

gi|62484382|ref|NP_724962.2| LASAQ--ERRRANASVQVKVLD-----NDNYPQFERTYTVQVPEQWGGCTEDNTVAHIRADADQGNNAAIRVAITGGNTQSFSIDEMSDDVSLVKPLDYESVRSRLVIRAQGGSPSRN--ITQLLVNVIDANDNAPRFYTSQ 693
gi|31210749|ref|XP_314341.1| MATPQ--ERRKSAITVLVKILDD-----NDNYPQFERTYTVQVREDQWAN--ENVAIAHQASDADQGNNAAIRVAITGGNTQSFSIDEMSDDVSLVKPLDYENVRSLVIRAQGGSPSRN--ITQLLVNVIDANDNAPRFYTSQ 713
gi|189518225|ref|XP_687264.3| QGKEP--GPRSAATVHIHVEDE-----NDNYPQFSEKRYVVQVPEVAVN--TKVAQVEA--DRDEGNARVHYSITSGAVKQOFFITHTPTGAIQVNPPLDYETITREYNLRIRKADGGRPPLINGTGMVVVQVVDVNDNAPMVFVSTP 416
gi|189537376|ref|XP_001920772.1| QGREP--GPRTAATVHIHVEDE-----NDNYPQFSEKRYVVQVSENAVAN--TQVAVVKA--DKDAGNAKVVHYSIINGIKGQFVIHSPITGVLDVVSPLDYEMIREYTLRKAQDGGRPPLINGTGMVVVQVVDVNDNAPMVFVSTP 565
gi|115648153|ref|NP_034016.2| QGRNP--GPLSASATVHIHVEDE-----NDNYPQFSEKRYVVQVPEVAVN--TAVLRVQA--DRDQGNAAIHYSIVSGNLKGQFVHLHSLGSLDVINPLDFEAIREYTLRKAQDGGRPPLINSSGLVSVQVLDVNDNAPMVFVSTP 584
gi|109481140|ref|XP_001070474.1| QGRNP--GPLSASATVHIHVEDE-----NDNYPQFSEKRYVVQVPEVAVN--TPVLRVQA--DRDQGNAAIHYSIVSGNLKGQFVHLHSLGSLDVINPLDFEAIREYTLRKAQDGGRPPLINSSGLVSVQVLDVNDNAPMVFVSTP 584
gi|7656967|ref|NP_055061.1| QGRNP--GPLSASATVHIHVEDE-----NDNYPQFSEKRYVVQVPEVAVN--TAVLRVQA--DRDQGNAAIHYSIVSGNLKGQFVHLHSLGSLDVINPLDFEAIREYTLRKAQDGGRPPLINSSGLVSVQVLDVNDNAPMVFVSTP 569
gi|73969260|ref|XP_538324.2| QGRNP--GPLSASATVHIHVEDE-----NDNYPQFSEKRYVVQVPEVAVN--TPVLRVRA--DRDQGNAAIHYSIVSGNLKGQFVHLHSLGSLDVINPLDFEAIREYTLRKAQDGGRPPLINSSGLVSVQVLDVNDNAPMVFVSTP 669
gi|194666763|ref|XP_600703.4| GSYSPF--FRSKD--SAHSVYLAISTPWEAAVVKPRGRMFLGGDLTAKVTRAAA--AGELPPPGSLRHLHSLVQVPGIVSGNKGQFVHLHSLGSLDFINPLDFETIREYTLRKAQDGGRPPLINSSGLVSVQVLDVNDNAPMVFVSTP 622
gi|193207741|ref|NP_506256.3| KGTPK--RES--TAMVETITVIVN--DNAVVFASDSVNVITILENITIP--AVLATVKA--DEDFGTNGKVHYSMASSSGIGGLIDYISTGEVTLRBRIDAKNS--PIITAVIRAKDGAQP--ALSTIVPLTINVIDINDHAPITLAAQ 483



gi|62484382|ref|NP_724962.2| FQESVLENVVGVNIRVQAYDSDEGANAEITYSISERD-----DNFPLAVDPRTGWQVNIKPLDREEQGRFAPQVAVKDGVPKSA--SSVVIIVQVNDNDPAFNPKYYEANGEDQPPGTPVITVATDPPEDSR 826
gi|31210749|ref|XP_314341.1| FQEAVLESVPGVNIIRVQAYDSDEGANSEITYSIQNRD-----DGMPLAVDPRTGWIHTKALDREEQSRYSQVAVDGGIPPKSASTSVIVITQVNDNDPFPKYYEAMLAEDQPPGTPVITVATDPPEDSR 846
gi|189518225|ref|XP_687264.3| FQATVLENVPIGYSVIHIQAIADSDSGENARLDYSITDIT-----PGPFVFINNSTGWIIVSDELDRSTEFYTFGVEARDNGVPMSSASVSIIVLVDVNDNIPFTFEKMYSLKINEDAVVGTSVLVTALDRDVSVP 549
gi|189537376|ref|XP_001920772.1| FQASVLENVPIGYSVIHIQAIADSDGNAHLEYKLTDTIS-----PGPFVFINNSTGWIIVSDELDRSTEFYTFGVEARDNGVPMSSASVSIIVLVDVNDNIPFTFOHLYNKLKVNEDAVVGTSVLVTAVDRDVSVP 698
gi|115648153|ref|NP_034016.2| FQAAVLENVPLGHSVLHIQAVDADAGENARLYRLVDTASILVGGSSVDSENPASAPDFPFQIHNSSGWIIVCAELDREIEHYSGFVEAVDHGSPMSSASVSIIVLVDVNDNIPMFTQPVYELRLNEDAAGVSSVLTLRARDANSV 734
gi|109481140|ref|XP_001070474.1| FQAAVLENVPLGHSVLHIQAVDADAGENARLYRLVDTASILVGGSSVDSENPASAPDFPFQIHNSSGWIIVCAELDREIEHYSGFVEAVDHGSPMSSASVSIIVLVDVNDNIPMFTQPVYELRLNEDAAGVSSVLTLRARDANSV 734
gi|7656967|ref|NP_055061.1| FQATVLENVPLGYVPHVHIQAVDADSGENARLHYRLVDTASFLGGSSAGPKNPAPFPDFPFQIHNSSGWIIVCAELDREIEHYSGFVEAVDHGSPMSSASVSIIVLVDVNDNIPMFTQPVYELRLNEDAAGVSSVLTQARDANSV 719
gi|73969260|ref|XP_538324.2| FQAAVLENVPLGHSVLHIQAVDADAGENARLYRLVDTASSLGSGGPGTDPGSPDFPFQIHNSSGWIIVCAELDREIEHYSGFVEAVDHGSPMSSASVSIIVLVDVNDNIPMFTQPVYELRLNEDAAGVSSVLTLRARDANSV 819
gi|194666763|ref|XP_600703.4| FQAAVLENVPLGHSVLHIQAVDADAGENARLYRLVDTASASVGGGGAAPAAPAAPADPFQIHNSSGWIIVCAELDREIEHYSGFVEAVDHGSPMSSASVSIIVLVDVNDNIPMFTQPVYELRLNEDAAGVSSVLTLRARDANSV 772
gi|193207741|ref|NP_506256.3| KMTILEENVAIGEVEGRVYAIIDSDSGNPIIKIYSMEGSE-----DFIIDEESGLIKRTRKLDRETTARYSLKVRADMDGSPSLNLTSTTIAVVLKIDINDNAPTFDKKEYVNTISEEMQSSQIITLKAVDNEDQK 613



