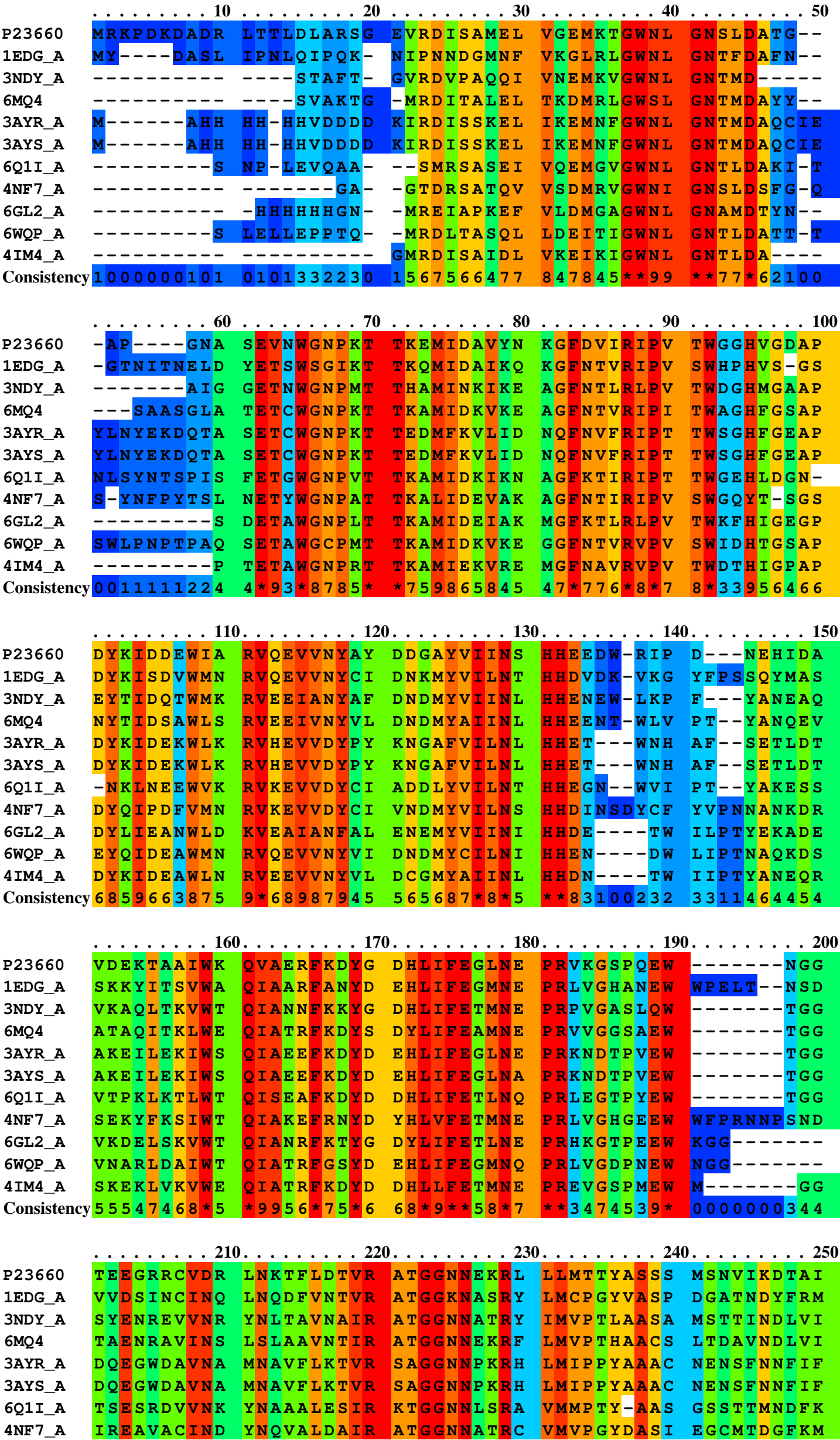


Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved



6GL2_A	TQEGRD	AVNQ	YHQVSV	DAIR	ATGGNN	AKRK	IMVST	TYAAS	TASNAL	NDYLV
6WQP_A	NQEARQ	VINS	YNQTFV	NTVR	ATGGNN	AIRC	LMVPT	TYAAS	CSSTTV	NDFVL
4IM4_A	TYENRD	VINR	FNLAVV	NTIR	ASGGNN	DKRF	ILVPT	TNAAT	GLDVAL	NDLVI
Consistency	549545	5994	584557	579*	77**8*	45*3	89775	66963	354546	5455

