterus_variegatus
MAAPANLP GPTSGRQRRL
>Erinaceus_europaeus
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Heterocephalus_glaber
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>Trichechus_manatus_latirostris
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>Orycteropus_afer_afer
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>Homo_sapiens	MNNTWWGEGER-VGVEG-----
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>Orcinus_orca	MNNTWWGEGVR-VGVEG-----
>Pteropus_alecto	MNNTWWGEGVR-VGVEG-----
>Dasypus_novemcinctus	MNNTWWGEGVR-VGVEG-----
>Galeopterus_variegatus	MNNTWWGEGVR-VGVEGRRRIYSSSESI AVLPLPPARAPAWRRGVAGLF
>Monodelphis_domestica	MNNTWWGEGVR-VGVEG-----
>Condylura_cristata	MNNTWWGEGVR-VGVEG-----
>Ochotona_princeps	MNNTWWGEGVR-VGVEG-----
>Equus_przewalskii	MNNTWWGEGVR-LGVEG-----
>Ictidomys_tridecemlineatus	MNNTWWGEGVR-VGVEG-----
>Tupaia_chinensis	MNNTCWGEGVRRVGVEG-----
>Trichechus_manatus_latirostr	MNNTWWGEGVR-VEVEG-----
>Orycteropus_afer_afer	MNNTWWGEGVK-VRVER-----

>Homo_sapiens
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>Rhinolophus_ferrumequinum
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>Dasypus_novemcinctus
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>Sarcophilus_harrisii
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>Monodelphis_domestica
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>Condylura_cristata
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>Manis_javanica
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>Homo_sapiens
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>Lipotes_vexillifer
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>Sarcophilus_harrisii
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>Galeopterus_variegatus
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>Monodelphis_domestica
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>Ornithorhynchus_anatinus
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>Manis_javanica
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>Dipodomys_ordii
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>Homo_sapiens

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>Lipotes_vexillifer

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>Monodelphis_domestica

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>Condylura_cristata

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>Oryctolagus_cuniculus

-----MAQPTASAKLVRP IRAVCRILQIPESDPSNLRP

>Geraotherium_simum_simum

-----MAQPTASAKLVRP IRAVCRILQIPESDPSNLR

>Manis_javanica

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>Ictidomys_tridecemlineatus

-----MAQPTASAKLVRP IRAVCRILQIPESDPSNLRP

>Tupaia_chinensis

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>Orycteropus_afer_afer

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>Monodelphis_domestica
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>Oryctolagus_cuniculus
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>Ceratotherium_simum_simum
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>Manis_javanica
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>Ictidomys_tridecemlineatus
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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>Balaenoptera_acutorostrata_s
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>Galeopterus_variegatus
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>Equus_asinus
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>Dipodomys_ordii
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>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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HG0481 ENSG00000198963 RORB

>Homo_sapiens
MVFSAEQLFADHLLHSC
>Ursus_maritimus
MVFSAEQLFADHLLHSC
>Balaenoptera_acutorostrata_s
MVFSAEQLFADYLPSC
>Rousettus_aegyptiacus
MVFSAEQLFADHLLHSC
>Monodelphis_domestica
MVFSAEQLIFGCSL-HSC
>Condylura_cristata
MVFSAKQLFAFHLLHSC
>Elephantulus_edwardii
MVFSAEQLFTDHLHPSC
>Ceratotherium_simum_simum
MIFSAEQLFADHLLHSC
>Manis_javanica
MVLSEQLFADHLLQCC
>Loxodonta_africana
MVFSAEQLFTDHLHLC
>Peromyscus_maniculatus_baird
MLLSAEQLFADRLLPSC
>Tupaia_chinensis
MVFSAEQLFTDYLLHSC
>Trichechus_manatus_latirostr
MVSSAEQLFTNHLLHSC
>Orycteropus_afer_afer
MVFSAEQPFVDHLVHSC

>Homo_sapiens

-----MGSEAPASGCGAVRSSQREAAASR-----

>Odobenus_rosmarus_divergens

MLTPAVGSPSFFFFFFFFGRPRRLRTGCGMGSEAPASGSGGAVRSSQGEAAAAASR-----

>Physeter_catodon

-----MGSEAPASGSGGAVRSSQGEAAAAASR-----

>Pteropus_alecto

-----MGSKAPASGSGGAVRSSQGEAAAAASR-----

>Dasypus_novemcinctus

-----MGSGAPASGCGWAVSSSQGEAGAAASQ-----

>Galeopterus_variegatus

-----MGSEAPASGCGGAVRSSQGEAAAAASR-----

>Monodelphis_domestica

-----MGSEVPESGCGWAENSSQGEETAGAATAEATAAAAAASCP-----

>Condylura_cristata

-----MGSEAPANGSSGAVRSSQGEAAAFSR-----

>Oryctolagus_cuniculus

-----MGSEAPASGCGGAVRSGQGEAAAAVSR-----

>Equus_asinus

-----MGSEAPASGGGGAVRSGRGEAEAAARR-----

>Manis_javanica

-----MGSEAPASCSGDGAVRSSQGEAAVACR-----

>Rattus_norvegicus

-----MGSEAPASGCGGAVRSTQREAAVAALR-----

>Trichechus_manatus_latirostr

-----MGSEALASGCGGAVRSSQGEVAAAACR-----

HG0483 ENSG00000164463 CREBRF

>Homo_sapiens
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>Ailuropoda_melanoleuca
MERGRGPCSGTGPSP
>Orcinus_orca
MERGRGPCSGTGPSP
>Rousettus_aegyptiacus
MERGRGPCSGTGPSP
>Dasypus_novemcinctus
MERGRGPCSGTGPSS
>Sarcophilus_harrisii
MERGRGPRTGTGPSP
>Galeopterus_variegatus
MERGRGPCSGTGPSP
>Macropus_eugenii
MERGRGPRSGTGPSP
>Oryctolagus_cuniculus
MERGRGPCSGTGPSP
>Equus_przewalskii
MERGRGPCSGTGPRP
>Manis_javanica
MERGRGPCSGTGPRP
>Ictidomys_tridecemlineatus
MERGRGPCSGTGPIIP
>Trichechus_manatus_latirostr
MERGRGPCSGTAPSP

>Homo_sapiens
MNQLASISLTNHRKMRDCLGATTSTMSPCTG-
>Canis_lupus_familiaris
-----MRDCLGTSNSTMSPCTG-
>Eptesicus_fuscus
-----MRDCLGTSTSTMRPCTG-
>Galeopterus_variegatus
-----MRDCLGTSTSTMGPCTG-
>Monodelphis_domestica
-----MRDCPGSASSTMSTACTD
>Elephantulus_edwardii
-----MRDYLSANTSTMSPCTG-
>Ceratotherium_simum_simum
-----MRDCLSTSPSTMSPCTG-
>Manis_javanica
-----MRDCLGTSTSTRNPCTG-
>Loxodonta_africana
-----MRDCLGASTSTMSPCTG-
>Chinchilla_lanigera
-----MRDCLGSSSSTMSPCTG-
>Tupaia_chinensis
-----MQDCFGASSAMSPCTG-
>Trichechus_manatus_latirostr
-----MRDCLGASTSTMSPCTG-
>Orycteropus_afer_afer
-----MRDCLGASTSIMSPCTG-

>Homo_sapiens
MSGDNYGEVILSHTLGFLVVSFSKTVDLNLLAQA
>Mustela_putorius_furo
MSRDNY-----
>Orcinus_orca
MRRDNY-----
>Pteropus_alecto
MSRDNY-----
>Monodelphis_domestica
MSRDNY-----
>Macropus_eugenii
MSRDNY-----
>Erinaceus_europaeus
MSRDNY-----
>Ochotona_princeps
MSGDNYGEVILSHTLGFLVVSFSETVDLNLRA--
>Equus_caballus
MSRDNY-----
>Manis_javanica
MSRDNY-----
>Microtus_ochrogaster
MSGDNYGEVRLSHALGFLVVSFSKTVDLNLLGRA
>Tupaia_chinensis
MSGDNYGEVALSHTLGFL-VSFSETVDLNLRA--
>Trichechus_manatus_latirostr
MSGDNY-----

HG0485.2 ENSG00000183715 OPCML

>Homo_sapiens

MQEGASGSARLES

>Mustela_putorius_furo

MQEGASGSARLES

>Orcinus_orca

MQEGASGSARLES

>Ochotona_princeps

MQEGASGSARLES

>Equus_asinus

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>Mesocricetus_auratus

MQEGASGSARLES

HG0486 ENSG00000067900 ROCK1

>Homo_sapiens

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>Canis_lupus_familiaris

MRLWASERLWVAVAPGPGSGE-RRSPQ

>Lipotes_vexillifer

MRLWASERLWVAVAPGPGSGE-RRSPQ

>Myotis_brandtii

MRLWASERLWVALAPGPGSGE-RRSPQ

>Dasypus_novemcinctus

MRLWASERLWVAVAPSPGSGE-WRSPQ

>Sarcophilus_harrisii

MRLWDSVRLRVAVAPRARPGERRAQ-

>Sorex_araneus

MRLWASERLWVAVAPGPGSPAERRSPQ

>Ochotona_princeps

MRLWACERLWVAVVPGPGSGEPRC-PQ

>Equus_asinus

MRLWASERLWVAVAPGPGSGE-RRSPQ

>Dipodomys_ordii

MRLWASGRLWVAVAPGPGSGERRWSPQ

>Tupaia_chinensis

MRLWASERLWVAVAPGPGSGE-RRSPQ

>Orycteropus_afer_afer

MRLWASERLWVAVAPGPGSGE-RRSPQ

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>Homo_sapiens
-----MEHFWKDVLDPAGWPAGF
>Mustela_putorius_furo
-----MEHFWKDALDPAGWPLGC
>Lipotes_vexillifer
-----MEHFWKDALDPAGWPVGC
>Rousettus_aegyptiacus
-----MEPFWKDALDPAGWPVGC
>Monodelphis_domestica
MNP CNFAHAYRATCTYTHILSFILTLSAFEFCISMEHFRKDALCPVGWPTGC
>Condylura_cristata
-----MEHFWKDALDPAGWPVCC
>Oryctolagus_cuniculus
-----MEHFWKDTLDPAGWPVGC
>Ceratotherium_simum_simum
-----MEHFWKDALDPAGWPAGC
>Manis_javanica
-----MDHFWKDALDPAGWRVGC
>Ictidomys_tridecemlineatus
-----MEHFWKDTLAPAGWPTGC
>Tupaia_chinensis
-----MEHFWKDDLDPAGWPVGC
>Trichechus_manatus_latirostr
-----MEHLWKDAFDPAGWPVGC
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>Homo_sapiens

-----MWQTEQSHNAFSAGLKTAHRPELPLYLKLHRWLVKFN-----

>Canis_lupus_familiaris

-----MWQTEQSHNAFSAGLKTAHRPELPLYLKLHRWLVKFNRLVL

>Balaenoptera_acutorostrata_s

-----MWQTEQSHNAFSAGLKTARRPGTSTILLKIT-----

>Myotis_lucifugus

-----MWQTEQSHNAFSAGLKTAHRPELPLHYLKLHRWLVKFD-----

>Dasypus_novemcinctus

-----MWQTEQSHNAFSAGLKTALRPELPLYLKLHRWLVKFN-----

>Sarcophilus_harrisii

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>Condylura_cristata

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>Oryctolagus_cuniculus

-----MWQTEQSHNAFSAGLRTAHRPELPLYDLKLHRWLVKLN-----

>Equus_przewalskii

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>Manis_javanica

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>Callospermophilus_lateralis

-----MWQTEQSHKAFSEGLDTAHRPELPLHYLKLHRWLVKFN-----

>Tupaia_chinensis

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HG0488.2 ENSG00000116194 ANGPTL1

>Homo_sapiens
MQLPLKSQMNKLLH
>Felis_catus
MQLPLKSQMNKLLH
>Balaenoptera_acutorostrata_s
MQLPLKSQTNKLLH
>Rousettus_aegyptiacus
MQLPLKSQMNKLLH
>Galeopterus_variegatus
-----MNKLLH
>Oryctolagus_cuniculus
MQLPLKSQMNKLLN
>Equus_caballus
MQLPLKSQTSKLLH
>Loxodonta_africana
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>Marmota_marmota_marmota
MQLPLKSQMNKLLH
>Tupaia_chinensis
MQLPLKSQMKLLH

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>Homo_sapiens
-----MLWEKPLPTCPLAWHCPL
>Odobenus_rosmarus_divergens
-----MPWEKPLPTCPLAWRCPL
>Balaenoptera_acutorostrata_s
-----MPWEKPLPICSLTWHCLL
>Myotis_brandtii
-----MGGAPPTCLLAWHCPL
>Dasypus_novemcinctus
-----MGEPLPSCPPTWHCPL
>Galeopterus_variegatus
-----MPWEKPLPTCPLAWHCLF
>Monodelphis_domestica
-----MASAWESPLPAYPLAWHCPL
>Condylura_cristata
-----MPWEKPLPIRPLAWHCPL
>Equus_asinus
-----MPWEKPLPTCPLAWHCLL
>Loxodonta_africana
-----MPWEKLLSTHPPTWHCPL
>Heterocephalus_glaber
MLSAGLGTOGTQPQPREVKPGFLAPFHRGTAGPRLLSEQEQLMAWEKPLPTCPLSWHCPL
>Tupaia_chinensis
-----MPWEKPLLICPLAWHCPL

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HG0490.1 ENSG00000152413 HOMER1

>Homo_sapiens
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>Odobenus_rosmarus_divergens
MAPFILLGRMNRSCPAFASSSPPLLCSES
>Myotis_lucifugus
MAPFI-LGRMNRSCPAFASSPPLLGSES
>Dasypus_novemcinctus
MAPFILLGRMNRSCPAFASSSPPLCS--
>Galeopterus_variegatus
MAPFILLERINRSCPAFASSSTPPLCFES
>Monodelphis_domestica
MASFILFWRMNRSSPAFSSCPPLSSDS
>Sorex_araneus
MAPFILLGRMNRSCPVFSSSPPLLCSES
>Manis_javanica
MVPFILLGRMNRSCPAFASSSPPLLCSES
>Loxodonta_africana
MAPFILLGRVNRSCPVFSSSLPPLLCSES
>Dipodomys_ordii
MAPFLLLGRMNRSCLAFASSSTPPLR-SES
>Tupaia_chinensis
MAPFI-LGRMNRSCPAFASSSPPLSSES
>Orycteropus_afer_afer
MAPFILLGSMRSCPVFSSSLPPLLCSES

HG0490.2 ENSG00000152413 HOMER1

>Homo_sapiens

MPPLFERFGIYKREIILPKRTN

>Acinonyx_jubatus

MPPLLERFGIYEREILLPKGNT

>Balaenoptera_acutorostrata_s

MPPLFEHFGISQREIILPKGNT

>Pteropus_vampyrus

MPPLFEHFGIYGREIILPKGNT

>Galeopterus_variegatus

MPPLFERFGVYQREIILPKRTN

>Condylura_cristata

MPPLFERFGVYEREIILPKGNT

>Ceratotherium_simum_simum

MPPLFERFGIYEGEIILPKGNT

>Manis_javanica

MSPLFERFDIYKREIILPKGNT

>Dipodomys_ordii

MPPLFERFGVYERELILPKRNN

>Tupaia_chinensis

MPPLFERFGIYEREIILPKRTN

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>Homo_sapiens
-----MQDTGLRRPEWGTR-----
>Mustela_putorius_furo
-----MQDTGLRRPEWGTRMPDIIRYQLA
>Orcinus_orca
-----MQDTGLRRPEWGTR-----
>Rousettus_aegyptiacus
MKAASGSMQDTGLLRAELGTR-----
>Monodelphis_domestica
-----MQDTGLRRPELGTR-----
>Condylura_cristata
-----MEDTGLRRPEWGTR-----
>Ochotona_princeps
-----MQDTGLRRLDWGTR-----
>Elephantulus_edwardii
-----MQDTWLRSEWGPR-----
>Ceratotherium_simum_simum
-----MQDTGLRRPEWGPR-----
>Loxodonta_africana
-----MQDTGLRPEWGTR-----
>Ictidomys_tridecemlineatus
-----MQDTGLRRPEWGTR-----
>Trichechus_manatus_latirostr
-----MQGTGLRPPELGTR-----
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>Homo_sapiens
-----MEYLFESWMYFSHLLAS-----
>Mustela_putorius_furo
-----MEYLFESWIYFSHSHLAS-----
>Orcinus_orca
-----MEYLLASWMYFSHSHLAS-----
>Pteropus_alecto
-----MEYLFECWMYFSHCHLAS-----
>Galeopterus_variegatus
-----MEYLFESWMYFPHGLAS-----
>Monodelphis_domestica
-----MECLDFWIIHYSHSHLAS-----
>Erinaceus_europaeus
-----MDYLFESWMYFSHSHRAS-----
>Equus_asinus
MPPGTADYFKVPPPCSYHCTLIWKIMEYLCESWMIISHSHLASWNFLWC
>Loxodonta_africana
-----MMEYLFESWTYFSHSHLAS-----
>Heterocephalus_glaber
-----MEYLFESWMYFSHGHLAS-----
>Trichechus_manatus_latirostr
-----MEYLFESWTYFSHSHLAS-----
>Orycteropus_afer_afer
-----MYFSHSHLAY-----

HG0493 ENSG00000164707 SLC13A4

>Homo_sapiens

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>Canis_lupus_familiaris

MPPSITLPRCLSAGPRTMLSNPT

>Balaenoptera_acutorostrata_s

MPPFIILSRFLFAGHKMTLTNPT

>Rhinolophus_ferrumequinum

MSRFTILCRFLSAGHKMTLTNPT

>Dasypus_novemcinctus

MPPFTILSQYLFAGHKTMLINPT

>Galeopterus_variegatus

MPPFIILSQFLSAGHKTMLINPT

>Monodelphis_domestica

MPQFVILGQFPFPAQKTLLINPT

>Oryctolagus_cuniculus

MPPHRTLSQFLFAGHKTMLINPT

>Ceratotherium_simum_simum

MPPFIIFSHFLFAGHKTMLANPT

>Manis_javanica

-----MLTDPS

>Peromyscus_maniculatus_baird

-----MLLNPT

>Tupaia_chinensis

MPPFIILSQFLFAGHKTMLINPT

>Homo_sapiens
-----MHAAVENIPELKKCNYVLCVLNAQKN---P---DPVGKRDEMWRE
>Mustela_putorius_furo
-----MLDAVENTPELKKCNGMLC--VCVKYQKSP---DPVGNRDEMWRE
>Orcinus_orca
-----MFDAVENTPELKKCNWMLCVR-----
>Rousettus_aegyptiacus
-----MLDPVENIPELKKCNWMLCVLNTRRAQTSWVIETKCGEND-----
>Dasypus_novemcinctus
MRNFAGNCHLGEQPESPHHPNSDVSQKLETSAVSISDGNRLLDVGNTPALKKCSWMLCVC-----
>Monodelphis_domestica
-----MQSTVENIPELKKCNWMLCVCSIQGAPIS-----CG-----
>Condylura_cristata
-----MLDAVENTPELKKCNWMCVCVCVKYQKSP---DPMGNKDEMWRE
>Ceratotherium_simum_simum
-----MLDAVENTPELKKCNWMLC--VC-----
>Loxodonta_africana
-----MLDAVENTPELKKCNWMCVCEIPE---EP---RPSG-----
>Nannospalax_galili
-----MLDAVENTPELKKCNWMLLNTRS---P---DPVGNRDEMWRE
>Trichechus_manatus_latirostr
-----MLDAVENTPELKKCNWMLCVC-----
>Orycteropus_afer_afer
-----MLGAVENTPEVKCNWVLCVC-----

>Homo_sapiens
-----MHEGATEAQRW
>Felis_catus
-----MHEGPTEAQRW
>Balaenoptera_acutorostrata_s
-----MHEGPTEAQRW
>Rousettus_aegyptiacus
-----MHEGPTEAQRW
>Galeopterus_variegatus
-----MHEGPTEAQRW
>Erinaceus_europaeus
-----MYEGPTEAQKRW
>Oryctolagus_cuniculus
MVGLRQRSGEIRGVLGARDWRPMHEGSTAREPW
>Equus_asinus
-----MHEGPTEAQRW
>Loxodonta_africana
-----MHEGPTTAQRW
>Ictidomys_tridecemlineatus
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>Homo_sapiens
-----MVWEAELKCPGLW
>Mustela_putorius_furo
-----MVWEAELKAGLW
>Orcinus_orca
-----MVWEAELKAGLP
>Eptesicus_fuscus
-----MVWEAELKAGLW
>Dasypus_novemcinctus
MVGLRQRSGGTRGSPGRPGLTDARGARGGAGAAVMWEAELKAGLR
>Galeopterus_variegatus
-----MVWEVEPKCPGLR
>Monodelphis_domestica
-----MVMVWEVELKSVGLW
>Condylura_cristata
-----MVWDAELKAGLW
>Equus_przewalskii
-----MVWEAELKAGLW
>Loxodonta_africana
-----MVWEAELKAGLW
>Nannospalax_galili
-----MHEGPAAEQEAVVMWEAELKCPGLW
>Tupaia_chinensis
-----MVWEEELKCARLW
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>Homo_sapiens
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>Canis_lupus_familiaris
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>Physeter_catodon
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>Pteropus_alecto
MSSSPRRVHCLWHDQNKGELLLHRVFQ
>Monodelphis_domestica
MGSSPRRVLYLWHDQNKDYWK-----
>Oryctolagus_cuniculus
MSSFPRRVHCLWHDQHKGELLLHRVFQ
>Equus_asinus
MSSFPRRVHCLWHDQNKGELLLHRVFQ
>Manis_javanica
MSSSPRRVHCLWHDQNKESFR-----
>Loxodonta_africana
MSSSPRRVLCWHDQNKGELLLHRVFQ
>Octodon_degus
MSSFPRRVPCWHDQNKGELLLHRVFQ
>Trichechus_manatus_latirostr
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>Homo_sapiens
-----MIYAGAEAAARNRAVKRASAY
>Mustela_putorius_furo
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>Pteropus_alecto
-----MIYAGAEAAARNRAVKRASAY
>Galeopterus_variegatus
-----MIYAGAEAAARNRAVKRASAY
>Monodelphis_domestica
-----MIYSGADRARNLAVKKASAY
>Condylura_cristata
-----MIYAGAEAAARNRAVKRASAY
>Oryctolagus_cuniculus
-----MIYAGAEAAARNRAVKRASAY
>Equus_asinus
-----MIYAGAEAAARNRAVKRASAY
>Loxodonta_africana
-----MIYAGAEAAARNRAVKRASAY
>Peromyscus_maniculatus_baird
-----MIYAGAEAAARNRAVKRASAY
>Tupaia_chinensis
-----MIYAGAEAAARNRAVKRASAY
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>Homo_sapiens
-----MRQAAHRPRPP
>Mustela_putorius_furo
-----MRQAAHRPRPP
>Balaenoptera_acutorostrata_s
-----MRQAAHRPRPP
>Rousettus_aegyptiacus
-----MRQAAHRPRPP
>Dasypus_novemcinctus
-----MRQAAHRPRPP
>Monodelphis_domestica
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>Equus_przewalskii
-----MRQAAHRPRPP
>Manis_javanica
-----MRQAAHRPRPP
>Mus_musculus
-----MRQAAHRPRPP
>Tupaia_chinensis
-----MRQAAHRPRPP

HG0499 ENSG00000011258 MBTD1

>Homo_sapiens
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>Mustela_putorius_furo
MLMLLISWGHP
>Orcinus_orca
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>Myotis_lucifugus
MLMLLISWGHP
>Dasypus_novemcinctus
MLMLLISWGHP
>Sarcophilus_harrisii
MLMLLISWGHP
>Oryctolagus_cuniculus
MLMLLISWGHP
>Equus_caballus
MLMLLISWGHP
>Manis_javanica
MLMLLISWGHP
>Mus_musculus
MLMLLISWGHP

>Homo_sapiens
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>Ailuropoda_melanoleuca
MLPSPGLWGLSCFLMAAASAG
>Pteropus_vampyrus
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>Dasypus_novemcinctus
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>Sarcophilus_harrisii
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>Monodelphis_domestica
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>Ceratotherium_simum_simum
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>Manis_javanica
MLPSPGLWRLSCFLMAAAAAG
>Loxodonta_africana
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>Rattus_norvegicus
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HG0501 ENSG00000110400 NECTIN1

>Homo_sapiens

MTRATCGGHLPSL

>Mustela_putorius_furo

MTRATCGGHPPSL

>Pteropus_vampyrus

MTRATCGGHLPSF

>Sminthopsis_crassicaudata

MTRLTCGGHLPRL

>Monodelphis_domestica

MTRLTCGGHLPRL

>Condylura_cristata

MTRATCGGHLPSL

>Ochotona_princeps

MTRATCGGHLPSL

>Ceratotherium_simum_simum

MTRATCGGHLPSL

>Manis_javanica

MTRATCGGHLPSL

>Marmota_marmota_marmota

MTRATCGGHLPSL

>Homo_sapiens
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>Canis_lupus_familiaris
MSEQHDYPLTSRLSFF-----
>Rhinolophus_ferrumequinum
-----MQQNPYL
>Galeopterus_variegatus
-----MQQSPRL
>Monodelphis_domestica
-----MQQNPYL
>Erinaceus_europaeus
MSEQYDYLLTSKLFFF-----
>Oryctolagus_cuniculus
-----MQQNPYL
>Equus_caballus
-----MQQNPYL
>Microtus_ochrogaster
MSEQHAYPLNYKLFFF-----
>Orycteropus_afer_afer
-----MQQNPYL

HG0503 ENSG00000141564 RPTOR

>Homo_sapiens

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>Felis_catus

MGRSWLWLQQLRRVRDPQG

>Orcinus_orca

MGRSWLWLQQLRRVRDPQG

>Rhinolophus_ferrumequinum

MGRSWLWLQQLRRVRDPQG

>Galeopterus_variegatus

MGRSWLWLQQLRRVRDPQG

>Monodelphis_domestica

MGRSWLQLQQLGRMWGPQG

>Ceratotherium_simum_simum

MGRSWLWLQQLRRLRDPQG

>Manis_javanica

MGRSWLPLQQLRRVRDPQG

>Loxodonta_africana

MGRSWLCLQQLRRVRDPQG

>Ictidomys_tridecemlineatus

MGRSWLLPQQLRRVRDPQG

>Homo_sapiens
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>Mustela_putorius_furo
MQTDCRNREERLLLISEEYNQMRHLSQPG-----
>Myotis_lucifugus
MQTDCRNREERLLLISEEYNQMRHLSQPG-----
>Galeopterus_variegatus
-----MKYLSQPGDCFGSCNHLCSKVGKIIQFLPCWTWKERGCVFIPTH
>Condylura_cristata
MQTDCRNREERLLLISEEYNQMRHLSQPG-----
>Oryctolagus_cuniculus
-----MKYLSQPGDCFGSCNHLCSKVGKIIQFLPCWTWKERGCVFIPTH
>Manis_javanica
MQTDCTHREERLLLISEEYNQMRHLSQPG-----
>Peromyscus_maniculatus_baird
MQADCRSRGERLLLISEEHDQMRYSQLGDCFGSCNHLCSKVGKIIQFFPCWTWKERGICALIPTH
>Tupaia_chinensis
-----MRHLSQPGDCFGSCNHLCSKVGKIIILFLPCWTWKEQGCVFIPTH

HG0505 ENSG00000157470

>Homo_sapiens
MGSRGAPTPRADVNY
>Odobenus_rosmarus_divergens
MGSRGAPAPRADVNY
>Lipotes_vexillifer
MGSRGAPAPRADVNY
>Rhinolophus_ferrumequinum
MGSRGAPAPREDVNY
>Dasypus_novemcinctus
MGCRGAPAPRADVNY
>Monodelphis_domestica
MGSRIPPAPSADVNY
>Condylura_cristata
MGPRGAPDSRADVNY
>Oryctolagus_cuniculus
MGSRGAPGPRAADVNY
>Manis_javanica
MGSRRAPAPCAADVNY
>Rattus_norvegicus
MGSRGAPDPRADVNY

>Homo_sapiens
MAAIRDSQAMGTTTDIISFDHCS
>Ursus_maritimus
MAAIRDSQAMGTTTDIVSSFDHCS
>Physeter_catodon
MAAIRDSQAMGTTTDIISFDHCS
>Miniopterus_natalensis
MAAIRDSQAMGTTTDIISFDHCS
>Galeopterus_variegatus
MAAIRDSQAMGSTTDIISFDHCS
>Trichosurus_vulpecula
MAAIGDSPAMELTPDFVSSFDQCS
>Oryctolagus_cuniculus
MAAIRDSQAMGTTTDI-ISFDHCS
>Equus_asinus
MAAIRDSQAMGTTTDI-ISFDHCS
>Manis_javanica
MAAIRDSQAMGTTTDTISFDHCS
>Mesocricetus_auratus
MAAIWDSQAMGTTTDV-ISFDHCA

HG0506.2 ENSG00000177853 ZNF518A

>Homo_sapiens

MSLHSIVSCLNYR

>Mustela_putorius_furo

MSWHSIVSCLNYK

>Balaenoptera_acutorostrata_s

MSRHSIVSCSNYK

>Miniopterus_natalensis

MSQHNIVSCLNYK

>Dasypus_novemcinctus

MCQHSIVSCLNVE

>Galeopterus_variegatus

MSWHSIVSCLNYK

>Equus_asinus

MSRHSIVSCLNYK

>Manis_javanica

MSQHSIVSCLNYK

>Loxodonta_africana

MSQHNIVSCLNFK

>Marmota_marmota_marmota

MSRHSIISCLNYR

HG0507 ENSG00000060237 WNK1

>Homo_sapiens

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>Odobenus_rosmarus_divergens

MTAAPLLLQPSRPPLAAGWMRTVRR

>Rousettus_aegyptiacus

MTAAPLLLQPSRPPLAAGWMWTARR

>Monodelphis_domestica

MTAVPQLLVPARPPPAAGWMRSVRR

>Oryctolagus_cuniculus

MTAAPLLPQPSRPPLAAGWMRTVQR

>Loxodonta_africana

MTAAPLLLQLSWPPLAAGWMRTVRR

>Rattus_sp.

MTAALLLPQPYRPPLAAGWMRTVRR

>Trichechus_manatus_latirostr

MTAALLLLQPSWPTVAAGWMRTVRR

>Orycteropus_afer_afer

MTAAPLLLQSSWLPLAAGWMRTVRR

HG0508 ENSG00000061936 SFSWAP

>Homo_sapiens
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>Acinonyx_jubatus
MAAVSSLGPGCGAFD
>Pteropus_alecto
MAAVSRLGPGCGACD
>Dasypus_novemcinctus
MAAVLRLVLGCGTFD
>Monodelphis_domestica
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>Oryctolagus_cuniculus
MAAVLRLGPGCGAFD
>Equus_asinus
MAAVLRLGPGCGAFD
>Manis_javanica
MAAMPRLGLGCGASD
>Marmota_monax
MAAVLRLRTGCGAFD

>Homo_sapiens

-----MCWWEFGARWSYRFRGNFEPFRIT

>Canis_lupus_familiaris

MPRPAPRGRQDWGFPRLRANTPCRCTCMCPWNLGALWSCRLRGSCPEL---

>Balaenoptera_acutorostrata_s

-----MCRWDSGALWSSRSCGSFEPF---

>Pteropus_alecto

-----MCPWDFGALWSYCLRGNFEPS---

>Dasypus_novemcinctus

-----MCWWNFGALWSYRLCGSIKPF---

>Galeopterus_variegatus

-----MCWWNFGALCSYRLGNFEPF---

>Ornithorhynchus_anatinus

-----MYWWSIGALWSCGLCGNFDPF---

>Ceratotherium_simum_simum

-----MCRWNF-----

>Peromyscus_maniculatus_baird

-----MCWWKFGAGWSYCLRGHFEPF---

HG0510 ENSG00000134769 DTNA

>Homo_sapiens

MVLKSSCCPFIEF

>Acinonyx_jubatus

MVLESSCCFFIEF

>Balaenoptera_acutorostrata_s

MVLKSSCCFFIEF

>Pteropus_alecto

MVLESSCCFFIEF

>Dasypus_novemcinctus

MVLESSCCCFIEF

>Monodelphis_domestica

MVLESSCCAFIEL

>Ceratotherium_simum_simum

MVLESSCCFFIEF

>Tupaia_chinensis

MVLESSCCFFIEF

>Orycteropus_afer_afer

MVLESSCCSFIEF

>Homo_sapiens
MAETSSSPFSSSLVPPARRRERSTAADPAQALPLSQPSRHTMGPEAGLLHSSD----DAGGGPGDSQLPP
>Felis_catus
-----MGPEAGLQHSSD----DAGGGPGDSQLPP
>Balaenoptera_acutorostrata_s
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>Rhinolophus_ferrumequinum
-----MGPEAGLQHSSD----DAGGGPGDSQLPP
>Dasypus_novemcinctus
-----MGPEAGLQYSSD----DAGGGPGDSQLPP
>Sarcophilus_harrisii
-----MGPEAAGQRGSGSGRSGGPTGPGDSQLPP
>Oryctolagus_cuniculus
-----MGPGAASRHSSD----DAGGGPGDSQLPP
>Equus_asinus
-----MGPEAGLRHSSD----DAGGGPGDSQLPP
>Marmota_marmota_marmota
-----MGPEAGLRHSSD----DAGGGPGDSQLPP

>Homo_sapiens
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>Canis_lupus_familiaris
MSCLQQRHNAKGKLRHWKERE---
>Balaenoptera_acutorostrata_s
MSSFHQRHSAKGKLRHWKERE---
>Miniopterus_natalensis
MSCFHQRHSAKGKLRHWKERQ---
>Monodelphis_domestica
MSCFYQKNSREGKLRHQEGRRINK
>Equus_przewalskii
MSCFHQRHSAKGKLRHWKERE---
>Manis_javanica
MSCFRQRHSAEGRLRHWKERE---
>Mesocricetus_auratus
MSCFHQRHSAKGKLRHWKERE---

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>Homo_sapiens
-----MLSAAAVWWGRSAGRKAVTKQNGGS
>Leptonychotes_weddelii
-----MLSAAAVWWGKSAGLKAVTKQNGGS
>Physeter_catodon
--MVLFLCLGFSDAISCCCLEGKSAGLKAVTKQNGGS
>Pteropus_alecto
-----MLSAAAVWWGRSAGLKAVSPQHGGG
>Galeopterus_variegatus
-----MLSAAAVWWGRSAGRKAVAKQNGGS
>Oryctolagus_cuniculus
-----MLSAAAVRWGESAGRKAVTARSGGS
>Elephantulus_edwardii
MRLCCFFVSGSQMLSAAAVQWKSAGLQAVTTQNGGS
>Equus_przewalskii
-----MLSAAAVEWQGSAGLKAVAKQNGGS
>Loxodonta_africana
-----MLSAAV-----
>Cavia_porcellus
-----MLSAAAVRWGKRAGRRAVPKQNSGS
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>Homo_sapiens
MPFTAAVSSFFSFG
>Panthera_tigris
MPFTAAVSSFFSFG
>Lipotes_vexillifer
MPFTAAVSSFFSFG
>Myotis_brandtii
MPFTAAVSSFFSFG
>Sorex_araneus
MPFTAAVSSFFSFG
>Elephantulus_edwardii
MPFTAAVSSFFSFG
>Ceratotherium_simum_simum
MPFTAAVSSFFSFG
>Loxodonta_africana
MPFTAAVSSFFSFG
>Ictidomys_tridecemlineatus
MPFTAAVSSFFSFG

HG0513 ENSG00000126860 EVI2A

>Homo_sapiens

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>Odobenus_rosmarus_divergens

-----MCHLWFGFKSGKLAVHILFFF-----

>Physeter_catodon

-----MCHLWLVES-----

>Miniopterus_natalensis

MCFSCSEKEMCHLWFGKSGKLAVHVLFCRFTLTFLFLQVCSTWKLCLKTRKEVAY

>Manis_javanica

-----MCHLWFGFKTGKLAVHILFYCRFTFKVHDL-----

>Loxodonta_africana

MCFSCSRKEMCHPSVVL-----

>Chinchilla_lanigera

MCLSCSGKEMCHLWFGFKSGKLAVRTLFCRCTLHFVFSKSILL-----

HG0514 ENSG00000147570 DNAJC5B

>Homo_sapiens

MKKRRDLKRDNQLAGKVTNEK

>Panthera_tigris

---MPPVQRDNQLADEVTNEK

>Physeter_catodon

---MTPVQRDNQLADRVTNQK

>Myotis_lucifugus

---MGPLQRDNQLADRVVTNEK

>Ornithorhynchus_anatinus

MSSFRRVFQRDNQLAARVTNDK

>Ceratotherium_simum_simum

---MPPVQRDNQLADRVVTNEK

>Microtus_ochrogaster

---MPPVQRDNQLADKVTNEK

>Tupaia_chinensis

---MAHMQRDNQLAGRVTNEK

HG0515 ENSG00000170471 RALGAPB

>Homo_sapiens

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>Leptonychotes_weddellii

MRAPPVASGAIWIVL

>Balaenoptera_acutorostrata_s

MRAPPVASGAIWIVL

>Myotis_brandtii

MRAPPVASGAIWIVL

>Monodelphis_domestica

MRAGPLGAGTIWIVL

>Erinaceus_europaeus

MRAPPVASGAIWIVL

>Mesocricetus_auratus

MRAPPVASGAIWIVL

>Tupaia_chinensis

MRAPPVASGAIWIVL

>Homo_sapiens
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>Panthera_tigris
MRMSLK-LSAGSWNRASVR-----
>Rousettus_aegyptiacus
MRMSLK-LFA-----
>Monodelphis_domestica
MRMSLKLLFARSWTRSCIQ-----
>Oryctolagus_cuniculus
MRMSGK-LLAGSWGASVQ-----
>Manis_javanica
MRMSLK-LFAPSWNRASVQGCVLR
>Chinchilla_lanigera
MRMSLE-LFA-----

HG0517 ENSG00000086717 PPEF1

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>Canis_lupus_familiaris
-MDCVLSLQVRLKDSATNKVKI--
>Monodelphis_domestica
-MDCVLSLLVRPKDSTMVKVEIWE
>Oryctolagus_cuniculus
-MDCVLSQQIRLRVSAANKVKI--
>Ceratotherium_simum_simum
-MDCVLSLQIRLKDTAASKMKI--
>Mus_musculus
-MDCALSLQVRMDSATSEMKI--
>Tupaia_chinensis
MMDSVLNLQVLKYSATSKAKI--
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>Homo_sapiens

-----MEGHRKKQDLELSKNIPASSLTL-----KVYSG----VFRGSLFQYYRDSLYYMAGGG-----

>Canis_lupus_familiaris

MSLFSPNKGRYMEGWRRKQDLELSKNIPASSLTF-----KV-----

>Pteropus_vampyrus

-----MEGWVRKQDLELSKNIPASSLTL-----KLYSG----VFCGHYPS-TTEIPYITWQEGWVNLGIVKTKNN-----

>Sarcophilus_harrisii

-----MEGSGRKQDLELNKNITASLIDF-----KKCILESFVVHCSSAA----EVPD----NYMAGGVGKLKNCEDYKTIQDPSLYLRICTQ

>Oryctolagus_cuniculus

-----MEGSGRKQDLELSKDIPASSLTL-----KIYSG----VSCGSLKCYRDS-----

>Equus_asinus

-----MEGWGRKQDLELSTNIFIDFQSIFWSLLWFTIPVLQRFHILHGRRG-----G-----

>Chinchilla_lanigera

-----MEGWGRKQDLELSKNIPASSLTL-----KVYCG----IFCGSLVQSYRDSLYITWQEV-----

HG0519 ENSG00000127074 RGS13

>Homo_sapiens

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>Acinonyx_jubatus

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>Pteropus_vampyrus

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>Trichosurus_vulpecula

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>Loxodonta_africana

MVDCCTGYICQRNVSTYTT-NMRKK---

>Cavia_porcellus

MVDSSTRYIC-----

>Orycteropus_afer_afer

MVDCSSGYIC-----

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>Homo_sapiens
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>Panthera_tigris
----MNNFRFTELRGFHLL-CPRSPLPESRAQAQNL-----
>Lipotes_vexillifer
----MNNFRFTELSRFHSL-CPWSPLPESLTQSQRPLSSSKCAFEE
>Rousettus_abyssiacus
MGSAMNNFRFTKLSGFCPLSVPRSPLESPAQSQNIQLSNNKPAFEE
>Monodelphis_domestica
----MNNWRFPGLPDFS-----
>Manis_javanica
----MNNFRFTELSGFHSL-CPRSQPKSPTQSQRQLSNSRHAFEE
>Tupaia_chinensis
----MNHSKFTELSGFHSL-CPRNLLPEFLTQSQNIPLSNRMGALEE
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HG0521 ENSG00000038274 MAT2B

>Homo_sapiens

-----MWRTARDSGIGIKMLI

>Myotis_lucifugus

-----MLKTARVSGIGIKMLI

>Sarcophilus_harrisii

-----MWETARDPETGI----

>Ceratotherium_simum_simum

-----MWKTARDSGIGIKMLI

>Ictidomys_tridecemlineatus

MKHETSHWVFWKLPRGISCQLTALWKTARDSGIGIKMLI

HG0522 ENSG00000140396 NCOA2

>Homo_sapiens

MAAAASATASAAKVSADGSRHLTA

>Rousettus_aegyptiacus

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>Monodelphis_domestica

MAAT--ASAPAGKVSAGSRHLID

>Ochotona_princeps

MAAAASATATAAKVSADGSRHLTA

>Dipodomys_ordii

MAATVSAPAWAAKVSADGSRHLTA

HG0523 ENSG00000075213 SEMA3A

>Homo_sapiens

MGCSWYSYKVNMLAAHIYP

>Monodelphis_domestica

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>Trichosurus_vulpecula

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>Mus_musculus

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HG0524 ENSG00000107929 LARP4B

>Homo_sapiens

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>Macropus_eugenii

MRTGRSVGDLESRG

>Manis_javanica

MRTGRSVGATESRG

>Microtus_ochrogaster

MRTGRSVGDLESRG

>Homo_sapiens
MTSPEIAVVQRKQSRGIELLQNA RVSNIVSAAASYLTKVEEILYFQLRKLKIPPA SDDQAPLDTEHCAFL LQVTSCLVTTHPGLTKLFORSERRGSWSYTSTTKDS
FFPARSVT
>Canis_lupus_familiaris
-----MICHSSHFLPC--DRTAGVDSCSADPRGGGFWSHASTTEDS
FSTRSVA-
>Ornithorhynchus_anatinus
-----MTSCLVTT-----

>Mus_musculus
-----MLLERRKWK-----VASRFHCDLLSVTSCLVTTQPCLTRLLCRSEGLGFLT TQCC---

HG0526 ENSG00000143569 UBAP2L

>Homo_sapiens

MRLEPERGERERARASEAWALPEYSTL

>Felis_catus

MRLEPERGERGRARASAAWAPPEYSTL

>Monodelphis_domestica

MRLGP-GGWREREGASAAWAPPEHSTL

>Chinchilla_lanigera

MRLQPEGGERERARASAAWALPEYSTL

HG0527 ENSG00000198382 UVRAG

>Homo_sapiens

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>Monodelphis_domestica

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>Oryctolagus_cuniculus

MS----GPGLCRVEGLHCGNMALP

>Chinchilla_lanigera

MS----APGLGPVEGLHCGNMALP

>Homo_sapiens

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>Ornithorhynchus_anatinus

--MLLVDDHVSSEKQTYQSLIMLIITYT-----

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>Homo_sapiens
-----MLAQLRNIREINSTQCV
>Canis_lupus_familiaris
-----MLAQLRNIREINSTQCV
>Lipotes_vexillifer
-----MLAQLRNIREINSTQCV
>Pteropus_alecto
-----MLAQLRNSREINSAQCV
>Dasypus_novemcinctus
-----MLAQLRNIRQIDLLQCV
>Galeopterus_variegatus
-----MLAQLRNIREINSTQCV
>Sorex_araneus
-----MLAQLRNIRETNST---
>Oryctolagus_cuniculus
-----MLAQLRNIREINSTQCV
>Elephantulus_edwardii
-----MLAQLRNTSKINSALCV
>Equus_asinus
MREPLIHRMLAQLRNIREINSTQCV
>Manis_javanica
-----MLAQLRNIREINSTKSV
>Loxodonta_africana
-----MLAQLRNIREINSTQCV
>Cricetulus_griseus
-----MLAQLRNIREINSTQCF
>Tupaia_chinensis
-----MLAQLRSIREINSTKCV
>Trichechus_manatus_latirostr
-----MLAQLRNIREINSTQCV
>Orycteropus_afer_afer
-----MLAQLRNIREINSTQSV
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>Homo_sapiens	
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>Felis_catus	
-----	MERGAPSSFKPG
>Lipotes_vexillifer	
-----	MERGAPSSLKPG
>Myotis_brandtii	
-----	MERGAPSSLKPG
>Dasypus_novemcinctus	
-----	MERGALSSLKPG
>Galeopterus_variegatus	
-----	MERRAPSSLKPG
>Condylura_cristata	
-----	MERGAPSSLKPG
>Oryctolagus_cuniculus	
-----	MERGAPSSLKPG
>Elephantulus_edwardii	
-----	MERGAPSSLKPG
>Ceratotherium_simum_simum	
-----	MERGAPSSLKPG
>Manis_javanica	
-----	MERGAPSSLKPG
>Loxodonta_africana	
-----	MERGAPSSLKPG
>Dipodomys_ordii	
-----	MERGAPSSLKPG
>Tupaia_chinensis	
-----	MERGAPSSLKPG
>Trichechus_manatus_latirostr	
-----	MERGAPSSLKPG
>Orycteropus_afer_afer	
-----	MERGAPSLKPG

>Homo_sapiens
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>Felis_catus
MRAQPGWWSAHAWFRGKRNL-----
>Balaenoptera_acutorostrata_s
MRAQPGWWSAHA-----
>Pteropus_alecto
MRARPGWWSAHA-----
>Dasypus_novemcinctus
MRAQPGW-----
>Galeopterus_variegatus
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>Condylura_cristata
MRAQPGWWRNAHA-----
>Oryctolagus_cuniculus
MRAQPGWWSAHAWPRG-----
>Elephantulus_edwardii
MRAQPGCWSAHASSWGQRNAL-----
>Equus_caballus
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>Manis_javanica
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>Loxodonta_africana
MRAQPGWWRCAHA-----
>Nannospalax_galili
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>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
MRAQPGWGRSAHA-----

>Homo_sapiens
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>Mustela_putorius_furo
-----MSCPELSQAR
>Physeter_catodon
-----MSCPELSRAR
>Pteropus_vampyrus
-----MSCPELSRAR
>Dasypus_novemcinctus
-----MSCPELPQAR
>Galeopterus_variegatus
-----MSCPEVSQAR
>Erinaceus_europaeus
-----MSCPELSLAR
>Oryctolagus_cuniculus
-----MSCPELPQAR
>Elephantulus_edwardii
-----MSCCHILT---
>Equus_asinus
-----MSCPELSRAR
>Manis_javanica
-----MSCPELSQAR
>Loxodonta_africana
-----MSCCLKVP---
>Cricetulus_griseus
-----MSCPELSQAR
>Trichechus_manatus_latirostr
-----MSCPELP---
>Orycteropus_afer_afer
-----MSCCLELS---

>Homo_sapiens
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>Acinonyx_jubatus
MKIPLHFSTAFSTVVG
>Lipotes_vexillifer
MKIPLHFSTAFSTVVG
>Eptesicus_fuscus
MKIPLHFSTAFSTVVG
>Dasypus_novemcinctus
MKIPLHFSTAFSRVVG
>Galeopterus_variegatus
MKIPLHFSAAFSAVVG
>Condylura_cristata
MKIPLNFSTAFSTVVG
>Oryctolagus_cuniculus
MKIPLHFSTAFSTVVG
>Ceratotherium_simum_simum
MKIPLHFSTAFSTVVG
>Manis_javanica
MKIPLHFSTAFLL----
>Loxodonta_africana
MKIPLHFSTAFSPVVG
>Ictidomys_tridecemlineatus
MKIPLHFSIAFSTVVG
>Tupaia_chinensis
MKITLHFSTAFSTVVG
>Trichechus_manatus_latirostr
MKIPLHFSTAFSPVVG
>Orycteropus_afer_afer
MKIPLHFSTAFSPVVG

>Homo_sapiens
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>Felis_catus
MPALGPLSPHSLGTQAGV
>Physeter_catodon
MLALGPLSPHSLGTEAGV
>Myotis_davidii
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>Dasypus_novemcinctus
MPALGPPSPHSLGTQAGV
>Erinaceus_europaeus
MPALGSLSHHQLGTQAGV
>Ochotona_princeps
MPALGAPSPHCSLDTQAGV
>Elephantulus_edwardii
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>Ceratotherium_simum_simum
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>Manis_javanica
MPAQGPLSPHSLGTQAGV
>Loxodonta_africana
MPALGPPSPHSLGTQAGV
>Cavia_porcellus
MPALGTPSPQHSLGTQAGV
>Tupaia_chinensis
MPTLGSPSPHSLGTQAGV
>Trichechus_manatus_latirostr
MPALGPPSLHHSVGTQAGV
>Orycteropus_afer_afer
MPALGAPSPHSLGTQAGV

>Homo_sapiens
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>Acinonyx_jubatus
MTSAIGQS-----
>Orcinus_orca
MTSAIG-----
>Eptesicus_fuscus
MTSAIGQSWESKWEKLFPLYSFGLDSFPGLQSLSWAVGQATGFFQG
>Dasypus_novemcinctus
MTSAIG-----
>Galeopterus_variegatus
MTSAIG-----
>Condylura_cristata
MTSAIGYS-----
>Oryctolagus_cuniculus
MTSAIGWS-----
>Elephantulus_edwardii
MTSAIGWS-----
>Ceratotherium_simum_simum
MTSAIGQS-----
>Manis_javanica
MTSAIGWS-----
>Loxodonta_africana
MTSAIG-----
>Cavia_porcellus
MTSAIGWS-----
>Tupaia_chinensis
MTSAIG-----
>Orycteropus_afer_afer
MTSAIG-----

>Homo_sapiens	-----MSVFPWDSLEIVQ
>Phoca_largha	-----MPVFPWDSLDIVQ
>Balaenoptera_acutorostrata_s	-----MPVFPWDSLEIVQ
>Myotis_davidii	-----MPVFPWDSLEIVQ
>Dasypus_novemcinctus	-----MPVFPWDSVEIVH
>Galeopterus_variegatus	-----MTVCPWDSLEIAQ
>Condylura_cristata	-----MPVFLWDSLEIVQ
>Oryctolagus_cuniculus	-----MPAFPGDSLEIVQ
>Ceratotherium_simum_simum	-----MPVFSWDSLEIVQ
>Manis_javanica	-----MPVFPWDSLEIVQ
>Loxodonta_africana	-----MPVFPWDSLEIVH
>Nannospalax_galili	MTASPLPLASVVQPAVGTPSFSAHATLHRYLEYRRKIIMPVLPWDSLEIVQ
>Tupaia_chinensis	-----MPVFPWDSLEIVQ
>Trichechus_manatus_latirostr	-----MPVFPWDSLEIVH
>Orycteropus_afer_afer	-----MPVFPWDSLEIVH

>Homo_sapiens
MCLLALDASPLRGGIVRDCGRLH
>Felis_catus
MCLLALGASPLGGIVRDCGRLL
>Balaenoptera_acutorostrata_s
MCLLALGASPLGGIARDGRLH
>Miniopterus_natalensis
MCLLALGASPLGGIVRDCGRLL
>Dasypus_novemcinctus
MCPLALDASPLGGIVRDCGRLH
>Galeopterus_variegatus
MCLLALGASPLGGIVRDCGRLH
>Sorex_araneus
MCLLALGASPLGGIVRDCGRLL
>Oryctolagus_cuniculus
MCLLALSASPLGGIVRDCGRLQ
>Ceratotherium_simum_simum
MCLLALSASPLGGIVRDCGRLL
>Manis_javanica
MCLLALGASPLGGIVRDCGRLL
>Loxodonta_africana
MCPLALGASPLRGGIVRDCSRLH
>Peromyscus_maniculatus_baird
MCLLALVASPLRGGMVRDCGRLH
>Tupaia_chinensis
MCLLALGASPLGGIARDGRLH
>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
MCPLALGASPLGGIVRDCSWLH

>Homo_sapiens
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>Canis_lupus_familiaris
MWTNPLEPAPFQGP
>Physeter_catodon
MWTNPLEPAPFRGP
>Miniopterus_natalensis
MRTNPLEPAPFRGP
>Dasypus_novemcinctus
MWTNPLEPLPFRGP
>Galeopterus_variegatus
MWTSPLEPAPFRGP
>Condylura_cristata
MWTNPLEPAPFRGP
>Ochotona_princeps
MWTNPLEPAPFRGP
>Elephantulus_edwardii
MWTNPLESAPFRGP
>Equus_asinus
MWTNPLEPAPFRGP
>Loxodonta_africana
MWTNPLKPAPFRGP
>Chinchilla_lanigera
MRTNPLEPAPSRGP
>Tupaia_chinensis
MWTNPLEPAPFRGP
>Trichechus_manatus_latirostr
MWTNPLEAAPFRGP


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>Homo_sapiens
-----MAHQLESILAMRKRM
>Acinonyx_jubatus
-----MAHQLESILAMKKRT
>Lipotes_vexillifer
-----MAHQLESILAMKKRT
>Myotis_brandtii
-----MAHQLESILAMKKRT
>Dasypus_novemcinctus
-----MAHQLESIFAMKKRT
>Galeopterus_variegatus
-----MAHQLESILAVRKRT
>Erinaceus_europaeus
-----MAHQLESIFVMKKRT
>Elephantulus_edwardii
-----MAHQLESILAMEKRM
>Equus_asinus
-----MAHQLESILAMKKRT
>Manis_javanica
-----MAHQLESILAMGKRT
>Loxodonta_africana
-----MAHQLESILAMIKRM
>Nannospalax_galili
-----MAHQLQSILAMKKRT
>Tupaia_chinensis
-----MAHQLESILAMKKRT
>Orycteropus_afer_afer
MIRAEGFLAAEGIKLMAHLLLESILAMKKRM
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>Homo_sapiens
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>Panthera_tigris
MSGGTVESVETPRGLSDRSLKRKKAKQINKTHPP
>Tursiops_truncatus
MSGGTVESVETPRGLSDSSLKRKKAKQINKTHPP
>Miniopterus_natalensis
MSRGTVESVETPRGLSDRSLKRKKAKQINKTHPP
>Dasypus_novemcinctus
MSGGTEETVETPRGLSDRSLKRKKAKQINKTHPP
>Condylura_cristata
MSGGAVESVETSRGLSDRSLKRKKAKQINKTHPP
>Oryctolagus_cuniculus
MSGGTEESVETPRRLDSSSKRKKAKQTNKTHPP
>Elephantulus_edwardii
MSGGIEQSVESPREIRDRSLKRKKAKQINKTHPP
>Equus_przewalskii
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>Manis_javanica
MSGGTVESVETPRGLSDSSLKRKKAKQINKTHPP
>Loxodonta_africana
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>Marmota_marmota_marmota
MSGGIEQSVETPRGFRDRSLKRKKAKQINKTHPP
>Tupaia_chinensis
MSGGTAESVETPRGLSARSLEREKTKQINKTHPP
>Trichechus_manatus_latirostr
MSGGTEESVETPRGLSDRSLKRKKAKQINKTHPP

>Homo_sapiens
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>Mustela_putorius_furo
MEMKRQGGHVRGAGDARPE
>Orcinus_orca
MEMKRQGGHVRDAGDARPE
>Pteropus_vampyrus
METKRQGGHVRGAGDARPE
>Dasypus_novemcinctus
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>Sorex_araneus
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>Ochotona_princeps
METERQGGHVWGAGDARPE
>Elephantulus_edwardii
METKRQGGHVRGAGDARPE
>Ceratotherium_simum_simum
METKRQGGHVRGAGDARPE
>Loxodonta_africana
METKRQGGHVRGAGDARPE
>Marmota_marmota_marmota
METELQGGHVRGAGDARPE
>Tupaia_chinensis
METERQGGHVRGAGDARPE
>Trichechus_manatus_latirostris
METNRQGGHVRGAGEARPE
>Orycteropus_afer_afer
METKRQGGHVRGAGDARPE

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>Homo_sapiens
-----MEPAQSGPFSQDSPQVLCGC
>Leptonychotes_weddelii
MSGAPETPGPSSSSMEPAQSGPCSPVSPLVLCGC
>Orcinus_orca
MFGTPETPGPSSSSMEPSQSGPCLLDSPPVLCGC
>Eptesicus_fuscus
MSGAPETPGPSSSSMEPAQSGPCSPDSPPVLCGC
>Dasypus_novemcinctus
-----MDPGQNWTCSPDSTPFLCGC
>Condylura_cristata
MSGAPETPGPSSSSMEPAQSGPCSPDSPLILCGC
>Elephantulus_edwardii
-----MEPIQSGPCSQDLPPVLCGC
>Equus_asinus
MFGAPETPGPSSSSMEPAQSHPCSPDSPPVLCGC
>Marmota_marmota_marmota
-----MEPAQSGQCSPDSPPVLCGC
>Tupaia_chinensis
-----MEPVQSGPCSPDSPPVQCGC
>Trichechus_manatus_latirostr
MSGAPEKPGPSSSSMEPAQSGPCSPDSPSVLCGC
>Orycteropus_afer_afer
-----MEPAQSDSCSPASPPVYSGC
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>Homo_sapiens
-MVLLEASLRGRPEATVPPR
>Felis_catus
-MAVLEASLRGRPDATVPPR
>Eptesicus_fuscus
MMAVLEASLQGSPEAVVPPR
>Dasypus_novemcinctus
-MGVLEAFPRGRPQATVPPR
>Galeopterus_variegatus
-MAVLEALLPGRPEAAVPPR
>Condylura_cristata
-MAILEAWVRPAATVPPR
>Oryctolagus_cuniculus
-MAILEASFRGRPEATVPPR
>Ceratotherium_simum_simum
-MAVLEASLRDRPEAAVPPR
>Manis_javanica
-MAVLEVPLRGRPEATVPLR
>Loxodonta_africana
-MAVLGALFRGRPEATVPPR
>Mus_musculus
-MGTLEVSLRGGPEATVPPR
>Tupaia_chinensis
-MAVLDAWLWRPAATVPPR
>Trichechus_manatus_latirostr
-MAVLGALFRGRPEAAVPPR
>Orycteropus_afer_afer
-MAVLEALLRGRPEATVPPR

>Homo_sapiens	-----MGDGRWLSFC
>Ailuropoda_melanoleuca	-----MGDGRWLSFC
>Lipotes_vexillifer	-----MGDGRWLSFC
>Rousettus_aegyptiacus	-----MGDGRWLSFC
>Dasypus_novemcinctus	
MACFPRNVTSDLGTERQWDELLARGEVEAASAILEM	MGDGRWLWFYC
>Galeopterus_variegatus	-----MGDRRWLSFC
>Condylura_cristata	-----MGDGRRLWSFC
>Ochotona_princeps	-----MGEGRWLWPFC
>Ceratotherium_simum_simum	-----MGDGRWLC SFC
>Manis_javanica	-----MGDGRWLSFC
>Loxodonta_africana	-----MGDGRWLSFC
>Marmota_marmota_marmota	-----MGDGRWLSFC
>Trichechus_manatus_latirostr	-----MGDGRGLWSFC
>Orycteropus_afer_afer	-----MGDGRWLSFC

>Homo_sapiens	-----MEQKECQDPAQADAGQPQHRQPTRR-
>Panthera_tigris	-----MEREECQDPAQTDVGQPQHRQPARR-
>Orcinus_orca	-----MEQKECQDPAQTDVGQPQHRQPTRR-
>Rousettus_aegyptiacus	-----MERKECQDPAQADVGQPRHRQPTRR-
>Dasypus_novemcinctus	-----MEQRECQDPAQTDVGQPQHRHLTRR-
>Galeopterus_variegatus	-----MEQKECQDPVQTDVSGQPQHRQPTRC-
>Erinaceus_europaeus	-----MEHKECQDPAQTDVGQPQHQQPTRR-
>Ochotona_princeps	MLSGAVRDKQKEAPGERGGRRDGAAGARAACWAERCGKPKQAVSMEQKECQDPAQTDVGQPQPRQPTRR-
>Ceratotherium_simum_simum	-----MEREECQDPGQTDVGQPQRRQQTRR-
>Manis_javanica	-----MERKECQDPAQTDVGQPQHQPAPHR-
>Loxodonta_africana	-----MDQRECEDPAQTDVGHPQHRQLTPRR-
>Microtus_ochrogaster	-----MEQKECQDPVHPDRDQPQHQQPTRR-
>Tupaia_chinensis	-----MEQKECQDPAQADVGQPRHRQPTRR-
>Orycteropus_afer_afer	-----MERGECQDLAQTDVGLPQHHPQPTCR-

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>Homo_sapiens
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>Acinonyx_jubatus
MCVLWTWAWLECSRVLKILL
>Balaenoptera_acutorostrata_s
MCVLWTWAWLECSRVLKILL
>Pteropus_alecto
MCVVWTWAWLECSRVLKTLL
>Dasypus_novemcinctus
MCVLWTWALLECSRVLKILL
>Galeopterus_variegatus
MCILWTWAWLECSRVLKILL
>Erinaceus_europaeus
MCVLWTWAWLECSRVLKILL
>Oryctolagus_cuniculus
MCVLWTWAWLECSRVLKILL
>Ceratotherium_simum_simum
MCVLWTWAWLECSRVLKILL
>Manis_javanica
MCVLWTWAWLECSRVLKIPL
>Loxodonta_africana
MYFLWTWAWLECTRVLKILL
>Chinchilla_lanigera
MCILWTWAWLECASVLKILL
>Tupaia_chinensis
MCALWTCTWLECSRVLKILR
>Trichechus_manatus_latirostr
MCVLWTWAWLECTKVLKILL

>Homo_sapiens
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>Mustela_putorius_furo
MRLPNNFHNNNPSRKRRKRKRIRRRWGWTRNTSRRRDASSVPNVRR
>Physeter_catodon
MRLPNNFHNNNPSRKRRKRKRIRRRWGWTRNTSRRRDASSVPNVRE
>Pteropus_alecto
MRLPNNFHNNNPSRKRRKRKRIRRRWGWTRNTSRRRDASSVPNVRG
>Dasypus_novemcinctus
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>Condylura_cristata
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Equus_asinus
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>Manis_javanica
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>Loxodonta_africana
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>Octodon_degus
MRLPNNFHNNNPSRKRRKRKRIRRRWGWTRSTSRRRDASSVPNVRG
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Panthera_tigris
MALTSRPSADLAPGLIQSLV-ASCFPPPGAQW-----
>Orcinus_orca
MALTSRPSADLAPGLQPRV-ASCLPPPGAQ-----
>Pteropus_alecto
MALTSRPSADLAPGLNQPLV-ASCFPPAGARWW-----
>Dasypus_novemcinctus
MALSSRPGAGLA-GPSRPLL-AARSPPPGARW-----
>Galeopterus_variegatus
MALTSHPADLAPGLFPPLL-APCFPPPGVRW-----
>Oryctolagus_cuniculus
MALPSPPGTDLAAGLLQPLL-ASRSPCCGARW-----
>Equus_przewalskii
MALTSRPSADLAPGLLQPLL-ASRVPPPGALWQW-----
>Manis_javanica
MALTGPSGADLARGLLPL-R-ASCCPVLGHGELGAQP
>Loxodonta_africana
MALTSWPSADLAPGLSQPLVAAG-CPPPGAPW-----
>Cavia_porcellus
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>Tupaia_chinensis
MALTSPPSAHLAPGLFQPLR-AACFPPPGARW-----
>Trichechus_manatus_latirostr
MALTSRPSADLAPGLSQPLVAARCCPPPGAPW-----
>Orycteropus_afer_afer
MALTSWPSADLAPGFSQPLLVAR-CPPPRARW-----

>Homo_sapiens	-----MNSPLELCRIPVPPPPLEN
>Canis_lupus_familiaris	-----MLPLEE-----TGPRV--PGTSWHIFWELLSWKIFKSQGMNSTLELCRIPVPPPPLEN
>Orcinus_orca	-----MNSTLELCRIPVPPPPLEH
>Myotis_lucifugus	-----MNSTLELCRIPVPPPPLEN
>Galeopterus_variegatus	-----MNSILELCCIPVPPPPLEN
>Erinaceus_europaeus	-----MNSTLDFCCIPVPPPPLEN
>Ochotona_princeps	-----MNSTLELCLIPVPPPPLEN
>Elephantulus_edwardii	-----MSQQMNSTREICHIPVPPPPLEN
>Ceratotherium_simum_simum	-----MNSTLELCRIPVPPPPLEN
>Manis_javanica	-----MNSTLELCCIPVPPPPLEN
>Loxodonta_africana	-----MNSTLEICHIPVPPPPLEN
>Mus_musculus	-----MNSTLELCRIPVPPPPLEN
>Tupaia_chinensis	MFSLHGDRNPCTLHRGGRAAAVFQPMAEAVVESVDLPNERVACYAAVGRLLREAVAVGSRQRGDSWKIFNPQQMNSALELCCIPVPPPPLEN
>Trichechus_manatus_latirostr	-----MNSTLETCRIPVPPPPLEN

>Homo_sapiens
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>Acinonyx_jubatus
-MQLWALSPWIVILCQ-
>Balaenoptera_acutorostrata_s
-MQLWALSPWIVILCQ-
>Pteropus_alecto
-MQLWVLSPWIVILGQ-
>Dasypus_novemcinctus
-MQLWALSPWIIILCQ-
>Condylura_cristata
-MQLWALSPWIVILCQ-
>Oryctolagus_cuniculus
-MQLWVLSPWIVFCVSK
>Ceratotherium_simum_simum
-MQLWALSLWMVILCQ-
>Manis_javanica
-MQLWVLSPWIVILCQ-
>Loxodonta_africana
-MQLWALSPWIVILCH-
>Heterocephalus_glaber
MMQLWALSPWIVILCQ-
>Tupaia_chinensis
-MQLWALPPWIVILCQ-
>Trichechus_manatus_latirostr
-MQLWALSPWIVILCQ-
>Orycteropus_afer_afer
-MQLWSLLPWIVTLCH-

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>Homo_sapiens
-----MTFKCASSVKYKENLYG
>Canis_lupus_familiaris
-----MTFKCSSSVKYKENLYG
>Lipotes_vexillifer
-----MTFKCASSVKYKENLYG
>Myotis_brandtii
MFVRCCLICFGVLCPFVELLMTFKCASSVKYKENLYG
>Galeopterus_variegatus
-----MTFKCASSVKYKENLYG
>Sorex_araneus
-----MTFKCASSVKYKENLYG
>Oryctolagus_cuniculus
-----MTFKCASPVKYKENLYG
>Elephantulus_edwardii
-----MTFTCVSSVKYKENLYG
>Equus_asinus
-----MTFKCASSVKYKENLYG
>Manis_javanica
-----MTFKCSSSVKYKENLYG
>Loxodonta_africana
-----MTFKCASSVKYKENLYG
>Nannospalax_galili
-----MTFKCASSDKYKENLYG
>Tupaia_chinensis
-----MTFNCASSVKNKENLYG
>Orycteropus_afer_afer
-----MTFKCATSVKYKENLYG
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>Homo_sapiens

MFSTRMQSFLLVK

>Odobenus_rosmarus_divergens

MFSTRMQSFLLVK

>Orcinus_orca

MFSTRMQFLLVK

>Myotis_lucifugus

MFSTRMQSFLLVK

>Sorex_araneus

MFSTRMQSFLLVK

>Ceratotherium_simum_simum

MFSTRMQSFVLR

>Loxodonta_africana

MFSTRMQSFLLVK

>Trichechus_manatus_latirostr

MFSTRMQSFLLVK

>Orycteropus_afer_afer

MFSTRMQSFLLVK

>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Orcinus_orca
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>Rousettus_aegyptiacus
MSEPALRSRPGREWQVVSAD-----
>Galeopterus_variegatus
MSEPAPRSCPGREWRAVSAEQKVAPVRGRFQ
>Condylura_cristata
MSEPALRSRPEREWQAVSEK-----
>Ochotona_princeps
MSEPVLCSCPGREWPAVSAE-----
>Equus_asinus
MSEPALRSRPGREWQAVSAE-----
>Manis_javanica
MSEPALRSLPGREWQAVSAE-----
>Loxodonta_africana
MSEPAPCSRPGREWQAVSAE-----
>Fukomys_darlingi
MSEPALRSCPGREWQAVSAE-----
>Tupaia_chinensis
MSEPALRSWPREWQAVSAESKVARSSGRFQ
>Trichechus_manatus_latirostr
MSEPAPGSRPGREWQAVSAE-----
>Orycteropus_afer_afer
MSELAPRSRPGREWQAVSVEQKVETVSGLFQ

>Homo_sapiens	-----MMVSSCQRRLWLPRER
>Acinonyx_jubatus	-----MTKLIMVSSCQRRLWMPRER
>Physeter_catodon	-----MVSSCQRRLWMPRER
>Rousettus_aegyptiacus	MRLSSASSCHAAMGGVLHYVDISSLSAIAKNQWCPASLLRFIHSTNLGTRITYGNSFYTWELKYRFYICCLTCFLLSFCRLIMVSSCQRRLWMPRER
>Dasypus_novemcinctus	-----MVSSCQRRLWVPRKM
>Galeopterus_variegatus	-----MVSSCQRRLWMPRER
>Condylura_cristata	-----MMVSSCQRRLWI PRDR
>Elephantulus_edwardii	-----MVSSCQRKLWMPRER
>Ceratotherium_simum_simum	-----MVSSCQRRLWMPGER
>Manis_javanica	-----MVSSCQRRLWMPRER
>Loxodonta_africana	-----MISSCRRRLWMPRER
>Nannospalax_galili	-----MVSSCQRRLWI PRER
>Tupaia_chinensis	-----MVSSCQRRLWMPRER
>Orycteropus_afer_afer	-----MVSSCRRRLWMPRER

>Homo_sapiens
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>Leptonychotes_weddelii
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>Physeter_catodon
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>Rhinolophus_ferrumequinum
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>Dasypus_novemcinctus
MYTMVIRQSIYQEGHSSVRLIPVT-----
>Galeopterus_variegatus
MYTMVIRQSIYQEGHPPIRLIPVT-----
>Condylura_cristata
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>Oryctolagus_cuniculus
MCTMVTRQSTYQERGHSSVRLIPVT-----
>Equus_asinus
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>Manis_javanica
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>Loxodonta_africana
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>Ictidomys_tridecemlineatus
---MVIRQSIHQEGHSSVRLIPVT-----
>Tupaia_chinensis
---MVRQSTCHEKGHAIVRPFVPT-----
>Orycteropus_afer_afer
---MVIRQSLYQEGHISKV--EPCDLMNPW

>Homo_sapiens
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>Felis_catus
---MTEWSFELDFCVPYGVGPDPRALGVGWRCYCKMQVG
>Physeter_catodon
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>Rousettus_aegyptiacus
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>Galeopterus_variegatus
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>Condylura_cristata
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>Oryctolagus_cuniculus
---MTAWSVELDFCVPDGVGPDPRALGVGWRCYCKMQVG
>Elephantulus_edwardii
---MTEWSFELDFCVLYGIGPDPRALGVGWRCYCKMQVG
>Ceratotherium_simum_simum
---MTAWSFELDFCVPYGVGPDPRALGVGWRCCKMQVG
>Manis_javanica
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>Loxodonta_africana
---MTEWSFELDFCVPYGVGPDPRALGVGWRCYCKMQVG
>Chinchilla_lanigera
---MTEWSFELDFCVPAGIGPDPRALGVGWRCFCCKMQVG
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Ursus_maritimus
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>Orcinus_orca
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>Myotis_lucifugus
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>Dasypus_novemcinctus
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>Galeopterus_variegatus
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>Erinaceus_europaeus
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>Equus_caballus
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>Manis_javanica
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
MGPASHSHLLSTGRG

>Homo_sapiens
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>Pteropus_vampyrus
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>Dasypus_novemcinctus
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>Galeopterus_variegatus
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>Sorex_araneus
MLLPNILLTGTPGVGKTTLGKELASRSGLKYVNVGDAREV
>Ochotona_princeps
MLRPNILLTGTPGVGKTTLGKELASRSGLKYVNVGDAREV
>Elephantulus_edwardii
MLLPNILLTGTPGVGKTTLGKELASRSGLKYINVGDAREV
>Equus_przewalskii
MLLPNILLTGTPGVGKTTLGKELASRSGLKYINVGDAREV
>Loxodonta_africana
MLQPNILLTGTPGVGKTTLGKELASRSGLKYVNVGDAREV
>Marmota_marmota_marmota
MLLPNILLTGTPGVGKTTLGKELASRSGLKYINVGDAREV
>Trichechus_manatus_latirostr
MLQPNILLTGTPGVGKTTLGKELASRSGLKYINVGDAREV
>Orycteropus_afer_afer
MLRPNILLTGTPGVGKTTLGKELASRSGLKYINVGDAREV

HG0557 ENSG00000012232 EXTL3

>Homo_sapiens
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>Ailuropoda_melanoleuca
MHICWSAKPRNKSYGS
>Balaenoptera_acutorostrata_s
MHMCWSAKPRNESYGS
>Eptesicus_fuscus
MHICWSAKPRNKSYGC
>Galeopterus_variegatus
MHTCWSAEPRNKSYGR
>Condylura_cristata
MHVCWPAKRRSKSHGR
>Equus_asinus
MHICWSAKPRNKSYGS
>Manis_javanica
MHTCLSAKPRNKSYGS
>Loxodonta_africana
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>Ictidomys_tridecemlineatus
MHICWSAKPRNKSYGL
>Tupaia_chinensis
MNICWSAKPRNKSYGS
>Trichechus_manatus_latirostr
MHICWPAKPRNKSYGT
>Orycteropus_afer_afer
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HG0558 ENSG00000029363 BCLAF1

>Homo_sapiens
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>Canis_lupus_familiaris
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>Balaenoptera_acutorostrata_s
MVFLPCLSREMAAV-----
>Miniopterus_natalensis
MVFLPFLSRVMAAV-----
>Dasypus_novemcinctus
MVFLPFLSREMAAV-----
>Galeopterus_variegatus
MVFLSFLSREMAAVWLQRR
>Condylura_cristata
MVFLPFLSREMAAV-----
>Ochotona_princeps
MVFLSFSSREMAAV-----
>Ceratotherium_simum_simum
MVFLPFSSREMAAV-----
>Manis_javanica
MVFLPFLSREMAAV-----
>Loxodonta_africana
MVFLSVLSREMAAV-----
>Chinchilla_lanigera
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>Tupaia_chinensis
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HG0559 ENSG00000078747 ITCH

>Homo_sapiens
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>Panthera_tigris
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>Balaenoptera_acutorostrata_s
MHLTVAFWRQLNPKK
>Miniopterus_natalensis
MHLTVAFWRQLNPKK
>Dasypus_novemcinctus
MHLTVAFWRQRFNPKK
>Galeopterus_variegatus
MHFTVAFWRQLNPKK
>Condylura_cristata
MHLTVAFWRQLNPKK
>Oryctolagus_cuniculus
MPFTVAFWRQLNQKK
>Equus_asinus
MHLTVAFWRQLNPKK
>Loxodonta_africana
MHVTVAFWRQLNPKK
>Dipodomys_ordii
MHFTVAFWRQLNPKK
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
MHLTVAFWRQHLNPKK

>Homo_sapiens
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>Leptonychotes_weddellii
MDAVPGRQPEPQPTCHSG
>Balaenoptera_acutorostrata_s
MDAVPGRQPEPQSTCHSG
>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
MDAVPGKQPEPQPTCHSG
>Galeopterus_variegatus
MDAVPERQPEPQTTCHSG
>Condylura_cristata
MDAVPGRQPEPQPTCHSG
>Ochotona_princeps
MDVEPGRRPAPQPTCHSG
>Elephantulus_edwardii
MDAVPGRQPEPQPTRHS-
>Ceratotherium_simum_simum
MDAVPGRQPEPQPTCHSG
>Manis_javanica
MDDLPGKRLEPQPTCHSG
>Dipodomys_ordii
MDAVPGRQPEPQPTCHSG
>Orycteropus_afer_afer
MDVILRRQPEPQPTCHSG

>Mustela_putorius_furo

>Orcinus_orca

>Myotis_lucifugus

>Dasypus_novemcinctus

>Galeopterus_variegatus

>Erinaceus_europaeus

>Oryctolagus_cuniculus

>Elephantulus_edwardii

>Ceratotherium_simum_simum

>Manis_javanica

>Dipodomys_ordi i

-----KSPSSSTWTSPLHPHHRHRLSSPLLLAPLCPFKSAWPSLPRDAGMEQTLICAGMESEF

>Homo_sapiens
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>Mustela_putorius_furo
MRRRRRTAPRRKRLMAAAELRETSAGQGPVAVAGRGLRL
>Physeter_catodon
MRRRRRTAPRRKRLMAAAELRETSAGQGPVAVAGRGLRL
>Rousettus_aegyptiacus
MRRRRRTAPRRKRLMAAAELRETSAGQGPVADRGLRL
>Dasypus_novemcinctus
MRRRRRTAPRRKRLMAAAELRETSAGQGPVAVAGRGLRL
>Erinaceus_europaeus
MRRRRRTAPRRKRLMAAAELRETSAGQGPVAVAGRGLRL
>Oryctolagus_cuniculus
MRRRRRTAPRRKRLMAAAELRETSAGQGPAAAGRGLRL
>Equus_asinus
MRRRRRTAPRRKRLMAAAELRETSAGQGPVADRGLRL
>Manis_javanica
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>Loxodonta_africana
MRRRRRTAPRRKRLMAA-ALRETSAGQGPVAVAGRGLRL
>Octodon_degus
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
MRRRRRTAPRRKRLMAA-ALRETSAGQEPVAVAGRGLHL

>Homo_sapiens

-----MRRFLGVLEPRREARSER-----

>Leptonychotes_weddellii

-----MRRFLGVVEPRREARTER-----

>Physeter_catodon

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-----MRRFLGVVDPREARTGR-----

>Galeopterus_variegatus

-----MRRFLGVVERREARTGRQSRGR-----

>Oryctolagus_cuniculus

-----MRRFVGVEPRREARTGR-----

>Elephantulus_edwardii

-----MRRFLGVE-QRREARSGG-----

>Ceratotherium_simum_simum

-----MRRFLGVLEPRREARTGR-----

>Manis_javanica

-----MRRFLGAVESRREARTGR-----

>Loxodonta_africana

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>Tupaia_chinensis

-----MRRVLGDVEPRREAQKER-----

>Orycteropus_afer_afer

-----MRRFLGVVEPRREARTGR-----

>Homo_sapiens
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>Leptonychotes_weddellii
-----MDNLLDFA
>Lipotes_vexillifer
-----MDDSIRLINHTMDNLLDFA
>Rousettus_aegyptiacus
-----MDNLLDFA
>Dasypus_novemcinctus
-----MDNLLDFA
>Galeopterus_variegatus
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>Sorex_araneus
-----MDNLLDFA
>Ochotona_princeps
-----MDNLLDLA
>Ceratotherium_simum_simum
-----MDNLLDFA
>Loxodonta_africana
-----MDNVDLA
>Chinchilla_lanigera
-----MDNLLDFA
>Tupaia_chinensis
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>Trichechus_manatus_latirostr
-----MDNVDLA

>Homo_sapiens
-----MAAGAGYWRRLPQSRSSRR
>Odobenus_rosmarus_divergens
-----MAAKAGYWRRLPQSWSSRR
>Balaenoptera_acutorostrata_s
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>Pteropus_alecto
-----MAAEAGYWRRLPQSRSSRR
>Dasypus_novemcinctus
-----MAAEAGYWRRLPQSGSSRR
>Galeopterus_variegatus
-----MAAEAGCWRRLPQSRSSRR
>Condylura_cristata
-----MAAEAGYWRRLPQSWSSRR
>Oryctolagus_cuniculus
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>Elephantulus_edwardii
-----MAAEAGYWHRLPKSGSSRR
>Ceratotherium_simum_simum
-----MAAEAGYWRRLPQSWSSRR
>Ictidomys_tridecemlineatus
-----MAAEAGYWRRLPQSRSSRR
>Trichechus_manatus_latirostr
-----MAAEAGYWRRLPQSWSSRR
>Orycteropus_afer_afer
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>Homo_sapiens
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>Leptonychotes_weddellii
MRVLAFCVLRCPST
>Lipotes_vexillifer
MRVLAFCVLRCPST
>Rousettus_aegyptiacus
MRVLAFCVLRCPST
>Dasypus_novemcinctus
MRVLAFCVLRCPST
>Condylura_cristata
MRVLAFCVLRCPST
>Ochotona_princeps
MRVLAFCVLRCPST
>Elephantulus_edwardii
MRVLALYVLRCPST
>Equus_asinus
MRVLAFCVLRCPST
>Fukomys_damarensis
MRVLAFCVLRCPST
>Tupaia_chinensis
MRVLAFCVLRCPST
>Trichechus_manatus_latirostris
MRVLAFCVLRCPST
>Orycteropus_afer_afer
MRVLAFCVLRCPST

>Homo_sapiens
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>Canis_lupus_familiaris
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>Balaenoptera_acutorostrata_s
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>Pteropus_alecto
MHLLQKQPRPWLRMLKEEDMEAGRP-----
>Dasypus_novemcinctus
MHLLQKQPRPWLRMLEEEDTEAVGPERLSSRS-----
>Condylura_cristata
MHLLQKQPRPWLSRMLKEEDTEARRP-----
>Oryctolagus_cuniculus
MHLLQKQPRPWLRRPLKEEDEEAGRL-----
>Ceratotherium_simum_simum
MHLLQKQPRPWLRMLKEEDTEAARP-----
>Manis_javanica
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>Loxodonta_africana
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>Marmota_marmota_marmota
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>Tupaia_chinensis
MHLLQKQPRPWLRMLKEEDTEAGQP-----
>Trichechus_manatus_latirostr
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>Homo_sapiens
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>Canis_lupus_familiaris
-MRGLPGAPSPGLGTRRM
>Physeter_catodon
-MRGLPGAPSPGLGTRRM
>Rousettus_aegyptiacus
-MRGLPGAPSPGLGTRRM
>Dasypus_novemcinctus
-MRGLPGVPSPGLGTRRM
>Galeopterus_variegatus
MMRGLPGAPSPGLGTRRM
>Condylura_cristata
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>Ochotona_princeps
-MRGLPGAPSPGLGTRRM
>Ceratotherium_simum_simum
-MRGLPGAPSPGLGTRRM
>Manis_javanica
-MLGLPGAPSPGLGTRRM
>Nannospalax_galili
-MRGLLGAPSPGLGTRRM
>Trichechus_manatus_latirostr
-MRGLPGAPSPGLGTRRM
>Orycteropus_afer_afer
-MRWLLGAPSPGLGTRRM

>Homo_sapiens
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>Canis_lupus_familiaris
MKGLKP--GITYAKFPQSPSPSVS
>Physeter_catodon
MKEIKP--GITYAEPLQSSPSVS
>Pteropus_alecto
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>Galeopterus_variegatus
MKEIKP--GIAYAELMPQSPSPSVS
>Condylura_cristata
MKESKPTNKTTAEPMRQSSPSVS
>Oryctolagus_cuniculus
MKEIKP--GIPYAEPMPSPSPSVS
>Equus_asinus
MKEIKP--GTTYAGPLQSSPSVS
>Manis_javanica
MKEIKP--GITYAEPLQSSPSVS
>Heterocephalus_glaber
MKEIKP--GLTHAEPMPQSSPSVS
>Tupaia_chinensis
MKEIKP--GITYAKPMPQLSPSVS
>Trichechus_manatus_latirostr
MKEIKQ--GITYAEPKLQLSPSVS
>Orycteropus_afer_afer
MKEIKQ--GITYAEPKLQLSPSVS

HG0568.2 ENSG00000138271 GPR87

>Homo_sapiens

MFRFHALPENPLPCRP

>Canis_lupus_familiaris

MLIFHAVPENPLLCQP

>Miniopterus_natalensis

MFIFHALPENPHPCQP

>Ceratotherium_simum_simum

MFLFHALPESPLLCQP

>Manis_javanica

MLIFHAFPENPLPCQP

>Tupaia_chinensis

MILFSALPENPLSCQP

>Homo_sapiens	-----MATGLMGHEGVATVIW
>Acinonyx_jubatus	-----MAAGLKGHEGVVTVIW
>Orcinus_orca	-----MAAGLKGHEGAVTVIW
>Myotis_brandtii	-----MAAGLKGHEGVVTVIW
>Galeopterus_variegatus	-----MAAGLKGHEGVITVTW
>Erinaceus_europaeus	
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>Elephantulus_edwardii	-----MAAGLKGHKGVVTVIW
>Ceratotherium_simum_simum	-----MAAGLRGHEGVVTVIW
>Manis_javanica	-----MAAELKGHKEVVTVIW
>Loxodonta_africana	-----MAAGLKGHKGVVTVIW
>Marmota_marmota_marmota	-----MAAGLRGHEGAVTVIW
>Trichechus_manatus_latirostr	-----MAAGLKGHRGVITVIW
>Orycteropus_afer_afer	-----MAAGLKGHRGVVTVIW

>Homo_sapiens
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>Ursus_maritimus
MRPARAEDQQPARR-----
>Rousettus_aegyptiacus
MRPARAQDQQPARR-----
>Dasypus_novemcinctus
MRPAPAEDQQPARR-----
>Condylura_cristata
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>Ochotona_princeps
MRPAGAEDQQPAGH-----
>Elephantulus_edwardii
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>Equus_asinus
MRPAGAEDQQPARR-----
>Loxodonta_africana
MRPAGAEDQQPARR-----
>Octodon_degus
MRPAPAQDQQPARR-----
>Tupaia_chinensis
MRPARAEDQQPARC-----
>Trichechus_manatus_latirostr
MRPAGAEDQQLARR-----
>Orycteropus_afer_afer
MRSAGAEDQQPAWR-----

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>Homo_sapiens
-----MARNASPPWWGKET
>Canis_lupus_familiaris
-----MARNASPPWRWGKET
>Orcinus_orca
-----MARNASPPWRWGKET
>Pteropus_alecto
-----MARNASPPWRWGKET
>Galeopterus_variegatus
MSAECKRPVISRGGEDVCHQNVTEEIRCMARNASPPWWGKET
>Erinaceus_europaeus
-----MARNASPPWRWGKET
>Ochotona_princeps
-----MARNASPPQWGKET
>Equus_asinus
-----MARNASPPWRWGKET
>Manis_javanica
-----MARNASPPWRWGKET
>Loxodonta_africana
-----MARNASPPWRWGKET
>Mesocricetus_auratus
-----MARNASPPWRWGKET
>Trichechus_manatus_latirostr
-----MARNASPPWRWGKET
>Orycteropus_afer_afer
-----MARNASPPWRWGKET
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>Homo_sapiens
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>Canis_lupus_familiaris
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>Physeter_catodon
MRIRVLTTPPFPAASWFSVFGVPVPMSCCGASAAFG--
>Myotis_brandtii
MRFRVTLTPRFPLAWFYCGSGPVPMSCGAPAAFG--
>Dasypus_novemcinctus
-----MSCCGTSAAFG--
>Galeopterus_variegatus
-----MPYCGASAAFG--
>Condylura_cristata
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>Oryctolagus_cuniculus
MRFRVTLTPRFPLARSYRSGPVPMSCCGSSVALGL--
>Ceratotherium_simum_simum
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>Manis_javanica
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>Marmota_marmota_marmota
MRIRVTLTPRFPLCWFYRSGGPVPMSCCGASAAFG--
>Tupaia_chinensis
-----MSRCGAPAAFG--
>Trichechus_manatus_latirostr
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>Homo_sapiens

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>Leptonychotes_weddellii

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>Galeopterus_variegatus

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>Condylura_cristata

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>Oryctolagus_cuniculus

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>Elephantulus_edwardii

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>Ceratotherium_simum_simum

-----MKSLGGKVAGQGQWWSRAASWRQHELRG

>Manis_javanica

-----MKSLGGKSAGQGRWWSRAASQRQHELGV

>Loxodonta_africana

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-----MKSLGGKGAGQGRWWSRAASRRQHELRG

>Orycteropus_afer_afer

-----MKSLGGKGAGQGRWWSRAASWRQHELRG

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>Homo_sapiens

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>Canis_lupus_familiaris

MRTMPAGPRGEGM

>Miniopterus_natalensis

MRTMPAGPRGKGM

>Dasypus_novemcinctus

MRTMPAGPRGEGM

>Galeopterus_variegatus

MRTMPAGPRGEGM

>Condylura_cristata

MRTMPTGPRGEGM

>Equus_asinus

MRTMPAGPRREGM

>Cricetulus_griseus

MRTMPAGPCGEGM

>Tupaia_chinensis

MRTMPAGPRGEGM

>Homo_sapiens
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>Panthera_tigris
MEEDGKNLFNGLKDWSLL
>Pteropus_vampyrus
---MEKNLFNGLKEWRLL
>Dasypus_novemcinctus
MEEDGKKLFNGLTEWRLL
>Galeopterus_variegatus
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Ceratotherium_simum_simum
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>Manis_javanica
MEEDRKNLFNGLKEWRLL
>Psammomys_obesus
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>Tupaia_chinensis
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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>Homo_sapiens	-----MMAILWMGRDLERTSSLSCNSSQYPT-----
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>Felis_catus	
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>Pteropus_vampyrus	-----MMAILWMGRNLERTSSLSCNFSQYPT-----
-	
>Dasypus_novemcinctus	-----MMAILWMGRDLERTSSLSATSVTIPHKSSQVTEKWKSN
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>Galeopterus_variegatus	-----MGRDLERTSSLSCNFSHYPT-----
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>Oryctolagus_cuniculus	-----MERDLRTSSLSCNFSQYLT-----
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>Elephantulus_edwardii	-----MMAILWMGRDLERTSTLSCNVSQYPT-----
-	
>Ceratotherium_simum_simum	-----MGRDLERTSSLSCNFSQYPT-----
-	
>Manis_javanica	-----MGRDLERTSSLSCNFSQYPT-----
-	
>Peromyscus_maniculatus_baird	-----MGRDLERTLGLSCNFSQYPT-----
-	
>Tupaia_chinensis	-----MILWMERGLGRMCSLPCSFSQYPT-----
-	
>Trichechus_manatus_latirostr	-----MMAILWMGRDLERT----CSFSQYPT-----
-	
>Orycteropus_afer_afer	-----MMANLWMGRDLERTSSLSCNFSHYPT-----
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>Homo_sapiens
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>Ailuropoda_melanoleuca
-----MKLESCLKT DSPSCEL
>Lipotes_vexillifer
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>Rhinolophus_ferrumequinum
-----MKLNSLQKTDNPSCDL
>Dasypus_novemcinctus
---MYSKINGFIALNGFEPKLYSLKKT DSTSCEL
>Oryctolagus_cuniculus
-----MKLCSLRET DSPSCEL
>Elephantulus_edwardii
-----MTLYTLKQTDSSSCEL
>Ceratotherium_simum_simum
-----MKLDCLKT DSPSCEL
>Loxodonta_africana
-----MKLHSLKKT DSPSCEL
>Chinchilla_lanigera
-----MKLYPLKKT DSPSCEP
>Tupaia_chinensis
-----MKLYSLKKT DSRLCEL
>Trichechus_manatus_latirostr
-----MKLRSLKKT DSPSEL
>Orycteropus_afer_afer
-----MKLYSLKKT DSPSEL
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>Homo_sapiens
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>Ursus_maritimus
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>Lipotes_vexillifer
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>Myotis_brandtii
MLSIRVGRGAACLTGQGLWASWRCV
>Dasypus_novemcinctus
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>Galeopterus_variegatus
MLSSRVGLGAAHLTTGQGLWAPWGRV
>Oryctolagus_cuniculus
MLSSRAGLGPAGLSTGQAPWASWGCA
>Elephantulus_edwardii
MLSSRVGLEAACLTGQGWAPWGCV
>Equus_asinus
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>Manis_javanica
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>Mus_musculus
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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>Homo_sapiens
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>Ailuropoda_melanoleuca
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>Orcinus_orca
MSRGWPGRSRYGGGLRHCRKWA
>Rousettus_aegyptiacus
MSRGWPGRSRYGGGLRHCRKWA
>Dasypus_novemcinctus
MSRDWPGRSRYGGGLRHCRKWA
>Condylura_cristata
MSRGWPGRSRYGGGLRHCRKWA
>Oryctolagus_cuniculus
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>Equus_asinus
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>Ictidomys_tridecemlineatus
MSRGWPGRSRYGGGLRHCRKWA
>Tupaia_chinensis
MSRGWPGRSRYGGGLRHCRKWA
>Trichechus_manatus_latirostr
MSRGWPGWSRYGGGLRHCRKWA
>Orycteropus_afer_afer
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HG0579 ENSG00000010818 HIVEP2

>Homo_sapiens

MPIDCGVRVEGSKEKEQSASLQTPWNMEATKL

>Felis_catus

-----MEANKL

>Balaenoptera_acutorostrata_s

MPIDYGVGVEGSKEKEHSASLQTPWNMEASKL

>Myotis_lucifugus

-----MEASKL

>Galeopterus_variegatus

MTIDYGVGVEGSREKEQSASLQTPWNMEATKL

>Ochotona_princeps

-----MEAAKL

>Ceratotherium_simum_simum

-----MEASKL

>Manis_javanica

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>Loxodonta_africana

-----MEATKL

>Nannospalax_galili

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>Tupaia_chinensis

MPIDCGEGVGSKEKEQSAGLQTPWNMEATKL

>Orycteropus_afer_afer

MPVDCGEGVEGSKEKEKS-SLQTSGNMEATKL

>Homo_sapiens
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>Acinonyx_jubatus
-----MCSSYCILTVTKPQI-----
>Balaenoptera_acutorostrata_s
-----MCNGYCILTVTKPQILMISLGGKGYIYKKPLNIVIKYIFS
>Rhinolophus_ferrumequinum
-----MCNSYCILTVTKPQI-----
>Galeopterus_variegatus
-----MCSIYCILTVTKPQI-----
>Erinaceus_europaeus
MIKLKRSVVKLLYLLTQADLCSSCCALTVSKPQI-----
>Equus_caballus
-----MCNSYCILTVNKPQI-----
>Manis_javanica
-----MCNSYCILTVTKPQI-----
>Mesocricetus_auratus
-----MCSSYCILIVTKPQI-----
>Tupaia_chinensis
-----MCSNYCILIVTKPQI-----
>Trichechus_manatus_latirostr
-----MCNSYCILTVTHPQI-----
>Orycteropus_afer_afer
-----MCNSYCIMTVTQPQI-----

>Homo_sapiens
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>Canis_lupus_familiaris
-----MNALASRAVL--SCDRWWQPEPALLPPG
>Orcinus_orca
-----MNALASRAVR--TCDRLWQPQPALLPPG
>Rhinolophus_ferrumequinum
-----MKALASRAVR--TCDRLWQPEPALLPPG
>Dasypus_novemcinctus
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>Galeopterus_variegatus
-----MNALASRAVR--TCDRFWQPEPALLPPG
>Erinaceus_europaeus
-----MTAPAPRTVRSPTRDRLWQPEPALLPPG
>Oryctolagus_cuniculus
-----MNALASRAVR--TYDRFWQPEPALLPPG
>Equus_caballus
-----MNALASRAVR--TCDRLWKTEPALLPPG
>Loxodonta_africana
-----MNAPDSRTAR--TYDRFWLREPALLSPG
>Ctenomys_sociabilis
-----MNALASRTVR--TCDRFWQPEPALLPPG
>Tupaia_chinensis
-----MNTLDSRAVR--TCDRFWKPEPALLSPG

>Homo_sapiens
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>Felis_catus
MEAV-ASAATVGAAREKVAV
>Physeter_catodon
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>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
MEAV-SWAATVGAAREKVAV
>Galeopterus_variegatus
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>Condylura_cristata
---MEVVAATVGAAREKVAA
>Oryctolagus_cuniculus
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MEVV-ACAATVGAGREKVAV
>Loxodonta_africana
MEAV-SSAATVGAARETVAV
>Ictidomys_tridecemlineatus
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>Orycteropus_afer_afer
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>Acinonyx_jubatus
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>Orcinus_orca
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>Myotis_brandtii
MAVGWDRHTSMTI
>Galeopterus_variegatus
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>Oryctolagus_cuniculus
MAVGWDRNTSMTI
>Elephantulus_edwardii
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>Ceratotherium_simum_simum
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>Loxodonta_africana
MAVGWDSNRSITI
>Cricetulus_griseus
MAVGWDRSTSMTI
>Tupaia_chinensis
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>Orycteropus_afer_afer
MAVGWDRNTSITI

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>Leptonychotes_weddellii
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>Balaenoptera_acutorostrata_s
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>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
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>Galeopterus_variegatus
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>Condylura_cristata
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Ceratotherium_simum_simum
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>Dipodomys_ordii
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>Orycteropus_afer_afer
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>Galeopterus_variegatus
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>Sorex_araneus
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Ceratotherium_simum_simum
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>Mus_musculus
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>Orycteropus_afer_afer
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>Homo_sapiens
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>Balaenoptera_acutorostrata_s
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>Erinaceus_europaeus
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>Oryctolagus_cuniculus
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>Elephantulus_edwardii
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>Tupaia_chinensis
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HG0586.2 ENSG00000108375 RNF43