gi|62484382|ref|NP_724962.2| LHYEITAGNTRGRFAITSONGRGLITIAQSLDYKQEKRFLLITVAATDSGGRSDTATVHINIDANFNAPFENAPYSASVFEADAPVGTIVLVVSA--SDSDVGVNAQITYSINLEESINGLSPDPFSSINPQTGAIVINAFLDRETTSGVLLT 976
gi|31210749|ref|XP_314341.1| LHYEITAGNTRGRFAITSONGRGLITIAQPLDYKQERRFALTTIATDSGQRDITIAVNNINIDANFNAPFENAPYSASVFEADAPVGTIVLVVSA--SDSDVGVNAQITYLLNDESINLGLANPFTTINAGTGAITINAKLDRETTSGVLLT 996
gi|189518225|ref|XP_687264.3| VHYQISSGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLTITASDG--TRFDTA--QVFINVDANTHRPVPQANANVQITFSDQPTGSSVTVVISA--DEDTGENARITVYMEDNVP-----QFRIDPDSGAIITQMEIDYEDQAAVTLA 691
gi|189537376|ref|XP_001920772.1| VHYQISSGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLTITASDG--TRFDTA--QVFINVDANTHRPVPQANANVQITFSDQPTGSSVTVVISA--DEDTGENARITVYMEDNVP-----QFRIDPDTGAIITQMEIDYEDQAAVTLA 840
gi|115648153|ref|NP_034016.2| ITYQLTGGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLAVTASDG--TRSHTA--QVFINVDANTHRPVPQSSHYTVSVSEDRPVGTSIAITSA--DEDTGENARITVYLEDVVP-----QFRIDPDTGIIYTMELDYEDQAAVTLA 876
gi|109481140|ref|XP_001070474.1| ITYQLTGGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLAVTASDG--TRSHTA--QVFINVDANTHRPVPQSSHYTVSVSEDRPVGTSIAITSA--DEDTGENARITVYLEDVVP-----QFRIDPDTGIIYTMELDYEDQAAVTLA 876
gi|7656967|ref|NP_055061.1| ITYQLTGGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLAVTASDG--TRSHTA--QVFINVDANTHRPVPQSSHYTVSVSEDRPVGTSIAITSA--DEDTGENARITVYLEDVVP-----QFRIDPDSGIIYTMELDYEDQAAVTLA 861
gi|73969260|ref|XP_538324.2| ITYQLTGGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLAVTASDG--TRSHTA--QVFINVDANTHRPVPQSSHYTVSVSEDRPVGTSIAITSA--DEDTGENARITVYLEDVVP-----QFRIDPDTGIIYTMELDYEDQAAVTLA 961
gi|194666763|ref|XP_600703.4| ITYQLTGGNTRNRFAITSSQSGGLIITLALPLDYKQERYVLLAVTASDG--TRSHTA--QVFINVDANTHRPVPQSSHYTVSVSEDRPVGTSIAITSA--DEDTGENARITVYLEDVVP-----QFRIDPDTGIIYTMELDYEDQAAVTLA 914
gi|193207741|ref|NP_506256.3| IIVRLEEADREVFSILDIDQDQAILSVSGELKR--DDHKVVRVEISATDQGGLOGRCVNVVIFDDVNV--SAPVYNDPFPVVKIP--EHSPTGIVPVIITLKAEDHDRDNRIVYSIDSSQF-----FRIDPSSGDISVSDLDREDRATFSVI 753



gi|62484382|ref|NP_724962.2| VTAKDGGNPSLSDTIDVEIGVITVDVNDNAPAFKSPLYQASILEDALVGTSVIQVAASDPDVLNNGRIKMLLSDRDIED--GSFVIDPSTGIRITNKGLDRESVAVFHLTAIAVDKGGP--PLSSIVVEQIRLEDVNDSPPTFASDKITLYVE 1123
gi|31210749|ref|XP_314341.1| VTAKDGGNPSLSDTIDVEIGVITVDVNDNAPVFKVPLVQAITPEDALIGTSVVOIAA--DLDMGLNNGRVKALQKQMDME--GSFVVDPISGVIRITNKGLDRESVAVFHLTAIASDKGTP--TMSSSVEQIRLEDVNDSPPTFASDKITLYVE 1143
gi|189518225|ref|XP_687264.3| IIAARDNGIPQKSDITVVEIILLDANDNSPRFRGRDKYQGTVFEDAPIYTSVLQISASDRDSGSGNRVSYTFQGGDDGE--GDFMIEQYSGIIRTHRKLDRDNVAVYVNLRAVAVDRGVF--PLKAAVEIQVSVLIDINDNAPVFEKDELYIVDK 838
gi|189537376|ref|XP_001920772.1| IIAARDNGIPQKSDITVVEIILLDANDNVPQFLRDIYQGTVFEDAPVYTSVLQVSA--DRDSGSGNRVSYTFQGGDDGE--GDFMIEPESGIRITARKLDRDNVALYTLKAFVAVDKGVF--PLKAAVVIQVSVLIDINDNAPVFEKDELYIVDK 987
gi|115648153|ref|NP_034016.2| IIAQDNGIPQKSDITVLEIILLDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSA--DRDSGPNGRLLYTFQGGDDGD--GDFVIEPESGIVIRTQRRLDRDNVAVYVNLWALAVDRGSPNPLSASVEIQVSVLIDINDNAPVFEKDELELVE 1024
gi|109481140|ref|XP_001070474.1| IIAQDNGIPQKSDITVLEIILLDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSA--DRDSGPNGRLLYTFQGGDDGD--GDFVIEPESGIVIRTQRRLDRDNVAVYVNLWALAVDRGSPNPLSASVEIQVSVLIDINDNAPVFEKDELELVE 1024
gi|7656967|ref|NP_055061.1| IMAQDNGIPQKSDITVLEIILLDANDNAPQFLWDFYQGSIFEDAPPSTSVLQVSA--DRDSGPNGRLLYTFQGGDDGD--GDFVIEPESGIVIRTQRRLDRDNVAVYVNLWALAVDRGSPNPLSASVEIQVSVLIDINDNAPVFEKDELELVE 1009
gi|73969260|ref|XP_538324.2| IIAARDNGIPQKSDITVLEIILLDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSA--DRDSGPNGRLLYTFQGGDDGD--GDFVIEPESGIVIRTQRRLDRDNVAVYVNLWALAVDRGSPNPLSASVEIQVSVLIDINDNAPVFEKDELELVE 1109
gi|194666763|ref|XP_600703.4| IIAARDNGIPQKSDITVLEIILLDANDNAPRFLRDFYQGSVFEDAPPSTSVLQVSA--DRDSGPNGRLLYTFQGGDDGD--GDFVIEPESGIVIRTQRRLDRDNVAVYVNLWALAVDRGSPNPLSASVEIQVSVLIDINDNAPVFEKDELELVE 1062
gi|193207741|ref|NP_506256.3| VIASDHA--SPPLNTSTQIEVILLDDINDNSGFLSS--YAAIIS--EDIPVGTSLQVSA--IDADI--GPNGRLLVYFLNSSSSPSIQLFRLDRSGLRVS--SKLRDRE--FAVIVL--IFARDR--PL--SL--SASEI--ITV--LID--IND--NAP--VFEKDELYIVDK 902



gi | 62484382 | ref | NP_724962.2 | ENSPVGSLVGEIHAHDPDEGVNAIVHYSIIGGDDSNAPSLVLRPGSD-RAQLLIMTELVDYESTRKRFEVLVRAASPLLRNDAHIEILVTDVNDNAPVLRDFQVIFN----NFRDHFPSGEIGRIPAFDADVSDKHLVIRLSCNANLLRL 1268
gi | 31210749 | ref | XP_314341.1 | ENSPVGSLVGEIYAHDPDEGVNAIVHYSIIGGDDSNAPSLVLRPGSD-RAQLLIMTELVDYESTRKRFEILIRAAASPLLRNDAHIEILVTDVNDNAPVLRDFQVIFN----NFRDCFPSPGIVGRIPAFDADVSDKHLVIRLSCNANLLRL 1288
gi | 189518225 | ref | XP_687264.3 | ENSPVGSLVAVRITAMPDDEGTNAQIILYQIVEGNVPEVFDLDFIFG----DLKALVDLDYETQ-KEYVIVVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 982
gi | 189537376 | ref | XP_001920772.1 | ENSAVGSLARVSAATDDEGTNAQIILYQIVEGNVPEVFDLDFIFG----DLIALDLDYETQ-MEYVIVVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1131
gi | 115648153 | ref | NP_034016.2 | ENSPVGSLVAVRIRANDPDEGPNQAIMYQIVEGNVPEVFDLDFIFG----DLRALVELDFEVR-RDYMVLVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1168
gi | 109481140 | ref | XP_001070474.1 | ENSPVGSLVAVRIRANDPDEGPNQAIMYQIVEGNVPEVFDLDFIFG----DLRALVELDFEVR-RDYMVLVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1168
gi | 7656967 | ref | NP_055061.1 | ENNPVGSVAVRIRANDPDEGPNQAIMYQIVEGNVPEVFDLDFIFG----DLRAMVELDFEVR-REYVVLVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1153
gi | 73969260 | ref | XP_538324.2 | ENSPVGSLVAVRIRANDPDEGPNQAIMYQIVEGNVPEVFDLDFIFG----DLRALVELDFEVR-REYVVLVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1253
gi | 194666763 | ref | XP_600703.4 | ENSPVGSLVAVRIRASDPDEGPNQAIMYQIVEGNVPEVFDLDFIFG----DLRALVELDFEAR-DEYVVLVQVATSAPLVSRATVHRLLDQNDNPPVLDQNFIEIFNNYVTKNSNSPSPGIVGRIPAHDPDLSLNYTFVCGNELSLLL 1206
gi | 193207741 | ref | NP_506256.3 | ENSPVGSLVGTIVARDADGDNADISFRIFGADAKLFDIIEADAEQNGVVRILTRAFDFYEAANKFFELQASSGQLSITVPRVIRHVSVDVNDNPKALKDFVILMN----RFDNVQMARQIGFIPAFDQNAILEVFLFEND---LIEA 1045