	260	270	280	290	300
P23660	PEDD-----H	IGFSIHAYTP	YAFT---YNA	NADWELFHWD	DSHDGELVSL
1EDG_A	PNDISGNNNK	IIVSVHAYCP	WNFAGLAMAD	GGTNAWNIND	SKDQSEVTWF
3NDY_A	PNN----DSK	VIVSLHMYSP	YFFA-----M	DINGTSSWGS	DYDKSSL DSE
6MQ4	PNN----DSK	IIVSLHMYSP	YYFA---MV--	SNSTPTWGT	DSDKSSLSYE
3AYR_A	PED----DDK	VIASVHAYAP	YNFA---LNN-	GEGAVDKFD	AAGKRDLEWN
3AYS_A	PED----DDK	VIASVHAYAP	YNFA---LNN-	GEGAVDKFD	AAGKRDLEWN
6Q1I_A	VPD----DKN	VIASVHAYSP	YFFA---MDT	SSNSVNTWGS	SYDKYSL DVE
4NF7_A	PNDT--ASGR	LILSVHAYIP	YYFA-----L	ASDTYVTRFD	DNLKYDIDSF
6GL2_A	PNG----DKN	VIVSVHSYFP	YQFC-----L	DGTDSTWGTE	ADKTALLAEL
6WQP_A	PTDT--VANK	LIVDIHSYSP	YNFA-----L	NT-SGTSSFT	QSDISQLQWT
4IM4_A	PNN----DSR	VIVSIHAYSP	YFFA-----M	DVNGTSYWGS	DYDKASLTSE
Consistency	8560000546	88688*6*5*	93*8000113	2444433235	5445458433

	310	320	330	340	350
P23660	MTNLKENYLD	KDIPVIITEY	GAVNKDND	DRAKWVSSYI	EYAEELLGIP
1EDG_A	MDNIYNKYTS	RGIPVIIGEC	GAVDKNN-LK	TRVEYMSYYV	AQAKARG-IL
3NDY_A	FDAVYNKFKV	NGRAVIGEM	GSINKNN-TA	ARVTHAEYYA	KSAAKARG-LT
6MQ4	LDAVYNKFIK	NGRAVIGEF	GSIDKSN-LS	SRVTHAQYYA	QEATKRG-IP
3AYR_A	INLMKKRFVD	QGIPMILGEY	GAMNRDN-EE	DRATWAEFYM	EKVTAMG-VP
3AYS_A	INLMKKRFVD	QGIPMILGEY	GAMNRDN-EE	DRATWAEFYM	EKVTAMG-VP
6Q1I_A	LDSYLNTEFKS	KGVPVVIGQF	GSINKNN-TS	SRAELAEYYV	TAAQKRG-IP
4NF7_A	FNDLNSKFLS	RNIPVVVGET	SATNRNN-TA	ERVKWADYYW	GRAARYSNVA
6GL2_A	DKIRDKFIVE	DNRAVVMGEW	GSTFSDN-PE	DRLAHAEFYA	RACAER-GIC
6WQP_A	LQEIYNSFGA	KGIPVIIGQF	GALNKNN-IN	GRVLWGENYL	RIAKSY-NIR
4IM4_A	LDAIYNRFVK	NGRAVIGEF	GTIDKNN-LS	SRVAHAEHYA	REAVSRG-IA
Consistency	5535465755	5756898884	876676*035	5*644775*5	4474555094

	360	370	380	390	400	
P23660	CVWWDNGY-Y	SGNEL	FGIFDRNTCT	WFTDVTVD	AIENAK----	
1EDG_A	CILWDNNN-F	GTGEL	FGFFDRRSCQ	FKFPEIIDGM	VKYAFGLIN-	
3NDY_A	PIWWDNGYSV	GKAET	FGIFNRSNLT	WDAPEVMKAF	IKGIGGSS--	
6MQ4	VCWWDNGYYG	GKDNS	YALLNRS	SLTWYYPEIVQAL	VKGS	GYTV--
3AYR_A	QIWWDNGVVF-	GTGER	FGLLDRKNLK	IVYPTIVAAL	QKGRGLEVNV	
3AYS_A	QIWWDNGVVF-	GTGER	FGLLDRKNLK	IVYPTIVAAL	QKGRGLEVNV	
6Q1I_A	CVWWDNNYAE	NKGET	FGLLNRSTLN	WYFSDIKDAL	IRGYK---	N-
4NF7_A	MVLWDNNIYQ	NNSAGSDGEC	HMYIDRNSLQ	WKDPEIIST	IMKH-----	
6GL2_A	PIWWD-----	NVDE	FGIFNRNTLE	WNYPEIAEAI	VK-----	
6WQP_A	CIWWDNNAFD	SGEN	FGLLNRGTLT	WQYPELLEAM	MK-----	
4IM4_A	VFWWDNGYYN	GDAET	YALLNRK	TLSSWYYPEIVQAL	MRGAG---	
Consistency	377**85321	4000044583	76767*5675	6357695587	6832200110	

		410
P23660	-----	
1EDG_A	-----	
3NDY_A	-----	
6MQ4	-----	
3AYR_A	VHAI EKETEE	
3AYS_A	VHAI EKETEE	
6Q1I_A	VH-----	
4NF7_A	-----	
6GL2_A	-----	
6WQP_A	-----	
4IM4_A	-----	
Consistency	0000000000	