

gi | 128485706 | ref | NP_081399.3 | MAFILRRRAFCHKILWIPGAVVALKIHHPASHPAKAVTDRLSVCFCSLQPELFRVRFHAYCKNFHSEKGNDFHPVGEPPWSSQAQEWNPQGSQLEDEEMLFRRLSYFTSFEVLSFISALDLPVPLAMAALLRICEIGRRDGEORL 149
gi | 34873428 | ref | XP_214418.2 | MAFL-LRRRAFCHMSVFWMPGAVVALKIHHPANNVQKAVRDCLRVWFCSLQPDLEFRVRFYHAYCKSFHSENGNDFLHPVGEPPWSSQAQVWNPQBOTLKNEDDEMLSRRLNSFASFEVLSFIHLDLPVPLASAAALLRICEIGKRDDGEORL 148
gi | 40068497 | ref | NP_076996.2 | MALTLRLKRLNLYRLSDFQMRALAAALKNKPLNHHVHVVKERLCPWLCRQPEPPGVFRFHAAHCKKFKHSENGNDFLHPGGPVFVQVSDCDRLLEONVKNNEESQMFVRRLSNLTSSSEVLSFISIMEPLPTMAAGALORICEVEKKDDGOGL 149
gi | 114599023 | ref | XP_517625.2 | -----MHRALAAALKNQPLNHHVHVVKERLCPWLCRQPEPPGVFRFHAAHCKKFKHSENGNDFLHPGGPVFVQVSDCDRLLEONVKNNEESQMFVRRLSNLTSSSEVLSFISIMEPLPTMAAGALORICEVEKKDDGOGL 132
gi | 74003089 | ref | XP_545176.2 | MALTLRLRNLCHLSDFRIRHGALAAALRNHPVSRVHKIAEERRPPWFCLPSPVVRVRFHAAHCKKFKHSENGNDFLHPAGELVFPFPAHDWDTPEQNPVSRVDEQTFVFRNLNLTSSSEVLSFVSTLQALPDLAAGALORICDMERKDDGOGL 150
gi | 194676663 | ref | XP_001789483.1 | MALVTLRRLNLYRLSDFRIHGALAAALTKQVNVHVKIVKHELCPWFWGQHPGPIRVRFHAAHCKKFKHSENGNDFLHPVGEPPGVQVHNWDRFVHSVKNVDEQMFYRKLNSFTSSGEILRFVSTLELPDMMAGALHRIICEVEKDDGOGL 149
gi | 50735005 | ref | XP_419017.1 | -----MQLSLVNETVHLCGDGTG--SSAQRER-----WMDEQVFRFTLKSHTSQEIKFKLRCLVMSDITMASGALORICEVEVDGDLGN 79
gi | 125822502 | ref | XP_001338251.1 | --MVLTFPMAKTLALRLRVLSSLDYGIKACAGKPLSPFPIQTTCFPFCSFHSARAVCTIERTDPLFASGSRVPRQELCLGSG--LSLHMVLSNNEHAFMKRLSSCTSQVVLHLLREVSVLSASAASILHRLADLHDAPEKSW 146
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 128485706 | ref | NP_081399.3 | PEGVLENRAFQALCLRCRDPFSLHTNAGLVLTALCSLLNLLPADPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLAMLQASCEILKLVVRLQSKSVEIFAPBEITISVYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKSISH 299
gi | 34873428 | ref | XP_214418.2 | PKEVLENRVFQALCLRCRDPFSLHTNAVLTVLSLV---IDPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLAMLQASCEILKLVVRLQSKSVEIFAPBEITISVYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKSISH 294
gi | 40068497 | ref | NP_076996.2 | PKEILENSIFQALCFQPEKPEPSQLNSTSLVTALQALTL--LLHVDPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLITLHSSGCVLLELIINOLQEGKLETFPEPIDIVALYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKLISQ 298
gi | 114599023 | ref | XP_517625.2 | PKEILENSIFQALCFQPEKPEPSQLNSTSLVTALQALTL--LLHVDPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLITLHSSGCVLLELIINOLQEGKLETFPEPIDIVALYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKLISQ 281