>Homo_sapiens

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>Canis_lupus_familiaris

MLFGEKKNFC

>Miniopterus_natalensis

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>Condylura_cristata

MLFGEKKNFC

>Equus_asinus

MLFGEKKNFC

>Tupaia_chinensis

MLFGEKKNFC

>Homo_sapiens
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>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
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>Condylura_cristata
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>Equus_asinus
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>Manis_javanica
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>Loxodonta_africana
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>Marmota_marmota_marmota
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>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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-----MRFSWKLFKRKMEGAV
>Lipotes_vexillifer
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>Myotis_davidii
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>Dasypus_novemcinctus
-----MRFPWKSLKRKMEGAV
>Galeopterus_variegatus
-----MRFPWKSFKRKMEGAI
>Condylura_cristata
-----MRFSWKLFKRKMEGAA
>Ochotona_princeps
-----MRLPWKSFKRKMEGAV
>Ceratotherium_simum_simum
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>Manis_javanica
-----MRSPWKLFKRKMEGAI
>Mesocricetus_auratus
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>Tupaia_chinensis
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>Pteropus_alecto
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>Galeopterus_variegatus
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>Condylura_cristata
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>Equus_caballus
-----MDTIQPPREFAPPAGKPLGANLGDRERSAPIVL-----
>Manis_javanica
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-----MDTIQPPREFAPPAGKPLGANLGDERSAPIGTRRHRFLRLIEISVF
>Orycteropus_afer_afer
-----MMDTIQPLREFIPPAGKPLGANLGDRESEAPIVL-----
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>Lipotes_vexillifer
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>Condylura_cristata
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>Equus_asinus
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>Manis_javanica
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>Ictidomys_tridecemlineatus
MQRPFPCSKQRWKYLGFR-----
>Tupaia_chinensis
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>Orycteropus_afer_afer
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>Homo_sapiens
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>Galeopterus_variegatus
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>Equus_asinus
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>Manis_javanica
-----MDLHSGSSPAFRILPPNSRPGAPSLGADVAV
>Loxodonta_africana
-----MDL-LGSSPAFGYWLPNTRPALPV-----
>Marmota_marmota_marmota
-----MDLHLCSSPAFPILPPNTRPGAPSLGADVVL
>Tupaia_chinensis
-----MDLHSGSSPALPTSPNTRPGSRSGADVVL

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>Felis_catus	
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	MAFVSPDALVTDLDEY
>Rhinolophus_ferrumequinum	
	MAFVSSDALVTDLDEY
>Condylura_cristata	
	MAFLSPDALVTDLDE-
>Oryctolagus_cuniculus	
	MAFVSPDALVTDLNEY
>Elephantulus_edwardii	
	MAFVSSDALVTDLDSRF
>Equus_asinus	
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>Chinchilla_lanigera	
	MAFVSPDALVTDLDEY
>Trichechus_manatus_latirostr	
	MAFVSPDALVTDLDTKY
>Orycteropus_afer_afer	
	MAFVSPEALVIVLDTKY

>Homo_sapiens
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>Leptonychotes_weddeli
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>Physeter_catodon
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>Galeopterus_variegatus
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>Condylura_cristata
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>Oryctolagus_cuniculus
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>Equus_asinus
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>Manis_javanica
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>Ictidomys_tridecemlineatus
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>Tupaia_chinensis
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>Orycteropus_afer_afer
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>Homo_sapiens

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>Acinonyx_jubatus

MWPKPDASLGHLDS

>Balaenoptera_acutorostrata_s

MWPKPDASLGRLDS

>Pteropus_alecto

MWPKPDSSLGHLDS

>Galeopterus_variegatus

MWPKLDTSLGHLDS

>Condylura_cristata

MWPKPDASLGHLDS

>Equus_asinus

MWPKADASLGRLDS

>Manis_javanica

MWPKPEASLGRLDS

>Fukomys_darlingi

MWPKLDNSLGHEDS

>Tupaia_chinensis

MWPKLDTSSGHLDS

>Orycteropus_afer_afer

MWPKPDTSLGHSDSP

>Homo_sapiens
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>Canis_lupus_familiaris
MAELQEILARQALPSGGKSRA-----
>Pteropus_alecto
MEEPQEILARQALPSKGKSRE-----
>Oryctolagus_cuniculus
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>Ceratotherium_simum_simum
MEEPQEILARQALPSRGKSRA-----
>Ictidomys_tridecemlineatus
MEQPQETLARQALPSRGQSGA-----
>Orycteropus_afer_afer
MEDPQEILAGQALPSRGKSCV-----

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>Homo_sapiens

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>Acinonyx_jubatus

MHTDVSSLQPFA

>Galeopterus_variegatus

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>Cavia_porcellus

MDTEVSNFQPFA

HG0592 ENSG00000133401 PDZD2

>Homo_sapiens

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>Mustela_putorius_furo

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>Balaenoptera_acutorostrata_s

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>Dasypus_novemcinctus

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>Tupaia_chinensis

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>Elephantulus_edwardii

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>Loxodonta_africana

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>Erinaceus_europaeus
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>Manis_javanica
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>Heterocephalus_glaber
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-----MSMVALKMNSLFSPDTLI
>Orycteropus_afer_afer
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>Condylura_cristata
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>Homo_sapiens
MRAGPSHRPVSHCPMLC
>Felis_catus
MRAGPSHRHVSDCLMLC
>Rousettus_aegyptiacus
MRAGPSHRHVSDCPMLC
>Dasypus_novemcinctus
MRAGPSHRHVSDCLMLC
>Condylura_cristata
MRAGPSHRHVSGCPMLC
>Ochotona_princeps
MRAGPSQRHVSHCPMLC
>Elephantulus_edwardii
MRAGPSHRHVSDCLMLC
>Equus_asinus
MRAGPSHRHVSDCPMLC
>Manis_javanica
MRAGPSHRHVNGCPMLC
>Nannospalax_galili
MRAGPSHRHVSHCPMLC
>Tupaia_chinensis
MRAGPSHRHVSHCPMLC
>Trichechus_manatus_latirostr
MRAGPSYRHVSDCPMLC

>Homo_sapiens
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>Canis_lupus_familiaris
MNQDKTSKCKYQKNYSTSW
>Physeter_catodon
MNQNKSSCKYQKNYNTSQ
>Eptesicus_fuscus
MNQDKTSKCKYQKNYNTSQ
>Dasypus_novemcinctus
MNQDKPSCKYQKNYNTSQ
>Galeopterus_variegatus
MNQEKTSKCKYQKNYNTSQ
>Condylura_cristata
MNQDTSKCKYQRNCHTSQ
>Oryctolagus_cuniculus
MNQDKTFCKYQKNYNTFP
>Ceratotherium_simum_simum
MNQDKTSKCKYQKNYNTSQ
>Manis_javanica
MNQDKTSKCKYQKNYNTSQ
>Marmota_marmota_marmota
MNQDKTSRCKYQKNYNTSQ
>Tupaia_chinensis
MNQGKTSKCKYQKKYSTSQ

>Homo_sapiens
MQEETFRRKTGREKLRLTLNLPNRASLR
>Panthera_tigris
MQEETFHRKTGREKL RPTIALPNRASLR
>Lipotes_vexillifer
MQGGTFHRKTGRGELRPASNLP SRASLR
>Miniopterus_natalensis
MQEEAFHRKTGRAKLRLTSLPSRVSLR
>Dasypus_novemcinctus
MQEETFHRKTGREKL RPTLNLPNRASLR
>Erinaceus_europaeus
MQEETFHRKTGREKLRLTFNLPNRASLR
>Oryctolagus_cuniculus
MQEEAFRRNAGRETLRLAARPPSGASPR
>Ceratotherium_simum_simum
MQEETFHRKTGREKLRLTLNLRIRASLR
>Manis_javanica
MQEEIFHRKSGREKLRLTVKLPNRVSLR
>Loxodonta_africana
MQEEAFHRKIGREKL RPTLNLLTRASLR
>Heterocephalus_glaber
MQEEAFHRKTGREKLRLTLNLPHRASLR
>Tupaia_chinensis
MQEETFHRKTGREKLRLSLNLPNRASLR

>Homo_sapiens
MSVTQRRCEAEGPSGGAAAASTSSSGSSPSPAVRSNWSPALRERTTKQPQRLSLRPRLLSARLRGQLPLAGLGWRARRAAAE-----RRAVC-----SRSPRTLHP
LASGLGGRSGIPATSNCP EIMQKVSQGS--
>Mustela_putorius_furo

-----MQKVSQGS--
>Lipotes_vexillifer

-----MQKVSQGS--
>Rousettus_aegyptiacus

-----MQKVS KAPDQ
>Dasypus_novemcinctus

-----MQKVSPSS--
>Condylura_cristata

-----MQKVSQGS--
>Ochotona_princeps
MSVTQRQCEAEGPSGGAAAASTSS--SSSGAARAELSRALRERSTKRAPRLALGPRLLSAGLLGQLPPQRA-WLLPGEAGGGGGGTPGCLLARPPPPHRAHSLHP
LAAGLGS RAGILATSDCPEIMQKVSQGS--
>Ceratotherium_simum_simum

-----MQKVSQGS--
>Loxodonta_africana

-----MQKVSQAS--
>Ictidomys_tridecemlineatus

-----MQKVSQGS--
>Trichechus_manatus_latirostr

-----MQKVSQAS--
>Orycteropus_afer_afer

-----MQKVSQAS--

>Homo_sapiens
-----MLFSCPFSPNHQQ
>Acinonyx_jubatus
-----MLFPCPFSPNHQQ
>Tursiops_truncatus
-----MLFPCPFSPNHQQ
>Myotis_davidii
-----MLFPCPFSPNHQQ
>Galeopterus_variegatus
MGVEKRPQGVERRRLTLPTT--TRLKQGYNITYPLMLLLYPFSPNHQQ
>Condylura_cristata
-----MLFPCPFSPNHQQ
>Elephantulus_edwardii
-----MLFLCPFFPNHQL
>Equus_asinus
-----MLFPCPFSPNHQQ
>Dipodomys_ordii
-----MCFPCPFSPNHQQ
>Tupaia_chinensis
-----MLFLCPFSPNHQQ
>Trichechus_manatus_latirostr
MGVKERPQGVGRGLIPPTPVPPHPKEGCNITYLLMLFPCPFSPNHQQ

HG0604.2 ENSG00000003147 ICA1

>Homo_sapiens

MSDPEGRSDRGREAPGGRGSEVII

>Odobenus_rosmarus_divergens

MKELEGRSDRGQREAPGGRGSEVII

>Tursiops_truncatus

MKELEGRSDRGREAPRGSEVII

>Rousettus_aegyptiacus

MRELEGRSDRGREAPGGRGSEVII

>Condylura_cristata

MKELEGRSDRGREAPGGRGSEVII

>Ceratotherium_simum_simum

MRELEGRSDRGREAPGGRGSEVII

>Ictidomys_tridecemlineatus

MWDLEGHSDRGREAPGGQSEV--

HG0604.3 ENSG00000003147 ICA1

>Homo_sapiens

MATWNTCRRAGAGSLWAADPSGGYPRRWGSRRDPGE

>Galeopterus_variegatus

MDTWNTCGRAGAGSPRAADPSKGYPKRWGSRKDPRE

>Ceratotherium_simum_simum

MDTWNTCGRAGRGHPRQMRAGGYPRRWGSRKDPRE

>Mus_musculus

MDTWNTC-----

>Orycteropus_afer_afer

MDTWNTCRKAGAGSPWTAGPRGGYPRRWGSRKDPRE

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>Homo_sapiens
MKKNQPLEDQHSRDYGGPSVFSVTGAMLT SVSWTHSDSGAFT
>Felis_catus
-----MLTSVSWTHSDSGAFT
>Physeter_catodon
-----MLTSVSWTHSDSGAFT
>Miniopterus_natalensis
-----MLTSVSWTHSDSGAFT
>Condylura_cristata
-----MLTSVSWTHSDSGAFT
>Oryctolagus_cuniculus
-----MRTSVSWTHCDSGAFT
>Ceratotherium_simum_simum
-----MLTSVSWTHSDSGAFT
>Manis_javanica
-----MLTSVSWTHSDSGAFT
>Loxodonta_africana
-----MLTSVSWTHSDSGAFT
>Nannospalax_galili
-----MLTSISWTHSDSGAFT
>Tupaia_chinensis
-----MLTSVSWTHSNSGAFT
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HG0606 ENSG00000055130 CUL1

>Homo_sapiens
MRFHSLHLKDILSELL
>Odobenus_rosmarus_divergens
MRFHSLHLKDILSELL
>Balaenoptera_acutorostrata_s
MRFHSLPLKDVSELL
>Cynopterus_sphinx
MKVHSLQLKDILSELL
>Dasypus_novemcinctus
MRSHSLHLKDILSELL
>Galeopterus_variegatus
MRFHFLHLKDILF---
>Ceratotherium_simum_simum
MRFHSLHLKDILSELL
>Manis_javanica
MRFHSLHLKDILSALL
>Heterocephalus_glaber
MRFHSLHLKDILSELL
>Tupaia_chinensis
MRFASLRLKDILSELL
>Trichechus_manatus_latirostr
MRAPSLHLKDTASELL

>Homo_sapiens
MRFQRPPCPLSHWPCLRPPPPQTAPVFFPRGEGIWTSPPRCLKEEKGMFCLVLLEATKGCWGC-----
>Odobenus_rosmarus_divergens
-----MFCFVLFLLEATKGCWGYF-----
>Orcinus_orca
-----MFCFVLFLLEATKGFWGC-----
>Miniopterus_natalensis
-----MFCFVLFLLEATKGCWGYF-----
>Dasypus_novemcinctus
-----MFCFVLFLLEATKGCWGYV-----
>Galeopterus_variegatus
-----MAAKSRGACRKAMFCFVLFLLEATKGCWGYF-----
>Condylura_cristata
-----MFCFVLFLVEATKGVGDTSDCYEGRKAC-----
>Oryctolagus_cuniculus
-----MNWWVCDGS-----LFVAGECYFACLSSL-----AGCVLFCAFFLLEATKGCWGYF-----
>Ceratotherium_simum_simum
-----MFCFVLFLLEATKGCWGYF-----
>Ictidomys_tridecemlineatus
-----MFCFVLFLLEATKGCWGYF-----
>Orycteropus_afer_afer
-----MFYFVFFLLEAAKGCWGDF-----

HG0608 ENSG00000084731 KIF3C

>Homo_sapiens

MNDPPAWGEDSR

>Leptonychotes_weddellii

MNDPPARGEDSR

>Orcinus_orca

MNDPPAGGEDSR

>Rousettus_aegyptiacus

MNDPPAGGEDSR

>Galeopterus_variegatus

MNDPPSVGEDSR

>Condylura_cristata

MNDPPAGGADSR

>Elephantulus_edwardii

MNDPPAGGDSR

>Loxodonta_africana

MNDPPAEGEDSR

>Peromyscus_maniculatus_baird

MNDPPAGGEDSR

>Trichechus_manatus_latirostr

MNDPPASGEDSR

>Orycteropus_afer_afer

MNDPPAWGEDSR

>Homo_sapiens
----MATQPCDSMSPRFQDPPWPHDSLTPMTL
>Ailuropoda_melanoieuca
----MATQPCDSMSPRFQDPPWPHDP-----
>Physeter_catodon
----MATQPCDSMSPFQDPPWPHDS-----
>Pteropus_alecto
----MATQSCDSMSPFQDPPWPHDA-----
>Galeopterus_variegatus
----MATQPCDSMSPFQDPPWPHDSLAPMAL
>Oryctolagus_cuniculus
----MATQPCDSMSPPFQDPPWPHDSLTPMAS
>Ceratotherium_simum_simum
----MATQPCDSMSPFQDPPWPHDP-----
>Manis_javanica
MWDSMATQPCDSMSPRFQDPPWPHDL-----
>Loxodonta_africana
----MATQPCDMSPRFQDPPWPHDSVTPMPS
>Rattus_norvegicus
----MATQPCGMSPPFQDPPWPHDYLTPTS
>Tupaia_chinensis
----MAIQPCDSMSPRFQDPPWPHDSLTPAL

HG0610 ENSG00000106069 CHN2

>Homo_sapiens
MGWGPRLRAAGRGQRRRPARG
>Odobenus_rosmarus_divergens
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>Orcinus_orca
MGWGPRLRAAGSGQRRRPARG
>Myotis_lucifugus
MGWGPRLRAAGRGQRRRPARG
>Dasypus_novemcinctus
MGWGPRLRAAGRGQRRRPARG
>Sorex_araneus
MGWGPRLRAAGPGQRRRPARG
>Ochotona_princeps
MGWGPRLRAAGPGQRRRLRQG
>Elephantulus_edwardii
MGWGPRLRAAGPGQRRPA-HRG
>Equus_asinus
MGWGPRLRAAGRGQRRRPARG
>Loxodonta_africana
MGWGPRLRAAGRGQLRRRPARG
>Ictidomys_tridecemlineatus
MGWGPRLRAAGGQRRRPARG

HG0611 ENSG00000108309 RUNC3A

>Homo_sapiens
MAMEGLRGPVGQRAQP
>Odobenus_rosmarus_divergens
MAVQASRGPGGQRAQP
>Orcinus_orca
MALEGSRGPGGQRAQP
>Eptesicus_fuscus
MAVEGSRGPDGQKAQP
>Galeopterus_variegatus
MAAEGSRRPGGQRAQP
>Sorex_araneus
MAAEGSRGPGGQRAQP
>Ochotona_princeps
MALEGSRGSGGQSAQP
>Elephantulus_edwardii
MAAEGSRGPGGRRAP
>Equus_asinus
MAVEGSRGPGGQRAQP
>Manis_javanica
MALEGSRGPGGQRAQR
>Ictidomys_tridecemlineatus
MAMERSMGPGGQRAQP

>Homo_sapiens
-----MAASRALWPRPQRRGAAGLQGVNSGDVRACV-----

>Mustela_putorius_furo
-----MAASLALWPSHQRRRAAGLEGVNSGDVSACDCWGGEM-----

>Lipotes_vexillifer
-----MAASLALWPSQRRRAAGLEGVNSGDVSACDCWGGEM-----

>Rousettus_aegyptiacus
-----MAASLALWPSHQRRRAAGLEGANS GDVSACDCWGGEM-----

>Condylura_cristata
-----MAASPAWWPSHRRRAAGLQSVHSGDVSACDCWGGEM-----

>Ochotona_princeps
-----MASSRALGPDQRREAAESEG VNPRDVRAWDCRGEM-----

>Elephantulus_edwardii
-----MAASLAWWPRRWRRSAAWLQGVSSPGPECV-----

>Manis_javanica
-----MAASVSLRPSRQRRRAAGLEGNSGDWSACDCWGGEMRSARSASPAAAGRRGGRAAGLLPASLV TLLFAALGEL AERLRRRMCVFLSG
GRRLF

>Rattus_norvegicus
MGANTNVHTRRRSAQPRGCAAEAWWPCHRRRGAAGLEGVNSGDVRACDCWGGEM-----

>Trichechus_manatus_latirostr
-----MAASPALGPRHQRRRAAGLEGVNSGDVSACDCWAGEM-----

>Orycteropus_afer_afer
-----MAASPALWPRHQRRRAAGLEGVDSGDL SACDCWAGEM-----

>Homo_sapiens
MLRAAAARRGESAGL
>Odobenus_rosmarus_divergens
MLRAAAARRGESGL
>Eptesicus_fuscus
MLRAAAARRGESAGL
>Dasypus_novemcinctus
MLRAAAARRGESAGL
>Galeopterus_variegatus
MLRAAAARRGESAGL
>Condylura_cristata
MLRVAAARRGESAGL
>Oryctolagus_cuniculus
MLRAAAARRGESAGL
>Manis_javanica
MLRAAAARRGESAGL
>Loxodonta_africana
MLRVAAARRGESGL
>Ictidomys_tridecemlineatus
MLRAAAARRGESAGL

HG0612.3 ENSG00000110422 HIPK3

>Homo_sapiens

MKMSVSLSGGRLL

>Ursus_maritimus

MGMSVFLSGGRRLF

>Lipotes_vexillifer

--MSVFLSGGRRLF

>Eptesicus_fuscus

--MSVSPSGGRLL

>Mesocricetus_auratus

--MSVFLSGGRLL

HG0613 ENSG00000114861 FOXP1

>Homo_sapiens
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>Canis_lupus_familiaris
MVRASIPSLICQP-----
>Balaenoptera_acutorostrata_s
MVRASIPCLICQP-----
>Pteropus_alecto
MVRASIPSLICQP-----
>Galeopterus_variegatus
MVRALIPSLICFQPCTAGCDAC
>Ochotona_princeps
MVRASIPSLICQP-----
>Ceratotherium_simum_simum
MVRASIPSLICQP-----
>Loxodonta_africana
MVRASIPSRFCCQP-----
>Jaculus_jaculus
MVRALPSLICRP-----
>Tupaia_chinensis
MVRASILSLICQP-----
>Orycteropus_afer_afer
MVRASVRSPICQP-----

>Homo_sapiens	
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>Odobenus_rosmarus_divergens	
-----	MDSSQ
ADLLICSSWTMFLINTCLSA	
>Galeopterus_variegatus	
-----	MDSSW
EALLISSWTMFLINICLSA	
>Erinaceus_europaeus	
-----	MDTSSW
TASLLHSSWTMDD-HLCLSA	
>Oryctolagus_cuniculus	
-----	MFPGQCWGLMFLLLPLPWFESGQCHSLSGYLGWLSLCSAGVQAAGGFLSVGEQNLWMD-SW
KASLAGSSWKKFLISIC---	
>Elephantulus_edwardii	
-----	MDFSW
DALLTCSSWTMFLINICLSA	
>Ceratotherium_simum_simum	

----MCSSWTMFLINNCLSA	
>Chinchilla_lanigera	
-----	MDSSG
KALLICSSWTMFLINICLSA	
>Tupaia_chinensis	

-----MLLITICLSA	
>Trichechus_manatus_latirostr	
-----	MDSSW
EALLTCSSWTMFHI-ICLSA	
>Orycteropus_afer_afer	
-----	MDSSW
EVLLTCSSWTMFLINICLSA	

>Homo_sapiens
MKTDSLRSQSLKLSAL
>Acinonyx_jubatus
MKTDSLRSQSFKLSAL
>Pteropus_alecto
MKTDSLRSQSFKLSAL
>Galeopterus_variegatus
MKTDSLRSQSFKLSAL
>Erinaceus_europaeus
MKTDSLRSQSFKLSAL
>Ochotona_princeps
MKTESLRSQSFKLSAL
>Equus_asinus
MKTDSLRSQSFKLSAL
>Manis_javanica
MKTDSLRSQSFKLSAL
>Loxodonta_africana
MKTDSLRSQSFKLSAL
>Marmota_marmota_marmota
MKTDSLRSQSFKLSAL
>Orycteropus_afer_afer
MKTDSLRSQSFKLSAL

>Homo_sapiens

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECQLYPRRSQQ--QQVPVVD
FQAELRQAFLAETPRGG

>Leptonychotes_weddellii

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECQLYPRRSQQ--QQIPVVD
FQAELRQAFLAETPRGG

>Tursiops_truncatus

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECHLYPRRSQQQQQVPVVD
FQAELRQAFLAETPRGG

>Miniopterus_natalensis

-----MGAC-----SRRPASRRPSSTMSRGACAGPLRRIRFKGQGLCFLAL--RPRGPPDACPPSRCQQFPRRSPP--PRARAAD
FAAELRPAFVAETPRGG

>Galeopterus_variegatus

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECHLYPRRSQQ--QPVPVVD
FQVELRQAFLAETPRGG

>Erinaceus_europaeus

-----MERARDRLNLRRT--TEQQVPEVEVQVKRRRTASLSNQECHLYPRRSQQ--QQVPVVD
FQAELRQAFLAETPRGG

>Ochotona_princeps

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECQLYPRRSQQ--QQVPVLD
FQAELRQAFLAETPRGG

>Equus_przewalskii

-----MERPRDLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECQLYPRRSQQ--QQIPLLD
FQAELRQAFLAETPRGG

>Ictidomys_tridecemlineatus

-----MERARDRLHLRRT--TEQHVPEVEVQVKRRRTASLSNQECHLYPRRSQQ--QQVPVVD
FQAELRQAFLAETPRGG

>Trichechus_manatus_latirostr

-----MERVRDLHLRRT--TEQHVPEVEVQVKRRRTASLNNQECQLYPRRSQQ--QQVPVVD
FQAELRQAFLAETPRGG

>Orycteropus_afer_afer

MTDNFSTGLVQGEFLPHNAVVMWEYTGRLSLMPDNIGSSPPP--RSAAVKWGGKDRHLRRT--TEQHVPEIEVQVKRRRTASLSNQECQLYPRRSQQ--QQVPVLD
FQAELRQAFLTETPRGG

>Homo_sapiens
MRATWVKKLPVNSHHFCPSLGNTFRECCGDRNMGEKQSG
>Mustela_putorius_furo
-----MGEKQSG
>Physeter_catodon
-----MEEKQSG
>Miniopterus_natalensis
-----MEEKQSG
>Galeopterus_variegatus
-----MGEKQSG
>Oryctolagus_cuniculus
-----MGEKQLG
>Equus_asinus
-----MGEKQSG
>Loxodonta_africana
-----MGKKQSG
>Dipodomys_ordii
-----MGETQSG
>Tupaia_chinensis
-----MGEIQSG
>Orycteropus_afer_afer
-----MGEKQSG

HG0618 ENSG00000137817 PARP6

>Homo_sapiens
MPISLALVRLVVRGAA--
>Leptonychotes_weddellii
MPIPLACVQLVVRGAA--
>Balaenoptera_acutorostrata_s
MPISLAWQLVVRGAA--
>Eptesicus_fuscus
MPISLAWQLVVRGAA--
>Dasypus_novemcinctus
MPISLALVQLVVRGAA--
>Condylura_cristata
MPISLARVQLVVRGAA--
>Oryctolagus_cuniculus
MPIILLAWRLVAWRGAAEH
>Ceratotherium_simum_simum
MPISLAWQLVVRGAA--
>Manis_javanica
MPISLAWQLVVRGAA--
>Loxodonta_africana
MPISLAWQLVVRGAA--
>Heterocephalus_glaber
MPISLAWQLVVRGAA--

>Homo_sapiens
MEKAARGAVYTD
>Felis_catus
MEKAARGALHTD
>Lipotes_vexillifer
MEKAARGALDTD
>Miniopterus_natalensis
MEKAARGALYTD
>Galeopterus_variegatus
MEKAARGALHTN
>Condylura_cristata
MEKAARGALHTD
>Elephantulus_edwardii
MEKAARGALHTD
>Equus_asinus
MEKAARGALHVD
>Manis_javanica
MEKAARGALHTN
>Chinchilla_lanigera
MEKAARGALHTD
>Trichechus_manatus_latirostr
MEKAARIALYTD

HG0620 ENSG00000145555 MY010

>Homo_sapiens
MCHQLFSACERCAQ-
>Odobenus_rosmarus_divergens
MCHQLFSARERCAQK
>Physeter_catodon
MCHQLFSARERGAQE
>Rousettus_aegyptiacus
MCHQLFSARERCAPK
>Galeopterus_variegatus
MCHQLFSARERFAQE
>Oryctolagus_cuniculus
MCHQLFPARERSVQK
>Ceratotherium_simum_simum
MCHQLFSARERGAQK
>Manis_javanica
MCHQLFSARQRCAQE
>Rattus_norvegicus
MCHQLFSAREHFAQK
>Tupaia_chinensis
MCHQLFTAREHLAQK
>Trichechus_manatus_latirostr
MCHQLFSARERCALK

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>Homo_sapiens
MPLSPPPPLLKPRLMDARECR|A
>Odobenus_rosmarus_divergens
MLLSPPP--PKPGLMDARECR|A
>Pteropus_alecto
--MLSSPPPLLKPRLMDAGECR|A
>Dasypus_novemcinctus
-----MDTRECR|A
>Condylura_cristata
-----MDARECR|A
>Oryctolagus_cuniculus
-----MKPGLMDARECR|A
>Equus_caballus
--MLLPPTPLKPRLMDARECR|A
>Loxodonta_africana
---MLLSPLLKSQLMDAGECR|A
>Rattus_norvegicus
MVLSPPRPLRKPG|MDAGECR|A
>Tupaia_chinensis
-----MDARECR|A
>Orycteropus_afer_afer
MLLS---PPPKPRLMDARECR|A
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HG0621.2 ENSG00000146352 CLVS2

>Homo_sapiens
MAGPGENLGQRWP
>Odobenus_rosmarus_divergens
MAGPGEDLGRRWP
>Orcinus_orca
MAGPGENLGQRWP
>Rousettus_aegyptiacus
MAGPGEDPGQPWP
>Galeopterus_variegatus
MAGPGEHLGQRWP
>Oryctolagus_cuniculus
MAGPGEDLGQWS
>Ceratotherium_simum_simum
MAGPGEDLGQRWP
>Loxodonta_africana
MAGPSEDLEQRWL
>Ictidomys_tridecemlineatus
MAGPGDGLGQRWP

HG0621.3 ENSG00000146352 CLVS2

>Homo_sapiens

MPPKLPSYP-----NEAGKGAERARELSECLRRSEICAGIIREELG

>Odobenus_rosmarus_divergens

MPRKLPSPAES--GREERGACAS-----

>Galeopterus_variegatus

MPPKLPSQPNKA--GREELSACAS-----

>Condylura_cristata

MPPEPPAEASGPEAGGTRLRGCLNATDVAILLKRVGERAAECVRELSECLRRREIEAGIMREELG

>Marmota_marmota_marmota

MPQKLPSFPRQGEKS-----

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>Homo_sapiens
MKIHLPLSWLLMGV-GVLLRFPGWKIISPGPSYIS-----
>Leptonychotes_weddelii
MKIHLPLSWPLVGA-GVLLGFPGWEITSPGPSYISRPVWRAPQG
>Orcinus_orca
MKLHLPLSWPRVGA-GVLLGFPGWKISSGPSYIS-----
>Pteropus_alecto
MKIHLPLSWPVVGA-GMLLGFPGWKIISPSPSYIS-----
>Dasypus_novemcinctus
MRIHLPLSWLLVRV-GVLLGFPGWKIISPSPSYIS-----
>Galeopterus_variegatus
MKIHLLLSWPLVGA-GVLLGFPGWKIISPSPSYIS-----
>Condylura_cristata
MKIHLPLSWPLVGG-GVLLGFPGWKISSPVLA I-----
>Oryctolagus_cuniculus
MKIHLPLSWLLAGGQGCYLG SQVGRLSHPAQTI-----
>Ceratotherium_simum_simum
MKIHLPLSWPLVGA-GVLLGFPGWKIISPSPVYIS-----
>Loxodonta_africana
MKIHLPLSWLLR-GRGCYLG SQVGRLSHPAQAI-----
>Jaculus_jaculus
MKIHLPLSWPLVGA-GALLGFPGWKIISPSPSYITG-----
```

>Homo_sapiens
MTIFARLHCTFSQVSSSLMCD-TSSWTRYFS-----
>Felis_catus
MVIPVRLHCTFSQVCSSSLMCN-PSTWTCYFS-----
>Orcinus_orca
MTIPVRLHCTFSQVSSSLMCN-PSTWTCYFS-----
>Pteropus_vampyrus
MIIPVRLH-----
>Dasypus_novemcinctus
-----MFSQVSSSLMCS--STWTCYFS-----
>Condylura_cristata
MIITVSLHCTFSNVSSLLLMCS-PSIWTFYFS-----
>Oryctolagus_cuniculus
----MSLHSTFFQVFSSSLMSNHTSTWTCYFS-----
>Equus_asinus
MIIPVRLHCTFSQVSSSLMCN-PSTWTCYFS-----
>Loxodonta_africana
-----MCN-TTTWTCYFS-----
>Dipodomys_ordii
-----MCN-TSTWTCYFR-----
>Tupaia_chinensis
MIPPVRLHCTFSQVSS-SRMCG-TSPWTCCFSLDVASNE

>Homo_sapiens
MALRSIKSIAGSCLCSRQRCGSSAAIFPEGIFRCLSPKFGQEFPE
>Acinonyx_jubatus
MALRSIKSIAGSCLCSRLRRCGSSAAIFPEGIFRCLSPKFGQEFPE
>Tursiops_truncatus
MALRSIKSIAGSCLCFRQRCSSGAAIFPEGIFRCLSPKFGQEFPE
>Eptesicus_fuscus
MALWSIKSIAGSCLCSRQRCSSSAAIFAEGLFRCLSPKFGQEFPE
>Dasypus_novemcinctus
MALWSIKSIAGSCRCREKRCSSAAIFPEGILQCLSPKFGQEFPE
>Galeopterus_variegatus
MALRSIKSIAGSCLCSRQRCNSSAAIFPEGIFRCLSPKFGQEFPE
>Oryctolagus_cuniculus
MALRSIKSIAGSRLCSRQRCSCGAAIFPKGIFRCLSPKLGQEFPE
>Ceratotherium_simum_simum
MALRSIKSIAGSCLCSRHRRCSSAAIFPEGIFRCLSPKFGQEFPE
>Manis_javanica
MALWSIKSIAGSCLCSRQRHWSSGAAIFPEGIFQCLSPKFGQEFPE
>Marmota_marmota_marmota
MALRSIKSIAGSCLCYRQRCSSSAAIFPEGIFRCLSPKFGQEFPE
>Tupaia_chinensis
MALRSIKSIAGSCLCSRQRCSSAAAIFPEGIFRCLSPKFGQEFPE

HG0625 ENSG00000164050 PLXNB1

>Homo_sapiens

MLLSPDPAGPAR

>Mustela_putorius_furo

MLLSPDPAGPAR

>Lipotes_vexillifer

MLLSPDPAGLAR

>Pteropus_vampyrus

MLLSPDPAGPAR

>Oryctolagus_cuniculus

MLLSPDPAGPAR

>Elephantulus_edwardii

MLLSPDPAGPAR

>Ceratotherium_simum_simum

MLLSPDPAGPAR

>Loxodonta_africana

MLLSPDPADPAR

>Dipodomys_ordii

MLLSPNPAGPAR

>Tupaia_chinensis

MLLSPDPAGPAR

>Orycteropus_afer_afer

MLLSPDPASPAR


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>Homo_sapiens
-----MDKPFPPQGFSHVP
>Acinonyx_jubatus
-----MDKPFPPQGFSDVP
>Physeter_catodon
-----MDKPFLQGFSQDVP
>Miniopterus_natalensis
-----MDRSFPQGFSDVP
>Galeopterus_variegatus
MTSAFPSMDKPFPPQGFSDVP
>Erinaceus_europaeus
-----MDKPFPPQGFSDVP
>Oryctolagus_cuniculus
-----MDKPFSQGFSDVP
>Equus_asinus
-----MDKPFPPQGFSDVP
>Manis_javanica
-----MDKPFSQGFSDVP
>Heterocephalus_glaber
-----MDKPFPPQGFSDVP
>Trichechus_manatus_latirostr
-----MDKPFPPQGFSDVP
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HG0627 ENSG00000169760 NLGN1

>Homo_sapiens
MRGLPLWIYLAEGYRPAANWI
>Odobenus_rosmarus_divergens
MRGFPLWIYLTGCRPAANWI
>Balaenoptera_acutorostrata_s
MRGLLLWIYLTGYPAPANWI
>Rhinolophus_ferrumequinum
MRGLPLWIFLTGYPAPANWI
>Sorex_araneus
MRGLPLWICLTGYPAPANWI
>Equus_asinus
MKGLRLWI-----
>Manis_javanica
MRVLPLWIYLTGYPRTANWI
>Loxodonta_africana
MKGLPPWIPLTQGYRPAKWI
>Marmota_marmota_marmota
MRGLPLWICLAEGYRPAANWI
>Tupaia_chinensis
MRGLAPRTRLPEGYRPTVNW
>Orycteropus_afer_afer
MRGLPPWIYLTGYPATNWI

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>Homo_sapiens
MKQEKYIDAALQPLQMFQDNIPDRNIDPLD
>Felis_catus
MKLEKYIDAALQPLQMFEDNIPERN-----
>Lipotes_vexillifer
-----MQHCVQPLQMFEDNIPERN-----
>Dasypus_novemcinctus
-----MFGDNIPQRS-----
>Galeopterus_variegatus
MKLEKYIDAALQPLQMFQDNIPERN-----
>Oryctolagus_cuniculus
MKLEKCIDAAALQPLQMFQNNIPERN-----
>Ceratotherium_simum_simum
MKLEKYIDAALQPLQMFEDNTPERN-----
>Loxodonta_africana
MKLEKYIDAALQPLQMFQDNIPERN-----
>Heterocephalus_glaber
MKLEKHTDAALKPLQMFQDNIPERKLIPVD
>Tupaia_chinensis
MKLEKHTDAALQPLQMFQDTIPERR-----
>Trichechus_manatus_latirostr
MKLEKYVDAALQPLQMFQDNIPERN-----
```

HG0629 ENSG00000170961 HAS2

>Homo_sapiens
MLFLNFLFFLAGRLKFI
>Odobenus_rosmarus_divergens
MLFLNFLFFLAGRLKFI
>Lipotes_vexillifer
MLFLNFLFFLAGRLKFI
>Myotis_brandtii
MLFLNFLFFLAGRLKFI
>Dasypus_novemcinctus
MLFLNFLFFLAGRLKFI
>Galeopterus_variegatus
MLFLNFLFFLAGRLKFI
>Condylura_cristata
MLFLNFLFFLAGRLKFI
>Ceratotherium_simum_simum
MLFLNFLFFLAGRLKFI
>Mus_musculus
MLFLNFLFFLAGRLKFI
>Tupaia_chinensis
MLFLNFLFFLAGRLKFI
>Orycteropus_afer_afer
MLFLNFLFFLAGRLKFI

HG0630 ENSG00000171552 BCL2L1

>Homo_sapiens

MIPPAGAG--FFASHREAG

>Canis_lupus_familiaris

MIPPAGAG--FFASRREAG

>Lipotes_vexillifer

MIPPAGAG--FFASRREAG

>Pteropus_vampyrus

MIPPAGAG--LFASRREAG

>Dasypus_novemcinctus

MIPSAGAA--FFANRREAG

>Galeopterus_variegatus

MIPPAGAV--FFASRREAG

>Oryctolagus_cuniculus

MIPPAGAV--CFASRREAG

>Equus_caballus

MILPAA---AFFASHREAG

>Heterocephalus_glaber

MIPPAGAG--FFASRREAG

>Tupaia_chinensis

MIPPAGAA--YFASRREAG

>Trichechus_manatus_latirostr

MIPPAGAVLLFFASRREAG

>Homo_sapiens
--MSPPCSQAYARRPDRAVSGPWTLT
>Physeter_catodon
MDMSPPCSQACAGRP---VSGPWTLT
>Cynopterus_sphinx
MDMSLSCLQACAGKPDRAVSGPWTQL
>Dasypus_novemcinctus
--MSPPCTQACAQRPERAFSGPWTLT
>Oryctolagus_cuniculus
MAGSPPSLEAHGQIPDWAAAGPWTLT
>Equus_asinus
MDMSPPCSHVCARRPERAVSGPWTLF
>Manis_javanica
MDVSPPCSQECARRSDRAVPGPWTLF
>Loxodonta_africana
--MSPPCSRSCAWRLDRAVSEPWTLT
>Ictidomys_tridecemlineatus
--MSPPCSQAYAQRLNRVVSGPWTLF
>Trichechus_manatus_latirostr
--MSPPCSQLCAWRPDRAVSGPWTLT
>Orycteropus_afer_afer
--MSPPYSQTFSWRLDRAVSGTWALL

```
>Homo_sapiens
MTVRATMGQEDQWKTP
>Ursus_maritimus
-----MGQEDQWKTP
>Orcinus_orca
MTVKKMMGQEDQWKTP
>Dasypus_novemcinctus
MTSKTMMGQEDQWKTP
>Galeopterus_variegatus
MTMKAMMGQEGRWKTP
>Oryctolagus_cuniculus
MTVKVMMGQEDQWKTP
>Equus_caballus
MTVKKMMGQEDQWKTP
>Loxodonta_africana
MTAKTMMGQEDQWKTP
>Dipodomys_ordii
MTMKAKMGQEDQWKSP
>Trichechus_manatus_latirostr
-----MGQEDQWKTP
>Orycteropus_afer_afer
MTVKTMMGQEDQWKTP
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HG0632.2 ENSG00000181315 ZNF322

>Homo_sapiens

MYVFFHLDSRVGNTK-----

>Canis_lupus_familiaris

MLLSFQLDSRVGNTK-----

>Rhinolophus_ferrumequinum

MLLFIHLDSRVGNTK-----

>Condylura_cristata

MLLIFHLDCRAGNTKQGISVYDGETL

HG0633 ENSG00000186174 BCL9L

>Homo_sapiens
MLRGWEAGTQAPSDPRIASPGPGWY
>Mustela_putorius_furo
MLGGWEAGTQAPSDPRIPSPGPGWY
>Orcinus_orca
MLRGWKAGTQAPSDPRIPTPGPGWY
>Pteropus_vampyrus
MLRGWKAGTQAPSNPRIPSPGPGWY
>Dasypus_novemcinctus
MLGDWEAGTQAPSDSRRPSLGPLWY
>Condylura_cristata
MFRGWEAGTQAPSDPRIPSPGPGWY
>Oryctolagus_cuniculus
MLRSWEAGTQAPRDSRTPSPGPGWD
>Equus_asinus
MLRGWEAGTQAPSDPRRP-PGPGWY
>Manis_javanica
MLRGWEAGTQAPSDPRIPSPGPGGY
>Marmota_marmota_marmota
MLRRREAGTQAPSDPRIPSPGPGWY
>Tupaia_chinensis
MLRGWETGTQAPSDPRIPSPGPGWC

>Homo_sapiens
-----MPESERNVATKASE
>Ursus_maritimus
-----MATSSMPESERSAATKASE
>Physeter_catodon
-----MATSSMPESERNAATKASE
>Rousettus_aegyptiacus
-----MATSSMPESERNAATKASE
>Dasypus_novemcinctus
MPIDSSAAGGKRMATSSMPESEKNADTKASE
>Galeopterus_variegatus
-----MATSSMPESEKNAATEASE
>Condylura_cristata
-----MATSSMPESERNAAAKTSE
>Ceratotherium_simum_simum
-----MATSSMPESERNAATKASE
>Manis_javanica
-----MATSSMPESERNAATQASE
>Cavia_porcellus
-----MATSSMPESERNAAKKASE
>Tupaia_chinensis
-----MATSSMPVSERNVATKASE

>Homo_sapiens	
MAAETGYWRCLPESRTCAEEAVHLWPAVLRDPRWGNPGDGAWPCYMRGPRLE	
>Leptonychotes_weddellii	
-----MPAPRLE	
>Rousettus_aegyptiacus	
-----MPAPRLE	
>Dasypus_novemcinctus	
-----MPAPRLE	
>Condylura_cristata	
-----MPAPRLE	
>Oryctolagus_cuniculus	
-----MPAPRLE	
>Elephantulus_edwardii	
-----MPAPRLE	
>Manis_javanica	
-----MPAPRLE	
>Fukomys_darlingi	
-----MTAPRLE	
>Trichechus_manatus_latirostr	
-----MPAPRLE	
>Orycteropus_afer_afer	
-----MPAPQLE	

>Homo_sapiens	MAQPRSL
FRAPDGLDRGAAQ	
>Felis_catus	MAQPESR
LRAPDRLDRGAAQ	
>Physeter_catodon	MAKPESR
LRAPDRLEGGAAQ	
>Rhinolophus_ferrumequinum	MAQPESR
LRTPDPLDRGAAQ	
>Erinaceus_europaeus	MAQPQSR
LGAPDWLDQRAAQ	
>Oryctolagus_cuniculus	
MPIPRARKPGQSEDPGPGGHPGAAPVSEDRLPLLPGRHTEHRLRTEHQNARLQGLRRAGNREPPPLPGLRGCLRPFHRLACLDIRSTCRGCSAVLPMAQPESR	
LRAPDGLDGGVAQ	
>Ceratotherium_simum_simum	MAQPESR
LRAPDRLDRGAAQ	
>Manis_javanica	MAQPESR
LVAPDRLDRGAAQ	
>Loxodonta_africana	MAQPQSR
PRAPDGLDGGAAQ	
>Cavia_porcellus	MAQPESR
FRAPDGRDRRAAQ	

HG0637 ENSG00000005102 MEOX1

>Homo_sapiens
MFSVIGDKYTYRGSQ
>Odobenus_rosmarus_divergens
MFSVIGDKYTSRGPQ
>Lipotes_vexillifer
MFSVIGDKYTYRGPH
>Pteropus_vampyrus
MFSVIGDKYTYRGPD
>Dasypus_novemcinctus
MYSVIGDKYTHKGP-
>Galeopterus_variegatus
MFSVISDKYTYKGPQ
>Equus_asinus
MFSVIGDKYTYRGPD
>Marmota_marmota_marmota
MFSAIGNKMYKGPQ
>Tupaia_chinensis
-----MYKGPQ
>Trichechus_manatus_latirostr
MFSVISDKYTYKGPQ

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>Homo_sapiens
MSSTSWPLTQLQQSQLHQLENKWDLHELHSELKYRLRC
>Mustela_putorius_furo
MSSRSWPFITLQQSHLHLEDKWDLHKFQILN-----
>Physeter_catodon
MSSTSWPLITLQQSHLHLENK-----
>Myotis_davidii
MSSTSWPLITLQQSHLHLENKWDICMNSRL-----
>Dasypus_novemcinctus
MSPTSWPLIQHQSHLHWPEKWKGLHEFQTP-----
>Galeopterus_variegatus
MSPTSQPIKLQQSQLHWLKNKWDRTNSQLN-----
>Condylura_cristata
MSSTSWPLIELLQSHLHLENK-----
>Ceratotherium_simum_simum
MSSTSWPLIHLQQSHLHLENKWFHEFQILN-----
>Manis_javanica
MSSTSWPLTQLQ-FHLHCLENKWDLREFQTLN-----
>Marmota_marmota_marmota
MSPTSWPLTQLQQSQLHWLENKWDLHKFQTELKFRLQC
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>Homo_sapiens

MGAAVPASEVTA

>Canis_lupus_familiaris

MGAAVPASEVTA

>Orcinus_orca

MGAAVPASEVTA

>Myotis_brandtii

MGAAVPASEVTA

>Dasypus_novemcinctus

MGAAVPASEVTA

>Galeopterus_variegatus

MGAAVPASEVTA

>Equus_przewalskii

MGAAVPASEVTA

>Loxodonta_africana

MGAAVPASEVTA

>Rattus_norvegicus

MGAAVPASEVTA

>Tupaia_chinensis

MGAAVPASEVTA

```
>Homo_sapiens
-----MLFRCEIFFLFLLFGS
>Canis_lupus_familiaris
-----MLFRCEIFFLFLLFGS
>Balaenoptera_acutorostrata_s
-----MLFRCEIFFLFLLFGS
>Miniopterus_natalensis
-----MLFRCEIFFLFLLFGS
>Galeopterus_variegatus
-----MLFRCEIFFLFLLFGS
>Oryctolagus_cuniculus
-----MLFRCEIFFLFLLFGS
>Elephantulus_edwardii
MCSCLGMLFRCEIFF-----
>Ceratotherium_simum_simum
-----MLFRCEIFFLFLLFGS
>Loxodonta_africana
-----MLFRCEILFL--LFGS
>Orycteropus_afer_afer
-----MFFRCEIFFLFLIFGS
```


>Homo_sapiens
MILDQMKPEEPSSSKIAG-
>Leptonychotes_weddeliii
MFLDQMKPEEPSSCKIIG-
>Physeter_catodon
MFLDQMKLEEPSSCKILG-
>Miniopterus_natalensis
MFLDQMKPEKPSSCKILG-
>Dasypus_novemcinctus
MFLDQMKPEEPSSSKILGE
>Galeopterus_variegatus
MFLGQMKPEEPSSSKIG--
>Ceratotherium_simum_simum
MFLDQMKPEEPSNCKILV-
>Manis_javanica
MFLDQLKPEEPSGHRILD-
>Loxodonta_africana
-----MTSEEPSSSKILGD
>Tupaia_chinensis
MFLDQMKTEEPSSSHTAG-

HG0642 ENSG00000100815 TRIP11

>Homo_sapiens

MAAGVELAGVTHGTEESH

>Ursus_maritimus

MAAGVELAGVALGTEESH

>Orcinus_orca

MAAGVELAGVANGTGESH

>Myotis_lucifugus

MAAGVELAGVAHRTGASH

>Condylura_cristata

MAAGVELAGVAHGAGESH

>Ceratotherium_simum_simum

MAAGVELAGVAHGTGESH

>Manis_javanica

MAAGVELAGIAHGIGESH

>Loxodonta_africana

MAAGVELAGVAHGTGESH

>Heterocephalus_glaber

MAASVELAGTAFGTEESH

>Trichechus_manatus_latirostr

MAAGVELAGVARGIGESH

>Homo_sapiens
-----MLFPTALMVPSDRLALL-----
>Acinonyx_jubatus
-----MVPSDRLAFL-----
>Physeter_catodon
-----MLPAA-----RWPGPQCPERALMVPSDRLAFL-----
>Myotis_davidii
-----MVPRDRLAFL-----
>Dasypus_novemcinctus
-----MVPSDRLAFL-----
>Condylura_cristata
-----MLPAA-----RWPGPQCPERALMVPSDRLAFL-----
>Oryctolagus_cuniculus
-----MVPGDRPALLTRGHQLS-----
>Equus_asinus
-----MVPSNRLAFL-----
>Manis_javanica
MMALPPSTSSGSLWHLFTLLWGRSGSSVGSHLTPLLHVPLLPVALMVP GDKWAFL-----
>Fukomys_damarensis
-----MVPSDRSAFL-----

>Homo_sapiens
-----MLSAGRWRRLHRKTLPGFEESDCY
>Mustela_putorius_furo
-----MLSAGRWR-----
>Balaenoptera_acutorostrata_s
-----MLSAGRWRRLNRKTLSGSEESDWY
>Pteropus_alecto
-----MLSASEWRSLNRKTVSGFEESIDWC
>Oryctolagus_cuniculus
-----MLSAGQRRSLNRKTHAGVEAS-----
>Equus_asinus
-----MLSAGRWRRLNRKTLSGYEGVE---
>Loxodonta_africana
-----MLCAGWWRRLNRKTYSGFEESDCC
>Cricetulus_griseus
-----MLR-----KVREKGLQLPRCSLWRRLNRKTLPCFEK-----
>Tupaia_chinensis
-----MLSAGQWRRLNRKTLPGVKESGGWY
>Trichechus_manatus_latirostr
MTEGGVRRGKGEKENITTPMMHPGMTTFPMFPGGAGREETACPLMLSAGWWRRLNRKTPFGFEGSSDCC

>Homo_sapiens
MVALEAAAAGAELYSQAWHQ RCH
>Canis_lupus_familiaris
MVALEVGAAGAERHSQAWPP RCH
>Rousettus_aegyptiacus
MVALEVGAAGAELYSQAWHQ RCH
>Dasypus_novemcinctus
MVALEVGAAGAELHSQAWH RCH
>Condylura_cristata
MVALEVGAAGAE LSSQAGHQ RCH
>Elephantulus_edwardii
MVALEVGPAGAELDSQARH RCH
>Ceratotherium_simum_simum
MVALEVGAAGAELYSQAWHQ RCH
>Manis_javanica
MVALEVGAARAELDSQARHQ RCR
>Loxodonta_africana
MVALEVGAAGTE LYSQAWHQ RCH
>Heterocephalus_glaber
MVALEVGAAGAELYSQVWH RCH

>Homo_sapiens
MEQWEREAGRFCKSPSGLTPSRRPRQGSEDPGEQMEEWSSL
>Balaenoptera_acutorostrata_s
---MGPGSRRFPRKSPSVPTSSRRTRQGSEEPGEQMEEWSSL
>Rousettus_aegyptiacus
-----MEEWSSL
>Condylura_cristata
-----MEEWSSL
>Ochotona_princeps
-----MEEWSSL
>Elephantulus_edwardii
-----MEWSSL
>Ceratotherium_simum_simum
-----MEEWSSL
>Dipodomys_ordii
---MGTGSGQVPSQIPLRLKPPRPHRQGSEEPGEQMEEWSSL
>Trichechus_manatus_latirostr
-----MEEWSSL
>Orycteropus_afer_afer
-----MEEWSSL

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>Homo_sapiens
MGVGGAGPEEMGRAGGAVVRAP
>Felis_catus
-----MGRAGGAVVGAP
>Balaenoptera_acutorostrata_s
-----MGRAGGAVVGDP
>Pteropus_alecto
-----MGRADGAVVGAP
>Oryctolagus_cuniculus
-----MGRAGGAVVGVL
>Equus_asinus
-----MGRAGGAVVGAP
>Manis_javanica
-----MGRAGGAVVGAL
>Dipodomys_ordii
MGVAGLELEAMGRAGGAVVGAP
>Tupaia_chinensis
MGVAGAEPEAMGRAGGAVVGAP
>Trichechus_manatus_latirostr
-----MGRAGGAVVGAS
```

HG0648 ENSG00000114331 ACAP2

>Homo_sapiens
MTSGRGALRSSAQR-
>Odobenus_rosmarus_divergens
MTSGRGALRSSAQR-
>Orcinus_orca
MTSGRGALRSSAQR-
>Rousettus_aegyptiacus
MTSGRGVLPSSAQL-
>Dasypus_novemcinctus
MTGGRGALRSSVQR-
>Condylura_cristata
MTSGRGALRSSAQR-
>Ochotona_princeps
MTSGRGALRSPAQRS
>Elephantulus_edwardii
MTSGLGALRSSAQH-
>Ceratotherium_simum_simum
MTSGRGALRSSARP-
>Ictidomys_tridecemlineatus
MTSGRGALRSSAQC-

HG0649.1 ENSG00000114439 BBX

>Homo_sapiens

MWRIHWDIEKYQRRIVPL

>Panthera_tigris

MWRIHWDIEKYQRRVLP

>Balaenoptera_acutorostrata_s

MWRSHWDIEKYQRRIVPL

>Rousettus_aegyptiacus

MWRIHWDIEKYQRRIVPL

>Dasypus_novemcinctus

MWRIHWDIEKYQRRIVPL

>Condylura_cristata

MWRSHWDIETYQRRFVPL

>Oryctolagus_cuniculus

MWRSHWDIEKYQRRIVPL

>Ceratotherium_simum_simum

MWRIHWDIEKYQRRIVPL

>Manis_javanica

MWRIHWDIEKYQRRIVPL

>Cavia_porcellus

MWRIHWDIEKYQRRIVPL

```
>Homo_sapiens
----MESLDLTGTLRKTPSL
>Canis_lupus_familiaris
----MESLDLTGTLRKTPSL
>Balaenoptera_acutorostrata_s
----MESLDLTGTLRKTPSL
>Myotis_brandtii
----MESLDLTGTLRKTPSL
>Dasypus_novemcinctus
MEITMESLDLTGTLRKTPAL
>Condylura_cristata
----MESLDLTGTLRKTPSL
>Equus_asinus
----MESLDLTGTLRKTPRL
>Manis_javanica
----MESLDLTGTLRKTPSL
>Microtus_ochrogaster
----MESLDLTGTLRKTPSL
>Tupaia_chinensis
----MESLDLTGTLGKTPSL
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HG0650 ENSG00000115226 FNDG4

>Homo_sapiens

MGRPLGTEQPPEA

>Canis_lupus_familiaris

MGRPLGTEQPPEA

>Orcinus_orca

MGRPLGTEQPPEA

>Miniopterus_natalensis

MGRPLGTEQPPEA

>Dasypus_novemcinctus

MGRPLGTEQPPEA

>Sorex_araneus

MGRPLGTEQPPEA

>Equus_asinus

MGRPLGTEQPPEA

>Peromyscus_maniculatus_baird

MGRPLGTEQPPEA

>Tupaia_chinensis

MGRPLGTEQPPEA

>Orycteropus_afer_afer

MGRPLGTEQPPEA

```
>Homo_sapiens
MIPFSGTVFSLGSCPAGPLSACVPDHGSLQYPLTIYQQDC---
>Felis_catus
MMPFSGTVFSLGSHLAC-LSTCVPDHAFLLQYPLTIHRQGC---
>Physeter_catodon
MTPFSGTVFSLISCLL---PVCLCP-----
>Miniopterus_natalensis
MMPFSGTVFSLGSCFACSVSACVPGHAFLLQYPLTIYQQDC---
>Oryctolagus_cuniculus
MMDFSGTVCSPGSGPSCSLSAGGPDHAFHGAP-----
>Ceratotherium_simum_simum
MMPFSETVFSLGSLACSLSACVPDHAFLLQYPLTIYQQDC----
>Manis_javanica
MMPFSGTVVTLGSLAYSLSACVPDHALLHYPLKTHQQDC---
>Loxodonta_africana
MIPFSGMVFLGSLTCSLSACVPDHACPAVSFHDFAAGLLKV
>Cavia_porcellus
-----MIFSLGSALACALSACIPDHASLQFLTIYQQDC---
>Orycteropus afer afer
MMPFSGTIFSLGSLVCSLSACVPDHACPAVSFNDLSARLLKV
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>Homo_sapiens
MMEGEKPLSVATESGERLLQ-----
>Odobenus_rosmarus_divergens
-MGSAKPLPVATESGERLLQ-----
>Balaenoptera_acutorostrata_s
MMEREEPLPVTESGERLLQ-----
>Myotis_lucifugus
MMEREKPLPVAIESGERLLQSPLP----
>Galeopterus_variegatus
MMEREKPLPVATESGERLLQ-----
>Erinaceus_europaeus
-MEREKPLPVATESGERLLQ-----
>Oryctolagus_cuniculus
-MERERSLPVATERGERLRQSQUALQNV-
>Loxodonta_africana
MMERESPPPVATEGGESLLQ-----
>Mus_musculus
MMEREKPLPVAESGASYCSRCSRMSE
>Orycteropus_afer_afer
-MARENPPPVATESGEGLLQWLVLQNV-

HG0653 ENSG00000120334 CENPL

>Homo_sapiens
MIRESGMGDSVITAFY
>Ursus_maritimus
-----MGDSVITAFY
>Lipotes_vexillifer
-----MVDSVITAFY
>Pteropus_alecto
MIREAGLGDSVITAFH
>Dasypus_novemcinctus
MIREAGMGDSVISAFC
>Oryctolagus_cuniculus
MIAESGMGDSVDTAFY
>Ceratotherium_simum_simum
-----MGDSVITAFY
>Manis_javanica
MIGAAGMGDSVITAFY
>Loxodonta_africana
MICEAGMRDSVVAAFY
>Fukomys_damarensis
-----MGDRVTTAFY

HG0654 ENSG00000133794 ARNTL

>Homo_sapiens

-----MWNPGPSLVFGRS

>Acinonyx_jubatus

-----MWNPRPSLVSGRS

>Galeopterus_variegatus

MLLDPSFTFQMWNPRPLLVFGRS

>Elephantulus_edwardii

-----MWNPGPLLVFRRS

>Manis_javanica

-----MWNPRPSLVSEERS

>Loxodonta_africana

MVLDSSLTFQMWNPRPLLVFERS

>Ictidomys_tridecemlineatus

MLLDPTSTTFQMWNPRPSLVFGRS

>Tupaia_chinensis

MLLDPRLTFQMWNPRPSLVVGRS

>Trichechus_manatus_latirostr

MLLDPSLTFQMWNPRPLLIFGRS

>Orycteropus_afer_afer

-----MWNPRPFLVFGRS

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>Homo_sapiens
-----MWQEPGATSELLWTLPLV-----
>Canis_lupus_familiaris
-----MWQKPRGPSELFWTLPLA-----
>Physeter_catodon
-----MWQEPPAPSELFWTLPLA-----
>Rhinolophus_ferrumequinum
-----MWQKPRLSAELFWTLPLLRGL-----
>Condylura_cristata
MREITDTFTAKPRTFLYNQWMKGFSQTAFSLFLED-YPPRSTIPVETARHTMWQKPRAPSELIWTLPLA---
>Ochotona_princeps
-----MWQEPGAPSE-FWTLPLA-----
>Ceratotherium_simum_simum
MREITDTFTGKPRTFLYNQWMKGFSQTLFSPFSLRIKPLQSSIPVQTARHTMWQKPRAPSELFWTLPLA---
>Loxodonta_africana
-----MWQKPGAPSELVWTL LLP-----
>Peromyscus_maniculatus_baird
-----MWQKPRAPSELLWTLPLA-----
>Trichechus_manatus_latirostr
-----MWQKPGAPSELVWTLHLPL-----
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HG0656 ENSG00000150776 C11orf57

>Homo_sapiens

MGIFPLSSTWKPQPPLQAP

>Panthera_tigris

MGVFSLTSLWKLHPPLRAL

>Lipotes_vexillifer

MGVFSLSSTWKPQPPLQPL

>Rousettus_aegyptiacus

MGVFSLSSFWKPRSPQLAL

>Dasypus_novemcinctus

MGVFSLSSAWRPQPPL---

>Galeopterus_variegatus

MGVFSLSSTWKPQHPLQAP

>Oryctolagus_cuniculus

MGVFSLSSTWKPQRPRQAP

>Equus_caballus

MGVFFLSSTWKPQLPLQAR

>Marmota_marmota_marmota

MGVFSLFSTWKPQPPFQAP

>Tupaia_chinensis

MGVFPLFSTWKLQTSLQAP

HG0657 ENSG00000151276 MAG11

>Homo_sapiens
MQTKLAGACAGLAGKPRKFVL
>Ursus_maritimus
MQTKLAGACAGLAGKPRKFVL
>Balaenoptera_acutorostrata_s
MQTKLAGACAGLAGKPRKFVL
>Pteropus_vampyrus
MQTKLAGACAGLAGKPRKFVL
>Condylura_cristata
MQTKLAGAFAELAGKPRKFVL
>Ochotona_princeps
MQTKLAGARAGLAGKPGKFVG
>Equus_asinus
MQTKLAGACAGLAGKPRKFVL
>Manis_javanica
MQTKLAGACARLAGKPRKFVL
>Ictidomys_tridecemlineatus
MQTKLAGACAGLAEEPRKFVL
>Tupaia_chinensis
MQTKLAGACAGLAGKPRKVVL

>Homo_sapiens
-----MHLKILKKRHKMFK
>Canis_lupus_familiaris
-----MHLKILKKRRKMFK
>Balaenoptera_acutorostrata_s
-----MHLKILKKRHKMFK
>Rhinolophus_ferrumequinum
-----MHLKILKKRRKMFK
>Condylura_cristata
-----MHLKILKKRHKMFQ
>Equus_asinus
-----MHLRVLKKRRKTFK
>Manis_javanica
MMRPCLSRSSRRRRRRPGGAAEPGDPARASDPVTQDSMHKILKKRRKMSK
>Loxodonta_africana
-----MHLKTLKKRRKMFK
>Dipodomys_ordii
-----MHLKILKKRHKMFA
>Tupaia_chinensis
-----MHLKILKKRHKAFR

>Homo_sapiens
----MEVYVTEEAALLPHALGP
>Odobenus_rosmarus_divergens
MRRGMEVYVTEEAALLPHAPGP
>Balaenoptera_acutorostrata_s
----MEVYVTEEA--EPHAPGP
>Rousettus_aegyptiacus
MRRGMEVYVTEEAALLPHAPGP
>Erinaceus_europaeus
----MEVYLTEEAALLPHAPGP
>Equus_asinus
MRRGMEVYVTEEAALLPHAPGP
>Manis_javanica
MRRGMEVYVTEEAALLPHAPGP
>Fukomys_darlingi
MRLEMEVYVTEEAALLPHAPGP
>Trichechus_manatus_latirostr
MRRGMEVYVTEEAALLPHSPGP
>Orycteropus_afer_afer
MRRGMEVYVTEEAELLPHAPGP

HG0659.2 ENSG00000158856 DMTN

>Homo_sapiens

MRTRQPGGTRQLLSRPQARSAQQPRRA

>Mustela_putorius_furo

M RTPQPGGTHSLLSWPGARSAQEPGRA

>Balaenoptera_acutorostrata_s

M RTPQPGGAPFLLSRPRARSAQEPDRA

>Pteropus_alecto

MRTLQPSGTPFLHSRPRARSAQKPGRA

>Condylura_cristata

MRTLQRSGPPSLLSRPRARSAPEPGRA

>Equus_asinus

M RTPPRPGGTPFLLSRPRARSAQEPRSA

>Manis_javanica

MRPPQPAGTPFLLSPHRVRSQEPGRA

>Trichechus_manatus_latirostr

MRTLQLGGTPFLLSRPRTRSAQERSRA

HG0660 ENSG00000165861 ZFYVE1

>Homo_sapiens

-----MEDETIKPNQRCC

>Canis_lupus_familiaris

-----MEDKTIKPNQRCC

>Lipotes_vexillifer

-----MEDETIKPSQRCC

>Rhinolophus_ferrumequinum

-----MEDETIKPNQRCC

>Dasypus_novemcinctus

-----MEDETIKPNQYCC

>Ceratotherium_simum_simum

-----MENKTIKPNQRCC

>Loxodonta_africana

-----MEDETIKPSQCCC

>Fukomys_darlingi

MSLHFTEDIKPNQHCC

>Tupaia_chinensis

-----MEDETIKPNQHCC

>Trichechus_manatus_latirostr

-----MEDETVRPNQSCC

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>Homo_sapiens
-MDFLLEIRTEACTEEMFLREMNRNNPL
>Acinonyx_jubatus
MMDFLLEIGTEVFTEEM-FLREMNRNNPF
>Physeter_catodon
MMDFLLEIHLEVVT EEMFLREMSRNNPF
>Rousettus_aegyptiacus
MMYFFWR--IRTVTEEMFLREMNRNKPF
>Galeopterus_variegatus
MMNFLLEIRTQAFTEEMFLREMNRNNPF
>Oryctolagus_cuniculus
-MGLLLGSRTGARM EEMFLRGMNRNNPF
>Equus_asinus
MMDFSLKIRAEAFREKRLFLREMNRNLF
>Manis_javanica
MMDFLLE--TEVFTEEMFLREINRNNPF
>Loxodonta_africana
-----MNRNNPF
>Tupaia_chinensis
MMDLLSEIRSEAFVEEMFLREMNRNSF
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HG0662 ENSG00000166897 ELFN2

>Homo_sapiens

MVAAPGRTVLPAPASGR

>Canis_lupus_familiaris

MVAAPGRTVPPAPASRC

>Orcinus_orca

MVAAPGRTVLPAPASGR

>Miniopterus_natalensis

MVAATGRTVLPASSC

>Galeopterus_variegatus

MVATPGRTVLPAPASGC

>Erinaceus_europaeus

MVATPGRTVLPAAASGL

>Oryctolagus_cuniculus

MVAAPGRTVLPAPTSGR

>Manis_javanica

MVAAPGRTVLPAPASGH

>Ictidomys_tridecemlineatus

MVAAPGRTVPPAPASGR

>Tupaia_chinensis

MVAAPGRTVLPASGR


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>Homo_sapiens
MSGASSDRGLSCVSAARVLVGRACSSGARASRPDLGPRQGWKMEEAEVEATEC
>Odobenus_rosmarus_divergens
MSGASSDRGRV-----ASVPSACSSRARASRPALGPRQGWEMMEQPEAEATEC
>Orcinus_orca
-----MVERAEAGATEC
>Rousettus_aegyptiacus
-----MMEPADAEAEIEC
>Dasypus_novemcinctus
-----MEEAEAGATEC
>Condylura_cristata
-----MMEQAEAEVSEC
>Oryctolagus_cuniculus
MSGASLDRGPCVSAARVLVPGRARP-----GQPWGPREGWKMMGEAE--ATEC
>Equus_asinus
MSGASSDWSRV-----ASVPSACSPAGARTRPALGPRQGWEMMEPAEAQATDC
>Manis_javanica
MSGASS-DSRV-----ASVPSACSPRARASLPALGPRQGWEMERAEAEATVS
>Chinchilla_lanigera
-----MGCVSAARMPASGR-----AHPGPHGARQGSEMMDKAETAR---
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HG0664 ENSG00000169085

>Homo_sapiens

-----MIPEPDWIRMPRD

>Felis_catus

-----MIPEPDWIRKPRD

>Balaenoptera_acutorostrata_s

-----MIPEPDWIRKPRD

>Myotis_davidii

MLQRRRLKDELTAACLLWTCTMIPEPDWIRKPCN

>Galeopterus_variegatus

-----MIPEPDWIRKPHD

>Oryctolagus_cuniculus

-----MIPEPDWISDARD

>Equus_caballus

-----MIPEPEWIRKPRD

>Manis_javanica

-----MIPEPDWIRKPRD

>Chinchilla_lanigera

-----MIAEPDWIRRPRD

>Tupaia_chinensis

-----MSSQPPACLLWTCTMIPEPDWIRKARD

HG0665 ENSG00000169515 CCDC8

>Homo_sapiens

MSAKMWIWTSSWKP

>Ailuropoda_melanoleuca

MSAKMWIWTSSWKP

>Balaenoptera_acutorostrata_s

----MWIWTSSWKP

>Rhinolophus_ferrumequinum

----MWIWTSSWKP

>Galeopterus_variegatus

MSAKMWIWTSSWKP

>Equus_caballus

MSAKMWIWTSSWRP

>Manis_javanica

MSAKMWIWTSSWKP

>Loxodonta_africana

----MWTWMSSWKP

>Marmota_monax

MSAKMWIWTSSWKP

>Tupaia_chinensis

----MWIWTSSWKP

HG0666 ENSG00000171943 SRGAP2C

>Homo_sapiens

MSDPRPASGRCSSPG

>Ailuropoda_melanoleuca

MSDPRPASGRCSSPG

>Physeter_catodon

MSDPRPASGRCSSPG

>Rousettus_aegyptiacus

MSDPRPASGRCSSPG

>Condylura_cristata

MSDPRPASGRCSSPG

>Oryctolagus_cuniculus

MSDPRPASGRCSSPG

>Ceratotherium_simum_simum

MSDPRPASGRCSSPG

>Manis_javanica

MSDPRPASGRCSSPG

>Loxodonta_africana

MSDPRPASGRCSSPG

>Cricetulus_griseus

MSDPRPASGRCSSPG

>Homo_sapiens
MCQYTVRISLICTVWGPHRLMLNFAN
>Acinonyx_jubatus
MCQLYSRISLICTVWGPH-----
>Physeter_catodon
MCQLYSRISLICTVWGPH-----
>Myotis_brandtii
MCQLHSRISLICTVWGPH-----
>Galeopterus_variegatus
-----MLNFAN
>Condylura_cristata
MCQLYSRISLICTVWGPH-----
>Ceratotherium_simum_simum
MCQLYSRISLICTVWGPH-----
>Manis_javanica
MCQLYSRISLICTVWGPH-----
>Rattus_sp.
-----MLNFAN
>Tupaia_chinensis
-----MLNFAN

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>Homo_sapiens
-----MLRKSVGFSVREGRSS-ALIWVTEANMSKTLVN

>Ailuropoda_melanoleuca
MGPFSSISWGICTGQRLPAMRYELKPISLFSYMLRKSVGFSVREGRSSAALIWVTEAGWGKTLVN

>Lipotes_vexillifer
-----MLRKSVGFLAVREGRSSAALIWVTEASLSKSLVN

>Rousettus_aegyptiacus
-----MLRKSVGFSVREGRSSAALIWVTEAGLSKTLVN

>Galeopterus_variegatus
-----MLRKSVGFSVREGRSS-ALIWVTEAGLSKTSVN

>Sorex_araneus
-----MCTGRRLPAMRCELKPISLFSYMLRKSVGFSVREGRSSAALIWVTEAGLSKTLVN

>Ceratotherium_simum_simum
-----MLRKSVGFSVREGRSSAALIWVTEAGLSKTLVN

>Manis_javanica
-----MLRKSVGFSVREGRSSAALIWVTEAGLSKTLVN

>Chinchilla_lanigera
-----MMRKSVGFSVREGRSSAALIWVTEAGLSKTLVN
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HG0668 ENSG00000182944 EWSR1

>Homo_sapiens
MVAPGVARFAPAQCGA
>Tursiops_truncatus
MVAPEVAGFAPAQCGA
>Eptesicus_fuscus
MVAPEVAGFAPAQCGA
>Condylura_cristata
MVAPEVADFAPAQCGA
>Ochotona_princeps
MVAPEVASFAPAQCGA
>Ceratotherium_simum_simum
MVAPEVAGFAPAQCGA
>Loxodonta_africana
MVAPEVAGLAPAQCGA
>Marmota_marmota_marmota
MVAPEVASFAPAQCGA
>Trichechus_manatus_latirostr
MVAPEVAGFAPAHCGA
>Orycteropus_afer_afer
MVTPEVAGFAPAQCGA

HG0669 ENSG00000183876 ARSI

>Homo_sapiens
MVESTFWKLPRRVSGWPG
>Mustela_putorius_furo
MVESTFWKQPRRVSGWPG
>Myotis_lucifugus
MVESTFWKSPRRVPGWPG
>Dasypus_novemcinctus
MVESTFWKPPSRVSGWPG
>Condylura_cristata
MVQSTFGELPRRVSGWPG
>Oryctolagus_cuniculus
MVESAFWEPPRRVSGWPG
>Ceratotherium_simum_simum
MVESTFWKPPRRVSGWPG
>Loxodonta_africana
MVESTFWKPPSRVSGWPG
>Cavia_porcellus
MVESTFWRPPRYVPGWPG
>Tupaia_chinensis
MVESTFCKSPRRVSGWPD

>Homo_sapiens	
APGGGGAGADPTSG	MISLARS
>Leptonychotes_weddellii	
APGGGGAGADPTSG	MISLARS
>Lipotes_vexillifer	
APGGGGAGANPTSG	MISPARS
>Eptesicus_fuscus	
APGGGGAGTNPTSG	MISPVRS
>Dasypus_novemcinctus	
APGGGGAGANPTSG	MISLARF
>Oryctolagus_cuniculus	
APGGGGAGANPTSG	MISPARS
>Equus_caballus	
MRVLMsRGWRRRKSGSKSEPETRQTGLHALLPAHPAAPASVHKAEAQRPQAKARAAPVPPQVSPSTPSPVPGLLVRPRPPPRGLPAGEAPRPLSRCVRMISLVR	
APGGGGAGANPTSG	
>Loxodonta_africana	
APGGGGAGANPTSG	MISLARS
>Marmota_marmota_marmota	
APGGGGAGADPTSG	MISLARS
>Tupaia_chinensis	
APGGGGAGADPTSG	MISLARS

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>Homo_sapiens
-----MPKVSGSRDTVCIKQKFASC
>Odobenus_rosmarus_divergens
MQGSDSTPIISGSRDTVCIKQKFASC
>Orcinus_orca
MQGLDSMPIISGSRDTVCIKQKFASC
>Pteropus_vampyrus
MRGLHGVPMLSGSRHTVCIKQKFASR
>Dasypus_novemcinctus
MQGLDSLPIVISASRDTVCMKQKFANC
>Galeopterus_variegatus
MQGLDSMPTISGSRNTVCIKQKFASG
>Ceratotherium_simum_simum
MQGLDSMPVISGSRDTVCIKQKFASC
>Manis_javanica
MQGSDSMPIVSGSRDTVCIKQKFASC
>Cavia_porcellus
MQGI-GLHADSGNRDTVCMKQKFASC
>Trichechus_manatus_latirostr
MQGLDSMPIISGNRDTVCIKQKFASC
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HG0672 ENSG00000196369 SRGAP2B

>Homo_sapiens

MSDPRPASGRCSPPG

>Ailuropoda_melanoieua

MSDPRPASGRCSPPG

>Physeter_catodon

MSDPRPASGRCSPPG

>Rousettus_aegyptiacus

MSDPRPASGRCSPPG

>Condylura_cristata

MSDPRPASGRCSPPG

>Oryctolagus_cuniculus

MSDPRPASGRCSPPG

>Ceratotherium_simum_simum

MSDPRPASGRCSPPG

>Manis_javanica

MSDPRPASGRCSPPG

>Loxodonta_africana

MSDPRPASGRCSPPG

>Cricetulus_griseus

MSDPRPASGRCSPPG

HG0673 ENSG00000266028 SRGAP2

>Homo_sapiens
MSDPRPASGRCSSPG
>Odobenus_rosmarus_divergens
MSDPRPASGRCSSPG
>Physeter_catodon
MSDPRPASGRCSSPG
>Rousettus_aegyptiacus
MSDPRPASGRCSSPG
>Condylura_cristata
MSDPRPASGRCSSPG
>Oryctolagus_cuniculus
MSDPRPASGRCSSPG
>Ceratotherium_simum_simum
MSDPRPASGRCSSPG
>Manis_javanica
MSDPRPASGRCSSPG
>Loxodonta_africana
MSDPRPASGRCSSPG
>Cricetulus_griseus
MSDPRPASGRCSSPG

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>Homo_sapiens
-----MFFSLAQPKMTNV
>Ailuropoda_melanoleuca
-----MFFSLAQPKMTNV
>Lipotes_vexillifer
MLFSLLEGGSQVLCMFFSLAQPKMTNV
>Myotis_davidii
-----MFFSLEQLKMTNV
>Erinaceus_europaeus
MLICLLLERGSKVVCVFFSLAQPKMTNV
>Ochotona_princeps
-----MFFSLTQPKMTTV
>Elephantulus_edwardii
-----MLFSLAQPKMTNV
>Equus_asinus
-----MFFSLAQPKMTNV
>Orycteropus_afer_afer
-----MFFFLAQPKMTNV
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HG0674.2 ENSG00000116793 PHTF1

