```
P28340.2  1     M    DGKRRPGPGPGVPPKRARGGlwDDDDAPRPSQFEEDLALMEEME-AEHRLQEQEEEELQSVLE[12]DPRWLRPT  83
P52431.2  1     M    DCKRRQGPGPGVPPKRARGHlwDEDE-PSPSQFEANLALLEEIE-AENRLQEAEEE-LQLPPE[12]DPRWRRPT  81
P54358.2  1     M    DGKRKFNGTSNGHAKKPRNP--DDDE---EMGFEAELAAFENSEdMDQTLLMGDGPENQTTSE    --RWSRPP  65
P90829.1  1     M[ 1]-SKRPGGSSFQPEVKRKRES--DEFEQCYVSRFENELPSVPTID--------------------    KTGWARPA  51
P15436.4  1     M[47]DSFRKYNS----QGFKAKDT--DLMGTQLESTFEQELSQMEHDM------ADQEEHDLSSFER    -----KKL  102

P28340.2  84    PPALDPQTEPLIFQQLEIDHYVGPaQPVPGGPPPSRGSVPVLRAFGVTDEGFSVCCHIHGFAPYFYTPAPPGFGPEHMGD  163
P52431.2  82    LRALDPSTEPLIFQQLEIDHYVGSaPPLPEGPLPSRNSVPILRAFGVTDEGFSVCCHIQGFAPYFYTPAPPGFGAEHLSE  161
P54358.2  66    PPELDPSKHNLEFQQLDVENYLG--QPLPGMPGAQIGPVPVVRMFGVTMEGNSVCCHVHGFCPYFYIEAPSQFEEHHCEK  143
P90829.1  52    VDKDLGISKSIACQILEVETYHED-------GSATSYDRTNVKLYGVTKSGNSICVIVTDYFPHFYFQAPQGFGVEHIGT  124
P15436.4  103   PTDFDPSLYDISFQQIDAEQSVLN-------GIKDENTSTVVRFFGVTSEGHSVLCNVTGFKNYLYVPAPNSSDANDQEQ  175

P28340.2  164   LQREL-NLAISRDSRGGR---ELTGPAV---LAVELCSRESMFGYHG-HGPSPFLRITVALPRLVAPARRLLEQGIRVAG  235
P52431.2  162   LQQEL-NAAISRDQRGGK---ELSGPAV---LAIELCSRESMFGYHG-HGPSPFLRITLALPRLMAPARRLLEQGVRVPG  233
P54358.2  144   LQKAL-DQKVIADIRNNK---DNVQEAV---LMVELVEKLNIHGYNG-DKKQRYIKISVTLPRFVAAASRLLKKEVIMSE  215
P90829.1  125   AQSAIcNMVAAAKRRGGSgqaQLPGKVVdnlVHVEIVHGENLYYFRGaDTKVPFVKVSGSTEAL-HKARMELKNGVNLMG  203
P15436.4  176   INKFV------------HylnETFDHAId---SIEVVSKQSIWGYSG-DTKLPFWKIYVTYPHMVNKLRTAFERGHLSFN  239

P28340.2  236   LGTPSFAP-YEANVDFEIRFMVDTDIVGCNWLELPAGKYALRLKEKA----TQCQLEADVLWSDVVSHPPEGPWQRIAPL  310
P52431.2  234   LGTPSFAP-YEANVDFEIRFMVDADIVGCNWLELPAGKYVRRAEKKA----TLCQLEVDVLWSDVISHPPEGQWQRIAPL  308
P54358.2  216   IDFQDCRA-FENNIDFDIRFMVDTDVVGCNWIELPMGHWRIRNSHSKPlpeSRCQIEVDVAFDRFISHEPEGEWSKVAPF  294
P90829.1  204   KGPVNVGNlYESNINVIVMFLAKTNIVGCGWIEIPAGKCRILSNSEKS---SRCQIEVTVPVKNLIVHESDGEWAGIAPI  280
P15436.4  240   SWFSNGTTtYD-NIAYTLRLMVDCGIVGMSWITLPKGKYSMIEPNNRV---SSCQLEVSINYRNLIAHPAEGDWSHTAPL  315

P28340.2  311   RVLSFDIECAGRKGIFPEPERDPVIQICSLGLRWGEPEPFLRLALTLRPCAPILGAKVQSYEKEEDLLQAWSTFIRIMDP  390
P52431.2  309   RVLSFDIECAGRKGIFPEPERDPVIQICSLGLRWGEPEPFLRLALTLRPCAPILGAKVQSYEREEDLLQAWADFILAMDP  388
P54358.2  295   RILSFDIECAGRKGIFPEAKIDPVIQIANMVIRQGEREPFIRNVFTLNECAPIIGSQVLCHDKETQMLDKWSAFVREVDP  374
P90829.1  281   RTLSLDIECIGRRGVFPEAIKDPIIQIANLVKIEGEAEPFVRNCFVLGTCAPVVGSNIIQCVNEKVLLEKWAEFVREVDP  360
P15436.4  316   RIMSFDIECAGRIGVFPEPEYDPVIQIANVVSIAGAKKPFIRNVFTLNTCSPITGSMIFSHATEEEMLSNWRNFIIKVDP  395

