

CLUSTAL X (1.83) multiple alignment of all 182 non-redundant SET-domain hits.

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XP_387621 Fg      -PVKFARSAIH--NWGLYA--MENIAKDDMIIEYVGQVRQQISEIRENR-----YLKSGIGS-----SYLFRID-----DNT
XP_961572 Nc      -PVKFARSAIH--NWGLYA--MENINKDDMIIEYVGEEVRQQIAELREAR-----YLKSGIGS-----SYLFRID-----DNT
XP_750524 Af      -PVRFARSAIH--NWGLYA--EENISANDMIIEYVGKVRQQVADMREKQ-----YLKSGIGS-----SYLFRID-----ENT
XP_449333 Cg      -PVTFARSAIH--NWGLYA--LEPINAKEMVIEYVGGERIRQPVAMRERR-----YIKNGIGS-----SYLFRID-----EHT
NP_983083 Ag      -PVTFARSAIH--NWGLYA--LEPISAKEMIEYVGGERIRQPVAMREKR-----YLKSGIGS-----SYLFRVD-----EST
NP_011987 Sc      -PVMFARSAIH--NWGLYA--LDSIAAKEMIEYVGGERIRQPVAMREKR-----YIKNGIGS-----SYLFRVD-----ENT
EAK99965 Ca      -PVTFARSAIH--NWGLYA--MEPIAAKEMIEYVGGERIRQQVAEHREKS-----YIKTGIGS-----SYLFRID-----DNT
XP_001411780 Mg   -PVKFERSAIH--NWGLYA--MEHIPKDDMIIEYVGEEVRPSVAQVREAR-----YDRSGIGS-----SYLFRID-----EDA
BAC65717 Mm      -----KSHIH--DWGLFA--MEPIAADEMVIIEYVGQNIHQVIADMRER-----YDEGIGS-----SYLFRVD-----HDT
NP_821172 Mm      -----KSRIH--EWGLFA--MEPIAADEMVIIEYVGQNIHQVMADMRER-----YVQEGIGS-----SYLFRVD-----HDT
NP_587812 Sp      -QLHFGPSRIH--TLGLFA--MENIDKNDMVIIEYIGEIIRQVRADNREKN-----YVREGIGD-----SYLFRID-----EDV
BAB10481 At      -HLRFQQSKI--DWGLVA--LEPIEAEDFVIEYVGELIRSSISEIRERQ-----YEKMIGS-----SYLFRID-----DGY
NP_001074518 Mm   -----RSPIH--GRGLFC--KRNIDAGEMVIEYAGNVIRSIQTDKREKY-----YDSKGIG-----CYMFRID-----DSE
NP_083550 Mm      -----RSIH--GRGLFC--KRNIDAGEMVIEYSGIVIRSVLTDKREKF-----YDGKGIG-----CYMFRMD-----DFD
NP_476769 Dm      -----RSHIH--GRGLYC--TKDIEAGEMVIEYAGELIRSTLTDKREKY-----YDSRGIG-----CYMFKID-----DNL
NP_001074852 Mm   -----RSRIQ--GLGLYA--ARDIEKHTMVIIEYIGTIIRNEVANRKEKL-----YESQNRG-----VYMFRMD-----NDH
AAH58659 Mm      -----RSRIQ--GLGLYA--AKDLEKHTMVIIEYIGTIIRNEVANRREKI-----YEEQNRG-----IYMFRIN-----NEH
NP_726773 Dm      --VYLARSKI--GLGLYA--ARDIEKHTMIEYIGEVIRTEVSEIREKQ-----YESKNRG-----IYMFRID-----EDR
AAK01237 At      -RLAFGKSGIH--GFGIFA--KLPFRAGDMMIEYTGELVRPSIADKREQL-----IYNSM-VGAG-----TYMFRID-----DER
AAF29390 At      -RLAFGKSGIH--GFGIFA--KLPFRAGDMMIEYTGELVRPPIADKREHL-----IYNSM-VGAG-----TYMFRID-----NER
BAA97320 At      -RVCFGRSGIH--GWGLFA--RRNIQEGEMVLEIRGEQVRGI IADLREAR-----YRR--EGKD-----CYLFKIS-----EEV
NP_194520 At      -RVCFGRSGIH--GWGLFA--RRNIQEGEMVLEIRGEQVRGSIADLREAR-----YRR--VGKD-----CYLFKIS-----EEV
CAA71599 At      -RVLLGISDIS--GWGAFL--KNSVSKHEYLGEYTGELISHKE--ADKRG---KIYD-RENC-----SFLFNLN-----DQF
AAD09108 At      -RILLGKSDVA--GWGAFL--KNSVSKNEYLGEYTGELISHHE--ADKRG---KIYD-RANS-----SFLFDLN-----DQY
NP_031996 Mm      -----SDVA--GWGTFI--KESVQKNEFISEYCGELISQDE--ADRRG---KVID-KYMS-----SFLFNLN-----NDF
NP_031997 Mm      -----SDVA--GWGIFI--KDPVQKNEFISEYCGEIIISQDE--DDRRG---KVID-KYMC-----SFLFNLN-----NDF
NP_524021 Dm      -HLLMAPSDIA--GWGIFI--KEGAQKNEFISEYCGEIIISQDE--ADRRG---KVID-KYMC-----SFLFNLN-----NDF
AAC39446 At      -KILIGKSDVH--GWGAFT--WDSLKKNEYLGEYTGELITHDE--ANERG---RIED-RIGS-----SYLFTLN-----DQL
XP_381075 Fg      -GLALQSQLEGVGYGLFT--VEPIAQDDFIIIEYVGELITHDEGEVARRG---DVFEESNI-----SYVFTLLEN-----EGI
EAA35807 Nc      --VLLGKSQLEGCGYGLFT--AEDISQDEFVIEYTGELITHDEGEVARRG---EGFGSQGTS-----SYLFTLLEH-----EGI
XP_369092 Mg      -PLCLGESGIEGCGYGLFT--AVDIAADEFIIIEYVGELIQHDEGEVARRG---NVFEESNV-----SYLFTLLED-----DGI
XP_385734 Fg      --ANVSVIKTEKKGFGLRA--DSDLQPNDFVFEYIGEVINEPTFRRMIMQ-----YDEEGI-----KHFFYMSLN-----KSE
XP_957740 Nc      --ADVSVIKTEKKGFGLRA--NTDLQVNDFIFEYIGEVINEPTFRSRMVK-----YDKEGI-----KHFFYMSLT-----KSE
EAL91994 Af      --ANVAVIKTEKKGFGLRA--ETDLRPHQFIFEYIGEVINEAQFRRMIMQ-----YDEEGI-----KHFFYMSLS-----RGE
XP_363735 Mg      --ANVSVIKTENKGYGLRA--DANLEPNDFVFEYIGEVIGEEELFRSRLMK-----YDTQRL-----KHFFYMSLT-----RTE
NP_594980 Sp      --AKVDVFLTEKKGFGLRA--DANLPKDTFVFEYIGEVIPEQKFRKMRMQ-----YDSEGI-----KHFFYFMLQ-----KGE
XP_445194 Cg      --ANIAVFKTKMKGYGVRA--ESDIEINDFIIEYKGEVIEEEEFDRDLVD-----YDQKKF-----RHFFYFMLQ-----SGE
NP_012367 Sc      --APIAIFKTKHKGYGVRA--EQDIEANQFIIEYKGEVIEEMEFRDLID-----YDQRHF-----KHFFYFMLQ-----NGE
NP_984733 Ag      --ADIAVFQTEKKGYGVRA--ERDIEANEFIIEYIGEVISEADFRDRMVD-----YDMRGF-----KHFFYFMLQ-----AGE
EAK95292 Ca      --SKVKVIQTELKGYGLIA--EQDIEENQFIIEYIGEVIDEISFRQRMIE-----YDLRHL-----KHFFYMMLS-----NDS