>Homo_sapiens

MRPAWPAASPPASRWDPGH

>Lipotes_vexillifer

MRPAWPGASPPASWPGRGH

>Nannospalax_galili

MRPTRPAASPPASRPGPSH

>Tupaia_chinensis

MRPAGPVASPRASRTGRGH

```
>Homo_sapiens
-----MQSISLQVLWKEHLLNSV-----
>Canis_lupus_familiaris
-----MQSISLQILWKVHLHSLCMMK RTPVQ
>Orcinus_orca
-----MQSISLQILWKVHLHSLCMMKQIPIR
>Myotis_brandtii
MPNQPAVCVVSSGGAMQSISLQILWKVHFHLLCVRKQIPIQ
>Galeopterus_variegatus
-----MQSISLQILWKVHLH-----
>Oryctolagus_cuniculus
-----MQNISLQILWKVHLH-----
>Ceratotherium_simum_simum
-----MQSISLQILWKVHLHSLCMMKQIPIQ
>Fukomys_damarensis
-----MELSRRAMQSISLQILWKVHLH-----
>Orycteropus_afer_afer
-----MQSISLQILWKVHLH-----
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HG0676 ENSG00000058673 ZC3H11A

>Homo_sapiens

MAIMLLCLLQLAAPLCSYSITIRFYLFWLNTP

>Felis_catus

MAIMLLCLLQLAAPLCSYSITIRFYLFWLNTP

>Eptesicus_fuscus

MAVMLLCLLQLAAPLCSYSITIRFYLFWLNTP

>Oryctolagus_cuniculus

MALPPLCLPQLAALLCSYSVTLRFYLFWLNTP

>Equus_caballus

MAIMLLCLLQLAAPLCSYSVTIRFYLFWLNTP

>Loxodonta_africana

MAITLLCLLQLAAPLRSYSITVRFYLFWLNTP

>Cricetulus_griseus

MAIMLLCLLQLAAPLCSYSVTIRFYLFWLNTP

>Trichechus_manatus_latirostr

MAIMLLCLLQLAAPLCSYSVTVRFYLFWLNTP

>Orycteropus_afer_afer

MAIMLLCLLQLAAPLYSYSITIRFYLFWLNTP

HG0677 ENSG00000064989 CALCRL

>Homo_sapiens
-MIHQPLVLPSVKTLDGPTFRS
>Ailuropoda_melanoleuca
-MIHQPLVLPPVKTLDGPTFRS
>Balaenoptera_acutorostrata_s
MMIHQPLVLPPVKTMDGPTFRS
>Rousettus_aegyptiacus
-MIHQPLVLPPVKTLDGPTFRS
>Dasypus_novemcinctus
-MTHQPLVLPPVKTLDVPTFRS
>Galeopterus_variegatus
MMIYQPLVLSPVKTLDGPTFRS
>Ochotona_princeps
-MIHPPLILPPKTVDDPTFRS
>Equus_asinus
-MMHQPLVLPPVKTLDGPTFRS
>Nannospalax_galili
-MIHQPLVLPAVKTS DGPTFRS

>Homo_sapiens
-----MGLARSAASPRSSKYTEQGPR--
>Canis_lupus_familiaris
MRAGQQWEVCEARTGSHWTFGRNRWGAGTRRRGCGATRPLQKHKL MGLALLVASSRSSKYGKRGPGR--
>Orcinus_orca
-----MGLARSAVSPRSSKYTERAPR--
>Eptesicus_fuscus
-----MGLARSAASPLSFKSTERGPGR--
>Galeopterus_variegatus
-----MGLARSAASLR-SKCIERGPPK
>Condylura_cristata
-----MGLACSAASPLSSKYTEWGPC--
>Ochotona_princeps
-----MGLARSPASPRSSKYRERGPALK
>Ictidomys_tridecemlineatus
-----MGLARSAASPRSFKYTERGPGR--
>Tupaia_chinensis
-----MGLAHSAAASPRSSKYTERGPC--

HG0678.2 ENSG00000108947 EFNB3

>Homo_sapiens

MPPPPGPRLPQSPT

>Mustela_putorius_furo

MPPPPGPRLPQSPT

>Physeter_catodon

MPPPPGPRLPQSPT

>Myotis_davidii

MPPPPGAWLPQSPT

>Oryctolagus_cuniculus

MPPPPGPRLPQSPT

>Mesocricetus_auratus

MLPPPGPRLPMSPT

HG0679 ENSG00000100281 HMGXB4

>Homo_sapiens
MAAIGGVEAGSGRAE
>Odobenus_rosmarus_divergens
MAAVGGAEAGSGRAE
>Rousettus_aegyptiacus
MAVVGAEAGSGRAK
>Dasypus_novemcinctus
MAAVGGAEAGSRRAE
>Condylura_cristata
MAAVGGAEAGSGPAE
>Ochotona_princeps
MAAVGGAEAGSGRA-
>Ceratotherium_simum_simum
MAAVGGAEAGSGRAE
>Manis_javanica
MAAVGGAEAGSGRAE
>Ictidomys_tridecemlineatus
MAAVGGAEAGSGRAE

HG0680 ENSG00000100678 SLC8A3

>Homo_sapiens

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>Odobenus_rosmarus_divergens

MPRTRLRPAGSPRGR

>Eptesicus_fuscus

MPRTRLRPAGSPRGR

>Erinaceus_europaeus

MPGTRLRPGGCPRGR

>Oryctolagus_cuniculus

MPRTRLRPAGSPRGR

>Equus_przewalskii

MPRTRLRPAGSPRGR

>Marmota_marmota_marmota

MPRTRLRPAGSPRGR

>Trichechus_manatus_latirostr

MPRTRLRPAGSPRGR

>Orycteropus_afer_afer

MPRTRLRPAGSPRGR

>Homo_sapiens
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>Mustela_putorius_furo
-----MLPPLAKMNTTEK-----
>Balaenoptera_acutorostrata_s
-----MRHRCADSQRPEIHCGEMLPPLAKMNTTEK-----
>Cynopterus_sphinx
-----MRRRRQPPEVHCGKMLPPLAKMNTTEK-----
>Dasypus_novemcinctus
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>Erinaceus_europaeus
-----MRCRRVADNHPPVIHSGKMLPPLAKMNTTEK-----
>Manis_javanica
-----MLPPLAKMNTTEK-----
>Ictidomys_tridecemlineatus
-----MSHCRFADSQPPEIHCGEMLLPLAKMNTTEK-----
>Orycteropus_afer_afer
-----MFPPLAKMNTTEENEGN-----

HG0682 ENSG00000105829 BET1

>Homo_sapiens

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>Ailuropoda_melanoleuca

MSWRFGRSWCFSGPWY

>Lipotes_vexillifer

MSWRFGRSWCFAGPRY

>Myotis_davidii

MSWRYRGRSW-----

>Dasypus_novemcinctus

MPWHFRGRSWSSGGPWD

>Oryctolagus_cuniculus

MSWRLG-----

>Ceratotherium_simum_simum

MSWRFGRSWCFAGPWS

>Ictidomys_tridecemlineatus

MSWRFGARSWCCSGPWD

>Tupaia_chinensis

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>Homo_sapiens
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>Canis_lupus_familiaris
-----MEALFPCQIPYWYIS
>Myotis_brandtii
MKHTRRRSLTPEQKRVFIRMDALFPCHIPYCCSS
>Erinaceus_europaeus
-----MEALFSCHTPYCSIS
>Oryctolagus_cuniculus
-----MESLFPCQIPYYCTA
>Equus_caballus
MKHTRRPSFTRQRRRVFIRMEALFPCQIAYCCIS
>Loxodonta_africana
-----MEALFPCQIHYYIS-
>Tupaia_chinensis
-----MEALFPCQIPYCCIS
>Orycteropus_afer_afer
-----MEALFP-----
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>Homo_sapiens
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>Felis_catus
MRGLCHSPHCPLP-----
>Pteropus_vampyrus
MRGLCHSPHCPLP-----
>Erinaceus_europaeus
MRGLCHSPHCPLP-----
>Oryctolagus_cuniculus
MRGLCHSPHCPLP-----
>Ceratotherium_simum_simum
MRGLCHSPHCPLP-----
>Manis_javanica
MRGLCHSPHCPCLDGVTGKKRRIQCWLPRCTKRFI-----
>Ictidomys_tridecemlineatus
MRGLCHSPHCPLPWRSNRKKKKKAYTM-LATENLFECNEIKGRRSHTIRPPPLRLRGLRRMSGASVSPGAGRSLEDSF
>Tupaia_chinensis
MRGLCHSPHCPLP-----

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>Homo_sapiens
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>Odobenus_rosmarus_divergens
MASGWRAAVPAVAPGRSPPL-----
>Physeter_catodon
MASGWRAEVPVARGRQLPV-----
>Pteropus_vampyrus
MASGWRAAPVAVLGQRPPV-----
>Galeopterus_variegatus
MASDWSAALRAAAPGRRPPA-----
>Erinaceus_europaeus
MASGSGARLSAAAPGRRPQV-----
>Equus_asinus
MASGWRSAVPVAVAPGRRLPV-----
>Marmota_monax
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>Tupaia_chinensis
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>Homo_sapiens
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>Leptonychotes_weddellii
-----MTVRQQRDGRSCGGGCRSPSSRGRSGG

>Balaenoptera_acutorostrata_s
-----MTVRQQRDGRSCGGGCRSPSSRGRSGG

>Miniopterus_natalensis
-----MTVRQQRDGRSCGGGCRSPSSRGHRGD

>Condylura_cristata
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>Oryctolagus_cuniculus
-----MTVRQQRDGRSCGGGCRSPSSRGRSGG

>Ceratotherium_simum_simum
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>Manis_javanica
-----MTVRQQRDGRSCGGGCRSPSSRGRSGA

>Octodon_degus
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>Homo_sapiens	-----MQFSRARETLHRSGK
>Acinonyx_jubatus	-----MQFSPARETLHRSGE
>Balaenoptera_acutorostrata_s	-----MQFSPARETLYRSGE
>Myotis_brandtii	-----MHFSPARETLHGSGE
>Condylura_cristata	-----MQFSWARATLHRSGE
>Ceratotherium_simum_simum	-----MRFSRASETLHRSGE
>Manis_javanica	-----MQSSRASATLHRSGA
>Mus_musculus	
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>Tupaia_chinensis	-----MQFSRAKETLHRSGE

>Homo_sapiens
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>Chinchilla_lanigera
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>Trichechus_manatus_latiostr
MVFIGCEHSSWERFRISLSFLIFSSLRRKLSKTSKCGTEDLDEASKQRNRKIGSLSQCSFSRR

>Homo_sapiens

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>Ailuropoda_melanoieuca

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>Myotis_lucifugus

-----MPKMPGLQACTLLRGR

>Dasypus_novemcinctus

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>Oryctolagus_cuniculus

-----MLQMSGLOACTVLRGR

>Equus_caballus

-----MSGLOACTVLRGR

>Manis_javanica

MALGAARFSAPPGAPSAAGDAKMSGLOQTCTVLRER

>Loxodonta_africana

MAHRGARSSALFRASPAAGDTKMSGLOACTDLRGR

>Trichechus_manatus_latirostr

-----MSGLOACTDLRGR

>Homo_sapiens
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>Leptonychotes_weddellii
-----MNVCNDIS-----
>Balaenoptera_acutorostrata_s
-----MNVCNDIS-----
>Pteropus_alecto
-----MNVCNDIS-----
>Oryctolagus_cuniculus
-----MNVCN AIS-----
>Ceratotherium_simum_simum
-----MNVCNDIS-----
>Fukomys_darlingi
-----MTVCNDSS-----
>Tupaia_chinensis
-----MNVCHDTS-----
>Trichechus_manatus_latirostr
-----MNVCN DIPDKKL IYKKERK

HG0690 ENSG00000125931 CITED1

>Homo_sapiens

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>Leptonychotes_weddellii

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>Orcinus_orca

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>Rhinolophus_ferrumequinum

MFPAQLQKGHR

>Galeopterus_variegatus

MFPAQLQKGHR

>Oryctolagus_cuniculus

MLPAQLQKGHR

>Equus_caballus

MFPAQLQKGHR

>Manis_javanica

MLPAELQKGHR

>Ictidomys_tridecemlineatus

MFPAQLQKGHR

HG0691 ENSG00000129535 NRL

>Homo_sapiens

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>Myotis_davidii

-----MVPPVSGEAVLAWLGH

>Galeopterus_variegatus

-----MGPLVSGEAVPVWL--

>Oryctolagus_cuniculus

-----MEPPVSGKTVAAWL--

>Elephantulus_edwardii

-----MGPPVLEEAVPVWF--

>Ceratotherium_simum_simum

-----MGPPVSGEAVPTWL--

>Loxodonta_africana

-----MGPPVSGEAVPAWLGH

>Ictidomys_tridecemlineatus

-----MGPPISGEAVPVWL--

>Trichechus_manatus_latirostr

-----MGPPVSGEAVPAWL--

>Homo_sapiens
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>Ailuropoda_melanoleuca
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>Pteropus_alecto
MALRAAWACGGAVRWSPALPGDTATCQETGLGSEVGCFWF
>Dasypus_novemcinctus
MALRSLAGGGAVGRGSVFPGDVNTGWLGAH----GLMWF
>Galeopterus_variegatus
MALRGNLSSGGVVQWSLMLPGDT-----GPSFEVGNFWF
>Equus_asinus
MAPRGAWACGVAVRWSPALHGDTAACREAGPGSECGSFWF
>Manis_javanica
MALRSVLACGGAVRWSPALPRDTTTCWPTGPGSEVGSVWF
>Ictidomys_tridecemlineatus
MALRGAPAGGGVFLGSPAFLRDT-----GPSFAVGSEFWF
>Tupaia_chinensis
MALWGGPAGGGAGQWGPALPGDT-----GPSFETGSFWF

HG0692.2 ENSG00000130338 TULP4

>Homo_sapiens

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>Felis_catus

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>Dasypus_novemcinctus

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>Galeopterus_variegatus

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>Homo_sapiens
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>Phoca_largha
MKREGGAAAPGRPRAGHAAQGP-----
>Physeter_catodon
MKREGGAAVPERPRAGDAARGP-----
>Pteropus_alecto
MKLEGGAAAPGRPRAGDAARGP-----
>Dasypus_novemcinctus
MSREGGAAAPGRPRAGAAARGP-----
>Ceratotherium_simum_simum
MKRVGGAAAPGRPRAGDATRGP-----
>Manis_javanica
MKREGGGAAPGRPRAGDAAQGPWMPL
>Ictidomys_tridecemlineatus
MKRADGAAAPGQPRAGNAAQGPWMPL
>Tupaia_chinensis
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HG0694 ENSG00000133265 HSPBP1

>Homo_sapiens

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>Felis_catus

MAAPSRVRCGRLCL-

>Physeter_catodon

MAAPSVRCGRVCL-

>Rousettus_aegyptiacus

MAAPTRGRCGQLCL-

>Dasypus_novemcinctus

MAAPSRVRCGPLCF-

>Condylura_cristata

MAAPSRVRCGRLCLY

>Oryctolagus_cuniculus

MAAPSRVRCGRL---

>Equus_przewalskii

MAAPTRVRCGRLCL-

>Marmota_marmota_marmota

MAAPSRVRCGRLCL-

>Homo_sapiens
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>Mustela_putorius_furo
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>Physeter_catodon
MESELLGVKREDRGRGVRVAQQVAAGDGGGGWGVR
>Galeopterus_variegatus
MESELWGGKREDRGRGVRVAQRVAAGDGGGGWGVR
>Oryctolagus_cuniculus
MECELWGGKREARGHGVRVAQQVAAGGGGRGVR---
>Elephantulus_edwardii
MESELWGGKREEGGRGVRVAQQVAAGGEGGGWGVR
>Ceratotherium_simum_simum
MESELWGVERDRGRGVRVAQQVAAGDGGGGWGVR
>Marmota_marmota_marmota
MESELWGGKREDRGRGVRVAQQVAAGDRGGGGWGVR
>Tupaia_chinensis
MESELWGGREDRGRGVRVAQQVAAGDGGGGWGVR

>Homo_sapiens

-----MLEAWNLSHYLKLLNNRRKWN-----

>Physeter_catodon

-----MKILNNRRKWN-----

>Myotis_brandtii

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>Condylura_cristata

-----MLETWDLNLSYFLKVTHTKNTSEVAANTIKNTSAVSWKMGVCICVVREREKITTY

>Oryctolagus_cuniculus

-----MLKAGHLDSLHCLKLLN-RRKWN-----

>Ceratotherium_simum_simum

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>Loxodonta_africana

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>Trichechus_manatus_latirostr

-----MLEAWNLSLHCLKLLTNRRKWD-----

>Homo_sapiens
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>Acinonyx_jubatus
MDWLPDQVPCSWQEYGAE
>Lipotes_vexillifer
MDWLPDQVPCSWQEYAE
>Eptesicus_fuscus
MDWLSQVPCSWQEYGAQ
>Dasypus_novemcinctus
MDWLPDRVPCSW-----
>Condylura_cristata
MDWLPYPICSWQECEAE
>Equus_caballus
MDWLPDQVPCSWQEYGAE
>Chinchilla_lanigera
MDWLRDRVPCSWQEYGEE
>Tupaia_chinensis
MDWLPDRVPCIRQDCEE-

>Homo_sapiens
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>Mustela_putorius_furo
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>Balaenoptera_acutorostrata_s
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>Miniopterus_natalensis
MTHREKRWWSQGGQLELSPLL---RGR-----
>Ceratotherium_simum_simum
MTHREKRWWSRGQLKLPQVL---NGW-----
>Manis_javanica
MTHREKRWCSQGGQLKLSHAV---NGR-----
>Loxodonta_africana
MTHREKRWWNQGQLKLPQVL---NGW-----
>Peromyscus_maniculatus_baird
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>Trichechus_manatus_latirostr
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>Homo_sapiens

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>Tursiops_truncatus

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>Myotis_davidii

MEEDV-HRSWQSPGTADRLGAAA

>Galeopterus_variegatus

MEEDA-AGGQQLGTEDRVGAAA

>Condylura_cristata

MEEDA-TRGPESPGTEDRLGAAA

>Oryctolagus_cuniculus

MEEDAPGGGRRSLGTEDRVGAAA

>Equus_asinus

MEEDA-TRSQKSRGTQDRVGAAA

>Fukomys_darlingi

MEEDA-TGGSQLGTTEGRAGAAA

>Tupaia_chinensis

MEEDA-IGGRQSLGVEDRVGAAA

>Homo_sapiens
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>Odobenus_rosmarus_divergens
-----MADRCFRPVGN DGLS
>Lipotes_vexillifer
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>Myotis_ricketti
-----MADQCFGPAGN DGLS
>Erinaceus_europaeus
MQDG-GGRALRGAAAPAGHGR-----
>Ceratotherium_simum_simum
-----MADRYFGPVGN DGLS
>Manis_javanica
-----MADRYFGPVGN DGLS
>Ictidomys_tridecemlineatus
MQDG-GGGVLRGAAAPAGED-----
>Trichechus_manatus_latirostr
MQDGDGGGALRGAADPAGESR-----

>Homo_sapiens
-MDC-LS-PSFHPGETVQI
>Canis_lupus_familiaris
-MDC-LS-LSFHPGETPQV
>Balaenoptera_acutorostrata_s
-MDC-FS-LSFHPGETAQV
>Rhinolophus_ferrumequinum
-MDCFFS-LSFHPGEASQV
>Dasypus_novemcinctus
MMDC-LS-LSFCPPGGLQI
>Galeopterus_variegatus
-MDC-LS-LSSPPGETLQI
>Equus_asinus
-MDCFSRDAFHPGETP--
>Manis_javanica
-MEC-FS-PSFHLGKAPQV
>Peromyscus_maniculatus_baird
-MDC-LS-VSFHPGQAFQI

HG0702 ENSG00000167377 ZNF23

>Homo_sapiens

MELALGQQEPVSEVGD

>Miniopterus_natalensis

MELALGQQEPVSEVGD

>Dasypus_novemcinctus

MELALGQQEPVSEVGD

>Galeopterus_variegatus

MELALGQQEPVSEVGD

>Manis_javanica

MELALGQQEPVSEVGD

>Loxodonta_africana

MELALGQQEPVSEVGD

>Cavia_porcellus

MELALGQQEPVSEVGD

>Tupaia_chinensis

MELALGQQEPVSEVGD

>Trichechus_manatus_latirostr

MELALGQQEPVSEVGD

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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Lipotes_vexillifer
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>Rousettus_aegyptiacus
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>Condylura_cristata
MWRDSLCTAAGYVLGRWDAAALSSLLSEAAAMMEV
>Ceratotherium_simum_simum
MWRDSLCTAAGYAFGRDAAALSSLLSEAAAMMEV
>Ictidomys_tridecemlineatus
MWRDSLCTAAGYAFGRWDAAALSSLLSEAAAMMEV
>Trichechus_manatus_latirostr
MWRNSLCTAAGYAIGRRDTAALSSLLSEAAAMMEV
>Orycteropus_afer_afer
MWRNSLCTAAGYALGRRDTVALSSLLSEAAAMMEV
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>Homo_sapiens
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>Leptonychotes_weddellii
MESGGRPGRGGVCSAPGLQ
>Lipotes_vexillifer
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>Pteropus_vampyrus
MESGGRLGKGGASSPAPGLQ
>Erinaceus_europaeus
MESGGRPGRGGASSAAGLQ
>Oryctolagus_cuniculus
MESGRRPGRGGASLPAPGLQ
>Mus_musculus
MESGGRRSRGGASTAAPGLQ
>Trichechus_manatus_latirostr
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>Orycteropus_afer_afer
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HG0704.2 ENSG00000272325 NUDT3

>Homo_sapiens

MRRPRRASGGAV

>Physeter_catodon

MRRPRRASGGAV

>Pteropus_alecto

MRRPRRASGGAV

>Oryctolagus_cuniculus

MRRPRRASGGAV

>Elephantulus_edwardii

MRRPRRASGGAV

>Heterocephalus_glaber

MKRPRRASGGVV

>Orycteropus_afer_afer

MRRPRRASGGAV

>Homo_sapiens
-MAAPGSDRLLGLRRE
>Acinonyx_jubatus
-MAAPGGDRLLGLRQE
>Balaenoptera_acutorostrata_s
-MAAPGSDRLLG----
>Miniopterus_natalensis
-MAAPGSDRLLGLRRE
>Galeopterus_variegatus
-MAAPGQYRLLGLRQE
>Erinaceus_europaeus
-MAAPGSDRLRGLRQK
>Ceratotherium_simum_simum
MMAAPGSDRLLGLQQE
>Loxodonta_africana
-MAAPGADGLLGLRLK
>Ictidomys_tridecemlineatus
-MAAPGSDRLLG----

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>Homo_sapiens
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>Canis_lupus_familiaris
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>Orcinus_orca
MRAPSHSLCRSFTVE-----
>Rousettus_aegyptiacus
MRAPSHCLCRSFAVERPVETCDPFSLSKSLVMSPICPWLQEKRL
>Condylura_cristata
MRVPSHSLCRSFTGEGDC-----
>Ceratotherium_simum_simum
MRAPSHSLCRSFAGKGDC-----
>Loxodonta_africana
MRAPSHSLCRSVAGEGDC-----
>Peromyscus_maniculatus_baird
MRARSHSLCRSFPGEEDC-----
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>Homo_sapiens
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>Leptonychotes_weddellii
-----MGFPGHTTYK

>Physeter_catodon
-----MVTFVILTQSPPL--PLPQSSSAECGSRGFLLLSSSMGFPGHTTYK

>Rousettus_aegyptiacus
-----MGFPGHTTYK

>Galeopterus_variegatus
-----MGFPGHTAYK

>Sorex_araneus
-----MGLPGHTTYK

>Ochotona_princeps
-----MGFPGHTTYK

>Equus_caballus
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>Dipodomys_ordii
-----MGFPGHTTYK

>Homo_sapiens

-----MGAQARKEIMKRHMC

>Felis_catus

-----MKRHMC

>Myotis_davidii

-----MKRHMC

>Galeopterus_variegatus

-----MKKHMC

>Erinaceus_europaeus

-----MKRRMC

>Equus_asinus

-----MKSHMC

>Manis_javanica

-----MKRPLC

>Fukomys_damarensis

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>Tupaia_chinensis

-----MKKHMC

HG0708 ENSG00000184613 NELL2

>Homo_sapiens

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>Ursus_americanus

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>Balaenoptera_acutorostrata_s

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>Pteropus_alecto

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>Elephantulus_edwardii

MMCALEGLSSSRAGILAFSS

>Loxodonta_africana

MMCALEGLSSSLAWAVLAFSS

>Ctenomys_sociabilis

-MSAAQAPSSARAGGRPFLS

>Trichechus_manatus_latirostr

MMCALEGLSSSRAGVLFVSS

>Orycteropus_afer_afer

MMCALEDLSSRA-----

>Homo_sapiens
-----MRLFLFEADTSS-----
>Acinonyx_jubatus
-----MRLFLFEADTSA-----
>Tursiops_truncatus
-----MKLFLFEADTSA-----
>Eptesicus_fuscus
-----MRLFLFEADTSA-----
>Dasypus_novemcinctus
-----MRLFLYEADTSA-----
>Galeopterus_variegatus
MSPGEMRLFLFEADTSS-----
>Condylura_cristata
-----MRLFLFEADTSAEPQVLLGKGSGCFQGENSVEKRSSTGQQRSSRNQ
>Oryctolagus_cuniculus
-----MRLFLFEADTSS-----
>Dipodomys_ordii
-----MRLFLFEADTSS-----

HG0710 ENSG00000196505 GDAP2

>Homo_sapiens

MGPPECSKVSSEY

>Mustela_putorius_furo

MGPPECSKVCSEY

>Orcinus_orca

MGPPECSKVYSEY

>Oryctolagus_cuniculus

MGPPECSEVSSEY

>Ceratotherium_simum_simum

MGPPECSEVS SAY

>Loxodonta_africana

MGTPECS DISSEY

>Chinchilla_lanigera

MGPPECSKLSRDY

>Tupaia_chinensis

MGPPECTKVTS DY

>Orycteropus_afer_afer

MGTPKCSNVSSEY

HG0711 ENSG00000198300 PEG3

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>Canis_lupus_familiaris
MSTLGWRRRAPGALWVC
>Balaenoptera_acutorostrata_s
MSTVGWRRRVPGAVWGH
>Pteropus_alecto
MSTLGWWCRQARGAV---
>Galeopterus_variegatus
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>Equus_asinus
MSTLGWRRRAPGAMWAR
>Manis_javanica
MSTLGWRRRSP-----
>Loxodonta_africana
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>Nannospalax_galili
MSTLGWRRRAPGAVVWH

>Homo_sapiens
MKGRCPFKVCFYSPWTLA-----
>Canis_lupus_familiaris
MKGRCPFKVCFAAQPVDFSLNTNPRSWLYLSMSRTEPGRLPVGFQRPSAGRGGRWGSESGI
>Orcinus_orca
MKGRCPFKVCF AARGL-----
>Pteropus_alecto
MKGRCPFKVCLAARGL-----
>Oryctolagus_cuniculus
MKGRCPFKVCCAVRGL-----
>Ceratotherium_simum_simum
MKGRCPFKVCF AARGL-----
>Manis_javanica
MKGRCPFKVCF AARGL-----
>Loxodonta_africana
MKGRCPFKVCF AAGGL-----
>Nannospalax_galili
MKGRCPFKVCF AARGL-----

>Homo_sapiens
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>Panthera_tigris
MPDSFDTLQRQRPEGGGRGGGGRRGGGRRDVSREGGQCSGPPL-----
>Balaenoptera_acutorostrata_s
MPDSFDTLQRQRPEGGGRGGRRGRGGGEEKGAM-----
>Miniopterus_natalensis
MPDSFDTLQRQRPEGGSGGERG-----GRGDVS-----
>Oryctolagus_cuniculus
MPDSFDTLQRQRDLEQRQPPEREQREAM-----
>Manis_javanica
MPDSFDTLQRQRAERGGRRGGARRGGGDASF---AGSARNTGPPLTLRPLSSPQRRELPRASSRDSAFWTWKCQ
>Loxodonta_africana
MPDSFDTLQRQRAGEQREEEEDGEEEE-EEEAL-----
>Rattus_norvegicus
MPDTFDTLQRQRALDRREKRGDRGGP-----

HG0714 ENSG00000051825 MPHOSPH9

>Homo_sapiens

-----MTRIHFSTAQEPLFSNKRI

>Acinonyx_jubatus

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>Pteropus_alecto

MKHLKMTRIQLQTVKEPTFSNKRA

>Oryctolagus_cuniculus

MKRLRKTRIQLFPQTVKEPFSNKRV

>Equus_asinus

MKHLKMTRTQLQTVKKPTFSNKRV

>Loxodonta_africana

MKHLKMTRIQLQTVKEPFSNKRA

>Fukomys_damarensis

-----MTRIQLFPQTVKEPLFSNKRL

>Tupaia_chinensis

MKHLKMTRIRFLQTVKQPLFSNKRD

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>Homo_sapiens

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>Felis_catus

MCYLCSWCVGGLL

>Lipotes_vexillifer

MCYLCSWCVGGLL

>Myotis_brandtii

MCYLCSRCVGGLL

>Galeopterus_variegatus

MCYRCSWCVGGLL

>Condylura_cristata

MCYRCSWCVGGLL

>Ceratotherium_simum_simum

MCYLCSWCVGGLL

>Nannospalax_galili

MCYLCSWCMGGLL

HG0716 ENSG00000075413 MARK3

>Homo_sapiens

MSPGTRRG TARARPGI

>Odobenus_rosmarus_divergens

MSPGTRRG TARARPGI

>Orcinus_orca

MSPATRRG TARARPGI

>Rousettus_aegyptiacus

MSPGARRG TARARPGI

>Galeopterus_variegatus

MSPGTRRG TARARPGI

>Oryctolagus_cuniculus

MSPGSRRG TARARPGI

>Marmota_monax

MSPGARGG TARARPRI

>Tupaia_chinensis

MSPGTLRG TARARPGI

HG0717 ENSG00000083857 FAT1

>Homo_sapiens

MLKIPGRQSWYFKPGS

>Mustela_putorius_furo

MLKIGGRQSWYFRYGF

>Lipotes_vexillifer

MLKIRGQSWYFIHGL

>Miniopterus_natalensis

MLKIPGRQSWYFRRGF

>Galeopterus_variegatus

MLKIGGRQSWHFRHG-

>Condylura_cristata

MLKIAGRQSWYFRRGF

>Ceratotherium_simum_simum

MLKIRGRQSWYFRPGF

>Rattus_norvegicus

MLKIQGRQSWYFEPGS

>Homo_sapiens

-----MMGEDKQLQAPARSAQLASG-ERPAVLCCRASAQSPGRA-----PDADCRHQNARDEEDRRSAAS-----

>Acinonyx_jubatus

-----MMGETKKLQAPACSAQSGSR-KED--FR----AVLPDLGPEREMLTIGRPECLE-----

>Rousettus_aegyptiacus

MISLNSKIPPRPRAPVHKAAPVTRGAPKKGRMLGEDKQLQAPACSAQFGSS-KE--ALRCSSSRPRPMRAERETPTVGRPECRE-----

>Galeopterus_variegatus

-----MGEDANYK-PQRSARKPAPGRRPAAHRHPASAQNPGLAPMLS-----AFQNAQNEEDRRSAVSQPPGLVS
MAPAIAGTVAC

>Ceratotherium_simum_simum

MVES-----R---RTQSSCSHSGPEEGEGDGRQATTSPSMQCASWAPGKRSAAQRCASASNGGRARDADFQ-----PSKMLR
MRK-TGGAL--

>Manis_javanica

-----MMGKEERLQAPACSAQCGGWKERPAAFRCPASAQKAGAA-----

>Ictidomys_tridecemlineatus

-----MTGEDKQLQAPACSAQRGL----PRVWRCRLPGLSPESG-----

>Trichechus_manatus_latirostr

-----MMGEDEQLQAPA-----

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>Homo_sapiens
MTGQRPLLQQPAHCLDALIQGHQLQLDHIDGSQIPEVMGWPGHW
>Odobenus_rosmarus_divergens
-----MGWPGQW
>Rousettus_aegyptiacus
-----MGWPGQW
>Sorex_araneus
-----MGWPGRW
>Equus_asinus
-----MPEGMGWPGRW
>Manis_javanica
-----MGWSGQW
>Ictidomys_tridecemlineatus
-----MDWPGQW
>Orycteropus_afer_afer
-----MGWPGQW
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HG0720 ENSG00000087053 MTMR2

>Homo_sapiens

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>Mustela_putorius_furo

MAASGLPPGPALA

>Orcinus_orca

MAASGLPPGPALA

>Pteropus_alecto

MAASGLPPGPALA

>Oryctolagus_cuniculus

MAASGLPPGPALA

>Loxodonta_africana

MAASGLPPGPALA

>Marmota_marmota_marmota

MAASGLPPGPALA

>Trichechus_manatus_latirostr

MAASGLPPRPALA

HG0721 ENSG00000095951 HIVEP1

>Homo_sapiens

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>Ailuropoda_melanoleuca

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>Balaenoptera_acutorostrata_s

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>Cynopterus_sphinx

MDIKFMELPFCDLLFLQFLRRKRG

>Dasypus_novemcinctus

-----MELPFCDLLFLQFLRGKSCP

>Ceratotherium_simum_simum

MDLEFMELPFCDLLFLQFLRRKRG

>Ictidomys_tridecemlineatus

MYIEFMEPPFCDLLFLQFLRRRSS

>Tupaia_chinensis

MSAEFMELFCDLLFLQFLRRKSL

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>Homo_sapiens

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>Ailuropoda_melanoleuca

MRPQPRRSPRALAPGAPR

>Balaenoptera_acutorostrata_s

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>Rousettus_aegyptiacus

MRPQPRRSPRAPRAGAPC

>Dasypus_novemcinctus

MRPQAPRSPRALAPGALC

>Condylura_cristata

MRPQPHRSPRAPLASGAPC

>Oryctolagus_cuniculus

MRPQPHGSPHAPLDPGALC

>Chinchilla_lanigera

MRPQPRGSPRAPLAGAPC

>Homo_sapiens	
ITDLKPKNKMR	M
>Ailuropoda_melanoleuca	
ITDLEPKNKM	M
>Balaenoptera_acutorostrata_s	
ITDLGPKNKM	M
>Eptesicus_fuscus	
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>Ceratotherium_simum_simum	
ITDLGPKNKM	M
>Manis_javanica	
ITDLGPKNMM	M
>Loxodonta_africana	
ITNLGPKNKMR	M
>Marmota_marmota_marmota	
ITDLEPKNKM	M

>Homo_sapiens
-----MDV-----SFLCPKTHPSPSLFSKGGAGEPPPTLGPPLPLPALPGRHHSPEGTGL-CCAS--EQKSQSQQSRLTTCKPQWLPACACCEVGD
GQEAG
>Lipotes_vexillifer
-----METHA-----SLLCPKTHPAPP-----

>Rousettus_aegyptiacus
MLCVRVSRGVVWLRVGVYYRVQTVVCDHCQ----SVYPRGCMST-PCSA-PRHTPAPP-----

>Galeopterus_variegatus
-----MDGC-----LFLALPQDTPQPLLSLGRGVGEPPPTQGPPRSLPALPSRHHSPEGTGL-CCASEQKPQNKQSSQPATTCKPQWLLFACCEVGD
GQEAG
>Condylura_cristata
-----MHA-----SSSL-----

>Oryctolagus_cuniculus
-----MDA-----SLLCPKTHPSPSLVWEGGWGASPYPGASPPSPCPAVTT-PQRAQS--CAE--PPSTAPE----PAEPRGWRPA--CHSGCP
LRAAG
>Ceratotherium_simum_simum
-----MHA-----SLLCPKTHPSPSLV-----

>Trichechus_manatus_latirostr
-----MDV-----SLLCPETHPGPSLVWEGGLGSH-PCPGASLAPRPAGQSPPPRGHSVPQCLRVKAPEGAQQADDL-----QATVAALCGL----

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>Homo_sapiens
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>Mustela_putorius_furo
-----MCFQTHQ-----
>Myotis_lucifugus
---MELCLFSRTCFCACQGNVKKLLGVEMLEEHLPSC-----
>Oryctolagus_cuniculus
-----MCFEACQWNLTLPFCFEMLEPPHLCVYLPS-
>Ceratotherium_simum_simum
-----MCFEAHQ-----
>Manis_javanica
MEEGTLCPFSRMRFAQHCNMILLLCVEMLEEHPLLCWHLPY
>Marmota_marmota_marmota
-----MCFQAHQWNLILLFCVEMLEETHLCLHPPSS
>Tupaia_chinensis
-----MCFQAHQWNMLLFCVEMLKK-LHLCLHLPPF
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>Homo_sapiens

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>Leptonychotes_weddellii

MWLRRGWRTRWRRRLLLRRRRRSGAEEGTGPDSARQRD

>Lipotes_vexillifer

MWLRRGWRTRWRRRLLLRRRRRSGAEEGTGPDSARQRD

>Rousettus_aegyptiacus

MWLRRGWRTRWRRRLLLRRRRRSGAEEGTGPDSARQRD

>Condylura_cristata

MWLRRGWRTRWRRRLLLRRRRRSGAEEGTGPDSARQRD

>Oryctolagus_cuniculus

MWLRRGWRTRWRRRLLLRRRRRSGSEEGTGPDSARQRD

>Equus_asinus

MWLRRGWRTRWRRRLLLRRRRRSGAEEGTGPDSARQRD

>Heterocephalus_glaber

MWLPRGWRTRWRRRLLLRWRWRSGSEEGTGPDSALQRD

HG0726.2 ENSG00000115504 EHBP1

>Homo_sapiens

MQSSFALDPLHY

>Oryctolagus_cuniculus

MQSSFALDPLLY

>Loxodonta_africana

MQSSFALDPLLY

>Fukomys_darlingi

MQSSFALDPLPY

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>Homo_sapiens

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>Felis_catus

-----MEKFTPPKMKMRTFEKVI

>Balaenoptera_acutorostrata_s

-----MKMRTFEKVI

>Condylura_cristata

-----MKMWVIEGI-

>Equus_przewalskii

-----MKMRTFENVI

>Marmota_marmota_marmota

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>Orycteropus_afer_afer

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>Balaenoptera_acutorostrata_s

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>Rhinolophus_ferrumequinum

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>Dasypus_novemcinctus

MLLKRTVEYKIITITEKQVGFGNKILTMLFAFG-----

>Oryctolagus_cuniculus

MLLKRTVEYKFMT-TVEQAGFGDTMF-----

>Equus_asinus

MLLKRTVEYKIITTEKQVGFGETIL-----

>Manis_javanica

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>Homo_sapiens

-----MAAVFAVVTLTILGFRL

>Felis_catus

-----MAVVFTGVTLILGFRL

>Lipotes_vexillifer

-----MAGVLAGVTILILGFRL

>Pteropus_alecto

-----MAVVFAGVTILILGFRL

>Dasypus_novemcinctus

-----MAAVSAGVTILILGFRL

>Erinaceus_europaeus

-----MAGVFVGVTILILGFQL

>Manis_javanica

MAAASREPAVAGHARWGPRAGMAGVFAGVTILILGFRL

>Peromyscus_maniculatus_baird

-----MAAAFTRVTLTILGFRS

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>Homo_sapiens
MQARGEGAARTMLRRVR-----
>Mustela_putorius_furo
-----MLRRTR-----
>Physeter_catodon
-----MLRQPRPSISNR
>Rhinolophus_ferrumequinum
-----MLRRVR-----
>Galeopterus_variegatus
-----MLRLPR-----
>Condylura_cristata
-----MLRRER-----
>Ochotona_princeps
-----MLRRVR-----
>Nannospalax_galili
MQAPGKGAARTMLRRVR-----
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>Homo_sapiens
MAPSRRSGERQGCKSGFQTGSVNGKGVGGLTAQACSFGLYN--SNSASKTWSLTETYFTPLE-----
>Panthera_tigris
MAPRRRR--REEAKCGLRIGSVNKGAKDGTAAHSLSTPQHSNGEGASKTWPLDETYFTLQKVGRSKKKRGTGGGTA
>Rousettus_aegyptiacus
MAPSRTSGENQEDKSRI-----NKGAKDRIAQAYSFGTL-----
>Dasypus_novemcinctus
MAPSRRSEKRGKNSCFRTGTVNECAKALTAQA-----
>Oryctolagus_cuniculus
MAPSGRSGERQGTKCCFRSASANKSAKDLTAQACTSDL-----
>Equus_caballus
MAPSRSS-----
>Loxodonta_africana
MAPSRRN-----
>Heterocephalus_glaber
MAPSSRREESPKGNFSFQTATVNKGAENLTAQAYCFGL-----

>Homo_sapiens

-----MDRCVYALILENLN-FF----F-----

>Ailuropoda_melanoleuca

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>Orcinus_orca

-----MDKCMYALIL-----

>Miniopterus_natalensis

-----MDQCMYALILENLE-GI----NFGFKYLAWVQYLKKADDQFSH-----

>Ceratotherium_simum_simum

-----MDRHMYALILENLK-CF----FKGRSQ-LWLQGFGMGTMP-----

>Manis_javanica

-----MDRCMKALILPNLK-FF-----

>Loxodonta_africana

-----MDRCMYALIFEGLK-FFSKEGVNFGFQCLAWVQCLKKADN-----

>Rattus_norvegicus

MRVITLGQQRDHTWTLFRRPANMDRYVHSPILENLNLFRRKKATLAGSV--WRIPCFAKADDLLATDHADHCLELD

>Homo_sapiens
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>Leptonychotes_weddellii
MLGGGMPELPVENYPNEKY-----VGWGP-----
>Orcinus_orca
MFGGGMPELPAENYPSKRN-----M-----
>Myotis_brandtii
MLAGGMPELPAENHPDKKY-----VG-----
>Galeopterus_variegatus
MLGGGMPELPAEYYPTRRN-----M-----
>Manis_javanica
-----MPELPAESYPYEKH-----VGWGP-----
>Chinchilla_lanigera
MLGRGMPELSAEIVSNQEKRCCKDLNLYLGLQEKDTPKAQHSIHLEGKY
>Tupaia_chinensis
MLGKGMPELPAENYPKIN-----VQEMPPNRPQH-----

HG0734 ENSG00000139318 DUSP6

>Homo_sapiens

MCPAPPPLPPLLSPSSRRARCCSLFALGLIRSGNSFPFL

>Ursus_maritimus

MCPAPPPPPPLSPSSRRARCCSLFALGLIRSGNSFPFL

>Rousettus_aegyptiacus

MCPAPPPPPPLSPSSRRARCCSLFALGLIRSGNSFPFL

>Sorex_araneus

MCPAPPPPPPLSPSSRGARCCSLFALGLIRSGNSFPFL

>Equus_asinus

MCPAPPPPPPLSPSSRRARCCSLFALGLIRSGNSFPFL

>Loxodonta_africana

MCPAPPPPPPLSPSSCGARCCSLFALGLIRSGNSFPFL

>Ctenomys_sociabilis

MCLLLLHRLLFFLLPSRRARCCSLFALGLIRSGNSFPFL

>Trichechus_manatus_latirostr

MCPAPPPPPPLSLSSRGARCCSLFALGLIRSGNSFPFL

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>Homo_sapiens

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>Ursus_maritimus

MDRVLGCPDEGSGRFGE

>Orcinus_orca

MHRVPGCPDEGSGGFGE

>Miniopterus_natalensis

MDQVPSCPDGSGGRFRN

>Dasypus_novemcinctus

MERVSGCRKEGSGMFGE

>Oryctolagus_cuniculus

MGRIPGCPDEGSGRVGE

>Equus_asinus

MDRVPGCPDEGSGRFGE

>Mus_musculus

MDRVLGCGDAGSGRSAE

>Homo_sapiens

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>Felis_catus

MWEPAGTFAGDTERGPEVEEPR-----AAPQELRARPWRRRRPLGWRRTMRSDGSGAGGRCRAATGSVSAAHCAACEQV

>Physeter_catodon

MWEPAGVFAGYTERGPEVGEPR-----AAPQELRATLWRRRRPLGWRRTMRSDGSGAGGRFCAAPGSESAADCAACEQV

>Pteropus_alecto

MWEPAAVAFAGDTEFGQEEVESR-----PAPQDLRARLWQQRWLCWKRTMRSDGSGTAGRCCAALGCVFATDCAACEQI

>Dasypus_novemcinctus

MWDPAGVFAGDTRA-----

>Galeopterus_variegatus

MCEPAGAFAGDTQAGAGSGAADG-RAAGAPG-----

>Equus_asinus

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>Balaenoptera_acutorostrata_s

MLPTSEASRGSWLGS

>Rousettus_aegyptiacus

MLSPSEASRGSWPGS

>Dasypus_novemcinctus

MLPTSETAKESWPGS

>Equus_asinus

MLPPSEASGGSWPGS

>Manis_javanica

MLPPSEASRGSWPGS

>Cavia_porcellus

MLPTSKCSGGSWPGS

>Tupaia_chinensis

MLPTSKACGGSWPGS

HG0738 ENSG00000143393 PI4KB

>Homo_sapiens

MEPGSGRCC

>Odobenus_rosmarus_divergens

MEPGSGRCC

>Galeopterus_variegatus

MEPGSGRCC

>Erinaceus_europaeus

MEPGSGRCC

>Ochotona_princeps

MEPGSGRCC

>Ceratotherium_simum_simum

MEPGSGRCC

>Loxodonta_africana

MEPGSGRCC

>Mesocricetus_auratus

MEPGSGRCC

HG0739 ENSG00000144331 ZNF385B

>Homo_sapiens
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>Panthera_tigris
MICSDALPVGCFLAPHFTEAPG-----
>Rousettus_aegyptiacus
MICSDALPVCCFLAPHFTGAPG-----
>Dasypus_novemcinctus
MICSGALPVGCFLAPHFTGAPG-----
>Ochotona_princeps
MICSDALPVGSFLALHFTEAPG-----
>Elephantulus_edwardii
MICSDPLPVGCFLAPHFTGAPG-----
>Ictidomys_tridecemlineatus
MICSDTLPVGCFLAPHFTGAPG-----
>Orycteropus_afer_afer
MICSDALPVGCFLAPHFTEAPASNDGIIYL

HG0740 ENSG00000144331 ZNF385B

>Homo_sapiens

MFYISTPSNIKLMFMG

>Mustela_putorius_furo

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>Pteropus_alecto

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>Oryctolagus_cuniculus

MFCISTSSKIKLVFMG

>Equus_asinus

MFCIATSSKIKLMFMG

>Mus_musculus

MLYISGSSEIKLIFMG

>Trichechus_manatus_latirostr

MFCVSTSSEIKLMFMG

>Orycteropus_afer_afer

MFCVSTSSEIKLIFMG

HG0741 ENSG00000144834 TAGLN3

>Homo_sapiens

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>Myotis_brandtii

-----MQHRQLTVKAAVLSAC

>Condylura_cristata

-----MQPQLSVKAAFFPAC

>Elephantulus_edwardii

-----MMQHQP LHVRAALLFAC

>Equus_caballus

-----MQHQQLNVKAAFLPAC

>Ictidomys_tridecemlineatus

-----MQHPQL-----

>Trichechus_manatus_latirostr

-----MQHQQLNLKAALLSAC

>Orycteropus_afer_afer

-----MMQHQQQLNVKAALLSAC

>Homo_sapiens
-----MFCKFP-----GGHEAPDTWIGLNKPLEFKTF
>Odobenus_rosmarus_divergens
-----MLCEYT-----GGHKAPDTWIGFNLKPLEFKTF
>Lipotes_vexillifer
-----MLCKAA-----GGHEAFDTWVGLNLKPLEFKTF
>Miniopterus_natalensis
-----MFALADTWIGLNKSLEFKTF
>Dasypus_novemcinctus
MGWRVAGTAFSSRRTQLAAVTAENSANAPRQQLPAAGILFPS--DQPSLLPFFPSDTWIGLNKPLEFKTF
>Elephantulus_edwardii
-----MGLNLKPLEFKTF
>Equus_caballus
-----MLAQRASACTLRPRLERRSLCIHLTDRDTWIGLNKPLEVKTF
>Nannospalax_galili
-----MLKLWRTGIGAFHLSDRDTWIGLNKPLEFKTF

HG0743 ENSG00000154814 OXNAD1

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>Homo_sapiens
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>Felis_catus
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>Rousettus_aegyptiacus
METLSVFQLVCI-----
>Galeopterus_variegatus
-----MFQLVYPKVS-----
>Manis_javanica
METLFVFQPVYIQRSQFNTRTKILHVSQPASHSFNDS-----
>Loxodonta_africana
MEKLPLFQLVCIKRSQYNTRTNILHKS--ASHTLNDSQNLMDI
>Ictidomys_tridecemlineatus
-----MFQPVYIQRQCQNTSRL-CVSEPAIP-----
>Orycteropus_afer_afer
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HG0744 ENSG00000163053 SLC16A14

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Balaenoptera_acutorostrata_s

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>Rousettus_aegyptiacus

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>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

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>Ictidomys_tridecemlineatus

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HG0745 ENSG00000163145 C1QTNF7

>Homo_sapiens

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>Canis_lupus_familiaris

-----MLRRALYFSSRYFLYCFEAASNKTHIFLL-----

>Lipotes_vexillifer

MNSKLQKSHAQTGTLFFIKFFLCGFEAALNDKHIFLL-----

>Pteropus_alecto

-----MLRRDLYFSSSYFLHCFAAALNNKHIFLL-----

>Galeopterus_variegatus

-----MLRQALYFSSSYFLHCFGAALNNRHIFLLYIF---

>Manis_javanica

-----MLRRALYFSSSYFLYCFEAALNNKHVFLLYIF---

>Loxodonta_africana

-----MLRRALYFSSSYFLHCFEAALNNKHLFLLYIF---

>Tupaia_chinensis

-----MIRRAFSSSYFLHWFGAALNNKHIFLLHIFEGF

HG0746 ENSG00000164741 DLC1

>Homo_sapiens

MISTTKWELRFWRN-----

>Leptonychotes_weddellii

MISTTKCELIFWRNSRGRTSFLA

>Lipotes_vexillifer

MISTTKCELIFWRN-----

>Myotis_brandtii

MISTTKCELIFWRN-----

>Ochotona_princeps

MISTTKCELRFWRNSLGDGLLR-

>Equus_przewalskii

MISTTKCELIFWRN-----

>Manis_javanica

MISTTKCELIFWRN-----

>Trichechus_manatus_latirostr

MISTTKCELIFWRN-----

HG0747 ENSG00000168036 CTNNB1

>Homo_sapiens

MIFSMNLGFCRSIHLQSQNPPGI-----

>Odobenus_rosmarus_divergens

----MNLGFCRSIHLQSQNPPGI-----

>Tursiops_truncatus

----MNLGFCRSIHLQSQNPPGL-----

>Erinaceus_europaeus

----MNLGFCRSIHLQSQNPPGI-----

>Ochotona_princeps

----MNLGFCRSVHLQSQNPPGILTFTKQLF

>Jaculus_jaculus

----MNLGFCRSIHLQSQNPPGI-----

>Trichechus_manatus_latirostr

----MNLGFCRSIHLQSQNPPGI-----

>Orycteropus_afer_afer

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>Homo_sapiens
MLWPFPLPTENGQTET-----
>Ursus_maritimus
MLWCFLLPIQNGT-----
>Tursiops_truncatus
MLWCFPLPTRNGTQETAEEKITASLQMRDFQVYIVSNCRKITISFSTV
>Eptesicus_fuscus
MLWRFPLPTQNGQTET-----
>Galeopterus_variegatus
MLWSFPLPTESGTQET-----
>Manis_javanica
MLWHFPLPIQKRTQET-----
>Heterocephalus_glaber
MLWPFPLPTENETQETM-----
>Tupaia_chinensis
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HG0749 ENSG00000169760 NLGN1

>Homo_sapiens

MVGFTWRWLWVPRILDRGCIWREKRINRHVLEVSUGE-----

>Mustela_putorius_furo

MVGFTWRWLWVPRILDRGFIWREKRINRHVLEVSUGE-----

>Physeter_catodon

MVGFTWRWL-----

>Myotis_brandtii

MVGSPWRWLWVPRILDPGCSWREKRINRHVLEVSUGE-----

>Condylura_cristata

MIGFTWRWLWVSRIQDRGCIWREKRINRHVLEVSUGE-----

>Oryctolagus_cuniculus

MVGFTWRCLWVPRNLDRGCIWKEKRINRHVLEVSUGELKKKKKRRGYN

>Equus_caballus

MVGFIWRWLWVPRILDPGCIWREERINRHVLEVSUGE-----

>Chinchilla_lanigera

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>Homo_sapiens	-----MVAPRAGEAVEGGGVRP
>Mustela_putorius_furo	-----MVAPRAGEVLEGGGARP
>Lipotes_vexillifer	-----MVAPRAGEAVEGGGARP
>Myotis_lucifugus	
MVTLTDVGYAVRDDVGAPLASACDATAARSPPRSRVTWGTASASQQPQRQRPAGEVKM	MVAPRAGEAVEGGGARP
>Dasypus_novemcinctus	-----MVAPRAGEAVEGGGARP
>Oryctolagus_cuniculus	-----MVAPRAGEAVEGGGARP
>Equus_caballus	-----MVAPRAGEAVEGGGARP
>Chinchilla_lanigera	-----MVAPRAGEAVEGGGVRS

>Homo_sapiens
MGSLPYAFVLVLQKGNLTEDHAVLKKY-----K-----
>Acinonyx_jubatus
MESLPYAFVLFSQKRKLDRGSCCP-----
>Myotis_brandtii
MGSLPYAFVLSSQKGKLDRRSCR-----
>Galeopterus_variegatus
-----MHLFWFCKKGNLTEDHAVLKKY-----NIPPE---VDGYERYFVIMCLMK
>Oryctolagus_cuniculus
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>Ceratotherium_simum_simum
-----MHFYFHKKGNLTEDHAVLKKY-----NITEE---VD-----
>Manis_javanica
-----MHLFCFHKKGNLTEDHAVLKKY-----NITEE---AD-----
>Fukomys_darlingi
-----MHLFWFYKKGNLTEDHAVLKKY-----K-----

>Homo_sapiens
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>Ailuropoda_melanoleuca
-----MAAAAFHDAGCSANKIREETVGMQVQWGHSRGCAIEARGSPGGSQSCWVSLRLLWEDPAFGERPLLPAGGSGLPPSLISIS
>Lipotes_vexillifer
-----MPILKMAA-AFHNDSCSAN-----
>Rousettus_aegyptiacus
-----MAAAAFRNDSCFANKICAETVGRKVQWG-----
>Oryctolagus_cuniculus
-----MAATAFRSKLLC-----EWDPGGNRIGRCRKAALRLP-----
>Elephantulus_edwardii
-----MPILKMSAIAFPSNNGSAEKIRAETVGR-----
>Ceratotherium_simum_simum
-----MAASAFHNDSCSANKIRAETVRRQTQWGRARVDL-----
>Marmota_marmota_marmota
-----MKNGVASFRVDSSFAIKIRAETLDGQVQPGRAEVAL-----

>Homo_sapiens
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>Mustela_putorius_furo
MGSRFLRGCDSGGGCCPRAERSEGVNEMCSSEHCF
>Balaenoptera_acutorostrata_s
MGNCFLGGCGSGGGWSRRA-----
>Rousettus_aegyptiacus
-----MIEGALLHNTKHSKGVNEMCSSGCHF
>Condylura_cristata
-----MHSSGCHF
>Ochotona_princeps
-----MCGSGCCF
>Heterocephalus_glaber
-----MSSSGCRF
>Tupaia_chinensis
-----MCSLECCF

>Homo_sapiens
-----MRQECSPYVTRHRFQMGRGLAQHPEPKQE
>Felis_catus
-----MKQECSPSVTRHRFQVGRGLAQHPEPK--
>Rousettus_aegyptiacus
-----MRQECSPYVTRHRFQVGRGLAQHPEPK--
>Erinaceus_europaeus
-----MRQECSPYVTRHGFQVGRGLAQHPEPK--
>Oryctolagus_cuniculus
MYIACWHCLGDGPQFAKPQRALLGPWHSLLKAMRRECSFYVTRHKFQVGRGLAQHPEPKQE
>Equus_caballus
-----MRQECSPYVTRHRFQVGRGLAQHPEPK--
>Manis_javanica
-----MRQECSPYVTRHRFQVGRGLAQHPEPK--
>Mus_musculus
-----MRQECSPYVTRHKFQVGRGLAQHPEPKQE

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>Homo_sapiens

MPVWKNFDVPVSSFYRVFHSFAISEKWD-----

>Ursus_maritimus

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>Physeter_catodon

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>Miniopterus_natalensis

MPAGEHLDVPVSSFYSVFHSFATSAKNAIKRKYFVK

>Oryctolagus_cuniculus

MPVWTNADVPVSSFQSVSILWPSQRKWC-----

>Equus_caballus

MPVWTHVDVPVSSFYSVFHSFAISEKMALKENIL--

>Loxodonta_africana

MPAQKSFDPASSFCTVVHILFNKK-LLFHF-----

>Heterocephalus_glaber

MLLWKNFDIPVSSFYSMFHSFATLEKMKANIM--

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>Homo_sapiens
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>Mustela_putorius_furo
-----MVACGASPDHPGPEMQ
>Orcinus_orca
-----MVACGAPHRHSGPEMW
>Rhinolophus_ferrumequinum
-----MVACGIPYHHLGSEMQ
>Galeopterus_variegatus
MQREEMVVCVPHHHSGPEMQ
>Equus_asinus
-----MVACGAPHHPPGPEMW
>Loxodonta_africana
-----MVARGAPHHHSAPKMR
>Marmota_marmota_marmota
-----MVACGASHHHPGPEIR
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HG0757.1 ENSG00000177301 KCNA2

>Homo_sapiens

MLLCFLGPVAAP-----

>Ailuropoda_melanoleuca

MLLCFLGPQAAP-----

>Balaenoptera_acutorostrata_s

MLLCFLGP-----

>Rousettus_aegyptiacus

MLLCFLGPSAAP-----

>Equus_asinus

MLLCFLGP-----

>Loxodonta_africana

MLLCFLGPLAAP-----

>Mus_musculus

MLLCFLGPLSAPSSLLQAAGRH

>Tupaia_chinensis

MLLCFLGPLAAP-----

HG0757.2 ENSG00000182255 KCNA4

>Homo_sapiens

MNLKGEPGESS

>Equus_asinus

MNLRGEPGESA

>Trichechus_manatus_latirostr

MNLRGEPGESS

HG0758 ENSG00000179299 NSUN7

>Homo_sapiens

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>Ailuropoda_melanoleuca

MLKVQGRPFPGTSEL

>Orcinus_orca

MLKVQGKPFPGTSEL

>Rousettus_aegyptiacus

MLTVQGKPFPGTSEL

>Oryctolagus_cuniculus

MLKVGGKPFPGTSEL

>Ceratotherium_simum_simum

MLKVQGKPFPGTSGL

>Loxodonta_africana

MLKVQGKPLPGTSEL

>Cavia_porcellus

MHKIRGKPFPGTSEV

>Homo_sapiens	-----MAAWASE
PPPGQPMR-----	
>Panthera_tigris	-----MAAWAME
PAPGHPVR-----	
>Orcinus_orca	-----MAAWVSE
PAPGQPVSTG-----	
>Rousettus_aegyptiacus	-----MVAWAAE
PGPGQPVR-----	
>Oryctolagus_cuniculus	
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PPPPQPMSSLHPSTG	
>Ceratotherium_simum_simum	-----MAAWASE
PAPGQPMR-----	
>Ctenomys_sociabilis	-----MAAWASE
PPSGQPMR-----	
>Tupaia_chinensis	-----MAAWASE
PPPGQPMRTG-----	

>Homo_sapiens

MFNKEIKCLNSHQKKKKPQKQNKNS-KSK-----NKKERGKKIQNKQTNKQGRTNL-Y---FKAAGTSHP--CLPPREGGLWPVVEELQGGSSGGQRPSDVLGA
TGQEAETQRGQRDSGPPRAARGWGARGSGTGAK

>Felis_catus

MFNKEIKCLNSHQKKKKKKKTQKPKISKKAKTKRERERERGKQNPQTNKQTRQNQPL---LQTSQRKPP--VSAARRGGSLARGGGVAGGIARGTEAE-----

>Pteropus_lecto

MCNKEIKCLNSHQKKKKTKQTNKKIPKSK-----NK--RERKKNPQTNKQTRHSQPL---LQSSRHEPP--ESAIQRGGLRPLVEELQGGSSGGQRPRDALGA
TGQEAEDTQGERDRGPPRAARGRGARGSGTGAK

>Condylura_cristata

MFNKEIKCLNSHQKKKKQKNSKKQKQ-----KEREGKKKSKTNKQTNQAEPTSPSNQPAQAT-R--VCHPERGVSGPWWRSCRGDQRQGGRG-----
--RVTP-----

>Oryctolagus_cuniculus

MFNKEIKCLNSHQKKKKQKTKKNSKS-----KNKKERG--KKAKTNKQTRQNQPL---LPTSRHQPA--VSATQGGSPARAAGVAGGIVRGTEAE-----

>Equus_asinus

MFNKEIKCLNSHQKKKKQNKISKKQK-----QKEREKKSKQTNKQGRTNL-Y---FKPAGASHP--CLPPREGGLWSVVEELQGGSSGGQRPSDALGA
TGQEAETQRGERDSGPPRAARGWGARGSGTGAK

>Cavia_porcellus

MFNKEIKCLTSHHKKKQKQQQNIYIYTSKSKNK---NRER---KKKPQNKQTNKAEPS---SAASQPAPATVSAAAGEGGLRPEVAEWQGGSSGGQRPSDVLGA
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>Tupaia_chinensis

MFNKEIKCFNSHQKKKQKQKNSKSKN-----KKRKREREKKSKTNKQTRQSQPL---LQPSRHQPP--CLPPERGVSGPWWRSCRGDQRQGD RG-----
--RVTS-----

>Homo_sapiens

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>Leptonychotes_weddellii

-----MTPRLAATRREIRCKHVCL-----

>Lipotes_vexillifer

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>Eptesicus_fuscus

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>Ochotona_princeps

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>Ceratotherium_simum_simum

-----MTPRLAATRREIRCKHVCSGTCVWVGWGGGGEERRNRFEKRSDFILPCG-PLLAFSIPPTPPPCFAILIGLPCFFLPRILLSPASPPP
RFACRYLS

>Manis_javanica

-----MTPRLAATRREIRCRRVCSRTRVWVGWGGGETGTALNDA-----VISICRAAPSPHSLPPTPLALSF-----

>Fukomys_damarensis

-----MTPRLAATRREIRCKHVCSGTRVWVGWGGGKGVKKPL-----

HG0762 ENSG00000187147 RNF220

>Homo_sapiens

MHHTLRLLPSVS

>Canis_lupus_familiaris

MHHTHRLPSVS

>Lipotes_vexillifer

MHHTHRLPSVS

>Myotis_lucifugus

MHHTHRLPSVS

>Equus_asinus

MHHTHRLPSVS

>Loxodonta_africana

MHHTPRLPSVS

>Marmota_marmota_marmota

MHHTLRLLPSVS

>Orycteropus_afer_afer

MHHTPRLPSVS

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>Homo_sapiens

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>Acinonyx_jubatus

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>Rousettus_aegyptiacus

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>Ochotona_princeps

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>Ceratotherium_simum_simum

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>Peromyscus_maniculatus_baird

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>Tupaia_chinensis

MLED SG SCFHPDDFFFLTLN

>Trichechus_manatus_latirostr

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>Homo_sapiens

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>Canis_lupus_familiaris

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>Tursiops_truncatus

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>Myotis_brandtii

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>Oryctolagus_cuniculus

-----MIVGQS-----

>Ceratotherium_simum_simum

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>Manis_javanica

-----MVEL-KKTTDQGWPKTVTGSLIIPGQDHCSVIR-----

>Ictidomys_tridecemlineatus

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>Homo_sapiens

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>Odobenus_rosmarus_divergens

-----MVRSLQGDIAFLAKEPET-----

>Lipotes_vexillifer

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>Dasypus_novemcinctus

-----MVRSLQGDTGRTFLAEGRDLKEAGVCW

>Equus_przewalskii

-----MVRCLQGDIGRTFLAERPET-----

>Manis_javanica

-----MVRSLQGDIGRAFLAERPET-----

>Loxodonta_africana

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>Nannospalax_galili

-----MVEFAYREALARAFLVEGPER-----

>Homo_sapiens	-----MMGTWRAALPFQPG
>Panthera_tigris	-----MGTWRAALPAQPG
>Dasypus_novemcinctus	-----MGTWRAVLPAQPG
>Oryctolagus_cuniculus	
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>Equus_przewalskii	-----MGTWRAALPAQPG
>Manis_javanica	-----MGTWRAALLAQPG
>Chinchilla_lanigera	-----MMGAWRAALPFQPG
>Orycteropus_afer_afer	-----MGTWRAPLPAQPG

>Homo_sapiens
-----MLDSFCNILVSRKHGIMATTESQ-----
>Canis_lupus_familiaris
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>Balaenoptera_acutorostrata_s
-----MAITESQRYKLHSVFF
>Rousettus_aegyptiacus
-----MAVTTSQ-----
>Equus_caballus
-----MTIAESQ-----
>Loxodonta_africana
-----MAIAESQ-----
>Dipodomys_ordii
-----MAITESQ-----
>Orycteropus_afer_afer
-----MAVTESQ-----

HG0767.2 ENSG00000197555 SIPA1L1

>Homo_sapiens

-----MERATQSCVFLPSS

>Galeopterus_variegatus

MITVLCNLLGDMERATQSSILILPSS

>Jaculus_jaculus

MLTVLCDLVGDMERAARSSILFLPSS

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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

MGYRQP-PPRLPSRTQQG

>Rhinolophus_ferrumequinum

MGCRQP--PRLPPRTRQG

>Galeopterus_variegatus

MGCRPPPPPPRLPPRTRQR

>Condylura_cristata

MGCRQP-PPRLPSRTRQG

>Ochotona_princeps

MGCRQP-PPQLLPTRTRQG

>Equus_caballus

MGCRQP-PPRLPSRTRQG

>Mus_musculus

MGYRPP-PTRLTPRTRQG

HG0769.1 ENSG00000280165 PCDH20

>Homo_sapiens
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MNREGVSSAALPTGAR
>Pteropus_alecto
MNGEGVSSGALPSGAR
>Condylura_cristata
MNREGVSSVALPTGAR
>Oryctolagus_cuniculus
MNGEGVSSAALPAGAR
>Equus_asinus
MNREGVSWAALPSGAR
>Mus_musculus
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>Tupaia_chinensis
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>Homo_sapiens
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>Lipotes_vexillifer
-----MTVPRYHLTFLPPELLSLTDEPVTIG
>Myotis_lucifugus
-----MTVPFCPSPFCTPS-APVLIGEPVTIG
>Nannospalax_galili
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>Orcinus_orca

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>Pteropus_alecto

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>Ceratotherium_simum_simum

MWLFVRGKNSHCSVPEPACG-EAPPMVPRRVGES

>Manis_javanica

-----MVPHRE---

>Loxodonta_africana

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>Orycteropus_afer_afer

MWIFACGRNSHCSVPEPACG-----

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>Homo_sapiens

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>Myotis_brandtii

MGPPDPGLRAARVPS----

>Dasypus_novemcinctus

MGPSGSGRRAARAPAWSQD

>Galeopterus_variegatus

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>Manis_javanica

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>Homo_sapiens

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>Peromyscus_maniculatus_baird

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>Homo_sapiens
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>Leptonychotes_weddellii
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>Pteropus_alecto
-----MLCDIDLSQRPRFGGE
>Condylura_cristata
-----MLCGRDLSQRPHFGGE
>Ceratotherium_simum_simum
-----MLCGSDLSQRPRLGGE
>Chinchilla_lanigera
-----MLCSDLSQTPRFGGE
>Tupaia_chinensis
-----MLCGTDLSQRPRFGGE

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>Homo_sapiens

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>Mustela_putorius_furo

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>Orcinus_orca

MCLPRPGGVSLTGRGMRGGRSPGP

>Myotis_lucifugus

-----MRGGRSPGP

>Condylura_cristata

MCLPRPGGVSLTGRGMRGGRWPGP

>Ceratotherium_simum_simum

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>Rattus_norvegicus

MCLPRPGGVSLTGRGMRGRRSLGP

HG0775 ENSG00000068001 HYAL2

>Homo_sapiens

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>Mustela_putorius_furo

-----MGFIKSPAGCPAGSSWCE-----

>Lipotes_vexillifer

-----MGFIKLPAGCPEGSSWCE-----

>Myotis_brandtii

-----MGFIKSPAGCPLGSSWRESLDWRGSNLRSGGLPYSS-----

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>Galeopterus_variegatus

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>Mus_musculus

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HG0776 ENSG00000082014 SMARCD3

>Homo_sapiens

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>Felis_catus

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>Rousettus_aegyptiacus

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>Dasypus_novemcinctus

MALGAAGVTGSGPGHRGGTG

>Ceratotherium_simum_simum

MALGAAGAVGSGPRHRGGTG

>Manis_javanica

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>Ictidomys_tridecemlineatus

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>Canis_lupus_familiaris

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>Myotis_davidii

----MPAQLPQGIPGLD

>Ceratotherium_simum_simum

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>Manis_javanica

----MLTQLPQGIPGLD

>Ictidomys_tridecemlineatus

----MPAQPPQGIPGLD

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>Homo_sapiens

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>Leptonychotes_weddellii

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>Rousettus_aegyptiacus

MRELGGGQTKMRIGTA

>Galeopterus_variegatus

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>Condylura_cristata

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>Ochotona_princeps

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>Octodon_degus

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>Homo_sapiens

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>Galeopterus_variegatus

MRRAGRPWRSGGGA---

>Erinaceus_europaeus

MRRAGRPWRSGGVV---

>Ochotona_princeps

MRRAGRPWESGGGAGPR

>Fukomys_damarensis

MRRAGRPWKSGGGAQRR

>Orycteropus_afer_afer

MRRAGRPWRGGDGALQR

>Homo_sapiens
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>Canis_lupus_familiaris
-----MPSLEQQQPG
>Dasypus_novemcinctus
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>Condylura_cristata
-----MPSLEQQQPG
>Ceratotherium_simum_simum
-----MPSLEQQQPG
>Manis_javanica
-----MPSLEQQQPG
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HG0781 ENSG00000100099 HPS4

>Homo_sapiens

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>Odobenus_rosmarus_divergens

MHLPDWAFLARSFL-KKFCREPEC--

>Myotis_lucifugus

MHLPYCTFLARS-LKGSFCREPES--

>Dasypus_novemcinctus

MHVPCGAFLERSFLKSLSCRQPY---

>Ceratotherium_simum_simum

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>Nannospalax_galili

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>Tupaia_chinensis

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HG0782 ENSG00000100368 CSF2RB

>Homo_sapiens

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>Panthera_tigris

MGLAWPPAEQAYRTPGH-----

>Myotis_davidii

MGLTWPPGTGEGHRVPGQ-----

>Oryctolagus_cuniculus

MGLAWPPPGREHKLPQG-----

>Ceratotherium_simum_simum

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>Manis_javanica

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>Tupaia_chinensis

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>Homo_sapiens
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>Felis_catus
MGVGDEEIIPPGHCPRAVRRPAAPARALSFLGSRMRAQRFPPPGSLRGTTKKVSSKMEFPAQGI
>Physeter_catodon
-----MEFPAQ--

>Pteropus_vampyrus
-----MEFPDQ--

>Condylura_cristata
-----MQLQAA--

>Ceratotherium_simum_simum
-----MRAQRLPSSGSFRGATEKDC-----

>Cricetulus_griseus
-----MEFPTQ--

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>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Orcinus_orca

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>Galeopterus_variegatus

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>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

MKGDPEKRRKLEAHWVV-----

>Dipodomys_ordii

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>Homo_sapiens

-----MSRPPITTNYR

>Rousettus_aegyptiacus

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>Galeopterus_variegatus

-----MNRPPISTNYR

>Oryctolagus_cuniculus

-----MNRPPITTSYR

>Equus_przewalskii

-----MNRPPVVTNYR

>Peromyscus_maniculatus_baird

-----MSRPPITTNYR

>Tupaia_chinensis

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>Equus_caballus

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>Marmota_marmota_marmota

MSSGCRSWD

>Orycteropus_afer_afer

MSSGCRSWD

>Homo_sapiens

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>Dasypus_novemcinctus

-----MLMATLKMAENLEPGT-----

>Galeopterus_variegatus

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>Oryctolagus_cuniculus

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>Equus_asinus

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>Manis_javanica

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>Peromyscus_maniculatus_baird

-----MAENLKPGTQETRAEA--EVR-----

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>Homo_sapiens

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>Myotis_lucifugus

MLSGELREGAG

>Erinaceus_europaeus

MLSGELREGAG

>Ochotona_princeps

MLSGELREGAG

>Equus_przewalskii

MLSGELREGAG

>Loxodonta_africana

MLSGELREGAG

>Rattus_norvegicus

MLSGELREGAG

HG0789 ENSG00000115355 CCDC88A

>Homo_sapiens

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>Ailuropoda_melanoleuca

MVSARGEASPACRW

>Pteropus_alecto

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>Sorex_araneus

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>Oryctolagus_cuniculus

MVSARGEASPACRW

>Ceratotherium_simum_simum

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>Ictidomys_tridecemlineatus

MVSARGEANPACRW

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>Ailuropoda_melanoieuca
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>Rousettus_aegyptiacus
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>Equus_asinus
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>Manis_javanica
----MLHPKP-----
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>Homo_sapiens
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>Mustela_putorius_furo
-----MWTLSPPLYR
>Physeter_catodon
-----MWTLSPPLHR
>Rhinolophus_ferrumequinum
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>Oryctolagus_cuniculus
-----MWTLSPPFHR
>Tupaia_chinensis
-----MWTLLSPPFYR

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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Oryctolagus_cuniculus

MRKLRPKEVTPLG

>Equus_asinus

MMKLRPKEVMPLG

>Chinchilla_lanigera

MRKLRPKEVIPFG

>Tupaia_chinensis

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>Trichechus_manatus_latirostr

MRKLSKEVMPLG

HG0792 ENSG00000132424 PNISR

>Homo_sapiens

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>Ursus_maritimus

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>Miniopterus_natalensis

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>Ochotona_princeps

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>Ceratotherium_simum_simum

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>Manis_javanica

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>Oryctolagus_cuniculus

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>Equus_caballus

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>Loxodonta_africana

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>Trichechus_manatus_latirostr

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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Myotis_brandtii

-----MLEHLIEKSFLAFLKIADNA--

>Oryctolagus_cuniculus

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>Equus_asinus

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>Heterocephalus_glaber

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>Homo_sapiens
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>Canis_lupus_familiaris
-----MAFRCQDNLKDR-----
>Lipotes_vexillifer
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>Erinaceus_europaeus
---MSMAFRRPDKLKDR-----
>Mus_musculus
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>Homo_sapiens	-----MSFSKCGM
VPLLY	
>Acinonyx_jubatus	-----MSFSKCGM
MPLPH	
>Myotis_lucifugus	-----MSFSKCGM
MPLPL	
>Dasypus_novemcinctus	
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VPLPY	
>Equus_asinus	-----MSFSKCGM
VPLSL	
>Loxodonta_africana	-----MSFSKCGM
IPLP-	
>Fukomys_damarensis	-----MSFAKCRM
VPLLC	

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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Rhinolophus_ferrumequinum
-----MLISGRTTGPS
>Galeopterus_variegatus
-----MLISRRVKGPS
>Condylura_cristata
-----MLISGRTEPS
>Manis_javanica
-----MLLSGRTKGPS
>Fukomys_darlingi
-----MLISGSKKRSS
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>Homo_sapiens
-----MSAAGSRGAAGTRLGAS-----
>Felis_catus
-----MSAAGSRGASGTRLGANQDAVVNHAQLLG-----
>Physeter_catodon
-----MSAGGSR-----
>Dasypus_novemcinctus
-----MSAAGSRGAVGARLGASWTVVVTHAQLLG-----
>Galeopterus_variegatus
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>Ceratotherium_simum_simum
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>Nannospalax_galili
-----MSAAGSRGAAGTRLGASWTARVHRAAFRLI-----

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>Homo_sapiens

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>Rhinolophus_ferrumequinum

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>Dasypus_novemcinctus

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>Manis_javanica

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>Chinchilla_lanigera

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HG0798.2 ENSG00000153707 PTPRD

>Homo_sapiens

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>Condylura_cristata

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>Homo_sapiens

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>Acinonyx_jubatus

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>Balaenoptera_acutorostrata_s

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>Rousettus_aegyptiacus

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>Equus_asinus

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>Mesocricetus_auratus

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>Homo_sapiens
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>Miniopterus_natalensis
-----MFSGRVSLGLSP

>Oryctolagus_cuniculus
-----MRRSPFLTTPPSAMFSGRVWLGGLPP

>Loxodonta_africana
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>Marmota_marmota_marmota
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>Trichechus_manatus_latirostr
-----MFSGQVSLGLPP

>Orycteropus_afer_afer
-----MFLGRVSLGLPP

>Homo_sapiens

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>Mustela_putorius_furo

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>Balaenoptera_acutorostrata_s

MFANHFEIAKCHIHGMHPAFI---LEFTPAWICH S----CICLRSLC

>Rhinolophus_ferrumequinum

MFANHFEIAKHHIQLSSLGNG-----

>Condylura_cristata

MFANHFEIAKHHIHGMYPAFS---LEFTRWLG LITVAPVFDLCVN---

>Equus_asinus

MFANHFEIAKRHIHGMHLAFI---LEITSAWFYHS----SVC LQSMY

>Cricetulus_griseus

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>Pteropus_vampyrus

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>Oryctolagus_cuniculus

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>Equus_asinus

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>Loxodonta_africana

MSLVPGATTAAA

>Ctenomys_sociabilis

MSLIPGATTAAA

>Trichechus_manatus_latirostr

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>Homo_sapiens

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>Pteropus_vampyrus

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>Erinaceus_europaeus

MLSRTWV L IVDYSWKQL ICLYVFV-----

>Equus_asinus

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>Nannospalax_galili

MLSRTWV I IAGYSWKQL IRSYVFV-----

>Trichechus_manatus_latirostr

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>Orycteropus_afer_afer

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>Homo_sapiens

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>Panthera_tigris

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>Myotis_davidii

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>Erinaceus_europaeus

-----MCFLNQANVSSMQITLKDNNRKEAN-----

>Ceratotherium_simum_simum

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>Dipodomys_ordii

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>Tupaia_chinensis

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>Homo_sapiens
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>Ailuropoda_melanoleuca
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GPGPKS-LP-AEDSRPPDTK
>Physeter_catodon
-----MFGHGGSSQMGTKGRFPRDGLGAQTSWSSGGLFWGGGW
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>Myotis_lucifugus
-----MFGHGG-----

>Galeopterus_variegatus
-----MQVRGLGS-----SGCLRGW-VPALLSLCPEAVCSDLTMFGHGGLSQRGTKGCFPGDGLGGQTSWSSASSFRVGAG
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>Oryctolagus_cuniculus
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>Trichechus_manatus_latirostr
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>Homo_sapiens

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>Orcinus_orca

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---PGRKVS AEDSQGTRETK

>Myotis_davidii

-----MQVRGLGSSCHPPSSCGLVPALS-VCP-GLCAQT-----

>Galeopterus_variegatus

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>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

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>Mustela_putorius_furo
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>Myotis_brandtii
MGSAVRIEVLKGPHFLE
>Condylura_cristata
MGAAAGVEMLKGPHFLK
>Manis_javanica
MGSAGVNMLKAPYFLK
>Loxodonta_africana
MGSAVRVEPRGPHFLK
>Mus_musculus
MGVAVGIEILKGPEFLK

>Homo_sapiens

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>Canis_lupus_familiaris

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>Rousettus_aegyptiacus

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>Dasypus_novemcinctus

-----MFLTECDLTGRLENIITFLNGAVWRNPKRNSIRAFWNISRKR

>Manis_javanica

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>Chinchilla_lanigera

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>Tupaia_chinensis

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>Homo_sapiens

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>Dasypus_novemcinctus

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>Oryctolagus_cuniculus

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HG0807.3 ENSG00000186487 MYT1L

>Homo_sapiens

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>Oryctolagus_cuniculus

MEKSRHREIK

>Equus_przewalskii

MEKSRHREIK

>Manis_javanica

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>Homo_sapiens

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>Miniopterus_natalensis

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>Equus_asinus

MPGPAPPTSSCWWW-

>Loxodonta_africana

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>Marmota_marmota_marmota

MPGLALRTSSCWWW

>Trichechus_manatus_latirostr

MPGPAPPTSSCWWW-

>Homo_sapiens
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>Dasypus_novemcinctus
-----MSFASQM
>Ochotona_princeps
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>Equus_caballus
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>Manis_javanica
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>Ictidomys_tridecemlineatus
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>Homo_sapiens
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>Canis_lupus_familiaris
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>Pteropus_vampyrus
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>Oryctolagus_cuniculus
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>Ceratotherium_simum_simum
MGARTRKTWPRAGSRF-----
>Manis_javanica
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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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-----MTLAWNLGPLKPTCSPL

>Equus_asinus

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HG0812 ENSG00000157368 IL34

>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Galeopterus_variegatus

MGLTATAPQLSSALPGR

>Equus_asinus

MGLTASAPRLPSALPGR

>Ctenomys_sociabilis

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>Tupaia_chinensis

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>Elephantulus_edwardii

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MK1GTQTTFAFDSR

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-----MEEPAAL
>Physeter_catodon
-----METPAAL
>Myotis_lucifugus
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>Equus_caballus
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>Manis_javanica
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>Peromyscus_maniculatus_baird
-----MDTPAAF

HG0815 ENSG00000163072 NOSTRIN

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>Ursus_maritimus
---MNVLGWDFLLRVFDD
>Rousettus_aegyptiacus
MNRMKVQGWDFLLRVFDD
>Equus_asinus
---MKVQGWDFLLGVFDD
>Manis_javanica
---MKVQGWDFLLGVFDD
>Nannospalax_galili
---MKVQDWDFLLGVFDD
>Tupaia_chinensis
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>Homo_sapiens
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>Mustela_putorius_furo
-----MFLADVSRSCP GAI

>Orcinus_orca
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>Rousettus_aegyptiacus
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>Dasypus_novemcinctus
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>Manis_javanica
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>Peromyscus_maniculatus_baird
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>Homo_sapiens

MTSSFRRLLPC

>Canis_lupus_familiaris

MTSSFRRLLPC

>Orcinus_orca

MTSSFRRLLPC

>Oryctolagus_cuniculus

MTSSFRRLLPC

>Ceratotherium_simum_simum

MTSSFRRLLPC

>Manis_javanica

MTSSFRRLLPC

>Rattus_norvegicus

MTSSFRRLLPC

>Homo_sapiens

-----MVRNKPHFSLGRLII-

>Mustela_putorius_furo

MFYLHASAFKSSLHY-SQGLHSSWSQARGQLCKNKPHFSLGKLIGV

>Miniopterus_natalensis

MKYVLLTCLSLSKFFALESEIALFLEPSMGPAVNKPHFSLGRLIGV

>Galeopterus_variegatus

-----MLRNKPHFSLGRLIAV

>Erinaceus_europaeus

-----MVRTTPHFSLGKRSGV

>Ceratotherium_simum_simum

-----MVRNKPHFSLGRLIGV

>Ictidomys_tridecemlineatus

-----MARMVRINSHFSLGRLIEV

HG0819 ENSG00000164188 RANBP3L

>Homo_sapiens

-----MKELSCVFNQMNWHLI

>Canis_lupus_familiaris

-----MKEELSCVFIQTNWHLYM

>Balaenoptera_acutorostrata_s

MCFEMKEELSCVFIQMNWHLYM

>Pteropus_vampyrus

MCFEMKEELSCVFIQMNWHL--

>Condylura_cristata

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>Equus_asinus

-----MKEELSCVFIQMNWHLYM

>Marmota_marmota_marmota

-----MNWHHFM

>Homo_sapiens
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>Acinonyx_jubatus
MLRSWGTLSGPLALPLGL-----
>Miniopterus_natalensis
MLRSWGTLSGPLALPLGL-----
>Equus_asinus
MLRSWGTLSGPFALPLGL-----
>Manis_javanica
MLRSWGTLLLEPLALPLGLGADKAGGSTEALLC
>Mus_musculus
MLRSWGTLSGPLVLPPGPQADTWGRSAGSLLC
>Tupaia_chinensis
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HG0821 ENSG00000165300 SLITRK5

>Homo_sapiens

MMTGPWRCETGR

>Mustela_putorius_furo

MMSGPWRCETGR

>Lipotes_vexillifer

MMSGPWRCETGR

>Pteropus_vampyrus

-MSGPWRCETGR

>Dasypus_novemcinctus

-MSGPWRCETGR

>Equus_caballus

MMSGPRRCETGR

>Ictidomys_tridecemlineatus

MMSGPWRCETGR

HG0822 ENSG00000166170 BAG5

>Homo_sapiens

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>Leptonychotes_weddellii

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>Balaenoptera_acutorostrata_s

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>Rousettus_aegyptiacus

MLGAQLRHRT

>Condylura_cristata

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>Equus_asinus

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>Oryctolagus_cuniculus

-----MAEDMPHSPAKKMKVFRSTRRL

>Mus_musculus

-----MAEKPLHVNKKTMETFQEFS--

>Trichechus_manatus_latirostr

-----MSEDRLHSSKKMKFFQEHS--

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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Condylura_cristata

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>Ochotona_princeps

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>Equus_przewalskii

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>Odobenus_rosmarus_divergens

MGGGLPESAGTMT

>Pteropus_alecto

MGGGLPEPAGTMT

>Galeopterus_variegatus

MGGGLPEPAGTMT

>Ceratotherium_simum_simum

MGGGLPEPAGTMT

>Loxodonta_africana

MGRGLPEPAGTMT

>Mus_musculus

MGGGLPEPAGTMT

>Homo_sapiens

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>Pteropus_alecto

MTLRRVVKKKREKRALGGEKGLTLWAPLKMARAASRAGETRTRTAL-----

>Dasypus_novemcinctus

MTLRRVVKKEK-PELSGVEKGLTLWASRKMARAAALRRAGETRPRTAL-----

>Equus_asinus

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>Manis_javanica

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>Loxodonta_africana

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>Homo_sapiens

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-----MCICEFAVEQLFIYSALCLC-----

>Orcinus_orca

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>Equus caballus

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>Trichechus_manatus_latiostr

-----MCICEFAVEQLFILPAPCLC-----

>Orycteropus afer afer

-----MCICEFTVEQLFIYPAPCLC-----

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>Homo_sapiens

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>Acinonyx_jubatus

MSWAARRCGHF

>Orcinus_orca

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>Ceratotherium_simum_simum

MSWAARRCGHF

>Trichechus_manatus_latirostr

MSWAAQRCDHF

>Orycteropus_afer_afer

MSWAAGRCGHF

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>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Physeter_catodon

MDSTCTLSSSELASVFR

>Miniopterus_natalensis

MDSTCTLSRTELASVFR

>Dasypus_novemcinctus

MDSTGTLGTSELAFVFR

>Manis_javanica

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>Ictidomys_tridecemlineatus

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>Homo_sapiens

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>Equus_przewalskii

-----MALEGGVQAEELWT-----

>Chinchilla_lanigera

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MQLSRFTSSNWLVL

>Condylura_cristata

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>Ochotona_princeps

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>Elephantulus_edwardii

MQLSRFVSNVSRVGR

>Mus_musculus

MQCSRHVSSSWLVGL

>Tupaia_chinensis

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>Homo_sapiens

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>Canis_lupus_familiaris

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>Fukomys_damarensis

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>Tupaia_chinensis

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>Homo_sapiens

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>Orcinus_orca

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>Ochotona_princeps

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>Equus_przewalskii

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>Mesocricetus_auratus

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>Tupaia_chinensis

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HG0833 ENSG00000176641 RNF152

>Homo_sapiens

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>Felis_catus

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>Ceratotherium_simum_simum

-----MNTPEYARCL

>Manis_javanica

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>Heterocephalus_glaber

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>Myotis_davidii

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>Ceratotherium_simum_simum

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>Manis_javanica

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>Erinaceus_europaeus

MKLPCLAAPLAAS

>Oryctolagus_cuniculus

MKLPCLAAPLAAS

>Loxodonta_africana

MKLPCRAPLAAS

>Mesocricetus_auratus

MRLPCLAAPLAAS

>Tupaia_chinensis

MKLPCLAAPLAAS

>Homo_sapiens

MSANMQNYRPGRS

>Mustela_putorius_furo

----MQNYRPGRS

>Lipotes_vexillifer

----MQNYRPGRS

>Rousettus_aegyptiacus

----MQNYRPGRS

>Condylura_cristata

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>Ceratotherium_simum_simum

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>Dipodomys_ordii

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>Homo_sapiens

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>Erinaceus_europaeus

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>Ceratotherium_simum_simum

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>Loxodonta_africana

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>Homo_sapiens
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>Myotis_lucifugus
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>Condylura_cristata
-----MVSPSSHRR-----
>Oryctolagus_cuniculus
-----MVSPSSRRRLCLLGASWRD-----
>Ceratotherium_simum_simum
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>Erinaceus_europaeus

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>Oryctolagus_cuniculus

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>Elephantulus_edwardii

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>Tupaia_chinensis

-----MARRRMRSASSATQVHK

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>Canis_lupus_familiaris
MITSLAASRGALAPWAGQ-----
>Balaenoptera_acutorostrata_s
MITGLAARRGALTPWAGQ-----
>Myotis_brandtii
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>Dasypus_novemcinctus
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>Equus_asinus
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>Manis_javanica
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HG0841 ENSG00000278259 MY019

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>Balaenoptera_acutorostrata_s

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>Myotis_brandtii

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>Galeopterus_variegatus

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>Ceratotherium_simum_simum

MTRWIALLP-VTQNP

>Chinchilla_lanigera

MTKWIALLP-GTQNP

>Homo_sapiens

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-----MKCAALPRTRRCGSQNTVRL

>Rousettus_aegyptiacus

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>Oryctolagus_cuniculus

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>Ictidomys_tridecemlineatus

-----MKCAALPRIRCCWNCNTVRL

>Orycteropus_afer_afer

-----MRAREDKARKCAALPRIRRCVGSRNTVRL

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>Homo_sapiens

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>Canis_lupus_familiaris

MSVEQLKSTDPHVP

>Oryctolagus_cuniculus

MSVEQLKSTDPHVP

>Equus_asinus

MNVEQLKSTDPHVP

>Peromyscus_maniculatus_baird

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>Tupaia_chinensis

MSVEQLKSTDPHVP

HG0844 ENSG00000091009 RBM27

>Homo_sapiens

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>Canis_lupus_familiaris

MPGGLGHREL

>Lipotes_vexillifer

MPGGLGHREL

>Dasypus_novemcinctus

MPGGLGHREL

>Galeopterus_variegatus

MPGGLGHREL

>Oryctolagus_cuniculus

MPGGLGHREL

>Homo_sapiens
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>Galeopterus_variegatus
-----MVALDFLHRLPVLDF
>Equus_asinus
-----MVALDCLPRLPVLDL
>Fukomys_darlingi
-----MVALDFLQRLTVLDF
>Orycteropus_afer_afer
-----MVVLDFLRLPILDF

>Homo_sapiens
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>Canis_lupus_familiaris
---MGKREKEDDPYDLEDLSAQK-----
>Pteropus_vampyrus
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>Condylura_cristata
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>Ceratotherium_simum_simum
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>Condylura_cristata

MALLPVLLASWGLGQ

>Equus_przewalskii

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>Trichechus_manatus_latirostr

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HG0848 ENSG00000111817 DSE

>Homo_sapiens

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>Pteropus_vampyrus

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MARRAR-----

>Ceratotherium_simum_simum

MARRAR-----

>Loxodonta_africana

MARRVR-----

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>Oryctolagus_cuniculus

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>Ctenomys_sociabilis

----MVTSAVGDFAVGRRGRPGPWEWFCAAIKIQGVEGTNRARHMQRSYLRNVSEKSENATEL

>Tupaia_chinensis

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>Canis_lupus_familiaris

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>Pteropus_vampyrus

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>Ceratotherium_simum_simum

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>Fukomys_damarensis

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>Tupaia_chinensis

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>Homo_sapiens

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>Leptonychotes_weddellii

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>Galeopterus_variegatus

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>Elephantulus_edwardii

MHSVDLT-----

>Equus_przewalskii

MHSVDLTQPGRTS

>Nannospalax_galili

MHSVDLTPPGRTS

>Homo_sapiens

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>Pteropus_vampyrus

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>Loxodonta_africana

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>Homo_sapiens

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>Felis_catus

----MYRACL THTQGCISKISKILL-----

>Oryctolagus_cuniculus

----MCTDCLTHTQGCTSKISK-----

>Ceratotherium_simum_simum

----MYRVCLTHTQGCISKISKMLLWRA-----

>Manis_javanica

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>Canis_lupus_familiaris
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>Pteropus_allecto
MGAASFGTAALREVGKQGASRKSSEQRVTRGRS-----SIC-----
>Ceratotherium_simum_simum
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>Manis_javanica
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>Mus_musculus
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>Pteropus_vampyrus

MAARWERNICVSRSFVRLA

>Equus_caballus

MAARWERNICVSRSFALRVA

>Manis_javanica

MAARWERIICVSRSFALRVA

>Cavia_porcellus

MAARGDRSICVSRSFALRV

HG0856 ENSG00000130055 GDPD2

>Homo_sapiens

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>Dasypus_novemcinctus

MGKAAQRNsspQAP

>Equus_asinus

MGKAAQRNssPRAP

>Ictidomys_tridecemlineatus

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>Trichechus_manatus_latirostr

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HG0857 ENSG00000130347 RTN4IP1

>Homo_sapiens

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>Myotis_lucifugus

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>Galeopterus_variegatus

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>Equus_asinus

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>Oryctolagus_cuniculus
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>Loxodonta_africana
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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Orcinus_orca
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>Rousettus_aegyptiacus
MRRGWTARSA-----
>Heterocephalus_glaber
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>Orycteropus_afer_afer
MRRGWTARSA-----

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>Oryctolagus_cuniculus

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MASPRSPAAPAIVSPGVA

>Manis_javanica

MASRLSPAAPAIVSPGVA

>Mesocricetus_auratus

MASPRSPAARAIVSPGAA

>Tupaia_chinensis

MASPLSPAARAIVSPGVA

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>Leptonychotes_weddellii

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>Myotis_lucifugus

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>Galeopterus_variegatus

MISGEEAPLLSAL-----ARGGSACAVGLSEAHAEEDRWLVRLDLV----

>Condylura_cristata

-----MRGGSACAVGSNEAHAAEARLLRVDHI-----

>Mus_musculus

MVSGNEGSFSV-----GACAVRGGSCALGWAKRTLRSFGVRGWCSESPRCH

>Homo_sapiens
-----MAPQGGEVGAA
>Leptonychotes_weddellii
-----MAPQGGEVGAA
>Orcinus_orca
-----MAPQGGEVGAA
>Oryctolagus_cuniculus
-----MTLGSQPPATSMAPQGGEVGAA
>Ceratotherium_simum_simum
MRARGQRGCPHTLPVAPLRAANPLTPHPAPGHRAPDPGLGAPSSASGHRSLRPSGPCAPVPGLQVPLGPQPPASPMAPQGGEVGAA
>Manis_javanica
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>Homo_sapiens

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>Ailuropoda_melanoleuca

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>Physeter_catodon

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>Ceratotherium_simum_simum

MAAGCGEGDALKAGVSPLPVL

>Marmota_monax

MAAGCGEGDASKAAVFFSFVL

>Tupaia_chinensis

MAAGCGEGSPLKAAVSRFRVL

HG0864 ENSG00000134533 RERG

>Homo_sapiens

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>Ailuropoda_melano-leuca

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>Myotis_davidii

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>Dasypus_novemcinctus

MVNPKAGTRKICSALWF---

>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

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HG0865 ENSG00000135540 NHL1

>Homo_sapiens

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>Mustela_putorius_furo

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>Miniopterus_natalensis

MPGRGVGLQVGMLGAHQRVGVPWFCSLQSPDKCS

>Oryctolagus_cuniculus

MPGRGAGLQFGVLGTPWSIGVPWFCSLQSTDKCA

>Manis_javanica

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>Cavia_porcellus

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>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Miniopterus_natalensis

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>Oryctolagus_cuniculus

MRRNSLGVQQTMIK

>Equus_asinus

MRKNSLGVHQTKLK

>Peromyscus_maniculatus_baird

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HG0867 ENSG00000137203 TFAP2A

>Homo_sapiens

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>Pteropus_vampyrus

MDQSRAPALGGASAR

>Oryctolagus_cuniculus

MDPSEAPALRGASAP

>Elephantulus_edwardii

MEPSGAPALGGASAP

>Tupaia_chinensis

MDPSEVPALQGASAW

>Trichechus_manatus_latirostr

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>Ursus_maritimus
-----MEKSQSEPGCVVEEGRAAAGK-EAGARAPCSLPGSPGPAGAPRPRPRAL
>Rousettus_aegyptiacus
-----MEKSQSEPGCGVHC GGGARRDQEGG-----
>Equus_caballus
-----MEKSQSEPRGAVEEGRAAAE-----PVARRCRLPGSPGPAGALWPRCL--
>Manis_javanica
-----MEKSLSSEPGCAVEEEPSAASTGKAARARQCRLPGSPGPAGAPGPLYL--
>Microtus_ochrogaster
-----MEKSQSELGCTVEEGRAAAGA-TGP-----
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HG0869 ENSG00000139910 NOVA1

>Homo_sapiens

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>Ailuropoda_melanoleuca

MSYNGTGIASSFALESS

>Physeter_catodon

MSFNGTGIASSFALESS

>Rousettus_aegyptiacus

MSYNGTGIASSFALESS

>Manis_javanica

MSYNGTGIASSFALESS

>Cavia_porcellus

MSYNGTGIASSFALESS

>Homo_sapiens
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>Balaenoptera_acutorostrata_s
MALGGTRRT-----
>Pteropus_vampyrus
MELGSTRRT-----
>Galeopterus_variegatus
MALGSTRKTWKYMRAQNYRRVFQKKFMRNN---
>Ceratotherium_simum_simum
MALGSTRRTCKEYLRAQSYKGCQQKNLWETIDQKH
>Marmota_marmota_marmota
MALGSTRSS-----

HG0871 ENSG00000141127 PRPSAP2

>Homo_sapiens

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>Ursus_maritimus

MSL-----LMALPFFCVLIQEEFCCQRIKGGCP

>Rousettus_aegyptiacus

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>Oryctolagus_cuniculus

-----MALPFFCVLIQEEFCCQRLKGGCP

>Equus_caballus

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>Mesocricetus_auratus

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>Homo_sapiens

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>Ursus_maritimus

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>Physeter_catodon

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>Cynopterus_sphinx

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>Dasypus_novemcinctus

-----MSSLSI-----

>Ceratotherium_simum_simum

-----MSSLSIQICYFG

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>Homo_sapiens

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>Rousettus_aegyptiacus

MLGSYALLLGDFL-----

>Galeopterus_variegatus

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>Manis_javanica

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>Ictidomys_tridecemlineatus

MLGSYALLLGVFLFKTKESSHFLCAACSSVCVYTIGSSTSRD

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>Homo_sapiens

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>Lipotes_vexillifer

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>Condylura_cristata

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>Oryctolagus_cuniculus

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>Ceratotherium_simum_simum

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>Mus_musculus

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>Condylura_cristata

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>Ceratotherium_simum_simum

MGDTPATDAGRQDLHP

>Loxodonta_africana

MGGTPATDAGRDLHL

>Orycteropus_afer_afer

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>Homo_sapiens

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>Dasypus_novemcinctus

-MAAPIRNSR-----

>Equus_caballus

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>Manis_javanica

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>Chinchilla_lanigera

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HG0877 ENSG00000146426 TIAM2

>Homo_sapiens

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>Felis_catus

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>Physeter_catodon

-----MLPCSQDPVKSTDH

>Pteropus_vampyrus

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>Cavia_porcellus

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>Homo_sapiens
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>Felis_catus
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MAAVAGPVVEKVSDETGLC-----
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>Equus_asinus
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HG0879 ENSG00000147145 LPAR4

>Homo_sapiens

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>Loxodonta_africana

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>Cricetulus_griseus

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>Trichechus_manatus_latirostr

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>Myotis_lucifugus

MGSAAGSPGARSSRRGS

>Equus_asinus

MGSAAGSPSARSCRRGS

>Ictidomys_tridecemlineatus

MGSAAGSPSARSSRRGP

>Orycteropus_afer_afer

MGSAAGSPSAHSSRRGL

>Homo_sapiens
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-----MAVGADSLRESLEEQRERSPGRLVAVLLYDAKDTGV
>Rhinolophus_ferrumequinum
-----MAVGADSLRESTEEQREKNSEVSSSELKRT-----
>Oryctolagus_cuniculus
-----MVGADSRQSRKRAKRKSPEMPEGAPTR-----
>Equus_caballus
MGREEGDFVFI L VFCKPPLARLPTCRHGNLKKVL IHWSEAENSVAFVCGECVRKSKEEQDSPVEFL I SMAVGADSFRESTKEQKEKNPEMSSYSALRR-----
>Manis_javanica
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>Homo_sapiens
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>Odobenus_rosmarus_divergens
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>Oryctolagus_cuniculus
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>Manis_javanica
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SGIYVVAVKPTHWACAVGVSGKRD
>Loxodonta_africana
-----MFHGNL~~R~~TRSPYGLDSQDGG~~S~~-----

>Fukomys_damarensis
-----MFPA~~N~~I-----

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>Homo_sapiens

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>Mustela_putorius_furo

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>Manis_javanica

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>Equus_asinus

MLGEAAWCFLS

>Microtus_ochrogaster

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>Tupaia_chinensis

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>Oryctolagus_cuniculus

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>Manis_javanica

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>Balaenoptera_acutorostrata_s

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>Ceratotherium_simum_simum

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>Tupaia_chinensis

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>Equus_asinus

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>Galeopterus_variegatus

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>Ochotona_princeps

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>Mus_musculus

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>Homo_sapiens
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>Pteropus_lecto
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>Heterocephalus_glaber
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>Orcinus_orca

-----MFCTRKNQQL

>Oryctolagus_cuniculus

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>Equus_caballus

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>Canis_lupus_familiaris

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>Rousettus_aegyptiacus

MADTMSRRRAGCP

>Galeopterus_variegatus

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>Oryctolagus_cuniculus

MADTMSRCRAGCP

>Ictidomys_tridecemlineatus

MADTMSRRRAGWP

HG0890 ENSG00000165813

>Homo_sapiens

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>Equus_caballus

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>Callospermophilus_lateralis

MERLAPEPELQRPR

>Trichechus_manatus_latirostr

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>Orycteropus_afer_afer

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>Tupaia_chinensis

-----MKQLCKGLKCLPESSIY-----

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>Rousettus_aegyptiacus
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>Loxodonta_africana
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>Homo_sapiens
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>Pteropus_vampyrus
MRVTSAPSARPPREAGPAE-----
>Oryctolagus_cuniculus
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>Homo_sapiens

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>Physeter_catodon

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>Rousettus_aegyptiacus

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>Equus_asinus

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>Heterocephalus_glaber

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HG0894.2 ENSG00000069424 KCNAB2

>Homo_sapiens

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>Ursus_maritimus

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>Rousettus_aegyptiacus

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>Equus_caballus

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>Cricetulus_griseus

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>Homo_sapiens

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>Lipotes_vexillifer

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>Manis_javanica

MNLRCPWPKRLEQLVS--

>Trichechus_manatus_latirostr

MNLRCPWPKRLEQLFSKK

>Homo_sapiens
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>Fukomys_damarensis
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>Trichechus_manatus_latirostr
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>Mustela_putorius_furo
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>Equus_caballus
MPCHCNWEKGKPDF-----
>Manis_javanica
MPCHCHREGGKPDF-----
>Tupaia_chinensis
MPRRCSGEGGKPDF-----


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>Homo_sapiens
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>Ailuropoda_melanoleuca
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>Balaenoptera_acutorostrata_s
MKSCCQACLEAP-----
>Manis_javanica
MKSCFQACPVPLQVSTDLS--AVCMGRLTLARSRPWGQLLFCEGTRGFVQRV-----
>Loxodonta_africana
MKSCFQACPESQVTTDFSAAAVHTGCLTYTNHPSRVWLIF-----
>Cavia_porcellus
MKSCVQVCWEPPPVTELSAAAVCTRHPKSVRSHPLRVQRMTF-----
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>Orcinus_orca
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>Pteropus_vampyrus
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>Elephantulus_edwardii
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>Equus_asinus
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>Trichechus_manatus_latirostr
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HG0900 ENSG00000173517 PEAK1

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>Mustela_putorius_furo

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>Pteropus_vampyrus

MVVAAAACSPLRYLPKLELML-----

>Dasypus_novemcinctus

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>Loxodonta_africana

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>Ictidomys_tridecemlineatus

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>Canis_lupus_familiaris
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>Myotis_davidii
-----MPTP----DSHGMHWQQGTSRAWVTEEGA
>Oryctolagus_cuniculus
-----MVAKWSSL----DSPAAGDPLDNV-----
>Equus_przewalskii
-----MVTKRPTL----DSHGMH-----
>Manis_javanica
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MASVLLLLWMSTAT

>Dasypus_novemcinctus

MASILLPFWMATT

>Condylura_cristata

MASVLLLFWMATTK

>Equus_caballus

MALTLLLFWMATT

>Jaculus_jaculus

MASVLLLFWMATT

HG0903 ENSG00000180616 SSTR2

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>Miniopterus_natalensis

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>Oryctolagus_cuniculus

MSQWILGLQGPLR

>Ceratotherium_simum_simum

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>Nannospalax_galili

MSQWILGLQGPLR

>Tupaia_chinensis

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>Homo_sapiens

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>Canis_lupus_familiaris

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>Ceratotherium_simum_simum

MYLIKGPVFVFLGSLLSSGNLEV-----

>Manis_javanica

MYLIKGPVFVFLGSLLSSGNLEV-----

>Chinchilla_lanigera

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>Canis_lupus_familiaris

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>Balaenoptera_acutorostrata_s

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>Equus_przewalskii

MVAPASLRVGGPAPLGAL

>Marmota_marmota_marmota

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>Tupaia_chinensis

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HG0907 ENSG00000186862 PDZD7

>Homo_sapiens

MELEARRAGLSRASRFLLDL

>Felis_catus

MEPGARGALCSRASRFLLDL

>Orcinus_orca

MEPGARGALLSRASRFPLDL

>Myotis_lucifugus

MEPGARRALLPRASRFLLDL

>Ceratotherium_simum_simum

MELGARRAFLLRASRFLLDL

>Ictidomys_tridecemlineatus

MELRALGAGLWRVGRFLLDL

HG0908.1 ENSG00000188554 NBR1

>Homo_sapiens

MHCGTKGLGHTVPWKL

>Felis_catus

MHCGSKGLRHSVPWKL

>Pteropus_alecto

MHCGSKGLRHCVPWKL

>Oryctolagus_cuniculus

MHCVTKGLRHSVPWKL

>Ceratotherium_simum_simum

MHCGSKGLRHSVPWKL

>Microtus_ochrogaster

MHCGTKGLHHSIPWKL

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>Homo_sapiens
MERNIQYQSGHNSHGNPVDRLTSAGLYMSTVMDWSVVMFSYLESRD
>Felis_catus
-----MDWSV-RFSHLESGE
>Rousettus_aegyptiacus
-----MDWSL-MFSYLESGE
>Oryctolagus_cuniculus
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>Ceratotherium_simum_simum
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HG0909 ENSG00000189079 ARID2

>Homo_sapiens

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>Rousettus_aegyptiacus

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>Erinaceus_europaeus

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>Ceratotherium_simum_simum

MTEPRRRRPRNGLRALVGSAGSGGRF-----

>Manis_javanica

MTEPRRRRPRNGLRALVGGAGSGGRFWTAIGAF

>Heterocephalus_glaber

MTEPRRRRPRNGLRALVGSAGRGGRF-----

>Homo_sapiens

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>Ailuropoda_melanoieuca

MLLMNPKSRLCDT-----

>Physeter_catodon

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>Oryctolagus_cuniculus

MLLIVPKSRAVFDTPKHRAAVFWVGKGLTGLSETCVPQRRLSTGTT----

>Equus_asinus

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>Marmota_marmota_marmota

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>Homo_sapiens

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>Felis_catus

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>Oryctolagus_cuniculus

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>Equus_przewalskii

MPRGAAVGLRGAAPAALGGISGLQLDRSCC

>Rattus_norvegicus

MPRVAAGGLREAGPAALEGEIKGLQLARSCC

>Homo_sapiens
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>Mustela_putorius_furo
-----MREG--GKEKENEKERMPEGPRLCRESQLDATV-----
>Tursiops_truncatus
-----MPEGPCLCRESQLDAKNSARPR
>Rousettus_abyssiacus
MKGGRKEEGEREKENEGGRKEEKENEKERMPEGPCLC-----
>Manis_javanica
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>Nannospalax_galili
-----MPEGPCLCWESQLDATVSA---

HG0913.1 ENSG00000204599 TRIM39

>Homo_sapiens

MRLSLKFALQLRHKE

>Acinonyx_jubatus

MRTSLKFALLLRHKE

>Physeter_catodon

MRTALKFALLLRHEE

>Equus_przewalskii

MRTSLKFALLLRHKE

>Loxodonta_africana

MRTSLEFALPLKHEE

>Ictidomys_tridecemlineatus

MRTSLKFVLLLRHEE

>Homo_sapiens
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>Oryctolagus_cuniculus
MPLPEIWREKMETRGGRSFGRRSGE-GRQVGPGTAMDAKSGRP-----
>Equus_caballus
-----METFGGETELWTTLRR-GSQSGT-----PDSGRNKMRTSLKFALLRLKE
>Manis_javanica
-----METGVGLSCGARSGE-GRRWDPGQW-----
>Loxodonta_africana
-----METGVGQSCGQRSGE-GCKMGPWTVVETQ-----

HG0914 ENSG00000227877 MRLN

>Homo_sapiens

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>Myotis_davidii

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>Ceratotherium_simum_simum

MVFFTEERDHLDFGLRFLNA-----

>Nannospalax_galili

----MGKRDHSDFGLGLLNP-----

>Homo_sapiens

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>Felis_catus

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>Balaenoptera_acutorostrata_s

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>Equus_caballus

-----MRLQNEFPGFTRRKSGAPGQKAEVRGLNWRENGFVVRDLRQRWLFKVHCPG-----

>Manis_javanica

-----MP SCL---GGGHFQKHRFLRPRNEFPGFGRRKSDAPGQKAEVRRLLNWRENGLLVREL RQPAVALGGPVSWGYHKDSFSSGS

>Peromyscus_maniculatus_baird

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>Homo_sapiens
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>Odobenus_rosmarus_divergens
MIHSAYASVENLWLDIPVGLGIQILGS-----
>Loxodonta_africana
MIHSAYASVENLWLDIPVGPGIQILGS-----
>Octodon_degus
MIHSAYAAVENLWLDIPVGPGIRILGYKQKLTLGDDFFYSLTHTLSRSFLFFFFVAVGGERTKQKTNKNQHPHPFTSNF
>Orycteropus_afer_afer
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HG0917 ENSG00000042980 ADAM28

>Homo_sapiens

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>Ailuropoda_melano leuca

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>Orcinus_orca

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>Equus_asinus

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>Mus_musculus

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>Homo_sapiens

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>Pteropus_vampyrus

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>Ceratotherium_simum_simum

MDLLLLPPRGYLERAGGA

>Manis_javanica

MGLLPLSPLGHLERAGGA

>Cavia_porcellus

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HG0919 ENSG00000051009 FAM160A2

>Homo_sapiens

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>Ursus_maritimus

MASYWLLQTG

>Sorex_araneus

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>Microtus_ochrogaster

MASYWLLQTG

>Orycteropus_afer_afer

MASYWLLQTG

HG0920 ENSG00000051382 PIK3CB

>Homo_sapiens

---MGATILRAPWL

>Canis_lupus_familiaris

---MGAVILRAPWL

>Pteropus_alecto

MTEMGATILRAPWL

>Condylura_cristata

---MGATILRAPWL

>Marmota_marmota_marmota

---MGTIILRAPWL

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>Leptonychotes_weddellii

MRKLRPREAHSPTARRSRIGNQTQVCWTPEPVPLTTG--

>Lipotes_vexillifer

MRKLPPGAHSLTARSSRIGNQTQVCSTPEPVPLTTG--

>Loxodonta_africana

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>Microtus_ochrogaster

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HG0922 ENSG00000079841 RIMS1

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Rousettus_aegyptiacus

----MKDWVRLPGSAAAAA---AAPPPA--AARRAPL

>Condylura_cristata

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>Nannospalax_galili

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>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Myotis_brandtii

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>Dasypus_novemcinctus

-----MSEFRCLLQHSLAKAIQQW

>Peromyscus_maniculatus_baird

-----ML--AQLRQPV-PPASAEVLAGRRLHHS LAKGTQHW

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Galeopterus_variegatus

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>Ceratotherium_simum_simum

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>Orycteropus_afer_afer

MTAAHRKQHCGRSAGAEETCLSVRCWRYPGLS-----

HG0925 ENSG00000088766 CRLS1

>Homo_sapiens

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>Pteropus_vampyrus

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>Erinaceus_europaeus

-----MEEAELPPDCRNSMEQRVACVPDC

>Manis_javanica

-----MVSQKRRADV RPWR-LQATCISGVCRGLKTGMEAAEVL RACGKSMERRSAGVPGC

>Marmota_marmota_marmota

-----MEASAAVLPRHFGVSM EKRLAGDPSC

HG0926 ENSG00000095397 WHRN

>Homo_sapiens

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>Balaenoptera_acutorostrata_s

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>Pteropus_vampyrus

MPRTPCRTAARLHRLQFGG-VWD

>Condylura_cristata

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>Equus_asinus

MPRTPCRTPARLHQLRFGG-LWD

HG0927 ENSG00000095951 HIVEP1

>Homo_sapiens

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>Mustela_putorius_furo

MAACGRHLPLLGAARERPELRSCEASST----

>Rousettus_aegyptiacus

MAACGRHLPLLGAARERPELRSCELSSKWIN-

>Marmota_monax

MAACGSHLPLLGALTAREQPELRSCDPSSTWIN-

>Tupaia_chinensis

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HG0928 ENSG00000102057 KCND1

>Homo_sapiens

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>Mustela_putorius_furo

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>Oryctolagus_cuniculus

MPQSPRQPCQGVPGPFSIPKNSGECDSRSRVGWPL

>Manis_javanica

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>Heterocephalus_glaber

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HG0929 ENSG00000102239 BRS3

>Homo_sapiens

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>Galeopterus_variegatus

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>Condylura_cristata

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>Oryctolagus_cuniculus

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>Ictidomys_tridecemlineatus

-----MSWIFFPFCSVLFS--

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>Balaenoptera_acutorostrata_s

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>Pteropus_vampyrus

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>Oryctolagus_cuniculus

MQRGREKRIEENSPEGQSRVLRCSQCRAHTDNRK--

>Equus_asinus

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HG0931 ENSG00000104951 IL411

>Homo_sapiens

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>Canis_lupus_familiaris

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>Pteropus_alecto

MCFLASPDKWPLTFLSVN-----

>Equus_przewalskii

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>Tupaia_chinensis

MHFLASPDWPLLKFLFIN-----

HG0932 ENSG00000105997 HOXA3

>Homo_sapiens

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>Felis_catus

MLRVGAHPAPRGPGRAAKPGRGPEPEPEPKPEPEPELAALIRS

>Pteropus_vampyrus

MLRVGAHPALRGPGRAAEPGRGPEPEP-----ALAALIRS

>Ceratotherium_simum_simum

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HG0933 ENSG00000106330 MOSPD3

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Rousettus_aegyptiacus

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>Galeopterus_variegatus

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>Fukomys_damarensis

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>Homo_sapiens

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>Tursiops_truncatus

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>Rousettus_aegyptiacus

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>Ceratotherium_simum_simum

MSGAGVPRTTAGLGL

>Ictidomys_tridecemlineatus

MSGAGVPRTPAGLGL

>Homo_sapiens
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>Eptesicus_fuscus
-----MGSRPRPYRPLQIKI-----
>Condylura_cristata
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>Oryctolagus_cuniculus
-----MGSRPRPYRPLQIKI-----
>Ictidomys_tridecemlineatus
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HG0936 ENSG00000108799 EZH1

>Homo_sapiens

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>Canis_lupus_familiaris

MEAEHLFCLCVLPFL

>Pteropus_vampyrus

MEAEHLFCLYVFPFL

>Galeopterus_variegatus

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>Ceratotherium_simum_simum

MEAEHLFCLCVLPFL

HG0937 ENSG00000109846 CRYAB

>Homo_sapiens

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>Ochotona_princeps

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>Equus_asinus

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>Marmota_monax

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>Homo_sapiens

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>Canis_lupus_familiaris

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>Myotis_lucifugus

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>Galeopterus_variegatus

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>Mesocricetus_auratus

-----MGSQGA WREV

>Homo_sapiens

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>Miniopterus_natalensis

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>Trichechus_manatus_latirostr

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>Homo_sapiens
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>Balaenoptera_acutorostrata_s
-----MGWTEERAHTSPHPTLSIWL-----
>Rousettus_aegyptiacus
-----MGWTEERAHTSPHLLPSGCNCQSQQTAVEEGRKPEGAKGEK---ELAGFPHPTESV-----TEHTDTGLLSCPR
>Equus_asinus
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>Chinchilla_lanigera
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HG0941 ENSG00000116285 ERRF11

>Homo_sapiens

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>Mustela_putorius_furo

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>Rhinolophus_ferrumequinum

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>Equus_asinus

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>Homo_sapiens

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>Myotis_brandtii

MEDAETRCHGSRVPAA-----

>Oryctolagus_cuniculus

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>Homo_sapiens
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>Balaenoptera_acutorostrata_s
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>Rousettus_aegyptiacus
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>Oryctolagus_cuniculus
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>Heterocephalus_glaber
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HG0944 ENSG00000120833 SOCS2

>Homo_sapiens

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>Ursus_maritimus

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>Miniopterus_natalensis

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>Equus_przewalskii

MVREHR-CGGVPGIFHVCVPPTQP-----

>Chinchilla_lanigera

MVQEHL-DGGVPGIFHFSVSPARPQGSSWD-----

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>Homo_sapiens

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>Myotis_lucifugus

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>Equus_przewalskii

MIAIAGENLIVYQLGQKMEFYGRGFLEA-----

>Manis_javanica

MIAIAGESLVVYQLGQKMEFHGRGFLEA-----

HG0946.1 ENSG00000127324 TSPAN8

>Homo_sapiens

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>Mustela_putorius_furo

MTSKRTYSPDSPCDI

>Pteropus_alecto

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>Dasypus_novemcinctus

MTSKRTYPPRDSPCDI

>Heterocephalus_glaber

MTSKRTYMPGDSLCDI

>Homo_sapiens
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>Rousettus_aegyptiacus
MCGLIFYPL-----
>Galeopterus_variegatus
MCGLIFYPL-----
>Ceratotherium_simum_simum
MRGLIFYPL-----
>Manis_javanica
MCWLIFYLL-----

>Homo_sapiens

-MTKREVARAEAPESGCGWDHLQYRK-----

>Physeter_catodon

-MTKTLVAGAEVPESGWLGLCLSYRKSIIYFLFFQMNEGRGYRVD

>Equus_asinus

-MTKRLVAGGEVRESGWWDY---LKSSTFISSFP-KGGE-----

>Loxodonta_africana

-MTKRLVAGAEVSESGLVGIFSVTGSKTFISSFP-KEGRGNRVD

>Nannospalax_galili

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HG0948 ENSG00000129595 EPB41L4A

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Miniopterus_natalensis

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>Equus_asinus

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>Marmota_marmota_marmota

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>Homo_sapiens
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>Canis_lupus_familiaris
-----MIPLPHHLC A A W L S
>Physeter_catodon
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>Myotis_lucifugus
-----MMPLPHHLC A A W L S
>Equus_asinus
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HG0950 ENSG00000132964 CDK8

>Homo_sapiens

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>Felis_catus

MSPALLRGLLLLLPHQSGWCCGRRRA

>Oryctolagus_cuniculus

MSPALSRGLLLLLPHPSRWCCGRRRA

>Ceratotherium_simum_simum

MSPALSRGLLLLRLPHQSGWCCGRRV

>Mus_musculus

MSPAPARGLL-PSPREAGWCCGRRV

HG0951 ENSG00000134061 CD180

>Homo_sapiens

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>Galeopterus_variegatus

MLSRQQYFLFQDHPLSTSLAAKLQGPL--

>Ceratotherium_simum_simum

MLSHQQHFLF-----

>Trichechus_manatus_latirostr

MRNSQQHFLF-----

HG0952 ENSG00000134453 RBM17

>Homo_sapiens

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>Canis_lupus_familiaris

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>Dasypus_novemcinctus

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>Condylura_cristata

MGRVGRAGRH

>Equus_caballus

MGRVGRAGRH

HG0953 ENSG00000134815 DHX34

>Homo_sapiens

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>Orcinus_orca

MNLCPSQRSIQES

>Cynopterus_sphinx

MNLCPSQRSIQDS

>Ceratotherium_simum_simum

MNLCPSQRSIQES

>Heterocephalus_glaber

MNLCPSLRSLQES

HG0954 ENSG00000134874 DZIP1

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Physeter_catodon

MVGPSRDSPVD-----

>Myotis_brandtii

MVGPSQGSLVD-----

>Ceratotherium_simum_simum

MVGPSRDSPVD-----

HG0955 ENSG00000134982 APC

>Homo_sapiens

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>Ceratotherium_simum_simum

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MLFPGSAVGCR

>Orycteropus_afer_afer

MLFPGNAVGCW

HG0956 ENSG00000136235 GPNMB

>Homo_sapiens
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>Canis_lupus_familiaris
MICPKAPLYLIKIRSGAQRPEEHCCS-----
>Dasypus_novemcinctus
MTCPEA-----
>Equus_asinus
MICPEA-QSFIKIRSGAQRPEEHG-----
>Manis_javanica
MICPKALN-----

>Homo_sapiens
MTRRSMVVRLGGLGARGRKPLLAKPRGGWQKVPHLGSLLLANRGSERRLYFDFSLQIRFFYMSGEDSCYQGGHTTFF
>Myotis_lucifugus
-----MSREDSCK-----
>Equus_asinus
-----MSGEDSCYK-----
>Manis_javanica
-----MSGEDSCFKER-----
>Ictidomys_tridecemlineatus
-----MSGEDRCYK-----

HG0958 ENSG00000137497 NUMA1

>Homo_sapiens

MNNHSCPFAPSLGGN-----

>Felis_catus

MNKHSCPFAPSLGRG-----

>Equus_asinus

MNKHSCPFAPSLGRG-----

>Cavia_porcellus

MNKHSCPFVPSSLGWKLIRIQPIRLSVS

>Tupaia_chinensis

MNKHSCPFASSLLKA-HSKARPLRIALP

>Homo_sapiens

-----MLPNDVFNVSYPALALFF-----IDPNSTFLL

>Leptonychotes_weddellii

-----MLPNDDFVNSYPALALFLFFSFLIDPNSTFLL

>Lipotes_vexillifer

MYRYHYRLSSGLEF--SICLDFLKVKSSNDFVNSYPALALFFSFHRP-----

>Ochotona_princeps

MGRFHYNCLLGLSSIFWVWRKSDQAMLPNVDFVNSSPLALFPPYILTLPF-----

>Trichechus_manatus_latirostr

-----MLPKDNFINSHLLSLSPFFSFIDNNSTFLL

>Homo_sapiens
MISLSLLSYLRAGSQKESDGATCCPLLCRY-----
>Myotis_lucifugus
MTYLSLLSYLRAGN-----
>Equus_przewalskii
MLYLSLLFYLRRTGS-----
>Manis_javanica
MVGLSLLSYVRAGNQAG-DRATCCSLFSEIKEEPEA---VSWTSCEYQKIEFGAVKRRPGDMVLTGASLELNQPSPGNKYVMASGPPQ
>Mus_musculus
MVCLSSLPLRTGSQKVSDRATCCSLLCIGLTGAWVSSLDGW-----

>Homo_sapiens
MARLEIAEGRREGEKWIPVLRSGLEGEVCKESALWKQPVNPAQGT-HSPDTHETLSVGTLEHLS
>Canis_lupus_familiaris
-----MASVSLYPHEEPVLWKQPANPAQSAGHSGTHETISADTLEYL-
>Myotis_brandtii
-----MLSEADHWRPVVLWKQPANPAQGTGLGPGTHETVSTDITLEHL-
>Oryctolagus_cuniculus
-----MGTLEHLP
>Nannospalax_galili
-----MLKHLS

>Homo_sapiens
-----MVSRLRGRRTWVRMRRLPPIPAWSQGGKMPGFVSLLVVHAADAWVAQR---LSTPYFSLFLSIPRCSFPRRSIDRTCSSLDDSE
GSSSISPSTPFILQMRLLKPRAR-----
>Physeter_catodon
-----MHVEISPTWRRGKWVPEFVSVLGTRARHAWVIQR---STMPNL-----

>Myotis_brandtii
-----MWRWPPPGNGGKGYLEHLFVGPA LGMPGKPR-----

>Ceratotherium_simum_simum
-----MWRFSPPGGEGKGCLDCVSVCGTHAGAAGI-----

>Ictidomys_tridecemlineatus
MCLLRWATSIVNPLPPGTAVVWCQRSPPGRTWVRCA--WRLLPPSRSERGVPGFVSLFVGSRLRCHLCRTPVSHSSPEH----LRHC-LSGRITALACSGFP---
-----DLRLRTRRAHWVLLFLWCW

HG0962.2 ENSG00000143319 ISG20L2

>Homo_sapiens

-----MLDSRIQQRMSPTSSFHP

>Dasypus_novemcinctus

-----MLVLGIQQRMIPTSSFHP

>Manis_javanica

-----MLVRGIQQRMSPLSSFHR

>Dipodomys_ordii

MQVPESLWTPRFSPDHMLDNGIQQRMSSSSFFHT

>Tupaia_chinensis

-----MLDAEIQQRMSPPASIHHP

>Homo_sapiens
MSESELGLSPARSQLLLVTQGRGSRERGSPSPACRIRG---C-----
--

>Myotis_lucifugus
MSESELGLSPARSQPLPVQTQPGSREPREAASGTHHPRR-----PELRGR-----
--

>Manis_javanica
MSESELRLYPTRSQLLRVQTQGRGSRERASPSRGRGTPG---QQSAPACRAPSPV-----AAGEGPGL-----
--

>Marmota_marmota_marmota
MSESELGLSPARSQQLRFRTSEGTRSEAHDPASAGRTPRLL---SAPACGALGVP-----AAGEGSLQNIRRVCGLLWLPGSRAASPRDALSSRTTAERD
RD

>Tupaia_chinensis
MSESKLGLYPARSQAFFPVQTQGRGSREREGSPTPGGLDSRAVGCSRVSRSRNPWNREIWTALQGYPRTPALLVSPVSC-----SESRGDALNPGTAE---
--

HG0964 ENSG00000145246 ATP10D

>Homo_sapiens
MAGVEAQPFTLRICA-----
>Mustela_putorius_furo
MAGVEA-----
>Balaeoptera_acutorostrata_s
MAGIEA-----
>Myotis_brandtii
MAGVEAPPVSALRICAWLLSCFLGLGIVVL
>Ceratotherium_simum_simum
MAGVEAQAASTRRICAWFFSCTLGLAIVML

HG0965 ENSG00000146006 LRRTM2

>Homo_sapiens

MKPMLSRGIS

>Leptonychotes_weddellii

MKPMLSRGIS

>Balaenoptera_acutorostrata_s

MKPMLSRGIS

>Erinaceus_europaeus

MKPMLSRGIS

>Orycteropus_afer_afer

MKPMLSRGIS

HG0966 ENSG00000148356 LRSAM1

>Homo_sapiens

MFVVGRRRLRTAGKQGTAVR-----

>Canis_lupus_familiaris

MLLVGRRRLMTAGEPCSAVLRFSVSDFVILV--CMTF-----

>Rhinolophus_ferrumequinum

MLLVGRRRRLTGGEPTALLPLEETSLWIQGSSCQVVCWDRP---

>Oryctolagus_cuniculus

MFLVGRLLRLTAGEPGASR-----

>Fukomys_damarensis

MFLMGRCLKLAAGKSGTARVTPE-----CQAPKPRAPPIL

HG0967 ENSG00000149925 ALDOA

>Homo_sapiens
MSGASGFPKYRSLPEDPWREKGRGH-----
>Lipotes_vexillifer
MSGASGFPKYRSPARGSVARKGQGSPEKVGDIGWG-----
>Ceratotherium_simum_simum
MSGASGFPKYRSLPGDLWRGKGRGHWRLGLTLAGGRAGAAL
>Manis_javanica
MSGASSFPKYRSLPGDLP-----
>Heterocephalus_glaber
MSGASGFPKYRSLGDPREKGRG-----

>Homo_sapiens
MRFSSLPQGLQPPALPEKRELWAFFLPVWSSSAFRTDRPWHRLPRDSCDAVCSCLLWSMAPTGFQDGS
>Rousettus_aegyptiacus
-----MVPTGLGEES
>Equus_asinus
-----MAPTGLWEES
>Fukomys_damarensis
-----MAPTGFQD--
>Tupaia_chinensis
-----MAPTGFQDES

HG0969 ENSG00000154645 CHODL

>Homo_sapiens

MRAGGRAAGLGRRE

>Physeter_catodon

MRSGGRAAGFGRPE

>Myotis_lucifugus

MRAGDRAAGLGQRE

>Dasypus_novemcinctus

MRAGGRAAGLARQE

>Chinchilla_lanigera

MRAGARATGLGRRE

HG0970 ENSG00000154727 GABPA

>Homo_sapiens

--MGRRFSRSTLTGQEASRRQSATGRV

>Miniopterus_natalensis

--MGRRFSRALTGQEASRRQSATGRL

>Oryctolagus_cuniculus

--MGRRFSRALTGQEASRRQSATGRL

>Manis_javanica

--MGHRFNRSFTFTEQVSRRRSATRRL

>Trichechus_manatus_latirostr

MHYGPRCTRSSLTGQEASRRRSATGRL

HG0971 ENSG00000155592 ZKSCAN2

>Homo_sapiens

MHSGKPHCAVTSCLEKRPGCILE--YTFTFSRAWHRFD-----

>Oryctolagus_cuniculus

MHPGKPSGRDTSCLGKRLGFFLDLSVPGHLFRGLG-----

>Ceratotherium_simum_simum

MHPGKPHRGDTSLEKRPSTLV--HRHLFKGLG-----

>Loxodonta_africana

MHPGKPHCGDTSLEKRSQFWTLG--YTVLFSRA-----

>Cavia_porcellus

MHSGKPHCQVTSCLEKRPQFWIWG--THSPFQGPTIDLINQPEVFLLLKLLNCGFGVRLDSF

>Homo_sapiens
MKNFNRKLLQKIRSFAANGEHLRQP-----
>Canis_lupus_familiaris
-MNFNRKLLQKIRSFSESGGFGISGSRDAPRREACSEWLLKTGTYPSPAHLPHF-----
>Balaenoptera_acutorostrata_s
MKNFNRKLLQKIRLFSANRAFPGISGSADVPRREVCSPVLLKTGTCLLQAF-LVSSRGSCNWFSNYAS
>Oryctolagus_cuniculus
MKDFNSERLLQELRSVSANAAFPRRAGCPAAPAFGRCHLRSRGS-----
>Heterocephalus_glaber
MKNFNRKLLQKIRSFKNGALLGISSPDALWREVCSEWL VETGTRPLPAK-RLPRF-----

HG0973 ENSG00000156535 CD109

>Homo_sapiens

-----MFATAARSAIVMGMGVEPPSPVSI

>Mustela_putorius_furo

-----MPAGAARSAIVMPVGGVEPPSPVSI

>Rousettus_aegyptiacus

-----MSARATRSAIVMRVGGVEPPSPVSI

>Marmota_marmota_marmota

-----MRVGRVEPPSPVSI

>Tupaia_chinensis

MLEPGWADRVRLSNPGGFAIFAGAARSAIVIRVGGVEPPSPVSI

>Homo_sapiens
MQTNDHPYADHFEYLQPCFCHCLCRKATCFKKKSSWSAY—ERVGCFLQ—————LIFPKQTIPPAISGFLKYILSLKRDQNLSKKYYRGKLINTTV
>Mustela_putorius_furo
—————MMVFLKYILSLKRDQNMSKNTALETs—————
>Miniopterus_natalensis
—————MSKNTTLGTS—————
>Equus_przewalskii
—————MWEFRLFVPQSFFFGFLERHQKRVEMETDGHPCADHFASFLKYILSVKRDQNMSKNTTLETs—————
>Dipodomys_ordii
—————MVGQFPFLCYF—————GALRCFLKYIF—————

HG0975.1 ENSG00000182158 CREB3L2

>Homo_sapiens

MRAGLLPSFWMHIPL

>Mustela_putorius_furo

MRAALLPSFWMRALL

>Equus_caballus

MRAYLLPSFWIHTLL

>Dipodomys_ordii

MRADLLPSLWMHIPR

>Tupaia_chinensis

MRADLLPLFWMLIPL

HG0975.2 ENSG00000157613 CREB3L1

>Homo_sapiens

MEASCAPGGAGGGGVG

>Odobenus_rosmarus_divergens

MEASCAPGGAGGGGVG

>Lipotes_vexillifer

MEASCAPGGAGGGGVG

>Ceratotherium_simum_simum

MEASCAPGGAGGGGVG

>Loxodonta_africana

MEASCAPGGAGGGGVG

>Homo_sapiens
-----MGLSLPICTMTAQD
>Canis_lupus_familiaris
-----MGLSLPICTMKALN
>Oryctolagus_cuniculus
MWPGGQRDTALWSGQGLHQPEQCPVAGALLLGLGCPEAEEAESGEQKGKSGKLGASPCLAVTGCGSTLHRQPVSAGLSLPICTMRALD
>Loxodonta_africana
-----MPGLSLPICTMRALD
>Chinchilla_lanigera
-----MASDFLYGPRLVLMGLSLPICTMTVLD

HG0977 ENSG00000158321 AUTS2

>Homo_sapiens

MLPS-LGGLAPLGSLRSPGLPWLHFLKIWEPGSEFSRRV

>Odobenus_rosmarus_divergens

MLPS-LGGLVPLRSLGSLGLPMMHFLKILEPGSEFSLRRV

>Rousettus_aegyptiacus

MLPS-LGGLVPLRSLGSPGLPMMHFLKIWEPGSEFSLRCV

>Galeopterus_variegatus

MLPS-LGGLAPRRSLWSPGLPWWHFLKILEPGSEFSRRV

>Chinchilla_lanigera

MLPSQGGGLAPLRSLPSPGLPMMQFLKNFAAWE-----

HG0978 ENSG00000159023 EPB41

>Homo_sapiens

MCHCGDGSMASPLAA

>Balaenoptera_acutorostrata_s

MCHCGDDSTASPLTAA

>Rousettus_aegyptiacus

MCHRGDGFMAPPLAV

>Equus_przewalskii

MCHCGDGSMALLAA

>Peromyscus_maniculatus_baird

MCHSDDGSTASP----

HG0979 ENSG00000159202 UBE2Z

>Homo_sapiens

MWEEVRVSGKWLFGADI

>Acinonyx_jubatus

-----MWLFQGDI

>Oryctolagus_cuniculus

MWEEVRVNGMWLFQGDI

>Equus_caballus

MWEEVRVNGMWLFRGDI

>Manis_javanica

MWEEVRVNGMWLFHGA I

HG0980 ENSG00000162670 BRINP3

>Homo_sapiens

MIQILGT-F-FCVLHRFVCHHAVKQVLRES

>Odobenus_rosmarus_divergens

MIQN-FE-I-FCMLFRFVCHHAVKQVLRES

>Equus_asinus

MIQIWGLFL-LRAI-----

>Chinchilla_lanigera

MIRFWGLFFSFCLLCRFVCHHAVSRC----

>Tupaia_chinensis

MIQMLGTFF-FCVLFRFVCHPCS-----

HG0981 ENSG00000163629 PTPN13

>Homo_sapiens

MLTAPGDRRAGEPC-SVAPRSAS---AAVRVAYRS

>Pteropus_vampyrus

MITGPRDRRAGKQH-TLAPRSASATSAALEARSRS

>Oryctolagus_cuniculus

MITAPRDRRAGALH-SQAPGSAS---AALGVGCRS

>Ceratotherium_simum_simum

MVTVSGDRRVGEQH-SLAPRPASASRAALGAGCRS

>Chinchilla_lanigera

MVSGPGDRRAGEQQRPRAPRSASDAPAALGAGCRR

HG0982 ENSG00000164116 GUCY1A3

>Homo_sapiens

MCGFARRALELLEIRKHSPEVCEATKHPSYQCP

>Mustela_putorius_furo

MWGFAGRARELPEIRKRSRRVWEANEHPSHQYP

>Dasypus_novemcinctus

MCGFARRALELLEIGKRSREVWEAIEHSSHQCP

>Oryctolagus_cuniculus

MCGFARRAPQLLRIPQRSPEVWAVHRAPQL---

>Ictidomys_tridecemlineatus

MCGFARRAPELQQIWKHGPQVWETAKHTGQQCP

HG0983 ENSG00000164128 NPY1R

>Homo_sapiens

MDSNMGKNKLNS

>Galeopterus_variegatus

MDSNMGKNKLNS

>Erinaceus_europaeus

MDSNMGKNKLNI

>Ochotona_princeps

MDSNMGYKNKLNS

>Ceratotherium_simum_simum

MDSNMGKNKLNI

HG0984 ENSG00000164185 ZNF474

>Homo_sapiens

-----MLKGKIKRSWRHLSFNEDFPTFQTAVLQ--

>Ailuropoda_melano leuca

-----MTTNITRSWRHLRFNEDFPAFQTAALQ--

>Orcinus_orca

-----MIKAKIER-----

>Mus_musculus

-----MSRSWRHLRFNGGFPTFRTAALQ--

>Tupaia_chinensis

MALCPHTVDSPRTAGTTRPGPTQRERGEAAGWRLLRLDGDFTFQTCPVMRL

HG0985 ENSG00000164604 GPR85

>Homo_sapiens

MKACLLVL---GRRTGKLLLKILYHLHKQNSSEMVK

>Pteropus_alecto

MKARLLIF---WR-----

>Elephantulus_edwardii

MSARIWGGFPWQGGGGGELSFKILNHPHKQNSSEMVK

>Loxodonta_africana

MSAWIFFLARWEE---EGEFKILYHPHKQNSSEMVK

>Ictidomys_tridecemlineatus

MSACF--W---GVGSGGWLLKILYHPHKQNSSEIVK

HG0986 ENSG00000164663 USP49

>Homo_sapiens

MVRGAGRDGPQNLKDEMGSKGREGAKRSWGSPDGCRTGVDCRGVIECACYGELLQKVCKGQGRNAVVKDQV

>Acinonyx_jubatus

-----MRWGVREENRVKGSWRSPAGGRTGLACTGVGVRCACCGEMLRKVCMGQGTGAVVKDQV

>Dasypus_novemcinctus

-----MKCACCGEILQKVWKGQGTKP-----

>Oryctolagus_cuniculus

-----MSNSSRARRAGIERACGRERLQKACEGQGRKAGVRDPV

>Cricetulus_griseus

-----MGSKRREAGRALMG-----VEPWAAQGWGLHMYLP-

HG0987 ENSG00000164932 CTHRC1

>Homo_sapiens

MQPAAASERGGARR

>Physeter_catodon

MQPAVASERGGAGL

>Oryctolagus_cuniculus

MQPAAVSQRGGARS

>Equus_asinus

MQPAAASERGGARL

>Dipodomys_ordii

MQPAAASERGAARH

HG0988 ENSG00000166130 IKBIP

>Homo_sapiens

-----MELAAERLSEATRMPGRGKGLGSGRCQVCEGARSPPRVPTNAKAATSCSPW

>Physeter_catodon

-----MAGRGRGLVSGRCQV-----

>Rousettus_aegyptiacus

MGSHVSQLEEFEGGCCEAAGMVGRKRGLVYGRR-----

>Equus_asinus

-----MRCEAARMAGRGRGLVSGRRQIREGARSPRLPAELRRPRPDPPG

>Ctenomys_sociabilis

-----MAGRKGLVSGRGRVCEEARPPRDAPVATSRESLK---

HG0989 ENSG00000166603 MC4R

>Homo_sapiens

-----MAASRKIIILNRLECIRLKLKQK

>Balaenoptera_acutorostrata_s

-----MRLKLKWK

>Myotis_lucifugus

MLVGASERQLMWACAHTLSPNGTAAPRRIILKRPECLRL-----

>Equus_caballus

-----MRPKLK--

>Trichechus_manatus_latirostr

-----MRLKLKQK

HG0990 ENSG00000166866 MY01A

>Homo_sapiens

MKLGHLYTCEGAWAGRGSKRENQKSGHWQEEGSLFPSFLAPWTAPIKPPLHP-GARTLMPHSCQIEISSTILQGQ----

>Canis_lupus_familiaris

-----MPPSCQIGISFTILQGTP----

>Dasypus_novemcinctus

-----MPPSCQIAISSTILQGGTEVTP

>Manis_javanica

-----MTPWTAPINQGTSPWGLGFLCPFVTLEFYPPFSKGHSEGTP

>Chinchilla_lanigera

-----MPPSCQTGISSTLLQGTLK---

HG0991 ENSG00000167654 ATCAY

>Homo_sapiens

MPSCTRAGLAFVCQ

>Odobenus_rosmarus_divergens

MSGCIRAGLAFVCA

>Myotis_brandtii

MPGCSRAGLAFVCA

>Equus_asinus

MLGCIRAGLAFVCA

>Manis_javanica

MPGCNRAGPAFVCA

HG0992 ENSG00000168000 BSCL2

>Homo_sapiens

MRHRYQLDRHFTF

>Rousettus_aegyptiacus

MSYRYQLDQHFVF

>Galeopterus_variegatus

MRYRYQLDHHFTF

>Equus_asinus

MRHRYQLDHHFMF

>Manis_javanica

MSYRYQLDHHFMF

HG0993 ENSG00000169306 IL1RAPL1

>Homo_sapiens

-----MYSEDLQATLQFLS

>Ochotona_princeps

MLLGEQEDLKTYMYPEDLQARLQFLS

>Loxodonta_africana

-----MYSEDLQARLRFLS

>Mesocricetus_auratus

-----MYSEDLQARLRFLS

>Orycteropus_afer_afer

-----MYSEDLQARLRFLS

HG0994 ENSG00000170852 KBTBD2

>Homo_sapiens

MLQITASRFS--FISEVFT

>Acinonyx_jubatus

MLQITASRVSPFFISEAFT

>Tursiops_truncatus

MLQITASRVSPFFISEAFT

>Rousettus_aegyptiacus

MLQITASRVSPFFISEAFT

>Geraotherium_simum_simum

MLQITASRVSPFFITEAFT

HG0995 ENSG00000171307 ZDHC16

>Homo_sapiens

MITADTYLVLPHWQECPCWYL--

>Galeopterus_variegatus

MIAADTYLVLSNWQKCPC-----

>Oryctolagus_cuniculus

MVAADTYLVLLHWQECLCRCL--

>Equus_asinus

MIAADTYLVLSHWQECPCYLWDR

>Peromyscus_maniculatus_baird

-MRAANTLVLSHWQECPCWLL--

HG0996 ENSG00000173890 GPR160

>Homo_sapiens

-----MKCRCIELTHIAYWYIKMKCKEPKIT

>Dasypus_novemcinctus

-----MKCKETKVR

>Galeopterus_variegatus

-----MAFWYSKMCKKNQK--

>Ochotona_princeps

-----MKGKEPKIT

>Fukomys_damarensis

MQVDAGSAFSTQRALSIHQAHRYRTYIAFWHSMCKCKEPTVT

HG0997 ENSG00000177728 TMEM94

>Homo_sapiens

MAAAPGGGDVK

>Felis_catus

MAAAPGGGDVK

>Oryctolagus_cuniculus

MAAAPGGGDVK

>Nannospalax_galili

MAAAPGGGDVK

>Trichechus_manatus_latirostr

MAAAPGGGDVK

>Homo_sapiens
MYWLLGKCRLPVENDILY-----
>Eptesicus_fuscus
MYWLLGKFSLLVENDILY-----
>Galeopterus_variegatus
MYWLLGKCRLLVENNILLIGSKCFLGSVLTENLSWAKHPYSE
>Condylura_cristata
MYWLLGKCRLLVGNDRSTNKI-----
>Loxodonta_africana
MYWLLGKCRLPVENNILY-----

HG0999 ENSG00000178401 DNAJC22

>Homo_sapiens

MEVGAGRDGPFSLCGQRK

>Canis_lupus_familiaris

MEVGAE-----

>Pteropus_alecto

MEVEAE-----

>Equus_asinus

MAVGAE-----

>Marmota_monax

MEVGAE-----

HG1000 ENSG00000179083 FAM133A

>Homo_sapiens

-----MLPIFFSATEQLPWYNKKDEYLLFIERMELA-----

>Myotis_davidii

MSGKPGLYPSARFANPCCRFFSATEQLPWYNPKDQCLLFIERI-----

>Oryctolagus_cuniculus

-----MLPIL-FCYRTTPLVNPDKDQCLLFTERKIPRSGMAGSHEDPEKRTGKQLER

>Manis_javanica

-----MKILQMASLGFFSATEHLPWYNQKDQCLLFMKRRT-----

>Chinchilla_lanigera

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HG1001 ENSG00000179761 PIPOX

>Homo_sapiens

MTIIEPRIESHARDARVRLAAELG

>Ailuropoda_melanoleuca

MTIIEPRIES-----

>Rousettus_aegyptiacus

MTIIEPRIES-----

>Oryctolagus_cuniculus

MTIIEPRIES-----

>Chinchilla_lanigera

MTIIEPRIES-----

>Homo_sapiens
-----MAAAAAGQLSWAGTALLELPQPTT-----
-
>Canis_lupus_familiaris
-----MAAAAAAMQLSWAGTTHPELPQQPQRMWPWP
S
>Pteropus_alecto
-----MPARPLSPLAGPKSPR-----RPLSHQEP IGLHLQPAPGRDGAVQLSWAGTTPLELPQPGM-----
-
>Condylura_cristata
-----MTLCSIMQNWLIWDFLVFLPAALPLSWAGTAPPELPQPAT-----
-
>Heterocephalus_glaber
MPQVVPKFIGLQEKGFPEGGDLPHWFGCLLRKRKDP I RSLVEKKKEKGFDDLVGVTFLGTMKLGSIVPNQLTCGFLVFLPSVEQLSWTGTALLKLPQPTA-----
-

>Homo_sapiens
-----MLIHPPGFHCLTSTVYISALQSVLRMKL-----
>Miniopterus_natalensis
-----MSAVCISALQSVLRMKL-----
>Oryctolagus_cuniculus
-----MLAIYISALQSVLRMKLN-----
>Ceratotherium_simum_simum
MRSSRDQELTWAKVLKALTAVLRPPLGTNSNALRTAVRLTQARRRRRKFPQIRAGSQSPTSAVYISALQSVLRMKP-----
>Peromyscus_maniculatus_baird
-----MMICPPGS-----

HG1004 ENSG00000185875 THNSL1

>Homo_sapiens

MFTSQWKLSTTHIN----

>Canis_lupus_familiaris

MFTSQWELSASHTC----

>Pteropus_vampyrus

MFTSQWELSTAHTS----

>Galeopterus_variegatus

MFTSQWELSTAHTS----

>Loxodonta_africana

MFTSQWELSTAHTSRKAK

HG1005 ENSG00000186472 PCLO

>Homo_sapiens

MEEAPAAGVTCERD

>Mustela_putorius_furo

MEEAPAAGVTCERD

>Myotis_lucifugus

MEEAPAAGVPCERD

>Galeopterus_variegatus

MEEAPAAGVTCERD

>Equus_asinus

MEEAPAAGVTCELD

>Homo_sapiens
-----MDVTLPVVRKQIY-
>Mustela_putorius_furo
-----MAARMDVTLPVVRKQRIY
>Balaenoptera_acutorostrata_s
MRGKWERFFLENVMTCPSTASQESAWFLEIYSDSTAARMDVTLPVVRKQRVY
>Loxodonta_africana
-----MAVGMDVTLPVVRKQRVY
>Cavia_porcellus
-----MATKMDVTLPVVRKQKVY

>Homo_sapiens
-----MGLFLAKVMTYASVPASQE
>Felis_catus
-----MMYPSVTASQE
>Equus_asinus
MGRACPLARRRGTAIDLGLWARIQEKWERFFLAKEMTCPSVTASQE
>Cavia_porcellus
-----MMTYLSVTSFQE

HG1007 ENSG00000188910 GJB3

>Homo_sapiens

-----MATDAPISRLRKRLRRATSPSGGWPGS--AWQRRV

>Mustela_putorius_furo

-----MAADAPISHMKKPRLRAATGPSEGGPGSGCPWH---

>Balaenoptera_acutorostrata_s

-----MKKKPRLRRASSPGEGCGNE-----

>Equus_asinus

MRFICSLALPMATDALISHLKTRRLRRATSPSTSGPGN--PWLPGA

>Chinchilla_lanigera

-----MAASAPTPCRSKPRLGRARIPSGAGPGA--TWLRRD

HG1008 ENSG00000198252 STYX

>Homo_sapiens

MAAGCKTPDPPLPCLRRR--RCWSHWDPVVCVC--

>Felis_catus

MAAGYEPPNLPLPRCRRR--RRRSRWDPLVCVC--

>Physeter_catodon

MAAGHEPPSPPLPGCRRRHRRRSRWDPLVCVC--

>Eptesicus_fuscus

MAAGYEPPNPPLPLCRRR--RRRSRDPLVCVCQL

>Sorex_araneus

MAAGHEPPNPPLPHCRRR--RRRSRWDPSVCEC--

HG1009 ENSG00000198909 MAP3K3

>Homo_sapiens

MPQRPAAGGAGAGAWGGGGPERSRPPRGARPAAVPAARAPGMQPLRR

>Odobenus_rosmarus_divergens

MPQRPAAGGAGAGAWGGGGPERSRPPRGARPAAVPAARAPGMQLRLRR

>Dasypus_novemcinctus

MPQRPAAGGAGAGAWGGGGPERSRPPRGARPATVPAARAPGMQLRLRR

>Oryctolagus_cuniculus

MPQSPVAAGAGAGAWAGGGPERSRPPRGARPAAVPAARAPGMQLRLRR

>Rattus_norvegicus

MPQRPAR--AGAGAWGGGGPERSRPPRGARPAAVPAACSPGMQPLRR

HG1010 ENSG00000203740 METTL11B

>Homo_sapiens

-----MTVSSSFRRRLIQNSKASFLSL--

>Galeopterus_variegatus

-----MTVSSSFRRRLIQNSQANFLSL--

>Ochotona_princeps

-----MTVSSSFRRRLIHRSSQASFLSQ--

>Equus_asinus

-----MTVSSSRKRRRLIQNSQASFLSL--

>Chinchilla_lanigera

MGQDWFKMTVSSSFRRRLIQNSHTSFFSLQE

>Homo_sapiens

-----MTIQRREEPLLSE-----

>Lipotes_vexillifer

-----MTIQSGEPLLSE-----

>Rousettus_aegyptiacus

MCLFSLPQKLKRKQAACPTLGCMTIQGRGEPLQNSE-----

>Manis_javanica

-----MTIQNGEPLLSEQDSPSKYLFF

>Ictidomys_tridecemlineatus

-----MTIQSGEPLLSE-----

HG1012 ENSG00000213694 S1PR3

>Homo_sapiens

MNVPGAPSRGFWS

>Balaenoptera_acutorostrata_s

MDVPRAPSGGFWS

>Condylura_cristata

MDVPGAPSAGIWN

>Equus_przewalskii

MGVPRAPSAGFWS

>Microtus_ochrogaster

MNVPGAPSRGLLR

HG1013 ENSG00000214022 REPIN1

>Homo_sapiens

MDGRRVPAQPAAEVRSLAQSEV

>Felis_catus

MDARRASHPAGEVRLASLRSEV

>Rousettus_aegyptiacus

MDARRASHPAGEVRLASLQSGA

>Dasypus_novemcinctus

MDGRRASHPAGEVRLASQQSEV

>Heterocephalus_glaber

MDGRRAPARPAGEVRLASLRSEG

HG1014.1 ENSG00000214595 EML6

>Homo_sapiens

MQIPDVKGGVAPPRASPGGRSPQVQ

>Mustela_putorius_furo

MQMPDLKGGVTLPRTPSPGGRSPQVQ

>Pteropus_vampyrus

MQISDLKGGATPARTSPRGRSPQVQ

>Manis_javanica

MQIPDLKGGVTPPRTSPGGRSPQVQ

>Mesocricetus_auratus

MQISDFKGGVTPGRTSPAGRSPQVQ

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>Homo_sapiens
--MAELTRVACQIKAI AE
>Mustela_putorius_furo
MVMAKLTRVLCQIKAVTE
>Myotis_lucifugus
MVMAKLSRVPCQIKAVTE
>Manis_javanica
--MAKLTPASCQIKAVTE
>Chinchilla_lanigera
--MAKLTRAACQIETVTE
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HG1015 ENSG00000240720 LRRD1

>Homo_sapiens

MKIKIKLQFCIGIKHISK

>Ursus_maritimus

MKIKIELQSCDVKHSSK

>Pteropus_alecto

MKIKIELQSCIGIKHISK

>Galeopterus_variegatus

MMMKIKLQSCIDRKISK

>Tupaia_chinensis

MKIKIKLPSCIGIKYNI-

HG1016 ENSG00000254004 ZNF260

>Homo_sapiens

---MLHFIPFCNHLISG

>Balaenoptera_acutorostrata_s

-MRMLYFIPICNQLITG

>Pteropus_alecto

-MRMLYFIMFCNHLISG

>Galeopterus_variegatus

MKRMLYFIPFCNHLI--

>Equus_asinus

-MRMLYFTPFCNHLISG

HG1017 ENSG00000255154 HTD2

>Homo_sapiens

MLHSSNSCLFRL

>Felis_catus

MLHSSNSCLFQP

>Balaeoptera_acutorostrata_s

MLHSSNSCLFQP

>Pteropus_vampyrus

MLHSSNSCLFQP

>Loxodonta_africana

MLHSSNSCLFWL

>Homo_sapiens
-----MPFPLNSCFFESGCGSSGHLAASSAQSTKCEPEGPP-----
>Ursus_maritimus
-----M--AMRSGQGYLTMPIPFSLNSCFFESGCGSGPQSVGPAGLP-----
>Myotis_brandtii
MI-----A-KRDLLPHLLAPAAHPNHL--ASSTKQG-----ADAPRVTCFSEHRSGLLASPARPPKCGPLRVTPSALSGLGSVNSRVR
>Manis_javanica
-----M--TMRTGQGHLAMQTRFPPNSCLFESGCGSPGHLVASAARVPKAWGLKNYPDQPL-----
>Rattus_norvegicus
MPSQKGRTLMEEMREGVALPGN---QSSPPLFALVAAKVWSENLATPWAANSNFFELWHSCGHLAVSSLWPEGQS-----

HG1019 ENSG00000019995 ZRANB1

>Homo_sapiens

MASLKLNISISGFPLISSFLDQTSL-YLLPISFAFQSSVLLNPRV---

>Odobenus_rosmarus_divergens

-----MSL-YLLLSFAF-----

>Lipotes_vexillifer

MTWLRLNISVRGFLI-----

>Orycteropus_afer_afer

MSWLKLNISIGGLPILTNPFLKTFSTDPLSLAYYLPCTAKYNFITS

HG1020 ENSG00000023902 PLEKH01

>Homo_sapiens

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>Orcinus_orca

MEGAEGRGAGVRVCASAREAG--L-

>Rhinolophus_ferrumequinum

MEGAEGRGASVRVCASAGEAG--P-

>Ochotona_princeps

MEGAEGRGAGVRVCASAREAG--L-

HG1021 ENSG00000064692 SNCAIP

>Homo_sapiens

MPTRSPPSRVSSPSLCWNPGMVWGPMRWQRLTLGSRNL---

>Panthera_tigris

-----MRWQRLTRGSRAFIKI

>Manis_javanica

-----MVWGPVSWQRSTRGSRAS---

>Mus_musculus

-----MVWGPMPRWQRLIHGSRKL---

>Homo_sapiens
-----MPGSPVPASESLGLHLSPLLYHLHH
HPCDPKSLNDSRRDSRQGLKG-PFTPYFWGPSVPPAKTSRYN-----FPKSHSGIRAKNGTQI
>Pteropus_alecto
-----MPGSPVPTSRSLGLCLSPLLYQLRH
PQ----S-LDSRRDSRQGLKGSPYTPTFQGGLLYHPPRPADLPLEAEVQAPKVLLPSCLCGLP-----
>Equus_asinus
-----MKGLCLSPLLYQPHH
HPRCPKSLNNSRTDSKQEKLGFPFTSTFDQGLLRHLPRPADLTLEVEVQAPEVLLPSCLCGHP-----
>Chinchilla_lanigera
MCISCVCVCVCVCVCVCDRDIQTHPTYTCTGFWSEIPRPHTHPSGVKRAIPGTQGTGTLPYFHGQEGAHRGWGGARGQDAWVSVPTSKSVGLCLSLLLYQPQH
HPCRPRALKLLNRLEAEAE--RSSFVPLLCAFACT-----TCKVSGPY--P-----

>Homo_sapiens
MGGHVPLQRTWGSSSPKRGTEKVPCLVPGR-----

>Felis_catus
MDGHVPRGRIWGPWSLKRGTGCAKVGNTFPPRPQVLPQAHLRAGFLKGPRAGVGRGR---GGAAEARSLGCAWASGRSGPGWAGDGSQGHGVGPGSAPREFLSWCQA
GDTVFL

>Pteropus_alecto
MDGHVPWRRIWGPWSPKRGIGG-----

>Equus_caballus
MGGHVPRRRTWGPWSPKRGTTGAKVGETFPPLPQVLSRAHLRAGFLRGPRAGGRSQQRRRAGAVPGRKAG----ACRAGPGMAVAVAVQVPAA----PRASS-----

HG1024 ENSG00000073464 CLCN4

>Homo_sapiens

MSLSVSASIRPSTQRRFR

>Equus_asinus

MSLSASVSIRPSTR-SRGFR

>Loxodonta_africana

MSLSGSVCISPSTQRRRGFP

>Heterocephalus_glaber

MNLSVSACIRPSTQRRSGGLR

HG1025 ENSG00000074621 SLC24A1

>Homo_sapiens

MSRSEGLWIPPGWASWRNLL

>Orcinus_orca

MSRFEGWLPPGWASWRNLL

>Myotis_davidii

MSRFEGWLISLWASWRNLP

>Rattus_norvegicus

MSRSEGLWIPPGWASWRNLS

HG1026.1 ENSG00000075035 WSCD2

>Homo_sapiens

MCVLSLKTPLLAQRSSPSVWEGW

>Orcinus_orca

-----MAQRSSPWLREGW

>Pteropus_alecto

-----MAQRSSL-----

>Manis_javanica

-----MAQRSSP-----

HG1026.2 ENSG00000179314 WSCD1

>Homo_sapiens

MTPPEALASLPPGR

>Eptesicus_fuscus

MMPPEAPASLPPGR

>Galeopterus_variegatus

MTSPEALASLPPGC

>Chinchilla_lanigera

MTPPEALASLLPGC

HG1026.3 ENSG00000179314 WSCD1

>Homo_sapiens

MVPFEHLLETGQEQ-----

>Rousettus_aegyptiacus

MVPFKHLETGQEEQ-----

>Ceratotherium_simum_simum

MVPSEHLLETGQEEQ-----

>Loxodonta_africana

MVPFKHLLKTGKRAHAGARSQDAGMTPPGVPACQPPGR

>Homo_sapiens
MRACRAARRGSRAPRRCNRTPRALAPGLRPLSIHSEVLD-----
>Balaenoptera_acutorostrata_s
-----MRRPLSIHSVLD-----
>Ceratotherium_simum_simum
-----MRRAPRRCNRTPRARPAPATFHSLGGAVLSAAETGSGAADSFTKKLRGPGRRLTAGPLQKLRSSGEGTGDSLGAQPAAN
>Ictidomys_tridecemlineatus
MRAGWAARRGSPSRARRRCNRTPSARPLRLATFPFTPRCLIERR-GEGLRCHGTTGLRIPVQRNSE-----DLGEKKEYHIGTL----

HG1028 ENSG00000076356 PLXNA2

>Homo_sapiens

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>Felis_catus

MNLDSMWIWSSP

>Tursiops_truncatus

MNLDSMWIWSFP

>Ceratotherium_simum_simum

MNLDSMWLWSSP

HG1029 ENSG00000079482 OPHN1

>Homo_sapiens
MERGYVSLPPWLNPSGA-----
>Pteropus_alecto
MEEGDVPLPPRLNPSGA-----
>Equus_asinus
MEEGYVSLPLLNSSGAYLDSKPVPLDQEELGAGGL
>Chinchilla_lanigera
MEEGYVSLPPGLNPSGT-----

>Homo_sapiens

-----MRTSFTCHLSEIYNPRRLVLPFYWDLRSSEMTVARSTEPAEVRPFLGMGCTERSD-----

>Mustela_putorius_furo

-----MRTSFTRHLSEICKYSFLLS--YRET-----

>Oryctolagus_cuniculus

MGPVHAVTTRVKLCSTCVCEDSGVWGAFSMRTSFTCHLRLGTRGGS-----SSRNAGNRESSGDQCGPL-----

>Ceratotherium_simum_simum

-----MRTSFTWHLSGICNHRSFALPDSEKCESCR-----GDCRQLLGAGRNTTVLEKGLYRKVKVAPGF

HG1031 ENSG00000082269 FAM135A

>Homo_sapiens

MLAGRAGPVAEPR-----

>Canis_lupus_familiaris

MLAGRFGPVAEPR-----

>Pteropus_alecto

MLAGRAGPVAERR-----

>Dasypus_novemcinctus

MLGGRAGPVAEPRRRTSSAAVVAVAAMAM

HG1032 ENSG00000084453 SLC01A2

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>Homo_sapiens
MQPSEPKKLNQRFKTYINKDSFIYNSASLMNKKLQLTRLRCLHTGYSICNFKNLLVLQYGSKNEW-
>Ceratotherium_simum_simum
-----MILQYRSSGEWS
>Manis_javanica
-----MILQYGSSD--
>Cavia_porcellus
MQPSEPKKLYQRIKSYVNKDPFIYISTSLKNKTLQFTCSQCFTCNS--TCNLF----FKKFDVLAD--
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HG1033 ENSG00000089225 TBX5

>Homo_sapiens

MPAPPPHRLPC

>Felis_catus

MPAPPPRRQLPC

>Miniopterus_natalensis

MPAPPPSRRLPC

>Heterocephalus_glaber

MPAPPPHRLPC

>Homo_sapiens
-----MQHLVSILPFMYCQTSTSVKITCLYKNLVTAEWNLSIL--
>Acinonyx_jubatus
MSVGQMQLVSIPLPFMYCQTNTSVKITCLYKNLVTVGWNLSIQ--
>Equus_asinus
-----MQHLVSVLPFMYCQTSTSVKLTCLYKNLVTVGWNLSIQD
>Manis_javanica
-----MQHLVSI SPFMYC-----

HG1035 ENSG00000093000 NUP50

>Homo_sapiens

MAARSVFGAVPPAVSG

>Leptonychotes_weddellii

MAAWSAFGAVPPAVSG

>Dasypus_novemcinctus

MAAQSVFAAVSPAISG

>Equus_asinus

MAAWSALGAVPPAVSG

HG1036 ENSG00000100813 ACIN1

>Homo_sapiens

-----MVI PGSRVSEYIRFKASARRRKPSLKAGREKGRCRADGKN

>Myotis_lucifugus

MF PENPKQGQPGSPRTSGPGPAPNTQAPQLSFRSEESRMTPIMVMPKSRASE-----

>Equus_asinus

-----MVMPESRASEQIRFKASVRRR-----

>Mesocricetus_auratus

MF PENPKQSQPSNPRTSGLKPAPNTQVPRRLSPREDAIRISPMVMRDSRSSE-----

HG1037 ENSG00000102710 SUPT20H

>Homo_sapiens

MVFTPLHQRT

>Canis_lupus_familiaris

MVFTPLHQRT

>Galeopterus_variegatus

MVFTPLHQRT

>Ceratotherium_simum_simum

MVFIPLHQRT

HG1038 ENSG00000104331 IMPAD1

>Homo_sapiens

MGRAGAGERAPV

>Orcinus_orca

MGRAGAGERAPV

>Eptesicus_fuscus

MGRAGAGERAPV

>Ictidomys_tridecemlineatus

MGRAGAGERAPV

HG1039 ENSG00000104804 TULP2

>Homo_sapiens

MFRDWPERQGTEASM

>Panthera_tigris

MFRNWPERQGEA--

>Orcinus_orca

MFRNWPERQGTEV--

>Equus_przewalskii

MFRNWPGRQGIEA--

>Homo_sapiens
MRKAHAWPPPACSLAVVRLRAARRGRQAG-----IQP--GR-----
>Odobenus_rosmarus_divergens
MRKAHA-----
>Heterocephalus_glaber
MRKAQAYPPPSRSLAGVRLRAGVAGRRGQ----SLGVALRAGSEGGDAGVQF
>Tupaia_chinensis
MREAHVWHPLACRLAGVRLRKRGGGQAGVQPRQCGLGPRVGAVECR-----

HG1041 ENSG00000106536 POU6F2

>Homo_sapiens

--MNSLGLCYPVCCLLSRC

>Acinonyx_jubatus

MGMNSLGLCYPVCCLLSRC

>Pteropus_alecto

--MNSLGLCDPVSCLLPRC

>Loxodonta_africana

--MNSLELCYPVCCLLSKC

HG1042 ENSG00000107249 GLIS3

>Homo_sapiens

MNRTGEAQRN---

>Odobenus_rosmarus_divergens

MSRTGEAQRNSTF

>Pteropus_vampyrus

MSRTGEAQRNSTF

>Equus_asinus

MNRTGEAQRNSTF

HG1043 ENSG00000107736 CDH23

>Homo_sapiens

MERGVAEPLDVWGAPSPSPRRA

>Manis_javanica

MESGGAESRDVWEALRPSPRRA

>Octodon_degus

MERGVAQRLHVGVPSPRRT

>Trichechus_manatus_latirostr

MEPWGAEPRDVWGALRPSP---

HG1044 ENSG00000109381 ELF2

>Homo_sapiens

-----MIMQTYNTGNHQ

>Ailuropoda_melanoleuca

MSIDFENMIMQTCNTGNHP

>Miniopterus_natalensis

-----MIMQTYNTGNHP

>Marmota_marmota_marmota

-----MIMQTYNIGNHL

>Homo_sapiens
-----MGGLEACRIADED
>Ailuropoda_melano leuca
MREARTGGGEPGRRWEGKESGEAWELGARRTRARTAGAARGRPMGGLEAGRIADEG
>Ceratotherium_simum_simum
-----MGGLEAGRIADEG
>Heterocephalus_glaber
-----MGGLEAGRIVDED

HG1046 ENSG00000112701 SENP6

>Homo_sapiens

MHSRLGGVGGRP

>Rousettus_aegyptiacus

MHSRLGGVGGRP

>Condylura_cristata

MHSRLGGVGGRP

>Marmota_monax

MHSRLGGVGGRP

HG1047 ENSG00000112769 LAMA4

>Homo_sapiens

MNVRRKPGQRSPQSRTARERRWPSAGGAHPNPSAF-----

>Odobenus_rosmarus_divergens

MDVRRKARQSPQSPPSPGQE--VAGSARPNPVCLLMLSLKLHPSIRPSARASGERESGREK

>Balaenoptera_acutorostrata_s

MGVGRKPGQRSPQSRPPGTGGRRSRGSPQTHPPLDA---EL-----

>Equus_przewalskii

MGVGRKPGQRSPQSRRRARRWPVLAGLAPTQSVF-----

HG1048 ENSG00000115295 CLIP4

>Homo_sapiens

MKTPISMHSQPTR

>Lipotes_vexillifer

MNTPISIHQPTL

>Loxodonta_africana

MKTPISIHSEPTL

>Fukomys_damarensis

MKTPISIHQPTL

HG1049 ENSG00000116212

>Homo_sapiens

MPRKELELWS-NAALRLNSGSATY

>Physeter_catodon

MQWQELELWS-DTALRLNSGSATY

>Pteropus_alecto

MQWKELELWS-NTALRLNSGSATY

>Manis_javanica

MQWKELELWSNTALRLNSGSATS

HG1050 ENSG00000116489 CAPZA1

>Homo_sapiens

-----MGNECNSLGKILDFKSPKANPTSWGAGAGAGVRRRHSRA-----

>Ursus_maritimus

-----MNGGNECNSVRKVLDLKSFKEKSYGRPRD--VQERRLSQPPPHP

>Galeopterus_variegatus

MEPRRQEQSKHAGKRATDERGNECNSERKTLDKSLKAKPTSWCAGCGRRHPRA-----

>Marmota_marmota_marmota

-----MGNDYN-----

HG1051 ENSG00000116852 KIF21B

>Homo_sapiens

MARGGARAQPRGAGRG--

>Odobenus_rosmarus_divergens

MARGGARAQPRGASPRG

>Rousettus_aegyptiacus

MARGGARDQPRGAAPGRG

>Heterocephalus_glaber

MARGGARDQPRGAGRD--

HG1052 ENSG00000118640 VAMP8

>Homo_sapiens

--MRGGRGQAESWSKQEVN----

>Balaenoptera_acutorostrata_s

--MRGGRGRAESWTSRK-----

>Rhinolophus_ferrumequinum

MGCEVSKGRAESWSKQEVN----

>Microtus_ochrogaster

----MGRRRAESWSKQEVKLWLR

HG1053 ENSG00000119522 DENND1A

>Homo_sapiens

MAFAGLERVH

>Mustela_putorius_furo

MAFAGLERVH

>Rousettus_aegyptiacus

MAFAGLERVH

>Erinaceus_europaeus

MAFAGLERVH

>Homo_sapiens
MGEGLDGLVGAENCRELLETDRNPGSRPRGLRTVGRLAGERGKDGAWPPGLPVPCELTPTVYCRELTRSHFEKKLERIPSG
>Panthera_tigris
-----MTRSHFENLER-SSSD
>Dasypus_novemcinctus
-----ML-----ERRPSGLTQA-----LDEDQISRERLQGSLSLF---
>Oryctolagus_cuniculus
-----MTRSHF-----

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>Homo_sapiens
-----MSLIAHLESGCVG
>Miniopterus_natalensis
-----MCVLSLQIAHLESGCVG
>Galeopterus_variegatus
-----MLMIAHLESGCAG
>Chinchilla_lanigera
MSGGICALPLGSREAEPLARGAPALASANTDTRSSGGGQPAQLDAGCLWTLRPSFPSIAHLESGCAG
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HG1056 ENSG00000128271 ADORA2A

>Homo_sapiens

MMLLPEPLQRAWFQETQSPL

>Acinonyx_jubatus

--MLPEPLKRVWFLETQSWL

>Galeopterus_variegatus

MTPCPEPLVRVWFLETLSRL

>Equus_caballus

--MPREPLERAWFLETQSWL

HG1057 ENSG00000131097 HIGD1B

>Homo_sapiens

-----MAQPPEMGYLGGSFQVEAVLGHGERGS

>Erinaceus_europaeus

-----MELVVQPSETGYPGR-FFQVEAVLGID-----

>Ictidomys_tridecemlineatus

-----MEEVALVAQTPETGYPGGSFQEETVLSMDWAEV

>Tupaia_chinensis

MLGRRDGEMVLAAPPEAGYLGRTSLQVQVMLGIARCS-

HG1058 ENSG00000131386 GALNT15

>Homo_sapiens

-----MESLFFSQGENRGKGREAIQFEVPVNGLSEGN

>Myotis_davidii

-----MRHLSRMESLLFPKEKRGQTV-----

>Galeopterus_variegatus

MRRGKETHGTHLSRMESLFFSQGENQGKGGGKQFNLKSL-----

>Marmota_marmota_marmota

MQRGKETHGTHLSRMDSFFPKEKNRVKGEQAIQFKVLVNGHSEGN

HG1059.1 ENSG00000132970 WASF3

>Homo_sapiens

MLLEGNFCNP

>Mustela_putorius_furo

MLPEGNFCNP

>Myotis_davidii

MLPEGNFCNP

>Equus_caballus

MLPEGNFCNP

HG1059.2 ENSG00000112290 WASF1

>Homo_sapiens

-----MMNWNNDERKHIRSQHSRPAL-----

>Galeopterus_variegatus

MPPSFDTLTPSLALAMMDWNNDERKAYPI-----

>Equus_caballus

-----MNWNDEKKARLNIHNL SYSRLID

HG1060 ENSG00000134242 PTPN22

>Homo_sapiens

MLCSGGSSGFLEVSRP

>Acinonyx_jubatus

MLCSGGSSGFLVVSRLP

>Orcinus_orca

MLCSGGSSGFSVLSRP

>Tupaia_chinensis

MLCSGGSSGFSVVSQP

HG1061 ENSG00000134802 SLC43A3

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>Homo_sapiens
MCCLCVLWVLGVTFSLGDGIQNSSAGAPLLHLLPGSYWDPENHPLMVFAQA-----
>Balaenoptera_acutorostrata_s
-----MVFTQA-----
>Marmota_marmota_marmota
-----MGFAQAPKSWNYRAP
>Tupaia_chinensis
-----MFFAQAENTQK-----
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>Homo_sapiens
MSQRTPCLGGRKGALALPD-TSDVYDTAPLSVAGSWRQTLWSRFGTARE---VGGGRASGSGL-----SLGAAQSTCIILLAH---GGLQL
PSH-----
>Mustela_putorius_furo
MSQRTPCLGGRKVLPP-----

>Loxodonta_africana
MSQQTPCLGRRNGALAAATDSSGDVYGTAPLSAARRWCRTLWSRFGNLRGKWEVGGETVVGCPFELPNRGALFCGRTEASHYSLNRSQPPCSLFELRGWGGGGLSL
LAETLPISVQQSCKGQQQEPTSGPVFLHTHSRLPGRGRYWWRARGLKVEAVYFSLCHQRYLKNASGG
>Chinchilla_lanigera
MSQRTPCLGGPKKDALATSDAVHDIYGTALLAAASLGRQTLW-----

HG1063 ENSG00000138162 TACC2

>Homo_sapiens

MELCEDAGVGAARR

>Odobenus_rosmarus_divergens

MELCEDAGVGAAGR

>Ceratotherium_simum_simum

MELCEDKGFGAAR-

>Manis_javanica

MELCEDAGVGAAR-

HG1064 ENSG00000139734 DIAPH3

>Homo_sapiens

MCWLRPRLQLRG-----

>Rousettus_aegyptiacus

MCWRRPRLQLRG-----

>Ceratotherium_simum_simum

MCWPRPRLQLRG-----

>Chinchilla_lanigera

MCWPRPRLQLRGWAGLG

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>Homo_sapiens
MQAQIYQAPQSTNTSPEEIKERNFKRKYQSLCKQSLVYSCLHQSTVRFMKKNKLRTTLYVHLQMPQLMLVGCLSAFCDNEHMDFCLLNSVDPFSQLPGAWIF-TS
NC-----
>Mustela_putorius_furo
-----MELLKISQRLNARKCPAVWVSFSS
RCKQIYPAPR
>Galeopterus_variegatus
-----MEAKELSQLILEGSLSVFCDNEHMDLCSLNLADHFS-----
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>Oryctolagus_cuniculus
-----MNTKGISQLIIQSSSVFCDDHMDVCSLNSTDHFS-----
-----
```