P28340.2  391   DVITGYNIQNFDLPYLISRAQTLKVQTFPFLGRVAGLCSNIRDSSFQSKQTGRRDTKVVSMVGRVQMDMLQVLLREYKLR  470
P52431.2  389   DVITGYNIQNFDLPYLISRAQALKVDRFPFLGRVTGLRSNIRDSSFQSRQVGRRDSKVISMVGRVQMDMLQVLLREHKLR  468
P54358.2  375   DILTGYNINNFDFPYLLNRAAHLKVRNFEYLGRIKNIRSVIKEQMLQSKQMGRRENQYVNFEGRVPFDLLFVLLRDYKLR  454
P90829.1  361   DIITGYNILNFDLPYILDRAKVLSLPQVSHLGRQKEKGSVVRDAAISSKQMGSRVNKSIDIHGRIIFDVLQVVLRDYKLR  440
P15436.4  396   DVIIGYNTTNFDIPYLLNRAKALKVNDFPYFGRLKTVKQEIKESVFSSKAYGTRETKNVNIDGRLQLDLLQFIQREYKLR  475

P28340.2  471   SYTLNAVSFHFLGEQKEDVQHSIITDLQNGNDQTRRRLAVYCLKDAYLPLRLLERLMVLVNAVEMARVTGVPLSYLLSRG  550
P52431.2  469   SYTLNAVSFHFLGEQKEDVQHSIITDLQNGNEQTRRRLAVYCLKDAFLPLRLLERLMVLVNNVEMARVTGVPLGYLLTRG  548
P54358.2  455   SYTLNAVSYHFLQEQKEDVHHSIITDLQNGDEQTRRRLAMYCLKDAYLPLRLLEKLMAIVNYMEMARVTGVPLESLLTRG  534
P90829.1  441   SYTLNSVSYQFLSEQKEDVEHNIIPDLQRGDEQTRRRLAQYCLKDAYLPLRLLDKLMSIINYIEMARVTGVPMNFLLTKG  520
P15436.4  476   SYTLNAVSAHFLGEQKEDVHYSIISDLQNGDSETRRRLAVYCLKDAYLPLRLMEKLMALVNYTEMARVTGVPFSYLLARG  555

P28340.2  551   QQVKVVSQLLRQAMHEGLLMPVVKSEGG--EDYTGATVIEPLKGYYDVPIATLDFSSLYPSIMMAHNLCYTTLLRPGTAQ  628
P52431.2  549   QQVKVVSQLLRQAMRQGLLMPVVKTEGS--EDYTGATVIEPLKGYYDVPIATLDFSSLYPSIMMAHNLCYTTLLRPGAAQ  626
P54358.2  535   QQIKVLSQLLRKAKTKGFIMPSYTSQGSD-EQYEGATVIEPKRGYYADPISTLDFASLYPSIMMAHNLCYTTLVLGGTRE  613
P90829.1  521   QQIKILSMMLRRCKQNNFFLPVIEANSGDgEGYEGATVIDPIRGFYNEPIATLDFASLYPSIMIAHNLCYTTLLKSPQ--  598
P15436.4  556   QQIKVVSQLFRKCLEIDTVIPNMQSQASD-DQYEGATVIEPIRGYYDVPIATLDFNSLYPSIMMAHNLCYTTLCNKATVE  634

P28340.2  629   KL   GLTEDQFIRTPTGDEFVKTSVRKGLLPQILENLLSARKRAKAELAKETDPLRRQVLDGRQLALKVSANSVYGFTG  705
P52431.2  627   KL   GLKPDEFIKTPTGDEFVKSSVRKGLLPQILENLLSARKRAKAELAQETDPLRRQVLDGRQLALKVSANSVYGFTG  703
P54358.2  614   KL[4]NLQDDQVERTPANNYFVKSEVRRGLLPEILESLLAARKRAKNDLKVETDPFKRKVLDGRQLALKISANSVYGFTG  694
P90829.1  599   --   GVENEDYIRTPSGQYFATKSKRRGLLPEILEDILAARKRAKNDMKNEKDEFKRMVYNGRQLALKISANSVYGFTG  673
P15436.4  635   RL[3]--IDEDYVITPNGDYFVTTKRRRGILPIILDELISARKRAKKDLRDEKDPFKRDVLNGRQLALKISANSVYGFTG  712

P28340.2  706   AQVGKLPCLEISQSVTGFGRQMIEKTKQLVESKYT---VENGYSTSAKVVYGDTDSVMCRFGVSSVAEAMALGREAADWV  782
P52431.2  704   AQVGKLPCLEISQSVTGFGRQMIEKTKQLVESKYT---VENGYDANAKVVYGDTDSVMCRFGVSSVAEAMSLGREAANWV  780
P54358.2  695   AQVGKLPCLEISGSVTAYGRTMIEMTKNEVESHYT---QANGYENNAVVIYGDTDSVMVNFGVKTLERSMELGREAAELV  771
P90829.1  674   ATVGKLPCLEISQSVTAFGRKMIDMTKLEVERIYKkgaLDGKCPADAKVIYGDTDSVMVKFGVETVAQAMEIGLDAAKEV  753