gi | 62484382 | ref | NP_724962.2 | NSSGGLVLSPOLNTVPKFAIMEVSVSDGINEAKAIMQLSVRLITEDMLFNSVTVRLNEMEEAFLSPLLNFFLDGLAAITCPKR-EHIFVFSIQDDIDVSSRILNVFSARRPVDVSHFEEFYTPQYLOQERVYLNRAILARLANAVRVLPP 1417
gi | 31210749 | ref | XP_314341.1 | NSSGGLVLSPOLNTVPKFAIMEVSVTDGINEAKAIMQLSVRLITEDMLFNSVTVRLNEMEEAFLSPLLNFFLDGLAAITCPKR-ENIFLFSIQDDIDVSGKILNVFSARRPVDVAFEEYYSQYLOQERIVYLNRAILARLANAVRVLPP 1437
gi | 189518225 | ref | XP_687264.3 | NPDTGELKLSKDLLDNNRPLEALMKVSVTDGIHQVAFCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTSR-EGVFIFFNQNDIDVSGNILLNVFSAALLPGGVPDRFPPSEELQEQIYLNRLLLQEISSONVLPF 1131
gi | 189537376 | ref | XP_001920772.1 | NQDTGELKLSKDLLDNNRPLEALMRVSVSDGLHQVAFCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTSR-DGIFIFNQNDIDVSGSILLNVFSAALLPGGAPGRYFPSEELQEQIYLNRLLLMLISTORVLPF 1280
gi | 115648153 | ref | NP_034016.2 | DPATGELQLSRDLDNNRPLEALMEVSVSDGIHVSVALCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTTK-DDIFVFNQNDIDVSSNILLNVFSAALLPGGTRGRFFPSEDLQEQIYLNRLLLTISAORVLPF 1317
gi | 109481140 | ref | XP_001070474.1 | DPATGELQLSRDLDNNRPLEALMEVSVSDGIHVSVALCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTTK-DDIFVFNQNDIDVSSNILLNVFSAALLPGGARGRFFPSEDLQEQIYLNRLLLTISAORVLPF 1317
gi | 7656967 | ref | NP_055061.1 | DPATGELQLSRDLDNNRPLEALMEVSVSDGIHVSVALCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTTK-DDVVFVFNQNDIDVSSNILLNVFSAALLPGGVRGQFPSEDLQEQIYLNRLLLTISAORVLPF 1302
gi | 73969260 | ref | XP_538324.2 | DPATGELQLSRDLDNNRPLEALMEVSVSDGIHVSVALCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTTK-DDVVFVFNQNDIDVSSNILLNVFSAALLPGGVRDKFFPSEDLQEQIYLNRLLLTISAORVLPF 1402
gi | 194666763 | ref | XP_600703.4 | DPATGELQLSRDLDNNRPLEALMEVSVSDGIHVSVALCTLRVTIITDDMLTNSITVRLNEMSQERFLSPLLSLFVKGVAAVLSTTK-DAVVFVFNQNDIDVSSNILLNVFSAALLPGGVRDKFFPSEDLQEQIYLNRLLLTISAORVLPF 1355
gi | 193207741 | ref | NP_506256.3 | EKYTGKILVKQEWKRN--MDVSKTKCVSDGANTECSTCRFTHVIVEPEWLSSEFTLSLARMVDDFDWPLVQFRFRDAMSILNWRKPSDTHVIGVQKHLDDVIYIN-----IATTDHGRVNRGWAETELVYKNSIKLEKMLLQVEVI 1186



gi | 62484382 | ref | NP_724962.2 | DDNLVREPCLVNFEELTLVKFGNAEFTHSDTVLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGTVRREGGYTCVCPSTHTGNCETGVGHRLPCPSEICEGGLSCLSNVPSSQPPPYTAT-----CELRARAF 1561
gi | 31210749 | ref | XP_314341.1 | DDNLVREPCLVNFEELTLVKFGNAEFTHSDTVLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYSCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1581
gi | 189518225 | ref | XP_687264.3 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1276
gi | 189537376 | ref | XP_001920772.1 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1425
gi | 115648153 | ref | NP_034016.2 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1462
gi | 109481140 | ref | XP_001070474.1 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1462
gi | 7656967 | ref | NP_055061.1 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1447
gi | 73969260 | ref | XP_538324.2 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1547
gi | 194666763 | ref | XP_600703.4 | DDNI CLRPEPCENYMKCVSLKFDSSAPFISSTVTLFRPIHPVNFACKCEPEGTGSKREYLCDETVLDCYSDPQNGGSMRREGGYTCVCEQYTGVCNCTISAGLKPCEISEVCGDGYSCLTSGGGHWPYTKT-----CELMRSRF 1500
gi | 193207741 | ref | NP_506256.3 | RDESANEPESHMAKCRQTKFVGMKAHEIDNFIARTLNTVNFVCECPSEFTSAGHGDIDRIDECYRGRCSNNDSTVAFENTYQCECPGWIQRHCEISVHALTCVPGYCMSDSLCELDGNQMKCRHCKVHGSDTDERCRLRSVSE 1336



gi | 62484382 | ref | NP_724962.2 | GRNSFLTFSFSLKQRHFRNLKRFATVQENGLLLYNGRYNELHDFIALEIHEGHVSFSFSLGDHSEIRIIVI--QEAQVSDGKWHQVEVVYLNRSVILVLDNCDTALASGQLGDRWSCANRITLKLDRKCSLLETCH-----RFLDLE 1702
gi | 31210749 | ref | XP_314341.1 | TRNSFLTFSFSLKQRHFRNLKRFATVQENGLLLYNGRYNELHDFIALEIHEGHVSFSFSLGDHSEIRIIVI--QQRKVSDDGNWHTVEVKNRITVLSLNDCTALALAG-LGERWNCANQITLVLDNRRCASLVEPCH-----RFFDLT 1721
gi | 189518225 | ref | XP_687264.3 | PGOSFITFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVPP--VPGGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAVAVRFGKDIGNYSCAAQGTQIGSKSLDLE 1424
gi | 189537376 | ref | XP_001920772.1 | PGOSFITFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVPP--VAGGVSDDGQWHTIHLHYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAVAVRFGKDIGNYSCAAQGTQIGSKSLDLE 1573
gi | 115648153 | ref | NP_034016.2 | PPOSFVTFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVPP--VPGGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAAVAVHFGSYVGNYSCAAQGTQIGSKSLDLE 1610
gi | 109481140 | ref | XP_001070474.1 | PPOSFVTFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVPP--VPGGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAAVAVHFGSYVGNYSCAAQGTQIGSKSLDLE 1610
gi | 7656967 | ref | NP_055061.1 | PPOSFVTFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVAPK--VPSGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAVAVRFGKDIGNYSCAAQGTQIGSKSLDLE 1595
gi | 73969260 | ref | XP_538324.2 | PPRSFTVFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVPP--VPGGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAVAVRFGKDIGNYSCAAQGTQIGSKSLDLE 1695
gi | 194666763 | ref | XP_600703.4 | PPOSFVTFRGLRQRFHFTVSEMFATRERNALLLYNRFNEKHDFIALEIIVEEQQLQTFSAGETITTVVAPK--VPGGVSDDGRWHSVQVYNNKPNIGHGLPHGSPGSEKMAVVVDDCDTAVAVRFGKDIGNYSCAAQGTQIGSKSLDLE 1648
gi | 193207741 | ref | NP_506256.3 | DGEGLLVNLDLPELQWIMKFRVYSIAHNGVLVFTG--DKRSDFVEYSVDRVLKQVFLGGEKIDAKMENDVENRINDGEWHVVALEYSNKRQIMSLDDCETN--PSLLLVNIPKCAIRAKLNLEKKECDEPTVPCY-----RYLDS 1475