>Homo_sapiens

MGIQRR-SGPLLTGLSVGLLLLF~~SW~~TLVQPTSL~~SALVHH~~PHLCQTTRDVHGRHYPGFFCPRLSDSP~~EEAYCCHLQAAGGSCCTRAE~~FEALYQVNL~~SALPPP~~I~~L~~R
GPGPLLVLGLYNLLVVTLM~~TVDLVHFC~~CGRGRSLGW--SHRRPPSGSSAASSLQVSAGTA

>Mustela_putorius_furo

MGFQRR-LG~~LLLTGLTVGL~~LLLF~~SWATLAQPTSLSALA~~HHPHLCQT~~TWDADGRRYPGFFCPRLSDTPEE~~AFCCHLQAAGGSCCTQAEFEALYQVNL~~SSLPPP~~I~~L~~R
GRGPLLALGLY~~LLLV~~ALMTADLVHFCRGRGGGRRR--RPSRLSSR~~SSAARPLQVP~~VGTD

>Pteropus_alecto

MGFPRR-----LPLR~~LLLLFGWMTLAQPASLSALA~~QYPHLCQTTRDADGRHYPGFFCPRLTDAPEEAYCCHLQAAGGSCCTRDEFEG~~LHQVNL~~SALPPP~~I~~L~~R~~
GPGPLLALS~~LYGLLAVL~~VTADLVHFCRSRRRG~~GW--GRRG~~PSFRSSAARPLQVSVGID

>Mesocricetus_auratus

MGLQRRSPGPLLTGLSVGLLLLF~~SQTNLAHPTDLSALA~~HHPNLCQTTRDAEGRHYPGFFCPRLSDTPEEAYCCHLQAAGRSCCTRDEF~~EALYQVNL~~SSLQPPP~~I~~L~~R~~
GPGPLLALGLYS~~LLMALMTAD~~FVHFCRGRGRRESLNSRSRGLRFRGSAARPLRVPVGTD

HG1067 ENSG00000143340 FAM163A

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>Homo_sapiens
MRLHARSRAVLGAPGRPRSLTCAAPAAGARKDALRPRGSRTRESLPERSCSAAGLMPLARRTPNCCLLRGSPRD
>Mustela_putorius_furo
-----MPMAMTHPQPLSARVQPA-
>Balaenoptera_acutorostrata_s
-----MTCPQLLSAQQAQPA-
>Myotis_lucifugus
-----MPLAMTQPQPLSAQAQPV-
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HG1068 ENSG00000144791 LIMD1

>Homo_sapiens

MPFTLGRWKSLLVLGRT

>Myotis_davidii

MTLTLGRWRVLLVLGWT

>Manis_javanica

MPLTPGRWKALPVLGWT

>Microtus_ochrogaster

MTFTLGRWESLSALGWT

HG1069 ENSG00000146414 SHPRH

>Homo_sapiens

MFGGWRMRARDLLGL

>Mustela_putorius_furo

-----MRARDLRGL

>Balaeoptera_acutorostrata_s

MFAGWRMRARDLRGH

>Manis_javanica

MLDGWRRRSRDLLGL

HG1070 ENSG00000147459 DOCK5

>Homo_sapiens

MAEASGARRSAGRRRPEPEEL

>Manis_javanica

MAGAPGARGSEARRRPAPQEL

>Loxodonta_africana

MAEEPGARSSAGRRRPAPEEL

>Heterocephalus_glaber

MAEEPGARKSA-RRRPQSQEL

HG1071 ENSG00000147573 TRIM55

>Homo_sapiens
-----MDTSAHRHVTAGC
>Oryctolagus_cuniculus
-----MDKSAHGHVTLGC
>Dipodomys_ordii
-----MDKSAHGHVTLGC
>Tupaia_chinensis
MLTPALCHLSGSILLSPAYMDKSAHRHVIPGC

HG1072 ENSG00000147874 HAUS6

>Homo_sapiens

MEGPPRPQADRREGS

>Felis_catus

MEGPPLPQAARREGA

>Myotis_lucifugus

MRGPPRPQAACREGA

>Galeopterus_variegatus

MDGPPRPQAARRGGS

>Homo_sapiens
-----MRRGK-DVIKCWRNTLIEAASSVAVWYGCRVLCDYTLMYSGSESL
RDLFCTLCIVGFGCLFV---
>Rousettus_aegyptiacus
-----MRREKVFKCWRNTFTEAASS---CGCVVWLLS-----SVGPF
ASVF-----
>Galeopterus_variegatus
MNSSLLINLSLNSSLFLCFTVSFTPLPHTPMSHNHACRVGNRTCQLSEDETVLCTYLSNCGRSGEERSLNARETPPLRHLLPVAVWCGCTVLCDCSLMYSGSESL
RNLFHSVSIVGFGCVCLFRA
>Trichechus_manatus_latirostr
-----MDSGSESL
RSLFCGLSIVGFGCMCLFRA

HG1074 ENSG00000150275 PCDH15

>Homo_sapiens

MRVDINASQKQVEHVNESSWN

>Myotis_lucifugus

MRLDINASQKQEV-----

>Equus_przewalskii

----MNASQKREE-----

>Orycteropus_afer_afer

MSLDISASEKQEE-----

>Homo_sapiens
-----MSNGAAGGGEL
>Mustela_putorius_furo
-----MSNGAAGGGEL
>Rhinolophus_ferrumequinum
-----MSNGAAGGGEL
>Chinchilla_lanigera
MKSPAPRGEVERQIPPCQSGSSSKALRAHPTHSVLTACVYMSNGAAGGGEL

HG1076 ENSG00000150967 ABCB9

>Homo_sapiens

MSSAETA-PQTRACCAPPRAHLVPGNRPGLALWMMMALPP

>Manis_javanica

MSCAEPAP-----

>Ictidomys_tridecemlineatus

MSCVEPAPWTT-----

>Tupaia_chinensis

MSGAEPAPPTTRALCSPLPTAHLVPGKRSSAPRTMTALPP

HG1077 ENSG00000151474 FRMD4A

>Homo_sapiens

MFLLSMLALPGAELASLLGEEK

>Myotis_brandtii

MFLGSILAPPGTKLASPLGEEK

>Oryctolagus_cuniculus

MFLVSMLALRGPEPASLLGEK-

>Fukomys_damarensis

MFPLSMLALWGAELASPPGEEE

HG1078 ENSG00000162607 USP1

>Homo_sapiens

MRAEGGAPLRNTPYNW

>Tursiops_truncatus

MRAERGETRLRNTLYDW

>Oryctolagus_cuniculus

MRARGGEPRLRNSVYNW

>Orycteropus_afer_afer

MQAEGGERLLRNTPYNW

HG1079 ENSG00000162975 KCNF1

>Homo_sapiens

MPA--PSPAAGCMPPRRAPAGCCPL

>Odobenus_rosmarus_divergens

MPG--RSPAAGCMPPRRAPAACRPL

>Oryctolagus_cuniculus

-----MPPRRAPAGGRPL

>Peromyscus_maniculatus_baird

MPAGSPAAATGCMAPLRRAPACCRPL

HG1080 ENSG00000164168 TMEM184C

>Homo_sapiens

MVQAE~~L~~RAIPR

>Balaenoptera_acutorostrata_s

MLQAE~~L~~RAIPR

>Miniopterus_natalensis

MVQAE~~L~~RAIPR

>Ochotona_princeps

MVQAE~~L~~RGIPR

HG1081 ENSG00000165392 WRN

>Homo_sapiens
MPGLQALLVVALHSHPAE-EDLLDWIFSGFLSDIVLYLPMKTLFFGLCK
>Pteropus_alecto
MPGFQALLSWLSTRHPAE-EDPFNCLFSGFYN-----
>Oryctolagus_cuniculus
MPGLQALVLWRPTSPPAEGEVPLTWLFSGAF-----
>Equus_asinus
MPGFRVLLPWGSTSHPAE-EDP-----

HG1082 ENSG00000165434 PGM2L1

>Homo_sapiens

MPFSEVGTPGPW

>Pteropus_alecto

MPFSEKGASGPW

>Dipodomys_ordii

MPFSEEGAPGPW

>Tupaia_chinensis

MPFSEKGTSGPW

HG1083 ENSG00000165804 ZNF219

>Homo_sapiens

MSVRRTAIPGTM

>Leptonychotes_weddellii

MSVRRTPIPGTM

>Myotis_davidii

MSVRRTPIPGTM

>Mus_musculus

MNVRRTPIPGTM

HG1084 ENSG00000165923 AGBL2

>Homo_sapiens

MG----PAPWEEEAGRYAALPVSDAPLASA

>Balaenoptera_acutorostrata_s

MGPAGVLAPPEEEAGRQAALPNSSASPV--

>Rousettus_aegyptiacus

MGPAMVLAPREEKAGRHAALPNSSASPM--

>Dasypus_novemcinctus

MGPARVLAPREEEAGRHAALPSSSASPV--

HG1085 ENSG00000166532 RIMKLB

>Homo_sapiens

--MNTSRGWGKGTEQSQLFHTLGSRSSFYHPLGSRHRDIN

>Pteropus_alecto

--MNPGRGWGKGTEQNQLSHTLGS--SLYHPLGSRHRDLN

>Loxodonta_africana

--MNTGRGWGKRTEQIKLFHTVGSRSRFYHPLGSRHRDLN

>Tupaia_chinensis

MDHEYCWGWTGTERASCP-TLWETSS-FCHLLGSRHRDIH

HG1086 ENSG00000167377 ZNF23

>Homo_sapiens

MLRSGRNINLCASRVWTVCSQAPDIGS

>Felis_catus

MLKSYRDSYLYAFQVWTVCLLTPNIGS

>Galeopterus_variegatus

MLRSCRDFYLY--EVWTVCSLPPDMGS

>Equus_asinus

MLRSCRGFYLYAFHVWTVYSLALNRGS

HG1087 ENSG00000168675 LDLRAD4

>Homo_sapiens

MLPEAGPAERTWTG

>Oryctolagus_cuniculus

MLPRAGLAERTCTG

>Rattus_norvegicus

MLPKAGPAERTWSG

>Tupaia_chinensis

MLLRAGPAE-----

HG1088 ENSG00000169740 ZNF32

>Homo_sapiens

-----MSRPGRPGP--RG-RPAASGEVGGPQS---RVPWTGERDAEVLRN^{SPWKNHMKRW}

>Canis_lupus_familiaris

-----M---LNSFQGLKDKRVFKNSPWKNHMKRW

>Ceratotherium_simum_simum

MLHQAIQISSIYLYPKLQLLLTSLFSLINSSALSCLFLLFCFVFCVCLFFPPQVLKHSPWKKHMKRW

>Ictidomys_tridecemlineatus

-----MQQVLRNSPWKNYMKRW

HG1089 ENSG00000169813 HNRNPF

>Homo_sapiens

MHLEFPRSPLRG

>Pteropus_alecto

MHLDFPRSPLRF

>Equus_asinus

MHLDFPRSPLRV

>Rattus_norvegicus

MHLDFPRSPLRF

HG1090.1 ENSG00000170458 CD14

>Homo_sapiens

MPCRILPVTVPLPETSFI AIFPGKEGGWLGGREVGR-----

>Orcinus_orca

-----MAPLLAKSFTAKFPRTADGVVGRKKCGEWQGSKRRERSDIPGLHKLSEAARG

>Rattus_norvegicus

MPLRLPVSVPCKTFHCNIY-----

>Tupaia_chinensis

MPCGILPVVAPLPETFFI AIFPRREVKGAAGRKRGVCVCV-----

HG1090.2 ENSG00000170458 CD14

>Homo_sapiens

MRFTISSTKHAVKYLRIFRDLVLVAGDQHKPRQ-GRSQRNESSRFSGI-----

>Felis_catus

MKFAIPSTKYPIIYLRIFR-----

>Orcinus_orca

MKFAISSTKYPVKYLRIFRELDLGDRRLTVITKTREN-----

>Manis_javanica

MKFAISSTKYPVKYLRIFGRLDLGEGRLIVTTKTRESQGNEVGRVSGMQAGKVRVLA

>Homo_sapiens
-----MRHLRRGRAGAKEGHPDMEPASSVSPDSARS-----

>Orcinus_orca
-----MGHTDKEPASLVNSDSGH-----

>Myotis_lucifugus
-----MGGAEAGQRDMEPVRSASPDGAC-----RPSCISRQEMATCSLENEPETEAAPGQRGQDSPLEVRGDS
PLTATDLGS
>Ceratotherium_simum_simum
MFILQAGRVRKERMKLQSTPSTASSEEGRAGAKAGHPDMEPASFVSPDSGHRALHLPAPGDGAAQPTCLAFRP-----

>Homo_sapiens

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>Ailuropoda_melanoleuca

-----MVRRRRPWGPTPRA

>Myotis_lucifugus

-----MVRQRPRGPTPRA

>Cavia_porcellus

MGVLGILVLLSLLARLPGNSPAQPLEPPPGGSVASLPRHMLFPAGGRRRAEKSETPPSTSASRPRGQSTKGGRRERGRSCRAKAPGPGRDSFSLTGDTLHTLDKD
PQESRHYPWQPHLTLDWCHGQPPRTYFGTQGRLGPSNAAMVRRRRPQGPTPPA

>Homo_sapiens

MYTVILTIALSHSYAKEEIIIRGYLPGPEETYVNFMNYYIRFPRSERKFLDII-----

>Panthera_tigris

-----MRAYLPSLEETSASQNVCVVSFPQSGRKLFEALSERWEADCFSTAA

>Dasypus_novemcinctus

----MFHMAHSRSYCAEEKVFMGGYLPKRKTSFHEMYILSVLRVK-----GSW-----

>Fukomys_damarensis

----MCRMAHSHSCWANEEMLIRGHLPGLOQETYNFESVFLTMVDG---FLPSVA-----

>Homo_sapiens
MGEPGEECERSGEEGRRQIGSGMCLRGRERALGPGVEKMRLWGCRGARSRW-----
>Panthera_tigris
-----MQLWGLPGRAVA-----
>Myotis_davidii
-----MLIEVHERALGPGIGKMQLGGPTVPSLAWR-----
>Marmota_marmota_marmota
-----MRLWGCRGSRSPGGNAAVPEVFGRDETLQGRVTCLQPASA

HG1095 ENSG00000179921 GPBAR1

>Homo_sapiens

MHLVHLCSSARTPDMVQTAAGLAAATP

>Ailuropoda_melanoleuca

-----MPSPARTPDSARSPAGLPAAVP

>Ceratotherium_simum_simum

-----MLSPARTPDVFRSPAGLAAATP

>Manis_javanica

-----MPSPARTPDIARSPAGLAAATP

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>Homo_sapiens
-----MDTVSTW-GLRYVAAALRFRNINWNQFAFEN-----
>Odobenus_rosmarus_divergens
-----MIL---IVPDLCIYCLTTNQFKSISWNQFAFENWTNTKT---
>Rousettus_aegyptiacus
MEKKRNMFLKNFLDAILIAFCMGIPTFIVLCFIVLHRCYFILFFYKVKARPITSKKITAGFVVILTLLWRSGETPALSLRFKII EWNQFAFENWTNTKT---
>Cavia_porcellus
-----MLEERIKSISWNQFAFENWMNTKDLIL
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HG1097 ENSG00000182481 KPNA2

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>Homo_sapiens
MPSSFFFLSPLPLAPKPYDSLPSQRVFQIHQWAHSLGSNQPIGMRSHREI
>Ursus_maritimus
-----MRGHREI
>Equus_asinus
-----MRSHREI
>Fukomys_damarensis
-----MRSHREI
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HG1098 ENSG00000183775 KCTD16

>Homo_sapiens

MKSCARKLWFEHGQFSPTVSYIHKHHMKWRSGSSVYFSQVPQ

>Odobenus_rosmarus_divergens

MENFARKFWLEHG-----

>Pteropus_alecto

MGSCARKLWFEHG-----

>Ochotona_princeps

MGNCARKLWFKRGQFSPTFSHIHKHQMWRFGSSVYIYHIPQ

HG1099 ENSG00000186334 SLC36A3

>Homo_sapiens

MVSSSSQSHCSLCPTAARAKLGEAKSPGKSWLGKQLRVKLRTILTEMGLS-----

>Mustela_putorius_furo

MVTSSSQSHSSLCPIALRAVLGGTGSPGESWRVANQMVRGPEGHNEMRLSKVPQKLSEA

>Galeopterus_variegatus

MVPSSAQSHCSLCPRAVRAESAEAESPGKSWQVAEQL-----

>Oryctolagus_cuniculus

MVPSSSQSHCSLGPTKARAALGEAKRPGESWQVAAGPRVSRGSPSPGPLEPGEAP----

HG1100 ENSG00000187815 ZFP69

>Homo_sapiens

-----MNSNLTNWLPKESA-----

>Felis_catus

MCGQCWFIPPLSFAPLEDCRGMHSRLLNWLPKEALLNLRKESVFQSC-----

>Miniopterus_natalensis

-----MHSNLCNRLPPKEAVLNLRQESVFQTHPSHISL

>Galeopterus_variegatus

MTG---ASGSLLSFVPLEENIDMYSNLPNWLPKETVLNLRGESVFQSC-----

HG1101 ENSG00000189334 S100A14

>Homo_sapiens

MSHQLLWGQL

>Manis_javanica

MSHQLLWGRL

>Nannospalax_galili

MSHQLLWGRL

>Tupaia_chinensis

MSHQLLWGRL

HG1102 ENSG00000196704 AMZ2

>Homo_sapiens

-----MKSHSTTFFQPGPDMSVLVS

>Galeopterus_variegatus

-----MPVLVR

>Ceratotherium_simum_simum

-----MPVLVR

>Tupaia_chinensis

MFCVRVKTPSTTRCQPDNMPVLVR


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>Homo_sapiens
MLGCKNAAQHGE MIFCPAGWCTLWSLTQTGAEGPTAVISRTKL-----
>Panthera_tigris
-----MVFSAAGWGLMWLAEP TRE-----
>Rousettus_aegyptiacus
-----MIFCTARWAIMWSLTQPGKKRASAMISRTKL-----
>Equus_caballus
-----MCCAAGCWGVMWSHSPPGPERPTAVMSRAKACVRGFPVGPSRVLLASSPC
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HG1104 ENSG00000205155 PSENEN

>Homo_sapiens

--MR-AVLPRPKTTISRETWGVSRKP-----

>Leptonychotes_weddellii

-----MSRKRPELQVAKASKRRK

>Oryctolagus_cuniculus

--MRTALPPRPEETNSRATCGLSRRP-----

>Ictidomys_tridecemlineatus

MRMRTAFPLQKERTTNSSETCGTSRKP-----

HG1105 ENSG00000213654 GPSM3

>Homo_sapiens

MRPPGVLPHEPPPLLQLEEFFVSVLPWGERD-----

>Rousettus_aegyptiacus

MRRPRVLPHELPPLLE-EILPV-FTPLGERQRSNKQFGWEKRTGG-S

>Equus caballus

-----MN--PLHDCSFSQSVLPWGERN-----

>Tupaia_chinensis

-----MLPWGERGQPS---WVGKENGGS

HG1106 ENSG00000215021 PHB2

>Homo_sapiens

MEMTCCLALPS--LGGQPSRKGRDFMRDSCARSSGP-----

>Odobenus_rosmarus_divergens

-----MRNSCARSSGPLWAPGRV

>Equus_asinus

--MTCCLALPKSLWEGRVPKKGGNFRMRNSCARSSGPQWPEGRV

>Marmota_monax

-----MRDSCARSSGPL-----

HG1107 ENSG00000217930 PAM16

>Homo_sapiens

--MRMPSAVSRTRSLRLSLTSDPPTLDPRPRGQEVGV-----

>Felis_catus

----MLCAASRTRSLP-----

>Myotis_brandtii

----MPSVASRTRSP-----

>Cavia_porcellus

MTMRMPSTPWTRSLLSFLTSDLPAALERGPRVQEAQARGPDA

HG1108 ENSG00000251247 ZNF345

>Homo_sapiens

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>Felis_catus

MAVENPQGSCKTVNQG-----

>Pteropus_alecto

MAVEHPQGTCKNVNQG-----

>Equus_asinus

MAVEHPQGTCKTVTQG-----

HG1109 ENSG00000278311 GGNBP2

>Homo_sapiens

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>Rousettus_aegyptiacus

MGNAARLFRPLLLLS--LPPVANVLRGGGCLSSRRLAVAGRSWEEAAAAAAGAAAAAAAGRRW

>Equus_asinus

MGNAARLSRPLLLLS--LPPVANVLRGGGCLRSRGLAVAGRSWEEAAAAAGAAE-AAAAAAAGRRW

>Microtus_ochrogaster

MGNAPRLSRPLLLRAPPFSPVANVLRGGGCLRSRGLAVAGRSWEEAAAAG-----AAAAAAAGKRW

HG1110 ENSG00000034152 MAP2K3

>Homo_sapiens

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>Tursiops_truncatus

MSVLRPGRARRPLD

>Ctenomys_sociabilis

MSTLGPGGARRPLD

HG1111 ENSG00000040531 CTNS

>Homo_sapiens

MEGGLSFAHERSREALAAPRVSVSLAADLIFPHAGAPISAPRPDPAALCP-----SKTRGNYSQSSSRDPAPRVWRSGDGPASPKV-----

>Pteropus_vampyrus

-----MACLILPHTRASIPA--KVPAPLRSS--STLHNCPAKPRENYSSHASLRDSKS-----GDSGQMASGLRSLSVKPAGEN
GYSLKRLHLVWSVSRASEVLSCLNLSRGVCRLLRGETVKAPFQELPLAC

>Ctenomys_sociabilis

-----MSDKPPGPLCPPCTTIRLSLVKTRKNYNCQGPSRRDLASTSQVTRVR-----

HG1112 ENSG00000068885 IFT80

>Homo_sapiens

MVTG-RY-----QVFESNRHRFPGT

>Miniopterus_natalensis

MVTGGREASW-----

>Microtus_ochrogaster

MVTG-RSGGFLVSGQSSESRRRFPGT

HG1113 ENSG00000072201 LNX1

>Homo_sapiens

MPSSFLQAPVHRS

>Peromyscus_maniculatus_baird

MPSFFLQPPVHRS

>Tupaia_chinensis

MPSSFLQAPVHRS

HG1114 ENSG00000073737 DHRS9

>Homo_sapiens

MGVTHRARREPEDSSHM

>Dasypus_novemcinctus

MGVTHSARREREDSSHM

>Jaculus_jaculus

MGVTHGVKRELQESSHV

HG1115 ENSG00000074219 TEAD2

>Homo_sapiens

MAGRPCPPACGSVGLSWSRPQLLP

>Odobenus_rosmarus_divergens

MAGRPCPPVCGSVGFSWSGLEFLP

>Physeter_catodon

MAGRPCPPVCGSVGLSWSWLEFVP

HG1116 ENSG00000084090 STARD7

>Homo_sapiens

MSGGSWPRDRETGSWPAI

>Oryctolagus_cuniculus

MRGGSWPRDRETLSGPAS

>Mesocricetus_auratus

MRGGSWPREREAGAGSAS

HG1117 ENSG00000089902 RCOR1

>Homo_sapiens

MRAKVALGSSLGA

>Oryctolagus_cuniculus

MRAKVALGSAPGA

>Manis_javanica

MRAKVALGTALGA

HG1118 ENSG00000090975 PITPNM2

>Homo_sapiens

MESMVPTPQLVSMLFPESPTIHLLSF

>Canis_lupus_familiaris

MEFTEPTPQLVPVLFESPTTCPLSF

>Mus_musculus

MESKEPTPPLLSVWFESPTTYPLSF

HG1119 ENSG00000092020 PPP2R3C

>Homo_sapiens

MKRNCERRR---FPQAGT-NELLGHVVRTRQRHTIKENAGLSWPLKSGLPRLPPSIKMVVGRPS

>Odobenus_rosmarus_divergens

MKRNCEAKKKKSLPRAGNAIGLLNHVVHTRQSPKLKK-----

>Ceratotherium_simum_simum

MKRNCEGRK---FFPRAGKA-----

HG1120 ENSG00000095585 BLNK

>Homo_sapiens

MLLPRRARNC

>Dasypus_novemcinctus

MLLPRRARNC

>Marmota_monax

MLLPRRARNC

HG1121 ENSG00000100350 FOXRED2

>Homo_sapiens

MEGLGIPG-SPKSQLETVESGQMSSE-DGFWAWP-----

>Balaenoptera_acutorostrata_s

-----MESGQMSSEVLGFWSWLRPKSQ

>Equus_asinus

MEGFRIPGGSPRSELETMESGPMSREGFGSWLCPK---

HG1122 ENSG00000100410 PHF5A

>Homo_sapiens

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>Acinonyx_jubatus

-----MEVKGRTEVP-----

>Ctenomys_sociabilis

MEASRTNHRDLEAGAIQVKGRTEVTQASGSPLG

HG1123 ENSG00000100884 CPNE6

>Homo_sapiens
MCEPVSRGCMCRHHFSV-----
>Manis_javanica
MRKPVSHGYMCLHHFLV-----
>Ctenomys_sociabilis
MCEPVSCGCMCRHHFCVDVGVHEPLQCVYLSVMPGVGAV

HG1124 ENSG00000100934 SEC23A

>Homo_sapiens

MLAGRRSSLRPGAGWRHP

>Oryctolagus_cuniculus

MLAGPRSSRRPGAGRCRP

>Tupaia_chinensis

MVAGLRSSQRPAGRRGP

HG1125 ENSG00000101574 METTL4

>Homo_sapiens

MNDKFSSMCMMSGFCTCISNLSVCMKCMFIEIQDI

>Felis_catus

MNVKFSFV-----

>Dasypus_novemcinctus

MNFKFSGYI-----

HG1126 ENSG00000101890 GUCY2F

>Homo_sapiens

MEFVNRLESLTGL

>Equus_przewalskii

MEFINRLQSLAGL

>Octodon_degus

MEFLNRLESLTGL

HG1127 ENSG00000103064 SLC7A6

>Homo_sapiens

MGGRAGSGAGAGPRSVGAEPGSSLPSPGAGCGPETARGWPIGAAREALRSLCGRGRQVELGLAAGDFISFSVLDPFMRRWLMKV

>Galeopterus_variegatus

-----MMRWLMKV

>Loxodonta_africana

-----MNGIRSCCGDFFFSVPDPFMMRRLMKV

HG1128 ENSG00000103852 TTC23

>Homo_sapiens

MVINLYKESPN-----

>Rousettus_aegyptiacus

MLINLFKESPNRYSGNQSVKSGC

>Fukomys_damarensis

MVINLYKESPN-----

HG1129 ENSG00000104432 IL7

>Homo_sapiens

MLMIPKIEPADQAQSRN

>Oryctolagus_cuniculus

--MNPKIEPAYQAQTRN

>Manis_javanica

--MNPKIEPADQAQSRN

HG1130 ENSG00000105559 PLEKHA4

>Homo_sapiens

MSERETGRDRDQRETQKVRVGREVV

>Equus_asinus

MSDRETGRDRD-----

>Manis_javanica

MSDRETGRDRD-----

HG1131 ENSG00000106780 MEGF9

>Homo_sapiens

MVRPVAVAAVAEASLVGLQRGEDD

>Manis_javanica

MVRPVAVAA--ATASLVRVQRGEDD

>Microtus_ochrogaster

MVRPVAAAAAATASLVGRQGGEDD

HG1132 ENSG00000109771 LRP2BP

>Homo_sapiens

MKTLIYHSTVIHLITWQSNTDRKIKLN---NS-----

>Rousettus_aegyptiacus

MKALIFHSPVIHLITWQSNTDRKIKPN---KIKCIPR

>Cricetulus_griseus

MKALTYHTVVIHLVTWQSNTDWKRKLSTTAKIQCIPIR

HG1133 ENSG00000111328 CDK2AP1

>Homo_sapiens

-----MSSIGYSNPGAWPDLGVWDLRA

>Manis_javanica

-----MSRTGCSYSGK-----

>Tupaia_chinensis

MDLKSMMSGIGCSRSGAWPDPSIWDLRA

HG1134 ENSG00000112984 KIF20A

>Homo_sapiens

----MSFFPLRQSKHPKPVTLCTPVKIVAKEGQELAAEASR-FPLGS----

>Ceratotherium_simum_simum

MAAEASGFPLGFLEK----KYLGFK--KKC-----

>Chinchilla_lanigera

MAARASVFPLGFLVN----KCLGFK--EKRWEESRAKQSKLATLGIADTR

HG1135 ENSG00000113597 TRAPPC13

>Homo_sapiens

MENKVFYAYVSKIEEMDLLKRSQFVKDTVGEFKVPPPERG

>Oryctolagus_cuniculus

-----MGLVKRSRWVRKGRSERRI-----

>Ceratotherium_simum_simum

-----MALVKRSCWMRR-----

HG1136 ENSG00000113749 HRH2

>Homo_sapiens

MGAGTSYGEYSCVST

>Myotis_lucifugus

MGAAVSYGEGCSHVST

>Manis_javanica

MGAAASYGEGHRHVHT

HG1137 ENSG00000115307 AUP1

>Homo_sapiens

MPGIVVSAGREL

>Pteropus_vampyrus

MPGIVVSAGREL

>Galeopterus_variegatus

MPGIVVPAGREF

HG1138 ENSG00000116871 MAP7D1

>Homo_sapiens

MRRGTPVLATGRRRRRR

>Elephantulus_edwardii

MRRGTPVLAAGRRRRRCR

>Cavia_porcellus

MRRGTPVLASGRRRRRR

HG1139.1 ENSG00000118308 LRMP

>Homo_sapiens

MQTQNCRSSGEAYHFPEKKNTFSVLPAS

>Canis_lupus_familiaris

MQTQNCRSSVEAYHFPEKKSTFSVSYA-

>Pteropus_vampyrus

MQTQNCRSSVEAYHFPEKKSTFSVSCA-

>Ceratotherium_simum_simum

MQTQNCRSVEAYHFPEKKSTFSVSCA-

>Manis_javanica

MQTRNCRSVEAYHFPEKKSTFSVSSA-

>Loxodonta_africana

MQTQNCRSSVEAYHFPEKKSTFSVSCA-

HG1139.2 ENSG00000118308 LRMP

>Homo_sapiens

MKEATLQKEAT

>Equus_asinus

MKEATLQKEAT

>Loxodonta_africana

MKEATLQKEAT

HG1140 ENSG00000118495 PLAGL1

>Homo_sapiens

MLPLPWSGVQLQGLC

>Tupaia_chinensis

MLPLPWGAQLQ---

>Trichechus_manatus_latirostr

MLPLPWSGVQLQWL

HG1141 ENSG00000121964 GTDC1

>Homo_sapiens

MHREPKSVTEIVVSLH-----

>Equus_przewalskii

MHREPKSVTEIVVVRGVCMSRI--

>Chinchilla_lanigera

MHREPKSVTEIVCV--VCLLSPVMH

HG1142 ENSG00000124613 ZNF391

>Homo_sapiens

-----MLDLQEAEEGSAQKYL-

>Odobenus_rosmarus_divergens

MVIQSEGGQLWMLDLQGTEEGSEQKYLGG

>Galeopterus_variegatus

-----MLDLQGAEEGIAPKHLR

HG1143 ENSG00000125245 GPR18

>Homo_sapiens

MPSFQGELMLSVTS

>Rousettus_aegyptiacus

MPSFQVELMLSMTS

>Galeopterus_variegatus

MPSFQGELLLSMIS

HG1144 ENSG00000128203 ASPHD2

>Homo_sapiens

MPPPAPAAPSPPR

>Ailuropoda_melano leuca

MPPPAPAAPSPPR

>Rhinolophus_ferrumequinum

MPPPAPAAPSPPR

HG1145 ENSG00000128585 MKLN1

>Homo_sapiens

-----MLENMGIGIRFWRRNVS-----

>Rousettus_aegyptiacus

MIGFITHSILENMGIGIRYVQRAEGAEVNQRMHR

>Ceratotherium_simum_simum

-----MGIGIRYVQRAEGAEVNHRMHC

HG1146 ENSG00000130413 STK33

>Homo_sapiens

MVISFLSAALTCEYVSSASLT

>Dasypus_novemcinctus

-----MCEYESSASLT

>Oryctolagus_cuniculus

-----MCEYKSSASLT

>Homo_sapiens
-----MPRPRSSLKKNVNRCLFVFCHPFFRTGDTNR
>Rhinolophus_ferrumequinum
MRSNSLLRRQQNLASPKAPAVAGFIRMLWPRSSLKDVN-----
>Ceratotherium_simum_simum
-----MLWPRSSLKSVN-----

HG1148 ENSG00000132938 MTUS2

>Homo_sapiens

MAVKLIFWGIGSHGLIGSHSAGT

>Mustela_putorius_furo

MAVKLLFWGSRSYGLIGSHSAGT

>Myotis_davidii

MSVKLVFWGSRSHGLIGSCSASP

HG1149 ENSG00000132975 GPR12

>Homo_sapiens

-----MILDCHPAVFKH

>Canis_lupus_familiaris

MVVSEWGLASVCVSFCMILDCHPAVSKH

>Galeopterus_variegatus

-----MILDCHPAVCKH

HG1150 ENSG00000135299 ANKRD6

>Homo_sapiens

MQTSFLCHLSVIQKCSSDL

>Leptonychotes_weddellii

MQTSSLCHLSIIQKHSAHL

>Tupaia_chinensis

MQTSLLCHPSVIQKHSSGL

HG1151 ENSG00000137168 PPIL1

>Homo_sapiens

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>Mustela_putorius_furo

MELALFSVLAISFFSSRIPASRPWKGDPSSSLQSPKSWHRKG

>Chinchilla_lanigera

MNLAFSSLLALSFF-----

HG1152 ENSG00000138658 ZGRF1

>Homo_sapiens

MTSRCFAGEIRKWILCNLTGGINS

>Ursus_maritimus

MTSRSFAGEIRKWILWT--GHINN

>Chinchilla_lanigera

MTSRSFAGEIRKWMLCS--GGINT

HG1153 ENSG00000138738 PRDM5

>Homo_sapiens

--MCRLPGAKRRC

>Canis_lupus_familiaris

MSMCRLPGAERWC

>Galeopterus_variegatus

--MCRLPGAERRC

HG1154 ENSG00000139725 RHOF

>Homo_sapiens
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>Balaenoptera_acutorostrata_s
MAKLKDSQLEE-----
>Nannospalax_galili
MAKLKDSQLEE-----

HG1155 ENSG00000141668 CBLN2

>Homo_sapiens

MKVVTPFNIKTWRELGKEKESKRREATGAFKGV-----

>Erinaceus_europaeus

---MKVLKKEWREFGKEKEGSPSRGASGASGA-----

>Cavia_porcellus

MKVVTPFKIKTWREFGKEKESKRDAAGAFEGLLAPSS

HG1156 ENSG00000144741 SLC25A26

>Homo_sapiens

MAAPSARGRDPLLLRLGL--

>Myotis_brandtii

MAAPSARGRDVLRDLSGL--

>Equus_asinus

MAAPSAWGRDPALLSLELYP

HG1157 ENSG00000148123 PLPPR1

>Homo_sapiens

MYLAPGSRTAQ

>Canis_lupus_familiaris

MHLAPGSRTAQ

>Pteropus_alecto

MHLAPGSRTAQ

HG1158 ENSG00000149571 KIRREL3

>Homo_sapiens

MVGANPRGPA-EAEHREPPRKRN

>Cavia_porcellus

MVGANQRGPAEAEHREPPRKRN

>Trichechus_manatus_latirostr

MVGASQRGPAALAESEPGQRN

HG1159 ENSG00000152822 GRM1

>Homo_sapiens

-----MSSKQTQH LAHRCQHDFHCTLDQFTLMHYR

>Myotis_lucifugus

---MCTLSPRASTTDSFQLTAGCHHDAHCPDLPFTLVHR-

>Heterocephalus_glaber

MPGSSDLGTTALSTPTQRP AHRCQH DVQCTLDQFTLIHL-

HG1160 ENSG00000154162 CDH12

>Homo_sapiens

-----MMCQRHAVFCF--EGGEMTGGNPGPPLARRSPLQLSSSRSESIIDLKGKCGGSHREGSRLF

>Rousettus_aegyptiacus

-----MCQRHAVFCF--EGGEMTGRESWAPIGWPLSAAVALQ-----PL-----

>Mus_musculus

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HG1161 ENSG00000154227 CERS3

>Homo_sapiens

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>Equus_caballus

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>Odobenus_rosmarus_divergens

MHSFCSKYDLNCILEIITYT

>Ceratotherium_simum_simum

MHAVCSKYDLNCILEFIYT

HG1163 ENSG00000157637 SLC38A10

>Homo_sapiens

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>Odobenus_rosmarus_divergens

--MRQPQGLAGSGG

>Ctenomys_sociabilis

MAMRRPHGLAGSGG

HG1164 ENSG00000162639 HENMT1

>Homo_sapiens

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>Dasypus_novemcinctus

MASGHAPPRPLGDAKPTARAGAQD-----

>Peromyscus_maniculatus_baird

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HG1165 ENSG00000162694 EXT2

>Homo_sapiens

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>Acinonyx_jubatus

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>Pteropus_alecto

-----MFPDTLASSACPFAISP-ITINPGASGSKA

HG1166 ENSG00000165071 TMEM71

>Homo_sapiens

-----MCVGI--CEKKEASYFSNNFVLCQLEEEAGNSLWKEHRICEV-----

>Panthera_tigris

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>Heterocephalus_glaber

-----MPFQQLSPQFHHQKQEAALYSSKCFAIYQLEEETGNSLWKDYTYGQIIFHNTCFALMEQKICEV

HG1167 ENSG00000165934 CPSF2

>Homo_sapiens

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>Odobenus_rosmarus_divergens

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>Pteropus_alecto

-----MRGNCSQIHKELFL-----

HG1168 ENSG00000166669 ATF7IP2

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-----MKHLNEGLITLNSAFVKSLSLHFAVLTLLV