gi | 74003089 | ref | XP_545176.2 | PKEILKNSVFQALCVLERESSLDPVPLVTALQALTL--LLHADPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLITLHSSGCVLLELIINOLQEGKLETFPEPIDIVALYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKLMSQ 299
gi | 194676663 | ref | XP_001789483.1 | PKEILLESFAFQALCDFRGRDPSLNSAGLVTAFAQALTL--LLCGDPOSSLMLSLVAECORRLRQGNLEVHHLVCLGESLITLHSSGCVLLELIINOLQEGKLETFPEPIDIVALYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKLMSQ 298
gi | 50735005 | ref | XP_419017.1 | PEDVLENEVFRALCFQPEKPEPSQLNSTSLVTALQALTL--RLRIDPHSLILIASLLSECEERLANRKLTVDSLQSLGESLITLHSSGCVLLELIINOLQEGKLETFPEPIDIVALYRILQVCPPEVDKHMPLNLTNNFSISVVPYLSPKLMSQ 228
gi | 125822502 | ref | XP_001338251.1 | S--YLSVAVFNKQLQRLEDNSALENEVVLGALLSCT--RLVLGSRSSLVLRVLEQCKRLDSEKLNKLVLCGISRASFALEGDSGLVQAMSQLOKTFEIQWKAALVAVYCMALAGLAEDVLYQDILLNEMNAQALRLVHQMDPEAVK 293
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 128485706 | ref | NP_081399.3 | VLTALVALDQTHALPLLILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVSIVVVCWDRLLSPSCIAELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 449
gi | 34873428 | ref | XP_214418.2 | VLTALVALDQTHARPLLILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 444
gi | 40068497 | ref | NP_076996.2 | MLTALVLDQSQAPPLIILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 448
gi | 114599023 | ref | XP_517625.2 | MLTALVLDQSQAPPLIILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 431
gi | 74003089 | ref | XP_545176.2 | MLGALVLDQSQAPPLIILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 449
gi | 194676663 | ref | XP_001789483.1 | MLTALVLDQSQAPPLIILKLGKVVVRYIPRFINEELRVLVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 448
gi | 50735005 | ref | XP_419017.1 | LILNSLVALHQTQVPLLILALCKHSVHKVYPIFSDLEASVLEAFVYFGHSDRFFTEALEQHVVAALCFSLDPAVASVVMGYCSRKRILSKPIFDVVAEIVFVCSSEKFSFSPQISELIEPFGKLNVPVPPNAPALFRKVENVLCARLHFFPPKML 378
gi | 125822502 | ref | XP_001338251.1 | LLGALVLRQEQALPLVIALCQAVHQVQSFADAEILTIVLVSALMHFGHSDHFFVEALERYVVKVAFVTAHAETIILKVMQFFQHRRLILSLPVFNAVAESFVYRAEYESTWVQSQITTLGVLGYLPPDAGRLFRKVESVLFHARFSQFPRAL 443
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 128485706 | ref | NP_081399.3 | LRLHSCALIERHPVNFMSKIFSPFFLQRLQKGE--SYLDRLSLAQLTQLFLTSLVLECPFYKPKLLPKYQVKSFLTPCCSLETPDLHLHYKSVVIGLIDLLGSRLYFASKVLPYVYITDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 598