NP_001074809 Mm   -----GWGLRA--AKDLPNTFVLEECYCEVLDHKEFKARVKE-----YARNKN-----IHFFYFMALK-----NDE
NP_572888 Dm      ---PCRVRTEKKKCGGITA--ELLIPPGEFIMEYVGVIDSEEFERRQHL-----YSKDRN-----RHFFYFMALR-----GEA
AAC34358 At      -YVKFERFQSGKKGYGLRL--LEDVREGQFLIEYVGVELDMQSYETROKE-----YAFKGQ-----KHFFYMTLN-----GNE
XP_132006 Mm      --PETKIIKTGKGWGLVA--KRDIRKGEFVNEYVGELIDEEECMARIKY-----AHENDI-----THFYMLTID-----KDR
NP_032765 Mm      -----GWGLRT--KTDIKKGEFVNEYVGELIDEEECRARIRY-----AQEHDI-----TNFYMLTLD-----KDR
NP_001001735 Mm   -----GWGLRT--KRSIKKGEFVNEYVGELIDEEECRLRIKR-----AHENSV-----TNFYMLTVD-----KDR
NP_733239 Dm      -----FGLVN--REPIAVGDFVIEYVGVEVINHAEFQRRMEQ-----KQRDRD-----ENYFVLGVE-----KDF
AAC23419 At      -VKMKMLIQTEKCGSGIVA--EEEIEAGEFIIIEYVGVIDDKTCEERLWK-----MKHRGE-----TNFYLCETI-----RDM
CAB75815 At      -IKMKMLVQTEKCGYGIVA--DEDINSGEFIIIEYVGVEIDDKICEERLWK-----LNHKVE-----TNFYLCQIN-----WNM
CAA18207 At      -EKKIKIVKTEHCGWGVEA--AESINKEDFIVEYIGEVISDAQCEQRLWD-----MKHKGM-----KDFYMCEIQ-----KDF
AAF04434 At      -YAKTKLIKCEGRGWGLVA--LEEIKAGQFIMEYCGEIVSWEAKKRAQT-----YETHGV-----KDAYIISLN-----ASE
XP_389092 Fg      --VGVEVIKTSDRGYGVRS--NRCFRPNQIIMEYAGEIITEECERRMTE-----VYKDNE-----CYLLMSFD-----QNM
EAA34880 Nc      -RIGVEVFKTEDRGYGVRS--NRCFEPHQIIMEYTGEEITDEECERRMNE-----EYKNNEVCFPRDCSS-----SCYLLMSFD-----QNM
XP_964116 Nc      ----FQMLTERTK----KG--GRYRIGVEIIMEYTGEEITDEECERRMNE-----EYKNNE-----CYLLMSFD-----QNM
EAL92920 Af      --IGVEVIKTADRGYGVRS--NRTFEPNQIIEYTGEEITQAECEKMRMT-----IYKNNE-----CYLLMYFD-----QNM
NP_524160 Dm      -----TADKGWGVRT--KLPIAKGTIIEYVGVEVTEKEFKQRMAS-----IYLNDT-----HHYCLHLD-----GGL
NP_619620 Mm      -----RAEEKGWGIRT--KEPLKAGQFIIIEYLGEVVSQEFRNRMIE-----QYHNHS-----DHYCLNLD-----SGM
NP_196541 At      --PPLVVVFDPLEGYTVEA--DGPIDKLTIFAETG--DVDYLNKREKD-----DCDSIMT-----LLLEDPSK-----TVI
NP_197821 At      --PPLMVVFDPEGYTVEA--DRFIKDWITIIEYVG--DVDYLSNREDDY-----DGDSMMT-----LLHASDPSQ-----CVI

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NP_084517	Mm	--EGMKIDLIDGKGRGVIA--TKQFSRGDFVVEYHG-LIEITDAKKREALY-----AQDPSTG-----CYMYFYQYL-----STY
NP_650354	Dm	-----GVVA--DRPFKRNEFVVEYVG-LISIGEAAEREKRY-----ALDENAG-----CYMYFYKHK-----SQY
XP_752474	Af	-VRLEIFHTGN-RGFGLRS--PDWIRAGQFIDCYLGEVITKQEADVRE-----EVVTSQHGH-----SYLFELDFHFD-----D--EI
NP_595186	Sp	-LPLEIFKTKE-KGWGVRs--LRFAPAGTFITCYLGEVITSAEAAKRD-----KNYD-DDGI-----TYLFDLDMFDD-----A--SE
XP_382954	Fg	-IPLEIFRTED-RGWGVRs--PVSIRKGQFVDRYLGEIITSTEADRRRS-----QSAISQRKD-----VYLFALDKFTD-----KGPSL
EAA28243	Nc	-VPLQIFRTKD-RGWGVKC--PVNIKRQGFVDRYLGEIITSEEADRRRA-----ESTIARRKD-----VYLFALDKFSD-----AGQPL
XP_370355	Mg	-LPLQIFRTDDGRGWGVRa--TVDIKCGQFVDTYIGEVITDSEAVERR-----KATRKKD-----LYLFDLDKFWQ-----DSDRL
NP_073561	Mm	-----GWGVKT--LVKIKRMSFVMEYVGEVITSEEAEERRGQ-----FYDNKGI-----TYLFDLDY-----ESDEF
NP_035644	Mm	-----GWGVRT--LEKIRKNSFVMEYVGEIITSEEAEERRGQ-----IYDRQGA-----TYLFDLDY-----VEDVY
NP_524357	Dm	----VLFKTANGSGWGVRA--ATALRKGEFVCEYIGEIIITSEANERGK-----AYDDNGR-----TYLFDLDYNT-----QDSEY
NP_766133	Mm	-----RTQDMGWGVRs--LQDIPLGTFVCEYVGEILSDSEADVRE-----ED-----SYLFDLDNK-----DGEVY
NP_665829	Mm	-----GWGVRA--LQTIPOGTFICEYVGEILSDAEADVRE-----DD-----SYLFDLDNK-----DGEVY
NP_569834	Dm	-----WGVRA--LANVPKGTfVGSYTGIEILTAMEADRRt-----DD-----SYFDFLDN-----G--H
AAD10665	At	-NKLQVFFTPNGKGWGLRT--LEKLPGKAFICEYIGEILTIPELYQRS-----FEDKP-----TLPVILDAHWE-----GDKAL
AAK92218	At	-NKLQVFFTPNGRGWGLRT--LEKLPGKAFVCELAGEILTIPELFQR-----ISDRP-----TSPVILDAYWG-----DDKAL
AAF63769	At	-CQLQVYFTQEGKGWGLRT--LQDLPKGTfICEYIGEILTNTELYDRNV----RSSSERH-----TYPVTLADADWK-----DEEAL
AAC17088	At	--AKLEVFRTEskGWGLRA--CEHILRGTFVCEYIGEVLDDQOEANKRRN-----QYNGGDC-----SYILDIDANIE-----EELDY
AAH45208	Mm	-----GWGLRT--LEFIPKGRFVCEYAGEVLGFSEVQRH-L-----QTSHDSN-----YIIAVREHI-----QIMET
NP_001097743	Dm	-KHLEIFDSPVYGSKGLRT--TAKITKGGYICEYAGELLTPPEARSHDN-----EKGLMN-----YILVLNEYT-----KQOVT
AAF00642	At	-VSLKIVRD-EKKGWCLYA--DQLIKQQGFICEYAGELLTTDEARNNIY-----DKLRSTQSF-----ASALLVvreHL-----ACLRI
NP_611966	Dm	--MKLQVFKTSNRGWGLRC--VNDIPKGAFICIYAGHLLTETMANEG----GQDAGDEYFADL-----DYIENSKD-----EAPY
NP_061365	Mm	--VRLQLFKTQNKGWGIRC--LDDIAKGSFVCiYAGKILTDdFADKE-----GLEMGEYFANL-----DHIEKSTHGIG-----EESCY
NP_001019872	Mm	--VRLQVFKSEKKGWGVRc--LDDIDKGTfVCIYSGRLRRATPEKTNIGE-GREQQHNSFSKK-----RKLEASQSQS-----KESLF