>Equus_caballus

-----MGKNIQDKDNLVHRKAIENAKVKHLYEGLITLNSAFVKI-----

HG1169 ENSG00000167637 ZNF283

>Homo_sapiens

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>Physeter_catodon

-----MYVSSKKVQI-----

>Rousettus_aegyptiacus

-----MNVLRKKAQV-----

HG1170 ENSG00000167858 TEK1

>Homo_sapiens

METALFTSLFCKSWKLQLG-----

>Myotis_lucifugus

METSLFTFLFCESRELQLGLGGSYSELV

>Equus_asinus

METALFTSQFCKSSGLPWEG-GSPPELV

HG1171 ENSG00000167968 DNASE1L2

>Homo_sapiens

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>Myotis_davidii

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>Cavia_porcellus

MLGQEWGWSFLTA-CLPKRIWLKEADSR----

HG1172 ENSG00000170381 SEMA3E

>Homo_sapiens

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>Rousettus_aegyptiacus

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>Loxodonta_africana

MNRLPK-----

HG1173 ENSG00000170464 DNAJC18

>Homo_sapiens

MGQHLNHIGHRTDLSITSKNPLQFNM--

>Odobenus_rosmarus_divergens

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>Balaeoptera_acutorostrata_s

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HG1174 ENSG00000173918 C1QTNF1

>Homo_sapiens
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>Mustela_putorius_furo
-----MCAGSVGGSAPCSH-----L-----AGVCSLRVCPAFLPLPLLSRNRASAGQRDLGPEEVTVPGRQGPAAACTRPLCTFFPE
DFFCPPGSL
>Ceratotherium_simum_simum
-----MRWERSRLRGRSH-----L-----AGVCSLRVCPAFFVSSFTFEKP-----RFRFWPK
RL-----

HG1175 ENSG00000174473 GALNTL6

>Homo_sapiens

MVLWVRSVARKEW

>Odobenus_rosmarus_divergens

MFLWVRSIAGKEW

>Marmota_marmota_marmota

MFLWVRSVAGKEW

HG1176 ENSG00000176472 ZNF575

>Homo_sapiens

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>Ailuropoda_melano leuca

MKFSNKKEAVHAASMD

>Heterocephalus_glaber

MKFNDRKDAVDAAVID

HG1177 ENSG00000178295 GEN1

>Homo_sapiens

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>Acinonyx_jubatus

MTEGRLPKPRRKGCPVF--

>Equus_asinus

MTEGRLPKPRGEGCPVCFK

HG1178 ENSG00000182670 TTC3

>Homo_sapiens

-----MCMRNITCTSNL

>Canis_lupus_familiaris

MRYLKWHVDFLIVKNLMCMKNVSCSTSNL

>Pteropus_alecto

-----MCMKNINCTSNL

HG1179 ENSG00000185933 CALHM1

>Homo_sapiens

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>Ceratotherium_simum_simum

MRWAPSVRSGPQGPSLRQW

>Tupaia_chinensis

MGWAPSGQSGPQGPWRRQ

HG1180 ENSG00000188674

>Homo_sapiens

MLQHASRSRERTKALEPVSGL-----

>Acinonyx_jubatus

MLQHASRSRERTKAPESVSGCL-----

>Rousettus_aegyptiacus

MLKHASRSRERTKALESAYRLREAGCSHRISGAV

HG1181 ENSG00000189058 AP0D

>Homo_sapiens

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>Ursus_maritimus

MDKTSHLCVWYRAKLLGQPS

>Pteropus_vampyrus

MDKTFHLCVLYRAKLLGQPS

HG1182 ENSG00000196155 PLEKHG4

>Homo_sapiens

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>Panthera_tigris

-----MKKAPRNLV

>Loxodonta_africana

-----MKKAPR---

HG1183 ENSG00000198133 TMEM229B

>Homo_sapiens

-----MKVACRDGKCLRRDTWKLPAPQPRIS

>Mustela_putorius_furo

-----MDRDTWKPPADQPRIS

>Cricetulus_griseus

MSGIELFRPHAMALLMVADMEHASLGFFPQGDRDTWKLPANQPRIS

HG1184 ENSG00000198894 CIPC

>Homo_sapiens

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>Physeter_catodon

-----MKRVLMNALPAQ

>Tupaia_chinensis

MGRAIQMKRVPM SALAAW

HG1185 ENSG00000198920 KIAA0753

>Homo_sapiens

-----MCL--LPS---AFFMCATALEIRTLRQLSLCSQEVSVFKQI-----

>Balaenoptera_acutorostrata_s

MPRPQFCRLLHSAALAPGLWRCQASWDCLTRVPPPTFAFDHVSSTALEIRNL----YTSTDVSVFKQIQSTILEFIQKLKLGIS-

>Manis_javanica

MEN----KIIRPLASKGKCWPHE-SCRCPGPISAGSFI--L-----QLQP-----LNSSDVSPVGI--ASLMCFLPSSFLIMSL

HG1186 ENSG00000204923

>Homo_sapiens

MGATVVLASPKT--

>Ursus_maritimus

MGATVALASPET--

>Ceratotherium_simum_simum

MGATVVLASPETYR

HG1187 ENSG00000213762 ZNF134

>Homo_sapiens

MAAAVMGPAQILCGC

>Ailuropoda_melano leuca

MAAAVMDPA-----

>Manis_javanica

MAAAVTDPA SILCGC

HG1188 ENSG00000214415 GNAT3

>Homo_sapiens

MSKPQLCSTFEKSEHIN

>Rousettus_aegyptiacus

MLKPELCSTFEKV----

>Condylura_cristata

MSKPELCSTFEDV----

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>Homo_sapiens

-----MELTSTTEFLHCKYTYVC---PPSQLSCQCLE-----

>Ailuropoda_melanoleuca

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>Marmota_marmota_marmota

-----MNCKHTYNTC---LPSHTSCECFERTGCGSFNFISRMTLIRHSMFFFA

HG1190 ENSG00000123684 LPGAT1

>Homo_sapiens

MHRCAGIVVRRRLRSSVSGKSY-----

>Galeopterus_variegatus

MNQCAGIAG-RPRCSVSGKSDREVPVLSFHS-GRHFGDTEGF

>Ictidomys_tridecemlineatus

MKQCAGMVVERTPSFSLSGKSDREVPASVLSLVYPRLGDTEGV

HG1191 ENSG00000164331 ANKRA2

>Homo_sapiens

MSESFFLGLFGHSWPVATERTFFPARVSPAGDSGL-LSRDAGTPVA--YF-----

>Oryctolagus_cuniculus

MSERFPPGLSEHCWPRRRSGRPLPRVCPAASSWPGTPAAYFLKIQISRIHWISLIMKKCFN

>Tupaia_chinensis

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>Homo_sapiens
-----MWNGVWGSAGLLSALGKGTGRDRDL-RSQPAAPAGQLA-----
>Oryctolagus_cuniculus
-----MWNGVLGSAGLLSALGEGTGRAGTSARROPAAPSARGRLCPLPAPHMPPAPLRGWPL
>Chinchilla_lanigera
MRPWSFPRPSHPLPASLLGNKGASGNWAPQAPGPAPAPALLMWNGVWGSAGPLSALGGGDQ-----GPGPAAPRPRGGLCQLPPLTPPHP-----

HG1193 ENSG00000177706 FAM20C

>Homo_sapiens

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>Dipodomys_ordii

MDLDPRGGAAFVPSSS

>Tupaia_chinensis

MDLDPRGGEAFVSNQG

HG1194 ENSG00000214694 ARHGEF33

>Homo_sapiens

MGTSRENKKKTSKNML

>Oryctolagus_cuniculus

MGTSREIMKKTSKNMM

>Fukomys_darlingi

MGTSREIRRKTSKNMV

Supplementary Figure S6

(a) *PTP4A1*

1 GCTAGCCTGTGTCGCCGCCGCTCGGGACCGGCTGT**ATGATTAGGCCACAATCTTCTGTG**
M I R P Q S S V
M I R P Q S S V

61 **TCGCCGCCGCTCGGGACCGGCTGTCAATGAGTAAACATATTCCTCAATTCTGTGGTGT**
S P P P R D R L S M S K H I P Q F C G V
S P P P R D R L S M S K H I P Q F C G V

121 **CTTGGTCACACATTTATGGAGTTTCTGAAGGGCAGTGGAGATTACTGCCAGGCACAGCAC**
L G H T F M E F L K G S G D Y C Q A Q H
L G H T F M E F S E G Q W R L L P G T A R

181 **GACCTCTA**^C**GCAGACAAGTGA**ACTGTAGAACTGATTACTGCTCCACCAAGAAGCCCCCA
D L Y A D K *
P L R R Q *

241 TAAGAGTGGTTATCCTGGACACAGAAGTGTTGAATTGAAATCCACAGAGCATTTTACAAG
301 AGTTCTGACCTGGATGGGGTAAACCTCAGTGCACCTCTTTTCTGTTGGCCTCAGTATTAC
361 TGGATTGAAGAATTGCTGCTTCTTGTTAGGAGGTTCAATTCACCTATCATTACTTACAAC
421 TTCATACTCAAAGCACTGAGAATTTCAAGTGGAGTATATTGAAGTAGACTTCAGTTTCTT
481 TGCATCATTTCTGTATTCAATTTTTTAATTATTTTCATAACCCTATTGAGTGTTTTTTAA
541 CTAAATTAACATGGCTCAAGCTT

(b) *MKKS*

1 GCTAGCTTGAATCTGAGCTTCATATCGAAAGAAGAG**ATGAAAAATACCAGTTGGATTAGA**
M K N T S W I R
M K N T S W I R K
61 **AAGAACTGGCTTCTTGTAGCTGGGATATCTTTCATAGGTGTCCATCTTGGAACATACTTT**
K N W L L V A G I S F I G V H L G T Y F
E L A S C S W D I F H R C P S W N I L F
121 **TTGCAGAGGTCTGCAAAGCAGTCTGTAAAATTTCACTCTCAAAGCAAACAAAAGAGTATT**
L Q R S A K Q S V K F Q S Q S K Q K S I
A E V C K A V C K I S V S K Q T K E Y
181 **GAAGAGTGA**AGTAAAATAAATATTTGGAATTACTAATTTGTCATTAAATCATTCTATGCT
E E *
E E *
241 GATTAGCTTCATAAACATTGAACTTTTTGATTTTATAGCCACAATGCTGCATATTCATAC
301 TTTAATTCCTAAAGAATAATTTTAAATGTTAAACGTGATAATGCAATAAATAGAAAAAT
361 GTGGTTTACAAAATAAAAACGGTCTTCACTAGTTACCACCTGAAGTAAGATGTCTCGTTA
421 AGCTT

(c) SLC6A8

1 GCTAGCCGCCCCGCGCGCCCCCGGGCCCCCGACACAC**ATGAGATTCTTCAGGCTCACTTTC**
M R F F R L T F
M R I L Q A H F Q

61 **AAGTGCTTCGTGGACTGCTTCTGA**CTGCGCCGCCCCGCGCCCCGCACCCCGCCGCCCCGCC
K C F V D C F *
V L R G L L *

121 GCCGCCCCGTCCCCGGCCCCGGCCGCCCCCGGCCCCGGCCGGCCCGCGCCCTCGGGGC

181 CCTCCCCGGTGCCGCCGGTGCCCCCGCCTGACCGCCGCCCCCGTGAGGCGCCGCGACC

241 CCGGCCCCGGCCGTGCGGCCCCGCCGAGGCC**ATGGAAGCTT**

(d) *FAM13B*

1 GCTAGCGAAGTACTGATCGAGTTCTGCATTTCTTCA^AATGAGGAACTACAGGCTGATCTTC
M R N Y R L I F
M R K L Q A D L L

61 ^ATGCCATTAATCTCAAACAGCCATAAATGACAAAAGAATGCTTGCTCAGTGAGGGTAGCTGG
C H N L K Q P *
P K S Q T A *

121 TGCAGAAGCCATTTTTTAAACTTAGGTATTTAAGTACTGAAAGAAAAGACAGCTTTGATT

181 TCTGGCTGCAAAAAGATATGAAAGCTT

(e) *MIEF1*

1 GCTAGCGGTGTGACACCCAGCCCCCTGCCAGTCCCCC**ATGGCCCCGTGGAGCCGAGAGGCG**
M A P W S R E A
M A P W S R E A

61 **GTGCTGAGTCTCTATCGGGCTCTGTTGCGCCAGGGCCGACAGCTTCGCTACACTGATCGA**
V L S L Y R A L L R Q G R Q L R Y T D R
V L S L Y R A L L R Q G R Q L R Y T D R

121 **GACTTCTACTTTGCCTCCATCCGCCGTGAATTCCGAAAAATCAGAAGCTAGAGGACGCT**
D F Y F A S I R R E F R K N Q K L E D A
D F Y F A S I R R E F R K N Q K L E D A

T
↓

181 **GAGGCCCGGGAGAGGCAGCTGGAGAAGGGCCTGGTCTTTCTCAACGGCAAATTGGGGAGG**
E A R E R Q L E K G L V F L N G K L G R
E A S G E A A G E G P G L S Q R Q I G E N

241 **ATCATT****TAG**GATCCTCCAAGGGAAAGAGGACAAAGGTGCCTTCTGTAGACACTCCTGCTC
I I *
I *

301 TCTTCCATCCCCATCTTACAGATGTATTAAGAAGCCTCAGATGAGCAATGGAAGCTT

(f) *EIF5*

```
1  GCTAGCCAGCCATTGGTACCTGTATTGGGGAAACATAGCATACAAGCAAGAAGCTTACAG
                                     C                                     A
                                     ↑                                     ↓
61  CCTCAGTGGCGAAAATTTTTTCATGTCAGAGACCGAGAACTCTTGCAGTCGTTTATGTCA
                                     M   S
                                     M   S   I

121 TCCCTTCTTCTCCAGACAGAAGATACCAAAAAGTTGCAATCAAAGATCTCTTCATCTTAT
    S L L L Q T E D T K K L Q S K I S S S Y
    P S S P D R R Y Q K V A I K D L F I L

181 TGATAAAAGCCACTAATAAGCCAAAATGTCCTCGAG
    *
    *
```

(g) MAPK6

1 GCTAGCGTCGGAGAAGTCCCGTTGTATCAGAGTAAG**ATGGACGGTAGCTTTGATTGTGAT**
M D G S F D C D
M D V A L I V I

A
↓

61 **TGTGGTGAGCTGGAGCCACCTGATCACTAA**CAAAAGACATCTTCTGTTAACCAACAGCCG
C G E L E P P D H *
V V S W S H L I T *

121 CCAGGGCTTCCTGTTGAAATAAATATATAGCAACAAAGGAAAAAAGAAGCAAAACGGAA
181 ATAGTGCTTACCAGCACCTTAGAATGATGCTGCTCAGGACCAGTCCAACACTGAATGTAT
241 CTGCACTGTGAGGAGAATGTTCATAGAAGCCTGTTGTGTGCATATTTATTCACATTTTGT
301 TTAAATGTTAAATCGTTTAGCACGGTAATCTGAGTGCACAGTATGTCATTTTCATTCCGTT
361 TGAGTTTCTTGTTTTTCGTTAAATGTCTGCAGAGTTGCTGCCCCCTTCTTGAACTATGAGT
421 ACTGCAATCTTTTTAATTCTCAATATGAATAGAGCTTTTTGAGCTTTAAATCTAAGGGGA
481 ACTCGACAGGCCTGTTTGGCATATGCAATGAACATCAAGAAACCATCTTGCTGTGGAAGC
541 ATAATTATTTTTCTTCTCCCTTTTTGAAAGATCTTTCCTTTTGATGCCAGTTTCTTCCT
601 TGTTTACACAAGTTCAATTTGAAAGGAAAAGGCAATAGTAAGGGTTTCAAAATGGAAGCT
661 T

(h) *MEIS2*

1 GCTAGCTTTGATTGACAGCTGGAGTGGCAAAAAGCC**A**TGA**AAC**CACGACAGTTCGGTTACA**C**
↓
M K H D S S V T
M K T R Q F G Y L

61 **TGTGGGCTGCTGACGGGCCGCTCGTAAC**CTTCAGTTCGGGGGCTTGACAATTTTTTTTCTT
C G L L T G R S *
W A A D G P L *

121 CTTTTTCTTCTTTTCTTTTCTTTCTTTTCTTTTCCAAGTGGGGAAGAGAAGAGAAAG
181 AGGGGGAAAGGAGGACCGAAGAGGAGGAGGAGGGGAGGGGGAGGAGGAGGAGGTGGAGG
241 AGGAGGAGGAAGATCAGGAGGAGGAGGAAGAAGAGGAAAAAAGAGAAAAAGAAGAAATAT
301 CACAGAAAAAAAAAATTCTTCGTTGTCTAGACTGGGCTTTTTTTTCCCCCTAAAAAATAGC
361 ATATTGGAGAATTGGGAGAAGTCTCTTTGGTTTGGAAAAAAAAAAGGAATCTTCAGCC
421 TAGATCACTTTCTTATCCGGACTGGGATATTAAATATAACGACACATCCAGGAGTTTATTG
481 GAGCGCAGACTG**ATGC**CTCGAG

(i) KAT6A

1 GCTAGCCAACAGGTTGTTTTGGTTTCTATAGTACAATTGGGGTGGCATTCTGTTTTGTGA

61 AAGGAGGAAGGACTTAGGCCAGAAAACATCATATGCT**ATGGTTAACTGGTTCCCAGCCTCC**

A
↓

M V N W F P A S
M V K L V P S L R

121 GAGAATCTTGT**TTTCCA**TTGGTGTA**AACTTACTCAGCATCAGGATAAGGGATAA**CGACTC

C
↑

E N L V F H G V K L T Q H Q D K G *
E S C F P R C K T Y S A S G K G *

181 TATGGATATACAGAATCCTTCACCA**ATGGTAAAAC**CTCGAG

(j) *SLC35A4*

1 GAGCTCTGCGCCTGCGCAACAAGTTCGGCGGGGAAGATGGCGGA^CAGACAAGGATTCTCTG
M A D D K D S L
M A T T R I L C

61 CCTAAGCTTAAGGACCTGGCATTCTCAAGAACCAGCTGGAAAGCCTGCAGCGGCCTGTA^A
P K L K D L A F L K N Q L E S L Q R R V
L S L R T W H F S R T S W K A C S G V I R

121 ^AGAAGACGAAGTCAACAGTGGAGTGGGCCAGGA^CTGGCTCGCTGTTGTCTCCCCGTTTCCTC
E D E V N S G V G Q D G S L L S S P F L
R R S H S G V G Q D G S L L S S P F L

181 ^CAAGGGATTCTGGCTGGCTA^CTGTGGTGGCCAAACTGAGGGCATCAGCAGTATTGGGCTTT
K G F L A G Y V V A K L R A S A V L G F
K G F L A G Y V V A K L R A S A V L G F

241 ^CGCTGTGGGCACCTGCACTGGCATCTA^CTGCGGCTCAGGCATA^CTGCTGTGCCCAACGTGGAG
A V G T C T G I Y A A Q A Y A V P N V E
A V G T C T G I Y A A Q A Y A V P N V E

301 AAGACATTAAGGGACTATTTGCAGTTGCTACGCAAGGGGCCCGACTAGCTCTAGGTGCCA^A
K T L R D Y L Q L L R K G P D *
K T L R D Y L Q L L R K G P D *

