

gi|24638969|ref|NP_525036.2|MSEPDPPQELGAEVVSGLVA--TSDDRLEMINAEVTLNLRDLN-MDRQTELOGVETYLEVS---QRCEMECTASHWMCCLAIYACRRSIPPTVTGNAVVKGCNCSLNNLRCKMKSIVYEFKIKIKWCMDA---LPG 129



gi|24638969|ref|NP_525036.2|EFVNEIEDLDRKFSIFMLHRRPRIIMDMIFSCPPNEKHKSKVYSLGHNHAHGKCSYIKLDDICWRLFPCAQNKPSNTVDLVTSNLIMCICDLIYN-NVLAERKTRDLIN---PKFEGFLSNWTDLDF--HNPCHILSNFCDM 268



gi|24638969|ref|NP_525036.2|TE---EAKAMKATFRQIMNSFFQASTIYGNKD---HMLGLLIANFERNLKSINISYEQYVLSGVEFDERLILSAYDAGEHTALNDQSLR---FPVTPPLIRKQ---DLPAQPMAGDKFEFVRN 380



gi|24638969|ref|NP_525036.2|AANNVQKLSAFCGRITP--HDFVKQAGEEVIKLLSITETEIKFLAKYPS---EAKS---RFLQAKSFFYLLDQLQAIRNRPDIDLRLKLLVQKSVLIFINIILMACCVLVLVLAQKTE-LKFPWVLDLQAF 510



gi | 24638969 | ref | NP_525036.2 | EFOKIIIEIVVRHGSHGCLNRSLIKHLNSIEETCLERLAWARNITVWEMIASAQLPLPTWLMVNLDR----- 577
gi | 33859602 | ref | NP_035379.1 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 109469134 | ref | XP_001055763.1 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 34577079 | ref | NP_002886.2 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 114681879 | ref | XP_001139919.1 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 73992372 | ref | XP_534412.2 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 119905907 | ref | XP_603207.3 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 118100471 | ref | XP_417312.2 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 677
gi | 189520777 | ref | XP_001333039.2 | YFYKVIIEVVIRS---EEGLSRDMVKHLNSIEEOILLESALWALWEALHANSANKVPECEEVIFPNNFETIGNGGNVOGHLPMMPMSPIIHPRVKEVRTDSG--SLRDMOPLSPIVHVERYSSPAAGSAKRRFLGDDPPKDLMDKIMAE 678
gi | 30682129 | ref | NP_566417.3 | DLKSVIEEFIRH---EDSLPRELRRHLNSLEERLLESVMWEKGSMSYNSLIVAR---PSLALEINQLGLLAEPMPSLDA TAALINFDGANHASVQKHETC-----PGQNGGIRPKRLCIDYRSILVERNSFTSPVKDRLLA 693
gi | 115477553 | ref | NP_001062372.1 | DLKSVIEEFIRH---EDTLPRELRRHLNSLEERLLESMAWEKGSMSYNSLIVAR---PILSAEINRLGLLAEPMPSLDA TAAHHNISLEGLPLLPFQKQHS-----PDKDE-VRSPKRACTERRNVLDVNSFTSPVKDRLLA 704
gi | 158295912 | ref | XP_316517.4 | RFFHIIIEVTVTAN---NDLILSDIVNHLRRIEQLVDSISWKSSEVLWECMEKENYITIPANKDVEQRA----- 596