AAK28971	At	-KLPLEIFKTKSRGWGVRc--LKSIPIGSFICEYVGEILLEDSEAErR-----IGNDEYLFDI-----GNRYESSG-----F
NP_181061	At	--IKLEIFKTKSRGWGVRs--LESIPIGSFICEYAGELLEDKQAESL-----TGKDEYLFDL-----G--EDDP-----F
NP_196900	At	--FNLEVFRSAKKGWAVRS--WEYIPAGSPVCEYIGVVRRTADVDTI-----SDN-EYIFEI-----DCQQENAPE-----F
AAK28974	At	-RNRLEVFRSLETGWGVRs--LDVLHAGAFICEYAGVALTREQANIL-----TMNGDTLVYP-----ARFSIPPVD-----F
NP_180887	At	--NRLEVFRSKETGWGVRT--LDLIEAGAFICEYAGVVVTRLQAEIL-----SMNGDVMVYP-----GRFTLPPLD-----F
AAK28966	At	-KVRLEVFKTANRGWGLRS--WDAIRAGSFICIYVGEAKDKSKVQQT-----MANDDYTFDT-----TNVYEIPL-----PL
NP_565056	At	--SRLEVFKTRNRGWGLRS--WDSLRAGSFICEYAGEVKDNGNLRGn-----QEEDAYVFDt-----SRVFNLPS-----PL
AAK28973	At	-KLHLEVFKTSNCGWGLRS--WDPiRAGTFICEFTGVSKTKEEVE-----EDDDYLFDT-----SRIYNLPT-----QV
NP_564036	At	--LHLEVFKTRNCGWGLRS--WDPiRAGTFICEFAGLRKTKKEEVE-----EDDDYLFDT-----SKIYNLPT-----QV
NP_178647	At	-RPGLILEDLsNGAENLKV--CEVKENGpALFRYVTVINNIpSMVDR-----CACGRRSCGS-----KHVFREKLS-----VSSL
EAA50044	Mg	---GLYVSHYGGKGFgIR--VTFYGRRHVfGELVGNLVKPGSFSDGMG-----LVFARDDLDEQ-----PVTAQ
XP_365330	Mg	---PSVVYFDGKELGLQAM-AEAYRKGTlIGEiVGRiVPPNTYNDGRA-----MMMVREDMDN-----EYVGQ
EAL89869	Af	---VQIFSTASGKNNGVVA--RVNFDrgAAiGEfVGLITNGISGVD-----VMVGgTKSR-----TYQ
XP_383195	Fg	---VQVFCTSNGRNGLQA--LVAFERGTAiGEfVGLITKDIEEQD-----VMSQAGGT-----RYQ
XP_357091	Mm	-CLMQTSFGDVP-HFGVFC--SDFIAKGVRfGPFGRVRVNASE-----VKAKGS-----
NP_031574	Mm	-LLFKYAANNsKEViGVVS--KEYIPKGTFRGPLiGEVYTNDT-----VPKNNEE-----
NP_001028453	Mm	-CLCTSTVPGLA--YGICA--AQRIQQGTWiGPFQGVLLSPEK-----VQTGVEP-----
EAL91753	Af	---VELVDYPQR-GIGVRA--LARFKGDILDEYVGELRPLDYTDdRVYG-----LLHESKMTEG-----HPL
XP_964337	Nc	-QIPRIQTdGSR-GEgVRA--IGSFKADECLGELVGELRPPRTAGTSCSS-----DHNHPNISSGQ---AQLLHDQLV
XP_449432	Cg	-YFDINETSW--GGRACFS--KRDLNNGQVVLEVEKAKFKAGLWFC-----DTCRDKYLSIHDNTTTVL---LPDNLKNSLTvQAFRH---QD-EAVDS
NP_015160	Sc	-FFQVRQTKW--GGRACFS--NGNIPKGTTVLQVSPKfLgAGLWFC-----EHCRtSYLQIPQSSesIL---LPSHLHRMLSIPLLRH---QE-EASDS
NP_982445	Ag	-LFEVKLTdY--GGRACFA--RQSQQRGDTVLKLTASSFGGGGLRFC-----EICKNAYMQMEERENVV---LPiGLRDLLSSALFRK---EQ-EGNYS
EAK94622	Ca	-WFiVDETKY--GGRGCFa--PKViPQ-HTViHSCQHvYS--LFFC-----EECKSTfTHQ-DVKEALT---CTPELQAFIDSTTIRS---SEVDPSed
NP_983709	Ag	-KVQVTWS--EKKGGLVA--RRPLAKGELVFAED-ALSFIPP-----LEKSTLVHLSKACG-----MSMWEEGYGLFCDAFP---LRYVGKFN
P38890	Sc	-KVEVKFiDD-EHGRGLFA--KRDFSKGQiILKENKPiViYIP-----LDKLFLiSNGKACARSW---ETVWEKCYELFCGAfP---LTMiGTfN
XP_446364	Cg	-KVEIRECEELRKGRGLYA--TRDiQQGELLFHEKVPiAMVPP-----MDKLELiRSGKSCS-----GSLWKKAfDLFiRTFP---LEYLGRFH
EAK96662	Ca	-NVHIIMTS--KRKGGLYA--KRDiAKGDLiWSEE-PLFFIPP-----LANVNLMKtASACTYN-----EHLWKiGYEKFLRVFP---LFMMGTYN
XP_385929	Fg	-LFVVSdVPP--KGGLIA--TTKiPKGTRIiAEPLLiKV-----PRIIK---EECGEEV---GIAETNGLCAGP-----
XP_391443	Fg	-MTELQEVPG--KGQGLIA--TRKiPKGTRIlSEKaiIRV-----PEiFANSDDDTSPYL---GIVRSNGL---P-----
NP_588413	Sp	-iYKVViPiPN--KGMGMiA--KVKiPVGTRIFAETPLiRT-----KSDAKEHPDTMGPFfL---GPfYSNALTID-----
EAA33925	Nc	-LYDiViPiPN--KGTGVIA--TQDiAKGTRIMAEKPLFiV-----PTNVMEHGTTfSPfL---AiCKTNMLGLGS-----
EAA49663	Mg	-PYVAVPVPG--KGiGLRA--TQPiRTGHlVtARTPAVMVDER-----TGLAD-AAKDH-----TNAYRTSiR-----
XP_362227	Mg	-VYKsVMVPG--KGVGLVA--ARTLYRGDRiMSSTPAiViDYG-----ETMPDGLYENY-----TNAFDiDADPDD-----
XP_366867	Mg	IMYELRNspG--KGKGLFA--SASVRQGDRIiAEAPLiTVDLARfRL-----PPAELEGADENNPLS---SRfLTNALGTDEDDRQ---Q---NP
XP_364335	Mg	-TYAVVPVPG--KGLGVVA--TRHiRAGEiLMADDPLLVADVA-----S--RG-SYSGG-----TNTfAVGVG-----
XP_370301	Mg	-SWEVKKVPg--KGLGMVA--KRRiPRGETFLVDYAAiLASVP-----GRVRS-STQGA-----TNTfSLEID-----
XP_368905	Mg	-LFERKEiPG--KGVGLVA--RRPiSRGQLiMAQRPAiLVDi-----KDIsDQTDs-----ANTNSfNLNiAG-----
XP_364537	Mg	-PfRAQAiPG--KGVGLVA--KRPiAKGELVMAETPAiLVHK-----LEEAQTGD-----LFTNSfQMALSGKA-----
EAA26997	Nc	KPFSESFiLS--KGPLTA--TiPLRRRKPLMSAAPVLLVHKD-----FFVDiWRKSERNK---FLLLASPFiDLGSNS---QA--TLQT

XP_363030 Mg PPFYKADIPG--KGKGVIA--KRKIALGETIMILPPTLLVSDA-----AYQAFGGARKALH--G--LDAAMKLDKNGFT-----YT
 NP_572675 Dm -PYRVEHSDIY--GRYLVA--NRQLEAGETLIREEPLAIGPCVSGDP-----VCLGLEDEAEQ-VHEVC--GILDVNCFEIGQ-NGA-----
 NP_609464 Dm -RTAVQWSPVC--GRYLVA--KGAIRGHGLLIEELPFAVGPKCNGPV-----VCLGLANRSEELIMQVV--GVLEVNAFEARSPKGY-----
 NP_649084 Dm -CFEIAATNEVL--GRHLRA--TRDIKIGEQLKEAPLVLGPKVASAP-----LCLGMKD--PEMDILRIA--AILDNTTFEVRQPRER-----