361 TGGAAGAGGCAGGATGAGCAGCTCAGCCTTCAGGTGGAGACACTTTATCTGGATTCCCCA

421 GCTGTCATCCATTTGCTATCTCCAACCTTCCTGCCACCTTCATCCTTGCCCTCCCTTCCTG

481 CAGATTGTGGACAGTAGTTCCTCAGCCTGCACCCTGGATTTCCTTCTCCCTTCCTAGCT

541 CCATGGGACTCGCCCCAAGACTGTGGCTTCAAGGACCACCAGCCCCTTACTCTTCAAGCC

601 CTGACTGTGGAGTTGGTAGATGCCTCTGATCCTCAGTATTCTCTCTGGCAATGTTCCACG

661 GCTTCTCCTTCCTGGGAGCTGGCTCCATAACTTGATTTTCCCCAAACGTGTTGCAATCCC

721 TGCTGCCCCTTAGCCACCCAGGGTCTTGTGTGGGTATGAGCTCGAG

(k) *LRRC8B*

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1  GCTAGCTCAGAAGGTGATCTCTTTAATGCTTTCTTTTAAGAATTTTCAAATTGAGACT
61 AATTGCAGAGGTTCCAGTTGACCAGCATT CATAGGAATGAAGACAAACACAGAGATGGTG
                                     M K T N T E M V
                                     M K T N T E M V
                                     A
                                     ↓
121 TGTCTAAGAACTTCAAAAGGTGTAGACCTCCTGACTGAAAGCATATTGGATT TATTTAAT
    C L R N F K R C R P P D *
    C L K T S K G V D L L N *
181 TTTTTTCACTGTATTTCTGTCCTCCTACAAGGGAAAGTCATGATTACACAAGCTT
```


(I) *CDH11*

1 GCTAGCCGTGTTGTCATTTGTTGAGTGACCAATCAG^A**ATGGGTGGAGTGTGTTACAGAAAT**
M G G V C Y R N
M G R S V L Q K L

61 **TGGCAGCAAGTATCCAA**^C**TGGGTGA**AGAAGAAGCTAACTGGGGACGTGGGCAGCCCTGACG
W Q Q V S N G *
A A S I Q R *

121 TGATGAGCTCAACCAGCAGAGACATTCCATCCCAAGAGAGGTCTGCGTGACGCGTCCGGG

181 AGGCCACCCTCAGCAAGACCACCGTACAGTTGGTGGAAGGGGTGACAGCTGCATTCTCCT

241 GTGCCTACCACGTAACCAAAA**ATGA**AAGCTT

(m) *PNRC2*

1 GCTAGCCTCTCAAACTTGTGTGCTGAGGAGACTCAG**ATGTTGGCCTCAGCTCCTAGGCTG**
M L A S A P R L
M L A S A P R L

A
↓

61 AACTCAGCAGATCGGCCCATGAAA**ACTTCTGTATTGAGACAAAGGAAGGGATCTGTCAGA**
N S A D R P M K T S V L R Q R K G S V R
N S A D R P M K N F C I E T K E G I C Q K

121 AAGCAACACTTGTTATCTTGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGAGATCCTG
K Q H L L S W A W Q Q G R G Q V V E I L
A T L V I L G L A A R K R T G S G D P A

T T
↑ ↑

181 CAATCT**G**AAAAGCAGACT**G**AAAG**GTGA**CAAAGAAGCTGAAG**ATGG**AAGCTT
Q S E K Q T E R *
I L K A D L K *

(n) *BACH2*

1 GCTAGCGCCCCACAAACTTTGGGGTCCA**C**GTCTGA**T**ATGGATTGCCAGAGCCTTCTCATC
M D C Q S L L I
M D C P E P S H L

61 TCTCCCTTCGCCCAGTTCCTGCATCCTAAACTCGAAGGCAGCACAGGACCTGGAAAAA
S P F A Q F P A S *
S L R P V P C I *

121 TTACATGGTGTGAACGGCATGTAAAGCTT

(o) *FGF9*

1 GCTAGCCTATAATAACGCCTAGGCATTTAAGTTGCT**ATGGTCATTCTGATCTCAAACCAA**
M V I L I S N Q
M V I L I S N Q

61 ^A
↓
ATGGAGAAACTACGGATTTTTTTTCCTTATTACGGTCGGATGGGATCA^T
↑
AAGACCTTCCTGC
M E K L R I F F P Y Y G R M G *
M E K T T D F F S L L R S M G *

121 CTGCTAAGAGCTGGGGATCTATCTATAGAGATACATAGATATGTTTATCAATATGTCAGT

181 GTGTGAGTATAAAGTGGTGGTTTCTTAGACTATCAGTGGTTTGACCTTGAACCTGTGCCA

241 GTGAAACAGCAGATTACTTTTATTTATGCATTTAATGGATTGAAGAAAAGAACCTTTTTT

301 TTCTCTCTCTCTCTGCAACTGCAGTAAGGGAGGGGAGTTGGATATACCTCGCCTAATATC

361 TCCTGGGTGACACCATCATTATTGTTTATTCTTGTGCTCCAAAAGCCGAGTCCTCTG**AT**

421 **GG**AAGCTT

(p) *PNISR*

1 GCTAGCCTAGAGTGGGGCATAACATAATCTTGCTGCT**ATGCTTCGAAGCTGTAGTCTGAAT**

M L R S C S L N

M L R S C S L I

A
↓

61 **CAACCTAAGTTTTAA**ACAGAAGGTGAACCTCTGAGAAAATCAAGTATATTTTAAAAGAAG

Q P K F *

N L S L *

121 GGATGTGGGAAGCTT

(q) TMEM184C

1 GCTAGCTTCCTGGTCTGTGCTGCTCTCCTGGAAGCC**ATGGTACAGGCAGAGCTCAGGGCG**
M V Q A E L R A
M V Q Q S S G R

A
↓

61 **ATCCCCAGGTGA**AGGGCAGCGGCTCTGCCTGGGATTCCACCGCAGTACAACCGGGTAGATG
I P R *
S P G *

121 CGGGGTGGAGAAGAAAGGATGTTGCCTGCACTGCTCGCCAATAGCACCCCTGAGAGGCTAC
181 ATTTGCAGAAGCAGCAGCAGCAGAAGACACAGCGCCGGTCCAGGAGGCGGCTCGAGCTGT
241 TCGTAAAGTCGCCCCGACAGCTTTTTCTCCGTAGTATGCGAGTTGACAAAACAGCCAGAGA
301 ACAGGGCTCCCCATTACAATCTTTTCGAGATCTTTTCCCTTGCTAACCGGATCTGATTG
361 TGCGAAAACATGCCTTGCAAAGCTT

Supplementary Figure S6. Nucleotide sequences of the 5'-UTRs and amino acid sequences of the CPuORFs analyzed in this study. **(a-q)** The 5'-UTRs of *PTP4A1* **(a)**, *MKKS* **(b)**, *SLC6A8* **(c)**, *FAM13B* **(d)**, *MIEF1* **(e)**, *EIF5* **(f)**, *MAPK6* **(g)**, *MEIS2* **(h)**, *KAT6A* **(i)**, *SLC35A4* **(j)**, *LRRC8B* **(k)**, *CDH11* **(l)**, *PNRC2* **(m)**, *BACH2* **(n)**, *FGF9* **(o)**, *PNISR* **(p)**, and *TMEM184C* **(q)**. The nucleotide sequences of the CPuORFs are shown in bold. The deduced amino acid sequences of the wild-type (WT-aa) and frameshift (fs) CPuORFs are indicated. The nucleotide sequences of other uORFs are underlined with a bold line. A dotted underline indicates the nucleotide sequences of other uORFs overlapping the CPuORFs. The initiation codons of these overlapping uORFs were changed to other codons, as indicated, while keeping the CPuORF amino acid sequence unaltered. The replaced nucleotides are shown as white letters in a black background. The nucleotides that were deleted and inserted in the frameshift mutants are shaded. The main coding sequences that were contained in the reporter constructs are boxed. The shaded boxes indicate the nucleotides changed to avoid the appearance of in-frame termination codons. Cloning sites were added at either end of the nucleotide sequences in controls to be subcloned into plasmid pGL4.10 with an SV40 promoter (pSV40:5'UTR::luc2) are underlined (Fig.2b).

Supplementary Table S1. CPU-ORFs extracted from *D. melanogaster*, *D. rerio*, *G. gallus*, and *H. sapiens*.

HG number	Species	Gene ID	Gene symbol	Gene description [†]	uORF-mORF fusion ratio	<i>K₁/K₂</i> analysis before manual validation			<i>K₁/K₂</i> analysis after manual validation			Previous report [‡]	CPUORF amino acid sequence
						Median pairwise <i>K₁/K₂</i> ratio	U-test <i>p</i> value	<i>q</i> value	Median pairwise <i>K₁/K₂</i> ratio	U-test <i>p</i> value			
HG0001	<i>D. melanogaster</i>	FBgn024734	PRL-1	PRL-1	0.00	0.06	0.0E+00	0.0E+00	0.06	0.0E+00	Crowe	MCMAIVLRVPYTMSEFLDSEAYCQAQHK*	
	<i>D. rerio</i>	ENSDDARG00000006242	ptp4a1	protein tyrosine phosphatase type IVA, member 1	0.04	0.10	0.0E+00	0.0E+00	0.10	0.0E+00	Crowe	MKLQSSSMKSHIPFCVLGHTFMFLKSGSDYCAQGHVYAEK*	
		ENSDDARG00000035676	ptp4a2b	protein tyrosine phosphatase type IVA, member 2b	0.00	0.22	0.0E+00	0.0E+00	0.22	0.0E+00	Crowe	MVGPFFCFRVDSDHTYMAFVTYVCFREFCQAQHLTFADIK*	
		ENSDDARG00000039997	ptp4a3	protein tyrosine phosphatase type IVA, member 3	0.00	0.07	0.0E+00	0.0E+00	0.07	0.0E+00	Crowe	MAFLORTGDYCHAQHLHI*	
		ENSDDARG00000054814	PTPA4a3	protein tyrosine phosphatase 4A3a	0.00	0.08	0.0E+00	0.0E+00	0.08	0.0E+00	Crowe	MEFWGGSGDYCQCHQHHTA*	
	<i>G. gallus</i>	ENSDDARG00000007143	ptp4a2a	protein tyrosine phosphatase type IVA, member 2a	0.04	0.14	0.0E+00	0.0E+00	0.14	0.0E+00	Crowe	MGSSBAPFCSLJECCTFMAYFVGVGVSVSGDFCOAQLHLYVDK*	
		ENSDDARG00000032026	PTPA4a2	protein tyrosine phosphatase type IVA, member 2	0.00	0.24	0.0E+00	0.0E+00	0.24	0.0E+00	Crowe	MPGVFCWNLRRITFMALLSVYAEFCQAQHSALADK*	
		ENSDDARG00000016271	PTPA1A1	protein tyrosine phosphatase type IVA, member 1	0.00	0.08	0.0E+00	0.0E+00	0.08	0.0E+00	Crowe	MIRLOSMSNMHPQCGVLGHTFMFLKSGSDYCAQAOHLYADK*	
		ENSDDARG00000012245	PTPA1A1	protein tyrosine phosphatase type IVA, member 1	0.00	0.09	0.0E+00	0.0E+00	0.09	0.0E+00	Crowe	MIRPQSSMSKHPCQVCGHTFMFLKSGSDYCAQAOHLYADK*	
	<i>H. sapiens</i>	ENSDDARG000000184007	PTPA4A2	protein tyrosine phosphatase type IVA, member 2	0.00	0.22	0.0E+00	0.0E+00	0.22	0.0E+00	Crowe	MAILSVRADEFQAQHSIFADK*	
HG0002	<i>D. rerio</i>	ENSDDARG00000003077	gpx9	glutathione peroxidase 9	0.04	0.07	0.0E+00	0.0E+00	0.07	0.0E+00	Crowe	MAANSVYDFVTLEEKYSDFIRKGLVLMNVATP*	
HG0003	<i>D. melanogaster</i>	FBgn0039280	Mocs2	Molybdenum cofactor synthesis 2	0.14	0.07	0.0E+00	0.0E+00	0.07	0.0E+00	Hayden	MNDAGPQVNVNHLFFAKSRELANTPRSTVEPTEITATELLOHLSVKFGLTSIRDNLIAHSEYIDNLSRDLFKEGDELAIPPLSGG*	
	<i>G. gallus</i>	ENSDDARG00000014906	Mocs2	molybdenum cofactor synthesis 2	0.02	0.07	0.0E+00	0.0E+00	0.07	0.0E+00	Hayden	MSCQVTLVYFARSALVGLRSESVSPQRTSLGLWEEWIKHPLRAVRDQVFAVRQEVLGDDLLVLTQGTDEVAIIPISGG*	
HG0004.1	<i>D. melanogaster</i>	FBgn028494			0.00	0.01	9.6E-86	1.2E-85	0.01	9.6E-86	Mackowiak	MLRRLVSTHFLKQP*	
	<i>D. rerio</i>	ENSDDARG000000076779	fam13b	family with sequence similarity 13, member B	0.00	0.00	0.0E+00	0.0E+00	0.00	0.0E+00	Mackowiak	MRNRYLIFCHMLKQP*	
HG0004.2	<i>G. gallus</i>	ENSDDARG00000041706			0.00	0.00	0.0E+00	0.0E+00	0.00	0.0E+00	Mackowiak	MRNRYLIFCHMLKQP*	
	<i>H. sapiens</i>	ENSDDARG00000031003	FAM13B	family with sequence similarity 13 member B	0.00	0.00	0.0E+00	0.0E+00	0.00	0.0E+00	Mackowiak	MRNRYLIFCHMLKQP*	
HG0004.3	<i>H. sapiens</i>	ENSDDARG000000136840	FAM13A	family with sequence similarity 13 member A	0.15	0.34	2.4E-05	1.3E-04	0.34	2.4E-05		MLEAALRPLWLDIGSCFSSHQRCAEWNFSILLSF*	
	<i>D. rerio</i>	ENSDDARG00000011055	fbxo9	F-box protein 9	0.16	0.04	0.0E+00	0.0E+00	0.04	0.0E+00	Crowe, Mackowiak	MAAIVWRARCFARCVRFSDRL*	
HG0005	<i>G. gallus</i>	ENSDDARG00000016320			0.22	0.04	0.0E+00	0.0E+00	0.04	0.0E+00	Crowe, Mackowiak	MAAIVRARSSYRCVYRFSDBREL*	
HG0006	<i>D. melanogaster</i>	FBgn020971	CG18624	GE013364p1	0.09	0.08	0.0E+00	0.0E+00	0.08	0.0E+00	Hayden, Mackowiak	MGSIGVVDLARKYGAFFVPTAVGSDIADWHSITROWKROQLQHLRAHQKQDR*	
HG0007	<i>D. melanogaster</i>	FBgn0204372	Gin3	GDI interacting protein 3	0.25	0.06	0.0E+00	0.0E+00	0.06	0.0E+00	Hayden	MSFNVEFNSQNSTQASRIARQVEQAFVTAALVDRNGE,ESLTGRFWENGPIAFDT,QAATLLKVLVLLTGCTAGVYSWSYGVKTEKQVYRPTSTLKEELKLVAKLKPKHSPRI*	
HG0008	<i>H. sapiens</i>	ENSDDARG000000175567	UCP2	uncoupling protein 2	0.00	0.30	1.3E-225	2.6E-223	0.30	1.3E-225	Crowe, Samandi	MTIRCFVSHPFSMENQGRAMITGSFEEDRTFREA*	
HG0009	<i>D. melanogaster</i>	FBgn0050100	CG30100	AT22563p2	0.07	0.05	0.0E+00	0.0E+00	0.05	0.0E+00	Hayden	MKMVQPSRQQLRYLKHLYRGNHLKTDKNYFLGRVHFDRNRSLTNPVEVFSFKRGTELLKGRIL*	
HG0010	<i>G. gallus</i>	ENSDDARG00000009013	MKKS	McKusick-Kaufman syndrome	0.00	0.11	1.1E-270	7.2E-269	0.11	5.4E-265	Akimoto	MMSLCTLWKDYKVLVMGISLGLVHWSFHKHSPLQVTKTEVPEPGVITYMOSDHKNKEK*	
	<i>H. sapiens</i>	ENSDDARG000000125863	MKKS	McKusick-Kaufman syndrome	0.00	0.10	0.0E+00	0.0E+00	0.10	0.0E+00	Akimoto	MSRLNLWRDYKVLVMVPLGLHLGWYRKSSPVFOIPKNDIDPEGDSLGLNLKCSQIQGK*	
HG0010.2	<i>G. gallus</i>	ENSDDARG00000009013	MKKS	McKusick-Kaufman syndrome	0.00	0.27	5.0E-187	2.3E-185	0.27	5.0E-187	Crowe, Akimoto, Mackowiak	MRKASWSKNNFLVAGLSLIGVHFGTLMVNFVAKKSARSHSETKRDNRHE*	
	<i>H. sapiens</i>	ENSDDARG000000125863	MKKS	McKusick-Kaufman syndrome	0.00	0.23	3.0E-245	7.0E-243	0.23	3.0E-245	Crowe, Akimoto, Mackowiak	MKNTSWIRKNVLAVGISFVGLHTYFLQRSAGSVKFSQSKSQSIEE*	
HG0011	<i>D. melanogaster</i>	FBgn0227360	Tin10	Translocase of inner membrane 10	0.03	0.05	3.5E-290	9.8E-290	0.05	3.5E-290	Hayden	MNRVSRMRKANGQYDSSAASDRPFIQ*	
HG0012	<i>D. melanogaster</i>	FBgn0204116	CG33713	QMS0135p	0.07	0.05	5.0E-301	1.4E-300	0.05	5.0E-301	Hayden	MATAAAYAAVYKSGKSHRFPVGNPITYTYGDELQYQREFGRFVVSANFDFKRTGCSKYQVGSFNSLTALKEIENQKHLEQNLNYSK*	
HG0013	<i>D. melanogaster</i>	FBgn0261381	mtTFB1	Mitochondrial Transcription Factor B1	0.21	0.05	4.3E-307	1.4E-306	0.05	4.3E-307		MSASEQGPQKYGESAPLKDQQLQFMKEEJENLDQVQKLRNRRNLTAGLGSVLYAYGYSPFVQDEKLD,DDPEEPKYSS*	
HG0014	<i>D. melanogaster</i>	FBgn0260392	CG42518	Uncharacterized protein, isoform A	0.27	0.04	0.0E+00	0.0E+00	0.04	0.0E+00		MMDLSPNNDIEKPKLADGLVQTSNPFPEPTISQNGIGQCHLTVOQLDIELPIYVRCVEXKPLENAVHLRESQDNKHIFELQKRFESAQEQRLQPGDFPKNEEQOQRELLRNQLKLQQLRYKYDTET*	
HG0015	<i>D. rerio</i>	ENSDDARG000000073737	sdcl1	ornithine decarboxylase 1	0.00	0.24	2.5E-211	4.1E-210	0.24	2.5E-211		MRKMSCLREHYTGPOLEAYLGYNFTGEPWALSDIC*	
HG0016	<i>G. gallus</i>	ENSDDARG00000010399	SELENOT	selenoprotein T	0.00	0.14	4.1E-254	2.4E-252	0.14	4.1E-254		MAYATGPLKFCIVCS*	
HG0017	<i>D. rerio</i>	ENSDDARG000000043154	ucp2	uncoupling protein 2	0.04	0.30	2.3E-104	3.0E-103	0.30	2.3E-104	Crowe	MFICTSSQRFSSMEERGNQIOVESHFNRDAPFAS*	
HG0018	<i>D. rerio</i>	ENSDDARG000000053291	pnrc2	proline-rich nuclear receptor coactivator 2	0.00	0.47	9.8E-87	1.1E-85	0.47	9.8E-87	Crowe, Samandi	MFNVSPPRONNAHHWIKTSDLAGHTCAARSRTTSRTWSIPGEELKSEKNHLNFFTTT*	
	<i>G. gallus</i>	ENSDDARG000000041122	PNRC2	proline rich nuclear receptor coactivator 2	0.00	0.34	0.0E+00	0.0E+00	0.34	0.0E+00	Crowe, Samandi	MLGSAAWLNTADRPMTKTSVPSQKSESRQHLGQAWKGERGQELSEVSEKTER*	
HG0019	<i>H. sapiens</i>	ENSDDARG000000189266	PNRC2	proline rich nuclear receptor coactivator 2	0.00	0.32	0.0E+00	0.0E+00	0.34	0.0E+00	Crowe, Samandi	MLASAPRLNSADRPMTKTSVLRQRKGSVRKQHLSSAWAQGRGQVVEILQSEKQTER*	
	<i>H. sapiens</i>	ENSDDARG000000178397	FAM220A	family with sequence similarity 220 member A	0.06	0.07	8.8E-203	1.5E-200	0.07	8.8E-203		MAALSGLAULSRSAARSYGVGKGLTRTLTUFFDLAWLRNFPYLYVASMLNLVRLQVHIEH*	
HG0020	<i>D. melanogaster</i>	FBgn0203436	CG12016	SD05789p2	0.07	0.07	1.1E-163	1.7E-163	0.07	1.1E-163	Hayden	MASNAGLQKILISAIAVFFYFFFWAVALPFMLDEGNPRLFFPLPKYAFVPTVYFGGLGAAPSFHWLSVRVKD*	
HG0021.1	<i>D. rerio</i>	ENSDDARG000000068708	ihf1	interferon-related developmental regulator 1	0.05	0.49	3.6E-60	3.5E-59	0.49	3.6E-60	Zhao, Samandi	MFRSRKSNKQDANTVATVPTVLYETQTKRHYSHWQIP*	
	<i>G. gallus</i>	ENSDDARG000000094446	IFRD1	interferon related developmental regulator 1	0.02	0.45	2.8E-89	8.7E-88	0.45	2.8E-89	Zhao, Samandi	MHLRLNSATNGISAAASSFACLRQSPRPPRPKASQSRWNKNSCSISG*	
HG0021.2	<i>H. sapiens</i>	ENSDDARG00000006652	IFRD1	interferon related developmental regulator 1	0.00	0.38	3.8E-79	2.9E-77	0.38	3.8E-79	Zhao, Samandi	MYFRSOLFQISAAATASHYPRRSTLTLAEDPSLSPRPHRTSKCSISG*	
	<i>D. rerio</i>	ENSDDARG000000038811	ihf2	interferon-related developmental regulator 2	0.00	0.27	8.4E-109	1.1E-107	0.27	8.4E-109		MVESGAATCTLRLPHFQKHLPSQGRHRLPDQNH*	
HG0022	<i>D. melanogaster</i>	FBgn0261359	CG33671	Mevalonate kinase	0.00	0.03	2.7E-164	4.2E-164	0.03	2.7E-164	Hayden	MSKYDSKYLEKLRKLOQTEYYSVDSGCGKFSAVVSPAFSGKTLQKHLNVLNSTALAELEKHAIFASQSYKYPEEWKVAQK*	
HG0023.1	<i>H. sapiens</i>	ENSDDARG000000175197	DDIT3	DNA damage inducible transcript 3	0.22	0.27	1.3E-37	5.8E-36	0.27	1.3E-37	Crowe, Jousse, Mackowiak, Samandi	MLKMSVGWQSGNSQSWNLRRRCRRCFIHHT*	
HG0023.2	<i>D. rerio</i>	ENSDDARG000000058936	ddit3	DNA-damage-inducible transcript 3	0.06	0.34	8.9E-49	7.8E-48	0.34	8.9E-49	Crowe, Jousse	MVMNSDQPSLQHTQTLNQKQPRKNNKKRSYWDKSPTHIQ*	
HG0024.1	<i>D. rerio</i>	ENSDDARG000000093406	C19H6orf2		0.00	0.48	2.9E-39	2.4E-38	0.48	2.9E-39		MGPPRCRSRRLPTEPDFGRFVLS*	
HG0024.2	<i>G. gallus</i>	ENSDDARG000000013628	C6orf62	chromosome 6 open reading frame 62	0.00	0.00	3.7E-13	2.2E-12	0.00	3.7E-13		MDWACASCFLLYT*	
	<i>H. sapiens</i>	ENSDDARG000000112308	C6orf62	chromosome 6 open reading frame 62	0.00	0.39	7.5E-12	1.0E-10	0.39	7.5E-12		MDFRDWSGVSCVLLHT*	
HG0024.3	<i>G. gallus</i>	ENSDDARG000000013628	C6orf62	chromosome 6 open reading frame 62	0.00	0.48	5.2E-47	7.4E-46	0.48	5.2E-47		MAGULLFLFDNSNTTFP*	
HG0025	<i>D. rerio</i>	ENSDDARG000000060054	epc1b	enhancer of polycomb homolog 1 (Drosophila) b	0.10	0.41	8.5E-29	5.5E-28	0.41	8.5E-29		MRTLGAGNIGKSGDRFMHLHL*	
HG0026	<i>D. rerio</i>	ENSDDARG000000097059	fam213ab	family with sequence similarity 213, member Ab	0.22	0.08	8.8E-63	7.9E-62	0.07	1.9E-51		MELVTVRAGSVGLVTLEALRSFTFLTPGPVCTALTQLADTDLRTDGDGRVFAKRELWESSGAVIMAVRRPQ*	
HG0027	<i>H. sapiens</i>	ENSDDARG00000017254	USP33	ubiquitin specific peptidase 33	0.00	0.47	1.0E-02	2.6E-02	0.47	1.0E-02		MEIRNRYGQPLQWAK*	
	<i>D. rerio</i>	ENSDDARG000000032103	mapk6	mitogen-activated protein kinase 6	0.00	0.07	0.0E+00	0.0E+00	0.07	0.0E+00		MDGSPDCDCELEPPDH*	
HG0028	<i>G. gallus</i>	ENSDDARG000000031448	MAPK6	Mitogen-activated protein kinase 6	0.00	0.07	0.0E+00	0.0E+00	0.07	0.0E+00		MDGSPDCDCELEPPDH*	
	<i>H. sapiens</i>	ENSDDARG00000069956	MAPK6	mitogen-activated protein kinase 6	0.00	0.07	0.0E+00	0.0E+00	0.07	0.0E+00		MDGSPDCDCELEPPDH*	
HG0028.2	<i>H. sapiens</i>	ENSDDARG00000069956	MAPK6	mitogen-activated protein kinase 6	0.00	0.35	9.1E-15	1.6E-13	0.35	9.1E-15		MFIEACCVHYHSFC*	
	<i>D. rerio</i>	ENSDDARG000000007523	hmt2a	lysine (K)-specific methyltransferase 2E	0.00	0.37	4.7E-64	4.7E-63	0.37	4.7E-6			

HG00445.2	<i>H. sapiens</i>	ENS000000003186	KAT5A	lysine acetyltransferase 6A	0.04	0.37	7.0E-26	2.1E-24	0.37	7.0E-26		MAAVSVWVGSAVRPCAPRSLFLPA*
D. rerio	ENS0000000018817		sortf	brain-derived neurotrophic factor	0.01	0.18	4.1E-213	7.1E-212	0.18	4.1E-213		MAFTRKTVLPASVYGVQV*
HG00446	<i>H. sapiens</i>	ENS000000176897	RDNF	brain-derived neurotrophic factor	0.00	0.19	2.0E-109	1.2E-107	0.19	2.0E-109		IMNTSKTHYLPASVGETR*
HG00447	<i>G. gallus</i>	ENS0000000015422	NRG1	neuregulin 1	0.00	0.34	1.3E-173	5.9E-172	0.34	1.3E-173		MLLLSLPLPLLIQILLPHONCFPLSRYPQMLKRVLPALGYWFT*
HG00448	<i>G. gallus</i>	ENS0000000039182			0.00	0.30	2.2E-39	2.7E-38	0.30	2.2E-39		MGCVLCODLM*
H. sapiens	ENS000000177565	TBL1XR1		transducin beta like 1 X-linked receptor 1	0.00	0.30	8.0E-29	2.6E-27	0.30	8.0E-29		MGVLCODLM*
D. rerio	ENS00000000044485	isaf4		spalt-like transcription factor 4	0.05	0.31	2.6E-32	1.8E-31	0.31	2.6E-32	Mackowiak	MINRNALLIIITLCALFLEGLISPLNFEN*
<i>G. gallus</i>	ENS00000000039238				0.00	0.46	1.7E-100	5.3E-99	0.46	1.7E-100	Mackowiak	MINRNALLIIIIAGHMRRGARRTGEAGGRDLDRFNFKIFP*
HG00500.1	<i>H. sapiens</i>	ENS000000074054	CLASP1	cytoplasmic linker associated protein 1	0.00	0.45	2.7E-143	3.7E-141	0.45	2.7E-143		MMVCHCSPOCFETALSNLQRTKQRPVRYVCEGVVITAL*
HG00500.2	<i>H. sapiens</i>	ENS000000074054	CLASP1	cytoplasmic linker associated protein 1	0.00	0.45	1.9E-06	1.2E-05	0.45	1.9E-06		MKYFRPSSRTSLCHSLLYLLV*
<i>G. gallus</i>	ENS00000000037162				0.01	0.38	4.3E-59	7.8E-58	0.38	4.3E-59	Crowe	MSCIIRAERQKIMMHYHRRNSCL*
H. sapiens	ENS000000116679	IVNS1ABP		influenza virus NS1A binding protein	0.00	0.37	4.9E-63	3.3E-61	0.37	4.9E-63	Crowe	MNVSSISEMMQIMMHYHRRNSCL*
HG00502	<i>H. sapiens</i>	ENS000000178235	SUTR1	SLIT and NTRK like family member 1	0.17	0.35	1.6E-124	2.0E-122	0.35	1.6E-124		MINNCVCGEGDCRQVFNVRSMGNCSL*
H. sapiens	ENS000000184564	SUTR1		SLIT and NTRK like family member 6	0.00	0.41	3.9E-05	2.3E-05	0.41	3.9E-05		MAVYMKCSQDRGVGRP*
HG00503.2	<i>H. sapiens</i>	ENS000000184564	SUTR1	SLIT and NTRK like family member 6	0.00	0.31	8.6E-19	2.0E-17	0.31	8.6E-19		MLSLSLTRKPNMLKWLNDTKSD*
<i>G. gallus</i>	ENS000000016222	NDP		NDP, norrin cystine knot growth factor	0.19	0.23	1.2E-108	5.8E-197	0.23	1.2E-108		MTAKRLKPDFSLSWRGTGSQYLEFF*
HG00504	<i>H. sapiens</i>	ENS000000124479	NDP	NDP, norrin cystine knot growth factor	0.00	0.29	2.2E-38	9.9E-37	0.29	2.2E-38		MTTRKLQPPDALSNGTGS*
<i>G. gallus</i>	ENS000000010533	ELAVL4		ELAV like RNA binding protein 4	0.00	0.06	3.0E-138	1.2E-138	0.06	3.0E-138		MLHVIFQRVSHDLKIRGGGVCCSA*
HG00505.2	<i>G. gallus</i>	ENS000000010533	ELAVL4	ELAV like RNA binding protein 4	0.00	0.00	1.3E-33	1.4E-32	0.00	1.3E-33		MSLLHRVAAL*
<i>G. gallus</i>	ENS000000011271	LUM		luciferan	0.01	0.32	1.6E-51	2.5E-50	0.32	1.6E-51		MGCPCTEGHLHFIKRAAFSYMPHKIDMTMT*
H. sapiens	ENS000000139329	LUM		luciferan	0.01	0.33	2.2E-15	4.0E-14	0.36	2.5E-09		MSWAVLSPHVHLHFVRECCHATPDQPHNDITFFRDROWAGSPHPPSALVSLRWQVPVPS*
HG00507	<i>H. sapiens</i>	ENS000000280987	MATR3	matrin 3	0.00	0.42	5.6E-41	2.7E-39	0.42	1.1E-33		MLGAQWRNRQPSRAECSLLVLSUKKLSLULGLVTFEAKLT*
HG00508	<i>H. sapiens</i>	ENS000000180332	KCTD4	potassium channel tetramerization domain containing 4	0.01	0.21	1.3E-146	1.8E-144	0.21	1.3E-146		MLPAFPFHQAGAE*
D. rerio	ENS00000000018060	pk3r2		phosphoinositide-3-kinase, regulatory subunit 2 (beta)	0.01	0.17	1.1E-275	2.3E-274	0.17	3.9E-270		MLHLSCLSIIMNLRGFKRVACTANTGOV*
<i>G. gallus</i>	ENS00000000003428				0.01	0.17	1.4E-168	5.6E-167	0.17	1.4E-168		MPTEHCWFMVFSLSLSIWNLRGFKRKRGGCT*
H. sapiens	ENS00000000000000	PIKC1R1		phosphoinositide-3-kinase regulatory subunit 1	0.00	0.48	1.3E-111	1.7E-110	0.48	1.3E-111		MSGVTKVSGRRCRSCQSRFVLTSC*
H. sapiens	ENS000000105847	PIKC1R2		phosphoinositide-3-kinase regulatory subunit 2	0.13	0.50	2.9E-07	1.9E-06	0.50	2.9E-07		MYAACCTLSLWVCSQSGSRQPWAPMALRVRA*
H. sapiens	ENS000000145675	PIKC1R1		phosphoinositide-3-kinase regulatory subunit 1	0.00	0.00	2.0E-04	8.8E-04	0.00	2.0E-04		MDSRMAHLS*
HG00509.5	D. rerio	ENS00000000038524	pk3r1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	0.18	0.26	6.7E-06	2.3E-05	0.26	6.7E-06		MGRVRCMHLEGAPNHITISFT*
<i>G. gallus</i>	ENS000000000014751				0.00	0.48	1.1E-19	8.7E-19	0.48	1.1E-19		MTADIEESCQWRVPVKWNQIO*
H. sapiens	ENS0000000049192	ADAMTS6		ADAM metalloproteinase with thrombospondin type 1 motif	0.00	0.47	9.0E-55	5.3E-53	0.47	9.0E-55		MNPDIIESAGCVKVKQWNQIO*
<i>G. gallus</i>	ENS000000000014751				0.00	0.35	1.6E-16	1.1E-15	0.35	1.6E-16		MVQFVSGVNPJAH*
H. sapiens	ENS0000000049192	ADAMTS6		ADAM metalloproteinase with thrombospondin type 1 motif	0.00	0.36	4.0E-29	1.3E-27	0.36	4.0E-29		MLRFVWYGDLSAHR*
<i>G. gallus</i>	ENS000000000004949				0.00	0.27	4.3E-12	2.5E-11	0.27	4.3E-12		MPFVKPMYTVLHCYCT*
H. sapiens	ENS000000166398				0.02	0.27	2.2E-51	1.3E-49	0.27	2.2E-51		MTVCLMEMPTLKLRFALHYFYT*
HG0061.2	<i>G. gallus</i>	ENS000000000004949			0.00	0.34	3.2E-06	1.2E-05	0.34	3.2E-06		MLQRKQLPQOTRKGEEGLQ*
H. sapiens	ENS000000166398				0.03	0.30	9.8E-10	1.0E-08	0.30	9.8E-10		MLDGRNYLSKQKRWRRRLTINA*
D. rerio	ENS000000000075689	gpbp11		GC-rich promoter binding protein 1-like 1	0.00	0.13	9.7E-04	2.6E-03	0.13	9.7E-04		MPFSTQGRHWYT*
<i>G. gallus</i>	ENS00000000010276	GPBP1L1		GC-rich promoter binding protein 1 like 1	0.00	0.12	1.8E-02	3.7E-02	0.12	1.8E-02		MPHFIEGRHWYT*
HG00602.2	<i>G. gallus</i>	ENS00000000010276	GPBP1L1	GC-rich promoter binding protein 1 like 1	0.00	0.38	5.3E-09	2.3E-07	0.38	5.3E-09		MSPCAPLGVSQVQ*
H. sapiens	ENS000000195952	GPBP1L1		GC-rich promoter binding protein 1 like 1	0.00	0.29	3.0E-14	5.1E-13	0.29	3.0E-14		MSYIKQHSHSATGGS*
<i>G. gallus</i>	ENS00000000002477				0.00	0.12	5.1E-09	2.4E-08	0.12	5.1E-09		MCACSIASFLLK*
H. sapiens	ENS000000162630	B3GALT2		beta-1,3-galactosyltransferase 2	0.00	0.12	5.9E-09	5.5E-08	0.12	5.9E-09		MCACSIASFLLK*
H. sapiens	ENS000000162630	B3GALT2		beta-1,3-galactosyltransferase 2	0.00	0.41	1.9E-11	2.4E-10	0.41	1.9E-11		MDTETRTQCHVQPGK*
HG0064.1	<i>H. sapiens</i>	ENS000000102678	FGF9	fibroblast growth factor 9	0.00	0.33	2.1E-133	2.7E-131	0.33	2.1E-133		MLVILSINGHLCRIFFPYPGRMG*
H. sapiens	ENS000000113578	FGF1		fibroblast growth factor 1	0.01	0.38	1.2E-14	2.1E-13	0.38	1.2E-14		MVCGCTQFFSWGFSLSHYQKGSRRERTSGNSLSRSGIRASPPFLGGHSLMLVNGNSLPPAAACLSQSW*
HG0064.2	<i>G. gallus</i>	ENS000000000029927	STRBP	Spermatid perinuclear RNA-binding protein	0.00	0.36	1.6E-85	4.3E-84	0.36	1.6E-85		MKRFRQAAQLSKLTPRRRKEKERS*
H. sapiens	ENS000000112182	BACH2		BTB domain and CNC homolog 2	0.22	0.18	5.0E-206	8.9E-204	0.18	5.0E-206		MDCQSLISPFQAQFPAS*
HG0067	<i>H. sapiens</i>	ENS000000168662	CACNG2	calcium voltage-gated channel auxiliary subunit gamma 2	0.00	0.01	2.6E-80	2.1E-78	0.01	2.6E-80		METGDQNFRRD*
D. rerio	ENS00000000071235				0.02	0.00	3.2E-298	8.1E-295	0.00	3.2E-298	Mackowiak	MRFFRLTKCFYDVC*
<i>G. gallus</i>	ENS0000000000041419				0.03	0.00	1.7E-293	1.3E-291	0.00	1.7E-293	Mackowiak	MRFFRLTKCFYDVC*
H. sapiens	ENS000000130821	SLC8A8		solute carrier family 8 member 8	0.02	0.00	2.0E-232	4.3E-230	0.00	2.0E-232	Mackowiak	MRFFRLTKCFYDVC*
<i>G. gallus</i>	ENS00000000010999	DICER1		dicer 1, ribonuclease III	0.00	0.42	2.9E-40	3.7E-38	0.42	2.9E-40		MMKSCSLSISTEAIEKIT*
H. sapiens	ENS000000100897	DICER1		dicer 1, ribonuclease III	0.03	0.27	1.1E-78	8.0E-77	0.27	1.1E-78		MSKSSDKSNTEISNIKT*
D. rerio	ENS000000000040926	nr2f2		nuclear receptor subfamily 2, group F, member 2	0.00	0.36	4.4E-41	3.7E-40	0.36	4.4E-41		MDDCKCPWTWPLRARLFGLLQ*
D. rerio	ENS000000000052695	nr2f1a		nuclear receptor subfamily 2, group F, member 1a	0.03	0.13	1.7E-126	2.3E-125	0.13	1.7E-126		MADCNLPWNWPPDNCIS*
H. sapiens	ENS000000175745	NR2F1		nuclear receptor subfamily 2 group F member 1	0.03	0.12	6.3E-162	9.8E-160	0.12	6.3E-162		MAGCVRPWTWPPDTRAP*
H. sapiens	ENS000000185551	NR2F2		nuclear receptor subfamily 2 group F member 2	0.20	0.07	1.5E-119	1.8E-117	0.07	1.5E-119		MADCCGLPWTWPPDSRLSSSTSTFTSSSSSSSSSSANSAAHL*
D. rerio	ENS00000000098240	meis2a		Meis homeobox 2a	0.00	0.39	2.0E-42	1.7E-41	0.39	2.0E-42		MHRDLSVLTCLMLGR*
H. sapiens	ENS000000134138	MEIS2		Meis homeobox 2	0.00	0.39	1.1E-68	8.0E-67	0.39	1.1E-68		MKHDSVSTCGLLTGRS*
H. sapiens	ENS000000143995	MEIS1		Meis homeobox 1	0.00	0.00	1.2E-08	1.1E-07	0.00	1.2E-08		MLSDSGALQV*
<i>G. gallus</i>	ENS00000000003960	STIM2		Stimulin-2	0.11	0.34	2.7E-35	3.0E-34	0.34	2.7E-35		MPDGSAGSVMMSGD*
H. sapiens	ENS000000104435	STIM2		stimulin 2	0.12	0.10	1.7E-101	1.7E-101	0.10	1.7E-101		MCSAGREGLSMBKILVICTPAPLADLYMLKSDSAGVMSGDLGSGSA*
D. rerio	ENS000000000004708	cspg2b		cspg2 binding protein	0.02	0.13	2.3E-203	3.7E-202	0.13	2.3E-203		MTSATAVVLGSLVITSTVAGKQWDRQRLREGVVDLERLEKRNLEALIEQIQLTRELTVERNRQAQEAESHDS*
D. rerio	ENS000000000078624	cgrf9b		Cdc42 guanine nucleotide exchange factor (GEF) 9b	0.06	0.06	1.9E-10	8.0E-10	0.06	1.9E-10	Mackowiak	MTLDVQTVAVTVAILLVNLVIFMGSS*
H. sapiens	ENS000000131089	ARHGEF9		Cdc42 guanine nucleotide exchange factor 9	0.01	0.04	8.1E-218	1.5E-215	0.04	8.1E-218	Mackowiak	MDSLTEQLTSPNLPAPLHYSVLHCMTLDVQTVVFAVNVLLVNLVIMFLEGT*
H. sapiens	ENS000000165699	TSC1		tuberous sclerosis 1	0.00	0.45	1.6E-49	8.8E-48	0.45	1.6E-49	Crowe	MKDTRLTALETEVVPVARTV*
D. rerio	ENS000000000004008	neurod6a		neuronal differentiation 6a	0.01	0.30	5.9E-120	8.1E-119	0.30	5.9E-120		MKTWVTHCLLTQFGDRTVKNYKNTANSTPGVAMMDAPLVTHGDGQAAALNHAPGRVVRSSRHMPDQGRNTOPLRASHVTSFCHVTSAADGMTSGWHQCHFS*
H. sapiens	ENS000000164600	NEUROD6		neuronal differentiation 6	0.00	0.47	5.9E-31	2.1E-29	0.47	5.7E-09		MGTSSGSHQKFLHLEINVEIQYTDMLTDLTKLRGRPKMKTQY*
<i>G. gallus</i>	ENS00000000005074				0.00	0.48	7.0E-33	7.1E-32	0.48	7.0E-33		MPFQPDPTTEKKVHLRLGRHCN*
<i>G. gallus</i>	ENS00000000005074				0.00	0.08	1.3E-10	6.8E-10	0.08	1.3E-10		MPSGGVLLKLGHCN*
<i>G. gallus</i>	ENS00000000016633	HMBOX1		homeobox containing 1	0.00	0.01	6.7E-05	2.2E-04	0.01	6.7E-05		MMVNTEDPQEL*
H. sapiens	ENS000000147421	HMBOX1		homeobox containing 1	0.00	0.37	1.4E-02	3.4E-02	0.37	1.4E-02		MVONADHLWKGY*
H. sapiens	ENS00000000004436	MBD5		methyl-CpG binding domain protein 5	0.00	0.30	4.9E-84	4.8E-82	0.31	2.0E-89		MSIFPWRWRVRLTKTDKDIHLEINCLHYTAESHTLVMSFSLLSRLHYWNFVEMKTSDEPTNCLTDSQWKIKRPFKECGL*
<i>G. gallus</i>	ENS000000000039403				0.01	0.29	4.2E-48	9.5E-47	0.29	4.2E-48		MYKLYMLCQDLSKQVQFOMANLNL*
H. sapiens	ENS000000179603	GRM8		glutamate metabotropic receptor 8	0.02	0.29	1.0E-68	8.8E-65	0.29	1.0E-68		MGPDSQKQVQPPVLLWQZ*
H. sapiens	ENS000000179603	GRM8		glutamate metabotropic receptor 8	0.00	0.09	8.7E-03	2.3E-02	0.09	8.7E-03		MTNRNLSISRT*
H. sapiens	ENS000000179603	GRM8		glutamate metabotropic receptor 8	0.09	0.34	1.0E-06	6.9E-06	0.34	1.0E-06		MEETVRLIGQLSPLSPEISHKCGRCARLTRRRRRRRR*
D. rerio	ENS000000000028228	zbtb18		zinc finger and BTB domain containing 18	0.06	0.41	7.1E-19	3.9E-18	0.41	7.1E-19		MMSEQLTGCHPVPSSNAGTGS*
D. rerio	ENS000000000028228	zbtb18		zinc finger and BTB domain containing 18	0.08	0.35	1.2E-02	2.2E-02	0.35	1.2E-02		MIVPVSIFYFFPPLSVQRVSKMNDGNGAASEP*
D. rerio	ENS000000000062379	hlc35a4		solute carrier family 35, member A4	0.01	0.07	5.5E-233	9.9E-232	0.07	5.5E-233	Andreev	MAEDIDPVTYKLDVHLKDQLEIEOKKVENVEOAGVPGGSLASPLFKGLAGVYVSRLSAVLGVALGTLSGFAQNYQVPIEATLRDLNSLKKRPRC*
H. sapiens	ENS000000176087	SLC35A4		solute carrier family 35 member A4	0.01	0.07	2.7E-235	1.6E-233	0.07	2.7E-235	Andreev	MADKDSLPLKDLAFKLNQLESQRRVEDEVENSGVGDDSLSPFLKGLAGYVVAKLRAVAFVAGTCTGTYGAQYAVPNVEKTLRDLQYLRKGPD*
<i>G. gallus</i>	ENS00000000008039	MFSB13A		major facilitator superfamily domain containing 13A	0.00	0.31	1.3E-53	2.2E-52	0.31	1.3E-53		MDWPRQRNCRCCKEATSLKHW

HG0092.2	<i>H. sapiens</i>	ENSNG00000166225	PRRS2	fibroblast growth factor receptor substrate 2	0.01	0.36	6.4E-07	4.4E-06	0.36	6.4E-07		MKGSHCHVRKSCGMSTSEONCISQKRPQG*
HG0093	<i>G. gallus</i>	ENSNGALG0000040486	Spt1	zinc finger E-box binding homeobox 2	0.13	0.26	1.7E-35	2.0E-34	0.26	1.7E-35	Crowe, Samandi	MLFLITSGQNYKQDFASACQ*
HG0094.1	<i>H. sapiens</i>	ENSNG00000169554	ZEB2	zinc finger E-box binding homeobox 2	0.22	0.44	2.7E-40	1.3E-38	0.44	2.7E-40	Crowe, Samandi	MLFLITSGQNYKQDFAACLM*
HG0094.1	<i>H. sapiens</i>	ENSNG00000112175	BMP5	bone morphogenetic protein 5	0.00	0.31	2.7E-60	1.7E-58	0.31	2.7E-60		MQQRLTLYQNWKSEFQLS*
HG0094.2	<i>H. sapiens</i>	ENSNG00000112175	BMP5	bone morphogenetic protein 5	0.00	0.15	8.4E-26	2.6E-24	0.15	8.4E-26		MDLQEGFQVNSGKHVLSNTT*
HG0095	<i>D. rerio</i>	ENSDDARG00000013708	usp9	ubiquitin specific peptidase 9	0.00	0.46	9.7E-57	6.9E-56	0.46	9.7E-57		MEERSLLGYAMSVATYVPVGVLSLSEVCRFSVAPEKLSSGVPA*
HG0096	<i>G. gallus</i>	ENSNGALG00000014186	MPPE1	metallophosphoesterase domain containing 1	0.01	0.42	6.1E-03	1.4E-02	0.42	6.1E-03		MVFSRCRCRKADIMIA*
HG0097	<i>G. gallus</i>	ENSNGALG000000037496			0.01	0.25	1.6E-37	1.8E-36	0.25	1.6E-37		MELOPRAGAADTPSAFLRSSHGERHGRFLVKMAWDRCNL*
HG0098	<i>H. sapiens</i>	ENSNG00000198739	LRRTM3	leucine rich repeat transmembrane neuronal 3	0.00	0.00	1.2E-06	8.1E-06	0.00	1.2E-06		MQKRNHEDPTI*
HG0099.1	<i>H. sapiens</i>	ENSNG00000168575	SLC20A2	solute carrier family 20 member 2	0.00	0.01	5.3E-105	5.6E-103	0.01	5.3E-105		MKRTNGSEKYRIGGIDITAFDREKYMGCFAD*
HG0099.2	<i>H. sapiens</i>	ENSNG00000144136	SLC20A1	solute carrier family 20 member 1	0.00	0.28	3.1E-03	9.5E-03	0.28	3.1E-03		MNLRFPSPPVNSAPCF*
HG0099.3	<i>H. sapiens</i>	ENSNG00000168575	SLC20A2	solute carrier family 20 member 2	0.00	0.45	1.0E-02	2.6E-02	0.45	1.0E-02		MLCMLVGHGTGLGRISH*
HG0099.4	<i>D. rerio</i>	ENSDDARG0000010941	hc20a1b	solute carrier family 20 (phosphate transporter), member 1b	0.00	0.36	5.5E-07	2.1E-06	0.36	5.5E-07		MDVRCILQIAKNTNRNRSILFRG*
HG0100.1	<i>D. rerio</i>	ENSDDARG00000104164	crebbp3b	CREB binding protein 3	0.48	0.48	5.0E-40	4.7E-39	0.48	5.0E-40		MNVLGVGLSWNEWRNRGALLSR*
HG0100.2	<i>D. rerio</i>	ENSDDARG00000104609	crebbp3a	CREB binding protein a	0.00	0.50	2.6E-33	1.8E-32	0.50	2.6E-33		MNMWVGVGLSWGEWWRNGALLLL*
HG0100.2	<i>D. rerio</i>	ENSDDARG00000001108	ep300b	ET1 binding protein p300 b	0.00	0.47	2.3E-13	1.0E-12	0.47	2.3E-13		MAEKTDASSEDSCRENSVAEAT*
HG0101	<i>H. sapiens</i>	ENSNG00000009920	NRP1	neurotrophin 1	0.00	0.45	2.0E-19	4.7E-18	0.45	2.0E-19		MARAVAPGRGTSYVGKGRGRS*
HG0102	<i>H. sapiens</i>	ENSNG00000182263	FIGN	figetin, microtubule severing factor	0.00	0.45	6.5E-32	2.4E-30	0.45	6.5E-32		MISNHRHLHLTASHQGHTRIDATLYRVLSPRVQV*
HG0103	<i>G. gallus</i>	ENSNGALG00000016558	VEGFD	vascular endothelial growth factor D	0.00	0.21	2.2E-93	6.6E-92	0.21	2.2E-93		MHFKRDASSCOMTTTA*
HG0103	<i>H. sapiens</i>	ENSNG00000165197	VEGFD	vascular endothelial growth factor D	0.00	0.48	1.7E-02	4.1E-02	0.48	1.7E-02		MPPEITFSSCLMSTA*
HG0104.1	<i>G. gallus</i>	ENSNGALG00000038097	EI24	EI24, autophagy associated transmembrane protein	0.00	0.32	3.0E-25	2.6E-24	0.32	3.0E-25		MNREAWRLFPSPCS*
HG0104.2	<i>H. sapiens</i>	ENSNG00000149547	EI24	EI24, autophagy associated transmembrane protein	0.02	0.47	5.5E-05	2.7E-04	0.47	5.5E-05		MLVLKQSSLSLCKSNKSRFSMRMDGLTGLSPVCS*
HG0105	<i>G. gallus</i>	ENSNGALG00000016176			0.00	0.33	6.9E-110	2.4E-108	0.33	2.0E-107		MWLDLADPELLFFRGAYGVREACGGYLAFFSLLPFFFFFVLGFGEPEPKMGNGASDRRGSPSLSVGRVPVLEV*
HG0105	<i>H. sapiens</i>	ENSNG00000135298	ADGRB3	adhesion G protein-coupled receptor B3	0.00	0.33	1.1E-87	9.3E-86	0.33	1.1E-87		MNGGDWRGRVSPSLGLRRVPVLVS*
HG0106	<i>H. sapiens</i>	ENSNG00000147548	NSD3	nuclear receptor binding SET domain protein 3	0.00	0.11	1.8E-29	6.2E-28	0.11	1.8E-29		MEQTEGPMRERES*
HG0107.1	<i>G. gallus</i>	ENSNGALG00000005601	ATP2B4	ATPase plasma membrane Ca2+ transporting 4	0.00	0.22	4.3E-81	1.1E-79	0.22	4.3E-81		MHFLTPSSQGLGLC*
HG0107.1	<i>H. sapiens</i>	ENSNG00000058698	ATP2B4	ATPase plasma membrane Ca2+ transporting 4	0.00	0.20	1.7E-80	1.4E-79	0.20	1.7E-80		MHFLTPSSQGLGLS*
HG0107.2	<i>G. gallus</i>	ENSNGALG00000030550			0.00	0.30	6.0E-44	7.8E-43	0.30	6.0E-44		MGRPRPYLSKMGILLI*
HG0107.2	<i>H. sapiens</i>	ENSNG00000070961	ATP2B1	ATPase plasma membrane Ca2+ transporting 1	0.00	0.31	1.2E-12	1.7E-11	0.31	1.2E-12		MDMEKLMVGORSRYFSKCCC*
HG0107.3	<i>D. rerio</i>	ENSDDARG00000005433	atp2b2	ATPase, Ca++ transporting, plasma membrane 2	0.01	0.28	3.5E-23	2.1E-22	0.28	3.5E-23	Crowe	MGNHVSDAGLOPW*
HG0107.3	<i>H. sapiens</i>	ENSNG00000157087	ATP2B2	ATPase plasma membrane Ca2+ transporting 2	0.00	0.41	9.9E-07	6.6E-06	0.41	9.9E-07	Crowe	MPVPGSSMGPTWEURLGLQP*
HG0107.4	<i>H. sapiens</i>	ENSNG00000070961	ATP2B1	ATPase plasma membrane Ca2+ transporting 1	0.00	0.00	6.5E-03	1.8E-02	0.00	6.5E-03		MSVWFKKDFFH*
HG0108.1	<i>G. gallus</i>	ENSNGALG00000007396	TAOK3	TAO kinase 3	0.00	0.29	5.8E-53	9.5E-52	0.29	5.8E-53		MKEETDOWLKAPTSS*
HG0108.2	<i>H. sapiens</i>	ENSNG00000135000	TAOK3	TAO kinase 3	0.01	0.32	8.1E-10	8.7E-09	0.32	8.1E-10		MNLSNMEYFVPHTKRY*
HG0108.3	<i>D. rerio</i>	ENSDDARG00000098304	taok1b	TAO kinase 1b	0.07	0.23	1.6E-02	2.9E-02	0.23	1.6E-02		MNSQRGLTCSRSTAR*
HG0109.1	<i>H. sapiens</i>	ENSNG00000048540	LMO3	LIM domain only 3	0.00	0.34	1.3E-34	5.1E-33	0.34	1.3E-34		MNGSHRGTSDCSHLOAFKGGEGVGLPGYSGEALQSSHCAY*
HG0109.2	<i>H. sapiens</i>	ENSNG00000048540	LMO3	LIM domain only 3	0.17	0.41	1.9E-23	5.3E-22	0.41	1.9E-23		MQHIFYGDYSGCCYEYDVRFMFFNMICANACCSLKSIXSYQEARGRWDFRITGRVREACGPIRHHFAHCEGLRVCALSCLAVLIPSTPCRHSDDLPLKMLHNSRSSAA*
HG0109.3	<i>H. sapiens</i>	ENSNG00000048540	LMO3	LIM domain only 3	0.08	0.43	1.7E-15	3.1E-14	0.43	1.7E-15		MHACLDGQVGRNLRNLMRYTSLQRGSH*
HG0110.1	<i>H. sapiens</i>	ENSNG00000019156	ZFHK4	zinc finger homeobox 4	0.00	0.34	5.2E-28	1.6E-26	0.34	5.2E-28		MPRPTTCSFFVFTQ*
HG0110.2	<i>D. rerio</i>	ENSDDARG00000073944	ZFH3 (1 of many)	zifh3-388b18.1	0.19	0.47	8.0E-08	3.1E-07	0.47	8.0E-08		MRSVLPAIFCTYVSRNKDRDTFFSLSPSPNSRQSGASVCSSTTKQGLNALNRNIEPRLTASA*
HG0111	<i>G. gallus</i>	ENSNGALG00000034944			0.04	0.25	5.3E-63	1.1E-61	0.25	5.3E-63		MEVISVWGPRPALWARVLLSDHMLPPE*
HG0112	<i>H. sapiens</i>	ENSNG00000105997	HOXA3	homeobox A3	0.00	0.32	2.6E-50	1.4E-48	0.32	2.6E-50		MKRSARGHWRVRSYT*
HG0113	<i>D. rerio</i>	ENSDDARG00000009727	hsb2	single-stranded DNA binding protein 2	0.00	0.40	4.7E-35	3.4E-34	0.40	4.7E-35		MGGIAPAVAMVYGLCPGRL*
HG0113	<i>G. gallus</i>	ENSNGALG000000023089	SBBP2	single stranded DNA binding protein 2	0.00	0.38	2.5E-05	8.8E-05	0.38	2.5E-05		MGCVCQGVAMATGLFPGRL*
HG0114.1	<i>G. gallus</i>	ENSNGALG00000003701	SGMS1	sphingomyelin synthase 1	0.01	0.46	1.3E-14	8.5E-14	0.46	1.3E-14		MKPRRSLMLWSRSDCCPL*
HG0114.2	<i>H. sapiens</i>	ENSNG00000198964	SGMS1	sphingomyelin synthase 1	0.00	0.36	3.6E-04	1.5E-03	0.36	3.6E-04		MTRFMLNNRRNPAQK*
HG0115.1	<i>G. gallus</i>	ENSNGALG00000010976	CCDC126	coiled-coil domain containing 126	0.00	0.41	5.0E-11	2.6E-10	0.41	5.0E-11		MESRPAKPRRCVQDDPARRLTL*
HG0115.2	<i>H. sapiens</i>	ENSNG00000169193	CCDC126	coiled-coil domain containing 126	0.02	0.01	6.5E-10	7.1E-09	0.01	6.5E-10		MSANRNVNRVDITLLMKNIQY*
HG0116	<i>G. gallus</i>	ENSNGALG00000030308			0.01	0.30	4.0E-38	4.6E-35	0.30	4.0E-38		MDQSSSDQETKGLL*
HG0117	<i>H. sapiens</i>	ENSNG0000010270	STARD3NL	STARD3 N-terminal like	0.00	0.35	1.3E-05	6.0E-05	0.35	1.3E-05		MLLFLPRDVGKRL*
HG0117.1	<i>H. sapiens</i>	ENSNG00000140945	CDH13	cadherin 13	0.07	0.49	2.4E-19	5.6E-18	0.49	2.4E-19		MLSAACAKINENANGR*
HG0117.2	<i>H. sapiens</i>	ENSNG00000140945	CDH13	cadherin 13	0.00	0.00	1.1E-03	4.0E-03	0.00	1.1E-03		MPFPFQSLARCSPPICAKRGSVRKESLV*
HG0118.1	<i>H. sapiens</i>	ENSNG00000183682	FAM19A1	family with sequence similarity 19 member A1, C-C motif of	0.00	0.22	2.2E-18	4.8E-17	0.22	2.2E-18		MTRFFPLPLWFL*
HG0118.2	<i>H. sapiens</i>	ENSNG00000183682	FAM19A1	family with sequence similarity 19 member A1, C-C motif of	0.00	0.38	1.3E-03	4.4E-03	0.38	1.3E-03		MHWSGDGPSATIN*
HG0119	<i>G. gallus</i>	ENSNGALG00000043570	SGK3	gamma-aminobutyric acid type A receptor alpha1 subunit	0.04	0.20	3.5E-51	5.4E-50	0.20	3.5E-51		MEMFTFSOEELRLDQYR*
HG0120	<i>H. sapiens</i>	ENSNG00000022355	GABRA1	gamma-aminobutyric acid type A receptor alpha1 subunit	0.08	0.46	1.5E-03	5.1E-03	0.46	1.5E-03		MKSPPHSHVCPGTYYYCLGKEFSKVV*
HG0121	<i>H. sapiens</i>	ENSNG00000122786	CALD1	caldesmon 1	0.00	0.50	6.8E-12	9.1E-11	0.50	6.8E-12		MCSLSDWDFWGPGRKGLEFY*
HG0122	<i>H. sapiens</i>	ENSNG00000169925	BRD3	bromodomain containing 3	0.00	0.40	4.5E-75	3.3E-73	0.40	4.5E-75		MLSCDRPSSCLEAGLQPSGLPCDPHHPHKAVALLGPEMGRFAVSGSVEAARASPSRCCDRK*
HG0123	<i>H. sapiens</i>	ENSNG00000173276	ZBTB21	zinc finger and BTB domain containing 21	0.03	0.41	3.1E-36	1.4E-34	0.41	3.1E-36		MTSSLVDDWDFVKMDGITAAAAAARASRV*
HG0124.1	<i>D. rerio</i>	ENSDDARG00000031763	smad6b	SMAD family member 6b	0.00	0.49	2.3E-13	1.0E-12	0.49	2.3E-13		MOYSIVPSKMLVLCRYTYVLCGAARAHSNANINARVAK*
HG0124.2	<i>D. rerio</i>	ENSDDARG00000052039	smad6a	SMAD family member 6a	0.09	0.14	3.5E-04	9.9E-04	0.14	3.5E-04		MMGIGNWLHCSPGQPRVCVSEEEH*
HG0125.1	<i>D. rerio</i>	ENSDDARG00000051926	lag1	pleiomorphic adenoma gene 1	0.00	0.33	2.7E-38	2.1E-37	0.33	2.7E-38		MNRKLKRIEIRFSEGEKRYRKDNVAFQGLMSLLC*
HG0125.1	<i>H. sapiens</i>	ENSNG00000181680	PLAG1	PLAG1 zinc finger	0.00	0.30	3.2E-09	3.3E-09	0.30	3.2E-09		MLKPRDWRKWEKLDSTLTHEESMLAKIK*
HG0126.1	<i>G. gallus</i>	ENSNGALG00000010899	GPRC2	glucose-6-phosphatase catalytic subunit 2	0.00	0.30	2.5E-10	1.2E-09	0.30	2.5E-10		INXCEQIAOMVQLFRRIA*
HG0126.2	<i>G. gallus</i>	ENSNGALG00000010899	GPRC2	glucose-6-phosphatase catalytic subunit 2	0.07	0.46	1.2E-15	8.2E-15	0.46	1.2E-15		MCFPRDSEPRVPMQAGYATLOYKAQPSGWY*
HG0127.1	<i>G. gallus</i>	ENSNGALG00000029709			0.00	0.33	3.4E-34	3.7E-33	0.33	3.4E-34		MQNSQTHEEKSPGRNVRGVAGVGNLHSHPTP*
HG0127.2	<i>H. sapiens</i>	ENSNG00000109452	INPP4B	inositol polyphosphate-4-phosphatase type II B	0.00	0.40	6.2E-09	5.8E-08	0.40	6.2E-09		MVLPGKRSSVFYEKLKGFTGGVLEICS*
HG0128	<i>D. rerio</i>	ENSDDARG00000091029	phox2bb	paired-like homeobox 2bb	0.00	0.25	4.1E-45	3.6E-44	0.25	4.1E-45		MRTICSRDLGLGSLGGS*
HG0128	<i>H. sapiens</i>	ENSNG00000109132	PHOX2B	paired like homeobox 2b	0.12	0.39	5.7E-33	2.2E-31	0.39	5.7E-33		MOESMIGRLDSSVPCCQPNRRMSYCHVKASNKNRFAVQVERAKFMRTICSRDLRGIS*
HG0129	<i>D. rerio</i>	ENSDDARG00000099437			0.00	0.14	2.5E-88	3.0E-87	0.14	2.5E-88		MPAVFLLRLSLVRLFGSLRSLASGVQLLRLLTATGHLGTVLRNIWERISSQSQSEALGCVLLCNMHKKVDN*
HG0130	<i>G. gallus</i>	ENSNGALG000000002993			0.00	0.31	1.7E-69	4.1E-68	0.31	1.7E-69		MSCWEIRRIFFSLVEEPCPGQWGLFLWRAKEAGSLSRTORELGHVLSAHLGNTVGVCKSRRIKAGIQTALIFVIFRRGMHLA*
HG0131	<i>G. gallus</i>	ENSNGALG00000013135	GALNT1	polypeptide N-acetylglucosaminyltransferase 1	0.00	0.35	1.1E-14	7.4E-14	0.35	1.1E-14		MAVNLQRRYTRVWSLKL*
HG0132	<i>H. sapiens</i>	ENSNG00000151067	CACNA1C	calcium voltage-gated channel subunit alpha1 C	0.00	0.32	1.0E-41	5.2E-40	0.32	1.0E-41	Crowe	MRYSPYTRGTSGSGKEQFLDFDAMGR*
HG0133.1	<i>D. rerio</i>	ENSDDARG00000051886	ankrd11	ankyrin repeat domain 11	0.00	0.00	4.1E-82	4.3E-81	0.00	4.1E-82	Mackowiak	NESTYVDQMAEA*
HG0133.1	<i>H. sapiens</i>	ENSNG00000167322	ANKRD11	ankyrin repeat domain 11	0.13	0.05	2.0E-09	2.0E-08	0.05	2.0E-09	Mackowiak	MEISQTVDEAPAA*
HG0133.2	<i>D. rerio</i>	ENSDDARG00000051886	ankrd11	ankyrin repeat domain 11	0.00	0.17	7.2E-03	1.5E-02	0.17	7.2E-03		MKTSIGREYDV*
HG0133.3	<i>H. sapiens</i>	ENSNG00000167522	ANKRD11	ankyrin repeat domain 11	0.00	0.36	3.2E-04	1.3E-03	0.36	3.2E-04		MGSARAPPLSRRAAQPSHEHYDPCSGTLHLHWI*
HG0134.1	<i>G. gallus</i>	ENSNGALG00000041267	BM11	Polycarb complex protein BM1-1	0.09	0.24	1.8E-02	3.7E-02	0.24	1.8E-02		MAWLTFIC*
HG0134.2	<i>H. sapiens</i>	ENSNG00000168283	BM11	BM1 proto-oncogene, polycarb ring finger	0.08	0.46	7.1E-07	4.9E-06	0.46	7.1E-07		MKRGDRGETMGMAWREPRSLAAPPSPA*
HG0135	<i>D. rerio</i>	ENSDDARG000000094132	lgf1	insulin-like growth factor 1	0.00	0.31	6.6E-08	2.6E-07	0.31	6.6E-08		MLPOLFPVENYSVM*
HG0135	<i>H. sapiens</i>	ENSNG00000117427	IGF1	insulin like growth factor 1	0.0							

HG0146.2	<i>G. gallus</i>	ENS GAL.G00000011855	RHOJ	ras homolog family member J	0.00	0.41	2.3E-08	1.1E-07	0.41	2.3E-08			MLWTALVWSSCDSLETV*
HG0146.3	<i>G. gallus</i>	ENS GAL.G00000014846	MEF2C	myocyte enhancer factor 2C	0.00	0.10	3.0E-10	1.5E-09	0.10	3.0E-10			MLTKRYVGRNRGTVN*
HG0149.2	<i>H. sapiens</i>	ENS G00000001189	MEF2C	myocyte enhancer factor 2C	0.00	0.34	9.3E-08	7.3E-07	0.34	9.3E-08			HWNLNKKWVNECRNLGTELCCK*
HG0150.1	<i>G. gallus</i>	ENS GAL.G00000032289	ICZF5	Zinc finger protein Pegasus	0.25	0.00	1.5E-48	2.2E-47	0.00	1.5E-48			MAAAEEGGGAGGRRRRHQGMEHKLT*
HG0150.2	<i>H. sapiens</i>	ENS G00000006574	ICZF5	IKAROS family zinc finger 5	0.00	0.26	2.0E-48	1.1E-46	0.26	2.0E-48			MAFVSPLLLYRSLQQLLYSSMLEVQEGKGTDLG*
HG0151	<i>G. gallus</i>	ENS GAL.G00000035504	ER81	ETS variant 1	0.00	0.32	1.1E-04	3.5E-04	0.32	1.1E-04			MFLNLEGNFLQPAARGLQADVSPDEISRSNAH*
HG0152	<i>D. rerio</i>	ENS DAR.G00000006468	ETV1	ETS variant 1	0.00	0.21	4.0E-35	1.6E-33	0.21	4.0E-35			MFLNLEGSFCSLSPSVAFSPVRCKASLVDHRX*
HG0153	<i>G. gallus</i>	ENS GAL.G00000003136	ICZF2	IKAROS family zinc finger 2	0.00	0.18	2.4E-31	2.4E-30	0.18	2.4E-31			MEEVPAQLATLAPLPQFF*
HG0154	<i>H. sapiens</i>	ENS G000000128573	FOXP2	forkhead box P2	0.02	0.46	1.7E-04	7.4E-04	0.46	1.7E-04			MPSVVDVIGORCTHSSVNTAVNSCLMVALTVS*
HG0155	<i>H. sapiens</i>	ENS G0000013635	TBR1	T-box, brain 1	0.00	0.44	3.9E-09	3.8E-08	0.44	3.9E-09			MAGAVSSAAQAARSVSLF*
HG0156	<i>H. sapiens</i>	ENS G00000156113	KCNMA1	potassium calcium-activated channel subfamily M alpha 1	0.06	0.45	1.5E-11	1.9E-10	0.45	1.5E-11			MAYDGLGQWWRRELPRAPAPAARC*
HG0157	<i>H. sapiens</i>	ENS G00000173926	MARCH3	membrane associated ring-CH-type finger 3	0.00	0.00	1.1E-30	3.9E-29	0.00	1.1E-30			MCGPGLGREDPPTLGNALARTAAAGTS*CYVDQSARTMELVECGSH*
HG0158	<i>H. sapiens</i>	ENS G00000198039	ZFP2	ZFP2 zinc finger protein	0.26	0.32	2.6E-22	7.1E-21	0.32	2.6E-22			MTYVGEVVALVBNPNSLQNLSPKNTSGLESLMKOKEPPEGGFDFGLGYCCQNLTFSPILISQSRGESID*
HG0159	<i>H. sapiens</i>	ENS G00000182197	EXT1	ectonuclein glycosyltransferase 1	0.01	0.08	7.8E-35	3.1E-33	0.08	7.8E-35			MOENYSPLANRPOCEFSFALSRALCNPKMKDRRGES*
HG0159.2	<i>H. sapiens</i>	ENS G00000182197	EXT1	ectonuclein glycosyltransferase 1	0.00	0.19	7.2E-08	6.7E-07	0.19	7.2E-08		Crowe	MCGFVRLRRSPCKMH*
HG0160	<i>D. rerio</i>	ENS DAR.G00000006089	btaf1	BTAF1 RNA polymerase II, B-TFIIID transcription factor-ase	0.00	0.33	9.3E-35	6.7E-34	0.33	9.3E-35			MAPHIKPAWLFLCDLQNYSPFVRLYKFRGSAEG*
HG0161	<i>G. gallus</i>	ENS GAL.G00000017191			0.02	0.25	2.7E-20	2.2E-19	0.25	2.7E-20			MCWLVFPVYTFPNS*
HG0162	<i>H. sapiens</i>	ENS G00000138347	MYPN	myopalladin	0.01	0.37	1.9E-13	3.0E-12	0.37	1.9E-13			MFRHMMYTAGNNLGPVS*
HG0163	<i>H. sapiens</i>	ENS G00000146285	SCML4	sex comb on midleg like 4 (Drosophila)	0.02	0.29	1.2E-25	3.6E-24	0.29	1.2E-25			MFAGAAGQGWRLTVSY*
HG0164	<i>H. sapiens</i>	ENS G00000151292	C5NK1G3	casein kinase 1 gamma 3	0.00	0.30	4.8E-39	2.3E-37	0.30	4.8E-39			MLPLWPIYSYLMVLFSDQYPSVCLSS*
HG0165	<i>H. sapiens</i>	ENS G00000177508	IRX3	iroquois homeobox 3	0.17	0.17	1.1E-58	6.7E-57	0.17	1.1E-58			MSIRASRPGNLRGOSVRT*
HG0166.1	<i>H. sapiens</i>	ENS G00000148948	LRRRC4C	leucine rich repeat containing 4C	0.00	0.01	2.6E-28	8.3E-27	0.01	2.6E-28			MKLQRRVREGDRS*
HG0166.2	<i>H. sapiens</i>	ENS G00000148948	LRRRC4C	leucine rich repeat containing 4C	0.00	0.35	4.8E-06	2.8E-05	0.35	4.8E-06			MODAASWNRQTOWIN*
HG0166.3	<i>H. sapiens</i>	ENS G00000148948	LRRRC4C	leucine rich repeat containing 4C	0.00	0.50	4.7E-04	1.8E-03	0.50	4.7E-04			MGNCEPHRHKESMIFLYKGESEPRRYVWNEKGFAGLVK*
HG0166.4	<i>H. sapiens</i>	ENS G00000148948	LRRRC4C	leucine rich repeat containing 4C	0.01	0.31	5.3E-10	3.3E-09	0.31	5.3E-10			MDEWGVRCGRABRGRGRWR*
HG0167	<i>D. rerio</i>	ENS DAR.G00000104025	klf4as		0.04	0.31	1.8E-33	1.3E-32	0.31	1.8E-33			MPHPRILGNPAWEKKC*
HG0168	<i>G. gallus</i>	ENS GAL.G00000006997	BRINP1	BMP/retinoic acid inducible neural specific 1	0.00	0.15	3.1E-10	1.5E-09	0.15	3.1E-10			MPAIWKEGDFLSEHKDC*
HG0169	<i>H. sapiens</i>	ENS G00000114933	INO80D	INO80 complex subunit D	0.00	0.47	2.0E-08	1.7E-07	0.47	2.0E-08			MYKLSFRRAEQLSGVMSSQCL*
HG0170	<i>H. sapiens</i>	ENS G00000180530	NRIP1	nuclear receptor interacting protein 1	0.00	0.07	3.1E-51	1.7E-49	0.04	2.7E-48			MKALRSAGIDSYGSPVLGTTAVRRTLUFANGEQMKKEKEYH*
HG0171.1	<i>H. sapiens</i>	ENS G00000177311	ZBTB38	zinc finger and BTB domain containing 38	0.00	0.00	2.8E-59	1.7E-57	0.00	2.8E-59			MYSKERTLMAVQLNQDSAEQDCHLQH*
HG0171.2	<i>H. sapiens</i>	ENS G00000177311	ZBTB38	zinc finger and BTB domain containing 38	0.00	0.10	5.2E-30	1.8E-28	0.47	2.6E-11			MNRNFFQSCFPVDKFSVITHSSCSAYDFCVYVTKTCEQEDREISWSPLYKMAECLVMLAH*
HG0171.3	<i>H. sapiens</i>	ENS G00000177311	ZBTB38	zinc finger and BTB domain containing 38	0.00	0.01	4.1E-18	8.9E-17	0.01	4.1E-18			MLAVLQKAFRAADLVFEEMDESEPRISK*
HG0171.4	<i>H. sapiens</i>	ENS G00000177311	ZBTB38	zinc finger and BTB domain containing 38	0.00	0.31	9.9E-03	2.6E-02	0.31	9.9E-03			MGDIRKICGADHKH*
HG0172.1	<i>H. sapiens</i>	ENS G00000196782	MAML3	mastermind like transcriptional coactivator 3	0.07	0.48	2.2E-12	3.1E-11	0.48	2.2E-12			MZLSQSGLTRTGGINTKTLFKWENAIKLAIVRCGVE*
HG0172.2	<i>H. sapiens</i>	ENS G00000196782	MAML3	mastermind like transcriptional coactivator 3	0.01	0.21	3.2E-06	1.9E-05	0.21	3.2E-06			MDYKKKASKERISP*
HG0173	<i>H. sapiens</i>	ENS G00000101746	NOL4	nucleolar protein 4	0.16	0.00	1.4E-02	3.4E-02	0.00	1.4E-02			MLIACRHRWYLS*
HG0174	<i>H. sapiens</i>	ENS G00000144355	DLX1	distal-less homeobox 1	0.01	0.39	2.1E-06	1.3E-05	0.39	2.1E-06			MRLTKRRAAPRALVORSPASQDSQSPVQDQSPISASST*
HG0175	<i>H. sapiens</i>	ENS G00000151320	NAKAP6	kinase anchoring protein 6	0.00	0.39	3.9E-12	5.4E-11	0.39	3.9E-12			MCKYHKQKTVYSGDAVLRSEV*
HG0176	<i>H. sapiens</i>	ENS G00000170962	POGFD	platelet derived growth factor D	0.20	0.01	1.3E-23	3.8E-22	0.01	1.3E-23			MQGEVWGLDG*
HG0177	<i>H. sapiens</i>	ENS G00000171843	MLLT3	MLLT3, super elongation complex subunit	0.09	0.46	5.3E-08	4.3E-07	0.46	5.3E-08			MLRNHLLYPGAAAAAFAFGAFENKRAQESAGGKQRQMSAIPPPLGALSFIAASS*
HG0178.1	<i>G. gallus</i>	ENS GAL.G000000029047	TMEM204	transmembrane protein 204	0.00	0.15	4.4E-45	5.8E-44	0.15	4.4E-45		Crowe, Mackowiak	MDLHVQFQITGALLIKVQEGG*
HG0178.2	<i>H. sapiens</i>	ENS G00000131634	TMEM204	transmembrane protein 204	0.05	0.24	6.4E-27	2.0E-25	0.24	6.4E-27		Crowe, Mackowiak	MGPEASSFTGLALLQVQEGG*
HG0178.2	<i>G. gallus</i>	ENS GAL.G000000029047	TMEM204	transmembrane protein 204	0.02	0.49	7.3E-09	3.4E-08	0.49	7.3E-09			MFDCRGSVSCSRLRPEAHONSHNKSHFL*
HG0179	<i>D. rerio</i>	ENS DAR.G00000036549	agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	0.00	0.09	8.0E-29	5.2E-28	0.09	8.0E-29		Mackowiak	MLSHIERLPCYNRLRDTAAQVYERKLEKVGAFPPTGSVVLSEGPCRKRL*
HG0179	<i>H. sapiens</i>	ENS G00000160216	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	0.12	0.08	8.3E-54	4.7E-52	0.08	8.3E-54		Mackowiak	MLRWVSVASPEFLNEVCRVWTVLSEGPCTRS*
HG0180.1	<i>H. sapiens</i>	ENS G00000112246	SIM1	single-minded family bHLH transcription factor 1	0.01	0.33	7.1E-35	2.8E-33	0.33	7.1E-35			MSIFRGQFGAFAGRRKGLWLRGTGPI*
HG0180.2	<i>H. sapiens</i>	ENS G00000112246	SIM1	single-minded family bHLH transcription factor 1	0.03	0.34	1.2E-06	7.9E-06	0.34	1.2E-06			MRTYKRWAPPKPLPLVGTGP*
HG0181.1	<i>H. sapiens</i>	ENS G00000143776	CDC42BP4	CDC42 binding protein kinase alpha	0.00	0.48	3.7E-15	6.6E-14	0.48	3.7E-15			MHSVFPLPLFFFFPSGSELLMGLYSMMQDPSFDQYVARVEF*
HG0181.2	<i>H. sapiens</i>	ENS G00000143776	CDC42BP4	CDC42 binding protein kinase alpha	0.00	0.04	4.3E-06	2.7E-05	0.04	4.3E-06			MYHMSIEBASIK*
HG0182	<i>G. gallus</i>	ENS GAL.G000000031991	decan	decan	0.06	0.05	1.1E-55	1.9E-55	0.05	1.1E-55			MDYNQKQKELLALKQPNHS*
HG0183	<i>H. sapiens</i>	ENS G00000114465	DCN	decorin	0.02	0.41	1.8E-12	2.8E-11	0.41	1.8E-12			MYWSAGLCSLRETLFFNCAME*
HG0184	<i>H. sapiens</i>	ENS G00000136542	GALNT5	polypeptide N-acetylglucosaminyltransferase 5	0.00	0.28	9.3E-07	6.2E-06	0.28	9.3E-07			MLCYEMPRRRLTRSGRN*
HG0185	<i>H. sapiens</i>	ENS G00000143033	MTF2	metal response element binding transcription factor 2	0.00	0.18	3.0E-04	1.2E-03	0.18	3.0E-04			MHRQSAIGNNGELY*
HG0186	<i>H. sapiens</i>	ENS G00000167552	TUBA1A	tubulin alpha 1a	0.08	0.41	3.3E-14	5.7E-13	0.41	3.3E-14			MASLGRQLGVWYTNKRPRPMPVTELYGSRRLCAAGSLTSTA*
HG0187.1	<i>G. gallus</i>	ENS GAL.G000000004058	GPR146	G protein-coupled receptor 146	0.25	0.40	5.2E-14	3.3E-13	0.40	5.2E-14			MDKMFLPASTGGQGTAYQKSW*
HG0187.2	<i>D. rerio</i>	ENS DAR.G000000059610	gpr146	G protein-coupled receptor 146	0.00	0.25	5.3E-04	1.5E-03	0.25	5.3E-04			MSMEIQNPMPP*
HG0187.3	<i>G. gallus</i>	ENS GAL.G000000004058	GPR146	G protein-coupled receptor 146	0.08	0.36	4.5E-06	1.7E-05	0.36	4.5E-06			MCMMYVGKSHVNTDSVP*
HG0188	<i>G. gallus</i>	ENS GAL.G00000162824	TAB3	TGF-beta activated kinase 1 and MAP3K7 binding protein 3	0.03	0.02	2.4E-33	2.5E-32	0.02	2.4E-33			MPAESEDHNNHWKC*
HG0188	<i>H. sapiens</i>	ENS G00000157625	TAB3	TGF-beta activated kinase 1 and MAP3K7 binding protein 3	0.00	0.27	4.9E-28	1.5E-26	0.27	4.9E-28			MTVVLDEHYVWKAG*
HG0189	<i>D. rerio</i>	ENS DAR.G00000001807	htraf2	tumor necrosis factor receptor superfamily, member 21	0.00	0.25	7.0E-24	4.3E-23	0.25	7.0E-24			MGIAIFVGNQALIPYLYKPVHSAGTKRREGTEFVH*
HG0190	<i>H. sapiens</i>	ENS G000000008949	CHD2	chromodomain helicase DNA binding protein 2	0.00	0.00	4.3E-08	1.9E-07	0.00	4.3E-08			MSFFPRTLY*
HG0191	<i>G. gallus</i>	ENS GAL.G00000036997			0.42	0.00	8.0E-16	6.0E-15	0.42	8.0E-16			MNRKRNPMYTVFLNQASPSISRT*
HG0192	<i>H. sapiens</i>	ENS G00000125107	CNOT1	CCR4-NOT transcription complex subunit 1	0.00	0.23	1.0E-18	2.3E-17	0.23	1.0E-18			MQKLPFSCQAISSQIQEYTHSKDLRSCMPNGAKTKCAMFQNRVPLVKN*
HG0193	<i>H. sapiens</i>	ENS G00000134853	PDGFRA	platelet derived growth factor receptor alpha	0.03	0.22	8.1E-06	4.6E-05	0.22	8.1E-06			MSFRMDYNIESTIKRG*
HG0194	<i>H. sapiens</i>	ENS G00000143507	DUSP10	dual specificity phosphatase 10	0.01	0.37	5.3E-11	6.4E-10	0.37	5.3E-11			MCESIAEEROMVEEYTYL*
HG0195	<i>H. sapiens</i>	ENS G00000165966	PDZRN4	PDZ domain containing ring finger 4	0.01	0.44	9.5E-05	4.3E-04	0.44	9.5E-05			MKNSSQVVRVVPFGTCLSVLKGLEDLTLSSAS*
HG0196	<i>H. sapiens</i>	ENS G00000189403	HMGCB1	high mobility group box 1	0.01	0.36	4.2E-09	4.0E-08	0.36	4.2E-09			MLQSGESEEAQSGSRSHSOSTLSSETAPQGVRAGRALGDSVPR*
HG0197	<i>H. sapiens</i>	ENS G00000196132	MYT1	myelin transcription factor 1	0.00	0.00	3.4E-04	1.4E-03	0.00	3.4E-04			MAFROLDKDRQ*
HG0198.1	<i>D. rerio</i>	ENS DAR.G00000018688	elk3	ELK3, ETS-domain protein	0.06	0.30	2.3E-03	5.6E-03	0.30	2.3E-03			MCVCYVRVRCARVPECRMVARGGKACHRRARLERGNRARREEVSLRALQLCLPAHRERRERKSE*
HG0198.2	<i>H. sapiens</i>	ENS G00000111145	ELK3	ELK3, ETS transcription factor	0.12	0.00	7.2E-05	3.4E-04	0.00	7.2E-05			MESRGLSPGSS*
HG0199	<i>G. gallus</i>	ENS GAL.G000000007989	ADNP	activity dependent neuroprotector homeobox	0.00	0.37	9.0E-03	2.0E-02	0.37	9.0E-03			MLRKGNCEQDMLLLCPGLFGTLQ*
HG0200	<i>G. gallus</i>	ENS GAL.G00000102015	NDS14	N-deacetylase and N-sulfotransferase 4	0.02	0.40	1.1E-17	8.0E-17	0.40	1.1E-17			MHCNCSHMNVSGEASFLRILVIMAL*
HG0201	<i>G. gallus</i>	ENS GAL.G00000114236	PAM	peptidylglycine alpha-amidating monooxygenase	0.00	0.30	8.1E-14	5.0E-13	0.30	8.1E-14			MFCOKLEACAPARNVWVW*
HG0202	<i>H. sapiens</i>	ENS G00000124786	BOX4	SRF-box 4	0.09	0.15	1.1E-46	6.4E-45	0.15	1.1E-46			MRSQSLLEIANGDYCYGFGANGRPQGVWVHEALVTADWLQPN*
HG0203	<i>H. sapiens</i>	ENS G00000128606	LRRIC17	leucine rich repeat containing 17	0.09	0.21	3.0E-14	5.1E-13	0.21	3.0E-14			MSLWHPPFKSLGTRTPAGSHCSRTALWKTQWISKEY*FHCBSVNTK*
HG0204	<i>H. sapiens</i>	ENS G00000182599	NFIA	nuclear factor 1 A	0.00	0.00	2.7E-09	2.7E-08	0.00	2.7E-09			MPLTPYSRHY*
HG0205	<i>H. sapiens</i>	ENS G00000184611	CNNH7	potassium voltage-gated channel subfamily H member 7	0.01	0.35	6.7E-04	2.5E-03	0.35	6.7E-04			MGRFEPVWRLMKCHERLARWPL*
HG0206.1	<i>G. gallus</i>	ENS GAL.G000000002069			0.00	0.48	3.4E-17	2.5E-16	0.48	3.4E-17			MVGAIQPRQPRFVWG/VGWQVSSACANDRDLWDGEIDPEWSGILLQREPHTGGLTWTS*
HG0206.2	<i>H. sapiens</i>	ENS G000000005238	FAM214B	family with sequence similarity 214 member B	0.00	0							

HG02251	H. sapiens	ENSNG00000118007	STAG1	stromal antigen 1	0.00	0.09	9.2E-07	6.1E-06	0.09	9.2E-07	MPPDGGLQLQR*
HG02252	H. sapiens	ENSNG00000150051	MXC	mohawk homeobox	0.21	0.30	5.2E-10	5.7E-09	0.30	5.2E-10	MPAOWROGNGMRRPRYCSRAARAGLGR*
HG02261	H. sapiens	ENSNG00000180592			0.07	0.06	1.7E-05	0.1E-05	0.06	1.7E-05	MERFIYRLYYLWEGRWQYKMLISGRFVWGEVGYOFLHLSGVNSGRWL*
HG02262	H. sapiens	ENSNG00000180592			0.09	0.44	1.9E-02	4.5E-02	0.44	1.9E-02	MAEQPIESADNMVKFKETPWLKNSLWYIKSOGAKQYFPLITRMLCLEEGONT*
HG02263	H. sapiens	ENSNG00000180592			0.26	0.40	8.1E-03	2.2E-02	0.40	8.1E-03	MRLGLPLSFQNLIDLENDTKICLNITKRLNIDFHPK*
HG02271	G. gallus	ENSNGALG00000031929			0.05	0.48	5.6E-04	1.6E-03	0.48	5.6E-04	MTALNNWHWFGYGVSSVY*
HG02272	H. sapiens	ENSNG00000275163			0.00	0.20	2.6E-04	1.1E-03	0.20	2.6E-04	MCKVSEEEPLFPVIASTGLQGTSLFLLGYVCFTHSLFCLRHFEH*
HG0228	D. rerio	ENSNDARG0000007887	ph21b	PHD finger protein 21B	0.05	0.39	2.1E-13	9.4E-13	0.39	2.1E-13	MSLTASKEARFTCAARVLAIVAFQNTSLTPQITRIASEVEEKSS*
HG0229	G. gallus	ENSNGALG00000005474			0.00	0.40	3.0E-03	7.7E-03	0.40	3.0E-03	MCHFWWTLPLFGV*
HG0230	G. gallus	ENSNGALG0000011007	CSBP1.3	oxysterol binding protein like 3	0.00	0.48	2.0E-05	7.2E-05	0.48	2.0E-05	MKMLLECWWRDFEOTLRSPLHLLDYLLMTF*
HG0231	H. sapiens	ENSNG00000152626	NETO1	neurotrophin 1	0.13	0.46	1.3E-04	4.4E-04	0.46	1.3E-04	MGEILLTHWATELGFSPRGRS*
HG0232	H. sapiens	ENSNG00000180875	GREM2	gremlin 2, DAN family BMP antagonist	0.20	0.34	9.4E-11	1.1E-09	0.34	9.4E-11	MGVCSLAAVELKAAAGDT*
HG0233	H. sapiens	ENSNG00000206432	TMEM200C	transmembrane protein 200C	0.17	0.45	1.2E-08	2.1E-07	0.45	1.2E-08	MSGGEESEAGCGMARDLTLTNGSWMLPPORRRLRAWGGRSPPRGC*
HG0234.1	G. gallus	ENSNGALG00000011250	ASIC4	acid sensing ion channel subunit family member 4	0.10	0.00	5.9E-03	1.4E-02	0.00	5.9E-03	MLTCLLELSIWILLAHDA*
HG0234.2	H. sapiens	ENSNG00000108684	ASIC2	acid sensing ion channel subunit 2	0.03	0.43	1.5E-04	6.5E-04	0.43	1.5E-04	MYVMGHYALVNLRAQRLVLSIFSLALFNLNYSVGCRGDFISIG*
HG0235.1	G. gallus	ENSNGALG00000035927			0.00	0.48	5.7E-08	2.5E-07	0.48	5.7E-08	MLATESIGNFTVGLARVLELTAKEARRGQTGMCPVLLHEQTTPRALGPCAKRA*
HG0235.2	H. sapiens	ENSNG00000101638	ST8SIA5	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase	0.03	0.37	9.2E-05	4.2E-04	0.37	9.2E-05	MPPAPAAPTRNFAPRSPPPA*
HG0236	G. gallus	ENSNGALG00000004437	LHFPL2	lipoma HMGC fusion partner-like 2	0.02	0.47	1.0E-07	4.6E-07	0.47	1.0E-07	MAVAGAGGQEGPGARAGGQGGSGAEPQTGWAGLRLAGGIARLKLWTKAKNRHWCWSSSGQSPRPSPVRSVMCMQCYQ*
HG0237	G. gallus	ENSNGALG00000012123	PAX6	paired box 6	0.00	0.35	1.3E-04	4.1E-04	0.35	1.3E-04	MCGVISGFEKAPARPHPLVLRREEVFGWMMTEVGR*
HG0238	H. sapiens	ENSNG00000049818	ARID1B	AT-rich interaction domain 1B	0.16	0.43	1.9E-05	1.0E-04	0.43	1.9E-05	MLGPGSASRFTVTHAREKKRVSKFPEKLTITMKAHSRSPRRA*
HG0239	H. sapiens	ENSNG00000146256	TENM4	tenascin transmembrane protein 4	0.00	0.33	1.4E-02	3.5E-02	0.33	1.4E-02	MGPRLALPGVQKQAKFYKDYLDZYD*
HG0240	G. gallus	ENSNGALG00000168342	NETO1	neurotrophin and toll-like 1	0.05	0.42	1.0E-08	2.4E-08	0.42	1.0E-08	MTDFPLFPMPOPKQPKWSEKCPNTPSSRSGGCSDLNLGASBETQ*
HG0241	H. sapiens	ENSNG00000198561	CTNND1	catenin delta 1	0.06	0.49	1.4E-03	4.8E-03	0.49	1.4E-03	MEVSGWLSLPLASSLLWGLCFHDFNLDWALCVKPSCDLLTV*
HG0242.1	G. gallus	ENSNGALG00000007112	LINS1	linex homolog 1	0.00	0.21	3.5E-08	1.6E-07	0.21	3.5E-08	MSRONLEEELCLALLDKNNKTDLQOSEIGEDLQRSVY*
HG0242.2	H. sapiens	ENSNG00000140471	LINS1	linex homolog 1	0.08	0.45	1.1E-02	2.7E-02	0.45	1.1E-02	MREEVPACTCELWRPRAGICVPSNGGVKRVLSIQPQTEETS*
HG0243.1	H. sapiens	ENSNG00000163697	APBB2	amyloid beta precursor protein binding family B member 2	0.04	0.43	3.8E-04	1.5E-03	0.43	3.8E-04	MLGSLSLQIQTITYFLHHC*
HG0243.2	H. sapiens	ENSNG00000163697	APBB2	amyloid beta precursor protein binding family B member 2	0.00	0.13	2.9E-17	5.9E-16	0.13	2.9E-17	MLWSDPLSRGTETGAWGKHKKLL*
HG0244	G. gallus	ENSNGALG0000010837	ASB5	ankyrin repeat and SOCS box containing 5	0.00	0.22	9.7E-05	3.2E-04	0.22	9.7E-05	MLTGLTSLRLKAVMKQ

HG0275.2	D. rerio	ENSDFAR000000045540	zsp6r2a	protein phosphatase 6, regulatory subunit 2a	0.03	0.29	2.8E-03	6.7E-03	0.29	2.8E-03		MLHGSVPFAPFCHSNACRPFVEE*
HG0276.1	G. gallus	ENSOGAL000000008912			0.13	0.38	7.7E-04	2.2E-03	0.28	7.7E-04		MDSSSSTVYNNVHHM*
HG0276.2	H. sapiens	ENSG000000073734	ABCB11	ATP binding cassette subfamily B member 11	0.12	0.30	6.9E-03	1.9E-02	0.30	6.9E-03		HMNKEGYGVGCT*
HG0277.1	H. sapiens	ENSG000000102531	FNDC3A	fibronectin type III domain containing 3A	0.10	0.02	5.4E-16	1.0E-14	0.02	5.4E-16		MAAAAFVVPYVKOKAGATRRGSEERG*
HG0277.2	G. gallus	ENSOGAL000000004169			0.06	0.00	7.2E-03	1.7E-02	0.00	7.2E-03		MAERSVGGRRRG*
HG0278.1	H. sapiens	ENSG000000119946	CNNM1	cyclin and CBS domain divalent metal cation transport med	0.20	0.22	2.0E-09	2.0E-08	0.22	2.0E-09		MPGHL0PPAGTSCPGGV*
HG0278.2	D. rerio	ENSDFARG000000078733	cnnm2b	cyclin and CBS domain divalent metal cation transport med	0.00	0.19	2.7E-03	6.5E-03	0.19	2.7E-03		MHKSRRRAEMKPDWL*
HG0279.1	H. sapiens	ENSG000000175928	LRRN1	leucine rich repeat neuronal 1	0.00	0.35	1.0E-13	1.6E-12	0.38	1.0E-13		MFTSARCPTYTHNVFTFC*
HG0279.2	G. gallus	ENSOGAL000000035099	Lm1	leucine rich repeat neuronal 1	0.28	0.47	2.3E-02	4.6E-02	0.47	2.3E-02		MSAPPLRGGELRGORPPGCRNVFRHGVDEPDTQRSS*
HG0280.1	H. sapiens	ENSG000000156299	TIAM1	T-cell lymphoma invasion and metastasis 1	0.00	0.26	2.2E-05	1.2E-04	0.26	2.2E-05	Crowe	MAHLEITKLPLPMGLAHSHRLR*
HG0280.2	D. melanogaster	Fbgr0085447	sif	still life	0.00	0.04	9.4E-08	9.7E-08	0.04	9.4E-08		MGAKESVAAAKMADGWHGVSSRRYNNRHNRQSLSNRGALSOADVSGMW*
HG0281.1	G. gallus	ENSOGAL000000006766	DEPCD5	DEP domain containing 5	0.01	0.12	4.8E-28	4.5E-27	0.12	4.8E-28		MCRMSSTVTFRNS*
HG0281.2	H. sapiens	ENSG000000100150	DEPCD5	DEP domain containing 5	0.04	0.11	1.0E-09	1.1E-08	0.11	1.0E-09		MTSLPQAVNS*
HG0282.1	D. rerio	ENSDFARG000000001328	cdon	cell adhesion associated, oncogene regulated	0.07	0.29	2.2E-10	1.2E-10	0.29	2.2E-10		MEGPRRCHNENVRRC*
HG0282.2	H. sapiens	ENSG000000144857	BOC	BOC cell adhesion associated, oncogene regulated	0.05	0.27	1.8E-02	4.2E-02	0.27	1.8E-02		MKCSRHLYRFAAR*
HG0283.1	G. gallus	ENSOGAL000000102070	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1	0.10	0.29	3.9E-31	3.9E-30	0.29	3.9E-31		MQVPGVPVSYAFSMASLC*
HG0283.2	H. sapiens	ENSG000000119682	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1	0.00	0.42	7.2E-24	2.1E-22	0.42	7.2E-24		MDRPLLTLLWRFSFMWKLEDKVKGAKSYLLW*
HG0284.1	H. sapiens	ENSG000000007168	PAFAH1B1	platelet activating factor acetylhydrolase 1b regulatory subu	0.13	0.10	4.4E-05	2.2E-04	0.10	4.4E-05	Crowe	MGVKDGRGAEAAVGRSGGMNLTC*
HG0284.2	G. gallus	ENSOGAL000000005834	PAFAH1B1	platelet activating factor acetylhydrolase 1b regulatory subu	0.03	0.18	1.5E-02	3.3E-02	0.18	1.5E-02		MPPGFVGVPFIWRNKLCSHGKLCNGS*
HG0285.1	G. gallus	ENSOGAL000000012156	DPP10	dipeptidyl peptidase like 10	0.20	0.13	9.2E-03	2.1E-02	0.13	9.2E-03		MLRGRRPAAGQEEHGAGDGLGFPAGAVAPRLPAFLFLYFSSSSAAPLRGEVGMRLAPGECPCGPQRQ*
HG0285.2	H. sapiens	ENSG000000175497	DPP10	dipeptidyl peptidase like 10	0.00	0.00	9.9E-03	2.6E-02	0.00	9.9E-03		HNQVNALFRA*
HG0286.1	H. sapiens	ENSG000000116698	SMG7	SMG7, nonsense mediated mRNA decay factor	0.00	0.00	5.8E-04	2.2E-03	0.00	5.8E-04		MSLSQAQYLR*
HG0286.2	D. rerio	ENSDFARG000000060767	smg7	SMG7 nonsense mediated mRNA decay factor	0.08	0.49	9.9E-03	2.0E-02	0.49	9.9E-03		MDNMAPGVDLACESVIV*
HG0287.1	H. sapiens	ENSG000000170325	PRDM10	PR/SET domain 10	0.00	0.33	1.7E-12	2.4E-11	0.33	1.7E-12		MLQTDLSVHETGCRMTVLYPLVLL*
HG0287.2	D. rerio	ENSDFARG000000104251	prdm10	PR domain containing 10	0.00	0.40	5.4E-07	2.0E-06	0.40	5.4E-07		MQGSLSCSYHSEGRPTSTIS*
HG0288.1	G. gallus	ENSOGAL000000000655	MAP3K13	mitogen-activated protein kinase kinase kinase 13	0.20	0.44	4.2E-03	1.2E-02	0.44	4.2E-03		MYRYNPAISRNDPVL*
HG0288.2	H. sapiens	ENSG000000073803	MAP3K13	mitogen-activated protein kinase kinase kinase 13	0.02	0.41	6.9E-04	2.8E-03	0.41	6.9E-04		MYCQQLALNERNVSPQLSSVPKPK*
HG0289	G. gallus	ENSOGAL000000009581	MPP5	membrane palmitoylated protein 5	0.00	0.45	1.1E-32	1.1E-31	0.45	1.1E-32		MDFTQGRNENWNISNS*
HG0289.1	H. sapiens	ENSG000000072415	MPP5	membrane palmitoylated protein 5	0.00	0.30	1.5E-16	2.9E-15	0.30	1.5E-16		MDFILOENENWLKGLD*
HG0290.1	H. sapiens	ENSG000000116539	ASH1L	ASH1 like histone lysine methyltransferase	0.00	0.48	1.9E-09	1.9E-08	0.48	1.9E-09		MLVSSFGDPTFLWNTVL*
HG0290.2	D. rerio	ENSDFARG000000070981	ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	0.04	0.28	6.6E-06	2.3E-05	0.28	6.6E-06		MEARLTREARSDEPELH*
HG0291.1	G. gallus	ENSOGAL0000000009173	GFR1A	GDNF family receptor alpha 1	0.24	0.41	2.2E-03	5.9E-03	0.41	2.2E-03		MDRNLLESHLGGFGISTC*
HG0291.2	H. sapiens	ENSG000000151892	GFR1A	GDNF family receptor alpha 1	0.14	0.44	3.0E-06	1.8E-05	0.44	3.0E-06		MELNFGRPECHSCPGIAAR*
HG0292.1	G. gallus	ENSOGAL000000006502	PCGF5	polycomb group ring finger 5	0.17	0.24	1.0E-28	9.6E-28	0.24	1.0E-28		MPKGVPURRAAPQLS*
HG0292.2	H. sapiens	ENSG000000118028	PCGF5	polycomb group ring finger 5	0.00	0.11	5.2E-06	3.0E-05	0.11	5.2E-06		MALSPRLRRWRDLGDEAAETNSQDMGKRNHQKE*
HG0293	G. gallus	ENSOGAL0000000012187	MGAT5	mannosyl (alpha-1,6)-glycoprotein beta-1,6-N-acetyl-gluc	0.00	0.33	4.8E-27	4.4E-26	0.33	4.8E-27	Mackowiak	MLRKAHPTTNRMELKYGYMLTKESE*
HG0293.1	H. sapiens	ENSG000000152127	MGAT5	mannosyl (alpha-1,6)-glycoprotein beta-1,6-N-acetyl-gluc	0.00	0.28	1.0E-23	2.8E-22	0.28	1.0E-23	Mackowiak	MEYRVKGNGLTQE*
HG0294.1	G. gallus	ENSOGAL0000000017038	LHPF	Ispcra HMGC fusion partner	0.05	0.41	7.3E-14	4.7E-13	0.41	7.3E-14		MGNRNLAFRRAPSPVRGCG*
HG0294.2	H. sapiens	ENSG000000183722	LHPF	Ispcra HMGC fusion partner	0.12	0.43	3.7E-04	1.5E-03	0.43	3.7E-04		MPRGKDKSLVCPDRGRCGRPPAMDHL*
HG0295.1	H. sapiens	ENSG000000116988	STAT6	signal transducer and activator of transcription 6	0.15	0.06	9.5E-36	3.9E-34	0.06	9.5E-36		MYTCALSYTSPFWWWWGGGASRASLALAGQSYRPMGPGSAR*
HG0295.2	G. gallus	ENSOGAL0000000003282	STAT5B	signal transducer and activator of transcription 5B	0.17	0.50	8.8E-05	2.9E-04	0.50	8.8E-05		MRACVPSLCPQLKACAGGRQKQPEHAARLQRTLVFKAENLASFLL*
HG0296	G. gallus	ENSOGAL000000006912	CEPB3	cytoplasmic polyadenylation element binding protein 3	0.23	0.17	2.1E-03	5.6E-03	0.17	2.1E-03		MQIARGRRRRRRRLVGGTGTFRSLSGQSESEFRCKRKEIWRNCGISLPYKHSHLD*
HG0297	G. gallus	ENSOGAL0000000001684			0.20	0.00	1.1E-05	4.0E-05	0.00	1.1E-05		MCFCFVLQRFWRLLFT*
HG0298	G. gallus	ENSOGAL000000042308			0.00	0.01	2.0E-04	6.2E-04	0.01	2.0E-04		MESIVWEGC*
HG0299	G. gallus	ENSOGAL0000000040465	Slp1	zinc finger E-box binding homeobox 2	0.00	0.39	1.2E-02	2.7E-02	0.39	1.2E-02		MLGKEKKNVRRGVTRQSVPRFVPFOVAERDGS*
HG0300	D. melanogaster	Fbgr0031688	CG31917	RES2906p2	0.00	0.02	0.0E+00	0.0E+00	0.02	0.0E+00	Hayden	MMVNVKGVLECCDPAKMGFLHLDEKALGRKFQGLDLENHFLSTDIEVLRQVDDLMRISFLHDKDA*
HG0301	D. melanogaster	Fbgr0036856	CG9666	isoform A, isoform A	0.15	0.05	0.0E+00	0.0E+00	0.05	0.0E+00	Hayden	MAFPTTSAQGAETNRKLEIQTKQLLAGGLSPNNMPMAPQLGGPTVMPDFQAQGVGIATNAT3SAFNPSTSTLGGFFIQDQSYGNSFPIVLPRLPLSPATTPPTPNAPSHSISK*
HG0302	D. melanogaster	Fbgr0031454	CG9660	CG9660	0.20	0.04	1.2E-269	3.2E-269	0.04	1.2E-269	Hayden	MDSDSTVTSLEENTETCTNPTRDLAIEGTLNPKFTPIERLDERVASTIQLQALRGQLDAAQLRDIEKAGSQIPEFADKVELLNKVKHVTISNVLVTSQERLTGLHKEKEQRRAQLDLSALSTNIS*
HG0303	D. melanogaster	Fbgr0260464	CG7071	CG7071, isoform A	0.00	0.05	1.4E-232	2.9E-232	0.05	1.4E-232	Hayden	MHTLDSHLHFPANCKLELQACHENAFAPFVGVGVNSIDDKVYKLGKEHARASANRAKARERQAQYKEKLGQESN*
HG0304	D. melanogaster	Fbgr0260467	CG7071	CG7071, isoform A	0.03	0.06	0.0E+00	0.0E+00	0.06	0.0E+00	Hayden	MKMMSVQRLRYVPLRLDRFVYVSEGEAFLEFVFRNRDSSEKFLPVQDTEYVSLSYKLSRCSATGRCGSAENLAAIDTEVSHLDDQVALLAKKAVERTASTQLQEARLAREQRRAEFLTNLHGYVRRNIESPEEKEIEALYSDQLKLNIAK*
HG0305	D. melanogaster	Fbgr0260390	Pjoc2	Phosphatohistidylphenylalanine decarboxylase	0.29	0.04	4.7E-246	1.1E-245	0.04	4.7E-246	Hayden	MTSQYDSQKLPVTPFRKSGVPLDNEGLCKQZPLVYASCLPRWAGDQTSQCRGDQVLYACRMENLMEKTEVPLKQFGDQSTYTDQKEPEVQKQ*
HG0306	D. melanogaster	Fbgr0259726			0.06	0.08	0.0E+00	0.0E+00	0.08	0.0E+00		MYAQVPRPKEDQLDQKEQQAQNRRTTALPKRTWQRNPLFOISFITSLLFFSKPLFDCFIADPLPPENKVPYHKH*
HG0307	D. melanogaster	Fbgr0037822	CG14683	Probable methyltransferase-like protein 15 homolog	0.12	0.06	1.1E-202	2.0E-202	0.06	1.1E-202		MSAQORFUKYLEKWPAKSKVGRDLQGEIRKQVTKLTSLEGGATDKELDQRNLSRLSNVYAKKPTFTFESTATGLTAQCSQVLSSEFLQYLNEDSKKKKK*
HG0308	D. melanogaster	Fbgr0264743	CG40041	LP2284p01	0.00	0.04	2.4E-197	4.3E-197	0.04	2.4E-197	Hayden	MPYIIRGNLASYSHYKWRVLVYSLGKADQLQNKFCSGYSDSTVLYVPHRSLALELGRFVVASSTAVQDQYENMYMTWRKEDEPEPELAEASVRENLSNIGREASLGNHYKHVDSPE*
HG0309	D. melanogaster	Fbgr0037689	CG8135	LMBR1 domain-containing protein 2 homolog	0.23	0.06	2.3E-243	5.2E-243	0.06	2.3E-243		MSVSEAEVQKIDUEPTTKGLFFHKTELLFRPLMLPKTQALREEMHRDTARLQKROKKKCSSTPTGSL*
HG0310	D. melanogaster	Fbgr0039339	CG5116	isoform A, isoform A	0.08	0.05	6.5E-119	8.7E-119	0.05	6.5E-119	Hayden	MLRHLKQDQREKHPFGDGYMDCMTRSLGTALCTGLFSCGYAQKIVQSKIRPKYKINLSSLVATGVSQYITSTRTKCAQAAWMFEDKSHVLEKTEP*
HG0311	D. melanogaster	Fbgr0263251	vnc	variable nurse cells	0.01	0.06	5.0E-128	6.8E-128	0.06	5.0E-128	Hayden	MSLQTGLAFITLASYVAIIILLVHMKAFSLKFLVRELLGOEPEEQDQPLAVHQNQCPHHGRARKARRD*
HG0312	D. melanogaster	Fbgr0038641	CG7708	High-affinity choline transporter 1	0.07	0.05	8.1E-98	1.0E-97	0.05	8.1E-98	Mackowiak	MGLHFHRTNPSPSQTSLRWGDCLLA*
HG0313	D. melanogaster	Fbgr0259725			0.12	0.06	9.8E-78	1.2E-77	0.06	9.8E-78		MSDTRDKCPKPNACRQACLTSKHHR*
HG0314	D. melanogaster	Fbgr0260468	CG7950	CG7950, isoform A	0.15	0.06	0.0E+00	0.0E+00	0.06	0.0E+00	Hayden	MSGVYLDVVKLRDPSVLTPTVPFCGCHSSLASIFGEIGGQTLLEIVKFSSSQKRSRLPVNVLDRVRAIILGYVEQPCPVQLVTSRRKPLDFEESPEEFVAFN*
HG0315	D. melanogaster	Fbgr0260234	CG42508	GHS2541p7	0.00	0.07	3.8E-68	4.5E-68	0.07	3.8E-68		MKPKPASANSTSYGRNKHQKSHGSKDKVGGKQSKDEKDKRHKDEKQVDEKDDKDLNSGFGDQYLRTPAEFEMKRLVFVATMLVMAWPHKEGFMVQMWQLSFREHQQ*
HG0316	D. melanogaster	Fbgr0041164	ami	armilage	0.10	0.07	6.3E-165	1.0E-164	0.07	6.3E-165		MSBPASGATIKKEEASGTVAIPNPFSEETAKEPKGEADKAESQSETTEGGAETTENHLKRLQNLRKLSYLSSETWMMYSLDKDAQ*
HG0317	D. melanogaster	Fbgr0258011	gemi1	gemi1	0.00	0.01	5.0E-17	5.0E-17	0.01	5.0E-17	Mackowiak	MEKSEIRLRGMSVYKSSSMTYMLATLKRLEITLRRHQREITGKWLNSYPLVL*
HG0318	D. melanogaster	Fbgr0035293	CG5687	CG5687, isoform A	0.00	0.04	1.7E-13	1.8E-13	0.04	1.7E-13	Mackowiak	MYKNNRGTQIQGRTFLRYSAALIPES*
HG0319	D. melanogaster	Fbgr0026778	Rad1	Radiation insensitive 1	0.00	0.07	5.4E-12	5.7E-12	0.07	5.4E-12	Hayden	MASEENSTSYFPHLVDQVFLYSKSSKNTKEERQGFYDLSLLGGELVLSRLHLDHNFSSFHAKNNRNSVCVEISKGYEYRPLGVPSYCKCFEQCHVLQPRGLYQDLPSGEGILEDDSEESRSVSYTCOHLALRHLFKHTGGKTEKILKDEKELATDVFQ*
HG0320	D. melanogaster	Fbgr0040993			0.00	0.06	1.0E-02	1.0E-02	0.06	1.0E-02	Hayden	MKTPDTAKLNNLSLKHLSKKQSGKSRNCSNCGLEFSLVTRLSVVP*
HG0321	D. rerio	ENSDFARG000000070426	chac1	ChaC, cation transport regulator homolog 1 (E. coli)	0.03	0.25	6.2E-160	9.2E-159	0.25	6.2E-160		MHQAKSVLRDCTTITAKGLSDTYRGIASQNPQLLDRRLKLAT*
HG0322	D. rerio	ENSDFARG000000070917	kltpa	kit ligand a	0.00	0.34	5.5E-27	3.4E-26	0.34	5.5E-27		MMILDMYLVDEENPPAPRRSKR*
HG0323	D. rerio	ENSDFARG000000071197	usp40	ubiquitin specific peptidase 40	0.02	0.03	7.8E-132	1.1E-130	0.03	7.8E-132	Mackowiak	MPFVKSSYARVSPVLNRELGTQKMR*
HG0324	D. rerio	ENSDFARG000000049065	rhf3-5	nuclear factor, interleukin 3 regulated, member 5	0.00	0.10	6.6E-97	8.1E-96	0.10	6.6E-97		MTVVVFHFHLFLTSLDT*
HG0325	D. rerio	ENSDFARG000000070738	znf219	zinc finger protein 219	0.13	0.07	2.2E-12	9.8E-12	0.07	2.2E-12		MYLIQVRNHHOVCH*
HG0326	D. rerio	ENSDFARG000000012848	arh2	ariadne homolog 2 (Drosophila)	0.00	0.00	5.5E-89	6.6E-88	0.00	5.5E-89		MSDGECCFFCFRCC*
HG0327	D. rerio	ENSDFARG000000022023	gtf2iiv1	GTF2I repeat domain containing 1	0.00	0.39	3.7E-20	2.2E-19	0.39	3.7E-20		MTNTFNLGNKREKRGKTHSSVKNREKGTQHQINHECTSDTYRPFEMTFSKVAVAF*
HG0328	D. rerio	ENSDFARG000000009996	usp8	ubiquitin specific peptidase 8	0.00	0.08	2.0E-63	2.0E-62	0.08	2.0E-63		MRNVAVASTTRMMNSPL*
HG0329	D. rerio	ENSDFARG000000036442	hsp11c	ATPase, Class VI, type 11C	0.00	0.43	2.2E-20	1.3E-19	0.43	2.2E-20		MRMRPEISQILWKRCSTFALHARGHNRLES*
HG0330	D. rerio	ENSDFARG000000039392	wnk1b	WNK lysine deficient protein kinase 1b	0.00	0.32	3.7E-37	2.8E-36	0.32	3.7E-37		MDEVSLTVYCHQGLPGLNPLTFYFVYKPTPLGSLGFLPKHCNC*
HG0331	D. rerio	ENSDFARG000000044899	mem183a	transmembrane protein 183A	0.02	0.34	6.3E-58	5.9E-57	0.34	6.3E-58		MYATLSVSSMAEDPGAFNFTLLDTFSLPLRWQ*
HG0332	D. rerio	ENSDFARG0000000102893	atg7	ATG7 autophagy related 7 homolog (S. cerevisiae								

HG0358	D. rerio	ENSDDARG00000062908	zc3h18	zinc finger CCHC-type containing 18	0.15	0.28	4.7E-06	1.6E-05	0.28	4.7E-06	MAALTVSQRVYAFFR*
HG0359	D. rerio	ENSDDARG00000071346	hoxc10a	homeobox C10a	0.07	0.30	3.3E-07	3.3E-07	0.30	3.3E-07	MSASYGPPPLRWKQCFEESKEQDKQ*
HG0360	D. rerio	ENSDDARG00000070801	gpat1	optic atrophy 1 (autosomal dominant)	0.04	0.10	7.6E-06	2.6E-05	0.10	7.6E-06	MCWPKDELFLGRDPPLVYIC*
HG0361	D. rerio	ENSDDARG00000071581	zzz3	zinc finger, ZZ-type containing 3	0.24	0.37	1.5E-03	3.9E-03	0.37	1.5E-03	MSCRFAEVRCPHTAAEERAPR*
HG0362	D. rerio	ENSDDARG00000078355	zc3h4	zinc finger CCHC-type containing 4	0.01	0.42	7.7E-04	2.1E-03	0.42	7.7E-04	MSFISHNRNCRTELRNVFLFLF*
HG0363	D. rerio	ENSDDARG00000059896	pou3f3b	POU class 3 homeobox 3b	0.22	0.31	2.3E-04	6.6E-04	0.31	2.3E-04	MRYNLPALKFKLQGGGQQQTSY*
HG0364	D. rerio	ENSDDARG00000040498	ppp3ca	protein phosphatase 3, catalytic subunit, alpha isozyme	0.00	0.42	9.3E-03	1.9E-02	0.42	9.3E-03	MPLHQLPVLATNRRR*
HG0365	D. rerio	ENSDDARG00000016132	keap1a	kelch-like ECH-associated protein 1a	0.00	0.17	3.3E-05	1.1E-04	0.17	3.3E-05	MPTWLATESYGLLTROKKHGLSLNDNLCLYFFMARGWW*
HG0366	D. rerio	ENSDDARG00000017803	gsk3b	glycogen synthase kinase 3 beta	0.00	0.20	8.8E-05	2.7E-04	0.20	8.8E-05	MELSGSERPRISVLKGNWKLIRAG*
HG0367	D. rerio	ENSDDARG00000034056	ckink1g2b	casein kinase 1, gamma 2b	0.03	0.22	8.1E-04	2.2E-03	0.22	8.1E-04	MFTVLPRTDFKETMRSTRGRSLVGFH*
HG0368	D. rerio	ENSDDARG00000058606	sik1	salt-inducible kinase 1	0.23	0.28	2.1E-03	5.2E-03	0.28	2.1E-03	MTCKCKCKXNLQCGRRWKLFS*
HG0369	D. rerio	ENSDDARG00000059278	hoxd4a	homeobox D4a	0.04	0.48	2.1E-02	3.8E-02	0.48	2.1E-02	MKSLLDWPSWSHGRLTLFS*
HG0370	D. rerio	ENSDDARG00000062693	rxrxnb	neurexin 3b	0.02	0.32	2.2E-02	3.8E-02	0.32	2.2E-02	MWONNRIRSMENLGNFNERRLKGTSVSKHF*
HG0371	D. rerio	ENSDDARG00000062765	hifc111	HuIf-Hirschhorn syndrome candidate 1-like 1	0.00	0.24	9.7E-03	1.9E-02	0.24	9.7E-03	MEHAGAGVRRWCT*
HG0372	D. rerio	ENSDDARG00000069467	gplf1b	immunoglobulin superfamily, member 98b	0.26	0.50	3.0E-02	5.0E-02	0.50	3.0E-02	MCQMGKRSYAAASANDGGLQ*
HG0373	D. rerio	ENSDDARG00000074611	wdr37	WD repeat domain 37	0.06	0.46	4.2E-03	9.4E-03	0.46	4.2E-03	MTVALRSAAEVALGFLFEVFLFTTLSSRLRMLCLLSFTLHGCFR*
HG0374	D. rerio	ENSDDARG00000075147	hrc38a	leucine rich repeat containing 38a	0.18	0.17	2.7E-03	6.5E-03	0.17	2.7E-03	MISWKLRLRVAAFRCTSLCRLSQRRQGMKPSRT*
HG0375	D. rerio	ENSDDARG00000076171	znf827	zinc finger protein 827	0.00	0.18	1.6E-02	3.0E-02	0.18	1.6E-02	MKGDLFSSYP*
HG0376	D. rerio	ENSDDARG00000077229	ano8b	anoctamin 8b	0.07	0.01	9.4E-05	2.9E-04	0.01	9.4E-05	MTHNNLHFTLTFI*
HG0377	D. rerio	ENSDDARG00000079549	cdcd42ep1a	CDC42 effector protein (Rho GTPase binding) 1a	0.00	0.28	2.5E-02	4.2E-02	0.28	2.5E-02	MQPPRFGIGVMHFHSHLSPNLSGYEQPMKAGTGS*
HG0378	D. rerio	ENSDDARG00000080009	bahcc1b	BAH domain and coiled-coil containing 1b	0.21	0.16	6.4E-05	2.0E-04	0.16	6.4E-05	MIGTYFFGRSQNCAECKT*
HG0379	D. rerio	ENSDDARG00000104372	gnb1b	guanine nucleotide binding protein (G protein), beta polypep	0.00	0.47	1.7E-02	3.0E-02	0.47	1.7E-02	MRGFDSHTVFFGGCHINKGHLRLRDTQNVRSQ*
HG0380	D. rerio	ENSDDARG00000053560	dp2ba	disco-interacting protein 2 homolog Ba	0.00	0.41	9.4E-03	1.9E-02	0.41	9.4E-03	MAEGVLRMDCYSFPNSRFMP*
HG0381	D. rerio	ENSDDARG0000006124	kdm5c	lysine (K)-specific demethylase 5C	0.00	0.04	3.0E-03	7.1E-03	0.04	3.0E-03	MACSSDRMNGG*
HG0382	D. rerio	ENSDDARG00000017242	rab39b	RAB39B, member RAS oncogene family b	0.00	0.29	4.4E-03	1.0E-02	0.29	4.4E-03	MTPEFTFADAGCGGLTRC*
HG0383	D. rerio	ENSDDARG00000032651	cue1b3b	CUE domain containing 1b	0.00	0.27	1.7E-02	3.1E-02	0.27	1.7E-02	MMALLSLPFLHWTSMKPSFQITWIKT*
HG0384	D. rerio	ENSDDARG00000054748	suedc1b	A kinase (PRKA) anchor protein 10	0.06	0.04	1.2E-02	2.7E-02	0.04	1.2E-02	MCLNMQKWRKQKFLSLQWTRFFN*
HG0385	D. rerio	ENSDDARG00000059540	akap10	A kinase (PRKA) anchor protein 10	0.00	0.15	3.2E-03	7.6E-03	0.15	3.2E-03	MNEGNESSGCCD*
HG0386	D. rerio	ENSDDARG00000060284	kcnn1a	chloride channel, voltage-sensitive 1a	0.00	0.25	5.9E-03	1.3E-02	0.25	5.9E-03	MCEEETERLSVCCVMCPHPRVGMRLQTSGLFLQ*
HG0387	D. rerio	ENSDDARG00000011051	cica	capicua transcriptional repressor a	0.16	0.28	1.2E-02	2.2E-02	0.28	1.2E-02	MQERNRVEDIDRLGLTGNOED*
HG0388	D. rerio	ENSDDARG00000077228	htrk3a	neurotrophic tyrosine kinase, receptor, type 3a	0.00	0.35	1.4E-02	2.6E-02	0.35	1.4E-02	MQPVEDSLGLAFEPFLH*
HG0389	D. rerio	ENSDDARG00000077361	bptf	bromodomain PHD finger transcription factor	0.08	0.36	1.5E-02	2.7E-02	0.36	1.5E-02	MAAASDLKRGAGRSP*
HG0390	D. rerio	ENSDDARG00000090035	rtnvr	reticulon 4 receptor	0.26	0.36	6.3E-03	1.3E-02	0.36	6.3E-03	MTERGTTGRRCSPRARTATVG*
HG0391	D. rerio	ENSDDARG00000090634	elna	elastin a	0.00	0.15	2.5E-02	4.4E-02	0.15	2.5E-02	MHRTKGFALS*
HG0392	D. rerio	ENSDDARG00000100003	glub	glutamate-ammonia ligase (glutamine synthase) b	0.00	0.04	4.1E-03	9.4E-03	0.04	4.1E-03	MRMRDQGPLPYKTLWKYSHSYSDLYFLIGL*
HG0393	G. gallus	ENS GAL.G00000002090	GPSM2	G protein signaling modulator 2	0.00	0.43	5.0E-36	5.8E-35	0.43	5.0E-36	MELKGPMKMLERVRSDSLRCV*
HG0394	G. gallus	ENS GAL.G00000002479	MAT1A	methionine adenosyltransferase 1A	0.00	0.39	1.6E-46	2.2E-45	0.39	1.6E-46	MKSPGMHTQDQADFDPT*
HG0395	G. gallus	ENS GAL.G00000004098	ESCO1	establishment of sister chromatid cohesion N-acetyltransferase	0.00	0.40	5.4E-03	1.3E-02	0.40	5.4E-03	MELHARBLKVPWRVRPLVKT*
HG0396.1	G. gallus	ENS GAL.G00000003423			0.00	0.43	2.9E-22	2.4E-21	0.43	2.9E-22	MKQDCKEPTWTFVSYNTYVQRN*
HG0396.2	G. gallus	ENS GAL.G00000003423			0.00	0.37	1.0E-04	3.3E-04	0.37	1.0E-04	MQKTKNKGKRDVKHDL*
HG0397	G. gallus	ENS GAL.G00000009438	SLC39A9	solute carrier family 39 member 9	0.00	0.17	3.1E-46	4.3E-45	0.17	3.1E-46	MAESPWDLGVCTG*
HG0398	G. gallus	ENS GAL.G000000005369	BTBD10	BTB domain containing 10	0.00	0.13	3.0E-52	4.9E-51	0.13	3.0E-52	MMEEKVRARAALNN*
HG0399	G. gallus	ENS GAL.G000000032659			0.00	0.43	4.8E-07	2.0E-06	0.43	4.8E-07	MTNHFCVCTTRIONS*
HG0400	G. gallus	ENS GAL.G000000004261	AQP9	aquaporin 9	0.00	0.19	1.3E-13	7.7E-13	0.19	1.3E-13	MISLVAQHEISYFSV*
HG0401	G. gallus	ENS GAL.G000000009057	TASP1	tsaspase 1	0.10	0.38	1.3E-16	9.5E-16	0.38	1.3E-16	MLQLNLFNGSMLFASRRC*
HG0402	G. gallus	ENS GAL.G000000035584			0.24	0.34	3.8E-03	9.5E-03	0.34	3.8E-03	MARCVWGREQPMLLI*
HG0403.1	G. gallus	ENS GAL.G00000007717	GCNT7	glucosaminyl (N-acetyl) transferase family member 7	0.00	0.12	3.9E-50	5.9E-49	0.33	5.1E-19	MNPPPNTPNPSRMLSGKEAFQHEIQSIPITCMPN*
HG0403.2	G. gallus	ENS GAL.G00000007717	GCNT7	glucosaminyl (N-acetyl) transferase family member 7	0.00	0.33	1.1E-02	2.4E-02	0.33	1.1E-02	MLSIAGNOVMFMFNPLQVEISQATE*
HG0404	G. gallus	ENS GAL.G000000080700	PDCD4	programmed cell death 4	0.00	0.32	1.4E-17	1.0E-16	0.32	1.4E-17	MEHSTRKDKTYLTRI*
HG0405.1	G. gallus	ENS GAL.G000000069185			0.00	0.46	5.3E-08	2.4E-07	0.46	5.3E-08	MLLSASWFLDLPFRPS*
HG0405.2	G. gallus	ENS GAL.G000000069185			0.00	0.40	2.9E-10	1.4E-09	0.40	2.9E-10	MPSRFSFSLSKLPLVL*
HG0406	G. gallus	ENS GAL.G000000004935	LSM14A	LSM14A, mRNA processing body assembly factor	0.23	0.34	1.4E-04	4.3E-04	0.34	1.4E-04	MKAAMMLGASGRFWCGV*
HG0407	G. gallus	ENS GAL.G00000015027	IAK2	Janus kinase 2	0.05	0.28	2.5E-25	2.1E-24	0.28	2.5E-25	MERARVLRGSRQLALRRAPAGYIMFYHCLCACFF*
HG0408	G. gallus	ENS GAL.G000000036255	WNT7B	Protein Wnt-7b	0.06	0.21	1.5E-10	7.7E-10	0.21	1.5E-10	MTGRSPSEAAAAARTAAAAHTLPREH*
HG0409	G. gallus	ENS GAL.G000000002315			0.00	0.32	1.1E-07	4.6E-07	0.32	1.1E-07	MVSTPCPEPLQK*
HG0410	G. gallus	ENS GAL.G000000008148	MYBPC3	myosin-binding protein C, cardiac-type	0.20	0.46	4.4E-11	2.4E-10	0.46	4.4E-11	MGASTEFWFVWGSQKPCSLICV*
HG0411	G. gallus	ENS GAL.G00000012166	SLC35F5	solute carrier family 35 member F5	0.00	0.27	7.8E-27	7.1E-26	0.27	7.8E-27	MAIPTLLTKWRLSSL*
HG0412	G. gallus	ENS GAL.G000000003446	PRLR	prolactin receptor	0.02	0.43	1.5E-05	5.4E-05	0.43	1.5E-05	MNERNKIFLCTHESFREPLM*
HG0413	G. gallus	ENS GAL.G000000005475			0.19	0.36	5.6E-13	3.2E-12	0.36	5.6E-13	MRSQCLWLLDFVSG*
HG0414	G. gallus	ENS GAL.G000000032599			0.18	0.17	2.7E-03	7.1E-03	0.17	2.7E-03	MMKALQWERAVVGG*
HG0415	G. gallus	ENS GAL.G000000034970			0.04	0.46	4.8E-07	2.0E-06	0.46	4.8E-07	MLSRITYMTREASLAKD*
HG0416	G. gallus	ENS GAL.G00000015874	TTK	TTK protein kinase	0.13	0.31	7.0E-06	2.6E-05	0.31	7.0E-06	MKQVSRGCVMLGR*
HG0417	G. gallus	ENS GAL.G00000001522	PHF20	PHD finger protein 20	0.00	0.48	8.0E-06	2.9E-05	0.48	8.0E-06	MTFSALTITDQGRHVVHGBELGE*
HG0418	G. gallus	ENS GAL.G00000010337	GPR149	G protein-coupled receptor 149	0.14	0.36	1.3E-06	5.1E-06	0.36	1.3E-06	MKQKIFSTTCSTLPLDPFSRA*
HG0419	G. gallus	ENS GAL.G00000012542	RASD2	RASD family member 2	0.03	0.48	1.7E-03	4.6E-03	0.48	1.7E-03	MGRPLPCSPSQSC*
HG0420	G. gallus	ENS GAL.G000000003363	PPP1R12B		0.00	0.38	4.4E-04	1.3E-03	0.38	4.4E-04	MPKIHNLNQGULTRAANSLSL*
HG0421	G. gallus	ENS GAL.G000000004032			0.21	0.05	2.8E-20	2.2E-19	0.05	2.8E-20	MEANLKRKKKDGKVSVMRMEIERRYLSSYLRLCAKIEKFFHHLEKESRAKGEPSLPEEFFAKEYAMANTETYNLKVALKMPPNKLQKVALKVSPPKPNLDSFVLRLVKROENLVEPTEDEQREYTLDEEGSHLRYKTIAPLVSAGVAILQ*
HG0422	G. gallus	ENS GAL.G000000050772	BOK	BOK, BCL2 family apoptosis regulator	0.00	0.44	7.2E-03	1.7E-02	0.44	7.2E-03	MKGKMKNRLWESSSWEL*
HG0423	G. gallus	ENS GAL.G000000006329			0.00	0.28	2.6E-03	6.9E-03	0.28	2.6E-03	MLSKLVGKGGHGLVSL*
HG0424	G. gallus	ENS GAL.G000000039553			0.00	0.27	2.8E-04	8.4E-04	0.27	2.8E-04	MTYVLSICRQRCLQ*
HG0425	G. gallus	ENS GAL.G000000043044			0.00	0.26	6.2E-07	2.5E-06	0.26	6.2E-07	MIQKTVRSQDCKMSSFYMLKGKGLKQLQEL*
HG0426	G. gallus	ENS GAL.G000000002192	PTPRC	protein tyrosine phosphatase, receptor type C	0.00	0.17	1.6E-03	4.4E-03	0.17	1.6E-03	MLLRKDTPDFQK*
HG0427	G. gallus	ENS GAL.G000000055950	ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1	0.01	0.45	1.3E-03	3.6E-03	0.45	1.3E-03	MKVYFLFELFASRGCCVWGYPALNPQKGSANSQK*
HG0428	G. gallus	ENS GAL.G000000069178	TCEA2	transcription elongation factor A2	0.00	0.04	1.9E-09	7.6E-09	0.04	1.9E-09	MSRPAAGRFAPLIK*
HG0429	G. gallus	ENS GAL.G000000006626	PDE8C	phosphodiesterase 6C	0.00	0.00	3.1E-12	1.8E-11	0.00	3.1E-12	MPLYSYMYVPSY*
HG0430	G. gallus	ENS GAL.G000000015490			0.00	0.39	2.1E-07	9.0E-07	0.39	2.1E-07	MLMSGTSASDALTLKTYFVAVMLRR*
HG0431	G. gallus	ENS GAL.G000000028542	FAM217B	family with sequence similarity 217 member B	0.00	0.33	6.8E-09	3.2E-08	0.33	6.8E-09	MPAAESKQVVMFAFGTLCVDRKVESRWKIM*
HG0432	G. gallus	ENS GAL.G000000040546			0.05	0.44	6.9E-03	1.6E-02	0.44	6.9E-03	MLENTSVSLVSEHPKN*
HG0433	G. gallus	ENS GAL.G000000002952	NRG4	neuregulin 4	0.00	0.43	9.6E-05	3.1E-04	0.43	9.6E-05	MQISGGVDSADCPVRV*
HG0434	G. gallus	ENS GAL.G000000008357	TPCN1	two pore segment channel 1	0.24	0.34	5.9E-05	2.0E-04	0.34	5.9E-05	MGARTFAFWWLEDHGRFRPGKR*
HG0435	G. gallus	ENS GAL.G00000010778	CHRM3	cholinergic receptor muscarinic 3	0.00	0.14	2.6E-07	1.1E-06	0.14	2.6E-07	MAKFSFSSVWYQLQAG*
HG0436	G. gallus	ENS GAL.G000000026736	OGN	osteolectin	0.10	0.16	8.1E-07	3.3E-06	0.16	2.5E-03	MLKLSAPCSRLRLTLGTGCWQSQIFPMESTFTNKLWGLKSHCSNLDVHCWVHNFTLLSVCMGLTYA*
HG0437	G. gallus	ENS GAL.G00000001728	NACC2	NACC family member 2	0.28	0.40	7.4E-04	2.1E-03	0.40	7.4E-04	MARGAAPARRPGPPSPGPRRPSAAAAARRKTMGRMTCPMLDTPALNA*
HG0438	G. gallus	ENS GAL.G00000008545	SENPS	SUMO1/iesntin specific peptidase 5	0.12	0.16	3.0E-05	1.0E-04	0.16	3.0E-05	MWYTRACCVTKEROFCFT*
HG0439	G. gallus	ENS GAL.G00000009172	OSBP6L	oxysterol binding protein like 6	0.14	0.04	1.6E-02	3.4E-02	0.04	1.6E-02	MOKSPICPHIVE*
HG0440	G. gallus	ENS GAL.G00000010090			0.00	0.28	5.3E-05	1.8E-04	0.28	5.3E-05	MMAGHLLTGFBSFKEIGHMLCM*
HG0441	G. gallus	ENS GAL.G00000010609	B4GALT4	beta-1,4-galactosyltransferase 4	0.00	0.40	2.4E-04	7.5E-04	0.40	2.4E-04	MSHRTTRSAALPTCSPELL*
HG0442	G. gallus	ENS GAL.G000000030									

HG0458	<i>H. sapiens</i>	ENS000000060339	CCAR1	cell division cycle and apoptosis regulator 1	0.05	0.35	6.3E-39	2.9E-37	0.35	6.3E-39		WMRRGAWNRKRLAKHAPKADGFEMASLAGLTRLSML*
HG0458	<i>H. sapiens</i>	ENS000000153848	ZNF148	zinc finger protein 148	0.00	0.30	5.3E-10	0.30	0.30	5.8E-09		MGRRNSTMSTFTHQHSPT*
HG0459	<i>H. sapiens</i>	ENS000000163848	ZNF148	zinc finger protein 148	0.00	0.47	1.3E-11	1.7E-10	0.47	1.3E-11		MGVCLTLYMESDGBD*
HG0459	<i>H. sapiens</i>	ENS000000163848	ZNF148	zinc finger protein 148	0.00	0.21	1.3E-05	7.3E-05	0.21	0.05		MSASLLWEEEEEKEEEEEKEEGEAGGVAVAEATAKVLPPIPPSPSSGQP*
HG0460	<i>H. sapiens</i>	ENS000000180008	SOC5A	suppressor of cytokine signaling 4	0.01	0.34	7.7E-46	4.0E-44	0.40	1.5E-38	Crowe, Samandi	MAMVMAAVTPTKTVKLSGRYQKVPVRRNLFLEMKMKQYL*
HG0461	<i>H. sapiens</i>	ENS000000066419	TNP03	transportin 3	0.02	0.35	8.0E-03	2.2E-02	0.35	8.0E-03		MAPVREPRWPRO*
HG0462	<i>H. sapiens</i>	ENS000000125686	MED1	mediator complex subunit 1	0.08	0.32	6.4E-18	1.4E-16	0.32	6.4E-18		MAAASSTLLFLPPGTSQ*
HG0463	<i>H. sapiens</i>	ENS000000129473	BCL2L2	BCL2 like 2	0.01	0.18	2.8E-30	9.8E-29	0.18	2.8E-30		MKGPSWGLLTAISAVS*
HG0464	<i>H. sapiens</i>	ENS000000188215	DCUN1D3	defective in cullin neddylation 1 domain containing 3	0.01	0.48	1.3E-10	1.5E-09	0.48	1.3E-10		MLRYMGQRGQRGPIQRGPL*
HG0465	<i>H. sapiens</i>	ENS000000132153	DHX30	DEXH-box helicase 30	0.00	0.35	2.8E-23	7.9E-22	0.35	2.8E-23	Crowe	MNRSKERIQLOFKSLONLRLSLL*
HG0466	<i>H. sapiens</i>	ENS000000139679	LPAR6	lysophosphatidic acid receptor 6	0.04	0.49	1.5E-12	2.2E-11	0.49	1.5E-12		MFLLGISEKKEIFKSPKDDPNQLNWR*
HG0467	<i>H. sapiens</i>	ENS000000163320	CGGBP1	COG triplet repeat binding protein 1	0.00	0.35	7.1E-15	1.3E-13	0.35	7.1E-15		MTSWHRRNRYVQAKFLPHHLLKN*
HG0467	<i>H. sapiens</i>	ENS000000163320	CGGBP1	COG triplet repeat binding protein 1	0.01	0.32	3.0E-07	2.2E-06	0.32	3.0E-07		MLRWFRSGDHSLLKTKTKTN*
HG0468	<i>H. sapiens</i>	ENS000000187778	ACR1S1	microspherule protein 1	0.00	0.09	7.2E-27	2.2E-25	0.09	7.2E-27	Samandi	MLPKVLELDQIDNPSTLVGVSHVENEGRRVRSQQSPSPGQPMWMLVDRSS*
HG0469	<i>H. sapiens</i>	ENS000000196399	SPRED2	sprouty related EVH1 domain containing 2	0.02	0.01	2.1E-19	5.1E-18	0.01	2.1E-19		MKGAKLPAAQASR*
HG0470	<i>H. sapiens</i>	ENS000000224470	ATXN1L	ataxin 1 like	0.00	0.39	1.4E-20	3.4E-19	0.39	1.4E-20		MWAPQPEAEFGTKQLGRSPF*
HG0471	<i>H. sapiens</i>	ENS000000023041	ZDHHC8	zinc finger DHHC-type containing 8	0.01	0.43	2.4E-19	5.6E-18	0.43	2.4E-19		MTKEHTWTCTGKWKACHRRKRSILLK*
HG0472	<i>H. sapiens</i>	ENS000000105991	HOXA1	homeobox A1	0.06	0.23	1.2E-25	3.5E-24	0.23	1.2E-25		MEEVKRLQASRRASQDQVQT*
HG0473	<i>H. sapiens</i>	ENS000000138650	PCDH10	protocadherin 10	0.00	0.42	1.3E-02	3.2E-02	0.42	1.3E-02		MKRGDACHPSCAKI*
HG0473	<i>H. sapiens</i>	ENS000000240184	PCDHGC3	protocadherin gamma subfamily C, 3	0.02	0.08	1.6E-10	7.1E-09	0.18	6.6E-10		MSDSAPSAQALTR*
HG0474	<i>H. sapiens</i>	ENS000000139083	ETV6	ETS variant 6	0.00	0.39	1.3E-08	1.1E-07	0.39	1.3E-08		MTASGWPWSLGLSGRGESQKNLRTS*
HG0475	<i>H. sapiens</i>	ENS000000109118	PHF12	PHD finger protein E12	0.02	0.42	6.9E-09	6.3E-08	0.42	6.9E-09		MAAPASLPQRTGCRQCRLL*
HG0476	<i>H. sapiens</i>	ENS000000130939	UBE4B	ubiquitination factor E4B	0.00	0.15	1.8E-05	9.6E-05	0.15	1.8E-05		MNNTWGEIGERVGVEG*
HG0477	<i>H. sapiens</i>	ENS000000166925	TSC22D4	TSC22 domain family member 4	0.01	0.17	8.4E-52	4.8E-50	0.17	8.4E-52	Mackowiak	MSDDPVRGSDGMAWPPC3SRGA*
HG0478	<i>H. sapiens</i>	ENS000000168214	RBFX	recombination signal binding protein for immunoglobulin kappa	0.00	0.10	1.3E-05	6.9E-05	0.10	1.3E-05		MISKRKENDDTLAEV*
HG0478	<i>H. sapiens</i>	ENS000000168214	HR	HR, lysine demethylase and nuclear receptor corepressor	0.00	0.07	1.1E-28	3.9E-27	0.07	1.1E-28	Crowe, Mackowiak	MAOPTASAKLVVRRVAVRCLQIPESDPSNLRP*
HG0478	<i>H. sapiens</i>	ENS000000168453	HR	HR, lysine demethylase and nuclear receptor corepressor	0.00	0.38	5.9E-05	2.9E-04	0.38	5.9E-05		MAORGPAALSAALVY*
HG0480	<i>H. sapiens</i>	ENS000000198018	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	0.00	0.20	1.2E-19	2.8E-17	0.20	1.2E-19		MPGTRPPSPQGRKRR*
HG0481	<i>H. sapiens</i>	ENS000000198963	RORB	RAR related orphan receptor B	0.01	0.38	1.0E-06	6.7E-06	0.38	1.0E-06		MYFSAEQLFADHLHSC*
HG0482	<i>H. sapiens</i>	ENS000000006717	TRAM1	translocation associated membrane protein 1	0.11	0.50	1.4E-17	2.9E-16	0.50	1.4E-17	Crowe	MGSEAPAGSCGSAVRSSQREAAASR*
HG0483	<i>H. sapiens</i>	ENS000000164463	CREBRF	CREB3 regulatory factor	0.07	0.22	3.8E-17	7.7E-16	0.22	3.8E-17	Mackowiak	MERGRGCSGTGSPSP*
HG0484	<i>H. sapiens</i>	ENS000000166444	ST5	suppression of tumorigenicity 5	0.00	0.41	9.3E-17	1.9E-15	0.44	2.7E-11		MNQLASISLTNRKMRDCLGATTSMTSPCTG*