gi | 24638969 | ref | NP_525036.2 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 825
gi | 33859602 | ref | NP_035379.1 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 825
gi | 109469134 | ref | XP_001055763.1 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 825
gi | 34577079 | ref | NP_002886.2 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 826
gi | 114681879 | ref | XP_001139919.1 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 826
gi | 73992372 | ref | XP_534412.2 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 826
gi | 119905907 | ref | XP_603207.3 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 826
gi | 118100471 | ref | XP_417312.2 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 826
gi | 189520777 | ref | XP_001333039.2 | GFKLKIAP--SSVTAESLSISPGQALLTMATAIVTGTGRKVTIPLHGIAN DAGEIILVPI SMNPTEESTAESPVSLTAOSLIGTSPKQTHLTKAQAHLTGVSFKPKRTGSLALFYRKVYHLASVRLRDLCLKLDVS--NELRRKIWTCFEH 810
gi | 30682129 | ref | NP_566417.3 | K-----PIKIIP--SGLENGTITIT---TVLSMATG-----NGQOLTIPLFVVKNEAGGIITVIQLQASDMNPLTAIVLLTASP-----SRPALAAPAISSDSQPPANPKRPTGSLALFYRKVYHLASVRLRDLCLKLDVS--SELRKGIWTCFEH 810
gi | 115477553 | ref | NP_001062372.1 | K-----LPPLOSFAFASPTRPNPAGGELCAETGIGVFLSKIAKLAIRIRGLCERLQLS--EQLVERVYSLVQO 768
gi | 158295912 | ref | XP_316517.4 | K-----LPPLOSFAFASPTRPNPAGGELCAETGIGVFLSKIAKLAIRIRGLCERLQLS--EQLVERVYSLVQO 771
ETAGVPLKGDMSYQVAYDRLCNLQNLGIDIEVVIKLIWTLIEH----- 641



gi | 24638969 | ref | NP_525036.2 | SIIHET--ELMKDRHLDQNLICAVYIIRVKRMEDPKFSDIMRARNQPOAVNSVYREVFIDIN-----EDGEPKVKDILIHFYNIHIVPLMRQV 707
gi | 33859602 | ref | NP_035379.1 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQERMKSRYRNPQANSVHYRVSLLKSIPGGVVVY-----NGDCEMTDGDIEDATKTP-----NCSSEFVKBERGDLIKFYNTIIVGRVKSF 940
gi | 109469134 | ref | XP_001055763.1 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQEIIMKSYRNPQANSVHYRVSLLKSIPGEVVAY-----NGDYEMTDGDIEDATKTP-----NCSSEFVKBERGDLIKFYNTIIVGRVKSF 940
gi | 34577079 | ref | NP_002886.2 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQEIIMKSYRNPQANSVHYRVSLLKSIPREVVAYN-----KNINDDFEMIDCDLEDAKTP-----DCSSGPVKBERGDLIKFYNTIIVGRVKSF 945
gi | 114681879 | ref | XP_001139919.1 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQEIIMKSYRNPQANSVHYRVSLLKSIPREVVAYN-----KNINDDFEMIDCDLEDAKTP-----DCSSGPVKBERGDLIKFYNTIIVGRVKSF 945
gi | 73992372 | ref | XP_534412.2 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQEIIMKSYRNPQANSVHYRVSLLKSIPREVVAYN-----KNINDDFEMIDCDLEDAKTP-----DCSSGPVKBERGDLIKFYNTIIVGRVKSF 945
gi | 119905907 | ref | XP_603207.3 | TLVHCP--DLMKDRHLDQLLCAFYIMAKVTKEER--TFQEIIMKSYRNPQANSVHYRVSLLKSIPREVVAYN-----KNINDDFEMIDCDLEDAKTP-----DCSSGPVKBERGDLIKFYNTIIVGRVKSF 945
gi | 118100471 | ref | XP_417312.2 | TLVHCA--DLMKDRHLDQLLCAFYIIRVKRMEDPKFSDIMRARNQPOAVNSVYREVFIDIN-----EDGEPKVKDILIHFYNIHIVPLMRQV 938
gi | 189520777 | ref | XP_001333039.2 | SLLHCT--DLMKDRHLDQLLCAFYIIRVKRMEDPKFSDIMRARNQPOAVNSVYREVFIDIN-----EDGEPKVKDILIHFYNIHIVPLMRQV 935
gi | 30682129 | ref | NP_566417.3 | VLAQRT--SLLPSRHIDQIILCCFYGVAKISQMSL--TFEIIINRYRKPQCKPKLVFRSVVVDALQC-----MEVDPADQENERTDQAANERSDADRTOVFESBERGLDIFYNNIIVSKMRSF 859
gi | 115477553 | ref | NP_001062372.1 | IIIQQT--ALFNRHIDQIILCCFYGVAKISQMSL--TFEIIINRYRKPQCKPKLVFRSVVVDALQC-----SRNGKTGEDVDIITFYNEVFIPTVKPL 862
gi | 158295912 | ref | XP_316517.4 | IITKCS--ELMRDRHLDQLLCAFYIIRVKRMEDPKFSDIMRARNQPOAVNSVYREVFIDIN-----EDGEPKVKDILIHFYNIHIVPLMRQV 920
TFRQIMHCKHSGQANSIYRVSFIRYESAAAPFDPSGKEVEBKAKDADECSNGGKNGTITTTTASNGEATGASERCPVTEAGTQVQYGREVYGDIIKIFYNDIIVVTVHHE 910