gi | 62484382 | ref | NP_724962.2 | GPLQVGGVLPRI PAHFVPIRSHDFVGCISDLRIDRFDVLDLNSVVDNGT---LAGCPQKAPLQKSE--PCFNNGTCREGWGCT-VSCCEPEGYAGNSCQDNIPAPWRFSGDGSLSNPFLLRP---IQLPWTISFSLRTRK--EAFLLGIQT 1840
gi | 31210749 | ref | XP_314341.1 | GPLQIGGLPKIPAYFQIRSHDFVGCISDLRIDRFDVLDLNSVVDNGT---VAGCPQKAAKSCASE--PCFNNGTCREGWGEGWECDCPDGFTGNACQESVALPWRFRHGDGILSNPFLLRP---IQLPWLTAFLSRLTRKR--DSFVMEIQV 1860
gi | 189518225 | ref | XP_687264.3 | GPLLGGVPLNLPEDFFVHNRDFVGCIMRNLITIDSKSVDMASVIANNGT---TEGCPAKNFICYEG--LCHGAQCEKWNVT-HFCCEPEGRGGKNCQDMPERHDFDGHAMMLWNPDMT---IAPVWYIATLMFRTRQTSTGTAHLMQVNA 1564
gi | 189537376 | ref | XP_001920772.1 | GPLLGGVPLNLPEDFFVQNRDFVGCINKLITIDSKIDMANFISDNGT---AAGCAAKRDFCSQA--VCONGGVVNRWNT-HTCNCPLEFGGKNCHEVMPAPLHFDGHALVSWSDLDIT---IAPVWYIATLMFRTRKS--TGVLQATA 1711
gi | 115648153 | ref | NP_034016.2 | GPLLGGVPLNLPEDFFVHNRDFVGCIMRNLISIDGRIVDMAAFIANNGT---RAGCASORNFCDGT---SCONGGT CVNRWNT-VLCECPLRFGGKNCQAMPHPORFTGESVVLWSDLDIT---ISVPWYIATLMFRTRKE--DGVLMETA 1748
gi | 109481140 | ref | XP_001070474.1 | GPLLGGVPLNLPEDFFVHNRDFVGCIMRNLISIDGRIVDMAAFIANNGT---RAGCASORNFCDGT---LCONGGT CVNRWNT-VLCECPLRFGGKNCQAMPHPORFTGESIVWSDDLIT---ISVPWYIATLMFRTRKE--DGVLMETA 1748
gi | 7656967 | ref | NP_055061.1 | GPLLGGVPLNLPEDFFVHNRDFVGCIMRNLISIDGRIVDMAAFIANNGT---REGCAARRNFCDGR--RCONGGT CVNRWNT-VLCECPLRFGGKNCQAMPHPOLFSGESVVSWSDDLIT---ISVPWYIATLMFRTRKE--DGVLMETA 1733
gi | 73969260 | ref | XP_538324.2 | GPLLGGVPLNLPEDFFVHNRDFVGCIMRNLISIDGRIVDMAAFIANNGT---RAGCAAQRNFCDGT---WCONGGT CVNRWNT-VLCECPLRFGGKNCQAMPHPORFTGESIVWSDDLIT---ISVPWYIATLMFRTRKE--DGVLMETA 1833
gi | 194666763 | ref | XP_600703.4 | GPLLGGVPLNLPEDFFVNRDFVGCIMRNLISIDGRIVDMAAFIANNGT---RAGCAAQRNFCDGT---WCONGGT CVSGWNT-VLCECPLRFGGKNCQAMPHPORFTGESVVSWSDDLIT---ISVPWYIATLMFRTRKE--DGVLMETA 1786
gi | 193207741 | ref | NP_506256.3 | NGLFLGGRP---GTSKQIEKAFSGCISDLSVDPKEDVDPSITKEMHKVGVVHEGCKHRKDFCSTSDGQGSATSKVNRWGG--RIGSCPQSVHSTGECVGALETQDLRGLHSLFEESFVLYPSQVSVPEVSEFRISRADMQVFALEFICQ 1621



gi | 62484382 | ref | NP_724962.2 | GQNSAAVCLRQGVLYIIFDGEF---MYLAGAFSLDGEWHRVEIKWQGG---SEIHFSVDYQORSQSVMPKQVQGLYVGVKIVMGSFDGSGIAPVPEAEP--FEGCIQDVRIGAGQVLSRPIITRENVEDGCEBRAQC--PDH--CF 1974
gi | 31210749 | ref | XP_314341.1 | GQNSAAVCLRQGVLYIIFDGEF---LQLAGADLADGRWHRVEIKWQGG---SEIHSVDYQORSQSVMPKQVQGLYVGVKIVMGSFDGSGIAPVPEAEP--FEGCIQDVRIGAGQVLSRPIITRENVEDGCEBRAQC--PDH--CF 1995
gi | 189518225 | ref | XP_687264.3 | GDTIQINLLLRDKVQFVLLGQKVAVLDFDVRVNDGGEWHLLVLELRSKDGKDKTYMAQVFLDYDMFKKSVIEIGNELPGLKLSFFPIGGLQQRDIVQGGFKGCMOGLRMGETAISTANINMHHAQKIRVEDGCDMSENC--DAINCP 1713
gi | 189537376 | ref | XP_001920772.1 | GEFKINLMVITNRHLRFQVFLGNRRVALLDFDQVYVDNGEWHHVLVELKSGDKGDKIKYMAVLSLDYGMFRTVIEIGNELPGLKLRNLFPIGGLKDDIVQGGFNGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--LANLCP 1860
gi | 115648153 | ref | NP_034016.2 | GTSRRLHLQILNSYIRFEVSYGPDVASMOLSKSRITDGGWHLLIELRSKAKGDKIKYLAVMITLDYGMDSSTVQIGNOLPGLKMRITVIGGVTEDKVSVRHRGFRGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--ASSPCP 1897
gi | 109481140 | ref | XP_001070474.1 | GTSRRLHLQILNSYIRFEVSYGPDVASMOLSKSRITDGGWHLLIELRSKAKGDKIKYLAVMITLDYGMDSSTVQIGNOLPGLKMRITVIGGVTEDKVSVRHRGFRGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--ASSPCP 1897
gi | 7656967 | ref | NP_055061.1 | GTSRRLHLQILNSYIRFEVSYGPDVASMOLSKSRITDGGWHLLIELRSKAKGDKIKYLAVMITLDYGMDSSTVQIGNOLPGLKMRITVIGGVTEDKVSVRHRGFRGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--ASSPCP 1882
gi | 73969260 | ref | XP_538324.2 | GTSRRLHLQILNSYIRFEVSYGPDVASMOLSKSRITDGGWHLLIELRSKAKGDKIKYLAVMITLDYGMDSSTVQIGNOLPGLKMRITVIGGVTEDKVSVRHRGFRGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--ASSPCP 1982
gi | 194666763 | ref | XP_600703.4 | GTSRRLHLQILNSYIRFEVSYGPDVASMOLSKSRITDGGWHLLIELRSKAKGDKIKYLAVMITLDYGMDSSTVQIGNOLPGLKMRITVIGGVTEDKVSVRHRGFRGCMOQVVRMGETSTNLANINIRHAKRIRHAKDGCNVDPAC--ASSPCP 1935
gi | 193207741 | ref | NP_506256.3 | R--SVHYNLVDDGHLKYNIDGSE---VELPAPEVITSKHWNVVIIFEADS---VATSNINGYSABAKASLSDMNLRLVFGIAPGTG--HPSRFEGCIRNVLVDGRSISVK---KKGKTRAGCIVVNRCSVDICP 1745