 NP_610944 Dm -PFKIAHNEQL--GRHLVA--TRTIKPYEIVLKEAPLVRGPAQISAP-----VCLGTQK--TEEEIMKAV--GALQINGHEVP-TTDP-----
 NP_001014717 Dm -NWTISSSTVA--GRGVFA--TRDIAAGELIFQERALVTGPTARKGQ-----SSCICTTDRFMDQLFRIV--GVLNNTAFEAAPC-RSG-----
 CAA15694 Dm -SWRVADSPIS--GRGIFA--TREIAAGEELFREHTLLVGPTAHRSMN----RTCTLR-EQMLDYFYRTI--CAFNTNAFESRS-NVD-----
 NP_572539 Dm -AWEIGVSKIA--GRGVVA--TRSLKRGEIIFRDSPLLIGLAAHEEDS----NACSVT-DKLIEIMNRTV--AVLRTNGFDKTTDRND-----
 NP_033892 Mm -NVEVFTSEGK--GRGLKA--TKEFWAADVIFAERAYSAVVFD-----SLINCH---ISHIF--GVINCNGFTLSDQRLQ-----
 NP_081072 Mm -GLERFCSAGK--GRGLRA--LRPFHVGDLFLSCPAYACVLTV-----GERGCE---LVVLF--AQVNCNGFTIEDEELS-----
 NP_081464 Mm -KVEKFTTANR--GNGLRA--VAPLRPGELLFRSDPLAYTVCK-----GSRGCDPSFDLFEAF--AKVICNSGFTICNAEMQ-----
 XP_360530 Mg -AVHGTGKGRS--GRSLRA--TRDFQPGDLIAEFDNPLAAFP-----RASTTCHHFLSLDVL--CKIQTNNSFDR---FDAD-----
 XP_381344 Fg -APFRVKSHRK--GRGIFS--TKSFAPGDVILPFT-PTILIP-----HINTICSHQKALTIL--CKIQTNAFHR---YDTD-----
 EAA36113 Nc -RIGGIPGVDR--GRSLFS--TERFGAGETIAIIENPLLALP-----NMRTTCNYKQAMEVL--CKIQTNAFNR---FDAD-----
 NP_650955 Dm -NFEIRELP GK--GRAMIA--TKNFAKDEVIFEEEPFVSQRQFSWNVAYG--YAKVRYCLTDSEKEQLDTV--IDGLYAKVGEF--EFLN-----
 NP_659167 Mm -----LTPQDREQLDTF--IDQLYKDIEAA--EFLN-----
 XP_384827 Fg -PVEIRDSPGR--GRGLFT--TKSVSAGDLLLVEKAFSYSYMDENRLW----DQITYMINLTSAPQDLV--DGG-LNSFG---SPT-----SCRER
 XP_380216 Fg -PVEIRESPPGR--GKALFT--TKAVSAGELLCKKAFSYSFAGDEQST----KQTKILMNLAAEFGLDHL--HAD-LNGFG---APR-----TGDEG
 EAL91344 Af -PVAVRPTESR--GRGLFT--TEAVKAGDLLFCEKAFAHAFHDADDP--RSIGLLINPQPAFIDLY--HDS-LNCFG---CPL-----DHDEQ
 XP_367445 Mg -RTRIAKTDNR--GRGLFA--TVPLCEGDVIFVEKAFFTVHRDAG-----DLAVLININKRYYDLF--DGGKLNFGF---CPR-----VQEG
 XP_366224 Mg -RTEERPSATH--GRGLFA--TERIAAGELVFVEKATVMPPQYDE-----RRLCRMH--AGDYRNCFS---APL-----GLAR
 EAA35550 Nc -NTRVADSGFH--GRGLFA--TRPLKAGDLVYVEKATLMPNQYDP-----DTMLKLY--PGQLKNCFS---SPL-----TYN
 AAF87042 At -GSIEIKKSELS--GRGLFA--TKNIVAGTLVLVTKAVAIERGILNGE----CGEKAQLIMWPEIALFR--PDEAFETCGDWWKSLD-----VMGKN
 XP_387208 Fg ---DYEIIPT-CKQLGVFA--KEDIAKGEAVLKEYSLLTANNRLKDSI----CDACSPPKMDIDIYENL--DEYDLWVMN---GTA-----RD
 XP_957213 Nc ---EYEIIPT-CNQLGLFA--KEDIAKGEAVLKEYSLLTANNRHKEST----CDACGPPKMDIDIFETL--PQHDLVVFN---GTA-----RD
 XP_365932 Mg ---GVAEQGT-CKQLGVFA--AADIGPGEVVLREFSALTANNRLQEPV----CDACGPSTMDVDIYRTL--ARHDTWVMN---GTA-----RD
 XP_367482 Mg ---NRYTIFTH-EASVTA--RRPIRKNEI IKALCGIQVVISP-----AEEASK-----
 EAA33797 Nc -NATNRYTIVTY-EASITA--RRFIQRNETIKYLAGIQVVITP-----EEELSK-----
 XP_386705 Fg -SSTNRYTIVSH-EAAVTA--RAAIRNEAIKYLSGVQVVITP-----EEMSK-----
 EAL93147 Af -TTTNRYTITEY-EAAVCA--RKFIKQGEIKYLSGTLVPMTR-----EERKK-----
 NP_588078 Sp -CSTNQYFSSSKPEACVIA--RESINAGEDITDLCGTI IKLSP-----KEERLD-----
 AAF45537 Dm --ACYRYTLEEQRGAKISS--TKRWSKNKDIECLVGICIAELTE-----AEEAAKN-----
 NP_659120 Mm -LPCNRYSE--QNGAKIVA--TKEWKRNDKIELLVGICIAELSE-----IENMKN-----
 NP_666289 Mm -----ME-TNGAKIVS--TRAWKKNEKLELLVGICIAELRE-----EDEDKR-----
 EAL85588 Af LMFWSPSELRELQGS AIVS--KIGKEGALRLAHIMGSLIMAYA-----FDIEKVEDEED--GVTDDQDQS-----
 XP_389160 Fg PMFWSENELDQLQASHMRH--KIGKADAVEIAHRMGSTIMAYA-----FDLENEETEE-----VEDREGKS-----
 XP_389761 Fg -----KALRWRFLKS-STPIEKDVPLVELNGAIGFQKDYCADPT-----NLWADLSSPL-----PFVFFHPVLP-----LY
 XP_363632 Mg --KQLSLARETVARWQYLMT-PTPVAKDVP LIELNGSIGFQKDYCADKH-----NRWDEFSSPL-----PFVFFHEMLP-----LY
 EAA28230 Nc --SRKTLGQGTVASWKCLKA-PSAIAHNVPVLVELNGIQIGISSYCADPD-----SRWQELTSPL-----PYVFFHPMLP-----IY
 EAL93416 Af ---PSINIEGQHPTWKVLRT-RESVSKDHIVGEITGKIGLLRDYCLDPS-----NRWQELRHPE-----PFVFFHPQLP-----IY
 NP_648681 Dm -----AQLIPYAG-AKVLIS-SVDLSPHAPIHELGRKYM LTTQFRTQNPTV-----NSFKAHKTPG-----QVFFVFLKGPE-----VC
 NP_082661 Mm ---QLGRVTRVQKHKRILRA-ARDLALDTLIEYRGKVM L RQQFEVNG-----HFFKKPY-----PFVLFYFNGVE-----MC
 XP_448906 Cg -ESSYARTFPAHTKLGVFT--KEYCNNGDLIEEFTQGVDFLKT YLDDTK-----NHYRIWGTAK-----NRVIFHPHWP-----LY
 NP_012954 Sc -DIAYSRTYPGFTKLGVYL--KKDCIKGDFIQEILGELDFYKNYLTDP-----NHYRIWGTAK-----RRVIFHSHWP-----IY
 NP_985624 Ag -EPHSRVRVHFPGPKLGVYS--QQPCA KDTLIAEFLGEVDFQRKYLEDP-----NNYRLLGIPN-----PKVLFHPHWP-----IY
 XP_446555 Cg --VLKPLASKDIQDFGVFT--SIPCSKKDYIQEYSGMISFSKQYVNNAE-----NKYDILGTPT-----RNILFHPHWP-----LY
 NP_012430 Sc -ADIEVRKSSNERDFGVFA--ADSCVKGELIQEYLGKIDFQKNYQTDPN-----NDYRLMGTTK-----PKVLFHPHWP-----LY
 EAA30745 Nc -WLEIRHTGTAEKGYGVFVK-TNEIPKAYLGHYVGEIIPGPTKGYNANN-----KYLYEPQVG-----WDTD