gi | 34873428 | ref | XP_214418.2 | LRLHSCSLIERHPVNFMSKIFSPFFLQRLQKGE--SYLDRLSLAQMTQLFLTSLVLECPFYKPKLLPKYQVKSFLTPCCSLETPMDLHLHYKSVVIGLIDLLGSRLYFASKVLPYVYITDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 593
gi | 40068497 | ref | NP_076996.2 | LKLLHSCSLNECHPVNFPLAKIFKPLFLQRLQKGE--SHLDTLSRAQLTQLFLASVLECPFYKPKLLPKYQVKSFLTPCCSLETPVDSLYRYVVKIGLNLGALRYFAPKVLTPYCYTIDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 597
gi | 114599023 | ref | XP_517625.2 | LKLLHSCSLNECHPVNFPLAKIFKPLFLQRLQKGE--SHLDTLSRAQLTQLFLASVLECPFYKPKLLPKYQVKSFLTPCCSLETPVDSLYRYVVKIGLNLGALRYFAPKVLTPYCYTIDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 580
gi | 74003089 | ref | XP_545176.2 | LKILHSCSLIECHPVNFMAKIFSPHFLQKLGEE--LYLDRLSLAQLTQLFLTSLVLECPFYKPKLLPKYQVKSFLTPCCSLETPVDFLFRVVKTKGLIDLLGALRYFASKVLPYCYTIDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 598
gi | 194676663 | ref | XP_001789483.1 | LRLHSCSLIECHPVNFMAKIFSPHFLQKLGEE--LYLDRLSLAQLTQLFLTSLVLECPFYKPKLLPKYQVKSFLTPCCSLETPMDFHLRYKSVMTGLIDLLGALRYFASKVLPYCYTIDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 597
gi | 50735005 | ref | XP_419017.1 | LNLHSCCVLIQRYVNFPLKIFSPYFLQELQAP--PGLDRVVASQSLTQLFLTSLVLECPFYKPKLLPKYQVNAFLTTCFLD---VHLFRVKSGLVLLKGMVPSSEVSPYVYITDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 523
gi | 125822502 | ref | XP_001338251.1 | LDLLHACVLIQRYVNFVSKVFSYFLQELQEGE--SGLSHVVAQLTQLYMSVKLECPFYDGRLLPKYQVKSFLAP---FETVPEVQFYNALKSGVLDLLGDSIVASVLPYCYTIDVEIKLDEDFVLPCHVDEDIHKRVALCIDG 590
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 128485706 | ref | NP_081399.3 | PQRFLDQSKHLLGKEAIKQRHLRLLGYQVVPYPYHELELLTSRLELVDYLQKLFQSSAVHW--- 661
gi | 34873428 | ref | XP_214418.2 | PQRFLDQSKHLLGKEAIKQRHLRLLGYQVVPYPYHELELLTSRLELVDYLQKLFQSSAVHW--- 656
gi | 40068497 | ref | NP_076996.2 | PRRFCSNSKHLGKEAIKQRHLRLLGYQVQIPYHEIGMLKSRRELVEYLQKLFQSNH--VHWLQ 662
gi | 114599023 | ref | XP_517625.2 | PRRFCSNSKHLGKEAIKQRHLRLLGYQVQIPYHEIGMLKSRRELVEYLQKLFQSNH--VHWLQ 645
gi | 74003089 | ref | XP_545176.2 | PRRFCLNSKHLGKEAIKQRHLRLLGYQVQIPYVEIEVLSRGLVEYLQKLFQSSAVHW--- 661
gi | 194676663 | ref | XP_001789483.1 | PRRFCLNSKHLGKEAIKQRHLRLLGYQVQIPYVEIEVLSRGLVEYLQKLFQSSAVHW--- 660
gi | 50735005 | ref | XP_419017.1 | QNRFCVNSHLLGEEAIKQRHLRLLGYQVQIPYVEIEVLSRGLVEYLQKLFQSSAVHW--- 586
gi | 125822502 | ref | XP_001338251.1 | SQRFANAKKLLGKEAIKQRHLRLLGYQVQIPYVEIEVLSRGLVEYLQKLFQSSAVHW--- 653
.....610.....620.....630.....640.....650.....660.....