gi | 62484382 | ref | NP_724962.2 | NRSQSSWDLSTCECDGSGVYVTDCAPICTVTRPCAS--GVCRANTSLPRGDCBCNS--SRHGDYCEKEIQQCPGGWGW--ERVCGPGRCDLAGEYHPDCKNTTGCYCKTNYHQPNETACLSDCDYSTGSGACNPLTGCCECREGVIG 2122
gi | 31210749 | ref | XP_314341.1 | NRSQSSWDLSTCECDGSGVYVTDCAPICTVTRPCAS--GVCRANTSLPRGDCBCNS--SRHGDYCEKEIQQCPGGWGW--ERVCGPGRCDLAGEYHPDCKNTTGCYCKTNYHQPNETACLSDCDYSTGSGACNPLTGCCECREGVIG 2143
gi | 189518225 | ref | XP_687264.3 | ENSQCTD---EHTCTCDPFGFRGDCVDAACHLNPCEHLSICVRKPS--SHGYTCBCSQD--YGYQYCNKVKPKPRGWWG--NPMCGPNCNDVSKGFNPDCNKTIGECRCKDNYQPKSDTFCPCDCFHGANRSCDPEGTGCPCKAGVIG 1858
gi | 189537376 | ref | XP_001920772.1 | SHSHCTDNWTSHTCTCDPFGFRGDCVDAACHLNPCEHLSICVRKPS--SHGYTCBCSQD--YGYQYCNKVKPKPRGWWG--NPMCGPNCNDVSKGFNPDCNKTIGECRCKDNYQPKSDTFCPCDCFHGANRSCDPEGTGCPCKAGVIG 2008
gi | 115648153 | ref | NP_034016.2 | PHSRCDTWDSYSICIDRQYFGKCKVDAACHLNPCKHVAACVRS--SPTPRGSCCECGPG--HYGYQYCNKVDLPCPKGWWG--NPVCGPCHCAVSKGFDPDCNKTNGCCOCKENYKPPADACLPCDFPHGSHSRACDMDTGCCACKPGVIG 2045
gi | 109481140 | ref | XP_001070474.1 | PHSRCDTWDSYSICIDRQYFGKCKVDAACHLNPCKHVAACVRS--SPTPRGSCCECGPG--HYGYQYCNKVDLPCPKGWWG--NPVCGPCHCAVSKGFDPDCNKTNGCCOCKENYKPPADACLPCDFPHGSHSRACDMDTGCCACKPGVIG 2045
gi | 7656967 | ref | NP_055061.1 | PHSRCDTWDSYSICIDRQYFGKCKVDAACHLNPCKHVAACVRS--SPTPRGSCCECGPG--HYGYQYCNKVDLPCPKGWWG--NPVCGPCHCAVSKGFDPDCNKTNGCCOCKENYKPPADACLPCDFPHGSHSRACDMDTGCCACKPGVIG 2030
gi | 73969260 | ref | XP_538324.2 | PHSRCDTWDSYSICIDRQYFGKCKVDAACHLNPCKHVAACVRS--SPTPRGSCCECGPG--HYGYQYCNKVDLPCPKGWWG--NPVCGPCHCAVSKGFDPDCNKTNGCCOCKENYKPPADACLPCDFPHGSHSRACDMDTGCCACKPGVIG 2130
gi | 194666763 | ref | XP_600703.4 | PHSRCDTWDSYSICIDRQYFGKCKVDAACHLNPCKHVAACVRS--SPTPRGSCCECGPG--HYGYQYCNKVDLPCPKGWWG--NPVCGPCHCAVSKGFDPDCNKTNGCCOCKENYKPPADACLPCDFPHGSHSRACDMDTGCCACKPGVIG 2083
gi | 193207741 | ref | NP_506256.3 | AESTCHRANWKKKCKKSKSVQDCTLPVCSVANVCSSITCVSN--TAGVECTCPAGKTKGNKQLEAPKQCPGSGWGWTFPRCRRCSCAQTKDYBAQCDKKTGACCKKSHFSTING--CVRCECG--FGADSTBCS--ADGHCKNDGAVG 1890



gi | 62484382 | ref | NP_724962.2 | RRCDSCS--NPYAEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2269
gi | 31210749 | ref | XP_314341.1 | RRCDSCS--NPYAEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2291
gi | 189518225 | ref | XP_687264.3 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 1973
gi | 189537376 | ref | XP_001920772.1 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2123
gi | 115648153 | ref | NP_034016.2 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2160
gi | 109481140 | ref | XP_001070474.1 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2160
gi | 7656967 | ref | NP_055061.1 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2145
gi | 73969260 | ref | XP_538324.2 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2245
gi | 194666763 | ref | XP_600703.4 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2198
gi | 193207741 | ref | NP_506256.3 | RRCNRC--NPFSEVTLGCEVYVYDACPFRSAGGVVWPRITPLGGVAIEGCPPFARGKQORSQDV--SGSWNTDMYNTSEFVLRRLQLSQLEKLELELNSFVAIKMAEQLRKACEAVDRRGAASKDKISGNRPNRRYKMESS--FLLSN 2001



gi | 62484382 | ref | NP_724962.2 | GGNVWS-HELEMDYLS-DELKFTVHDLRQLGADLLVTEGLLQELINYLMLSGSLNLSHSQDKYFIKLVDAAEVILDRKYEAERWRATELILQGGPDDLVDFAFNKYLVLVLAHQHDVYSPFEIVQPNMALGLDIVTESLFGVYEPQLS--E 2415
 gi | 31210749 | ref | XP_314341.1 | SASLWRBDDFELDYLINDGOSFVQSKLYGADLLIIDLRLHLMRYEAYQHGLNLSHSQDKHYVRNLVESAAGEILDRRYASEWKRVDLTLGRGPDLDVDAFNQYIVLVAHQHDVYNNPFEIVHKNMVLGMDIVTESLFGVYEQMVKQQQ 2441
 gi | 189518225 | ref | XP_687264.3 | -----SFFYGNQVKTIIYHLLSSILRYESQOQGFNLAAMRDAKFNENLVKAGSAILDASNKEHWDQIIRTEG-CTANLLKHFEYANTLAONMRKTYLKPFIIVTENMVFVAVDYLVTYVDA-KVYVNFQITD 2097
 gi | 189537376 | ref | XP_001920772.1 | -----YRLFNDVVRTAYHLLASVLEHESLQGGFELTATHDTDFNRNLIKAGSAILDPLNCEHWKIQRSBG-CTANLLHQFEYANTLVQNVKRTYLRPFIIITDNIIVALDFLDSTASQ-EKIPRFQEVK 2247
 gi | 115648153 | ref | NP_034016.2 | -----SILFGNDVVRTAYQLLARILQHESRQGGFDLAATREANFHEDVVHTGSAALLAPATRAAWEQIQRSEA-GAAQLLRHFAYFSNVARNVVRTYLRPFVIVIANMILAVDIFDKLNFITGAQVPRFEDIQ 2285
 gi | 109481140 | ref | XP_001070474.1 | -----SILFGNDVVRTAYQLLARILQHESRQGGFDLAATREANFHEDVVHTGSAALLAPDEAAWQIQRSEA-GAAQLLRHFAYFSNVARNVVRTYLRPFVIVIANMILAVDIFDKLNFITGAQVPRFQDVQ 2285
 gi | 7656967 | ref | NP_055061.1 | -----GLFGNDVVRTAYQLLGHVLEHESRQGGFDLAATQDADFHEVDVHTGSAALLAPATRAAWEQIQRSEB-GTAQLLRHFAYFSNVARNVVRTYLRPFVIVIANMILAVDIFDKLNFITGARVPRFDTIH 2270
 gi | 73969260 | ref | XP_538324.2 | -----AALFGNDVVRTAYQLLARVLLHESRQGGFELAAATRDADFHEVDVHTGSAALLAPDQAAWQIQRSEB-GAVQLLRGFAYFSNVARNVVRTYLRPFVIVIANMILAVDIFDKLNFITGARVPRFEDIR 2370
 gi | 194666763 | ref | XP_600703.4 | -----AALFGNDVVRTAYQLLGRVLLHESRQGGFELAAATRDADFHEVDVHTGSAALLAPATRAAWEQIQRSEP-GTAQLLRHFAYFSNVARNVVRTYLRPFVIVIANMILAVDIFDKLNFITGARVPRLEHLR 2323
 gi | 193207741 | ref | NP_506256.3 | -----GRNQTIAAALSRLLVDYVQSGPMFKGRAHIKDKMFKTEKLIESTLGRVMSEQPADEVSTL-----ISKLWNVAETVAEIHENVNFLSPFFVANDHIVFASDKLDFGNILPKFNFLVDLRF 2113