gi | 24638969 | ref | NP_525036.2 | VIDYLVNVTVDVSGRASLDQLSPHPKERA-----AQPKKVTGSHSLFVFSQMSKN--EIQQSPNQMVYVFCRSPAKDLQAMNEKVRGGKRLMSFGDEPGLGTMAEIKRSKISVAVMDDPELSEACQAVTIEGCVGGEGGEHE 844
gi | 33859602 | ref | NP_035379.1 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--ADSPAKRLCOENDVLLKRLQDVVERANH 1063
gi | 109469134 | ref | XP_001055763.1 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSRKVLNMMVNGEKRKRVAIISGD--AESPAKRLCOENDVLLKRLQDVVERANH 1063
gi | 34577079 | ref | NP_002886.2 | ALKYDLANQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--AESPAKRVCOENDVLLKRLQDVVERANH 1068
gi | 114681879 | ref | XP_001139919.1 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--AESPAKRVCOENDVLLKRLQDVVERANH 1068
gi | 73992372 | ref | XP_534412.2 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--AESPAKRLCOENDVLLKRLQDVVERANH 1068
gi | 119905907 | ref | XP_603207.3 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--AESPAKRLCOENDVLLKRLQDVVERANH 1068
gi | 118100471 | ref | XP_417312.2 | ALKYDLSNQDHIMDAPPLSPFPHIKQOP-----GSPRRISQOHSIYVSPHNG--AGLTPRALLYKFNQSPSKSLKIDINNMIRQGEQRTKKRVAIISGD--AESPAKRLCOENDVLLKRLQDVVERANH 1060
gi | 189520777 | ref | XP_001333039.2 | AFKVAL--TLDNRMEAPPLSPFPHIKQOP-----LSPRRISQOHSIYVSPHNS--SLSLTPSHAYTYRFTGSPSKELSDINMMIRQGG--VSKRAFTEGDETESPKCLRQENDVLLKRLQDVVERASL 1058
gi | 30682129 | ref | NP_566417.3 | LVELGP--VRNDRVAVANNKPEGQCPSPKVSVFPVDPMSPKKVSAAHNVYVPLRGSKMDALISHSKSYACVGES--HAFQSPSKDLKVINNRNLSNRRKRTLNFDAAEAGVSDSMVANSNLNQNQNQNGSDASSGGAAFLKT 1008
gi | 115477553 | ref | NP_001062372.1 | LVELGSGTSPNKKNEEKCAADGYPPEPRLRFPNLDMSPKKVSAAHNVYVPLRGSKMDALISHSKSYACVGES--HAFQSPSKDLKVINNRNLSNRRKRTLNFDAAEAGVSDSMVANSNLNQNQNQNGSDASSGGAAFLKT 1005
gi | 158295912 | ref | XP_316517.4 | ALQVYNAIVSQQESLFLSPTPKSQMNRNIQ-----KSPROITSSGINLYVETINNKISSLKDSVNVRLVFPSPGQSPIMHERKLPVLRGKVGETAARRLTPAPAYEPTRAIKLRLRDIKHIERHQDNEMSENE----- 918



gi	24638969	ref	NP_525036.2	T----	845
gi	33859602	ref	NP_035379.1	-----	1063
gi	109469134	ref	XP_001055763.1	-----	1063
gi	34577079	ref	NP_002886.2	-----	1068
gi	114681879	ref	XP_001139919.1	-----	1068
gi	73992372	ref	XP_534412.2	-----	1068
gi	119905907	ref	XP_603207.3	-----	1068
gi	118100471	ref	XP_417312.2	-----	1060
gi	189520777	ref	XP_001333039.2	-----	1058
gi	30682129	ref	NP_566417.3	RPIDG	1013
gi	115477553	ref	NP_001062372.1	RQFDC	1010
gi	158295912	ref	XP_316517.4	-----	918
				

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