 XP_001481661 Af -NKTQSKYIDESIGYGLFA--TGRIPAGEVVFADKVAKTADDLVAERVRA---EEWHRGFLCLP-----NPQPAYAQIWH-----MIAL
 XP_384009 Fg --GSTEVKSSPGAGRGLFT--TRDISPNEIIMCEKASLVCDTRPSQVERIL---LQGDYKGIG-----QKLIELDEVPOQT-----EDE
 BAB11411 At --PIRVGLTESAGRAVFA--TRKIGAGDLIHTAKPKLCLKKFLD VETR-----ADWSSFDDYFLTQK--NAFRIDLVA AAS-----VE
 NP_588361 Sp ---PLEIRDTERKGRGVFA--LEPIPAQT CIEISPVLMSKEEYEQHG-----QYTVTYVWS-----
 EAA34532 Nc ---NNFQVRLSRYGGFGTFA--TRDLKMG E VILNEKPLLRTPRDSFYTEFLK----EEDQAKFMQLYTPH--DGS DYHIRGILKAN-----SFAI
 XP_381576 Fg --EYFQVRRSDLAGWG AFA--VRELKEGDQILLEKP-LFTATNLTLFDGFA--EVAYSLHANNN-----VEVLIWKTNAFSTAN-----PSKG
 NP_193253 At --RSDDKYVS YRKLGLGVVC--NKEFG EEDFVVEFLGEVYPVWKWFQD GIR---SLQENKTD PAP-----EFYNIYLERPK-----YDL
 NP_594837 Sp --VPISSSKFCSSRFLVLS--TCEIPPNTPI MEVGRVCTQNEYKSDPKN----QYNILGAPK-----HVFFDSN-----SQ
 EAK95983 Ca ----ALFISNNGGSGGGS---LTIPENTPIIEYLGEIDL FKNYCRDSIN----QYRMWGSP-----KPPTQYSDET-----LD
 XP_713530 Ca -FDIGKRHFSDKCLKLGI VSS-IKLIGHEIGLTLFKNLIKVSKKNWKFID---DLVAIVFIN-----YFTLFN-----Y
 NP_542983 Mm -RVYVADSLISSAGEGLFS--KVAVGPNTVMSFYNGVRITHQEVDSRDWAL-----NTLSLD-----EETVIDVP-----EP
 NP_565457 At -RLASSAHQKQSCSLVS-FCSFASHTPWLCESLRRLHQSSSAQPSDRQ---VFQILLSLQSGSSNGDCSAGDSASLLSSVISPDLTG--MEPCSV
 CAE76340 Nc ----IEPDVTS SRKNLVHGRFAGITREEYETYVAGEMLIANPTEEDRQK---ACHDFFKH YAFQVKRPHLPSPITNTLSPITSSSTAS-----ASI

XP_387621	Fg	VIDATK-KGGIARFINHS-----FEGSK---RIVIYA-LRDIALNEELTYDYKFER
XP_961572	Nc	VIDATK-KGGIARFINHSCMP--N---CTAKI IK-----VEGSK---RIVIYA-LRDIAQNEELTYDYKFER
XP_750524	Af	VIDATK-RGGIARFINHSCTP--N---CTAKI IK-----VDGSK---RIVIYA-LRDIGRDEELTYDYKFER
XP_449333	Cg	VIDATK-KGGIARFINHCCEP--S---CTAKI IK-----VGGKR---RIVIYA-LRDIAANEELTYDYKFER
NP_983083	Ag	VIDATK-KGGIARFINHCCDP--S---CTAKI IK-----VGGMK---RIVIYA-LRDIAANEELTYDYKFER
NP_011987	Sc	VIDATK-KGGIARFINHCCDP--N---CTAKI IK-----VGGRR---RIVIYA-LRDIAASEELTYDYKFER
EAK99965	Ca	VIDATK-KGGIARFINHCSP--S---CTAKI IK-----VEGKK---RIVIYA-LRDIEANEELTYDYKFER
XP_001411780	Mg	VIDATK-KGGIARFINHSCMP--N---CTAKI IR-----VEGTK---RIVIYA-LRDIARNEELTYDYKFEL
BAC65717	Mm	IIDATK-CGNFARFINHSCNP--N---CYAKVIT-----VESQK---KIVIYS-KQHINVNEEITYDYKFPI
NP_821172	Mm	IIDATK-CGNLARFINHCTP--N---CYAKVIT-----IESQK---KIVIYS-KQPIGVDEEITYDYKFPL
NP_587812	Sp	IVDATK-KGNIARFINHSCAP--N---CIARI IR-----VEGKR---KIVIYA-DRDIMHGEELTYDYKFPE
BAB10481	At	VLDATK-RGGIARFINHSCNP--N---CYTKI IS-----VEGKK---KIFIYA-KRHIDAGEEISYNYKFPL
NP_001074518	Mm	VVDATM-HGNAARFINHSCNP--N---CYSRVIN-----IDGQK---HIVIFA-MRKIYRGEELTYDYKFPI
NP_083550	Mm	VVDATM-HGNAARFINHSCNP--N---CFSRVIH-----VEGQK---HIVIFA-LRRILRGEELTYDYKFPI
NP_476769	Dm	VVDATM-RGNAARFINHSCNP--N---CYSKVVD-----ILGHK---HIIIFA-LRRIVQGEELTYDYKFPF
NP_001074852	Mm	VIDATL-TGGPARYINHSCAP--N---CVAEVVT-----FERGH---KIIISS-NRRIQKGEELCYDYKFDF
AAH58659	Mm	VIDATL-TGGPA-----AEVVT-----FDKED---KIIIS-SRRIPKGEELTYDYQDF
NP_726773	Dm	VVDATL-SGGLARYINHSCNP--N---CVTEIVE-----VDRDV---RIIIFA-KRKIYRGEELSYDYKFDI
AAK01237	At	VIDATR-TGSIAHLINHSCVP--N---CYSRVIT-----VNGDE---HIIIFA-KRHIPKWEELTYDYRFFS
AAF29390	At	VIDATR-TGSIAHLINHSCNP--N---CYSRVIS-----VNGDE---HIIIFA-KRDVAKWEELTYDYRFFS
BAA97320	At	VVDATE-KGNIARLINHSCMP--N---CYARIMS-----VGDDDES--RIVLIA-KTTVASCEELTYDYLDFP
NP_194520	At	VVDATD-KGNIARLINHSCTP--N---CYARIMS-----VGDEES--RIVLIA-KANVAVGEELTYDYLDFP
CAA71599	At	VLDAYR-KGDKLKUFANHSPEP--N---CYAKVIM-----VAGDH---RVGIFA-KERILAGEELFYDYRYEP
AAD09108	At	VLDATQ-KGDKLKUFANHSAP--N---CYAKVMF-----VAGDH---RVGIFA-NERIEASEELFYDYRYGP
NP_031996	Mm	VVDATR-KGNKIRFANHSVNP--N---CYAKVVM-----VNGDH---RIGIFA-KRAIQAGEELFYDYRYSQ
NP_031997	Mm	VVDATR-KGNKIRFANHSVNP--N---CYAKVMM-----VNGDH---RIGIFA-KRAIQTGEELFYDYRYSQ
NP_524021	Dm	VVDATR-KGNKIRFANHSINP--N---CYAKVMM-----VTGDH---RIGIFA-KRAIQPGEELFYDYRY--
AAC39446	At	EIDARR-KGNEFKFLNHSARP--N---CYAKLMI-----VRGDQ---RIGLFA-ERAIEEGEELFYDYCYGP
XP_381075	Fg	WVDAAT-YGNLSRYINHASSEDKN---ITPRILY-----VNGEY---RIKFTA-MRDIAGEELFFNYGENF
EAA35807	Nc	WVDAAM-YGNLSRYINHASSENDKN---ITPKI IY-----VNNEY---RIKFTA-LRDIKAGEELFFNYGDNF
XP_369092	Mg	WVDAAV-YGNLSRYMNHASSEDKN---VVPKIVQ-----VNGDF---RIRFTA-LRDIKAGEELFFNYGENF
XP_385734	Fg	FVDATK-KGNYGRFCNHSCNP--N---CYVDKWV-----VGDKL---RMGIFT-SRKIQSGEELVFNYNVDR
XP_957740	Nc	FVDATK-KGNLGRFCNHSCDP--N---CYVDKWV-----VGDKL---RMGIFA-GRAIKAGEELVFNYNVDR