gi | 62484382 | ref | NP_724962.2 | YHRSK-VLKPNAFTTESVVLVPTDSTGFLQHSARQR-FVTSFPKYNNYILDNRKFDQHTKVLVPLEMLGITPPESDEISOSGRRGSSDHRRAIVAYAQYKDVGQLLPLDLYDETITRRWGVDELATPILSLQILVPSMEREQETORLEIPSR 2563
 gi | 31210749 | ref | XP_314341.1 | FKQAKGHPDLRGHPAETVILPDTSSFLQNSPKQKQPLISFPKYNNYIQDRSKFDRSTKVLVPLDMLGITAPDKNEVNVN-----QIAEHRAIFTYAQYKIDAGELPPTNFDETITRRWGVEMQIASSVLSIAIVTPELKDDEYTC 2579
 gi | 189518225 | ref | XP_687264.3 | -----QECPKDLKSSVLFPEFSFKS---SEHKDDPEFQIN-----SDEBEKQATNKRKRHV-----ETIIPFPVASVVIYKTLGQFLPEHYVDPDRSLR----- 2178
 gi | 189537376 | ref | XP_001920772.1 | -----EVFSKEMECVSLFENLLMSKSKDALSTDPSPQINSIVSVMMDGSDVDVLDLIPSIKRRSHA-----EQDPPAAVMVMYIRSLGHLLPESYVDPDRSLR----- 2341
 gi | 115648153 | ref | NP_034016.2 | -----BELPRELESSVSFPADTFKPPKKEGVPVRLINRRTTP-LIAQPEPRAERETSSSRRRRHP-----DEPGQFAVALVVIYRITLQGLLPEHYVDPDRSLR----- 2378
 gi | 109481140 | ref | XP_001070474.1 | -----EEFPRELESSVSFPADTFKPPKKEGPMVRLINRRTAP-LIAQPEPRERETFSRQRHRP-----DEPGQFAVALVVIYRITLQGLLPEHYVDPDRSLR----- 2378
 gi | 7656967 | ref | NP_055061.1 | -----EEFPRELESSVSFPADTFKPPKKEGFLIRPAGRRTP-QTRPFGGTEREAPISRRRRHP-----DDAGQFAVALVVIYRITLQGLLPEHYVDPDRSLR----- 2363
 gi | 73969260 | ref | XP_538324.2 | -----DEFPKELLESSVFSADFPKPPESKESPTVRPAARNAAP-QIAPPGPGAHREAPFRQRHRP-----DEPGQFAVALVVIYRITLQGLLPERVDPDRSLR----- 2463
 gi | 194666763 | ref | XP_600703.4 | -----GEVPRDLESSVFSADFPKPAERKEGPTARPAGRKTP-QMARPPQRTMEMAPSRQRHRP-----DEPGQFAIALVLIYRITLQGLLPEHYVDPDRSLR----- 2416
 gi | 193207741 | ref | NP_506256.3 | -----TGFPVRRAIVTGTITQVVVYSIVYPRCN---------- 2140



gi | 62484382 | ref | NP_724962.2 | KIFSSSSPSSSSSSGSTEQCFVEVDFVVKAPTSSSEQQIEDIRITAEHEIPPPVSSVEQDEASSDEGEEREPIHRLNLDIEFHGNSGEEVISPDSPMLNPNYEGVSSSTGSDPEPKGENEAVYRDRRLVKRQVEIITYPSEQMQTEQVYV 2713
 gi | 31210749 | ref | XP_314341.1 | -----PFPSSGGLEKSGGNQVETIAPPKAKVPERTESEKLSLNEIKISIHDMSDREEGLDLIDCHAP-----GVPMVNTAENSEDFHDDDLPEVTVLARSEQMS-----SIEKTAETAIRKRRTSIVSADGGIPESEVEMDSASRIN 2712
 gi | 189518225 | ref | XP_687264.3 | ----------VFNRPVINTPIVSA 2192
 gi | 189537376 | ref | XP_001920772.1 | -----LFPNRPVINTPIVSV 2355
 gi | 115648153 | ref | NP_034016.2 | -----LFPNRPVINTPVSA 2392
 gi | 109481140 | ref | XP_001070474.1 | -----LFPNRPVINTPVVA 2392
 gi | 7656967 | ref | NP_055061.1 | -----LPHRPIINTPMVST 2377
 gi | 73969260 | ref | XP_538324.2 | -----LFPNRPVINTPVSA 2477
 gi | 194666763 | ref | XP_600703.4 | -----LFPNRPVINTPVST 2430
 gi | 193207741 | ref | NP_506256.3 | -----LFPNRPVINTPVST 2140



gi | 62484382 | ref | NP_724962.2 | YRELGSPHLAQPIKLMWLVDVSAFPGPRSNPQCVRWNSFTHNQWTRLGCOEIPDFDGFNFPAQAAILVNCSTHISYAVIVDVIDPEDIPESLLVQITSYSAFLVSLPLLGLVLLALALLRGOQINSNTIHQNIIVLCVFCABELLFF 2863
 gi | 31210749 | ref | XP_314341.1 | -----VYVPLGQPHLKQAIKLMWLNIIPNRNFVSRNSPQCVRWNSHANLWTRIGCOEIPNYE-----MIGHNDTIIVNCTNQNLATYAVLVDIIDPEDIPESLLVQITSYSAFLVSLPLLGLVLLALALLRGLQINSNSIHQNLIFCFAELLFF 2859
 gi | 189518225 | ref | XP_687264.3 | -----VYVSEGQPLHPILEPITLIDYNLLETTEERTKPVCFVWNHSTIVYGGAGAWSKG-----CDIISRNHTHISCCNHMTSFVAVLMDISKRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2334
 gi | 189537376 | ref | XP_001920772.1 | -----VVHKDGEPLLSPQRPIILLNFRLLTEERTKPVCFVWNHSLMVAGGAWWSKG-----CELVFRNSTHISCCSHMSFAVLMDSKRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2497
 gi | 115648153 | ref | NP_034016.2 | -----MVISSEGTPLPSLQRPILVVEFSLLETEERSKPVCFVWNHSLDGGTGGWSAGK-----CELLSRNRTHVTCOCSHSASCVAVLMDISRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2534
 gi | 109481140 | ref | XP_001070474.1 | -----MVISSEGTPLPSLQRPILVVEFSLLETEERSKPVCFVWNHSLDGGTGGWSAGK-----CELLSRNRTHVTCOCSHSASCVAVLMDISRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2534
 gi | 7656967 | ref | NP_055061.1 | -----LVYSEGAPLPSPLERPVLVEHVLLETTEERTKPVCFVWNHSLAVGGTGGWSARG-----CELLSRNRTHVACQCSHTASFAVLMDSRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2519
 gi | 73969260 | ref | XP_538324.2 | -----VVYSEGAPLPSPLERPVLVEHVLLETTEERTKPVCFVWNHSLITIGGAGGWSAGK-----CELLSRNRTHVACRCSHTASFAVLMDSRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2619
 gi | 194666763 | ref | XP_600703.4 | -----VVYSEGAPLPSPLERPVLVEHVLLETTEERTKPVCFVWNHSLITIGRTGGWSAGK-----CELLSRNRTHVACRCSHTASFAVLMDSRRE--HGEVPLPKIVTYTYSASLVALLIFILLAILHKLRSNLHSIHKNLVAALFFSELVFL 2572
 gi | 193207741 | ref | NP_506256.3 | -----RCENPMIAIVANSDPVVIVEFEIEEDDKWYPECVFKDEKSGTWTARGAALIG-----LNLTHAAACENRIGVTFMVDQSSS--IVRVAQMDNMTSPAAGVALFCFLSILLTLRRSLKTHSVRIQGFILFFAINLNLFFV 2278