P15436.4  713   ATVGKLPCLAISSSVTAYGRTMILKTKTAVQEKYC---IKNGYKHDAVVVYGDTDSVMVKFGTTDLKEAMDLGTEAAKYV  789

P28340.2  783   SGHFPSPIRLEFEKVYFPYLLISKKRYAGLLFSsRPDAHDRMDCKGLEAVRRDNCPLVANLVTASLRRLLIDRDPEGAVA  862
P52431.2  781   SSHFPSPIRLEFEKVYFPYLLISKKRYAGLLFSsRSDAHDKMDCKGLEAVRRDNCPLVANLVTSSLRRILVDRDPDGAVA  860
P54358.2  772   SSKFVHPIKLEFEKVYYPYLLINKKRYAGLYFT-RPDTYDKMDCKGIETVRRDNSPLVANLMNSCLQKLLIERDPDGAVA  850
P90829.1  754   SKIFTPPIKLEFEKVYSPYLLINKKRYAGLYFT-KPDVHDKMDCKGLETVRRDNCPLVAKVLGVCLEKLLIERDQQSALD  832
P15436.4  790   STLFKHPINLEFEKAYFPYLLINKKRYAGLFWT-NPDKFDKLDQKGLASVRRDSCSLVSIVMNKVLKKILIERNVDGALA  868

P28340.2  863   HAQDVISDLLCNRIDISQLVITKELTRAASDYAGKQAHVELAERMRKRDPGSAPSLGDRVPYVIISAAKGVAAYMKSEDP  942
P52431.2  861   HAKDVISDLLCNRIDISQLVITKELTRAAADYAGKQAHVELAERMRKRDPGSAPSLGDRVPYVIIGAAKGVAAYMKSEDP  940
P54358.2  851   YVKQVIADLLCNRIDISHLVITKELAK--TDYAAKQAHVELAAKMKKRDPGTAPKLGDRVPYVICAAAKNTPAYQKAEDP  928
P90829.1  833   FAKRTISDLLCNKIDISLLIISKELTKSGDKYQAKQAHVELAARMKKRDAGSAPRLGDRVPYVFVAAAKNVPAYERAEDP  912
P15436.4  869   FVRETINDILHNRVDISKLIISKTLAP---NYTNPQPHAVLAERMKRRE-GVGPNVGDRVDYVIIGG--NDKLYNRAEDP  942
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P28340.2  943   LFVLEHSLPIDTQYYLEQQLAKPLLRIFEPILGEGRAEAVLLRGDHTRCKTVLTGKVGGLLAFAKRRNCCIGCRTVLS--  1020
P52431.2  941   LFVLEHSLPIDTQYYLEQQLAKPLLRIFEPILGEGRAESVLLRGDHTRCKTVLTSKVGGLLAFTKRRNCCIGCRSVID--  1018
P54358.2  929   LYVLENSVPIDATYYLEQQLSKPLLRIFEPILGDN-AESILLKGEHTRTRTVVTSKVGGLAGFMTKKTSCLGCKSLMPKG  1007
P90829.1  913   TFVLQNNIPLDTKHYLTNQLAKPLARIFEPILGD-RAEKILVEGEHTRVRTVVQSKVGGLAAFTTKSATCLGCKSVLPRA  991
P15436.4  943   LFVLENNIQVDSRYYLTNQLQNPIISIVAPIIGDKQANGMFVVKS---IKINTGSQKGGLMSFIKKVEACKSCKGPLRKG  1019

P28340.2  1021  -HQGAVCEFCQPRESELYQKEVSHLNALEERFSRLWTQCQRCQGSLHEDVICTSRDCPIFYMRKKVRKDLEDQEQLLRRF  1099
P52431.2  1019  -HQGAVCKFCQPRESELYQKEVSHLNALEERFSRLWTQCQRCQGSLHEDVICTSRDCPIFYMRKKVRKDLEDQERLLQRF  1097
P54358.2  1008  yEQACLCPHCEPRMSELYQKEVGAKRELEETFSRLWTECQRCQESLHEEVICSNRDCPIFYMRQKVRMDLDNQEKRVLRF  1087
P90829.1  992   eSENAVCKHCEPKLPTIFASRMNTMHELENHFGRLWTECQNCAKTMQDKVNCSARDCPIYYMREKVRNELSEASAVIERF  1071
P15436.4  1020  --EGPLCSNCLARSGELYIKALYDVRDLEEKYSRLWTQCQRCAGNLHSEVLCSNKNCDIFYMRVKVKKELQEKVEQLSKW  1097

P28340.2  1100  GPPGPEAW--  1107
P52431.2  1098  GPPGPEAW--  1105
P54358.2  1088  GLA---EW--  1092
P90829.1  1072  GDPCFQAPtk  1081
P15436.4        ----------
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*P28340: Human, P52431: Mouse, P54358: *Drosophila*, P90829: *c. elegans*, P15436: *s. cerevisiae*