EAL91994	Af	FVDATK-KGNLGRFCNHSCNP--N---CYVDKWV-----VGEKL---RMGIFA-ERAIQAGEELVFNYNVDR
XP_363735	Mg	YVDATK-KGNLGRFCNHSCNP--N---CYVDKWV-----VGDKL---RMGIFA-MRAIKAGEELCFNYNVDR
NP_594980	Sp	YIDATK-RGSLARFCNHSCRP--N---CYVDKWM-----VGDKL---RMGIFC-KRDIIRGEELTFDYNVDR
XP_445194	Cg	FIDATI-KGSLARFCNHSCNP--N---AYVNKWV-----VAGKL---RMGIFA-KRKILKGEETFDYNVDR
NP_012367	Sc	FIDATI-KGSLARFCNHSCSP--N---AYVNKWV-----VKDKL---RMGIFA-QRKILKGEETFDYNVDR
NP_984733	Ag	FIDATE-RGCLARFCNHSCNP--N---AYVSKWD-----VAGKL---KMGIFA-HRKILKGEETFDYNVDR
EAK95292	Ca	FIDATE-KGSLGRFINHSCNP--N---AFVDKWH-----VGDRL---RMGIFA-KRKISRGEETFDYNVDR
NP_001074809	Mm	IIDATQ-KGNCSRFMNHSCNP--N---CETQKWT-----VNGQL---RVGFFT-TKLVPSGSELTFDYQF--
NP_572888	Dm	VIDATS-KGNISRYINHSCDP--N---AETQKWT-----VNGEL---RIGFFS-VKPIQPGEEITFDYQYLR
AAC34358	At	VIDAGA-KGNLGRFINHSCNP--N---CRTEKWM-----VNGEI---CVGIFS-MQDLKKGQELTFDYNVVR
XP_132006	Mm	IIDAGP-KGNYSRFMNHSCQP--N---CETLKWT-----VNGDT---RVGLFA-VCDIPAGTELTFNYNLDC
NP_032765	Mm	IIDAGP-KGNYARFMNHCCQP--N---CETQKWS-----VNGDT---RVGLFA-LSDIKAGTELTFNY----
NP_001001735	Mm	IIDAGP-KGNYSRFMNHSCNP--N---CETQKWT-----VNGDV---RVGLFA-LCDIPAGMELTFNY----
NP_733239	Dm	IIDAGP-KGNLARFMNHSCNP--N---CETQKWT-----VNCIH---RVGIFA-IKDIPVNSELTFNYLWD-
AAC23419	At	VIDATH-KGNKSRYINHSCNP--N---TQMOKWI-----IDGET---RIGIFA-TRGIKKGEHLTYDYQFVQ
CAB75815	At	VIDATH-KGNKSRYINHSCNP--N---TEMOKWI-----IDGET---RIGIFA-TRFINKGELTYDYQFVQ
CAA18207	At	TIDATF-KGNASRFLNHSCNP--N---CVLEKWQ-----VEGET---RVGVFA-ARQIEAGEPLTYDYRFVQ
AAF04434	At	AIDATK-KGSLARFINHSCRP--N---CETRKWN-----VLGEV---RVGIFA-KESISPRTELAYDYNFEW
XP_389092	Fg	IIDAT--TGSIARFVNHSCNP--N---CRMIKWI-----VSGQP---RMALFAGDKPIMTGDELTYDYNFDP
EAA34880	Nc	IIDAT--TGSIARFVNHSCSP--N---CRMIKWI-----VSGQP---RMALFAGDRPIQTGEELTYDYNFDP
XP_964116	Nc	IIDAT--TGSIARFVNHSCSP--N---CRMIKWI-----VSGQP---RMALFAGDRPIQTGEELTYDYNFDP
EAL92920	Af	IIDAT--RGSIARFVNHSCNP--N---CRMEKWT-----VAGKP---RMALFAGDHGIMTGEELTYDYNFDP
NP_524160	Dm	VIDGQR-MGSDCRFVNHSCNP--N---CEMQKWS-----VNGLS---RMVLFA-KRAIEEGEELTYDYNF--
NP_619620	Mm	VIDSYR-MGNEARFINHSCDP--N---CEMQKWS-----VNGVY---RIGLYA-LKMPAGTELTYDYNF--
NP_196541	At	CPDKFGNISRFINGINNPNPAKN---CKCVRY-----INGEC---RVLLVA-TRDISKGERLYDYNGYE
NP_197821	At	CPDRRSNIARFISGINNHSPGRN---LKCVRFN-----INGEA---RVLLVA-NRDISKGERLYDYNGYE
NP_084517	Mm	CVDATQETNRLGRLIN-HSKCG-N---CQTKLHD-----IDGVP---HLILIA-SRDIAAGEELLYDYGDRS
NP_650354	Dm	CIDATVDTGKLGRLIN-HSRAG-N---LMTKVVL-----IKQRP---HLVLLA-KDDIEPGEELTYDY----
XP_752474	Af	YVDGQK-FGSPTRFMNHSCNPCK---LFPVTRT---Y---GDERLY---DLAFFS-LHNIPNTELTFDYNPNW

NP_595186 Sp YVDAQN-YGDVSRFFNHSCSPNIA---IYSAVRN-H---GFRTIY--DLAFFA-IKDIQPLEELTFDYAGAK
 XP_382954 Fg EVDGEF-MSGPTRFVNHSCEPNMR---IFARVGD-H---ADKHIH--DLALFA-IKDIPRGEELTFDYVDGV
 EAA28243 Nc EVDGEY-MSGPTRFINHSCDPNMA---IFARVGD-H---ADKHIH--DLALFA-IKDIPKGTELTFDYVNGL
 XP_370355 Mg VIDGEY-RSGPSRFFNHSCDPNMR---IFARVGA-H---AELNLH--DLAFFA-IRDISNGEELTFDYVDGQ
 NP_073561 Mm TVDAAR-YGNVSHFVNHSC-DPNL---QVFSVFIDN---LDTRLP--RIALFS-TRTINAGEELTFDYQ---
 NP_035644 Mm TVDAAY-YGNISHFVNHSC-DPNL---QVYNVFIDN---LDERLP--RIAFFA-TRTIWAGEELTFDY----
 NP_524357 Dm TIDAAN-YGNISHFINHSC-DPNL---AVFPCWIEH---LNVALP--HLVFFT-LRPIKAGEELSFDY----
 NP_766133 Mm CIDARF-YGNVSRFINHHC-EPNL---VPVRVFMH---QDLRFP--RIAFFS-TRLIQAGEQLGFDYGERF
 NP_665829 Mm CIDARY-YGNISRFINHLC-DPNI---IPVRVFMH---QDLRFP--RIAFFS-SRDIRTGEELGFDYGDRF
 NP_569834 Dm CIDANY-YGNVTRFFNHSC-EPNV---LPVRVFYEH---QDYRFP--KIAFFS-CRIDIDAGEEICFDY----
 AAD10665 At CLDGMF-YGNISRFLNHRCLDANL---IEIPVQVET---PDQHYY--HLAFFT-TRDIEAMEELAWDYGIDF
 AAK92218 At SLEGTH-YGNISRFINHRCLDANL---IEIPVHAET---TDSHYY--HLAFFT-TREIDAMEELTWDYGVVF
 AAF63769 At CLDATI-CGNVARFINHRCEDANM---IDIPIEiet---PDRHYY--HIAFFT-LRDVKAMDELTWVSTMIK
 AAC17088 At AIDATT-HGNISRFINHSC-SPNL---VNHQVIVES---MESPLA--HIGLYA-SMDIAAGEEITRDYGRRP
 AAH45208 Mm FVDPTY-IGNIGRFLNHSCEP-NL---LMIPVRID-----SMVP--KLALFA-AKDILPGEELS DY----
 NP_001097743 Dm IVDPSR-RGNIGRYLNHSCEP-NC---HIAAVRI-----
 AAF00642 At NIDATR-IGNVARFINHSCDGNL---STVLLRSSG-----ALLP--RLCFFA-AKDIAEEELSFSYGDVS
 NP_611966 Dm IMDAKT-TGNLGRYFNHSCSPNLF---VQNVFVD-T---HDLRFP--WVAFFS-AAHIRSGTELTWNYNVEV
 NP_061365 Mm IIDAKL-EGNLGRYLNHSCSPNLF---VQNVFVD-T---HDLRFP--WVAFFA-SKRIRAGTELTWDYNYEV
 NP_001019872 Mm LLDASK-EGNVGRFLNHSCCPNLW---VQNVFVE-T---HDRNFP--LVAFFT-NRYVKARTELTWDYGYEA