gi	62484382	ref	NP_724962.2	VGMQRRRLLESEFPCKLVAICLHYFWLAAFAWTVDVCVHLRYRMLTEMRDINHGPMPGFYFAMGYGAPAIIVGLSVGVRAHEYGNLFCWLSVYEPVWVWVLPVIGAGMNVNLLILFVSVKAAFTLKDHVLFVGFNLRLLWLWVSVSLPLMG	3013
gi	31210749	ref	XP_314341.1	VAIQARRDLLDNEFPCKLVAIALHYFWLAAFAWTVDVCVHLRYRMLTEMRDINHGPMPGFYHIGYGAPALLVGLSVGVRVHEYGNMFCWLSVYEVVWVWVLPVIGAIIVSVFDFILFLSVKAAFTIKDHVLFVGFNLRLLWLWVSVSLPLMG	3009
gi	189518225	ref	XP_687264.3	IGIN---QTDNPFVCTVIAAILLHYFYMCFAFWTFVVEGLHIYRMLTEVRNINHGMRFYAIGWGIPIAITGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2480
gi	189537376	ref	XP_001920772.1	IGIN---QTDSPFVCTVVAAILLHYSYMCAFAMFVVEGLHIYRMLTEMRNINQGHMRFYAIAGWGIPIAITGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2642
gi	115648153	ref	NP_034016.2	VGIN---QTEENPFVCTVVAAILLHYVSMGTFAWTLVENLHYRMLTEVRNIDTGPMPRFYVVGWGIPIAIVTGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2680
gi	109481140	ref	XP_001070474.1	VGIN---QTEENPFVCTVVAAILLHYVSMGTFAWTLVENLHYRMLTEVRNIDTGPMPRFYVVGWGIPIAIVTGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2680
gi	7656967	ref	NP_055061.1	IGIN---QTEENPFVCTVVAAILLHYVSMGTFAWTLVENLHYRMLTEVRNIDTGPMPRFYVVGWGIPIAIVTGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2665
gi	73969260	ref	XP_538324.2	IGIT---QTEENPFVCTVVAAILLHYVSMGTFAWTLVENLHYRMLTEVRNIDAGMPRFYVVGWGIPIAIVTGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2765
gi	194666763	ref	XP_600703.4	IGIT---QTEENPFVCTVVAAILLHYVSMGTFAWTLVENLHYRMLTEVRNIDAGMPRFYVVGWGIPIAIVTGLAVGLDPPQGYGNPDFCWLSDLIWISFAGPTAVVVLNIVIFVMAAKASCGRQRSEYKSGVTPALRMAFLLLLLIS	2718
gi	193207741	ref	NP_506256.3	IKTIA---INQAYCVRNAMLSEFSSAPFAWLFYGLYIYRMLADGSSSPS--LTTSLLVGIVFPCLI-----FTTFVTVQCSLSPHLWLFWCIILPGLLELLSFVAAATSVLVSLHKKYDVFAKYNVKKRAVQHFILHIFP	2413



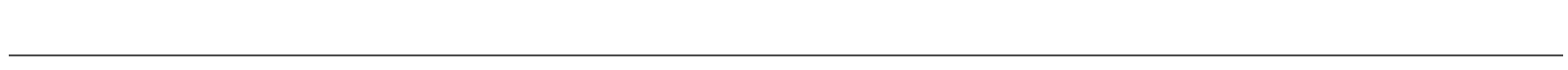
gi	62484382	ref	NP_724962.2	VMVLAVALAASEHSQLLSLLSGLVLLHALFCLIGYCIINRVRRENLRCLRCMGRKVPVLLDSSMVMVSNHNVNAAARPSNFLASG-YDTRTRRNIGISASSTSRSTAKTSSSPY	3130
gi	31210749	ref	XP_314341.1	IMVLAVALAASENSQLLNMLLSAVVIMHSLFIIGYCIINRVRRENLRHNAFLRCMGRKVPVLLDSSIAISNSQNVGSPKTPGFAGSSGGQYDTRARNIGISTSTTSRSSTAKTSSSPYR	3128
gi	189518225	ref	XP_687264.3	ATWLLGLMAVNSDVMTEFHYLFAIFSCLQGVFIFFHFIVFNKEVRKNLKNVFT-----GKRQLPDEESTTRTLLRLRLNLCNTYMEDGALFRSAIGESTVLSLETSVRSKSHS	2589
gi	189537376	ref	XP_001920772.1	ATWLLGLMAVNSDVLSEFHYLFAIFSLCLOGVFIFFHFICILNKDVRNKLKSVFT-----GKNIPAEDEPSVTRAILLRSNLNG-DVMEDGGLYRTTIGESSVLSQSSVRSKSHS	2781
gi	115648153	ref	NP_034016.2	ATWLLGLLAVNSDILSFHYLFAAFSLCLOGIFVLLFHCVAHREVRKHLRAVLA-----GKKLQDDSATTRAILLRSNLNNTYSEGPDMLRTALGESTASLDSTTRDEG	2785
gi	109481140	ref	XP_001070474.1	ATWLLGLLAVNSDILSFHYLFAAFSLCLOGIFVLLFHCVAHREVRKHLRAVLA-----GKKLHLEDSATTRAILLRSNLNNTYSEGPDMLRTALGESTASLDSTTRDEG	2785
gi	7656967	ref	NP_055061.1	ATWLLGLLAVNRDALSFHYLFAIFSCLQGFVLLFHCVLNQEVRKHLKGVLG-----GRKHLLEDSATTRAILLRSNLNNTYFEGDPMRLRDLGESTASLDSTIVRDEG	2770
gi	73969260	ref	XP_538324.2	ATWLLGLLAVNSDALAFHYLFAVCSCLQGLFVLLFHCVLNREVRKHLKGVLA-----GKKLHPDDSATTRAILLRSNLNHSYSEPNMFRALGESTASLDSTIVRDEG	2870
gi	194666763	ref	XP_600703.4	ATWLLGLLAVNGDALAFHYLFAVCSCLQGLAVLLHCFVFNREVRKHLRGLVLA-----GKKPYADDSATTRAILLRSNLNNTYGEEDVFRALGESTASLDSTIVRDEG	2823
gi	193207741	ref	NP_506256.3	LGMVLTGLFANQLPLPMEIMEIQSIYIYIAALVFLWCVDITTKAS-----DSNPEMVLDN	2471



gi	62484382	ref	NP_724962.2	-----SDGOLRQTSSTSNYNSASDAPSFRLRGFESSTI-----GRSRGGE	3170
gi	31210749	ref	XP_314341.1	-----SDGOFRETSSTSNYNSDGVASYMRGHVRESALRKIKNGGQRDGE	3174
gi	189518225	ref	XP_687264.3	-----VFYTHRDELQKPSVSGNAKAGLTDIDGS	2619
gi	189537376	ref	XP_001920772.1	REDGGTANLLHCFEEYANLVQNVKRYLRFLLIDNHLIVALDFLDSTASQEKIPRFQEVKEVFSKEMECSVLEFPNLLMSKKSADLSTDPSSQINSTVSMMDGSDVVDLIPILKKRSHAEQDPPAAVMVMIVRSLGHLLPESEYD	2931
gi	115648153	ref	NP_034016.2	-----VQKLSVSSGPARGNHGEPPDASFIPRN	2811
gi	109481140	ref	XP_001070474.1	-----VQKLSVSSGPARGNHGEPPDASFIPRN	2811
gi	7656967	ref	NP_055061.1	-----IQKLGVSSSGLVRSVSHGEPPDASLMPRS	2796
gi	73969260	ref	XP_538324.2	-----AQKLSVSSGPARGGHGEPPDSSFVPRN	2896
gi	194666763	ref	XP_600703.4	-----GQKLSVSSGPARGGHGEPPDASFVPRS	2849
gi	193207741	ref	NP_506256.3	-----QKSVMAESTMADPQCASPILLS	2492



gi	62484382	ref	NP_724962.2	-----	3170
gi	31210749	ref	XP_314341.1	-----	3174
gi	189518225	ref	XP_687264.3	-----	2619
gi	189537376	ref	XP_001920772.1	DRRSRLRLPNRPVINTPIVSVVVKDGEPLLSPLQRPILLFRLLLETQERIKPVCVYWNHSIMVAGGCAWSSKGCCLVFRNSTHISCCCHMSFAILLMDIKREHGDVLPKVVVTVYSASLVALLIFLLLAILRKLRSNLSIHKIL	3081
gi	115648153	ref	NP_034016.2	-----	2811
gi	109481140	ref	XP_001070474.1	-----	2811
gi	7656967	ref	NP_055061.1	-----	2796
gi	73969260	ref	XP_538324.2	-----	2896
gi	194666763	ref	XP_600703.4	-----	2849
gi	193207741	ref	NP_506256.3	-----	2492