HG0485	<i>H. sapiens</i>	ENS000000182687	NTM	neurotrophin	0.00	0.00	4.5E-16	8.6E-15	0.00	4.5E-16		MSGDNGEVLISHTLQFLVFSKTVDLNLQAQ*
HG0485	<i>H. sapiens</i>	ENS000000183715	OPCML	opioid binding protein/cell adhesion molecule like	0.03	0.00	2.4E-03	7.6E-03	0.00	2.4E-03		MQEGASGASRLES*
HG0486	<i>H. sapiens</i>	ENS000000067900	ROCK1	Rho associated coiled-coil containing protein kinase 1	0.00	0.16	2.0E-25	5.9E-24	0.16	2.0E-25		MRLWASERVLVAVAPGPGSERRSPQ*
HG0487	<i>H. sapiens</i>	ENS000000091831	ESR1	estrogen receptor 1	0.07	0.41	1.3E-11	1.6E-10	0.41	1.3E-11		MEHFVKDVLDPAGWPAGF*
HG0488	<i>H. sapiens</i>	ENS000000116194	ANGPTL1	angiotensinogen like 1	0.00	0.48	1.5E-09	1.5E-08	0.48	1.5E-09		MMVOTGSHNFA5AGLKTAAHPELPYLKHLRHWLVFN*
HG0488	<i>H. sapiens</i>	ENS000000116194	ANGPTL1	angiotensinogen like 1	0.00	0.24	1.1E-04	4.9E-04	0.24	1.1E-04		MLKPLKSGMNMH*
HG0489	<i>H. sapiens</i>	ENS000000143847	PTPRF4	PTPFR interacting protein alpha 4	0.00	0.48	6.5E-06	3.7E-05	0.48	6.5E-06		MLWEKPLTQPLAHLNPL*
HG0490	<i>H. sapiens</i>	ENS000000152413	HOMER1	homer scaffolding protein 1	0.00	0.48	6.0E-07	4.2E-06	0.48	6.0E-07		MAPFLFGRMRNCSLAFSSSSPPLCCSE*
HG0490	<i>H. sapiens</i>	ENS000000152413	HOMER1	homer scaffolding protein 1	0.00	0.45	6.3E-04	2.4E-03	0.45	6.3E-04		MPPLFERFGYKREILPKRNT*
HG0491	<i>H. sapiens</i>	ENS000000154114	TBCEL	tubulin folding cofactor E like	0.03	0.26	3.4E-12	4.8E-11	0.26	3.4E-12	Mackowiak	MQDTGLRRFWEGR*
HG0492	<i>H. sapiens</i>	ENS000000162670	BRINP3	BMP/retnic acid inducible neural specific 3	0.00	0.40	1.2E-06	7.6E-06	0.40	1.2E-06		MEYLFESWYMFYSHLLAS*
HG0493	<i>H. sapiens</i>	ENS000000164707	SLC13A4	solute carrier family 13 member 4	0.12	0.34	3.1E-17	6.3E-16	0.34	3.1E-17		MPPFILSQFLFAGHKTMLNPT*
HG0494	<i>H. sapiens</i>	ENS000000184226	PCDH9	protocadherin 9	0.00	0.44	1.7E-14	2.9E-13	0.44	1.7E-14		MHAAVENPELKKCNVYLCVLNAQKNPDPVKRDEMIRE*
HG0495	<i>H. sapiens</i>	ENS000000196730	DAPK1	death associated protein kinase 1	0.00	0.13	2.1E-08	1.8E-07	0.13	2.1E-08		MHEGATEAQERW*
HG0495	<i>H. sapiens</i>	ENS000000196730	DAPK1	death associated protein kinase 1	0.00	0.26	1.1E-05	6.2E-05	0.26	1.1E-05		MVWEAEKCPGLW*
HG0496	<i>H. sapiens</i>	ENS000000135913	USP37	ubiquitin specific peptidase 37	0.01	0.42	1.1E-02	2.8E-02	0.42	1.1E-02		MSSVPRRVLCVHKKDQNGELLHRRVF*
HG0497	<i>H. sapiens</i>	ENS000000147571	CRH	corticotropin releasing hormone	0.09	0.00	3.9E-04	1.5E-03	0.00	3.9E-04		MYAGAEARNRAVRKASR*
HG0498	<i>H. sapiens</i>	ENS000000055379	TSPDAP1	TSPD associated protein 1	0.00	0.00	4.8E-16	9.1E-15	0.00	4.8E-16		MROAAHRRRP*
HG0499	<i>H. sapiens</i>	ENS000000112558	MDJ1	ret1 domain containing 1	0.02	0.13	2.9E-03	6.8E-03	0.13	2.9E-03		MLMLLSWQSP*
HG0500	<i>H. sapiens</i>	ENS000000207778	PTPN21	protein tyrosine phosphatase, non-receptor type 21	0.00	0.24	6.4E-22	1.7E-20	0.24	6.4E-22		MLPSSHGHWRJCTLMAAAAAG*
HG0501	<i>H. sapiens</i>	ENS000000110400	NECTIN1	nectin cell adhesion molecule 1	0.11	0.19	5.4E-07	3.8E-06	0.19	5.4E-07		MTBATCGGHLPSL*
HG0502	<i>H. sapiens</i>	ENS000000126882			0.00	0.00	1.7E-22	4.6E-21	0.00	1.7E-22		MSEPHNYSLNKYLFTGRISVFVHVECEKKREPRAHQMOMPLY*
HG0503	<i>H. sapiens</i>	ENS000000141564	RPTOR	regulatory associated protein of MTOR complex 1	0.00	0.19	3.7E-18	8.2E-17	0.19	3.7E-18		MGRSRLWLQQLRRVRDPQG*
HG0504	<i>H. sapiens</i>	ENS000000144460	NYAP2	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase	0.00	0.28	2.6E-14	4.5E-13	0.36	3.7E-09		MTDCTDRNQRRELLISEEYNQMYRISQDGFCSNCHL3SKVGKIQFLPCWTKWKGCGVFPIH*
HG0505	<i>H. sapiens</i>	ENS000000157470			0.05	0.31	6.7E-07	4.6E-06	0.31	6.7E-07		MGSRGAPTPRADVNY*
HG0506	<i>H. sapiens</i>	ENS000000177853	ZNF518A	zinc finger protein 518A	0.00	0.18	4.0E-08	3.3E-07	0.33	1.1E-04		MAAIRDSQAMGTTDISDFHCS*
HG0506	<i>H. sapiens</i>	ENS000000177853	ZNF518A	zinc finger protein 518A	0.00	0.49	2.0E-02	4.7E-02	0.49	2.0E-02		MSLHSVSLCNLYR*
HG0507	<i>H. sapiens</i>	ENS000000060237	WNK1	WNK lysine deficient protein kinase 1	0.01	0.44	1.9E-08	1.7E-07	0.44	1.9E-08		MTAAPLLPPAPRPLAAGWMRTVR*
HG0508	<i>H. sapiens</i>	ENS000000061936	SFSWAP	splicing factor SWAP homolog	0.16	0.38	5.4E-10	5.9E-09	0.38	5.4E-10		MAAVLRJLGTGCVDF*
HG0509	<i>H. sapiens</i>	ENS000000060224	HADC4	halothane desatylase 4	0.10	0.30	2.0E-08	1.8E-07	0.30	2.0E-08		MCWHEFGARQWYSYFRGNFEPFRIT*
HG0510	<i>H. sapiens</i>	ENS000000134789	OTN1A	oxytocin receptor alpha	0.04	0.19	7.2E-05	3.4E-04	0.19	7.2E-05		MLKSKSCQEPF*
HG0511	<i>H. sapiens</i>	ENS000000143337	TOR1AIP1	torin 1A interacting protein 1	0.25	0.45	8.1E-15	1.4E-13	0.45	8.1E-15		MAETSSSPSSSLYPARRRERSTAADPAQALSPQSRHPMGEAGLLHSSDAGGSPSDSQLP*
HG0512	<i>H. sapiens</i>	ENS000000112319	EYA4	EYA transcriptional coactivator and phosphatase 4	0.00	0.34	6.1E-09	6.7E-08	0.34	6.1E-09		MSCFHORHSAKGLRWKERE*
HG0512	<i>H. sapiens</i>	ENS000000104313	EYA1	EYA transcriptional coactivator and phosphatase 1	0.02	0.43	3.6E-13	5.6E-12	0.43	3.6E-13		MLSAAAVWVGSRAGKAVTKONGGS*
HG0512	<i>H. sapiens</i>	ENS000000104313	EYA1	EYA transcriptional coactivator and phosphatase 1	0.00	0.00	3.4E-03	1.0E-02	0.00	3.4E-03		MPPTAAVSFFSFG*
HG0513	<i>H. sapiens</i>	ENS000000126860	EVI2A	ecotropic viral integration site 2A	0.02	0.20	1.5E-11	2.0E-10	0.23	1.6E-06		MCFCSGKEMCHLWFGKSGKLAHLFYCRFTLRILFSKILL*
HG0514	<i>H. sapiens</i>	ENS000000147570	DNAJC5B	DnaJ heat shock protein family (Hsp40) member C5 beta	0.00	0.39	6.0E-07	4.2E-06	0.39	6.0E-07		MKRKRDLKMRDQLAGAKVTNEK*
HG0515	<i>H. sapiens</i>	ENS000000170471	RALGAPB	Ral GTPase activating protein non-catalytic beta subunit	0.06	0.00	4.1E-03	1.2E-02	0.00	4.1E-03		MRAPPVASGAIWVL*
HG0516	<i>H. sapiens</i>	ENS000000041515	MYO16	myosin XVI	0.16	0.20	4.1E-09	3.9E-08	0.20	4.1E-09		MRMSLLKFGASWNRASMQ*
HG0517	<i>H. sapiens</i>	ENS000000086717	PPEF1	protein phosphatase with EF-hand domain 1	0.00	0.42	1.5E-04	6.4E-04	0.42	1.5E-04		MDCVLSPVQRKESTTSKVKP*
HG0518	<i>H. sapiens</i>	ENS000000111254	AKAP3	A-kinase anchoring protein 3	0.06	0.44	2.0E-04	8.6E-04	0.44	2.0E-04		MEGHRRKQDELKSNPABSLTKVYSGVFRGSLFYQYRDSLYMAGGG*
HG0519	<i>H. sapiens</i>	ENS000000127074	RGS13	regulator of G protein signaling 13	0.00	0.23	2.9E-08	2.4E-07	0.23	2.9E-08		MRDCTQTCGVNRYFTYTNMRRK*
HG0520	<i>H. sapiens</i>	ENS000000197415	VEPFI	ventricular zone expressed PH domain containing 1	0.00	0.48	1.3E-04	5.9E-04	0.48	1.3E-04		MNPNFTTLLSGHSLCPRLPESPAQSQMTSLNCKGAFEE*
HG0521	<i>H. sapiens</i>	ENS000000038274	MAT2B	methionine adenosyltransferase 2B	0.08	0.21	2.7E-04	1.1E-03	0.21	2.7E-04		MWTRARDSGIGKML*
HG0522	<i>H. sapiens</i>	ENS000000140396	NCOA2	nuclear receptor coactivator 2	0.00	0.25	1.4E-05	7.8E-05	0.25	1.4E-05		MAAASATASAAKVSADGSRHLTA*
HG0523	<i>H. sapiens</i>	ENS000000075213	SEMA3A	semaphorin 3A	0.10	0.04	1.1E-03	3.9E-03	0.04	1.1E-03		MGCWSY5YKYNMLLAHYPT*
HG0524	<i>H. sapiens</i>	ENS000000107929	LARP4B	LA ribonucleoprotein domain family member 4B	0.13	0.13	1.1E-03	4.1E-03	0.13	1.1E-03		MRTGRSVGLDESRR*
HG0525	<i>H. sapiens</i>	ENS000000136167	LCP1	lymphocyte cytosolic protein 1	0.07	0.35	1.7E-02	4.0E-02	0.35	1.7E-02		MTSPLEIAVORQKRSQIELLNQARVSNVSAASLYLKVEELFYQLRKLIPASDDAPLDEHCAFLQVTSCLVTYHPGLTKFCRSERRGSWSYSTTSDKSFSPARSVT*
HG0526	<i>H. sapiens</i>	ENS000000143569	UBAP2L	ubiquitin associated protein 2 like	0.06	0.40	8.3E-04	3.0E-03	0.40	8.3E-04		MRLPEPERGERARERASWALPEYSTL*
HG0527	<i>H. sapiens</i>	ENS000000198382	UVRRAG	UV radiation resistance associated	0.08	0.08	1.5E-04	6.6E-04	0.08	1.5E-04</		

HG0548	<i>H. sapiens</i>	ENS00000155744	FAM126B	family with sequence similarity 126 member B	0.00	0.30	1.5E-12	2.1E-11	0.30	1.5E-12			MSNPSELGRIPVPPPLEN*
HG0549	<i>H. sapiens</i>	ENS00000156236	USP16	ubiquitin specific peptidase 16	0.16	0.20	2.0E-04	8.5E-04	0.20	2.0E-04			MCGLWLSRNWLLQZ*
HG0550	<i>H. sapiens</i>	ENS00000156650	KAT6B	lysine acetyltransferase 6B	0.00	0.14	8.7E-24	2.5E-22	0.14	8.7E-24			MTTKCASSVYKKNLGY*
HG0550.2	<i>H. sapiens</i>	ENS00000156650	KAT6B	lysine acetyltransferase 6B	0.00	0.15	1.1E-06	7.2E-06	0.15	1.1E-06			MFTTRMSQLVKV*
HG0551	<i>H. sapiens</i>	ENS00000162951	LRRTM1	leucine rich repeat transmembrane neuronal 1	0.03	0.48	1.9E-15	3.4E-14	0.48	1.9E-15			MSPEALCSCPGREWQVASE*
HG0552	<i>H. sapiens</i>	ENS00000169641	LUZP1	leucine zipper protein 1	0.00	0.25	6.3E-16	1.2E-14	0.25	6.3E-16			MMVSSCORRLWLPRER*
HG0553	<i>H. sapiens</i>	ENS00000183475	ASB7	ankyrin repeat and SOCS box containing 7	0.00	0.49	6.0E-16	1.1E-14	0.49	6.0E-16			MVTRQSVHQEHGSHSRILPV7*
HG0554	<i>H. sapiens</i>	ENS00000186914	ARRHGFE12	Rho guanine nucleotide exchange factor 12	0.00	0.47	2.2E-09	2.2E-08	0.47	2.2E-09	Samandi		MTWSEFLDFDPVQDVGPPDRALGVGRRCYCKMQGV*
HG0555	<i>H. sapiens</i>	ENS00000204310	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	0.15	0.18	1.8E-16	3.5E-15	0.18	1.8E-16			MGPTTSHSLPSIGRG*
HG0556	<i>H. sapiens</i>	ENS00000273841	TAF9	TATA-box binding protein associated factor 9	0.00	0.12	1.5E-59	9.5E-58	0.11	2.2E-51			MLLPNLLTGTGPVGKTLTGKELASKSLYKYNGLDAREV*
HG0557	<i>H. sapiens</i>	ENS00000012232	EXTL3	exostosin like glycosyltransferase 3	0.00	0.30	1.6E-03	5.5E-03	0.30	1.6E-03			MHCWSAKPRNKSYGI*
HG0558	<i>H. sapiens</i>	ENS00000029363	BCLAF1	BCL2 associated transcription factor 1	0.01	0.35	2.9E-12	4.1E-11	0.35	2.9E-12			MVFLFLSREMAAVWLQRR*
HG0559	<i>H. sapiens</i>	ENS00000078747	ITCH	itchy E3 ubiquitin protein ligase	0.00	0.13	3.2E-20	7.8E-19	0.13	3.2E-20			MHTVVALWRQLNPRK*
HG0560.1	<i>H. sapiens</i>	ENS00000032051	JPH4	junctionophilin 4	0.11	0.42	3.1E-04	1.2E-03	0.42	3.1E-04			MDAVPRQRPQDPTCHYHSQ*
HG0560.2	<i>H. sapiens</i>	ENS00000032051	JPH4	junctionophilin 4	0.00	0.00	5.0E-03	1.4E-02	0.00	5.0E-03			MEOTLICAGMESF*
HG0561	<i>H. sapiens</i>	ENS00000100393	EP300	E1A binding protein p300	0.04	0.34	1.9E-04	6.1E-04	0.34	1.9E-04			MRRRRTPARRKRLMAAEARETSAGQGPVAVAGRGLRL*
HG0562	<i>H. sapiens</i>	ENS00000105821	DNAJC2	DnaJ heat shock protein family (Hsp40) member C2	0.07	0.45	8.4E-12	1.1E-10	0.45	8.4E-12			MRRFLGVLEPRREARSR*
HG0563	<i>H. sapiens</i>	ENS00000107249	GLIS3	GLIS family zinc finger 3	0.00	0.17	2.1E-08	1.8E-07	0.17	2.1E-08			MDDSLRHLTMDMLLDFA*
HG0564	<i>H. sapiens</i>	ENS00000109171	SLAIN2	SLAIN motif family member 2	0.05	0.37	4.6E-05	2.3E-04	0.37	4.6E-05			MAAGAGYWRRLPQSRSRRR*
HG0565	<i>H. sapiens</i>	ENS00000120533	ENVY2	ENVY2, transcription and export complex 2 subunit	0.00	0.00	1.8E-05	9.5E-05	0.00	1.8E-05			MKVLAFCVLRCPSY*
HG0566	<i>H. sapiens</i>	ENS00000124496	TRERF1	transcriptional regulating factor 1	0.00	0.31	4.9E-17	9.9E-16	0.31	4.9E-17			MHLLQKQPRPLWRLMKKEEDAEGRP*
HG0567	<i>H. sapiens</i>	ENS00000132155	RAF1	Raf-1 proto-oncogene, serine/threonine kinase	0.01	0.08	1.1E-35	4.6E-34	0.08	1.1E-35			MRGLLGAPSSQLGTRRM*
HG0568.1	<i>H. sapiens</i>	ENS00000138271	GPR87	G protein-coupled receptor 87	0.00	0.32	1.7E-22	4.7E-21	0.32	1.7E-22			MKEIKPGITYAETPQSSPSVS*
HG0568.2	<i>H. sapiens</i>	ENS00000138271	GPR87	G protein-coupled receptor 87	0.00	0.38	2.0E-04	8.4E-04	0.38	2.0E-04			MFRHALPENRLPCRP*
HG0569	<i>H. sapiens</i>	ENS00000139651	ZNF740	zinc finger protein 740	0.00	0.30	1.8E-10	4.0E-17	0.30	1.8E-10			MATGLMGHEGAVTVM*
HG0570	<i>H. sapiens</i>	ENS00000142214	RFX2	Rfx like without CNAK 2	0.02	0.36	7.3E-05	3.7E-04	0.36	7.3E-05			MRRPAREGQDPRR*
HG0571	<i>H. sapiens</i>	ENS00000153206	FEZF2	FEZ family zinc finger 2	0.13	0.00	3.0E-05	1.5E-04	0.00	3.0E-05			MARNASWWWQKET*
HG0572	<i>H. sapiens</i>	ENS00000159161	EYA3	EYA transcriptional coactivator and phosphatase 3	0.00	0.45	1.1E-22	3.1E-21	0.45	1.1E-22			MRRVRLTPRRPPLDWFYCGSLISMSCCOGATFAFL*
HG0573.1	<i>H. sapiens</i>	ENS00000162526	TSSK3	testis specific serine kinase 3	0.01	0.39	2.8E-11	3.4E-10	0.39	2.8E-11			MKSLRGKGAGQGRWRSRAASQRQHELRG*
HG0573.2	<i>H. sapiens</i>	ENS00000020620	TSSK2	testis specific serine kinase 2	0.00	0.27	1.1E-10	1.3E-09	0.27	1.1E-10			MKRTMPAGPHDGGM*
HG0574	<i>H. sapiens</i>	ENS00000164663	USP49	ubiquitin specific peptidase 49	0.00	0.28	1.7E-17	3.5E-16	0.28	1.7E-17			MEEDKKNLFGRLKRWRL*
HG0575	<i>H. sapiens</i>	ENS00000164663	USP49	ubiquitin specific peptidase 49	0.00	0.45	1.7E-02	4.0E-02	0.45	1.7E-02			MMALVMGRDLERTSSLCNSSOYPT*
HG0576	<i>H. sapiens</i>	ENS00000175029	CTBP2	C-terminal binding protein 2	0.00	0.37	3.8E-09	3.7E-08	0.37	3.8E-09			MKVYSKLTDSPSCEL*
HG0577	<i>H. sapiens</i>	ENS00000205010	GPR162	G protein-coupled receptor 162	0.00	0.49	1.9E-13	3.0E-12	0.49	1.9E-13	Crowe		MLSTGVSLGAACLLTGRLLWGSWECL*
HG0578	<i>H. sapiens</i>	ENS00000004897	CDC27	cell division cycle 27	0.05	0.22	6.1E-11	7.3E-10	0.22	6.1E-11			MSRGWPGRSRYRGLRHCRKWA*
HG0579	<i>H. sapiens</i>	ENS00000010818	HIVEP2	human immunodeficiency virus type 1 enhancer binding protein	0.08	0.25	1.5E-17	3.2E-16	0.28	9.6E-14			MPDCCGVRRVGECKEKGASLQTPWNMEATK*
HG0580	<i>H. sapiens</i>	ENS00000073711	PPP2R3A	protein phosphatase 2 regulatory subunit B'alpha	0.00	0.40	1.8E-04	7.9E-04	0.40	1.8E-04			MCSSYCLIVTKPD*
HG0581	<i>H. sapiens</i>	ENS00000097074	PPP1R15A	protein phosphatase 1 regulatory subunit 15A	0.14	0.39	3.3E-20	8.2E-19	0.39	3.3E-20	Crowe, Mackowiak		NNAALALTYRTGRRVWOTEPALLPPG*
HG0582	<i>H. sapiens</i>	ENS00000087338	GMC1L	germ cell-less, spermatogenesis associated 1	0.01	0.39	1.2E-17	2.5E-16	0.39	1.2E-17			METVASATYGAAREKVAV*
HG0583	<i>H. sapiens</i>	ENS00000087502	ERGIC2	ERGIC and golgi 2	0.04	0.18	4.1E-12	5.6E-11	0.18	4.1E-12			MAYGVNDHTSMT*
HG0584	<i>H. sapiens</i>	ENS00000082051	JPH4	junctionophilin 4	0.07	0.25	2.6E-05	1.4E-04	0.25	2.6E-05			MDAVPRQRPQPT*
HG0585	<i>H. sapiens</i>	ENS00000106038	EVX1	even-skipped homeobox 1	0.05	0.16	8.2E-03	2.2E-02	0.16	8.2E-03			MGLPFRGGAGRSARFTR*
HG0586.1	<i>H. sapiens</i>	ENS00000108375	RNF43	ring finger protein 43	0.00	0.08	7.3E-05	3.4E-04	0.08	7.3E-05			MGENDIPAAVDG*
HG0586.2	<i>H. sapiens</i>	ENS00000108375	RNF43	ring finger protein 43	0.00	0.00	1.4E-09	1.4E-08	0.00	1.4E-09			MLFGEKNFC*
HG0587	<i>H. sapiens</i>	ENS00000119138	KLF9	Kruppel like factor 9	0.22	0.42	4.0E-19	9.2E-18	0.42	4.0E-19			MPERCQAGAGVQKQPSVDGSKVS*
HG0588	<i>H. sapiens</i>	ENS00000120162	MOB3B	MOB kinase activator 3B	0.00	0.07	6.6E-29	2.2E-27	0.07	6.6E-29			MRFPWKSFKRMEGAV*
HG0589.1	<i>H. sapiens</i>	ENS00000121871	SLITRK3	SLIT and NTRK like family member 3	0.01	0.45	6.5E-10	7.1E-09	0.45	6.5E-10			MMDTQLRRFEAPPAG*
HG0589.2	<i>H. sapiens</i>	ENS00000121871	SLITRK3	SLIT and NTRK like family member 3	0.04	0.44	2.8E-06	1.7E-05	0.44	2.8E-06			MORPPCKSORWKHLNGLQA*
HG0589.3	<i>H. sapiens</i>	ENS00000121871	SLITRK3	SLIT and NTRK like family member 3	0.20	0.44	2.3E-12	3.3E-11	0.44	2.3E-12			MLDHSGSSAPFLTPYTRPGAPV*
HG0590	<i>H. sapiens</i>	ENS00000122557	HERPUD1	HERPUD family member 2	0.00	0.25	6.9E-23	1.7E-21	0.25	6.9E-23	Mackowiak		MKVYSSSVALTDLDT*
HG0591.1	<i>H. sapiens</i>	ENS00000127124	HIVEP3	human immunodeficiency virus type 1 enhancer binding protein	0.00	0.12	1.9E-37	7.8E-36	0.12	1.9E-37			MNAACFQREQSFSGHWRVCLQHRRRA*
HG0591.2	<i>H. sapiens</i>	ENS00000127124	HIVEP3	human immunodeficiency virus type 1 enhancer binding protein	0.01	0.35	3.3E-10	3.7E-09	0.35	3.3E-10			MWPKQDLSLCHWOYS*
HG0591.3	<i>H. sapiens</i>	ENS00000127124	HIVEP3	human immunodeficiency virus type 1 enhancer binding protein	0.00	0.49	1.4E-05	7.4E-05	0.49	1.4E-05			MEEPRGVLAQARPSSGKSGA*
HG0591.4	<i>H. sapiens</i>	ENS00000127124	HIVEP3	human immunodeficiency virus type 1 enhancer binding protein	0.06	0.19	1.3E-03	4.5E-03	0.19	1.3E-03			MDTDVSNLQPA*
HG0592	<i>H. sapiens</i>	ENS00000133401	PDZD2	PDZ domain containing 2	0.00	0.46	1.7E-18	3.7E-17	0.46	1.7E-18			MNTGKADGGGPGGTWGPVGSQPGQEDL*
HG0593	<i>H. sapiens</i>	ENS00000135048	TMEM2	transmembrane protein 2	0.01	0.44	1.4E-12	2.0E-11	0.44	1.4E-12			MERRSGPEDARDSSPSPWATV*
HG0594	<i>H. sapiens</i>	ENS00000136169	SETDB2	SET domain bifurcated 2	0.00	0.26	6.0E-11	7.3E-10	0.26	6.0E-11			MHFPHVDQKMLVFYFKMLLM*
HG0595	<i>H. sapiens</i>	ENS00000141098	GFOD2	glucose-fructose oxidoreductase domain containing 2	0.00	0.40	6.8E-13	1.0E-11	0.40	6.8E-13			MPACQEDCLTRTGRSYPCORLL*
HG0596	<i>H. sapiens</i>	ENS00000157483	MYO1E	myosin IE	0.11	0.24	1.9E-04	8.3E-04	0.24	1.9E-04			MSPLSGHWWL*
HG0597	<i>H. sapiens</i>	ENS00000163032	VSNL1	vasinin 1	0.07	0.26	5.9E-24	1.7E-22	0.26	5.9E-24			MGFFICSLRDLPERVAAAAGLARRDPRI*
HG0598	<i>H. sapiens</i>	ENS00000163788	SNRK	SNF related kinase	0.03	0.35	7.8E-10	8.4E-09	0.35	7.8E-10			MTTLKMNFLYSPDL*
HG0599	<i>H. sapiens</i>	ENS00000164930	FZD9	fizzled class receptor 9	0.00	0.36	4.8E-18	1.0E-16	0.36	2.2E-17			MNNMLILDDLLLRKGRVHPHSVVKSGP*
HG0600	<i>H. sapiens</i>	ENS00000173055	FAM222B	family with sequence similarity 222 member B	0.06	0.29	5.9E-05	2.8E-04	0.29	5.9E-05			MKQASHPRHPHSCPMCL*
HG0601	<i>H. sapiens</i>	ENS00000175893	ZDHHC21	zinc finger DHHC-type containing 21	0.00	0.42	6.9E-05	3.3E-04	0.42	6.9E-05			MNKKSKRCRFQKNYSTQ*
HG0602	<i>H. sapiens</i>	ENS00000179195	ZNF664	zinc finger protein 664	0.00	0.32	1.7E-20	4.3E-19	0.32	1.7E-20			MOEETFRKTRGKRLKLLTNPNRSLR*
HG0603	<i>H. sapiens</i>	ENS00000197329	PELL1	pellino E3 ubiquitin protein ligase 1	0.05	0.02	5.1E-21	1.3E-19	0.02	5.1E-21			MSYVQRRCEAEGSPGAAASTSSGQSPSPAVRSNVPALRERTTKQOPRLSLRPRLLSARLQGLPLAGLQWRARRAAAEARRVACSRSRPTTLHPLASLGGRSIPATSNCPMEQKVSGS*
HG0604.1	<i>H. sapiens</i>	ENS000000003147	ICA1	islet cell autoantigen 1	0.03	0.33	5.9E-04	2.2E-03	0.33	5.9E-04			MLSCFPSPNHOQ*
HG0604.2	<i>H. sapiens</i>	ENS000000003147	ICA1	islet cell autoantigen 1	0.13	0.48	1.8E-03	5.9E-03	0.42	7.4E-03			MSDPEGRSDRGREAPGGRGSEVI*
HG0604.3	<i>H. sapiens</i>	ENS000000003147	ICA1	islet cell autoantigen 1	0.22	0.35	6.2E-05	3.0E-04	0.35	6.2E-05			MATWNTCRRAGAGSLWAADPSGGYPRRVGSHRRDPE*
HG0605	<i>H. sapiens</i>	ENS000000053254	FOXN3	foxford box N3	0.00	0.09	1.4E-20	3.4E-19	0.09	1.4E-20			MKNQPLEDDHSRDYGGPSVSVTGAMLTSVSWTHSDSGAFT*
HG0606	<i>H. sapiens</i>	ENS000000055130	CUL1	cullin 1	0.00	0.48	4.4E-05	2.2E-04	0.48	4.4E-05			MRFHSLHLKDLSELL*
HG0607	<i>H. sapiens</i>	ENS00000074657	ZNF532	zinc finger protein 532	0.00	0.44	4.5E-11	5.5E-10	0.49	8.0E-09			MRFQRPPCLSHWPCRLPPPPQTPAVFVRPGIEWTSPPRCLKKEEGMFLVLFLEATKGQWCGP*
HG0608	<i>H. sapiens</i>	ENS00000084731	KIF3C	kinesin family member 3C	0.01	0.30	8.5E-04	3.1E-03	0.30	8.5E-04			MNDPPFAWEDSR*
HG0609	<i>H. sapiens</i>	ENS00000086539	SEMA4G	semaphorin 4G	0.00	0.16	7.5E-31	2.7E-29	0.16	7.5E-31	Crowe		MAFPCDSMSBPPFQDPPHSHSLTPTML*
HG0610	<i>H. sapiens</i>	ENS00000106059	CHN2	chitinase 2	0.22	0.38	1.2E-12	1.8E-11	0.38	1.2E-12			MKQSPRRRLRAAGRGWRVRRPHRG*
HG0611	<i>H. sapiens</i>	ENS00000108309	RUNDC3A	RUN domain containing 3A	0.01	0.29	2.7E-18	6.0E-17	0.29	2.7E-18			MAAMEGLRGPVGHQPCAL*
HG0612.1	<i>H. sapiens</i>	ENS00000110422	HIPK3	homeodomain interacting protein kinase 3	0.00	0.50	5.0E-14	8.4E-13	0.50	5.0E-14			MAASRALVPRPQRRGAAGLQGVNSGVDRACV*
HG0612.2	<i>H. sapiens</i>	ENS00000110422	HIPK3	homeodomain interacting protein kinase 3	0.00	0.14	6.8E-07	4.6E-06	0.14	6.8E-07			MLRAAAARRGESAGL*
HG0612.3	<i>H. sapiens</i>	ENS00000110422	HIPK3	homeodomain interacting protein kinase 3	0.06	0.20	9.2E-03	2.4E-02	0.20	9.2E-03			MKMSVLSGGRRLL*
HG0613	<i>H. sapiens</i>	ENS00000114861	FOXP1	forkhead box P1	0.00	0.17	2.7E-08	2.3E-07	0.17	2.7E-08			MVRASIPSLCOQP*
HG0614	<i>H. sapiens</i>	ENS00000122203	KIAA1191	KIAA1191	0.03	0.30	7.8E-29	2.6					

HG0634	<i>H. sapiens</i>	ENS00000198026	ZNF335	zinc finger protein 335	0.04	0.23	1.0E-20	2.6E-19	0.23	1.0E-20		MPESERNVATKASE*
HG0635	<i>H. sapiens</i>	ENS00000259332	STZ2-MTHF5	STZ2-MTHF5 readthrough	0.00	0.34	1.6E-08	4.1E-10	0.48	4.8E-08		MAAGYWRKLPBTRCTAAEAVHLWPAVLDRPWGNPGGAWPCYMRGPRL*
HG0636	<i>H. sapiens</i>	ENS00000002587	HS3T1	heparan sulfate-glucosaminase 3-sulfotransferase 1	0.08	0.32	1.8E-19	4.4E-18	0.32	1.8E-19		MAQPSRLFRPDGLDRGAQ*
HG0637	<i>H. sapiens</i>	ENS000000005102	MEOX1	mesenchyme homeobox 1	0.03	0.42	1.7E-02	4.1E-02	0.42	1.7E-02		MFVSDIGKYTYRGSQ*
HG0638	<i>H. sapiens</i>	ENS000000013561	RNF14	ring finger protein 14	0.00	0.45	3.3E-12	4.7E-11	0.45	3.3E-12		MSST5WPLTKLQGSGLHLENKWDHSELHSEKYRLRC*
HG0639	<i>H. sapiens</i>	ENS000000018236	CNTN1	contactin 1	0.00	0.00	5.2E-11	6.3E-10	0.00	5.2E-11		MGAAPVACEVA*
HG0640	<i>H. sapiens</i>	ENS000000062194	GPBP1	GC-rich promoter binding protein 1	0.00	0.00	5.5E-06	3.2E-05	0.00	5.5E-06		MLFRCEIFFLLFGS*
HG0641	<i>H. sapiens</i>	ENS000000010359	SGSM3	small G protein signaling modulator 3	0.00	0.41	1.9E-09	1.9E-08	0.40	2.2E-07		MLQDMKPEEPSSSKIAQ*
HG0642	<i>H. sapiens</i>	ENS0000000100815	TRIP11	thyroid hormone receptor interactor 11	0.00	0.44	1.1E-09	1.2E-08	0.44	1.1E-09		MAAGVELAGVTHGTEESH*
HG0643	<i>H. sapiens</i>	ENS000000010363	CSK	CSK, non-receptor tyrosine kinase	0.00	0.48	5.0E-08	4.1E-07	0.48	5.0E-08		MLFPTALMVPDRLLALL*
HG0644	<i>H. sapiens</i>	ENS0000000104299	INTS9	integrator complex subunit 9	0.00	0.48	3.3E-10	3.7E-09	0.48	3.3E-10		MLSAGRWRRLRHKTLPGFEFSDCY*
HG0645	<i>H. sapiens</i>	ENS0000000107282	APBA1	amyloid beta precursor protein binding family A member 1	0.03	0.42	4.7E-09	4.4E-08	0.42	4.7E-09		MVALEAAAGALYSQAWHQRC*
HG0646	<i>H. sapiens</i>	ENS0000000108312	UBTF	upstream binding transcription factor, RNA polymerase I	0.28	0.00	2.4E-07	1.8E-06	0.00	2.4E-07		MEQIEWEAGRPFKCSFISGLTPSHRPGGSEDPGQMEWSSL*
HG0647	<i>H. sapiens</i>	ENS0000000108395	TRIM37	TRIM37 with coiled-coil, ankryrin repeat and PH domains 2	0.00	0.34	1.6E-08	1.4E-07	0.34	1.6E-08		MTGVGAGCGGAGGAGGAGVVRAP*
HG0649	<i>H. sapiens</i>	ENS0000000114331	ACA2P	ACA2P with coiled-coil, ankryrin repeat and PH domains 2	0.02	0.35	2.9E-11	3.6E-10	0.35	2.9E-11	Mackowiak	MTISGALCARLSASQ*
HG0649	<i>H. sapiens</i>	ENS0000000114439	BBX	BBX, HMG-box containing	0.00	0.16	5.9E-03	1.7E-02	0.16	5.9E-03		MWRHWRDEKQYRRIVPL*
HG0649	<i>H. sapiens</i>	ENS0000000114439	BBX	BBX, HMG-box containing	0.00	0.12	4.1E-04	1.6E-03	0.12	4.1E-04		MESLDTLTKRLTPSL*
HG0650	<i>H. sapiens</i>	ENS0000000115226	FNDCC4	fibronectin type III domain containing 4	0.29	0.00	1.2E-10	1.4E-09	0.00	1.2E-10	Mackowiak	MGRPLTGQEPPEA*
HG0651	<i>H. sapiens</i>	ENS0000000115935	WIPF1	WAS/WASL interacting protein family member 1	0.01	0.45	2.0E-16	3.9E-15	0.45	2.0E-16		MPFSGTVFSLGSCAPGLSACVPHGSHLQYPLTYQQDC*
HG0652	<i>H. sapiens</i>	ENS0000000118515	SGK1	serum/glucocorticoid regulated kinase 1	0.18	0.37	9.6E-14	1.6E-12	0.37	9.6E-14		MMKEGKLSVATESGERLLQ*
HG0653	<i>H. sapiens</i>	ENS0000000120334	CENPL	centromere protein L	0.01	0.32	2.2E-04	9.4E-04	0.32	2.2E-04		MIRESGMGDSVITAFY*
HG0654	<i>H. sapiens</i>	ENS0000000133794	ARNTL	aryl hydrocarbon receptor nuclear translocator like	0.12	0.41	3.0E-03	9.5E-03	0.41	3.0E-03		MWNPGLSLVGRS*
HG0655	<i>H. sapiens</i>	ENS0000000143061	IGSF3	immunoglobulin superfamily member 3	0.00	0.22	8.6E-23	2.4E-21	0.22	8.6E-23		MWQEPGLVATSLTLPVA*
HG0656	<i>H. sapiens</i>	ENS0000000150776	C11orf57	chromosome 11 open reading frame 57	0.00	0.36	2.8E-13	4.3E-12	0.36	2.8E-13		MGIFLSSLTWKPPQLQAP*
HG0657	<i>H. sapiens</i>	ENS0000000151276	MAQ1	membrane associated guanylate kinase, WW and PDZ dom	0.00	0.28	1.7E-04	7.3E-04	0.28	1.7E-04	Crowe	MOIKLAGACAGLAGKPKRVFL*
HG0658	<i>H. sapiens</i>	ENS0000000153786	ZDHHC7	zinc finger DHHC-type containing 7	0.00	0.39	1.3E-02	3.3E-02	0.39	1.3E-02		MRHLKKWKKWPM*
HG0659	<i>H. sapiens</i>	ENS0000000158856	DMTN	desmin actin binding protein	0.00	0.24	1.2E-10	2.9E-10	0.24	1.2E-10		MEYYVTEAAALLPHALGP*
HG0659	<i>H. sapiens</i>	ENS0000000158856	DMTN	desmin actin binding protein	0.01	0.46	5.3E-09	5.0E-08	0.46	5.3E-09		MTRTPOGTROLLSRPOARSQQPRRA*
HG0660	<i>H. sapiens</i>	ENS0000000165861	ZFYVE1	zinc finger FYVE-type containing 1	0.00	0.30	1.4E-03	4.8E-03	0.30	1.4E-03		MEDETKPNQRCC*
HG0661	<i>H. sapiens</i>	ENS0000000166645	C18orf54	chromosome 18 open reading frame 54	0.00	0.33	1.6E-17	3.4E-16	0.29	8.9E-16		MDFLLEIRTEACTEEMFLREMNRPINL*
HG0662	<i>H. sapiens</i>	ENS0000000166897	ELFN2	extracellular leucine rich repeat and fibronectin type III dom	0.00	0.40	5.3E-08	4.3E-07	0.40	5.3E-08		MVAAPRTVLPAASGR*
HG0663	<i>H. sapiens</i>	ENS0000000168615	ADAM9	ADAM metalloproteinase domain 9	0.09	0.42	8.9E-11	1.1E-09	0.42	8.9E-11		MSGASDRGLSCVSAARVLVGRACSSGARASRPDLGPROGWMMEEAEATEC*
HG0664	<i>H. sapiens</i>	ENS0000000169085			0.01	0.25	1.9E-07	1.4E-06	0.25	1.9E-07		MIPEPDWIRMPD*
HG0665	<i>H. sapiens</i>	ENS0000000169515	CDCD8	coiled-coil domain containing 8	0.07	0.19	1.1E-05	6.0E-05	0.19	1.1E-05		MSAKMWITSSWKP*
HG0666	<i>H. sapiens</i>	ENS0000000171943	SRGAP2C	SLIT-ROBO Rho GTPase activating protein 2C	0.00	0.00	1.8E-05	9.7E-05	0.00	1.8E-05		MSDPRPASGRCSSPG*
HG0667	<i>H. sapiens</i>	ENS0000000182700	IGIP	igfa inducing protein	0.00	0.00	1.3E-11	1.7E-10	0.00	1.3E-11		MCQYTVRSISLCTVWGPHLRLNFAN*
HG0667	<i>H. sapiens</i>	ENS0000000182700	IGIP	igfa inducing protein	0.17	0.45	5.1E-04	2.0E-03	0.45	5.1E-04		MLRKSVGFSAREGSSALWTEANMSKTLWN*
HG0668	<i>H. sapiens</i>	ENS0000000182844	ENSR1	ENSR RNA binding protein 1	0.03	0.21	3.1E-20	7.7E-19	0.21	3.1E-20		MAAPVAPAPAGCA*
HG0669	<i>H. sapiens</i>	ENS0000000183876	ANS1	ankyrinlike family member 1	0.16	0.41	8.2E-06	4.8E-05	0.41	8.2E-06		MEESTFWKLPRVSCWQP*
HG0670	<i>H. sapiens</i>	ENS0000000187164	SHTN1	shodin 1	0.04	0.27	9.0E-07	6.1E-06	0.27	9.0E-07		MISLARSAPGGGAGADPTSG*
HG0671	<i>H. sapiens</i>	ENS0000000189194	PCDH18	protocadherin 18	0.01	0.36	2.5E-10	2.8E-09	0.36	2.5E-10		MPKVSQSDRTVCIKQFASC*
HG0672	<i>H. sapiens</i>	ENS0000000196369	SRGAP2B	SLIT-ROBO Rho GTPase activating protein 2B	0.00	0.00	1.8E-05	9.7E-05	0.00	1.8E-05		MSDPRPASGRCSSPG*
HG0673	<i>H. sapiens</i>	ENS0000000266028	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	0.00	0.00	1.8E-05	9.7E-05	0.00	1.8E-05		MSDPRPASGRCSSPG*
HG0674	<i>H. sapiens</i>	ENS0000000005576	PHTF2	putative homeodomain transcription factor 2	0.01	0.19	3.3E-04	1.3E-03	0.19	3.3E-04		MFFSLAQPMKTNV*
HG0674	<i>H. sapiens</i>	ENS0000000116793	PHTF1	putative homeodomain transcription factor 1	0.00	0.43	1.5E-03	5.2E-03	0.43	1.5E-03		MRPAPWAPASPASRWDPGH*
HG0675	<i>H. sapiens</i>	ENS0000000048991	R3HDM1	R3H domain containing 1	0.01	0.46	6.2E-03	1.8E-02	0.46	6.2E-03		MQSISLQVLWKEHLNSV*
HG0676	<i>H. sapiens</i>	ENS0000000005873	ZC3H11A	zinc finger CCHC-type containing 11A	0.00	0.23	2.0E-16	3.9E-15	0.23	2.0E-16	Mackowiak	MAIMLLCLQLLAAPLCSYITIRFYFLWNTP*
HG0677	<i>H. sapiens</i>	ENS0000000064989	CALCLRL	calcatonin receptor like receptor	0.06	0.34	3.3E-09	3.2E-08	0.34	3.3E-09		MIHQPLVPSVKTLDTGPTFRS*
HG0678	<i>H. sapiens</i>	ENS0000000090776	EFNB1	ephrin B1	0.07	0.40	7.1E-14	1.2E-12	0.40	7.1E-14		MGALARSASPSRKYTEGGPR*
HG0679	<i>H. sapiens</i>	ENS0000000108947	EFNB3	ephrin B3	0.08	0.06	1.2E-06	7.7E-06	0.06	1.2E-06		MPPRRPRPLRPSBT*
HG0679	<i>H. sapiens</i>	ENS0000000103291	HMCXB4	HMC-box containing 4	0.20	0.38	6.5E-06	3.7E-05	0.38	6.5E-06		MAAGGVKAGSGRAE*
HG0680	<i>H. sapiens</i>	ENS0000000100678	SLCA3A3	solute carrier family 8 member A3	0.01	0.00	1.2E-02	3.1E-02	0.00	1.2E-02		MPRTLRPLADSPRGR*
HG0681	<i>H. sapiens</i>	ENS0000000101349	PAKS	p21 (RAC1) activated kinase 5	0.00	0.21	7.2E-03	2.0E-02	0.21	7.2E-03		MLPLAKMITEEK*
HG0682	<i>H. sapiens</i>	ENS0000000105829	BET1	Bet1 golgi vesicular membrane trafficking protein	0.06	0.40	9.6E-04	3.5E-03	0.40	9.6E-04		MSWFRGRSVCWAGPWV*
HG0683	<i>H. sapiens</i>	ENS0000000111837	MAK	male germ cell associated kinase	0.02	0.39	1.2E-11	1.5E-10	0.38	2.5E-10		MKHTRRSRFTRETRTRVIRMEVLFPCPISCYIS*
HG0684	<i>H. sapiens</i>	ENS0000000113916	BCL6	B-cell CLL/lymphoma 6	0.00	0.21	2.8E-10	3.2E-09	0.21	2.8E-10		MRLGLCHSPHCLLH*
HG0685	<i>H. sapiens</i>	ENS0000000117262	GPR89A	G protein-coupled receptor 89A	0.08	0.38	1.1E-11	1.4E-10	0.38	1.1E-11		MASGWRAAVPAAPGRQTV*
HG0686	<i>H. sapiens</i>	ENS0000000118985	ELL2	elongation factor for RNA polymerase II 2	0.08	0.22	1.8E-07	1.4E-06	0.22	1.8E-07		MTVRQQRDQFSGGGCRSPSRGRSGG*
HG0687	<i>H. sapiens</i>	ENS0000000120549	KIAA1217	KIAA1217	0.05	0.45	4.1E-05	2.1E-04	0.45	4.1E-05		MOFSRARETLHRSQK*
HG0687	<i>H. sapiens</i>	ENS0000000120549	KIAA1217	KIAA1217	0.00	0.05	5.2E-03	1.5E-02	0.05	5.2E-03		MVFIGEHSS*
HG0688	<i>H. sapiens</i>	ENS0000000122420	PTGFR	prostaglandin F receptor	0.00	0.33	5.8E-09	5.5E-08	0.33	5.8E-09		MSGLDGBVLGR*
HG0689	<i>H. sapiens</i>	ENS0000000123352	SPTA2S2	spermatogenesis associated serine rich 2	0.00	0.25	2.3E-08	2.0E-07	0.25	2.3E-08		MMVTTLVYSYMLPKGDMNVNCDTS*
HG0690	<i>H. sapiens</i>	ENS0000000125931	CTED1	Caps300 interacting transactivator with Glu/Ric rich carb	0.00	0.18	6.0E-09	4.8E-07	0.18	6.0E-09		MCAPAKLQKQKTR*
HG0691	<i>H. sapiens</i>	ENS0000000129535	NRL	neural retina leucine zipper	0.22	0.48	5.6E-07	3.9E-06	0.48	5.6E-07		MIFPLCANSHLELSRTPRCMEPSWSWAVVWLVWH*
HG0692	<i>H. sapiens</i>	ENS0000000130338	TULP4	tubby like protein 4	0.00	0.41	1.5E-14	2.7E-13	0.41	1.5E-14		MALRGAAGGAGVWVSPAFFDQTPGSFEVESFWF*
HG0692	<i>H. sapiens</i>	ENS0000000130338	TULP4	tubby like protein 4	0.00	0.37	6.5E-03	1.8E-02	0.37	6.5E-03		MDLILRAFFKMEKDL*
HG0693	<i>H. sapiens</i>	ENS0000000131653	TRAF7	TNF receptor associated factor 7	0.05	0.37	4.1E-16	7.8E-15	0.37	4.1E-16		MKRAGGAAAPGRPRAGASQGP*
HG0694	<i>H. sapiens</i>	ENS0000000133265	HSPBP1	HSPA (Hsp70) binding protein 1	0.06	0.23	1.2E-09	1.2E-08	0.23	1.2E-09		MAAPSRVRCGRCLL*
HG0695	<i>H. sapiens</i>	ENS0000000133704	IPO8	importin 8	0.05	0.45	1.5E-07	1.1E-06	0.45	1.5E-07		MESELWGGKREDRGRVRAVQAQVAGDGGGGWGW*
HG0696	<i>H. sapiens</i>	ENS0000000138380	CARF	calcium responsive transcription factor	0.11	0.32	1.6E-05	8.8E-05	0.32	1.6E-05		MLEAVNLNLSHYLLNNRRKWN*
HG0697	<i>H. sapiens</i>	ENS0000000143344	RGL1	ral guanine nucleotide dissociation stimulator like 1	0.00	0.32	1.4E-07	1.0E-06	0.32	1.4E-07		MDWLPDRVPCSW*
HG0698	<i>H. sapiens</i>	ENS0000000157554	ERG	ERG, ETS transcription factor	0.00	0.49	1.6E-07	1.2E-06	0.49	1.6E-07		MTHREKRWQNGQQLKPSGEILVDGLAY*
HG0699	<i>H. sapiens</i>	ENS0000000160785	SLC25A44	solute carrier family 25 member 44	0.09	0.43	7.7E-12	1.0E-10	0.43	7.7E-12		MEDATGPRHSLTGTDRLGAAA*
HG0700	<i>H. sapiens</i>	ENS0000000165156	ZPK1	zinc fingers and homeoboxes 1	0.00	0.46	8.3E-06	4.7E-05	0.46	8.3E-06		MDSGQVGLVAGAAAPGASGASRLRDRARRLWAAGGNWSAESAGTGKEKTDCCFGPVNDGLS*
HG0701	<i>H. sapiens</i>	ENS0000000166202	TMEM100	transmembrane protein 100	0.05	0.46	7.2E-05	3.4E-04	0.46	7.2E-05		MLDGLSPFHGETGV*
HG0702	<i>H. sapiens</i>	ENS0000000167377	ZNF23	zinc finger protein 23	0.02	0.00	6.8E-05	3.2E-04	0.00	6.8E-05		MELALGDQEPVSEVGL*
HG0703	<i>H. sapiens</i>	ENS0000000171862	PTEN	phosphatase and tensin homolog	0.19	0.42	4.1E-10	4.6E-09	0.42	4.1E-10		MRCGRIRARRWDATASLLSEAAAMEY*
HG0704	<i>H. sapiens</i>	ENS0000000173598	NUDT4	nudix hydrolase 4	0.05	0.46	2.5E-07	1.9E-06	0.46	2.5E-07		MESGQLGRGAGFASIPWFO*
HG0704	<i>H. sapiens</i>	ENS0000000272325	NUDT3	nudix hydrolase 3	0.00	0.00	7.5E-05	3.5E-04	0.00	7.5E-05		MRRPRPASGGAV*
HG0705	<i>H. sapiens</i>	ENS0000000175224	ATG13	autophagy related 13	0.00	0.29	7.7E-09	7.1E-08	0.29	7.7E-09		MAAPSGDRLLGLRRE*
HG0705	<i>H. sapiens</i>	ENS0000000175224	ATG13	autophagy related 13	0.00	0.29	1.3E-12	1.9E-11	0.29	1.3E-12	Samandi	MRRNHSILCRSFAVERPVETCDPFLSNKSLVLLCCPGVSWVV*
HG0706	<i>H. sapiens</i>	ENS0000000178498	DTX3	deltex E3 ubiquitin ligase 3	0.05	0.00	3.8E-06	2.3E-05	0.00	3.8E-06		MFGPGHTYK*
HG0707	<i>H. sapiens</i>	ENS0000000179796	LRRCB8	leucine rich repeat containing 3B	0.00	0.01						

HG0727	H. sapiens	ENSOG00000115825	PRKD3	protein kinase D3	0.00	0.05	7.4E-17	1.5E-15	0.05	3.0E-11	MYKACTLKSFFVRHRRKVPHPRMQMRTFEKV*	
HG0728	H. sapiens	ENSOG00000116991	SIPA1L2	signal induced proliferation associated 1 like 2	0.00	0.28	1.2E-10	1.4E-09	0.28	1.2E-10	MLKRLTEAYNITTTTEKQVGFETV*	
HG0729	H. sapiens	ENSOG00000119383	PTPA	protein phosphatase 2 phosphatase activator	0.00	0.32	1.3E-08	1.1E-07	0.32	1.3E-08	MAAVFAVVLTLGFL*	
HG0730	H. sapiens	ENSOG00000125170	DOK4	docking protein 4	0.00	0.30	2.9E-08	2.4E-07	0.30	2.9E-08	MOARGEAGARTMLRRRV*	
HG0731	H. sapiens	ENSOG00000129255	MPDU1	mannose-6-pholich utilization defect 1	0.06	0.47	1.0E-06	6.7E-06	0.47	1.0E-06	MAPRRRSRGQGGKSGFGTGVNKGVLGAQACSFGLYNSNSASKTWSLTFTYPL*	
HG0732	H. sapiens	ENSOG00000135914	HTR2B	5-hydroxytryptamine receptor 2B	0.21	0.28	4.4E-07	2.9E-06	0.28	4.1E-07	MORCVYAILLENLFF*	
HG0733	H. sapiens	ENSOG00000136247	ZDHHC4	zinc finger DHHC-type containing 4	0.18	0.49	1.6E-06	1.0E-05	0.49	1.6E-06	MLRGMPLEPAENYPYTKRNVGWVP*	
HG0734	H. sapiens	ENSOG00000139318	DUSP6	dual specificity phosphatase 6	0.04	0.48	1.6E-04	6.8E-04	0.48	1.6E-04	MCAPPPPLPPLSPSSRRARCCSLFALGLRSGNSFFPL*	
HG0735	H. sapiens	ENSOG00000139579	NABP2	nucleic acid binding protein 2	0.22	0.49	1.2E-06	7.8E-06	0.49	1.2E-06	MORVPACRDGSGRSGG*	
HG0736	H. sapiens	ENSOG00000139626	ABHD13	aldehyde dehydrogenase domain containing 13	0.20	0.47	1.6E-02	3.9E-02	0.47	1.6E-02	MWEPAGAFAGDTRAGAGSGATARRSSGLDRGAGSGPWAGG*	
HG0737	H. sapiens	ENSOG00000141628	MAPK4	mitogen-activated protein kinase 4	0.00	0.40	3.2E-06	2.3E-05	0.40	3.2E-06	MLPSTKSSNSWFGS*	
HG0738	H. sapiens	ENSOG00000143393	PKA9	phosphatidylinositol 4-kinase beta	0.03	0.00	1.2E-08	1.1E-07	0.00	1.2E-08	MEFGSGRC*	
HG0739	H. sapiens	ENSOG00000144331	ZNF358B	zinc finger protein 358B	0.19	0.42	1.6E-06	1.0E-05	0.42	1.6E-06	MICSEALPAGCLAPHFTGAPG*	
HG0740	H. sapiens	ENSOG00000144331	ZNF358B	zinc finger protein 358B	0.00	0.34	1.0E-03	3.7E-03	0.34	1.0E-03	MFYISTPSNKLMMFG*	
HG0741	H. sapiens	ENSOG00000144834	TAGLN3	transgelin 3	0.04	0.35	9.4E-06	5.2E-05	0.35	9.4E-06	MRKSNQCALPGARQRLQFMNKGGLFAC*	
HG0742	H. sapiens	ENSOG00000154556	SORBS2	sorbin and SH3 domain containing 2	0.00	0.50	1.3E-04	5.8E-04	0.50	1.3E-04	MFCKPFGHEAPDTWGLNKLPEFKT*	
HG0743	H. sapiens	ENSOG00000154814	OXNAD1	oxidoreductase NAD binding domain containing 1	0.24	0.35	1.8E-07	1.4E-06	0.35	1.8E-07	MEKLSMFLQLYQKSCNSRRTKFCQSDAHLNDS*	
HG0744	H. sapiens	ENSOG00000163053	SLC16A14	solute carrier family 16 member 14	0.04	0.35	4.7E-14	8.0E-13	0.35	4.7E-14	MIGDIATLYTLQLRGLQAEQGVRRSGRAE*	
HG0745	H. sapiens	ENSOG00000163145	C1QTNF7	C1q and TNF related 7	0.00	0.31	4.7E-05	2.3E-04	0.31	4.7E-05	MLRRLVYSSSYLHCFGVASNNKHILL*	
HG0746	H. sapiens	ENSOG00000164741	DLC1	DLC1 Rho GTPase activating protein	0.03	0.08	5.4E-04	2.1E-03	0.08	5.4E-04	MISTTWLEIRFWN*	
HG0747	H. sapiens	ENSOG00000168036	CTNNB1	catenin beta 1	0.00	0.16	2.0E-04	8.5E-04	0.16	2.0E-04	MFFSMNLQCFRRHLQSNPPG*	
HG0748	H. sapiens	ENSOG00000168830	HTR1E	5-hydroxytryptamine receptor 1E	0.03	0.46	7.2E-04	0.4E-03	0.46	7.2E-04	MLWHPPLPTNCTQET*	
HG0749	H. sapiens	ENSOG00000169760	NLGN1	neuroligin 1	0.00	0.47	6.8E-04	2.5E-03	0.47	6.8E-04	MVGFWRWLVWPLRLDGCWRKRNHVLVSVGE*	
HG0750	H. sapiens	ENSOG00000170881	RNF139	ring finger protein 139	0.28	0.20	3.0E-06	1.8E-05	0.20	3.0E-06	MVAPRAGEAVEGGVRP*	
HG0751	H. sapiens	ENSOG00000171791	BCL2	BCL2 apoptosis regulator	0.01	0.38	4.1E-06	2.4E-05	0.38	4.1E-06	MGSLPYAFVLVLQKGNLTDHVAKKYK*	
HG0752	H. sapiens	ENSOG00000172269	DPAQT1	dolichyl-phosphate N-acetylglucosaminophosphotransferase	0.05	0.44	1.6E-07	1.2E-06	0.44	1.6E-07	MKSGITLLFHHPLHPLMLKMAAAAFRRSGNSGANKRAETVDRVRQGRRT*	
HG0753	H. sapiens	ENSOG00000173406	DAB1	DAB1, reelin adaptor protein	0.00	0.33	1.5E-04	6.7E-04	0.33	1.5E-04	MGRSFLGGCGSGCGSLGSHSKRVNEMSCSECH*	
HG0754	H. sapiens	ENSOG00000175182	FAM131A	family with sequence similarity 131 member A	0.05	0.28	2.5E-05	1.3E-04	0.28	2.5E-05	MRQECSPYVTRHRFGMRGLAQHPKQE*	
HG0755	H. sapiens	ENSOG00000176597	BGN7S	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase	0.00	0.49	1.2E-06	7.7E-06	0.49	1.2E-06	MPVWKNFDPVSSFYRVFHSASEKWD*	
HG0756	H. sapiens	ENSOG00000177051	FBXO46	F-box protein 46	0.06	0.40	3.4E-05	1.7E-04	0.40	3.4E-05	MQRAMVACGASHHLGPEMR*	
HG0757	H. sapiens	ENSOG00000177301	KCNA2	potassium voltage-gated channel subfamily A member 2	0.00	0.11	3.3E-15	5.9E-14	0.11	3.3E-15	MLLCFLGPVAP*	
HG0757.2	H. sapiens	ENSOG00000182255	KCNA4	potassium voltage-gated channel subfamily A member 4	0.00	0.16	5.5E-03	1.6E-02	0.16	5.5E-03	MLNKGPEGS*	
HG0758	H. sapiens	ENSOG00000179259	NOL1	NOL1 RNA methyltransferase family member 7	0.05	0.24	2.8E-12	3.4E-12	0.24	2.8E-12	MLQMKRGKPTGTSE*	
HG0759	H. sapiens	ENSOG00000180929	GPR62	G protein-coupled receptor 62	0.23	0.23	2.1E-10	2.3E-09	0.23	2.1E-10	MAWAVEPFGPGPM*	
HG0760	H. sapiens	ENSOG00000182463	TSHX2	teashirt zinc finger homeobox 2	0.22	0.36	3.9E-08	3.2E-07	0.36	3.9E-08	MMNEKCLNSHOKKXPKOKONOKNSKNKREKKGKQKQNTKNGQRTLYKKAAGTSHPCPLPRREGGLWPVVEELQGGSSGGORPSDVLGATGQEAETQGRQDQSGPQRAARQWGAISGTGAK*	
HG0761	H. sapiens	ENSOG00000185895	SLITRK2	SLIT and NTRK like family member 2	0.00	0.43	1.3E-10	1.5E-09	0.43	1.3E-10	MTWRLAATPREIRCKHVCSSRQACVGLGMGE*	
HG0762	H. sapiens	ENSOG00000187147	RNF220	ring finger protein 220	0.00	0.14	1.5E-08	1.3E-07	0.14	1.5E-08	MHHTLRLPSVS*	
HG0763	H. sapiens	ENSOG00000188050	RNF133	ring finger protein 133	0.00	0.41	2.0E-07	1.5E-06	0.41	2.0E-07	Crowe MLEDSGSCLYPEDDFVLVLN*	
HG0764	H. sapiens	ENSOG00000188725	SMIM15	small integral membrane protein 15	0.11	0.37	2.2E-09	2.2E-08	0.37	2.2E-09	MCTVELKTDYQGSSEVVIGSLITPGGS*	
HG0765	H. sapiens	ENSOG00000196123			0.08	0.44	1.1E-06	7.0E-06	0.44	1.1E-06	MVKSLLQOEYIAKFLAEGPET*	
HG0766	H. sapiens	ENSOG00000196189	SEMA4A	semaphorin 4A	0.15	0.20	6.0E-13	9.1E-12	0.20	6.0E-13	MMGTWRAALPFQPG*	
HG0767	H. sapiens	ENSOG00000197555	SIPA1L1	signal induced proliferation associated 1 like 1	0.00	0.28	5.5E-05	2.7E-04	0.28	5.5E-05	MLDSFCNLVSRKHMMATTESQ*	
HG0767.2	H. sapiens	ENSOG00000197555	SIPA1L1	signal induced proliferation associated 1 like 1	0.00	0.28	4.9E-03	1.4E-02	0.28	4.9E-03	MERATGSCVCLFUS*	
HG0768	H. sapiens	ENSOG00000130323	SYT13	synaptobrevin 3	0.13	0.31	1.3E-05	3.0E-06	0.31	1.3E-05	MCGRPHPPLPPYRHNQ*	
HG0769	H. sapiens	ENSOG00000220165	PCDH20	protocadherin 20	0.11	0.34	3.7E-07	2.7E-06	0.34	3.7E-07	MNREGVSSALALPSRL*	
HG0769.2	H. sapiens	ENSOG00000197991			0.00	0.46	2.3E-03	7.4E-03	0.46	2.3E-03	MMVPVFCFLALPLFEPFSLJEEPTG*	
HG0770	H. sapiens	ENSOG0000010165	METTL13	methytransferase like 13	0.00	0.45	4.3E-07	3.1E-06	0.45	4.3E-07	MWLFRRGNKSHCSVPEACGGGAPGMVSHRE*	
HG0771	H. sapiens	ENSOG0000013306	SLC25A39	solute carrier family 25 member 39	0.00	0.37	8.4E-07	5.7E-06	0.37	8.4E-07	MGPDPDGRRAARA*	
HG0772	H. sapiens	ENSOG00000064309	CDON	cell adhesion associated, oncogene regulated	0.03	0.22	1.5E-11	1.9E-10	0.22	1.5E-11	MTWGLSEFAAAQEVWRLSOPRGE*	
HG0773	H. sapiens	ENSOG00000065548	ZC3H15	zinc finger CCHC-type containing 15	0.04	0.47	8.6E-05	4.0E-04	0.47	8.6E-05	MLCDLDSQRPLRGQ*	
HG0774	H. sapiens	ENSOG00000066933	MYO9A	myosin IXA	0.00	0.42	1.9E-03	6.2E-03	0.42	1.9E-03	MCLLRPGGVSLTRGMRRRGRSPGP*	
HG0775	H. sapiens	ENSOG00000068001	HYAL2	hyaluronoglucosaminidase 2	0.02	0.48	1.3E-03	4.5E-03	0.48	1.3E-03	MGRKSSASCPTGSSWRK*	
HG0776	H. sapiens	ENSOG00000082014	SMARCD3	SWI/SNF related, associated, actin dependent regulator	0.16	0.33	2.2E-07	1.7E-06	0.33	2.2E-07	MLAAGAAGVSGPSRRHGGTG*	
HG0777	H. sapiens	ENSOG00000085444	ZNF213	zinc finger protein 213	0.20	0.25	5.9E-07	4.2E-06	0.25	5.9E-07	MPADZPGGVLGG*	
HG0778	H. sapiens	ENSOG00000089118	LHX5	LHX homeobox 5	0.02	0.17	4.1E-02	0.17	4.1E-02	0.17	4.1E-02	MNELRSGSCNMWMA*
HG0779	H. sapiens	ENSOG00000091140	DLD	aldehyde dehydrogenase	0.09	0.45	2.8E-05	1.4E-04	0.45	2.8E-05	MMREGRPWMSGGAQR*	
HG0780	H. sapiens	ENSOG00000092199	HNRNPCC	heterogeneous nuclear ribonucleoprotein C (C1C2)	0.02	0.00	1.8E-04	7.8E-04	0.00	1.8E-04	MPSLQGOQ*	
HG0781	H. sapiens	ENSOG00000100099	HP54	HP54, biogenesis of lysosomal organelles complex 3 subunit	0.00	0.50	9.0E-05	4.2E-04	0.50	9.0E-05	MHPLFLAFLERSLKRWFRCPO*	
HG0782	H. sapiens	ENSOG00000103068	CSF2RB	colony stimulating factor 2 receptor beta common subunit	0.08	0.35	2.8E-06	1.7E-05	0.35	2.8E-06	MGLAWLPAGEHRTSGH*	
HG0783	H. sapiens	ENSOG00000105053	VRK3	vaccinia related kinase 3	0.17	0.04	8.6E-07	5.8E-06	0.04	8.6E-07	MRAQRSPPSGFSRWATEKVAVKMEFPTG*	
HG0784	H. sapiens	ENSOG00000105851	PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit	0.11	0.43	7.3E-03	2.0E-02	0.43	7.3E-03	MKAPEKRNKLDAAHWA*	
HG0785	H. sapiens	ENSOG00000107242	PIPSK1B	phosphatidylinositol-4-phosphate 5-kinase type 1 beta	0.00	0.38	1.1E-03	4.1E-03	0.38	1.1E-03	MSRPPITTYNR*	
HG0786	H. sapiens	ENSOG00000107862	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor	0.00	0.00	4.4E-05	2.2E-04	0.00	4.4E-05	MSGSCRWSD*	
HG0787	H. sapiens	ENSOG00000108592	FTS3	FtsJ homolog 3	0.18	0.23	9.8E-11	1.2E-09	0.23	9.8E-11	MAENLEPTGGTGQAEAEVSVSLVRFQVWRKLRLW*	
HG0788	H. sapiens	ENSOG00000113739	STC2	stannocalcin 2	0.10	0.00	2.5E-08	2.1E-07	0.00	2.5E-08	MSELGREGAG*	
HG0789	H. sapiens	ENSOG00000115355	CCDC38BA	coiled-coil domain containing 38A	0.06	0.26	3.2E-07	6.9E-07	0.26	3.2E-07	MSARSGAGSCAPWY*	
HG0790.1	H. sapiens	ENSOG00000115568	ZNF142	zinc finger protein 142	0.00	0.47	2.9E-05	1.5E-04	0.47	2.9E-05	MTMLHPKPSRLQATFAPRWLL*	
HG0790.2	H. sapiens	ENSOG00000115568	ZNF142	zinc finger protein 142	0.00	0.20	6.9E-05	3.3E-04	0.20	6.9E-05	MWLTSSPPPYR*	
HG0791	H. sapiens	ENSOG00000131323	TRAF3	TNF receptor associated factor 3	0.00	0.32	6.1E-04	2.3E-03	0.32	6.1E-04	MMKMRPKEVMPLG*	
HG0792	H. sapiens	ENSOG00000132424	PNISR	PNN interacting serine and arginine rich protein	0.00	0.17	1.2E-05	6.7E-05	0.17	1.2E-05	MLRSCSLNQPK*	
HG0793	H. sapiens	ENSOG00000132698	RAB25	RAB25, member RAS oncogene family	0.00	0.26	4.4E-07	3.1E-06	0.26	4.4E-07	MRRGAGDLLRAEG*	
HG0794.1	H. sapiens	ENSOG00000135218	CD36	CD36 molecule	0.00	0.41	4.6E-04	1.8E-03	0.41	4.6E-04	MLEHLIEKSLFLAIKIAQ*	
HG0794.2	H. sapiens	ENSOG00000135218	CD36	CD36 molecule	0.00	0.17	6.0E-04	2.3E-03	0.17	6.0E-04	MSMAFRCCDNLKR*	
HG0795	H. sapiens	ENSOG00000137601	NEK1	NIMA related kinase 1	0.00	0.35	1.9E-05	9.8E-05	0.35	1.9E-05	MSFSKCOMVLLPY*	
HG0796	H. sapiens	ENSOG00000138074	SLCSA6	solute carrier family 5 member 6	0.03	0.33	2.7E-11	3.3E-10	0.33	2.7E-11	MRPSPSLGSLADPLFFPSEGLPRRAARSRLQTPSARCSPPRQDAEVAASQKLGPLHPPSEKAGMLISGTSKGPS*	
HG0797	H. sapiens	ENSOG00000140526	ABHD2	aldehyde dehydrogenase domain containing 2	0.01	0.34	5.0E-09	4.7E-08	0.34	5.0E-09	MAAGSGRAGAGTRILGAS*	
HG0798	H. sapiens	ENSOG00000142949	PTPRF	protein tyrosine phosphatase, receptor type F	0.06	0.00	5.2E-06	4.2E-05	0.00	5.2E-06	MTLTPGWSGGGSGGAPLVLISQGE*	
HG0798.2	H. sapiens	ENSOG00000153707	PTPRD	protein tyrosine phosphatase, receptor type D	0.00	0.47	1.6E-02	3.8E-02	0.47	1.6E-02	MLAPREAMCGSRRL*	
HG0799	H. sapiens	ENSOG00000143398	PIPK1A	phosphatidylinositol-4-phosphate 5-kinase type 1 alpha	0.01	0.35	1.6E-06	1.0E-05	0.35	1.6E-06	MPGEWGLVLQVEPARRY*	
HG0800	H. sapiens	ENSOG00000143812	C1orf43	chromosome 1 open reading frame 43	0.03	0.37	1.6E-02	3.9E-02	0.37	1.6E-02	MPGRVWLGLPP*	
HG0801	H. sapiens	ENSOG00000144278	GALNT13	polypeptide N-acetylglucosaminyltransferase 13	0.00	0.39	6.0E-04	2.3E-03	0.39	6.0E-04	MFANHFIAKCHIQFNI*	
HG0802	H. sapiens	ENSOG00000144283	PKP4	plakophilin 4	0.12	0.00	7.2E-05	3.4E-04	0.00	7.2E-05	MSLPGATTAA*	
HG0803	H. sapiens	ENSOG00000144802	NFKBIZ	NFKB inhibitor zeta	0.05	0.40	1.8E-05	9.5E-05	0.40	1.8E-05	MLSRITWVIADYSWKQLCSYVF*	
HG0804	H. sapiens	ENSOG00000144815	NXPE3	neurexophilin and PC-esterase domain family member 3	0.00	0.46	2.7E-03	8.4E-03	0.46	2.7E-03	MCFLNLQSLLCIRALKGTREANETESSAAQSKDMF*	
HG0805.1	H. sapiens	ENSOG00000145936	KCNMB1	potassium calcium-activated channel subfamily M regulator	0.04	0.49	8.8E-05	4.1E-04	0.49	8.8E-05	MFHGGGLPOMGTSCFPDGRGQGTSC*	
HG0805.2	H. sapiens	ENSOG00000145936	KCNMB1	potassium calcium-activated channel subfamily M regulator	0.06	0.49	6.4E-03	1.8E-02	0.49	6.4E-03	MVEOGLNSCLPGQWVPLRVVSRKCAQT*	
HG0806	H. sapiens	ENSOG00000147481	SNTG1	synaptrophin gamma 1	0.00	0.42	7.5E-					

HG0821	<i>H. sapiens</i>	ENS00000165300	SLITRK5	SLIT and NTRK like family member 5	0.04	0.07	2.5E-08	2.1E-07	0.07	2.5E-08		MMTOPWRCETGR*
HG0822	<i>H. sapiens</i>	ENS00000169170	BAG3	BCL2 associated thiogene 5	0.19	0.26	7.4E-03	2.9E-02	0.26	7.4E-03		MC2AGLRNRYT*
HG0823	<i>H. sapiens</i>	ENS00000166258	MYRFL	myelin regulatory factor-like	0.00	0.27	7.7E-07	5.2E-06	0.27	7.7E-07		HAEDILHNSKKMKFKQHS*
HG0824	<i>H. sapiens</i>	ENS00000167100			0.04	0.26	1.7E-04	7.3E-04	0.26	1.7E-04		MERLEPARSPRPQ*
HG0825	<i>H. sapiens</i>	ENS00000169180	XP06	exportin 6	0.00	0.00	3.6E-05	1.8E-04	0.00	3.6E-05		MGGLPESAGTMT*
HG0826	<i>H. sapiens</i>	ENS00000169851	PCDH7	protocadherin 7	0.00	0.45	6.2E-04	2.3E-03	0.45	6.2E-04		MTLRRVVKKCKPALS3VRRD*
HG0827	<i>H. sapiens</i>	ENS00000170365	SMAD1	SMAD family member 1	0.00	0.35	1.0E-08	9.2E-08	0.35	1.0E-08		MCIREFAVEQLFLYSAPCL*
HG0828	<i>H. sapiens</i>	ENS00000170390	DCLK2	doublecortin like kinase 2	0.00	0.17	6.8E-08	5.5E-07	0.17	6.8E-08		MTWAARRCGHF*
HG0829	<i>H. sapiens</i>	ENS00000171502	COL24A1	collagen type XXIV alpha 1 chain	0.12	0.29	3.4E-04	1.4E-03	0.29	3.4E-04		MDSTCTLSSELASVFR*
HG0830	<i>H. sapiens</i>	ENS00000171631	P2RY6	pyrimidinergic receptor P2Y6	0.25	0.41	6.6E-08	5.3E-07	0.41	6.6E-08		MALEGVGQAEEMGAVLSEPLPP*
HG0831.1	<i>H. sapiens</i>	ENS00000174482	LINGO2	leucine rich repeat and Ig domain containing 2	0.00	0.32	2.5E-03	8.0E-03	0.32	2.5E-03		MQLSRFVSSSWVLGL*
HG0831.2	<i>H. sapiens</i>	ENS00000174482	LINGO2	leucine rich repeat and Ig domain containing 2	0.21	0.44	1.3E-02	3.3E-02	0.44	1.3E-02		MRRSEGSTGESGHYQHEEPNNSNW*
HG0832	<i>H. sapiens</i>	ENS00000175048	ZDHHC14	zinc finger DHHC-type containing 14	0.13	0.37	1.8E-03	5.4E-03	0.37	1.8E-03	Crowe	MTVLGPGGLTWSSSASKLSPSREP*
HG0833	<i>H. sapiens</i>	ENS00000176641	BNF1	bin finger protein 152	0.00	0.37	6.7E-06	3.9E-05	0.37	6.7E-06		MSRRRRRGEDGTTDTTDMNTWSTGCL*
HG0834	<i>H. sapiens</i>	ENS00000182489	XKRX	XK related, X-linked	0.00	0.33	1.7E-02	4.2E-02	0.33	1.7E-02		MLAFVFLFKHSKYVDWNRGQSRKFKVXVLLGFFSQTPSRH*
HG0835	<i>H. sapiens</i>	ENS00000182901	RG57	regulator of G protein signaling 7	0.06	0.23	4.0E-04	1.6E-03	0.23	4.0E-04		MKLPCLAAPLAS*
HG0836	<i>H. sapiens</i>	ENS00000197461	PDGFA	platelet derived growth factor subunit A	0.27	0.12	2.3E-05	1.2E-04	0.12	2.3E-05		MSANNQNYRPRGR*
HG0837	<i>H. sapiens</i>	ENS00000198690	FAN1	FANCD2 and FANCI associated nuclease 1	0.02	0.40	1.0E-06	6.8E-06	0.40	1.0E-06		MRSYRIPLLVISQSESKPILLSFTLLNCFAGNQIFP*
HG0838	<i>H. sapiens</i>	ENS00000198707	CEP290	centrosomal protein 290	0.01	0.41	9.8E-03	2.6E-02	0.41	9.8E-03		MVSPSRRCRFGLLGTWLDPESAWNRRDLSGPAGSSLLVAVVRRLWPLGLV*
HG0839	<i>H. sapiens</i>	ENS00000198791	CNOT7	CCR4-NOT transcription complex subunit 7	0.04	0.42	5.2E-07	3.7E-06	0.42	5.2E-07		MQHPLPPPLPPPPPPPSAVSMARRRRSSASTQVHK*
HG0840	<i>H. sapiens</i>	ENS00000278195	SSTR3	somatostatin receptor 3	0.16	0.43	1.8E-06	1.1E-05	0.43	1.8E-06		MTSLAARREALTPWAGK*
HG0841	<i>H. sapiens</i>	ENS00000278259	MYO19	myosin XIX	0.03	0.16	6.9E-09	6.3E-08	0.16	6.9E-09		MTRWVLLVPPTAQNPQ*
HG0842	<i>H. sapiens</i>	ENS00000202746	HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein	0.03	0.37	1.1E-03	4.0E-03	0.37	1.1E-03		MKCAALPRRRRCWSRNTVRL*
HG0843	<i>H. sapiens</i>	ENS00000243093	DCUN1D1	defective in cullin neddylation 1 domain containing 1	0.12	0.44	1.0E-02	2.6E-02	0.44	1.0E-02		MRVEELRSTDPHF*
HG0844	<i>H. sapiens</i>	ENS00000291009	RBMY2	RNA binding motif protein 27	0.00	0.00	1.4E-03	4.8E-03	0.00	1.4E-03		MPGGLGHLREL
HG0845	<i>H. sapiens</i>	ENS00000299249	PA1AD	patatin domain containing 1	0.02	0.44	7.0E-04	2.9E-04	0.44	7.0E-04		MAALLRRLTVLDPF*
HG0846	<i>H. sapiens</i>	ENS00000302852	ARHGAP5	Rho GTPase activating protein 5	0.00	0.33	3.8E-05	1.9E-04	0.33	3.8E-05	Mackowiak	MCKRKEKEDPQVLEDVSAQK*
HG0847	<i>H. sapiens</i>	ENS00000306096	PLEKHA8	pleckstrin homology domain containing A8	0.28	0.13	1.8E-09	1.6E-07	0.13	1.8E-09		MALLVLWASLQGT*
HG0848	<i>H. sapiens</i>	ENS00000311817	DSE	dermatan sulfate epimerase	0.29	0.15	3.8E-04	1.5E-03	0.15	3.8E-04		MARRRGRLGSEGASGPGALE*
HG0849	<i>H. sapiens</i>	ENS00000311846	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	0.01	0.49	3.2E-03	9.9E-03	0.49	3.2E-03		MTCRMVTPSTCNFMVMTGGPGIRTSLRTSVVF*
HG0850	<i>H. sapiens</i>	ENS00000313916	BCL6	B-cell CLL/lymphoma 6	0.00	0.41	5.7E-03	1.6E-02	0.41	5.7E-03		MCQLSFAKEKILEW*
HG0851	<i>H. sapiens</i>	ENS00000321479	FGF12	fibroblast growth factor 12	0.00	0.19	3.9E-06	2.4E-05	0.19	3.9E-06		MHSVDLTLGRTS*
HG0852	<i>H. sapiens</i>	ENS00000321494	EEF1B2	eukaryotic translation elongation factor 1 beta 2	0.05	0.25	1.8E-07	1.4E-06	0.25	1.8E-07		MPLLIYFGTQRKWHGQFVGHJQGPQFVRGVEVGMKYFDL*
HG0853	<i>H. sapiens</i>	ENS00000321807	CCR2	C-C motif chemokine receptor 2	0.07	0.41	1.1E-04	4.9E-04	0.41	1.1E-04		MVRVGLTHQTGGISKISKLFWRPQNPVQCS*
HG0854	<i>H. sapiens</i>	ENS00000327249	ATP13A4	ATPase 13A4	0.00	0.42	5.6E-04	2.1E-03	0.42	5.6E-04		MAASFETAALRECNKGAANSNS*
HG0855	<i>H. sapiens</i>	ENS00000327804	METTL16	methyltransferase like 16	0.10	0.49	1.6E-02	3.9E-02	0.49	1.6E-02		MAARWERICVSRFSAMRLL*
HG0856	<i>H. sapiens</i>	ENS00000330055	GDPD2	glycerophosphodiester phosphodiesterase domain containi	0.04	0.33	1.8E-02	4.3E-02	0.33	1.8E-02		MCKPAPQNNSSIQAP*
HG0857	<i>H. sapiens</i>	ENS00000330347	RTNMP1	reticulon 4 interacting protein 1	0.00	0.29	3.7E-07	2.8E-06	0.29	3.7E-07		MORLRTGTLIRAHMRRAE*
HG0858	<i>H. sapiens</i>	ENS00000332702	HAPLN2	hyaluronan and proteoglycan link protein 2	0.04	0.23	1.8E-08	1.8E-07	0.23	1.8E-08		MRTQAPEGRCGAQVDF*
HG0859	<i>H. sapiens</i>	ENS00000332942	AP3B1	adaptor related protein complex 3 beta 1 subunit	0.12	0.05	2.6E-05	1.4E-04	0.05	2.6E-05		MRRGWTARSQAQVATPSPPEARAPPYEN*
HG0860	<i>H. sapiens</i>	ENS00000333056	PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit	0.00	0.24	5.9E-07	4.1E-06	0.24	5.9E-07		MASPLSPAAAIVSPGVA*
HG0861	<i>H. sapiens</i>	ENS00000334001	EIF2S1	eukaryotic translation initiation factor 2 subunit alpha	0.00	0.13	1.2E-07	9.3E-07	0.13	1.2E-07		MVNDEEPLVQRLRRMRGGSACAVE*
HG0862	<i>H. sapiens</i>	ENS00000334245	WNT2B	Wnt family member 2B	0.02	0.00	3.0E-08	2.5E-07	0.00	3.0E-08		MAPQGEVGA*
HG0863	<i>H. sapiens</i>	ENS00000334313	KIDINS220	kinase D interacting substrate 220	0.00	0.45	1.2E-03	4.3E-03	0.45	1.2E-03		MAAGCGEGDALAVAVSCFPVL*
HG0864	<i>H. sapiens</i>	ENS00000334533	RERG	RAS like estrogen regulated growth inhibitor	0.00	0.46	1.3E-03	4.7E-03	0.46	1.3E-03		MVNPKTGTKKIVSYL*
HG0865	<i>H. sapiens</i>	ENS00000335540	NHSL1	NHS like 1	0.00	0.39	1.3E-06	8.4E-06	0.39	1.3E-06		MPRRGVGLQFGLMGTQRQRVGPVPLCVLQSPQKY*
HG0866	<i>H. sapiens</i>	ENS00000336011	STAB2	stabilin 2	0.09	0.18	4.8E-05	2.3E-04	0.18	4.8E-05		MKRNLSGVGYTKLK*
HG0867	<i>H. sapiens</i>	ENS00000337203	TFAP2A	transcription factor AP-2 alpha	0.09	0.41	9.6E-03	2.5E-02	0.41	9.6E-03		MDPSRAPALRGASAP*
HG0868	<i>H. sapiens</i>	ENS00000337843	PAK6	p21 (RAC1) activated kinase 6	0.09	0.41	3.5E-08	2.9E-07	0.41	3.5E-08		MPEDLMKQSESPRGAEEGAAAGAGP*
HG0869	<i>H. sapiens</i>	ENS00000339910	NOVA1	NOVA alternative splicing regulator 1	0.04	0.35	1.1E-03	4.1E-03	0.35	1.1E-03		MSRNTOASBFALES*
HG0870	<i>H. sapiens</i>	ENS00000340993	TIGD7	tiger transposable element derived 7	0.01	0.30	2.5E-05	1.3E-04	0.30	2.5E-05		MAQOSTRIKTRILRL*
HG0871	<i>H. sapiens</i>	ENS00000341127	PRPSAF2	phosphoribosyl pyrophosphate synthetase associated prote	0.04	0.37	6.8E-05	3.9E-05	0.37	6.8E-05		MPAQGREPSRGTAESELEEFCCORIKGCGP*
HG0872	<i>H. sapiens</i>	ENS00000342583	SLC2A5	solute carrier family 2 member 5	0.16	0.30	1.2E-05	6.6E-05	0.30	1.2E-05		MLLAVIHGQSAPRMSLSIQCRTYFC*
HG0873	<i>H. sapiens</i>	ENS00000342875	PRKACB	protein kinase cAMP-activated catalytic subunit beta	0.00	0.48	1.2E-04	5.5E-04	0.48	1.2E-04		MLGYSALLGASLFTKESRFRLLCAACSSVCVYTIQSSPSPD*
HG0874	<i>H. sapiens</i>	ENS00000343515	ATP8B2	ATPase phospholipid transporting 8B2	0.22	0.24	9.2E-05	4.2E-04	0.24	9.2E-05		MGSTGPPGRASAE*
HG0875	<i>H. sapiens</i>	ENS00000345284	SCD5	stearoyl-CoA desaturase 5	0.09	0.26	1.3E-05	7.0E-05	0.26	1.3E-05		MGDTPATDAGRODLHP*
HG0876	<i>H. sapiens</i>	ENS00000345908	ZNF300	zinc finger protein 300	0.05	0.36	1.2E-03	4.3E-03	0.36	1.2E-03		MAAPCGNSRQPCFLNKASEDAERAKPSTERRLSGPVWCSRTSGRRVCQ*
HG0877	<i>H. sapiens</i>	ENS00000346426	TIAM2	T-cell lymphoma invasion and metastasis 2	0.00	0.33	3.3E-07	2.4E-06	0.33	3.3E-07		MKKRLTSWTHFACLLNLVCSQDHVKPTDF*
HG0878	<i>H. sapiens</i>	ENS00000346802	TMEM168	transmembrane protein 168	0.01	0.37	1.8E-04	7.8E-04	0.37	1.8E-04		MAAAGPVTEKVYADTGLY*
HG0879	<i>H. sapiens</i>	ENS00000347145	LPAR4	lysophosphatidic acid receptor 4	0.03	0.28	2.0E-07	1.5E-06	0.28	2.0E-07		MDKNMHFQRASCPFTCLLANYLQASASHL*
HG0880	<i>H. sapiens</i>	ENS00000351789	ZNF385D	zinc finger protein 385D	0.01	0.33	5.7E-05	2.8E-04	0.33	5.7E-05		MGSAGSGSPALSRRRS*
HG0881	<i>H. sapiens</i>	ENS00000353822	KCNJ16	potassium voltage-gated channel subfamily J member 16	0.00	0.45	1.8E-02	3.9E-02	0.45	1.8E-02		MAVGASGSRFRLTQPRKCEPMLSYGALTR*
HG0882.1	<i>H. sapiens</i>	ENS00000354832	CXXC1	CXXC finger protein 1	0.30	0.43	4.5E-06	2.6E-02	0.30	4.5E-06		MFPANIPANRYGVYQKDGGA*
HG0882.2	<i>H. sapiens</i>	ENS00000354832	CXXC1	CXXC finger protein 1	0.01	0.26	7.0E-03	1.9E-02	0.26	7.0E-03		MHWKGETEWRNRYNLQVILRKRSLYL*
HG0883	<i>H. sapiens</i>	ENS00000356011	PSD3	pleckstrin and Sec7 domain containing 3	0.00	0.00	1.5E-05	7.9E-05	0.00	1.5E-05		MLGEAAWCFLS*
HG0884	<i>H. sapiens</i>	ENS00000356463	SH3RF2	SH3 domain containing ring finger 2	0.00	0.16	2.9E-08	2.4E-07	0.16	2.9E-08		MWTLTLQVGTGLVK*
HG0885.1	<i>H. sapiens</i>	ENS00000357502	MUM1L1	MUM1 like 1	0.00	0.37	2.7E-07	2.0E-06	0.37	2.7E-07		MPTKPWKDSATTEVPSSWKALLDKQL*
HG0885.2	<i>H. sapiens</i>	ENS00000357502	MUM1L1	MUM1 like 1	0.00	0.43	3.6E-03	1.1E-02	0.43	3.6E-03		MAVWNASYFORLEDE*
HG0886	<i>H. sapiens</i>	ENS00000358850	B4GALT3	beta-1,4-galactosyltransferase 3	0.05	0.33	4.4E-05	2.2E-04	0.33	4.4E-05		MAAMMPARLLGWR*
HG0887	<i>H. sapiens</i>	ENS00000360959			0.00	0.43	1.5E-06	9.7E-06	0.43	1.5E-06		MVEICPPAELGRGLVSGTFQEPV*
HG0888	<i>H. sapiens</i>	ENS00000364023	SGMS2	sphingomyelin synthase 2	0.00	0.27	1.5E-05	8.2E-05	0.27	1.5E-05		MEETVIGWLPTSTCFRKRQSL*
HG0889	<i>H. sapiens</i>	ENS00000364091	WDR82	WD repeat domain 82	0.08	0.24	1.4E-04	6.2E-04	0.24	1.4E-04		MADTMSRRRAGCP*
HG0890	<i>H. sapiens</i>	ENS00000365813			0.11	0.18	2.5E-07	1.8E-06	0.18	2.5E-07		MEKLAPELQDQC*
HG0891	<i>H. sapiens</i>	ENS00000366211	SPIC	Sp1-C transcription factor	0.00	0.40	2.3E-06	1.1E-04	0.40	2.3E-06		MKHALYGLKCLPGLSTYFLFSSSNNC*
HG0892	<i>H. sapiens</i>	ENS00000368418	KCNQ4	potassium voltage-gated channel modifier subfamily G mem	0.28	0.43	1.3E-06	9.4E-06	0.43	1.3E-06		MCSPLCAEKOLETGSLROEDW*
HG0893	<i>H. sapiens</i>	ENS00000368769	TE72	telomeric proteinase dioxygenase 2	0.26	0.38	1.0E-02	2.7E-02	0.38	1.0E-02		MQYTSAPSAPRPFDAGPA*
HG0894.1	<i>H. sapiens</i>	ENS00000369282	KCNAB1	potassium voltage-gated channel subfamily A member regu	0.00	0.50	4.8E-04	1.9E-03	0.50	4.8E-04		MLRAPVHPACPGPDAGGASCGKPAL*
HG0894.2	<i>H. sapiens</i>	ENS00000369424	KCNAB2	potassium voltage-gated channel subfamily A regulatory be	0.00	0.29	2.2E-04	9.2E-04	0.29	2.2E-04		MALSPVVPVQEQNFPTVKNRASLDK*
HG0895	<i>H. sapiens</i>	ENS00000370035	UBE2E3	ubiquitin conjugating enzyme E2 E3	0.00	0.45	1.2E-02	3.0E-02	0.45	1.2E-02		MNLRCRWPWKLEQLFSKR*
HG0896	<i>H. sapiens</i>	ENS00000370365	SMAD1	SMAD family member 1	0.00	0.40	2.1E-03	6.9E-03	0.40	2.1E-03		MCFRRGGTGNACQISQL*
HG0897	<i>H. sapiens</i>	ENS00000371435	KSR2	kinase suppressor of ras 2	0.10	0.20	2.9E-05	1.5E-04	0.20	2.9E-05		MPQPCNWQEGCPDFF*
HG0898	<i>H. sapiens</i>	ENS00000371729	TMEM51	transmembrane protein 51	0.02	0.34	1.2E-07	9.4E-07	0.34	1.2E-07		MKSCLLACPESPQITGPTAAIRTGGLAIARNHPAGVOLIFSSVGREILVSAFKGLL*
HG0899	<i>H. sapiens</i>	ENS00000373320	STOX2	storkhead box 2	0.03	0.36	7.9E-05	3.7E-04	0.36	7.9E-05		MKGRHMRVGAPTQPSRAHQRPPEPRGGED*
HG0900	<i>H. sapiens</i> </											

HG0918	<i>H. sapiens</i>	ENS00000047648	ARHGAP6	Rho GTPase activating protein 6	0.11	0.43	2.8E-03	6.3E-03	0.43	2.6E-03	MDLLLLPPPGHLERTGGA*
HG0919	<i>H. sapiens</i>	ENS00000051009	FAM160A	family with sequence similarity 160 member A2	0.00	0.00	4.6E-05	4.6E-05	0.00	2.3E-04	MSGVNLLGTG*
HG0920	<i>H. sapiens</i>	ENS000000051362	PKICB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit	0.00	0.12	9.4E-06	5.2E-05	0.12	9.4E-06	MGATLAPRWL*
HG0921	<i>H. sapiens</i>	ENS000000058799	YIPF1	Yip1 domain family member 1	0.03	0.46	1.1E-04	4.9E-04	0.46	1.1E-04	MRPKLRPGARIGQRSSRIGNQTQLCTPEPVLPTTG*
HG0922	<i>H. sapiens</i>	ENS000000079841	RIMS1	regulating synaptic membrane exocytosis 1	0.03	0.34	2.2E-07	1.6E-06	0.34	2.2E-07	MQTMTKDWVLLALPGSAAAAAAMPPAAAARAPL*
HG0923	<i>H. sapiens</i>	ENS000000001138	CDH7	cadherin 7	0.14	0.30	1.7E-04	7.5E-04	0.30	1.7E-04	MTPLSCLRSSTDHGFHDLRLYLLHSLAKAIQW*
HG0924	<i>H. sapiens</i>	ENS000000081307	UBA5	ubiquitin like modifier activating enzyme 5	0.21	0.50	2.8E-04	1.1E-03	0.50	2.8E-04	MSATHRKRLRGRPVGVSETCLSVRRVVHVPRALG*
HG0925	<i>H. sapiens</i>	ENS0000000088766	CRLS1	cardiolipin synthase 1	0.30	0.49	3.3E-03	1.0E-02	0.49	3.3E-03	MEAAVAQCLSGCRVSMKRLASVPGC*
HG0926	<i>H. sapiens</i>	ENS0000000065397	WHRN	whirlin	0.00	0.34	5.8E-07	4.1E-06	0.34	5.8E-07	MPRTFCTPAPLHRLPLGVLWD*
HG0927	<i>H. sapiens</i>	ENS0000000095951	HIVEP1	human immunodeficiency virus type 1 enhancer binding protein	0.00	0.30	1.1E-05	6.1E-05	0.30	1.1E-05	MAACGCRPALLAGAAREPSTWIN*
HG0928	<i>H. sapiens</i>	ENS000000102057	KCNBD1	potassium voltage-gated channel subfamily D member 1	0.05	0.29	1.7E-03	5.7E-03	0.29	1.7E-03	MPQSPHLHCKGIPGSSAFPLETSAENSPRVSWPL*
HG0929	<i>H. sapiens</i>	ENS000000102239	BR53	bombesin receptor subtype 3	0.25	0.20	1.5E-03	5.1E-03	0.20	1.5E-03	MGKLAKHAGHRTLKRQSIWMSWIFFPSCVLS*
HG0930	<i>H. sapiens</i>	ENS000000102524	TNFSF13B	TNF superfamily member 13b	0.12	0.31	2.9E-04	1.2E-03	0.31	2.9E-04	MGKGRKEKQDSNIPG*
HG0931	<i>H. sapiens</i>	ENS000000104051	L4H1	interleukin 4 induced 1	0.02	0.45	4.2E-03	1.3E-02	0.45	4.2E-03	MCFLPSPOKWLKPLVINSYEDNTGQ*
HG0932	<i>H. sapiens</i>	ENS000000105997	HXXA3	hemidesmos A3	0.11	0.48	9.3E-05	4.3E-04	0.48	9.3E-05	MLRVRHAHPKAPRG*GRAAHPGRGPEVSEPEPEPALVRS*
HG0933	<i>H. sapiens</i>	ENS000000106330	MOSPD3	mollie sperm domain containing 3	0.05	0.34	7.1E-04	2.7E-03	0.34	7.1E-04	MTEAVRRKRYKGLSGTQWQ*
HG0934	<i>H. sapiens</i>	ENS000000107443	CNNJ	cyclin J	0.00	0.19	4.4E-05	2.2E-04	0.19	4.4E-05	MSGAGVRRITAGLGL*
HG0935	<i>H. sapiens</i>	ENS000000108518	PFN1	profilin 1	0.06	0.14	1.6E-03	5.5E-03	0.14	1.6E-03	MGSRPPRYRPLQIK*
HG0936	<i>H. sapiens</i>	ENS000000108799	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit	0.00	0.46	6.0E-03	1.7E-02	0.46	6.0E-03	MEAGHLFCCCVLPFS*
HG0937	<i>H. sapiens</i>	ENS000000109846	CRYAB	crystallin alpha B	0.03	0.44	1.1E-04	5.1E-04	0.44	1.1E-04	MTSHWPAGTCLCLSLFSYSTGVYSHQCPDHKS*
HG0938	<i>H. sapiens</i>	ENS000000111665	CDCA3	cell division cycle associated 3	0.13	0.33	9.1E-04	3.3E-03	0.33	9.1E-04	MGTTSAQPIGSGOGAWREV*
HG0939	<i>H. sapiens</i>	ENS000000111674	ENO2	enolase 2	0.22	0.49	4.9E-03	1.4E-02	0.49	4.9E-03	MGALEREPRQPLFLAPRRNRLAAILP*
HG0940	<i>H. sapiens</i>	ENS000000115556	PLCD4	phospholipase C delta 4	0.01	0.20	9.7E-03	2.5E-02	0.20	9.7E-03	MGWTGESSHLSPSYCFPPATCOSSQPAVEEGRKQASAGKEKRSQAGLPDPTASGSGGTARHRRKRTALLSCRP*
HG0941	<i>H. sapiens</i>	ENS000000116285	ERRF1	ERBB receptor feedback inhibitor 1	0.11	0.42	8.6E-04	3.1E-03	0.42	8.6E-04	MGRGAPGRSSRSSGGMKATG*
HG0942	<i>H. sapiens</i>	ENS000000117477	ELF1	ET1 like ETB transcription factor 1	0.04	0.47	6.5E-05	3.1E-04	0.47	6.5E-05	MEADAERCHGSGVSLVAAAAGAGSVFSAM*
HG0943	<i>H. sapiens</i>	ENS000000120680	SOCS2	suppressor of cytokine signaling 2	0.00	0.38	9.3E-04	3.4E-03	0.38	9.3E-04	MLRRLRSLREGRVGRKALLTRSHINGE*
HG0944	<i>H. sapiens</i>	ENS000000120833	SOCS2	suppressor of cytokine signaling 2	0.00	0.50	4.6E-04	1.8E-03	0.50	4.6E-04	MLKQERSGGVDFHVFYFPTTTPAAGVQGLTGPPAPSL*
HG0945	<i>H. sapiens</i>	ENS000000124782	RREB1	ras responsive element binding protein 1	0.00	0.43	1.4E-03	4.9E-03	0.43	1.4E-03	MIATAGESIVFWQWVRK*
HG0946.1	<i>H. sapiens</i>	ENS000000127334	TSPAN8	tetraspanin 8	0.00	0.43	5.8E-03	1.7E-02	0.43	5.8E-03	MTSKGTLYPGDSLCD*
HG0946.2	<i>H. sapiens</i>	ENS000000127334	TSPAN8	tetraspanin 8	0.00	0.08	3.4E-06	2.0E-05	0.27	7.4E-04	MCLGLFSLSLTFYSLLYFFAFSFCSEAVDTEISAGKLLQSDKQPVNTS*
HG0947	<i>H. sapiens</i>	ENS000000129226	CD68	CD68 molecule	0.14	0.49	1.3E-02	3.3E-02	0.49	1.3E-02	MTKREVARAEAPESGOWDHLQYRK*
HG0948	<i>H. sapiens</i>	ENS000000129595	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	0.01	0.12	1.8E-02	4.3E-02	0.12	1.8E-02	MKRGDAPPPSPASSAGAPAAPRG*
HG0949	<i>H. sapiens</i>	ENS000000131381	RBSN	rabenosyn, RAB effector	0.00	0.16	5.9E-05	2.9E-04	0.16	5.9E-05	MKPLPHLLCAA*
HG0950	<i>H. sapiens</i>	ENS000000132964	CKDK	cyclin dependent kinase 8	0.13	0.44	6.1E-04	2.3E-03	0.44	6.1E-04	MSLALRGLLLLLHPQSGWCCGRRA*
HG0951	<i>H. sapiens</i>	ENS000000134061	CD180	CD180 molecule	0.00	0.29	1.1E-02	2.8E-02	0.29	1.1E-02	MLSSQGHFLFDHPSEYLSGCGIARAFIV*
HG0952	<i>H. sapiens</i>	ENS000000134453	RBM17	RNA binding motif protein 17	0.05	0.00	7.1E-03	2.0E-02	0.00	7.1E-03	MGRVGRAGR*
HG0953	<i>H. sapiens</i>	ENS000000134815	DHX34	DEAH-box helicase 34	0.00	0.10	1.0E-04	4.7E-04	0.10	1.0E-04	MNCFPSQBSLQMS*
HG0954	<i>H. sapiens</i>	ENS000000134874	DZIP1	DAP interacting zinc finger protein 1	0.00	0.27	9.8E-05	4.4E-04	0.27	9.8E-05	MSGSPRNSPVDWMSGFSSA*
HG0955	<i>H. sapiens</i>	ENS000000134982	APC	APC, WNT signaling pathway regulator	0.00	0.17	1.2E-03	4.1E-03	0.17	1.2E-03	MLPFGTVGCG*
HG0956	<i>H. sapiens</i>	ENS000000136235	GPWMB	glycoprotein mb6	0.09	0.14	6.4E-05	3.1E-04	0.36	1.1E-02	MLPEALYLKIERAPOMPEEHCCSBBWATGPEEFVRK*
HG0957	<i>H. sapiens</i>	ENS000000136874	STX17	syntaxin 17	0.04	0.48	8.3E-03	2.2E-02	0.48	8.3E-03	MTRSRSMVLRGLGARGRKPLAKPRGQWQVPLHLSLLANGRSERLYDFDSLQIRFYMSGEDSCYQGGHTFTT*
HG0958	<i>H. sapiens</i>	ENS000000137497	NUMA1	nuclear mitotic apparatus protein 1	0.00	0.10	2.2E-05	1.2E-04	0.10	2.2E-05	MNNHSCFPAPSLGGN*
HG0959	<i>H. sapiens</i>	ENS000000137558	PH15	peptidase inhibitor 15	0.00	0.47	1.4E-03	4.9E-03	0.47	1.4E-03	MLPNDVFNVSYPALFFIDPNSTFL*
HG0960	<i>H. sapiens</i>	ENS000000140297	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	0.00	0.46	6.6E-04	2.5E-03	0.46	6.6E-04	MISLSSLVYLRSALGKESDGATCPOPLCRY*
HG0961	<i>H. sapiens</i>	ENS000000140853	NLRCS	NLR family CARD domain containing 5	0.09	0.04	4.2E-07	3.0E-06	0.04	4.2E-07	MARLBAEGRREGKEWIPVRLSGLEGEVKEWQSLQWPNPAQGTHTHETSLVGTLEHS*
HG0962.1	<i>H. sapiens</i>	ENS000000143319	ISG20L2	interferon stimulated exonuclease gene 20 like 2	0.11	0.11	4.8E-04	1.9E-03	0.11	4.8E-04	MVSRSLRGRRTVRCMRRLPPPAWSSQGMQGVSLVLLVHAADVAQRLSTPYTFLSIPRCSFRRRSIDRTCSLLDSEGSSISPTSPFLGMRLKPRAR*
HG0962.2	<i>H. sapiens</i>	ENS000000143319	ISG20L2	interferon stimulated exonuclease gene 20 like 2	0.00	0.36	5.6E-04	2.2E-03	0.36	5.6E-04	MLDSRHSRQMSPTSSFP*
HG0963	<i>H. sapiens</i>	ENS000000143667	OSR1	odd-skipped related transcription factor 1	0.13	0.49	6.2E-05	3.0E-04	0.49	6.2E-05	MSESELGLSPARSQLLLVGTQRGSRERGSPPACRIGC*
HG0964	<i>H. sapiens</i>	ENS000000145246	ATP10D	ATPase phospholipid transporting 10D (putative)	0.04	0.23	2.5E-04	1.0E-03	0.23	2.5E-04	MAGVEAQPAFTLRICA*
HG0965	<i>H. sapiens</i>	ENS000000146036	LRTM2	leucine rich repeat transmembrane neuronal 2	0.00	0.00	4.2E-07	4.3E-06	0.00	4.2E-07	MKQMLSRQSI*
HG0966	<i>H. sapiens</i>	ENS000000146335	LRSM1	leucine rich repeat and sterile alpha motif containing 1	0.05	0.43	5.4E-05	2.6E-04	0.43	5.4E-05	MFVAVGRRLRTAQCKGTAVR*
HG0967	<i>H. sapiens</i>	ENS000000149225	ALDOA	aldolase, fructose-bisphosphate A	0.11	0.49	8.3E-04	3.1E-03	0.49	8.3E-04	MUSGASGFYKYSLPEDPWKRGH*
HG0968	<i>H. sapiens</i>	ENS000000154319	FAM167A	family with sequence similarity 167 member A	0.02	0.27	3.8E-06	2.2E-05	0.32	4.8E-04	MRFSLSLQGLQPPALPEKRELWAFPLVWSSSAFRTRDPWRHLPRDSCDVCSCLLWSMPTQFGDGS*
HG0969	<i>H. sapiens</i>	ENS000000154645	CHODL	chondrolectin	0.15	0.30	4.2E-05	2.1E-04	0.30	4.2E-05	MIRAGGAGLGRRE*
HG0970	<i>H. sapiens</i>	ENS000000154727	GABPA	GA binding protein transcription factor alpha subunit	0.06	0.37	2.6E-03	8.2E-03	0.37	2.6E-03	MGRFRSRSTLTGGAEASRRGSATRGV*
HG0971	<i>H. sapiens</i>	ENS000000155592	ZKSCAN2	zinc finger with KRAB and SCAN domains 2	0.15	0.47	1.9E-03	6.2E-03	0.47	1.9E-03	MHSGKPHCAVCSLCKRPGFQILEYTFYSRAWHRFD*
HG0972	<i>H. sapiens</i>	ENS000000155926	SLA	Src like adaptor	0.27	0.42	9.4E-03	2.5E-02	0.42	9.4E-03	MKNFNRLKLLQKRFSFANGHELQRP*
HG0973	<i>H. sapiens</i>	ENS000000156535	CD109	CD109 molecule	0.16	0.24	6.9E-06	4.0E-05	0.24	6.9E-06	MFATARSAAVMGGVGEPPSPVSI*
HG0974	<i>H. sapiens</i>	ENS000000157578	LCASL	LCASL, lebercilin like	0.03	0.23	1.3E-02	3.3E-02	0.23	1.3E-02	MGTDNDHPYADHFYELQPCFCHLCKRCACTFKKKSWSYAYERGCFQLIFPKQTIIPASIGFLKYLILSKRDQNLKKYYRKGILNTTV*
HG0975.1	<i>H. sapiens</i>	ENS000000182158	CREB3L2	cAMP responsive element binding protein 3 like 2	0.02	0.38	1.4E-04	6.2E-04	0.38	1.4E-04	MIRAGLLPSFWMHPL*
HG0975.2	<i>H. sapiens</i>	ENS000000157613	CREB3L1	cAMP responsive element binding protein 3 like 1	0.19	0.00	7.0E-08	5.6E-07	0.00	7.0E-08	MEASCAPGAGGAGGGV*
HG0976	<i>H. sapiens</i>	ENS000000159036	EXTL1	exonuclease like glycosyltransferase 1	0.03	0.41	7.0E-03	1.9E-02	0.41	7.0E-03	MAISLPRCTMTAQD*
HG0977	<i>H. sapiens</i>	ENS000000158321	AUTS2	AUTS2, activator of transcription and developmental regulator	0.17	0.17	3.0E-04	1.2E-03	0.17	3.0E-04	MLPSLGLLAPLGLSLRSLQPLPWLHFKIWEPSSEFSPPRV*
HG0978	<i>H. sapiens</i>	ENS000000159023	EPB41	erythrocyte membrane protein band 4.1	0.01	0.40	2.7E-03	8.6E-03	0.40	2.7E-03	MCCHCGDGSMSGLMA*
HG0979	<i>H. sapiens</i>	ENS000000159202	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.00	0.37	1.2E-02	3.0E-02	0.37	1.2E-02	MWEVVRVSGWLFOAD*
HG0980	<i>H. sapiens</i>	ENS000000162670	BRINP3	BMP/retinoic acid inducible neural specific 3	0.00	0.16	3.8E-06	2.3E-05	0.16	3.8E-06	MIQLGTFFVCLHRFVCHAVKQVLRSE*
HG0981	<i>H. sapiens</i>	ENS000000163629	PTPN13	protein tyrosine phosphatase, non-receptor type 13	0.00	0.48	5.5E-03	1.6E-02	0.48	5.5E-03	MLTAPGDRRAGEPCSVAPRASAAVRVAYRS*
HG0982	<i>H. sapiens</i>	ENS000000164116	GUCY1A3	guanylate cyclase 1 soluble subunit alpha	0.00	0.47	3.0E-04	1.2E-03	0.47	3.0E-04	MCGFARRALELIRKHSPEVCATKHPSYQCP*
HG0983	<i>H. sapiens</i>	ENS000000164128	NPY1R	neuropeptide Y receptor Y1	0.00	0.12	8.7E-04	3.2E-03	0.12	8.7E-04	MDSNMGNKKNLS*
HG0984	<i>H. sapiens</i>	ENS000000164185	ZNF474	zinc finger protein 474	0.00	0.35	1.8E-03	5.9E-03	0.35	1.8E-03	MLKKGKRSWRHLSFNEDFPFTQTAVLQ*
HG0985	<i>H. sapiens</i>	ENS000000164604	GPR85	G protein-coupled receptor 85	0.05	0.20	8.8E-06	5.0E-05	0.20	8.8E-06	MKACLVLVLRGTQKLLKLYLHKQNSSEVMK*
HG0986	<i>H. sapiens</i>	ENS000000164663	USP49	ubiquitin specific peptidase 49	0.00	0.39	1.0E-04	4.7E-04	0.39	1.0E-04	MOVRAGRGDGNKLDEMGSKGREGAKRSWSPDGCRTGDCRQGVGIEACAYGELLQVKQVKGQGRNAVQDVQ*
HG0987	<i>H. sapiens</i>	ENS000000164932	CHTRC1	collagen triple helix repeat containing 1	0.21	0.34	6.8E-03	1.9E-02	0.34	6.8E-03	MQPAAPEGRGKARR*
HG0988	<i>H. sapiens</i>	ENS000000166130	IKBIP	IKBKB interacting protein	0.07	0.46	6.8E-04	2.5E-03	0.46	6.8E-04	MEIAAERLSAETRNMPQRKGLGSGRCQCEGARSPPRPVNTNAKAATSCPW*
HG0989	<i>H. sapiens</i>	ENS000000166603	MC4R	melanocortin 4 receptor	0.00	0.34	1.5E-02	3.7E-02	0.34	1.5E-02	MAASRKLINLECRKLKQ*
HG0990	<i>H. sapiens</i>	ENS000000166666	MYO1A	myosin 1A	0.23	0.41	5.1E-03	1.5E-02	0.41	5.1E-03	MLKGLHYTCGAWAGRGSKRENKQSGHWQEGSLFPLSLAPATAPKIPPLHPQARTLLMPSHQEISLTLQQQ*
HG0991	<i>H. sapiens</i>	ENS000000167654	ATCAY	ATCAY, catyixin	0.16	0.37	4.4E-04	1.7E-03	0.37	4.4E-04	MPSCTRAGLAFVQC*
HG0992	<i>H. sapiens</i>	ENS000000168000	BSC12	BSC12, seipin lipid droplet biogenesis associated	0.11	0.21	9.2E-05	4.2E-04	0.21	9.2E-05	MHRRYQRLDRHTF*
HG0993	<i>H. sapiens</i>	ENS000000169306	IL1RAPL1	interleukin 1 receptor accessory protein like 1	0.00	0.22	1.9E-03	6.3E-03	0.22	1.9E-03	MYSEDLQATLOFLS*
HG0994	<i>H. sapiens</i>	ENS000000170852	KBTBD2	kelch repeat and BTB domain containing 2	0.00	0.12	1.9E-07	1.4E-06	0.12	1.9E-07	MLQITASRFSISEVFT*
HG0995	<i>H. sapiens</i>	ENS000000171307	ZDHHC16	zinc finger DHHC-type containing 16	0.10	0.26	1.6E-03	5.4E-03	0.26	1.6E-03	MITADYLVLPHWQEOCPWYL*
HG0996	<i>H. sapiens</i>	ENS000000173890	GPR160	G protein-coupled receptor 160	0.00	0.46	9.1E-03	2.4E-02	0.46	9.1E-03	MKCRCELTHIAYWYKMKCKEKPIT*
HG0997	<i>H. sapiens</i>	ENS000000177728	TMEM84	transmembrane protein 84							

HG1016	<i>H. sapiens</i>	ENS000000254004	ZNF260	zinc finger protein 260	0.00	0.06	6.8E-07	4.5E-06	0.06	6.6E-07		MLHIFPHNHLISG*
HG1017	<i>H. sapiens</i>	ENS000000255154	HTD2	hydroxyacyl-thiester dehydratase type 2	0.00	0.21	2.6E-03	8.4E-03	0.21	2.6E-03		MLHSSNLSRL*
HG1018	<i>H. sapiens</i>	ENS000000259120	SMIM6	small integral membrane protein 6	0.12	0.47	1.6E-02	3.9E-02	0.47	1.6E-02		MFPLPNSOFFGSCSSGHQAASSAPQTKCEPGEPP*
HG1019	<i>H. sapiens</i>	ENS000000019995	ZNRAB1	zinc finger RANBP2-type containing 1	0.00	0.22	1.1E-03	4.0E-03	0.22	1.1E-03		MASLKLNISQIFLSSFLDQTSLYLLPSIFAQSSVLNRPV*
HG1020	<i>H. sapiens</i>	ENS000000023902	PLEKH01	pleckstrin homology domain containing O1	0.12	0.43	9.2E-03	2.4E-02	0.43	9.2E-03		MEKAGRGGAQVRCASANAREAGLE*
HG1021	<i>H. sapiens</i>	ENS000000046692	SNCAIP	synuclein alpha interacting protein	0.03	0.43	4.1E-04	1.6E-03	0.43	4.1E-04		MPTFRSPPSRVSSPLCWNQWGMWGMWRQRLTSLSRN*
HG1022	<i>H. sapiens</i>	ENS000000065357	DGKA	diacylglycerol kinase alpha	0.06	0.47	3.2E-04	1.3E-03	0.47	7.0E-03		MPGSPVASESLGLHLSPLLYHLHHPCDKPLNSDRSDRQGLKGFPTFYFWPGSPVPKATSRYNFKSHSGIRAKNGTOI*
HG1023	<i>H. sapiens</i>	ENS000000068001	HYAL2	hyaluronoglucosaminidase 2	0.01	0.45	1.3E-02	3.3E-02	0.45	1.3E-02		MGGHVLQRTYWGSSSPKRGKTGEKVELPVGK*
HG1024	<i>H. sapiens</i>	ENS000000073464	CLCN4	chloride voltage-gated channel 4	0.01	0.43	3.9E-03	1.2E-02	0.43	3.9E-03		MSLSVSASIRPTQSRRRFR*
HG1025	<i>H. sapiens</i>	ENS000000074621	SLC24A1	solute carrier family 24 member 1	0.00	0.36	1.5E-02	3.7E-02	0.36	1.5E-02	Crowe	MSRSEGLVWPGWASWRLL*
HG1026.1	<i>H. sapiens</i>	ENS000000075035	WSCD2	WSC domain containing 2	0.00	0.12	2.6E-03	8.2E-03	0.12	2.6E-03		MCVLSKTPLLAQRSSPSVWEGW*
HG1026.2	<i>H. sapiens</i>	ENS000000179314	WSCD1	WSC domain containing 1	0.00	0.32	1.5E-02	3.6E-02	0.32	1.5E-02		MTPPEALASLPPGR*
HG1026.3	<i>H. sapiens</i>	ENS000000179314	WSCD1	WSC domain containing 1	0.00	0.11	2.2E-04	9.4E-04	0.11	2.2E-04		MVFPFHLLETGGEQ*
HG1027	<i>H. sapiens</i>	ENS000000075223	SEMA3C	semaphorin 3C	0.04	0.16	2.1E-03	6.7E-03	0.16	2.1E-03		MKACRAANBQSSRRAPRCNRTPRALAPGLRPLSHSEVLD*
HG1028	<i>H. sapiens</i>	ENS000000076356	PLXNA2	plexin A2	0.05	0.06	1.0E-02	2.7E-02	0.06	1.0E-02		MNDSMMHWHS*
HG1029	<i>H. sapiens</i>	ENS000000079492	OPHN1	oligophrenin 1	0.06	0.46	1.0E-02	2.7E-02	0.46	1.0E-02		MERGYSVLPWWLNPSPA*
HG1030	<i>H. sapiens</i>	ENS000000082175	PGR	progesterone receptor	0.09	0.10	2.3E-04	9.8E-04	0.13	3.3E-03		MRTSFTHLSYEINPRLLYPHYWDLRSEEMTARSTPAEVRPFLMGCTGERSD*
HG1031	<i>H. sapiens</i>	ENS000000082269	FAM135A	family with sequence similarity 135 member A	0.00	0.33	2.6E-03	8.3E-03	0.33	2.6E-03		MLAGRAGPVAEPK*
HG1032	<i>H. sapiens</i>	ENS000000084453	SLCO1A2	solute carrier organic anion transporter family member 1A2	0.00	0.13	1.4E-02	3.4E-02	0.13	4.1E-02		MQPSPEKLNRPKTYINKDSFYNSALMNKKLQTLRLCHTGYSCFNKLLVLQYGSKNW*
HG1033	<i>H. sapiens</i>	ENS000000089225	TBX5	T-box 5	0.04	0.21	1.2E-03	4.1E-03	0.21	1.2E-03		MPAPPHPHRLPC*
HG1034	<i>H. sapiens</i>	ENS000000090487	SPG21	SPG21, maspardin	0.00	0.19	3.3E-05	1.7E-04	0.19	3.3E-05		MQHLVSLPFWYQTSVTGKTLXKVLTAEWNLIL*
HG1035	<i>H. sapiens</i>	ENS000000093000	NUP50	nucleoporin 50	0.11	0.30	1.8E-03	6.1E-03	0.30	1.8E-03		MAARSVFGAVPAAVSG*
HG1036	<i>H. sapiens</i>	ENS000000100813	ACIN1	apoptotic chromatin condensation inducer 1	0.02	0.44	8.7E-03	2.3E-02	0.44	8.7E-03		MVPGSRSEYVRFKASARRRKPSLKAGREKCRACRQDN*
HG1037	<i>H. sapiens</i>	ENS000000102710	SPT20H	SPT20 homolog, SAGA complex component	0.00	0.00	1.2E-04	5.6E-04	0.00	1.2E-04		MVFTPLHQRT*
HG1038	<i>H. sapiens</i>	ENS000000104331	IMPAD1	inositol monophosphatase domain containing 1	0.21	0.10	9.8E-05	4.5E-04	0.10	9.8E-05	Mackowiak	MKRTGAGERAPV*
HG1039	<i>H. sapiens</i>	ENS000000104804	TULIP2	tulip-like protein 2	0.01	0.01	4.6E-05	2.3E-04	0.01	4.6E-05		MFRDMPERQGTGASM*
HG1040	<i>H. sapiens</i>	ENS000000105223	PLD3	phospholipase D family member 3	0.00	0.24	5.1E-04	2.0E-03	0.24	5.1E-04		MKRXHAWPPFACSLAVRLRAARGRGAQGGPGR*
HG1041	<i>H. sapiens</i>	ENS000000106536	POU6F2	POU class 6 homeobox 2	0.16	0.20	6.5E-03	1.8E-02	0.20	6.5E-03		MNLSGLCYVPVCCLLSRC*
HG1042	<i>H. sapiens</i>	ENS000000107249	GLIS3	GLIS family zinc finger 3	0.00	0.13	2.3E-03	7.3E-03	0.13	2.3E-03		MNRTGEAQSDN*
HG1043	<i>H. sapiens</i>	ENS000000107736	CDH23	cadherin related 23	0.24	0.42	5.2E-03	1.5E-02	0.42	5.2E-03		MERGVAEPLDVWGAQSPSPRRA*
HG1044	<i>H. sapiens</i>	ENS000000109381	ELF2	EF1-like ETS transcription factor 2	0.00	0.11	2.4E-03	7.7E-03	0.11	2.4E-03		MMQTYNTNGHQ*
HG1045	<i>H. sapiens</i>	ENS000000110925	CSRNP2	cysteine and serine rich nuclear protein 2	0.00	0.27	3.1E-03	9.6E-03	0.27	3.1E-03		MGGLEACRIADE*
HG1046	<i>H. sapiens</i>	ENS000000112701	SENPE	SUMO1/centrin specific peptidase 6	0.15	0.00	5.5E-03	1.6E-02	0.00	5.5E-03		MHSRLGGVGGPR*
HG1047	<i>H. sapiens</i>	ENS000000112769	LAMA4	laminin subunit alpha 4	0.11	0.46	2.0E-02	4.6E-02	0.46	2.0E-02		MNVRRKPGQRSPQSRATERRRWPASGAHPNPSAF*
HG1048	<i>H. sapiens</i>	ENS000000115295	CLIP4	CAP-Gly domain containing linker protein family member 4	0.00	0.30	3.4E-03	1.0E-02	0.30	3.4E-03		MKTPSBMHSQPTR*
HG1049	<i>H. sapiens</i>	ENS000000116212			0.00	0.39	2.7E-03	8.4E-03	0.39	2.7E-03		MPRKELEWSNAALNLSGSATY*
HG1050	<i>H. sapiens</i>	ENS000000116489	CAPZA1	capping actin protein of muscle Z-line alpha subunit 1	0.00	0.13	9.0E-04	3.3E-03	0.13	9.0E-04		MQNECNSGLHLDLFRSPKANP*TSWAGAGAGVRRHRSRA*
HG1051	<i>H. sapiens</i>	ENS000000116882	PIF1B	kinesin family member 21B	0.02	0.22	6.3E-05	3.0E-04	0.22	6.3E-05		MARGCARADPRRAGK*
HG1052	<i>H. sapiens</i>	ENS000000116840	VAMP9	vesicle associated membrane protein 9	0.09	0.141	3.9E-03	1.1E-02	0.141	3.9E-03		MKRGQGAQESWHSQEVN*
HG1053	<i>H. sapiens</i>	ENS000000119522	DENND1A	DENN domain containing 1A	0.02	0.00	4.4E-03	1.3E-02	0.00	4.4E-03		MAFAGLERYH*
HG1054	<i>H. sapiens</i>	ENS000000120832	MTERF2	mitochondrial transcription termination factor 2	0.02	0.19	1.7E-03	5.7E-03	0.19	1.7E-03		MGEOTDGLVAAENCRELLETEDNRNPGSRPRGLRTVRLAGERGKDGAWPPQLVPVPCLELTPTYCRELTRSHFEKKLERPSGI*
HG1055	<i>H. sapiens</i>	ENS000000122299	ZC3H7A	zinc finger CCHC-type containing 7A	0.01	0.14	5.9E-04	2.2E-03	0.14	5.9E-04		MSLHLESQGVG*
HG1056	<i>H. sapiens</i>	ENS000000128271	ADORA2A	adenosine A2a receptor	0.00	0.38	4.7E-04	1.8E-03	0.38	4.7E-04		MMLPEPLORAWFQETQSL*
HG1057	<i>H. sapiens</i>	ENS000000131097	HIGD1B	HIG1 hypoxia inducible domain family member 1B	0.11	0.40	2.2E-03	7.2E-03	0.40	2.2E-03		MAQPPMGLVGGTSPQVEAVLGHGERS*
HG1058	<i>H. sapiens</i>	ENS000000131386	GALNT15	polypeptide N-acetylglucosaminyltransferase 15	0.00	0.43	1.2E-03	4.3E-03	0.43	1.2E-03		MESLFSQSGENRGKRGAEQFVFNGLSEGN*
HG1059.1	<i>H. sapiens</i>	ENS000000132970	WASF3	WAS protein family member 3	0.00	0.00	3.3E-05	1.7E-04	0.00	3.3E-05		MLLEGNFCNP*
HG1059.2	<i>H. sapiens</i>	ENS000000112290	WASF1	WAS protein family member 1	0.20	0.05	1.5E-02	3.7E-02	0.05	1.5E-02		MMNWNNDERHIRSHSRPLV*
HG1060	<i>H. sapiens</i>	ENS000000134242	PTPN22	protein tyrosine phosphatase, non-receptor type 22	0.00	0.37	1.7E-03	5.6E-03	0.37	1.7E-03		MLCSGSSGFLVESRPA*
HG1061	<i>H. sapiens</i>	ENS000000134802	SLCA3A3	solute carrier family 43 member 3	0.00	0.02	1.1E-05	6.2E-05	0.02	1.1E-05		MCCLCVLWLVGVTSLGDGQIGNSAGAPALHLLPGSYWDFENPLMVFAQA*
HG1062	<i>H. sapiens</i>	ENS000000137337	MDC1	mediator of DNA damage checkpoint 1	0.26	0.41	7.9E-04	2.9E-03	0.41	7.9E-04		MSCTRPLGLGPRRGAALJALDPTSDVYDTAPLVSWSWRGTLWSRFATREVGGRASGSLSLGAAGQSTCILLAHGGLQLPSH*
HG1063	<i>H. sapiens</i>	ENS000000138162	TACD3	transforming acidic coiled-coil containing protein 2	0.02	0.15	1.3E-02	3.3E-02	0.15	1.3E-02		MELCEDGVQVAAIR*
HG1064	<i>H. sapiens</i>	ENS000000139734	DIAPH3	diaphanous related form 3	0.14	0.21	7.1E-05	3.4E-04	0.21	7.1E-05		MCKLRLPRQLQ*
HG1065	<i>H. sapiens</i>	ENS000000140030	GPCR65	G protein-coupled receptor 65	0.00	0.10	5.1E-04	2.0E-03	0.16	2.7E-03		MQAQYQAPQSTNTPSEEMKERNFKRYGSLCKSLGVSYLGHSTVYRMKNNRLTLYVHQLMPLMLVGLSAFCNDHMFDFLLNSVDFPSQLGAWFTSNC*
HG1066	<i>H. sapiens</i>	ENS000000140533	UNC45A	unc-45 myosin chaperone A	0.26	0.32	1.2E-05	6.5E-05	0.32	1.2E-05		MQGRSRSLGLTGLSVLLGLLFSWTLVQPTLSALVHPHLCOITRDVHGRHYGPFRLRSDSPEEYACCHLQAAGSGCCTRAEYQVNLNLSAPPILRPGRLVLVGLYNLLVTLMTVDLVHFCGGRGRSLGWSHRRPPSGSSAASSLQVYAGTA*
HG1067	<i>H. sapiens</i>	ENS000000143340	FAM163A	family with sequence similarity 163 member A	0.04	0.35	1.4E-12	2.0E-11	0.35	1.4E-12		MRLHRSRAVLGAGPRRSLTCAAPAGAKRALKRPRGSRTRTESPERSCSAAGMLPARRTPNCCLLRCSRD*
HG1068	<i>H. sapiens</i>	ENS000000144791	LIMD1	LIM domains containing 1	0.00	0.33	9.4E-04	3.4E-03	0.33	9.4E-04		MFPTLGRWKLVLVLRGT*
HG1069	<i>H. sapiens</i>	ENS000000146414	SHPRH	SNF2 histone linker PHD RING helicase	0.21	0.19	2.7E-03	8.6E-03	0.19	2.7E-03		MFGGWMMRARDLLGL*
HG1070	<i>H. sapiens</i>	ENS000000147459	DOCK5	dedicator of cytokinesis 5	0.25	0.42	7.3E-03	2.0E-02	0.42	7.3E-03		MAEASGARRSAGRRRPEPEL*
HG1071	<i>H. sapiens</i>	ENS000000147573	TRIM55	tripartite motif containing 55	0.00	0.22	4.4E-04	1.7E-03	0.22	4.4E-04		MDTSARHHVTAGC*
HG1072	<i>H. sapiens</i>	ENS000000147874	HAUS6	HAUS augmin like complex subunit 6	0.15	0.25	1.4E-04	6.0E-04	0.25	1.4E-04		MEGPPRPQADRRREG*
HG1073	<i>H. sapiens</i>	ENS000000149187	CELP1	CUGBP Elav-like family member 1	0.09	0.33	1.7E-02	4.1E-02	0.33	1.7E-02		MKRGKDVICWRNLTUEAASSVAWVYGRVLYCDYTLMSYSGESRLDFCTLGVGFGLFV*
HG1074	<i>H. sapiens</i>	ENS000000150275	PCP1H15	proboscoidien related 15	0.00	0.41	8.8E-03	2.3E-02	0.41	8.8E-03		MNVDMHAKQDEVHNESSWV*
HG1075	<i>H. sapiens</i>	ENS000000150347	ARID5B	AT-rich interaction domain 5B	0.00	0.00	1.0E-02	2.6E-02	0.00	1.0E-02		MNSNAGAGGLL*
HG1076	<i>H. sapiens</i>	ENS000000150967	ABC9	ATP binding cassette subfamily B member 9	0.05	0.17	9.1E-04	3.3E-03	0.17	9.1E-04		MSAEATAPOTRACCAPPPHRLVPGNRPGLAWMMMLFP*
HG1077	<i>H. sapiens</i>	ENS000000151474	FRMD4A	FERM domain containing 4A	0.28	0.48	2.9E-03	8.9E-03	0.48	2.8E-03		MFLSMLALPQAEALSLGEEK*
HG1078	<i>H. sapiens</i>	ENS000000162607	USP1	ubiquitin specific peptidase 1	0.00	0.38	2.0E-03	6.7E-03	0.38	2.0E-03		MRAEGQAPRLRNTYVNW*
HG1079	<i>H. sapiens</i>	ENS000000162975	KCNF1	potassium voltage-gated channel modifier subfamily F member 1	0.29	0.37	2.6E-04	1.1E-03	0.37	2.6E-04	Crowe	MPAPSPAAQCMPPPRPAFAGCCPL*
HG1080	<i>H. sapiens</i>	ENS000000164168	TMEM184C	transmembrane protein 184C	0.03	0.04	3.8E-05	1.9E-04	0.04	3.8E-05	Mackowiak	MVQAEALRAIP*
HG1081	<i>H. sapiens</i>	ENS000000165392	WRN	Werner syndrome RecQ like helicase	0.01	0.45	4.2E-03	1.3E-02	0.45	4.2E-03		MPLGLQALLVAHSHPAEEDLDWIFSGFLSDVLYPMKTLFFGLCK*
HG1082	<i>H. sapiens</i>	ENS000000165434	PGM2L1	phosphoglucomutase 2 like 1	0.03	0.27	1.1E-02	2.8E-02	0.27	1.1E-02		MPFSEVGTGPWP*
HG1083	<i>H. sapiens</i>	ENS000000165804	ZNF219	zinc finger protein 219	0.00	0.14	2.6E-03	8.4E-03	0.14	2.6E-03		MSVRRTAIPGTM*
HG1084	<i>H. sapiens</i>	ENS000000165923	AGBL2	ATP/GTP binding protein like 2	0.13	0.08	1.2E-04	5.4E-04	0.08	1.2E-04		MGPAPWEEAGRYAALPVADAPLAA*
HG1085	<i>H. sapiens</i>	ENS000000166532	RIMB2	ribosomal modification protein rimb like family member B	0.03	0.33	3.2E-04	1.3E-03	0.43	6.7E-03		MNTSRVWGLRVYAAALFRNNWNGAFEN*
HG1086	<i>H. sapiens</i>	ENS000000167377	ZNF23	zinc finger protein 23	0.10	0.465	1.9E-02	5.8E-02	0.45	1.9E-02		MNLSRNNLQASQRYVYVCSQAPDGS*
HG1087	<i>H. sapiens</i>	ENS000000168675	DLRAD4	low density lipoprotein receptor class A domain containing 4	0.00	0.27	3.9E-04	1.5E-03	0.27	3.9E-04		MLPEAGAEWYNTG*
HG1088	<i>H. sapiens</i>	ENS000000169740	ZNF32	zinc finger protein 32	0.02	0.37	5.7E-05	2.8E-04	0.37	5.7E-05		MSRPGRPGPRPFAASGEVGGPQSRVYVNTQERDAELVNSPWNHMKRW*
HG1089	<i>H. sapiens</i>	ENS000000169813	HNRNP2	heterogeneous nuclear ribonucleoprotein F	0.00	0.12	1.2E-02	3.1E-02	0.12	1.2E-02		MHLEFPSPSLRG*
HG1090.1	<i>H. sapiens</i>	ENS000000170458	CD14	CD14 molecule	0.09	0.10	1.9E-03	6.3E-03	0.10	1.9E-03		MPCRILPVTLPLTSPFAIPFGKEGWLGRGVR*
HG1090.2	<i>H. sapiens</i>	ENS000000170458	CD14	CD14 molecule	0.05	0.37	1.1E-02	2.7E-02	0.37	1.1E-02		MKFTISTTHAKVYLRFDRDLVAGDQGHKPRGQSRQSNRESSRFSGI*
HG1091	<i>H. sapiens</i>	ENS000000172183	ISG20	interferon stimulated exonuclease gene 20	0.06	0.32	7.7E-05	3.6E-04	0.32	7.7E-05		MRLHRRGAGAKEHPDMEPASSVSPDSARS*
HG1092	<i>H. sapiens</i>	ENS000000173327	MAP3K11									

HG1115	<i>H. sapiens</i>	ENS00000074219	TEAD2	TEA domain transcription factor 2	0.28	0.24	2.9E-03	9.2E-03	0.24	2.9E-03		IAGRPPCPACGSGVLGWSRPLQLP*
HG1116	<i>H. sapiens</i>	ENS00000040490	STARD7	SAR related lipid transfer domain containing 7	0.18	0.37	5.9E-03	1.7E-02	0.37	5.9E-03		MSGGWRPWRPQVHSGWPAI*
HG1117	<i>H. sapiens</i>	ENS00000008902	RCOR1	REST corepressor 1	0.05	0.29	8.8E-03	2.3E-02	0.29	8.8E-03		MRKAVLGSGLG*
HG1118	<i>H. sapiens</i>	ENS00000009075	PITPNM2	phosphatidylinositol transfer protein membrane associated	0.24	0.38	3.4E-03	1.1E-02	0.38	3.4E-03		ME5MVPPTQLYSMLFPESPHTLLSF*
HG1119	<i>H. sapiens</i>	ENS00000009200	PPP2R3C	protein phosphatase 2 regulatory subunit B"gamma	0.00	0.26	2.3E-04	9.9E-04	0.39	2.8E-02		MKRNCERRRPQAGTNELGHVVVTRTORHTIKENAGLSWPLKSLPLRPPSKMVVGRPS*
HG1120	<i>H. sapiens</i>	ENS00000009585	BLNK	B-cell linker	0.02	0.00	7.3E-03	2.0E-02	0.00	7.3E-03		MLLPRRRANC*
HG1121	<i>H. sapiens</i>	ENS00000010030	FOXRED2	FAD dependent oxidoreductase domain containing 2	0.00	0.35	2.4E-03	7.6E-03	0.35	2.4E-03		MEGLGIPGSPKSOLETVESQMSSEDFGAWP*
HG1122	<i>H. sapiens</i>	ENS000000100410	PHF5A	PHD finger protein 5A	0.04	0.21	5.8E-03	1.6E-02	0.21	5.8E-03		MGVKRGTEVPKASGGRSL*
HG1123	<i>H. sapiens</i>	ENS000000100884	CPN6E	copine 6	0.00	0.25	1.3E-02	3.2E-02	0.25	1.3E-02		MCEPVSRGCMCRHFFSV*
HG1124	<i>H. sapiens</i>	ENS000000100934	SEC23A	Sec23 homolog A, coat complex II component	0.00	0.38	1.5E-02	3.6E-02	0.38	1.5E-02		MLAGRSSSLRPGAGWRHP*
HG1125	<i>H. sapiens</i>	ENS000000101574	METTL4	methyltransferase like 4	0.01	0.19	5.4E-05	2.6E-04	0.21	2.5E-03		MNDKFSMCMGCTCISNL5VCKMCMFIEQDI*
HG1126	<i>H. sapiens</i>	ENS000000101890	GUCY2F	guanylate cyclase 2F, retinal	0.00	0.22	1.0E-02	2.7E-02	0.22	1.0E-02		MEFVNRLESLTG*
HG1127	<i>H. sapiens</i>	ENS000000103064	SLC7A6	solute carrier family 7 member 6	0.04	0.15	2.1E-03	6.8E-03	0.15	2.1E-03		MCGRQSGAGAGQPSRVGAEGPCGSSLSPGAGCGPETARGWPGIAAREALRSLCGRGRQVELGAAGDFISFVLDPFMRRLWMKV*
HG1128	<i>H. sapiens</i>	ENS000000103852	ITTC23	tetratricopeptide repeat domain 23	0.00	0.05	1.9E-02	4.8E-02	0.05	1.9E-02		MRNLNWKESNP*
HG1129	<i>H. sapiens</i>	ENS000000104432	L7	interleukin 7	0.00	0.00	7.3E-03	2.0E-02	0.00	7.3E-03		MLMIPKEFPADDAQBRN*
HG1130	<i>H. sapiens</i>	ENS000000105559	PLEKHA4	pleckstrin homology domain containing A4	0.02	0.17	6.5E-03	1.8E-02	0.17	6.5E-03		M5ERETGRDRDRETKQVRVGREVV*
HG1131	<i>H. sapiens</i>	ENS000000106780	MEGF9	multiple EGF like domains 9	0.05	0.50	1.8E-02	4.3E-02	0.50	1.8E-02		MVRPVAAVAASVLGRQGEDD*
HG1132	<i>H. sapiens</i>	ENS000000109771	LRP2BP	LRP2 binding protein	0.00	0.25	3.7E-03	1.1E-02	0.25	3.7E-03		MKTLVHSTVHLITWQSDNRDKLNNS*
HG1133	<i>H. sapiens</i>	ENS000000111328	CDK2AP1	cyclin dependent kinase 2 associated protein 1	0.09	0.37	1.8E-02	4.2E-02	0.37	1.8E-02		MSSIGVSNPGAWPDLGVWNDLR*
HG1134	<i>H. sapiens</i>	ENS000000112984	KIF20A	kinesin family member 20A	0.00	0.10	6.2E-54	3.6E-52	0.10	6.2E-54		MSFFPLRQSKHPKPVTLCTPVKIVAKEGQELAAEASRPLGS*
HG1135	<i>H. sapiens</i>	ENS000000113597	TRAPPC13	trafficking protein particle complex 13	0.00	0.06	1.4E-03	4.7E-03	0.06	1.4E-03		MENKVFYAYVSKIEEMDLKRSQFVKDVTGEFVPPPERG*
HG1136	<i>H. sapiens</i>	ENS000000113749	HRH2	histamine receptor H2	0.00	0.32	1.1E-02	2.8E-02	0.32	1.1E-02		MGAGTVSYGEYCSCVST*
HG1137	<i>H. sapiens</i>	ENS000000115307	AUP1	ancient ubiquituous protein 1	0.22	0.31	9.6E-03	2.5E-02	0.31	9.6E-03		MPGIVVSAGREL*
HG1138	<i>H. sapiens</i>	ENS000000116871	MAP7D1	MAP7 domain containing 1	0.16	0.17	2.8E-03	8.8E-03	0.17	2.8E-03		MRRGTVPLATGRRRRRR*
HG1139	<i>H. sapiens</i>	ENS000000118308	LIMP	lymphoid restricted membrane protein	0.19	0.44	1.2E-02	3.0E-02	0.44	1.2E-02		MQTONCRSSSGEAYHFPEKNNFTSVLPAS*
HG1140	<i>H. sapiens</i>	ENS000000118328	LIMP	lymphoid restricted membrane protein	0.00	0.00	1.4E-03	6.1E-03	0.00	1.4E-03		MKEATLQKEA*
HG1140	<i>H. sapiens</i>	ENS000000118405	PLAGL1	PLAGL1 like zinc finger 1	0.00	0.16	2.8E-03	8.8E-03	0.16	2.8E-03		MLPLRWSVGQQLG*
HG1141	<i>H. sapiens</i>	ENS000000121964	GTOC1	glycosyltransferase like domain containing 1	0.00	0.23	3.3E-03	1.0E-02	0.23	3.3E-03		MHREPKSYTEHWWSLH*