 AAK28971 At TIDAAS-KGNVGRFINHSCSPNLY---AQNVLYD-H---EDSRIP--HVMFFA-QDNIPPLQELCYDYNAL
 NP_181061 At TINAAQ-KGNIGRFINHSCSPNLY---AQDVLYD-H---EEIRIP--HIMFFA-LDNIPPLQELS DYDNYKI
 NP_196900 At CIDAGS-TGNFARFINHSCSPNLF---VQCVLSS-H---QDIRLA--RVVLFA-ADNISPMQELTYDYGAL
 AAK28974 At AMDVSK-MRNVACYISHSKEPNVM---VQFVLHD-H---NSLMFP--RVMLFA-AENIPPMTELSLDYGVV-
 NP_180887 At SMDVSR-MRNVACYISHSKEPNVM---VQFVLHD-H---NHLMFP--RVMLFA-LENISPLAELSLDYGLA-
 AAK28966 At IISAKN-VGNVARFMNHSCSPNVF---WQPVSYE-N---NSQLFV--HVAFFA-ISHIPPMTELTYDYGVS
 NP_565056 At LISAKK-FGNVARFMNHSCSPNVF---WQPVIRE-G---NGESVI--HIAFFA-MRHIPPMaelTYDYGISP
 AAK28973 At LISAKE-KGNVGRFMNHNCWPNVF---WQPIEYDDN---NGHIYV--RIGLFA-MKHIPPMTELTYDYGISC
 NP_564036 At LISAKE-KGNVGRFMNHSCSPNVF---WQPIEYE-N---RGDVYL--LIGLFA-MKHIPPMTELTYDYGVSC
 NP_178647 At VISAKK-SGNVARFMNHSCSPNVF---WQSIARE-Q---NGLWCL--YIGFFA-MKHIPPTELRYDYGKSR
 EAA50044 Mg LYTGD--KGNIFRFINHRCS-PA---VKIEGKM-----ISGKYR--MMVVS--RDVTAGEELTANWGRGF
 XP_365330 Mg IWTGE--EGNIFRFTNHKCAN-AE---AEVKGKK-----ISGAYR--MVLVAT--QDILHGMEVCVDFGQKF
 EAL89869 Af IYQGE--MGNFTRFINHSCR--PN---SQFORFY-----WRGQER--IIVVSR---GVVAGREITVDYSDHY
 XP_383195 Fg IWQ GK--QGNFTRFANHSCK--PN---AQFEKFV-----WLGTOH--IVMNN-----TADIPLFRFNM IN
 XP_357091 Mm -----GNWMSYVNCARFPKEQ-----NLLAV-----QHQ--GQIFYESCRDIQRNQELLVWYNGY
 NP_031574 Mm -----KSNWMRYVNPASAREQ-----NLAAC-----QNG--MNIYFYTIKPIPANQELLVWYCRDF
 NP_001028453 Mm -----KSSWMRYIRCARHCGEQ-----NLTVV-----QYR--SNIFYRACIDIPRGTELLVWYNDY
 EAL91753 Af ALISAKQHGNWTRYLNHS-CKPST---TFLKMTVG-----KR----TIMAVQAVRDIDIFEEITVDYG---
 XP_964337 Nc ADIYPQQMGNVVRKVRHDGVSPSA---VFKVMKITG-----KWR-----VMLVAMRDIRDGDEITAKYGRGY
 XP_449432 Cg REYFGYVWFPKASYFNHSCDPN-----ITKT-----RID--RKMVFTLN RDVACGEELNIDYSGVL
 NP_015160 Sc REYFGYVWFPEASYFNHSCNPN-----ITKY-----RKG--NSMLFTMN RDIKKDEQICIDYSGVL
 NP_982445 Ag RDYLG YWVLP EASYFNHSCAPN-----LAKK-----RVG--REMYFVLTS DVAAGEQLCIDYKGIL
 EAK94622 Ca KEFLGFGVYPSASF FNHSCSPN-----IVKT-----RNN--SEMVF TSKDIEIGEELCISYGNYT
 NP_983709 Ag LNQVNGQIYM LLSHLNHSCEPN-----IYYELEG-----HH-----INVYARKEIKSDEELTVSYVNPL
 P38890 Sc INQYNGQVYH WISFINHDCEPN-----AYIEQVE-----EHE--E-LRLHARKPIKKGEQIRITYVNPL
 XP_446364 Cg INQLSGQLYFLYSFLNHNCEPN-----VRYDINN-----KL-----E-LKVYARKFIKKDEELVT TYVNPL
 EAK96662 Ca INNLD SNVFLTQSHLNHCASN-----TSVETEL-----NRT--AGLKVIAGRDIKS GEELTT TYVNPS
 XP_385929 Fg ----DEVFLATSRINHSCKPN-----AQNRWN-----QGL--GKITVHAVEDIEQGEITITYLGNP
 NP_391443 Fg ----MDVFLQASRINHACDNN-----AQKDYN-----EGI--KRHTVHALRDIEEGEITITYLGIL
 NP_588413 Sp ----EMFLLGSRMNHDCSPN-----VKHTWN-----PRL--DQVTVHAVRDIEAGEEILT TYIDLH
 EAA33925 Nc ----PPLFIEASRINHACNPN-----TQNSWN-----SRI--NRETIHAVRDIKKGEEITISYIGHF
 EAA49663 Mg ---RFHSTFVEVSRMNEHCSPN-----CAAYFD-----PMT--MSQRIYAIRDIMPGEELTVSYIDPV
 XP_362227 Mg ---QFYVVFPEISRCNHDCRPN-----ADYYD-----PET--LTQHVHAVRQINIGEEISLSYLDPL
 XP_366867 Mg HRKAVPAVFRNASRLNHS CVPN-----CHFSWD-----RVT--RTCLVHAITDVSPGDELTVAYDSRG
 XP_364335 Mg ---DYMGLYPEIARINHACSPN-----SFSRFH-----PSD--LTMDVGAMRDIMPGEEITISYIPLG
 XP_370301 Mg ---GYMGLFPTISRINHACGPN-----SQVKFD-----PAT--LSQKAFASHDIEAGEEITISYAEFG
 XP_368905 Mg ----HAGTFLGVSRLNHDCRPNNP-----TSLAFHV-----AKS--FVHTTHATRDIAAGEELTISYVDSY
 XP_364537 Mg ----HYGNFPNVSKLNHDCRPN-----MVFHI-----DNN--LVHRTHAVRDIKPGEELTISYVDQM
 EAA26997 Nc DHSKHYINYP SMFLPTHSCRPN-----IAFHI-----DGT--LALRTTVA--VAPGEELS IAYIDPL
 XP_363030 Mg EESQHLGVYAQAAAINHDCRPS-----IN YRLNDITQIQPGEELSVSYVDLM
 NP_572675 Dm ----ARTLYPSAFLLAHDCTPN-----TAHTDDPS-----S-----FEILLRTSRVREREAL TSYAYTL
 NP_609464 Dm ----LRCLFPYTGLAHNCVPN-----TSRSIYPS---E-G-----YKIRLRAMVDLEEGQPLHHSYTYTL

NP_649084 Dm ----IRALYPGAAMISHDCVPN-----MRHRFDDD-----MNIVFLAKRKIAKGEILSISYTQPL
 NP_610944 Dm ----VAVFYT-ASFTENSCLPN-----LAKSFNKN-----GHCILWAPREIKKNAHLSICYSDAM
 NP_001014717 Dm ---LLRGLFPLTAIMNHECTPN-----ASHYFENG-----R-----LAVVRAARDIPKGGEITTTYTKIL
 CAA15694 Dm ---LVRALFPLAGLLNHQCTPN-----AAHHFENG-----E-----TIVVCATERIPAGAEITMSYAKLL
 NP_572539 Dm ---NYRALYPLFGVVNHDCIPN-----AYYTFEEK-----TN-----NMIVRAAVDIPEGFEVTTYTKLF
 NP_033892 Mm ----GVGIFPNLGLVNHDCWPN-----CTVIFN-----NG-----KIELRALGKISEGEELTVSYIDFL
 NP_081072 Mm ----GSAIFPDVALMNHSCCPN-----VIVTYK-----GT-----LAEVRAVQEIHPGDEVFTSYIDL
 NP_081464 Mm ----GVGLYPSMSLLNHSCDPN-----CSIVFN-----GP-----HLLLRAVREIEAGEELTICYLDM