gi|62484382|ref|NP_724962.2| 3170
gi|31210749|ref|XP_314341.1| 3174
gi|189518225|ref|XP_687264.3| 2619
gi|189537376|ref|XP_001920772.1| VASIFLSEFIFLQGINQDTSPPFVCTVVAILLHYSYMCFAWMFVGLHIVRMLTEMRNINQGHMRFYVAIGWGPALITGLAVGLDPOGYGNPDFCWLSSVYDTLIWSTTGPISIVVLIINIVLIVLAAKASCGRRRQTEKSGAISALRVAF 3231
gi|115648153|ref|NP_034016.2| 2811
gi|109481140|ref|XP_001070474.1| 2811
gi|7656967|ref|NP_055061.1| 2796
gi|73969260|ref|XP_538324.2| 2896
gi|194666763|ref|XP_600703.4| 2849
gi|193207741|ref|NP_506256.3| 2492
.....3610.....3620.....3630.....3640.....3650.....3660.....3670.....3680.....3690.....3700.....3710.....3720.....3730.....3740.....3750

gi|62484382|ref|NP_724962.2| 3173
gi|31210749|ref|XP_314341.1| RRS 3177
gi|189518225|ref|XP_687264.3| LFRNG 2624
gi|189537376|ref|XP_001920772.1| LLLLLISATWLLGLMVAIVSIVLDFHFLFAISLCLGICIFFFHCILNKDVRRLKSVFTGKNIPAEPPSVIRANLLRSLNGDVVYMDGGLYRTTIGESSVLSQSSVRSCKSHSGSYLASTFREKKRISISNGGHVGHDEVDSTLFFHKS 3384
gi|115648153|ref|NP_034016.2| 2814
gi|109481140|ref|XP_001070474.1| 2814
gi|7656967|ref|NP_055061.1| 2799
gi|73969260|ref|XP_538324.2| TKR 2899
gi|194666763|ref|XP_600703.4| AKK 2852
gi|193207741|ref|NP_506256.3| PR 2494
.....3760.....3770.....3780.....3790.....3800.....3810.....3820.....3830.....3840.....3850.....3860.....3870.....3880.....3890.....3900

gi|62484382|ref|NP_724962.2| 3323
gi|31210749|ref|XP_314341.1| SRRQRKSDSGSEIDGRSELELASSHSSDDDESRRTARSSGTHRSTAVSSTPAYLNPITEHVQATPPPELVVQSSPOLFPVSNKPVYAPRWSSQLPDAYLOSPPNIGRWSQDTGSDNEHVHGQAKMTISPNPLPNPDLTDSYLLQOHKIN 3315
gi|189518225|ref|XP_687264.3| HRRHRRSDSGSEIDGRSELELASSHSSDDDESRVGRNSSTHRSTGVCSTSYLPNITEHVATPPPELVVQSSPOLFPVNTPTTRWPNQANNYMPPGNGRWSQETASDNEAHPHKSPTINGGSLPNPDIETSYLHQNR--MN 2731
gi|189537376|ref|XP_001920772.1| KKADSDSDSELSVDEHSSSYASSHSSDSEDEDIDMQPKWNNRQPLHSTPKGTKEVDIVSNHVK-----PYWPEAMTASDSEDPGGAELRVEKVVNVELHQENKLNHIG 3484
gi|115648153|ref|NP_034016.2| KKKEDSDSELSADEHSSSYASSHSSDSEDERHSHKTKWNNERTPIHSTPK-----VDGVSGHGK-----PYWPEEMPTASEDEMVRPEKLRVETKVNVELHQENKLNHIG 2917
gi|109481140|ref|XP_001070474.1| AHGPDSDSELSLDEHSSSYASSHTSDSEDDGGEAEDKWNPAAGPAHSTPK-----ADALANHVP-----AGWPDESLAGSDSEELDTEPHLKVETKVSVELHQAAGNHCG 2917
gi|7656967|ref|NP_055061.1| AHGPDSDSELSLDEHSSSYASSHTSDSEDDGGEAEDKWNPAAGPAHSTPK-----ADALANHVP-----AGWPEESLAGSDSEELDTEPHLKVETKVSVELHQAAGNHCG 2902
gi|73969260|ref|XP_538324.2| PPCHSDSDSELSLDEQSSSYASSHSSDSEDDGVGAEEKWDPARGAVHSTPK-----GDAVANHVP-----AGWPDESLAGSDSEDPGKPKLVETKVSVELHREOGSHRG 3002
gi|194666763|ref|XP_600703.4| HHGHDSDSELSLDEQSSSYASSHSSDSEDDGVGAEEKWDSARGPVHSTPK-----VDATANHVP-----AGWPDESLAGSDSEEPGDPQLKVEKVSVELHLDEQGNHCG 2955
gi|193207741|ref|NP_506256.3| PHGHDSDSELSLDEQSSSYASSRSDSEDDGGEAEDKWDPAQGPVHSTPK-----VDAVGNHVS-----AGWPDESLAGSDSEEPGELPRLKVEKVSVELHLDEQGNHCS 2586
HQHHEVPMDSSEWVDPVNPNSNHVHTSINEPDTPRRLLLPQNRDVINILSSPDC-----ILNEGVGHVYRNNMGSPLRRLRAQDEADDAVYTYTASRKY
.....3910.....3920.....3930.....3940.....3950.....3960.....3970.....3980.....3990.....4000.....4010.....4020.....4030.....4040.....4050



gi|62484382|ref|NP_724962.2| 3471
gi|31210749|ref|XP_314341.1| MPPSILENIRDAREGYEDSLYGRRGYFPDKYGSYKPPSHYGSEKDYPGGGSG-SQIIGHMRSFHPDAAY-LSDNIVDKRITLGSYLGAKSESFLYSKDRITPDIYGRSDGHYSLKROPAYADSLHSHVHLLKNDYHQOQQQQQHHLQ 3456
gi|189518225|ref|XP_687264.3| MPPSILENIQEN--VNIGYSNIDLSHSDRNYSNYGNADNYVPPADYAKRHTGSMQVINHMRAYHENFYALKESLYERSRILGYGTAGGAESPYHAGHPLT---APNDLYSPPG-AIHGMSFKSVQLLKNDYQQQRQQYKHHQ 2851
gi|189537376|ref|XP_001920772.1| -----EST--DKEQPTPAIQANSNHQPQRKGIILKNKITYPPLT--DKNMKNLLREKLSYDNPPTISSRAPSIITNDGGNG--HNVLIKPPRPVPPPREHLNGMAMNLSAIVNGNQSDSDGNETSI-- 3597
gi|115648153|ref|NP_034016.2| -----DLS--QSEGFPS--QENSNQLP--RRGILKNKITYPPLT--DKNMKNLLREKLSYDNPPTISSRAPSIITNDGGNG--HNVLIKPPRPVPPPREHLNGMAMNLSAIVNGNQSDSDGNETSI-- 3034
gi|109481140|ref|XP_001070474.1| DRPSDPESEGLAKPVAVLSSQPQQRKGIILKNKITYPPLT--EQLKSLREKLAECQSPSSRTSILGSGDGVHA--TDCVITIKTPRREPGRHLNGVAM--NVRTGS--AQANGSDSEKPHGT 3037
gi|7656967|ref|NP_055061.1| EYPPDQESGGAAR--LASSOPPEQRKGIILKNKITYPPLTLEQTLKRLREKLAECQSPSSRTSILGSG--G--PDCAITVKSPPGREPGRHLNGVAM--NVRTGS--AQANGSDSEKPHGT 3014
gi|73969260|ref|XP_538324.2| ERPPDQESGPPRPSGVLPSQPPEQRKGAVG--VAASTCWRDQGPAG--PEERGRWGLQVTPPRSGPPRG--RLAPFPVRVVPQGG--LAHHA--APTSCFOGAPP 3102
gi|194666763|ref|XP_600703.4| ERLPARDSG-GPRPAAVPPSQPPEQRKGIILKNKITYPPLT--EKTLSRLREKLAECQSPASSRSSEVGSGLRA--PDSAITVKTTPCREPGRHLNGVAMMNVRAQS--AQAHGSGSE 3071
gi|193207741|ref|NP_506256.3| -----KNTISTFNRE-----
.....4060.....4070.....4080.....4090.....4100.....4110.....4120.....4130.....4140.....4150.....4160.....4170.....4180.....4190.....4200