HG1142	<i>H. sapiens</i>	ENS000000124613	ZNF391	zinc finger protein 391	0.18	0.37	1.2E-02	2.9E-02	0.37	1.2E-02		MLDLOEAEAGSAQKYL*
HG1143	<i>H. sapiens</i>	ENS000000125245	GPR18	G protein-coupled receptor 18	0.00	0.24	1.2E-02	3.0E-02	0.24	1.2E-02		MPSFGGELMSVTS*
HG1144	<i>H. sapiens</i>	ENS000000128203	ASPHD2	aspartate beta-hydroxylase domain containing 2	0.27	0.00	2.3E-03	7.4E-03	0.00	2.3E-03		MPPPPAAPSPPPR*
HG1145	<i>H. sapiens</i>	ENS000000128585	MKLN1	muskelin 1	0.27	0.04	7.1E-03	2.0E-02	0.04	7.1E-03		MLENMGIGIRFWRNVN*
HG1146	<i>H. sapiens</i>	ENS000000130413	STK33	serine/threonine kinase 33	0.02	0.15	4.5E-03	1.3E-02	0.15	4.5E-03		MVISFLSAALTCEYVSASLT*
HG1147	<i>H. sapiens</i>	ENS000000131781	FM05	flavin containing monooxygenase 5	0.00	0.33	1.7E-02	4.1E-02	0.33	1.7E-02		MPRRPSLKNVNRCLVFCVCHPFRTGDTNR*
HG1148	<i>H. sapiens</i>	ENS000000132938	MTUS2	microtubule associated scaffold protein 2	0.00	0.41	1.8E-02	4.3E-02	0.41	1.8E-02		MAVKLIFWGISHGLGSHSAGI*
HG1149	<i>H. sapiens</i>	ENS000000132975	GPR12	G protein-coupled receptor 12	0.00	0.00	2.9E-03	9.1E-03	0.00	2.9E-03		MLDCHPAVFH*
HG1150	<i>H. sapiens</i>	ENS000000135299	ANKRD6	ankyrin repeat domain 6	0.01	0.37	1.8E-02	3.8E-02	0.37	1.8E-02		MQTSFLCHLSVQKGSDDL*
HG1151	<i>H. sapiens</i>	ENS000000137168	PRL1	peptidylprolyl isomerase like 1	0.04	0.46	4.1E-03	1.2E-02	0.46	4.1E-03		MKFAFSVSLRPSFSSTPSPASRHHWKGPSSLSWPPKSWYRKG*
HG1152	<i>H. sapiens</i>	ENS000000138358	ZGRF1	zinc finger GRF-type containing 1	0.01	0.41	1.8E-02	3.8E-02	0.41	1.8E-02		MTSRCFAGEIRHILCNLTGGNS*
HG1153	<i>H. sapiens</i>	ENS000000138738	PRDM5	PRDM5 domain 5	0.16	0.05	2.3E-03	7.4E-03	0.05	2.3E-03		MCLRPLGAKRR*
HG1154	<i>H. sapiens</i>	ENS000000139725	RHOF	ras homolog family member F, filopodia associated	0.00	0.21	8.9E-03	2.4E-02	0.21	8.9E-03		MAKPKDSOLEDWRRFLKFIWIFYDLESIFYLN*
HG1155	<i>H. sapiens</i>	ENS000000141668	CBLN2	cerebellin 2 precursor	0.08	0.27	7.4E-03	2.0E-02	0.27	7.4E-03		MKVVTFPNFKTWRELKGEKESKRREATGAFKGV*
HG1156	<i>H. sapiens</i>	ENS000000144741	SLC25A26	solute carrier family 25 member 26	0.18	0.18	8.8E-03	2.3E-02	0.18	8.8E-03		MAAPSARGDRPLLLRLG*
HG1157	<i>H. sapiens</i>	ENS000000148123	PLPPR1	phospholipid phosphatase related 1	0.03	0.15	1.4E-02	3.4E-02	0.15	1.4E-02		MYLAPSGRTAQ*
HG1158	<i>H. sapiens</i>	ENS000000149571	KIRREL3	kin of IRRE like 3 (Drosophila)	0.00	0.24	3.1E-03	9.6E-03	0.24	3.1E-03		MVGANPRGPAEAERHPPRRKN*
HG1159	<i>H. sapiens</i>	ENS000000152822	GRM1	glutamate metabotropic receptor 1	0.00	0.26	6.2E-03	1.8E-02	0.26	6.2E-03		MSKQTOHLAHRCDQHDHCTLDQFTLMHYR*
HG1160	<i>H. sapiens</i>	ENS000000154162	CDH12	cadherin 12	0.29	0.15	1.6E-02	3.9E-02	0.15	1.6E-02		MMCORHAVFCFEGEMGTGNPGPLARRSPLQSSSRSESDILKCKCGGSHRGSLR*
HG1161	<i>H. sapiens</i>	ENS000000154227	CERS3	ceramide synthase 3	0.13	0.35	1.4E-02	3.5E-02	0.35	1.4E-02		MHRCGDPPGLADPPRRPTEEVYKQEATSHOEPEAGI*
HG1162	<i>H. sapiens</i>	ENS000000155380	SLC16A1	solute carrier family 16 member 1	0.00	0.22	7.6E-03	2.1E-02	0.22	7.6E-03		MQVFCSKYLDLTGLEFIYT*
HG1163	<i>H. sapiens</i>	ENS000000157637	SLC38A10	solute carrier family 38 member 10	0.01	0.08	2.3E-03	7.6E-03	0.08	2.3E-03		MLARRPRLUASASQ*
HG1164	<i>H. sapiens</i>	ENS000000162630	HENMT1	HEN1 methyltransferase homolog 1	0.20	0.29	8.7E-03	2.3E-02	0.29	8.7E-03		MASGHAPORPLRDAKPTPWN*
HG1165	<i>H. sapiens</i>	ENS000000162694	EXTL2	extensin like glycosyltransferase 2	0.05	0.08	2.2E-03	7.2E-03	0.08	2.2E-03		MESPLTPRPPTTSVPGCMGSSACPAISSQALNPGVVDISD*
HG1166	<i>H. sapiens</i>	ENS000000165071	TMEM71	transmembrane protein 71	0.02	0.28	8.4E-03	2.3E-02	0.28	8.4E-03		MGCVCIEKEASYSNFVLCOLEEAGNSLWKEHRCIEV*
HG1167	<i>H. sapiens</i>	ENS000000165934	CPSF2	cleavage and polyadenylation specific factor 2	0.00	0.08	8.6E-03	2.3E-02	0.08	8.6E-03		MGFKLPAVLRPNINKELFRIPGVSSYIRLYRLQPL*
HG1168	<i>H. sapiens</i>	ENS000000166669	ATF7IP2	activating transcription factor 7 interacting protein 2	0.00	0.36	1.5E-02	3.8E-02	0.36	1.5E-02		MTCDITICKTNGEDQDKDLYHRKAENAKMKHLEGLTLNSAFVNLICRVYQTTS*
HG1169	<i>H. sapiens</i>	ENS000000167637	ZNF283	zinc finger protein 283	0.08	0.33	3.5E-03	1.1E-02	0.33	3.5E-03		MTARKKSMLSMIMNVSSKKDNFRSGSVRGTSGCQDLMGKF*
HG1170	<i>H. sapiens</i>	ENS000000167858	TEKT1	tektin 1	0.19	0.37	1.4E-02	3.4E-02	0.37	1.4E-02		METALFTSLFCXSWKLQGL*
HG1171	<i>H. sapiens</i>	ENS000000167968	DNASE1L2	deoxyribonuclease 1 like 2	0.06	0.15	1.5E-03	5.0E-03	0.15	1.5E-03		MLRGREGCWSYLRCLAFPEGILLREAESRRPN*
HG1172	<i>H. sapiens</i>	ENS000000170381	SEMA3E	semaphorin 3E	0.00	0.04	7.2E-03	2.0E-02	0.04	7.2E-03		MNSFAQVTEKYSFFLNPLA*
HG1173	<i>H. sapiens</i>	ENS000000170464	DNAJC18	DnaJ heat shock protein family (Hsp40) member C18	0.24	0.37	1.0E-02	2.6E-02	0.37	1.0E-02		MGGHNLHIGHORTDLSTISKNPLQFNM*
HG1174	<i>H. sapiens</i>	ENS000000173918	C1QTNF1	C1q and TNF related 1	0.30	0.43	2.3E-147	3.4E-145	0.43	2.3E-147		MGGHSRQGGKPRFRFWSQRPRRRRGGGAVGGDWLLVPPPTLLFCTAVLRKTFSPALFSPSLCIAPDLAGRRLGRREM*
HG1175	<i>H. sapiens</i>	ENS000000174473	GALNTL6	polypeptide N-acetylgalactosaminyltransferase-like 6	0.00	0.12	2.2E-03	7.0E-03	0.12	2.2E-03		MLVLRWSVARNKEV*
HG1176	<i>H. sapiens</i>	ENS000000176472	ZNF575	zinc finger protein 575	0.00	0.02	5.4E-03	1.6E-02	0.02	5.4E-03		MKNRQKKGAVDASMN*
HG1177	<i>H. sapiens</i>	ENS000000178295	GEN1	GEN1, Holliday junction 5' flap endonuclease	0.03	0.38	9.7E-03	2.5E-02	0.38	9.7E-03		MTKGLPLEPRRKGCPVCF*
HG1178	<i>H. sapiens</i>	ENS000000182670	TYTC3	tetratricopeptide repeat domain 3	0.00	0.01	7.6E-03	2.1E-02	0.01	7.6E-03		MCMRNITCTSNL*
HG1179	<i>H. sapiens</i>	ENS000000185933	CALHM1	calcium homeostasis modulator 1	0.28	0.36	1.6E-02	3.9E-02	0.36	1.6E-02		MRWAPSGGGGGQGPWSWRQ*
HG1180	<i>H. sapiens</i>	ENS000000188674			0.19	0.28	4.2E-03	1.3E-02	0.28	4.2E-03	Mackowiak	MLQHASRSRERTKALEPVSGL*
HG1181	<i>H. sapiens</i>	ENS000000189058	APOD	apolipoprotein D	0.00	0.43	1.2E-02	3.1E-02	0.43	1.2E-02		MDTTSHLCSIQTKLLGQPS*
HG1182	<i>H. sapiens</i>	ENS000000196155	PLEKHG4	pleckstrin homology and RhoGEF domain containing G4	0.00	0.00	7.2E-03	2.0E-02	0.00	7.2E-03		MEQDNSKAPLWQDILLMKAPR*
HG1183	<i>H. sapiens</i>	ENS000000198133	TMEM229B	transmembrane protein 229B	0.00	0.16	1.5E-02	3.7E-02	0.16	1.5E-02		MKVACRDGCKCLLRDTWKLPAQPRIS*
HG1184	<i>H. sapiens</i>	ENS000000198894	CIPC	CLOCK interacting pacemaker	0.01	0.16	1.4E-02	3.5E-02	0.16	1.4E-02		MGRNAVQMKRVPMNLPAAE*
HG1185	<i>H. sapiens</i>	ENS000000198920	KIAA0753	KIAA0753	0.00	0.11	2.1E-03	6.8E-03	0.11	2.1E-03		MCLLPFAFFMCATALEIRTLRLSLSCSVEVSFKQI*
HG1186	<i>H. sapiens</i>	ENS000000204923			0.00	0.21	6.5E-03	1.8E-02	0.21	6.5E-03		MGAIVVLASPKT*
HG1187	<i>H. sapiens</i>	ENS000000213782	ZNF134	zinc finger protein 134	0.29	0.01	3.7E-03	1.1E-02	0.01	3.7E-03		MAAAWMPDQILQCG*
HG1188	<i>H. sapiens</i>	ENS000000214415	GNAT3	G protein subunit alpha transducin 3	0.04	0.22	4.5E-03	1.3E-02	0.22	4.5E-03		M5KPKLCSTFEKSEHN*
HG1189	<i>H. sapiens</i>	ENS000000227999			0.00	0.34	7.0E-03	1.9E-02	0.34	7.0E-03		MELTSTELTLHCKYTYVCPSPQLSCQCLE*
HG1190	<i>H. sapiens</i>	ENS000000123684	LPGAT1	lysophosphatidylglycerol acyltransferase 1	0.11	0.41	1.3E-02	3.2E-02	0.41	1.3E-02		MHRCAGVVVRRLRSVSGSKY*
HG1191	<i>H. sapiens</i>	ENS000000164331	ANKRA2	ankyrin repeat family A member 2	0.05	0.11	5.2E-03	1.5E-02	0.11	5.2E-03		MESEFLGLFGHSWPVATERTFFPARVSPAGDSQLLRDAGTVAFY*
HG1192	<i>H. sapiens</i>	ENS000000168758	SEMA4C	semaphorin 4C	0.29	0.49	1.4E-02	3.4E-02	0.49	1.4E-02		MWNVGWGSAGLISALGKTGRDRDLRSQAPAAQGLA*
HG1193	<i>H. sapiens</i>	ENS000000177706	FAM20C	FAM20C, golgi associated secretory pathway kinase	0.29	0.47	2.1E-02	4.9E-02	0.47	2.1E-02		MDLDRGGAALVPSCS*
HG1194	<i>H. sapiens</i>	ENS000000214694	ARHGFE33	Rho guanine nucleotide exchange factor 33	0.00	0.19	6.5E-03	1.8E-02	0.19	6.5E-03		MGTSRENKKTSKNML*

* The gene description is based on information contained in Ensembl (<https://www.ensembl.org/index.html>) and Ensembl Metazoa (<https://metazoa.ensembl.org/index.html>).

Supplementary Table S2. Taxonomic range of sequence conservation of the CPuORFs.

HG number	Species	Gene ID	Taxonomic category **																			
			Metazoa																			
			Eumetazoa***																			
			Bilateria																			
			Protostomia										Deuterostomia									
			Ecdysozoa										Chordata									
			Arthropoda										Vertebrata									
			Insecta										Euteleostomi									
			Deuterostomia*										Sarcopterygii									
			Chordata*										Tetrapoda									
Actinopterygii*										Amniota												
Ostarioclupeomorpha										Eutheria												
Sarcopterygii*										Euarchontoglires												
Amphibia																						
Sauropsida*																						
Aves																						
Mammalia*																						
Eutheria*																						

HG0001	D. melanogaster	FBgn0024734	0	8	0	10	0	4	22	5	0	3	7	3	1	2	3	27	4	10	4
	D. rerio	ENSDARG00000006242	0	9	0	14	0	9	22	1	0	6	20	3	2	2	3	27	4	10	4
		ENSDARG000000035676	0	3	0	13	0	1	1	1	0	6	22	3	2	2	3	29	4	10	5
		ENSDARG000000039997	0	3	0	9	0	3	1	1	0	3	18	3	2	2	3	27	4	10	4
		ENSDARG000000054814	0	5	0	12	0	6	15	0	0	5	17	3	2	2	3	27	4	10	4
		ENSDARG000000087443	0	8	0	14	0	4	9	6	0	6	23	3	2	2	3	29	4	10	5
	G. gallus	ENSGALG000000003265	0	1	0	7	0	0	1	1	0	6	20	4	2	2	3	28	4	10	5
		ENSGALG000000016271	0	9	0	13	0	10	22	2	0	6	21	4	2	2	3	26	4	10	4
H. sapiens	ENSG000000112245	0	9	0	13	0	9	22	2	0	6	20	4	2	2	3	27	4	10	3	
	ENSG000000184007	0	1	0	0	0	0	0	0	0	5	16	4	2	2	3	29	4	10	4	
HG0002	D. rerio	ENSDARG000000003077	1	6	5	22	0	18	8	6	1	2	27	4	1	2	3	0	2	10	5
HG0003	D. melanogaster	FBgn0039280	0	8	3	11	3	10	22	4	1	2	15	3	1	2	2	5	1	1	2
	G. gallus	ENSGALG000000014906	0	7	3	12	3	9	23	2	1	2	14	3	1	2	2	5	1	1	2
HG0004.1	D. melanogaster	FBgn0028494	0	0	0	0	0	3	13	0	0	0	0	0	0	0	0	0	0	0	0
	D. rerio	ENSDARG000000076779	0	0	0	1	0	0	2	0	0	1	19	2	1	2	3	28	2	9	5
	G. gallus	ENSGALG000000041706	0	0	0	0	0	0	0	0	0	1	19	3	1	2	3	27	2	9	5
	H. sapiens	ENSG000000031003	0	0	0	0	0	0	0	0	0	1	19	3	1	2	3	28	2	9	4
HG0004.2	H. sapiens	ENSG000000138640	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	
HG0005	D. rerio	ENSDARG000000011055	0	1	0	0	0	7	12	4	0	1	23	3	1	2	3	5	2	4	4
	G. gallus	ENSGALG000000016320	0	1	0	1	0	6	12	5	0	1	23	4	1	1	3	4	2	4	4
HG0006	D. melanogaster	FBgn0029971	0	0	0	6	0	13	27	0	0	0	0	1	0	1	0	0	0	0	0
HG0007	D. melanogaster	FBgn0034372	0	0	0	3	0	11	27	0	0	0	0	1	0	0	0	0	0	0	0
HG0008	H. sapiens	ENSG000000175567	0	1	0	0	0	0	0	0	0	2	12	4	1	2	3	0	3	10	4
HG0009	D. melanogaster	FBgn0050100	0	0	0	0	0	14	26	0	0	0	0	1	0	0	0	0	0	0	0
HG0010.1	G. gallus	ENSGALG000000009013	0	0	0	3	0	0	1	5	0	0	2	0	1	2	3	7	3	5	4
	H. sapiens	ENSG000000125863	0	0	0	2	0	3	5	5	0	0	2	0	1	2	3	8	2	5	3
HG0010.2	G. gallus	ENSGALG000000009013	0	0	0	0	0	0	0	0	0	0	3	0	1	2	3	9	3	7	5
	H. sapiens	ENSG000000125863	0	0	0	0	0	0	0	3	0	0	3	0	1	2	3	10	3	7	4
HG0010.3	H. sapiens	ENSG000000125863	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	4
HG0011	D. melanogaster	FBgn0027360	0	0	0	0	0	10	24	0	0	0	0	1	0	1	0	0	0	0	0
HG0012	D. melanogaster	FBgn0064116	0	0	0	0	0	6	27	0	0	0	0	1	0	0	0	0	0	0	0
HG0013	D. melanogaster	FBgn0261381	0	0	0	0	0	6	27	0	0	0	0	0	0	1	0	0	0	0	0
HG0014	D. melanogaster	FBgn0260392	0	0	0	0	0	8	24	0	0	0	0	1	0	0	0	0	0	0	0
HG0015	D. rerio	ENSDARG000000007377	0	1	0	0	0	0	0	0	0	3	22	3	1	2	0	0	0	1	0
HG0016	G. gallus	ENSGALG000000010399	0	1	0	0	0	0	0	0	0	0	6	1	0	2	3	3	2	10	5
HG0017	D. rerio	ENSDARG000000043154	0	1	0	0	0	0	0	0	0	3	14	3	1	0	2	0	3	1	4
HG0018	D. rerio	ENSDARG000000053291	0	1	0	0	0	0	0	0	0	0	22	3	0	0	0	0	0	3	2
	G. gallus	ENSGALG000000004122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	28	4	10	5
	H. sapiens	ENSG000000189266	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	29	4	10	4
HG0019	H. sapiens	ENSG000000178397	0	0	0	4	0	0	1	5	0	0	0	0	1	1	2	0	2	6	3
HG0020	D. melanogaster	FBgn0035436	0	0	0	0	0	4	19	0	0	0	0	1	0	0	0	0	0	0	0
HG0021.1	D. rerio	ENSDARG000000068708	0	1	0	0	0	0	0	0	0	0	20	3	0	0	0	0	0	0	0
	G. gallus	ENSGALG000000009448	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	8	2	7	5
	H. sapiens	ENSG000000006652	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	3	2	10	4
HG0021.2	D. rerio	ENSDARG000000036811	0	0	0	0	0	0	0	0	0	0	18	2	0	0	0	0	0	0	0
HG0022	D. melanogaster	FBgn0061359	0	0	0	0	0	3	19	0	0	0	1	0	0	0	0	0	0	0	0
HG0023.1	H. sapiens	ENSG000000175197	0	0	0	0	0	0	1	0	0	0	0	0	0	2	2	2	1	8	3
HG0023.2	D. rerio	ENSDARG000000059836	0	0	0	0	0	0	0	0	0	0	11	3	0	0	0	0	0	0	0
HG0024.1	D. rerio	ENSDARG000000093406	0	1	0	0	0	0	0	0	0	0	15	2	0	0	0	0	0	0	0
HG0024.2	G. gallus	ENSGALG000000013628	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	24	0	0	0
	H. sapiens	ENSG000000112308	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	10	3
HG0024.3	G. gallus	ENSGALG000000013628	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	25	0	0	0
HG0025	D. rerio	ENSDARG000000060054	0	1	0	0	0	0	0	0	0	0	12	2	0	0	0	0	0	0	0
HG0026	D. rerio	ENSDARG000000087059	0	2	0	8	0	2	0	1	0	0	2	0	0	0	0	0	0	0	0
HG0027	H. sapiens	ENSG000000077254	0	1	0	0	0	1	1	0	0	0	1	0	0	1	0	0	0	0	0
HG0028.1	D. rerio	ENSDARG000000032103	0	0	0	0	0	0	0	0	0	2	17	3	1	2	3	29	3	11	5
	G. gallus	ENSGALG000000031448	0	0	0	0	0	0	0	0	0	2	17	4	1	2	3	28	3	11	5
	H. sapiens	ENSG000000069956	0	0	0	0	0	0	0	0	0	2	17	4	1	2	3	29	3	11	4
HG0028.2	H. sapiens	ENSG000000069956	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	29	2	10	4

[illegible]

HG0063.1	G. gallus	ENSGALG00000002477	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	19	3	6	3
	H. sapiens	ENSG00000162630	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	20	3	6	2
HG0063.2	H. sapiens	ENSG00000162630	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4	2	10	4
HG0064.1	H. sapiens	ENSG00000102678	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	16	1	10	4
HG0064.2	H. sapiens	ENSG00000113578	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2
HG0065	G. gallus	ENSGALG00000029927	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	25	1	2	1
HG0066	H. sapiens	ENSG00000112182	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	14	3	10	2
HG0067	H. sapiens	ENSG00000166862	0	0	0	0	0	0	0	0	0	0	7	4	0	1	2	8	1	6	3
HG0068	D. rerio	ENSDARG00000071235	0	0	0	0	0	0	0	0	2	2	14	1	1	2	1	1	1	2	2
	G. gallus	ENSGALG00000041419	0	0	0	0	0	0	0	0	2	2	15	2	1	2	1	1	1	2	2
	H. sapiens	ENSG00000130821	0	0	0	0	0	0	0	0	2	2	13	2	1	2	1	1	1	2	1
HG0069	G. gallus	ENSGALG00000010999	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	26	1	1	1
	H. sapiens	ENSG00000100697	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	16	1	10	2
HG0070	D. rerio	ENSDARG00000040926	0	0	0	0	0	0	0	0	0	0	15	2	1	0	0	1	0	4	2
		ENSDARG00000052695	0	0	0	0	0	0	0	0	0	1	14	3	1	2	1	1	0	5	2
	H. sapiens	ENSG00000175745	0	0	0	0	0	0	0	0	0	1	15	3	1	2	0	1	0	5	1
		ENSG00000185551	0	0	0	0	0	0	0	0	0	1	8	3	1	1	1	1	0	5	1
HG0071.1	D. rerio	ENSDARG00000098240	0	0	0	0	0	0	0	0	0	0	11	2	1	0	2	2	0	8	3
	H. sapiens	ENSG00000134138	0	0	0	0	0	0	0	0	0	1	11	3	1	0	2	2	0	8	2
HG0071.2	H. sapiens	ENSG00000143995	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	4	
HG0072	G. gallus	ENSGALG00000039690	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	14	0	5	4
	H. sapiens	ENSG00000104435	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2	15	0	7	4
HG0073	D. rerio	ENSDARG00000041708	0	0	0	0	0	0	0	0	1	12	3	0	2	2	5	0	3	2	
HG0074	D. rerio	ENSDARG00000078624	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0
	H. sapiens	ENSG00000131089	0	0	0	0	0	0	0	0	0	7	1	0	2	1	7	2	7	2	
HG0075	H. sapiens	ENSG00000165699	0	0	0	0	0	0	0	0	0	0	0	0	0	2	9	3	11	4	
HG0076	D. rerio	ENSDARG00000040008	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	8	2	9	5
	H. sapiens	ENSG00000164600	0	0	0	0	0	0	0	0	0	1	0	0	2	2	8	2	9	4	
HG0077.1	G. gallus	ENSGALG00000005074	0	0	0	0	0	0	0	0	0	0	0	0	0	2	26	0	0	0	
HG0077.2	G. gallus	ENSGALG00000005074	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	
HG0078.1	G. gallus	ENSGALG00000016633	0	0	0	0	0	0	0	0	0	0	0	0	0	2	26	0	0	0	
HG0078.2	H. sapiens	ENSG00000147421	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	2	
HG0079	H. sapiens	ENSG00000204406	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	9	1	10	3
HG0080.1	G. gallus	ENSGALG00000039403	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	0	7	5	
	H. sapiens	ENSG00000179603	0	0	0	0	0	0	0	0	0	0	0	0	0	2	8	2	11	4	
HG0080.2	H. sapiens	ENSG00000179603	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	
HG0080.3	H. sapiens	ENSG00000179603	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	
HG0081.1	D. rerio	ENSDARG00000028228	0	0	0	0	0	0	0	0	0	3	2	0	1	2	7	1	7	4	
HG0081.2	D. rerio	ENSDARG00000028228	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	
HG0082	D. rerio	ENSDARG00000062379	0	0	0	0	0	0	0	0	0	13	1	1	1	1	2	1	5	2	
	H. sapiens	ENSG00000176087	0	0	0	0	0	0	0	0	0	13	2	1	1	1	2	1	5	1	
HG0083.1	G. gallus	ENSGALG00000008039	0	0	0	0	0	0	0	0	0	0	0	0	0	1	26	0	0	0	
HG0083.2	H. sapiens	ENSG00000138111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	
HG0084.1	G. gallus	ENSGALG00000009207	0	0	0	0	0	0	0	0	0	0	0	0	0	1	26	0	0	0	
HG0084.2	H. sapiens	ENSG00000154447	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
HG0085	G. gallus	ENSGALG00000002003	0	0	0	0	0	0	0	0	0	0	0	0	0	2	12	2	0	0	
	H. sapiens	ENSG00000107779	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	11	2	9	3
HG0086	G. gallus	ENSGALG00000009835	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	24	0	0	
HG0087	H. sapiens	ENSG00000164548	0	0	0	0	0	0	0	0	0	5	0	1	1	1	8	1	8	2	
HG0088	H. sapiens	ENSG00000273079	0	0	0	0	0	0	0	0	0	0	0	0	0	2	14	0	8	3	
HG0089.1	G. gallus	ENSGALG00000002294	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	9	1	8	3
	H. sapiens	ENSG00000092421	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	10	1	9	3
HG0089.2	H. sapiens	ENSG00000092421	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	
HG0089.3	G. gallus	ENSGALG00000002294	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	
HG0090.1	G. gallus	ENSGALG00000008487	0	0	0	0	0	0	0	0	0	0	0	0	0	3	17	1	5	0	
	H. sapiens	ENSG00000172765	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	2	
HG0090.2	D. rerio	ENSDARG00000060954	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0	
HG0090.3	G. gallus	ENSGALG00000008487	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	
HG0091.1	H. sapiens	ENSG00000172209	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	15	0	6	3
HG0091.2	H. sapiens	ENSG00000172209	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	6	3	
HG0091.3	H. sapiens	ENSG00000172209	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	6	3	
HG0092.1	G. gallus	ENSGALG00000009966	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	18	1	3	0
HG0092.2	H. sapiens	ENSG00000166225	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	3	
HG0093	G. gallus	ENSGALG00000040465	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	9	0	9	4
	H. sapiens	ENSG00000169554	0	0	0	0	0	0	0	0	0	0	0	0	0	3	10	0	9	3	
HG0094.1	H. sapiens	ENSG00000112175	0	0	0	0	0	0	0	0	0	0	0	0	0	3	10	1	10	2	
HG0094.2	H. sapiens	ENSG00000112175	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	9	3	
HG0095	D. rerio	ENSDARG00000013708	0	0	0	0	0	0	0	0	1	15	3	1	2	0	0	2	1	1	
HG0096	G. gallus	ENSGALG00000014186	0	0	0	0	0	0	0	0	0	0	0	0	0	1	25	0	0	0	
HG0097	G. gallus	ENSGALG000000037496	0	0	0	0	0	0	0	0	0	0	0	0	0	3	8	2	10	3	
HG0098	H. sapiens	ENSG00000198739	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	2	11	4	
HG0099.1	H. sapiens	ENSG00000168575	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	3	11	4	
HG0099.2	H. sapiens	ENSG00000144136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3	
HG0099.3	H. sapiens	ENSG00000168575	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	
HG0099.4	D. rerio	ENSDARG00000010641	0	0	0	0	0	0	0	0	0	5	3	0	0	0	0	0	0	0	
HG0100.1	D. rerio	ENSDARG00000104148	0	0	0	0	0	0	0	0	0	21	3	0	0	0	0	0	0	0	
		ENSDARG00000104609	0	0	0	0	0	0	0	0	0	21	3	1	0	0	0	0	0	0	
HG0100.2	D. rerio	ENSDARG00000061108	0	0	0	0	0	0	0	0	0	9	2	0	0	0	0	0	0	0	
HG0101	H. sapiens	ENSG000000099250	0	0	0	0	0	0	0	0	0	1	0	0	0	2	8	2	9	3	

HG0102	<i>H. sapiens</i>	ENSG00000182263	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	2	7	1	7	4
HG0103	<i>G. gallus</i>	ENSGALG00000016558	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	21	1	0	0
	<i>H. sapiens</i>	ENSG00000165197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3	
HG0104.1	<i>G. gallus</i>	ENSGALG00000038097	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	19	3	0	0
HG0104.2	<i>H. sapiens</i>	ENSG00000149547	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	1	
HG0105	<i>G. gallus</i>	ENSGALG00000016176	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	8	1	7	4
	<i>H. sapiens</i>	ENSG00000135298	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	9	1	9	3
HG0106	<i>H. sapiens</i>	ENSG00000147548	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2	2	4	2	9	3
HG0107.1	<i>G. gallus</i>	ENSGALG00000003601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	8	1	5	3
	<i>H. sapiens</i>	ENSG00000058668	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	3	8	1	6	3
HG0107.2	<i>G. gallus</i>	ENSGALG00000030550	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	0	0	0	0
	<i>H. sapiens</i>	ENSG00000070961	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	4
HG0107.3	<i>D. rerio</i>	ENDSARG00000063433	0	0	0	0	0	0	0	0	0	0	0	0	11	2	0	0	0	0	0	0	0
	<i>H. sapiens</i>	ENSG00000157087	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0107.4	<i>H. sapiens</i>	ENSG00000070961	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3
HG0108.1	<i>G. gallus</i>	ENSGALG00000007396	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	20	0	0	0
HG0108.2	<i>H. sapiens</i>	ENSG00000135090	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3
HG0108.3	<i>D. rerio</i>	ENDSARG00000098304	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
HG0109.1	<i>H. sapiens</i>	ENSG00000048540	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	14	0	5	2
HG0109.2	<i>H. sapiens</i>	ENSG00000048540	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	6	3
HG0109.3	<i>H. sapiens</i>	ENSG00000048540	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	4
HG0110.1	<i>H. sapiens</i>	ENSG00000091656	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	6	3
HG0110.2	<i>D. rerio</i>	ENDSARG00000073944	0	0	0	0	0	0	0	0	0	0	0	7	1	1	1	0	0	0	0	1	0
HG0111	<i>G. gallus</i>	ENSGALG00000034944	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	19	0	0	0
HG0112	<i>H. sapiens</i>	ENSG00000105997	0	0	0	0	0	0	0	0	0	0	0	7	0	0	1	1	8	0	4	1	
	<i>D. rerio</i>	ENDSARG00000099727	0	0	0	0	0	0	0	0	0	0	0	8	0	1	1	1	1	1	1	5	3
HG0113	<i>G. gallus</i>	ENSGALG00000023089	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	1	2	6	4
	<i>G. gallus</i>	ENSGALG00000003701	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	20	0	0	0
HG0114.2	<i>H. sapiens</i>	ENSG00000198964	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2
HG0115.1	<i>G. gallus</i>	ENSGALG00000010976	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	20	0	0	0
HG0115.2	<i>H. sapiens</i>	ENSG00000169193	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4
HG0116	<i>G. gallus</i>	ENSGALG00000033038	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	19	0	0	0
	<i>H. sapiens</i>	ENSG00000010270	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1
HG0117.1	<i>H. sapiens</i>	ENSG00000140945	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	0	9	3
HG0117.2	<i>H. sapiens</i>	ENSG00000140945	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3
HG0118.1	<i>H. sapiens</i>	ENSG00000183662	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	5	1	10	3
HG0118.2	<i>H. sapiens</i>	ENSG00000183662	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2
HG0119	<i>G. gallus</i>	ENSGALG00000043570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	18	0	0	0
HG0120	<i>H. sapiens</i>	ENSG00000022355	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	2	2	2	7	4	
HG0121	<i>H. sapiens</i>	ENSG00000122786	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	7	4
HG0122	<i>H. sapiens</i>	ENSG00000169925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	4	9	4
HG0123	<i>H. sapiens</i>	ENSG00000173276	0	0	0	0	0	0	0	0	0	0	0	12	1	0	2	2	1	0	1	2	
HG0124.1	<i>D. rerio</i>	ENDSARG00000031763	0	0	0	0	0	0	0	0	0	0	0	12	2	0	0	0	0	0	0	3	3
HG0124.2	<i>D. rerio</i>	ENDSARG00000053209	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0	0
HG0125.1	<i>D. rerio</i>	ENDSARG00000051926	0	0	0	0	0	0	0	0	0	0	0	12	2	0	1	0	0	0	0	3	2
HG0125.2	<i>H. sapiens</i>	ENSG00000181690	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	11	4
HG0126.1	<i>G. gallus</i>	ENSGALG00000010899	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	19	0	0	0
HG0126.2	<i>G. gallus</i>	ENSGALG00000010899	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0
HG0127.1	<i>G. gallus</i>	ENSGALG00000029709	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	19	0	0	0
HG0127.2	<i>H. sapiens</i>	ENSG00000109452	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3
	<i>D. rerio</i>	ENDSARG00000091029	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	1	4	1	3	3	
HG0128	<i>H. sapiens</i>	ENSG00000109132	0	0	0	0	0	0	0	0	0	0	0	5	2	0	2	1	4	1	3	2	
	<i>D. rerio</i>	ENDSARG00000099437	0	0	0	0	0	0	0	0	0	0	0	14	2	1	2	1	0	0	0	0	0
HG0130	<i>G. gallus</i>	ENSGALG00000002993	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	0	9	3
HG0131	<i>G. gallus</i>	ENSGALG00000013135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	18	0	0	0
HG0132	<i>H. sapiens</i>	ENSG00000151067	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	1	6	0	7	3	
HG0133.1	<i>D. rerio</i>	ENDSARG00000051886	0	0	0	0	0	0	0	0	0	0	0	1	16	2	0	0	0	0	0	0	0
	<i>H. sapiens</i>	ENSG00000167522	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1
HG0133.2	<i>D. rerio</i>	ENDSARG00000051886	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
HG0133.3	<i>H. sapiens</i>	ENSG00000167522	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1
HG0134.1	<i>G. gallus</i>	ENSGALG00000041267	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	3	3	1	6	2	
HG0134.2	<i>H. sapiens</i>	ENSG00000168283	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2
HG0135	<i>D. rerio</i>	ENDSARG00000094132	0	0	0	0	0	0	0	0	0	0	0	7	0	0	1	0	2	0	0	1	
	<i>H. sapiens</i>	ENSG00000017427	0	0	0	0	0	0	0	0	0	0	0	7	0	0	1	0	2	1	5	3	
HG0136.1	<i>H. sapiens</i>	ENSG00000125845	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	2	10	4	
HG0136.2	<i>H. sapiens</i>	ENSG00000125845	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
HG0137.1	<i>H. sapiens</i>	ENSG00000181722	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	3	0	10	3	
HG0137.2	<i>H. sapiens</i>	ENSG00000181722	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2
HG0138.1	<i>H. sapiens</i>	ENSG00000185070	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	1	8	3
HG0138.2	<i>H. sapiens</i>	ENSG00000185070	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2
HG0139	<i>G. gallus</i>	ENSGALG00000006379	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	10	0	3	3	
HG0140	<i>H. sapiens</i>	ENSG00000009307	0																				

HG0145	<i>H. sapiens</i>	ENSG00000162599	0	0	0	0	0	0	0	0	0	0	0	0	4	4	0	0	0	6	1	2	1	
HG0146.1	<i>H. sapiens</i>	ENSG00000163681	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	5	4	
HG0146.2	<i>H. sapiens</i>	ENSG00000163681	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	
HG0146.3	<i>H. sapiens</i>	ENSG00000163681	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	
HG0147	<i>G. gallus</i>	ENSGALG00000004370	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	1	0	10	3	
	<i>H. sapiens</i>	ENSG00000108984	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	1	10	2	
HG0148.1	<i>G. gallus</i>	ENSGALG00000011855	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	16	0	0	0	
HG0148.2	<i>G. gallus</i>	ENSGALG00000011855	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	0	
HG0149.1	<i>G. gallus</i>	ENSGALG00000014645	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	11	2	0	1	
HG0149.2	<i>H. sapiens</i>	ENSG00000081189	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3	
HG0150.1	<i>G. gallus</i>	ENSGALG00000032289	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	15	0	0	0	
HG0150.2	<i>H. sapiens</i>	ENSG00000095574	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	8	4	
HG0151	<i>G. gallus</i>	ENSGALG00000035504	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1	1	
	<i>H. sapiens</i>	ENSG00000006468	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	0	9	3	
HG0152	<i>D. rerio</i>	ENSADARG00000015536	0	0	0	0	0	0	0	0	0	0	0	0	7	2	1	1	1	0	0	3	2	
HG0153	<i>G. gallus</i>	ENSGALG00000003136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	10	5	
HG0154	<i>H. sapiens</i>	ENSG00000128573	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	2	2	2	1	3	3	
HG0155	<i>H. sapiens</i>	ENSG00000136535	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	8	2	
HG0156	<i>H. sapiens</i>	ENSG00000156113	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	1	9	1	
HG0157	<i>H. sapiens</i>	ENSG00000173926	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	11	4	
HG0158	<i>H. sapiens</i>	ENSG00000198939	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	9	4	
HG0159.1	<i>H. sapiens</i>	ENSG00000182197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	9	3	
HG0159.2	<i>H. sapiens</i>	ENSG00000182197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	9	3	
HG0160	<i>D. rerio</i>	ENSADARG00000060089	0	0	0	0	0	0	0	0	0	0	0	0	12	2	1	1	0	0	0	0	0	
HG0161	<i>G. gallus</i>	ENSGALG00000017191	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	15	0	0	0	
HG0162	<i>H. sapiens</i>	ENSG00000138347	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	4	0	8	2	
HG0163	<i>H. sapiens</i>	ENSG00000146285	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	9	1	
HG0164	<i>H. sapiens</i>	ENSG00000151292	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	10	4	
HG0165	<i>H. sapiens</i>	ENSG00000177508	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2	1	0	1	2	0	5	1
HG0166.1	<i>H. sapiens</i>	ENSG00000148948	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	0	7	2	
HG0166.2	<i>H. sapiens</i>	ENSG00000148948	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2	
HG0166.4	<i>H. sapiens</i>	ENSG00000148948	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	
HG0167	<i>D. rerio</i>	ENSADARG00000104005	0	0	0	0	0	0	0	0	0	0	0	0	11	3	1	0	0	0	0	0	0	
HG0168	<i>G. gallus</i>	ENSGALG00000006997	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	10	2	0	0	
HG0169	<i>H. sapiens</i>	ENSG00000114933	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	11	1	2	0	
HG0170	<i>H. sapiens</i>	ENSG00000180530	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	9	4	
HG0171.1	<i>H. sapiens</i>	ENSG00000177311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	7	2	
HG0171.2	<i>H. sapiens</i>	ENSG00000177311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	6	1	
HG0171.3	<i>H. sapiens</i>	ENSG00000177311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	2	
HG0171.4	<i>H. sapiens</i>	ENSG00000177311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	1	
HG0172.1	<i>H. sapiens</i>	ENSG00000196782	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	7	3	
HG0172.2	<i>H. sapiens</i>	ENSG00000196782	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	
HG0173	<i>H. sapiens</i>	ENSG00000101746	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	6	3	
HG0174	<i>H. sapiens</i>	ENSG00000144355	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2	4	4	
HG0175	<i>H. sapiens</i>	ENSG00000151320	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	1	7	1	
HG0176	<i>H. sapiens</i>	ENSG00000170962	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	6	4	
HG0177	<i>H. sapiens</i>	ENSG00000171843	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	8	3	
HG0178.1	<i>G. gallus</i>	ENSGALG00000029047	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	9	0	0	1	
	<i>H. sapiens</i>	ENSG00000131634	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4	4	
HG0178.2	<i>G. gallus</i>	ENSGALG00000029047	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	2	
HG0179	<i>D. rerio</i>	ENSADARG00000036549	0	0	0	0	0	0	0	0	0	0	0	0	10	1	0	0	1	1	0	0	0	
	<i>H. sapiens</i>	ENSG00000160216	0	0	0	0	0	0	0	0	0	0	0	0	5	2	0	0	0	0	2	3	1	
HG0180.1	<i>H. sapiens</i>	ENSG00000112246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	8	3		
HG0180.2	<i>H. sapiens</i>	ENSG00000112246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
HG0181.1	<i>H. sapiens</i>	ENSG00000143776	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	5	4	
HG0181.2	<i>H. sapiens</i>	ENSG00000143776	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	
HG0182	<i>G. gallus</i>	ENSGALG00000031991	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	4	4	
HG0183	<i>H. sapiens</i>	ENSG00000011465	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	9	2	
HG0184	<i>H. sapiens</i>	ENSG00000136542	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	9	2	
HG0185	<i>H. sapiens</i>	ENSG00000143033	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	8	4	
HG0186	<i>H. sapiens</i>	ENSG00000167552	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	9	2	
HG0187.1	<i>G. gallus</i>	ENSGALG00000004058	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	9	0	0	0	
HG0187.2	<i>D. rerio</i>	ENSADARG00000059610	0	0	0	0	0	0	0	0	0	0	0	0	2	4	0	0	0	0	0	0	0	
HG0187.3	<i>G. gallus</i>	ENSGALG00000004058	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	
HG0188	<i>G. gallus</i>	ENSGALG00000016284	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	8	0	0	0	
	<i>H. sapiens</i>	ENSG00000157625	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	4	
HG0189	<i>D. rerio</i>	ENSADARG00000001807	0	0	0	0	0	0	0	0	0	0	0	0	2	9	0	1	0	0	0	0	0	
HG0190	<i>G. gallus</i>	ENSGALG00000006949	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	1	0	0	
HG0191	<i>G. gallus</i>	ENSGALG00000036097	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	7	2	0	0	
HG0192	<i>H. sapiens</i>	ENSG00000125107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	8	1	
HG0193	<i>H. sapiens</i>	ENSG00000134853	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2	1	5	2	
HG0194	<i>H. sapiens</i>	ENSG00000143507	0	0	0																			

HG0200	G. gallus	ENSGALG00000012015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	6	0	1	1
HG0201	G. gallus	ENSGALG00000015256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	7	1	0	0
HG0202	H. sapiens	ENSG00000124766	0	0	0	0	0	0	0	0	0	0	4	1	0	1	1	0	0	3	1	
HG0203	H. sapiens	ENSG00000128606	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	7	3	
HG0204	H. sapiens	ENSG00000162599	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	6	3	
HG0205	H. sapiens	ENSG00000184611	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	7	2	
HG0206.1	G. gallus	ENSGALG00000002069	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	7	0	0	0	
HG0206.2	H. sapiens	ENSG00000005238	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	4	
HG0207.1	G. gallus	ENSGALG00000007121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3	3	1	
HG0207.2	H. sapiens	ENSG00000106952	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	3	
HG0208	G. gallus	ENSGALG00000013272	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	0	0	0	
HG0209	H. sapiens	ENSG00000101040	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	7	2	
HG0210	H. sapiens	ENSG00000155849	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	7	2	
HG0211	H. sapiens	ENSG00000176204	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	6	3	
HG0212	D. rerio	ENSXDARG00000100244	0	0	0	0	0	0	0	0	0	0	1	3	1	1	1	2	0	0	0	
HG0213.1	G. gallus	ENSGALG00000001946	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	5	0	0	0	
HG0213.2	G. gallus	ENSGALG00000001946	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	
HG0214.1	G. gallus	ENSGALG00000012917	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	4	1	0	0	
HG0214.2	H. sapiens	ENSG00000040731	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	4	
HG0215	D. rerio	ENSXDARG00000079280	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0	0	0	0	0	
	G. gallus	ENSGALG00000016681	0	0	0	0	0	0	0	0	0	0	5	2	0	0	0	1	0	0	0	
HG0216.1	G. gallus	ENSGALG000000020922	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	5	0	0	0	
HG0216.2	H. sapiens	ENSG00000116667	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	10	2		
HG0217.1	H. sapiens	ENSG00000150394	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	5	2		
HG0217.2	G. gallus	ENSGALG000000005319	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0	0	0	
HG0218	D. rerio	ENSXDARG00000100149	0	0	0	0	0	0	0	0	0	0	7	0	0	1	0	0	0	0	0	
HG0219	D. rerio	ENSXDARG00000104082	0	0	0	0	0	0	0	0	0	0	3	3	0	0	0	0	2	0	0	
HG0220	G. gallus	ENSGALG000000008418	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	0	0	0	
HG0221	G. gallus	ENSGALG00000010859	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	3	
HG0222	G. gallus	ENSGALG00000011564	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	6	0	0	0	
HG0223	H. sapiens	ENSG00000091656	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	1	2	
HG0224	H. sapiens	ENSG00000118007	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	5	2	
HG0225	H. sapiens	ENSG00000150051	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	3	1	
HG0226.1	H. sapiens	ENSG00000180592	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	4	1	
HG0226.2	H. sapiens	ENSG00000180592	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	
HG0226.3	H. sapiens	ENSG00000180592	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	
HG0227.1	G. gallus	ENSGALG00000031929	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	5	0	0	0	
HG0227.2	H. sapiens	ENSG00000275163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	
HG0228	D. rerio	ENSXDARG00000087887	0	0	0	0	0	0	0	0	0	0	4	2	1	0	0	0	0	0	0	
HG0229	G. gallus	ENSGALG000000005474	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	0	0	0	
HG0230	G. gallus	ENSGALG00000011007	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	0	0	0	
HG0231	H. sapiens	ENSG00000150636	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	1	2	0	
HG0232	H. sapiens	ENSG00000180875	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	1	3	
HG0233	H. sapiens	ENSG00000206432	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	4	1	
HG0234.1	G. gallus	ENSGALG00000011250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	
HG0234.2	H. sapiens	ENSG00000108684	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	
HG0235.1	G. gallus	ENSGALG00000035927	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	
HG0235.2	H. sapiens	ENSG00000101638	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
HG0236	G. gallus	ENSGALG000000004437	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	0	
HG0237	G. gallus	ENSGALG00000012123	0	0	0	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	1	
HG0238	H. sapiens	ENSG00000049618	0	0	0	0	0	0	0	0	0	0	4	0	1	0	0	1	0	0	0	
HG0239	H. sapiens	ENSG00000149256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	4	1	
HG0240	H. sapiens	ENSG00000166342	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	1	1	
HG0241	H. sapiens	ENSG00000198561	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	1	2	
HG0242.1	G. gallus	ENSGALG00000007112	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	
HG0242.2	H. sapiens	ENSG00000140471	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
HG0243.1	H. sapiens	ENSG00000163697	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	1	
HG0243.2	H. sapiens	ENSG00000163697	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	3	
HG0244	G. gallus	ENSGALG00000010837	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	1	
HG0245	H. sapiens	ENSG00000091831	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2	1	
HG0246	H. sapiens	ENSG00000162676	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	2	
HG0247.1	D. rerio	ENSXDARG00000014746	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	
HG0247.2	H. sapiens	ENSG00000100320	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0248.1	G. gallus	ENSGALG000000004570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	
HG0248.2	H. sapiens	ENSG00000124151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	3	
HG0249	D. rerio	ENSXDARG00000062550	0	0	0	0	0	0	0	0	0	0	1	2	0	0	1	0	0	0	0	
HG0250	G. gallus	ENSGALG00000014861	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	
HG0251	H. sapiens	ENSG00000185053	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	1	
HG0252.1	G. gallus	ENSGALG00000009645	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	
HG0252.2	H. sapiens	ENSG00000119715	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	
HG0252.3	H. sapiens	ENSG00000196482	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	1	
HG0253.1	G. gallus	ENSGALG00000015184	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	
HG0253.2	H. sapiens	ENSG00000140332	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	2	
HG0253.3	H. sapiens	ENSG00000140332	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0254.1	G. gallus	ENSGALG00000035919	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	
HG0254.2	H. sapiens	ENSG00000072134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	
HG0255	G. gallus	ENSGALG00000012139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	
HG0256	G. gallus	ENSGALG00000039901	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	
HG0257	H. sapiens	ENSG00000198791	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	

HG0258.1	<i>G. gallus</i>	ENSGALG00000016797	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HG0258.2	<i>G. gallus</i>	ENSGALG00000016797	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0
HG0259	<i>G. gallus</i>	ENSGALG00000009936	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
HG0260.1	<i>G. gallus</i>	ENSGALG00000016890	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0
HG0260.2	<i>H. sapiens</i>	ENSG00000139793	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	4	
HG0260.3	<i>H. sapiens</i>	ENSG00000152601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2	
HG0260.4	<i>H. sapiens</i>	ENSG00000152601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	1	
HG0260.5	<i>H. sapiens</i>	ENSG00000152601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0260.6	<i>H. sapiens</i>	ENSG00000152601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0261.1	<i>G. gallus</i>	ENSGALG00000005867	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0	
HG0261.2	<i>G. gallus</i>	ENSGALG000000009520	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	
HG0261.3	<i>H. sapiens</i>	ENSG00000145416	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2		
HG0261.4	<i>H. sapiens</i>	ENSG00000165406	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
HG0262.1	<i>H. sapiens</i>	ENSG00000023445	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	
HG0262.2	<i>H. sapiens</i>	ENSG00000023445	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
HG0262.3	<i>G. gallus</i>	ENSGALG00000017186	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
HG0262.4	<i>H. sapiens</i>	ENSG00000023445	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
HG0263.1	<i>H. sapiens</i>	ENSG00000169826	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	
HG0263.2	<i>G. gallus</i>	ENSGALG00000002543	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	
HG0263.3	<i>G. gallus</i>	ENSGALG00000002543	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	
HG0263.4	<i>H. sapiens</i>	ENSG00000147408	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0264.1	<i>H. sapiens</i>	ENSG00000151458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	3		
HG0264.2	<i>H. sapiens</i>	ENSG00000151458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	3		
HG0264.3	<i>G. gallus</i>	ENSGALG000000011831	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	
HG0264.4	<i>H. sapiens</i>	ENSG00000151458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0265.1	<i>H. sapiens</i>	ENSG00000144285	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	2	
HG0265.2	<i>H. sapiens</i>	ENSG00000196876	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	
HG0265.3	<i>D. rerio</i>	ENSDARG00000018032	0	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0	
HG0266.1	<i>H. sapiens</i>	ENSG00000184185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	
		ENSG00000260458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	
HG0266.2	<i>G. gallus</i>	ENSGALG00000001181	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	
HG0267	<i>D. rerio</i>	ENSDARG00000028173	0	0	0	0	0	0	0	0	0	0	2	3	0	0	0	0	0	0	0	
		ENSDARG00000052330	0	0	0	0	0	0	0	0	0	0	9	2	0	0	0	0	0	0	0	
	<i>H. sapiens</i>	ENSG00000164889	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	3	
HG0268.1	<i>D. rerio</i>	ENSDARG00000011703	0	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0	
HG0268.2	<i>H. sapiens</i>	ENSG00000134852	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	
HG0268.3	<i>H. sapiens</i>	ENSG00000134852	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
HG0269.1	<i>G. gallus</i>	ENSGALG00000028685	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	
HG0269.2	<i>D. rerio</i>	ENSDARG00000061471	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	
HG0269.3	<i>G. gallus</i>	ENSGALG000000011686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
HG0270.1	<i>G. gallus</i>	ENSGALG00000015147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	
HG0270.2	<i>G. gallus</i>	ENSGALG00000015147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0	
HG0270.3	<i>H. sapiens</i>	ENSG00000128918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	1		
HG0271.1	<i>G. gallus</i>	ENSGALG00000004064	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0	
HG0271.2	<i>H. sapiens</i>	ENSG00000164850	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	
HG0271.3	<i>D. rerio</i>	ENSDARG00000074661	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	
HG0272.1	<i>D. melanogaster</i>	FBgn0034649	0	0	0	0	0	7	25	0	0	0	0	0	0	0	0	0	0	0	0	
HG0272.2	<i>D. melanogaster</i>	FBgn0034649	0	0	0	0	0	6	24	0	0	0	0	0	0	0	0	0	0	0	0	
HG0272.3	<i>H. sapiens</i>	ENSG00000143315	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	
HG0273.1	<i>G. gallus</i>	ENSGALG00000003293	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	
HG0273.2	<i>H. sapiens</i>	ENSG00000140943	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	1	
HG0273.3	<i>H. sapiens</i>	ENSG00000140943	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	
HG0274.1	<i>H. sapiens</i>	ENSG00000204256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	2	
HG0274.2	<i>D. rerio</i>	ENSDARG00000100129	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	
HG0275.1	<i>H. sapiens</i>	ENSG00000100239	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	
HG0275.2	<i>D. rerio</i>	ENSDARG00000045540	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	
HG0276.1	<i>G. gallus</i>	ENSGALG000000008912	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	
HG0276.2	<i>H. sapiens</i>	ENSG00000073734	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
HG0277.1	<i>H. sapiens</i>	ENSG00000102531	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	2		
HG0277.2	<i>G. gallus</i>	ENSGALG00000004169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
HG0278.1	<i>H. sapiens</i>	ENSG00000119946	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	
HG0278.2	<i>D. rerio</i>	ENSDARG00000078733	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	
HG0279.1	<i>H. sapiens</i>	ENSG00000175928	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2	
HG0279.2	<i>G. gallus</i>	ENSGALG00000035099	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
HG0280.1	<i>H. sapiens</i>	ENSG00000156299	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	
HG0280.2	<i>D. melanogaster</i>	FBgn0085447	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	
HG0281.1	<i>G. gallus</i>	ENSGALG00000006766	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0	
HG0281.2	<i>H. sapiens</i>	ENSG00000100150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	2	
HG0282.1	<i>D. rerio</i>	ENSDARG00000061328	0	0	0	0	0	0	0	0	0	0	9	2	0	0	0	0	0	0	0	
HG0282.2	<i>H. sapiens</i>	ENSG00000144857	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
HG0283.1	<i>G. gallus</i>	ENSGALG00000010270	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	
HG0283.2	<i>H. sapiens</i>	ENSG00000119682	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4	
HG0284.1	<i>H. sapiens</i>	ENSG00000007168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	4	
HG0284.2	<i>G. gallus</i>	ENSGALG00000005834	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	
HG0285.1	<i>G. gallus</i>	ENSGALG00000012156	0	0	0	0</																

HG0287.2	<i>D. rerio</i>	ENSDARG00000104251	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0	0	0	0	0	0
HG0288.1	<i>G. gallus</i>	ENSGALG00000006655	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
HG0288.2	<i>H. sapiens</i>	ENSG00000073803	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0
HG0289	<i>G. gallus</i>	ENSGALG00000009581	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	0	0	0	0
	<i>H. sapiens</i>	ENSG00000072415	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3	0
HG0290.1	<i>H. sapiens</i>	ENSG00000116539	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	10	3	0	0
HG0290.2	<i>D. rerio</i>	ENSDARG00000070981	0	0	0	0	0	0	0	0	0	0	0	0	4	1	0	0	0	0	0	0	0	0
HG0291.1	<i>G. gallus</i>	ENSGALG00000009173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14	0	0	0	0
HG0291.2	<i>H. sapiens</i>	ENSG00000151892	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	0
HG0292.1	<i>G. gallus</i>	ENSGALG00000006502	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0	0
HG0292.2	<i>H. sapiens</i>	ENSG00000180628	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
HG0293	<i>G. gallus</i>	ENSGALG00000012187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0
	<i>H. sapiens</i>	ENSG00000152127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	4	0
HG0294.1	<i>G. gallus</i>	ENSGALG00000017036	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0
HG0294.2	<i>H. sapiens</i>	ENSG00000183722	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0
HG0295.1	<i>H. sapiens</i>	ENSG00000166888	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	9	3	0	0
HG0295.2	<i>G. gallus</i>	ENSGALG00000003282	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	2	0
HG0296	<i>G. gallus</i>	ENSGALG00000006912	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	2	0	0
HG0297	<i>G. gallus</i>	ENSGALG00000031684	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	0
HG0298	<i>G. gallus</i>	ENSGALG00000042308	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0
HG0299	<i>G. gallus</i>	ENSGALG00000040465	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
HG0300	<i>D. melanogaster</i>	FBgn0031668	0	0	0	0	0	14	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0301	<i>D. melanogaster</i>	FBgn0036856	0	0	0	0	0	6	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0302	<i>D. melanogaster</i>	FBgn0031454	0	0	0	0	0	7	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0303	<i>D. melanogaster</i>	FBgn0260464	0	0	0	0	0	7	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0304	<i>D. melanogaster</i>	FBgn0260467	0	0	0	0	0	8	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0305	<i>D. melanogaster</i>	FBgn0050290	0	0	0	0	0	8	21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0306	<i>D. melanogaster</i>	FBgn0259726	0	0	0	0	0	5	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0307	<i>D. melanogaster</i>	FBgn0037822	0	0	0	0	0	7	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0308	<i>D. melanogaster</i>	FBgn0264743	0	0	0	0	0	1	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0309	<i>D. melanogaster</i>	FBgn0037689	0	0	0	0	0	8	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0310	<i>D. melanogaster</i>	FBgn0039339	0	0	0	0	0	7	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0311	<i>D. melanogaster</i>	FBgn0263251	0	0	0	0	0	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0312	<i>D. melanogaster</i>	FBgn0038641	0	0	0	0	0	11	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0313	<i>D. melanogaster</i>	FBgn0259725	0	0	0	0	0	2	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0314	<i>D. melanogaster</i>	FBgn0260468	0	0	0	0	0	0	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0315	<i>D. melanogaster</i>	FBgn0260234	0	0	0	0	0	1	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0316	<i>D. melanogaster</i>	FBgn0041164	0	0	0	0	0	2	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0317	<i>D. melanogaster</i>	FBgn0050011	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0318	<i>D. melanogaster</i>	FBgn0035293	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0319	<i>D. melanogaster</i>	FBgn0026778	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0320	<i>D. melanogaster</i>	FBgn0040993	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HG0321	<i>D. rerio</i>	ENSDARG00000070426	0	0	0	0	0	0	0	0	0	0	0	0	20	3	0	0	0	0	0	0	0	0
HG0322	<i>D. rerio</i>	ENSDARG00000070917	0	0	0	0	0	0	0	0	0	0	0	0	17	3	0	0	0	0	0	0	0	0
HG0323	<i>D. rerio</i>	ENSDARG00000071197	0	0	0	0	0	0	0	0	0	0	0	0	19	1	0	0	0	0	0	0	0	0
HG0324	<i>D. rerio</i>	ENSDARG000000094965	0	0	0	0	0	0	0	0	0	0	0	0	18	1	0	0	0	0	0	0	0	0
HG0325	<i>D. rerio</i>	ENSDARG00000079738	0	0	0	0	0	0	0	0	0	0	0	0	15	3	0	0	0	0	0	0	0	0
HG0326	<i>D. rerio</i>	ENSDARG00000012848	0	0	0	0	0	0	0	0	0	0	0	0	14	3	0	0	0	0	0	0	0	0
HG0327	<i>D. rerio</i>	ENSDARG00000022203	0	0	0	0	0	0	0	0	0	0	0	0	14	3	0	0	0	0	0	0	0	0
HG0328	<i>D. rerio</i>	ENSDARG00000099999	0	0	0	0	0	0	0	0	0	0	0	0	15	2	0	0	0	0	0	0	0	0
HG0329	<i>D. rerio</i>	ENSDARG00000036442	0	0	0	0	0	0	0	0	0	0	0	0	14	2	0	0	0	0	0	0	0	0
HG0330	<i>D. rerio</i>	ENSDARG00000039392	0	0	0	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0	0
HG0331	<i>D. rerio</i>	ENSDARG00000044899	0	0	0	0	0	0	0	0	0	0	0	0	14	2	0	0	0	0	0	0	0	0
HG0332	<i>D. rerio</i>	ENSDARG00000102893	0	0	0	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0	0
HG0333	<i>D. rerio</i>	ENSDARG00000042518	0	0	0	0	0	0	0	0	0	0	0	0	12	2	0	0	0	0	0	0	0	0
HG0334	<i>D. rerio</i>	ENSDARG00000075349	0	0	0	0	0	0	0	0	0	0	0	0	11	3	0	0	0	0	0	0	0	0
HG0335	<i>D. rerio</i>	ENSDARG00000034700	0	0	0	0	0	0	0	0	0	0	0	0	10	3	0	0	0	0	0	0	0	0
HG0336	<i>D. rerio</i>	ENSDARG00000028676	0	0	0	0	0	0	0	0	0	0	0	0	11	1	0	0	0	0	0	0	0	0
HG0337	<i>D. rerio</i>	ENSDARG00000054906	0	0	0	0	0	0	0	0	0	0	0	0	10	1	0	0	0	0	0	0	0	0
HG0338	<i>D. rerio</i>	ENSDARG00000000151	0	0	0	0	0	0	0	0	0	0	0	0	8	2	0	0	0	0	0	0	0	0
HG0339	<i>D. rerio</i>	ENSDARG00000063144	0	0	0	0	0	0	0	0	0	0	0	0	9	1	0	0	0	0	0	0	0	0
HG0340	<i>D. rerio</i>	ENSDARG00000017591	0	0	0	0	0	0	0	0	0	0	0	0	7	1	0	0	0	0	0	0	0	0
HG0341	<i>D. rerio</i>	ENSDARG00000039430	0	0	0	0	0	0	0	0	0	0	0	0	7	1	0	0	0	0	0	0	0	0
HG0342	<i>D. rerio</i>	ENSDARG00000045801	0	0	0	0	0	0	0	0	0	0	0	0	6	2	0	0	0	0	0	0	0	0
HG0343	<i>D. rerio</i>	ENSDARG00000057062	0	0	0	0	0	0	0	0	0	0	0	0	6	2	0	0	0	0	0	0	0	0
HG0344	<i>D. rerio</i>	ENSDARG00000032072	0	0	0	0	0	0	0	0	0	0	0	0	6	1	0	0	0	0	0	0	0	0
HG0345	<i>D. rerio</i>	ENSDARG00000035910	0	0	0	0	0	0	0	0	0	0	0	0	5	2	0	0	0	0	0	0	0	0
HG0346	<i>D. rerio</i>	ENSDARG00000041982	0	0	0	0	0	0	0	0	0	0	0	0	5	2	0	0	0	0	0	0	0	0
HG0347	<i>D. rerio</i>	ENSDARG00000063194	0	0	0	0	0	0	0	0	0	0	0	0	5	2	0	0	0	0	0	0	0	0
HG0348	<i>D. rerio</i>	ENSDARG00000036139	0	0	0	0	0																	

HG0358	<i>D. rerio</i>	ENSDARG00000062506	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0
HG0359	<i>D. rerio</i>	ENSDARG00000070348	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0	0	0
HG0360	<i>D. rerio</i>	ENSDARG00000070801	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0
HG0361	<i>D. rerio</i>	ENSDARG00000077581	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0
HG0362	<i>D. rerio</i>	ENSDARG00000078355	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0
HG0363	<i>D. rerio</i>	ENSDARG00000095896	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
HG0364	<i>D. rerio</i>	ENSDARG00000004988	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
HG0365	<i>D. rerio</i>	ENSDARG00000016132	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
HG0366	<i>D. rerio</i>	ENSDARG00000017803	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
HG0367	<i>D. rerio</i>	ENSDARG00000034056	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0368	<i>D. rerio</i>	ENSDARG00000058606	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0369	<i>D. rerio</i>	ENSDARG00000059276	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
HG0370	<i>D. rerio</i>	ENSDARG00000062693	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
HG0371	<i>D. rerio</i>	ENSDARG00000062765	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
HG0372	<i>D. rerio</i>	ENSDARG00000069467	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0373	<i>D. rerio</i>	ENSDARG00000074611	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
HG0374	<i>D. rerio</i>	ENSDARG00000075147	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0375	<i>D. rerio</i>	ENSDARG00000076171	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
HG0376	<i>D. rerio</i>	ENSDARG00000077229	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
HG0377	<i>D. rerio</i>	ENSDARG00000079549	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0378	<i>D. rerio</i>	ENSDARG00000080009	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0379	<i>D. rerio</i>	ENSDARG00000104372	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0
HG0380	<i>D. rerio</i>	ENSDARG00000005350	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0381	<i>D. rerio</i>	ENSDARG000000006124	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0382	<i>D. rerio</i>	ENSDARG00000017242	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0383	<i>D. rerio</i>	ENSDARG00000036501	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
HG0384	<i>D. rerio</i>	ENSDARG00000054748	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
HG0385	<i>D. rerio</i>	ENSDARG00000059549	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0386	<i>D. rerio</i>	ENSDARG00000062084	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
HG0387	<i>D. rerio</i>	ENSDARG00000071150	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
HG0388	<i>D. rerio</i>	ENSDARG00000077228	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
HG0389	<i>D. rerio</i>	ENSDARG00000077361	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0390	<i>D. rerio</i>	ENSDARG00000090035	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
HG0391	<i>D. rerio</i>	ENSDARG00000099634	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
HG0392	<i>D. rerio</i>	ENSDARG00000100003	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
HG0393	<i>G. gallus</i>	ENSGALG00000002090	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	0	0	0
HG0394	<i>G. gallus</i>	ENSGALG00000002479	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24	0	0	0
HG0395	<i>G. gallus</i>	ENSGALG00000014936	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22	0	0	0
HG0396.1	<i>G. gallus</i>	ENSGALG00000034253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	0	0	0
HG0396.2	<i>G. gallus</i>	ENSGALG00000034253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0
HG0397	<i>G. gallus</i>	ENSGALG00000009438	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0
HG0398	<i>G. gallus</i>	ENSGALG00000005369	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0	0	0
HG0399	<i>G. gallus</i>	ENSGALG00000032659	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0	0	0
HG0400	<i>G. gallus</i>	ENSGALG00000004261	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0
HG0401	<i>G. gallus</i>	ENSGALG00000009057	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0
HG0402	<i>G. gallus</i>	ENSGALG00000035584	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0
HG0403.1	<i>G. gallus</i>	ENSGALG00000007717	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0
HG0403.2	<i>G. gallus</i>	ENSGALG00000007717	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0404	<i>G. gallus</i>	ENSGALG00000008700	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0
HG0405.1	<i>G. gallus</i>	ENSGALG00000009185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0
HG0405.2	<i>G. gallus</i>	ENSGALG00000009185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0
HG0406	<i>G. gallus</i>	ENSGALG00000004935	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0
HG0407	<i>G. gallus</i>	ENSGALG00000015027	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0
HG0408	<i>G. gallus</i>	ENSGALG00000036255	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0
HG0409	<i>G. gallus</i>	ENSGALG00000002315	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0
HG0410	<i>G. gallus</i>	ENSGALG00000008148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0
HG0411	<i>G. gallus</i>	ENSGALG00000012166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0
HG0412	<i>G. gallus</i>	ENSGALG00000003446	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0
HG0413	<i>G. gallus</i>	ENSGALG00000005475	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0
HG0414	<i>G. gallus</i>	ENSGALG00000032599	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0
HG0415	<i>G. gallus</i>	ENSGALG00000034970	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0
HG0416	<i>G. gallus</i>	ENSGALG00000015874	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0
HG0417	<i>G. gallus</i>	ENSGALG00000001522	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0
HG0418	<i>G. gallus</i>	ENSGALG00000010337	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0
HG0419	<i>G. gallus</i>	ENSGALG00000012542	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0
HG0420	<i>G. gallus</i>	ENSGALG00000000336	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0421	<i>G. gallus</i>	ENSGALG00000003492	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0422	<i>G. gallus</i>	ENSGALG00000005772	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0423	<i>G. gallus</i>	ENSGALG00000006329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0424	<i>G. gallus</i>	ENSGALG00000039553	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0425	<i>G. gallus</i>	ENSGALG00000043044	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
HG0426	<i>G. gallus</i>	ENSGALG00000002192	0	0	0	0	0																

HG0434	G. gallus	ENSGALG00000008357	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0
HG0435	G. gallus	ENSGALG00000010778	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0
HG0436	G. gallus	ENSGALG00000026736	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0
HG0437	G. gallus	ENSGALG00000001728	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0438	G. gallus	ENSGALG00000008545	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0439	G. gallus	ENSGALG00000009172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0440	G. gallus	ENSGALG00000010090	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0441	G. gallus	ENSGALG00000015069	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0442	G. gallus	ENSGALG00000030250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0443	G. gallus	ENSGALG00000039454	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
HG0444	G. gallus	ENSGALG00000000558	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0445	G. gallus	ENSGALG00000004017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0446	G. gallus	ENSGALG00000006807	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0447	G. gallus	ENSGALG00000008784	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0448	G. gallus	ENSGALG00000011762	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0449	G. gallus	ENSGALG00000014106	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0450	G. gallus	ENSGALG00000015528	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0451	G. gallus	ENSGALG00000019489	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
HG0452	G. gallus	ENSGALG00000004227	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0453	G. gallus	ENSGALG00000005995	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0454	G. gallus	ENSGALG00000007186	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0455	G. gallus	ENSGALG00000010718	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0456	G. gallus	ENSGALG00000033256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0457	G. gallus	ENSGALG00000039538	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HG0458	H. sapiens	ENSG00000060339	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	11	4
HG0459.1	H. sapiens	ENSG00000163848	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	11	4	
HG0459.2	H. sapiens	ENSG00000163848	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4	
HG0459.3	H. sapiens	ENSG00000163848	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	
HG0460	H. sapiens	ENSG00000180008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	10	3	
HG0461	H. sapiens	ENSG00000064419	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	10	4	
HG0462	H. sapiens	ENSG00000125686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	11	3	
HG0463	H. sapiens	ENSG00000129473	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	11	3	
HG0464	H. sapiens	ENSG00000188215	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	9	4	
HG0465	H. sapiens	ENSG00000132153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	11	3	
HG0466	H. sapiens	ENSG00000139679	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	9	3	
HG0467.1	H. sapiens	ENSG00000163320	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	9	4	
HG0467.2	H. sapiens	ENSG00000163320	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	
HG0468	H. sapiens	ENSG00000187778	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	4	
HG0469	H. sapiens	ENSG00000198369	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	9	3	
HG0470	H. sapiens	ENSG00000224470	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	11	3	
HG0471	H. sapiens	ENSG00000023041	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	3	
HG0472	H. sapiens	ENSG00000105991	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	3	
HG0473.1	H. sapiens	ENSG00000138650	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	4	
HG0473.2	H. sapiens	ENSG00000240184	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	2	
HG0474	H. sapiens	ENSG00000139083	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	9	3	
HG0475	H. sapiens	ENSG00000109118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	3	
HG0476	H. sapiens	ENSG00000130939	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	4	
HG0477	H. sapiens	ENSG00000166925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	8	3	
HG0478	H. sapiens	ENSG00000168214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	7	3	
HG0479.1	H. sapiens	ENSG00000168453	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	8	3	
HG0479.2	H. sapiens	ENSG00000168453	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	2	
HG0480	H. sapiens	ENSG00000198018	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	4	
HG0481	H. sapiens	ENSG00000198963	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	2	
HG0482	H. sapiens	ENSG00000067167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	3	
HG0483	H. sapiens	ENSG00000164463	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	3	
HG0484	H. sapiens	ENSG00000166444	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	3	
HG0485.1	H. sapiens	ENSG00000182667	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	7	3	
HG0485.2	H. sapiens	ENSG00000183715	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	
HG0486	H. sapiens	ENSG00000067900	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0487	H. sapiens	ENSG00000091831	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0488.1	H. sapiens	ENSG00000116194	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0488.2	H. sapiens	ENSG00000116194	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	4	
HG0489	H. sapiens	ENSG00000143847	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0490.1	H. sapiens	ENSG00000152413	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0490.2	H. sapiens	ENSG00000152413	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	
HG0491	H. sapiens	ENSG00000154114	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	2	
HG0492	H. sapiens	ENSG00000162670	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	2	
HG0493	H. sapiens	ENSG00000164707	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	4	
HG0494	H. sapiens	ENSG00000184226	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9	1	
HG0495.1	H. sapiens	ENSG00000196730	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3	
HG0495.2	H. sapiens	ENSG00000196730	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	3	
HG0496	H. sapiens	ENSG00000135913	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7	2	
HG0497	H. sapiens	ENSG00000147571	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	4	
HG0498	H. sapiens	ENSG00000005379	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	2	
HG0499	H. sapiens	ENSG00000011258	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	2	
HG0500	H. sapiens	ENSG000000070778	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	6	1	
HG0501	H. sapiens	ENSG00000110400	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	2	
HG0502	H. sapiens	ENSG00000126882	0	0	0	0	0	0														

HG0504	<i>H. sapiens</i>	ENSG00000144460	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	4
HG0505	<i>H. sapiens</i>	ENSG00000157470	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	2
HG0506.1	<i>H. sapiens</i>	ENSG00000177853	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	3
HG0506.2	<i>H. sapiens</i>	ENSG00000177853	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	2
HG0507	<i>H. sapiens</i>	ENSG00000060237	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	2
HG0508	<i>H. sapiens</i>	ENSG00000061936	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	2
HG0509	<i>H. sapiens</i>	ENSG00000068024	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	2
HG0510	<i>H. sapiens</i>	ENSG00000134769	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	6	1
HG0511	<i>H. sapiens</i>	ENSG00000143337	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	2
HG0512.1	<i>H. sapiens</i>	ENSG00000112319	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	1
HG0512.2	<i>H. sapiens</i>	ENSG00000104313	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	3
HG0512.3	<i>H. sapiens</i>	ENSG00000104313	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	1
HG0513	<i>H. sapiens</i>	ENSG00000126860	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5	1
HG0514	<i>H. sapiens</i>	ENSG00000147570	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	2
HG0515	<i>H. sapiens</i>	ENSG00000170471	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	2
HG0516	<i>H. sapiens</i>	ENSG00000041515	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2
HG0517	<i>H. sapiens</i>	ENSG00000086717	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	3
HG0518	<i>H. sapiens</i>	ENSG00000111254	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	2
HG0519	<i>H. sapiens</i>	ENSG00000127074	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	1
HG0520	<i>H. sapiens</i>	ENSG00000197415	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	1
HG0521	<i>H. sapiens</i>	ENSG00000038274	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1
HG0522	<i>H. sapiens</i>	ENSG00000140396	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	2
HG0523	<i>H. sapiens</i>	ENSG00000075213	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1
HG0524	<i>H. sapiens</i>	ENSG00000107929	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
HG0525	<i>H. sapiens</i>	ENSG00000136167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
HG0526	<i>H. sapiens</i>	ENSG00000143569	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
HG0527	<i>H. sapiens</i>	ENSG00000198382	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
HG0528	<i>H. sapiens</i>	ENSG00000204767	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
HG0529	<i>H. sapiens</i>	ENSG00000112851	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	4
HG0530	<i>H. sapiens</i>	ENSG00000128594	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	4
HG0531	<i>H. sapiens</i>	ENSG00000146834	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	4
HG0532	<i>H. sapiens</i>	ENSG00000105221	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	3
HG0533	<i>H. sapiens</i>	ENSG00000114209	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	4
HG0534	<i>H. sapiens</i>	ENSG00000117408	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	3
HG0535	<i>H. sapiens</i>	ENSG00000118407	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	4
HG0536	<i>H. sapiens</i>	ENSG00000181751	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	4
HG0537	<i>H. sapiens</i>	ENSG00000184481	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	4
HG0538	<i>H. sapiens</i>	ENSG00000006116	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0539	<i>H. sapiens</i>	ENSG00000115966	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0540	<i>H. sapiens</i>	ENSG00000120519	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0541.1	<i>H. sapiens</i>	ENSG00000122584	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0541.2	<i>H. sapiens</i>	ENSG00000122584	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	2
HG0542	<i>H. sapiens</i>	ENSG00000126581	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0543	<i>H. sapiens</i>	ENSG00000131931	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0544	<i>H. sapiens</i>	ENSG00000136802	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0545	<i>H. sapiens</i>	ENSG00000142784	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0546	<i>H. sapiens</i>	ENSG00000148143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0547	<i>H. sapiens</i>	ENSG00000149596	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0548	<i>H. sapiens</i>	ENSG00000155744	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0549	<i>H. sapiens</i>	ENSG00000156256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0550.1	<i>H. sapiens</i>	ENSG00000156650	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0550.2	<i>H. sapiens</i>	ENSG00000156650	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	0
HG0551	<i>H. sapiens</i>	ENSG00000162951	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0552	<i>H. sapiens</i>	ENSG00000169641	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0553	<i>H. sapiens</i>	ENSG00000183475	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0554	<i>H. sapiens</i>	ENSG00000196914	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	4
HG0555	<i>H. sapiens</i>	ENSG00000204310	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0556	<i>H. sapiens</i>	ENSG00000273841	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	3
HG0557	<i>H. sapiens</i>	ENSG00000012232	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0558	<i>H. sapiens</i>	ENSG00000029363	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0559	<i>H. sapiens</i>	ENSG00000078747	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0560.1	<i>H. sapiens</i>	ENSG00000092051	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0560.2	<i>H. sapiens</i>	ENSG00000092051	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	3
HG0561	<i>H. sapiens</i>	ENSG00000100393	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	2
HG0562	<i>H. sapiens</i>	ENSG00000105821	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0563	<i>H. sapiens</i>	ENSG00000107249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0564	<i>H. sapiens</i>	ENSG00000109171	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0565	<i>H. sapiens</i>	ENSG00000120533	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0566	<i>H. sapiens</i>	ENSG00000124496	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0567	<i>H. sapiens</i>	ENSG00000132155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0568.1	<i>H. sapiens</i>	ENSG00000138271	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0568.2	<i>H. sapiens</i>	ENSG00000138271	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1
HG0569	<i>H. sapiens</i>	ENSG00000139651	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	2
HG0570	<i>H. sapiens</i>	ENSG00000152214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0571	<i>H. sapiens</i>	ENSG00000153266	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0572	<i>H. sapiens</i>	ENSG00000158161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	4
HG0573.1	<i>H. sapiens</i>	ENSG00000162526	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	3
HG0573.2	<i>H. sapiens</i>	ENSG00000206203	0	0	0	0															

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[illegible]

[illegible]

HG1159	<i>H. sapiens</i>	ENSG00000152822	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1160	<i>H. sapiens</i>	ENSG00000154162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1161	<i>H. sapiens</i>	ENSG00000154227	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1162	<i>H. sapiens</i>	ENSG00000155380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1163	<i>H. sapiens</i>	ENSG00000157637	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1164	<i>H. sapiens</i>	ENSG00000162639	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1165	<i>H. sapiens</i>	ENSG00000162694	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1166	<i>H. sapiens</i>	ENSG00000165071	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1167	<i>H. sapiens</i>	ENSG00000165934	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1168	<i>H. sapiens</i>	ENSG00000166669	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1169	<i>H. sapiens</i>	ENSG00000167637	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1170	<i>H. sapiens</i>	ENSG00000167858	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1171	<i>H. sapiens</i>	ENSG00000167968	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1172	<i>H. sapiens</i>	ENSG00000170381	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1173	<i>H. sapiens</i>	ENSG00000170464	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1174	<i>H. sapiens</i>	ENSG00000173918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1175	<i>H. sapiens</i>	ENSG00000174473	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1176	<i>H. sapiens</i>	ENSG00000176472	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1177	<i>H. sapiens</i>	ENSG00000178295	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1178	<i>H. sapiens</i>	ENSG00000182670	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1179	<i>H. sapiens</i>	ENSG00000185933	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1180	<i>H. sapiens</i>	ENSG00000188674	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1181	<i>H. sapiens</i>	ENSG00000189058	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1182	<i>H. sapiens</i>	ENSG00000196155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1183	<i>H. sapiens</i>	ENSG00000198133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1184	<i>H. sapiens</i>	ENSG00000198894	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1185	<i>H. sapiens</i>	ENSG00000198920	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1186	<i>H. sapiens</i>	ENSG00000204923	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1187	<i>H. sapiens</i>	ENSG00000213762	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1188	<i>H. sapiens</i>	ENSG00000214415	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HG1189	<i>H. sapiens</i>	ENSG00000279909	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
HG1190	<i>H. sapiens</i>	ENSG00000123684	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HG1191	<i>H. sapiens</i>	ENSG00000164331	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HG1192	<i>H. sapiens</i>	ENSG00000168758	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HG1193	<i>H. sapiens</i>	ENSG00000177706	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HG1194	<i>H. sapiens</i>	ENSG00000214694	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2

** Numbers of orders from which uORF-tBLASTn and mORF-tBLASTn hits were extracted are indicated.

* Orders included in lower taxonomic categories were excluded.

***The category 'Ctenophora' was omitted from animal taxonomic categories because no sequences were classified to this category.

Supplementary Table S3. Numbers of bases and sequences of EST/TSA and RefSeq and their assembly.

	Species	Sequences	Bases
Plant			
Original EST/TSA	1,134	72,369,635	53,793,063,962
Assembled EST/TSA	1,134	44,000,517	22,309,227,524
RefSeq RNA	74	3,218,211	5,490,948,218
Assembled EST/TSA/RefSeq	1,143	47,218,728	27,800,175,742
Animal			
Original EST/TSA	1,765	174,758,651	142,647,705,501
Assembled EST/TSA	1,765	94,795,989	49,197,476,441
RefSeq RNA	332	10,679,878	28,758,793,440
Assembled EST/TSA/RefSeq	1,920	105,475,867	77,956,269,881
Eukaryota other than animals and plants			
Original EST/TSA	619	14,932,588	11,598,150,341
RefSeq RNA	303	3,047,192	4,604,373,881
Organism other than Eukaryota			
Original EST/TSA	37	21,275	19,198,153
RefSeq RNA	12,812	21,415	31,025,423

Supplementary Table S4. Estimation of the number of potential “spurious” CPuORFs for each species.

Species	(1): all uORF [*]	(2): uORFs that overlap with mORFs ^{**}	(3): (1)-(2)	(4): (2) & uORFs with FR ≥ 0.3
<i>D. melanogaster</i>	17,035	6,320	10,715	2,493
<i>D. rerio</i>	39,616	6,037	33,579	4,086
<i>G. gallus</i>	8,929	3,246	5,683	1,511
<i>H. sapiens</i>	44,085	23,380	20,705	3,814

^{*} When multiple uORFs in a transcript shared the same stop or start codon, they were counted as one.

^{**} uORFs that overlapped with an mORF between splice variants according to genomic information of the original species. The fusion ratio (FR) was calculated as shown in Supplementary Fig. S3b

Supplementary Table S5. Information regarding the constructs.

Gene symbol	Gene ID	Refseq ID	Construct
<i>PTP4A1</i>	ENSG00000112245	NM_003463.4	<i>pSV40:5'UTR (PTP4A1) ::luc2</i>
<i>MKKS</i>	ENSG00000125863	NM_170784.2	<i>pSV40:5'UTR (MKKS) ::luc2</i>
<i>SLC6A8</i>	ENSG00000130821	NM_005629.3	<i>pSV40:5'UTR (SLC6A8) ::luc2</i>
<i>FAM13B</i>	ENSG00000031003	NM_016603.3	<i>pSV40:5'UTR (FAM13B) ::luc2</i>
<i>MIEF1</i>	ENSG00000100335	NM_019008.5	<i>pSV40:5'UTR (MIEF1) ::luc2</i>
<i>EIF5</i>	ENSG00000100664	NM_001969.4	<i>pSV40:5'UTR (EIF5) ::luc2</i>
<i>MAPK6</i>	ENSG00000069956	NM_002748.3	<i>pSV40:5'UTR (MAPK6) ::luc2</i>
<i>MEIS2</i>	ENSG00000134138	NM_170674.4	<i>pSV40:5'UTR (MEIS2) ::luc2</i>
<i>KAT6A</i>	ENSG00000083168	NM_006766.5	<i>pSV40:5'UTR (KAT6A) ::luc2</i>
<i>SLC35A4</i>	ENSG00000176087	NM_080670.3	<i>pSV40:5'UTR (SLC35A4) ::luc2</i>
<i>LRRC8B</i>	ENSG00000197147	NM_015350.2	<i>pSV40:5'UTR (LRRC8B) ::luc2</i>
<i>CDH11</i>	ENSG00000140937	NM_001797.3	<i>pSV40:5'UTR (CDH11) ::luc2</i>
<i>PNRC2</i>	ENSG00000189266	NM_017761.3	<i>pSV40:5'UTR (PNRC2) ::luc2</i>
<i>BACH2</i>	ENSG00000112182	NM_021813.3	<i>pSV40:5'UTR (BACH2) ::luc2</i>
<i>FGF9</i>	ENSG00000102678	NM_002010.2	<i>pSV40:5'UTR (FGF9) ::luc2</i>
<i>PNISR</i>	ENSG00000132424	NM_001322405.2	<i>pSV40:5'UTR (PNISR) ::luc2</i>
<i>TMEM184C</i>	ENSG00000164168	NM_018241.3	<i>pSV40:5'UTR (TMEM184C) ::luc2</i>