 XP_360530 Mg ----GTFLDPVLAMANHSCVPN-----AVLFW-----RR-----KAYLRAEMPIKQGEISISYIDYT
 XP_381344 Fg ----GIFLGTKLAMANHSCIPN-----AMVQFI-----GR-----RAILRAEKPIKIDDEIEISYTDYT
 EAA36113 Nc ----GIYLHPSLSMVNHSCVPN-----AYIAFE-----KR-----KAFLKAERDLEPGDEILISYIGMA
 NP_650955 Dm ----GSGLYLLQSKINHSCVPN-----ACSTFP-----YSN----DIVVLKALAPIQQGEEICISYLDEC
 NP_659167 Mm ----GSGFLVLQSCCNHSCVPN-----AETSFP-----ENN----FVLHVTALEDIKPGEEICISYLDCC
 XP_384827 Fg PLFTTAGVWLLAARINHSCVGN-----CRRSFIGD-----IQI---VR---AARDIPAGTELTFPYCPTG
 XP_380216 Fg FKYTTSGIWLASRINHSCVGN-----CRPSFIGD-----MQI---VR---ATKDVPAKTEIFFCYRPPV
 EAL91344 Af -KFHSCGVWLLASYINHSCSN-----ARRSFIGD-----MMI---VR---AAQDLAAGTEITFWYQSP
 XP_367445 Mg GPESSTGMWLHAAYANHTCIPN-----ATRAFIGD-----MMI---VR---AARDIPAGAEIFMGYASLA
 XP_366224 Mg QPPSARGLWPLAAAMNHACVAS-----TVRAFVGD-----VFI---TR---ALRDIEPGEELTQQYVVPV
 EAA35550 Nc SVCMAGKLWAHSSLMNHSCVPN-----TMSFVGD-----MLI---CR---ATRDVQEGEELFQQYVVPV
 AAF87042 At KEYYGVLWTLASFINHSCIPN-----ARRLHVG-----YVI---VH---ASRDIKTGEEISFAYFDVL
 XP_387208 Fg GRPDVAAPHYPWCLANHDCDPN-----VTWEWGR-----MVL---EARKERVVGGIKKGEEILNHYCDVN
 XP_957213 Nc GRPEVAAPHYPWCLANHDCDPN-----VTWEWGR-----MTL---FARETRVVGNIKAGEEILNHYCDVD
 XP_365932 Mg GRPDVAAPHYPWCLANHDCDPN-----VTWEWSGR-----MVL---RAKEERVWGIKAGDEILNHYCDVN
 XP_367482 Mg ---STSLFMGPARFANHDCGAN-----ARLKT-----ADQ---SIMEVQALRNIEVGEEITVTYGDNY
 EAA33797 Nc ---STSLFMGPARFANHDCNAN-----ARLIT-----RGQ---AGIEIIACRNIEVGEEITVTYSESY
 XP_386705 Fg ---CTSLFMGPARFANHDCDAN-----AKLMR-----TSH---AGIEIVATRPIDAGEEITVTYGDNY
 EAL93147 Af ---TPSFFLGPARFANHDCNAN-----GKLV-----RGS---EGMQVVATRDIIYIGEEITVSYGDDY
 NP_588078 Sp ---SMCLFLGPARFVNHCNAN-----CRFNT-----SGK---R-IWLCVRDIKPGEEITTFYSSNY
 AAF45537 Dm ---CAQLWLGPAAYNHDCRAN-----CKFLA-----TGR---DTACVKVLRDIEVGEEITCFYGEDF
 NP_659120 Mm ---CAQLWLGPAAFINHDCRPN-----CKFVS-----TGR---DTACVKALRDIEPGEEISCYYGDF
 NP_666289 Mm ---SAQLWLGPAAFINHDCRPN-----CKFVP-----SDG---NTACVKVLRDIEPGDEVTCFYGEGF
 EAL85588 Af ----SKGMVPLADILNADADRNN-----ARLF-----QED---DSLVMKAIKPIRVGEEIFNDYGELP
 XP_389160 Fg ----MMGMVPMADILNADAEFN-----AHVN-----HEE---ESLTVTSLRPKAGEEILNYYGPH
 XP_389761 Fg IDTRQEGSLA---RYVRRSCKPN-----AQLDTYLSDES-----E-YHFVIVSDRHSANEQITLP-----
 XP_363632 Mg IDTRQEGSRA---RYVRRSCKPN-----AVLDTFLSGGS-----E-YHFWLVSDRSIAANEQITIA-----
 EAA28230 Nc IDTRKEGSA---RYVRRSCKPN-----AMLETYLSDG-----E-LHFVLVTDQVAAREEITLP-----
 EAL93416 Af IDSRHEGSIL---RYVRRSCRPN-----VTIKTYITNEV-----E-YHFCFVAKEDISANSEITAM-----
 NP_648681 Dm VDTRTYGND---RFVRRSCRPN-----AELQHYFEKG-----T-LHLYIVALTHIRAQTEITIR-----
 NP_082661 Mm VDARTFGND---RFIRRSCTPN-----AEVRHMIADG-----M-IHLCIYAVSAITKDAEVTIA-----
 XP_448906 Cg IDARSKGNLT---RFLRRGCKPN-----VELVTVCLPSAG-EKD---IKFILRATRDIDEGEELLID-----
 NP_012954 Sc IDARLSGNST---RYLRRSCQPN-----VELVTIKLQD---NRNDKR-IKFVLRALRDISEDEELYIK-----
 NP_985624 Ag IDARLCGNLT---RYLRRSCYPN-----VELVTIKMPADD-RQAS-K-VKFVLRALRDLERGEELHIK-----
 XP_446555 Cg INTSGTKGAHNVEHLRSCNPN-----VELVTVRIMDNK-PR-----IKFVIRAIRDIAEGEELQIA-----
 NP_012430 Sc IDSRETGGLT---RYIRRSCEPN-----VELVTVRPLDEK-PRGD-C-VKFVLRAIRDIRKGEEISVE-----
 EAA30745 Nc RIIDAGKMGWTRFMNSSCDPN-----VSESIQIG-----V-RVIAFPANKTLKSGDELCTYYGDDY
 XP_001481661 Af QPENAKVLVLGLAFVNHACIAN---SLYYTLRYPRD---ENGEEDI-GRVVRASRDIRPGEEITVAYFYAK
 XP_384009 Fg DISNASTGLWVRSYNHSCIPN-----AKKDLIG-----DLILFRATRRIASGEEITHAYDEST
 BAB11411 At GEGAVGHAVYMPFYNHDCDPN-----AHIIWLHN-----ADARLNTLRDVEEGEELRICYIDAS
 NP_588361 Sp --EKQGLALGLGSMFHNHSDRPN-----VYWKDNRN-----NYISYTLREIKTNEELCISYGDHL
 EAA34532 Nc NPYSSDIISVYTSRLNHACRSVAN---VLFDFDF-----QDP---ECITLTVSKPVKAGSELFISYGGSP
 XP_381576 Fg RCYDEAGLFPIASRFNHACEPMNS---VKWHYN-----HADG---NLKMTIQAKIEAGKELTITLPYFS
 NP_193253 At VVVDAMHMANYASRICHSCRPN-----CEAKVAVDG-----HYQIGIYSVRAIEYGEETFDYNSVT
 NP_594837 Sp LVVDSRVAGSKARFARKGCQSN---SVVSSVYMN---GSNSVP---RFILYSTTHIAPETEIIIGD-----
 EAK95983 Ca IVLDSRFVGNESRFIRKACPSSAN---CRIETVYVP---EQNKFR---PLVFTSKPITLKSQDEELRLP-
 XP_713530 Ca QRQELGIALDPFALINHSCIPN-----CCQITNDCN-----EFQIVSTLPIINNGEELTVTYVSLG
 NP_542983 Mm YNHVSKYCASLGHKANHSFTPN-----CVYDLFVHP-----RFG---PIKCIRTLRAVEAEELTVAYGYDH
 NP_565457 At SNEKRSVRAYGTSFFNHDCLPN-----ACRFDYVDS---ASDGN---TDIIIRMIHDVPEGREVCLSYFPVN
 CAE76340 Nc STSTPPTPTTNGSLINHCTSPSAY---VARKRTERG---PNCWEG---LAHFVKPKHIIKEGEQLTWDYGKKE