

gi	189528839	ref	XP_001923676.1	-----
gi	189528837	ref	XP_001921577.1	-----
gi	189528842	ref	XP_001345438.2	-----
gi	189528833	ref	XP_001345556.2	-----
gi	189528835	ref	XP_001345541.2	-----
gi	189528831	ref	XP_001345569.2	-----
gi	189528829	ref	XP_001921519.1	-----
gi	189528827	ref	XP_697477.3	-----
gi	153945757	ref	NP_001093623.1	-----
gi	167963454	ref	NP_001108172.1	-----
gi	167621474	ref	NP_001108028.1	-----
gi	167963486	ref	NP_001108188.1	-----
gi	125816799	ref	XP_001332356.1	-----
gi	165972457	ref	NP_001107101.1	-----
gi	189519439	ref	XP_001922903.1	-----
gi	66932947	ref	NP_000005.2	-----
gi	114643413	ref	XP_001139819.1	-----
gi	73997689	ref	XP_534893.2	-----
gi	157954061	ref	NP_001103265.1	-----
gi	28274695	ref	NP_783327.1	-----
gi	6978425	ref	NP_036620.1	-----
gi	118083282	ref	XP_416476.2	-----

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

MIKKFKALKKPPDDKGRYWA GGS LAMKHLGWCWRK EPTG SCHVLLAMEHRRSLAVQKPH LLLKMGARQIMQTAGIPHORSRAGTAE TTPARGLPKILSSSEVAFLTVQIKGPTQYF SKRSTVTLVKNTONLIFVQTDKPIYELGQKGPKEI

gi	189528839	ref	XP_001923676.1	-----
gi	189528837	ref	XP_001921577.1	-----
gi	189528842	ref	XP_001345438.2	-----
gi	189528833	ref	XP_001345556.2	-----
gi	189528835	ref	XP_001345541.2	-----
gi	189528831	ref	XP_001345569.2	-----
gi	189528829	ref	XP_001921519.1	-----
gi	189528827	ref	XP_697477.3	-----
gi	153945757	ref	NP_001093623.1	-----
gi	167963454	ref	NP_001108172.1	-----
gi	167621474	ref	NP_001108028.1	-----
gi	167963486	ref	NP_001108188.1	-----
gi	125816799	ref	XP_001332356.1	-----
gi	165972457	ref	NP_001107101.1	-----
gi	189519439	ref	XP_001922903.1	-----
gi	66932947	ref	NP_000005.2	-----
gi	114643413	ref	XP_001139819.1	-----
gi	73997689	ref	XP_534893.2	-----
gi	157954061	ref	NP_001103265.1	-----
gi	28274695	ref	NP_783327.1	-----
gi	6978425	ref	NP_036620.1	-----
gi	118083282	ref	XP_416476.2	-----

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

ELDNCRVSGWRVASNSWSLPSHVSPFRAFTRTYTGKPVPGLETVSMCRKLFHSAYCQKQEFCEKFSQQLNSNGCIIQOVKSNLLQIKNMGYEMOLIVEAKTREERTEFVFTGYETCSINIVTRLRFVKVDENFRRGIPFFGQVLLIDGK

gi | 189528839 | ref | XP_001923676.1 | 450
gi | 189528837 | ref | XP_001921577.1 |
gi | 189528842 | ref | XP_001345438.2 |
gi | 189528833 | ref | XP_001345556.2 |
gi | 189528835 | ref | XP_001345541.2 |
gi | 189528831 | ref | XP_001345569.2 |
gi | 189528829 | ref | XP_001921519.1 |
gi | 189528827 | ref | XP_697477.3 |
gi | 153945757 | ref | NP_001093623.1 |
gi | 167963454 | ref | NP_001108172.1 |
gi | 167621474 | ref | NP_001108028.1 |
gi | 167963486 | ref | NP_001108188.1 |
gi | 125816799 | ref | XP_001332356.1 |
gi | 165972457 | ref | NP_001107101.1 |
gi | 189519439 | ref | XP_001922903.1 |
gi | 66932947 | ref | NP_000005.2 |
gi | 114643413 | ref | XP_001139819.1 |
gi | 73997689 | ref | XP_534893.2 | DVVPIPNKRIFISTSRANLYLNTTNEOGLVQFVSVNNTNIMANKTIVMVLRVNGHVMPLLYTCQVLHQOLEGICLKALQGNVNFVSAEAVQFLALCGNEVARVPEIGRKMVIKILLVEVSRSRPLHYFSETLRIVLTKSMPEGIEQEKI 450
gi | 157954061 | ref | NP_001103265.1 |
gi | 28274695 | ref | NP_783327.1 |
gi | 6978425 | ref | NP_036620.1 |
gi | 118083282 | ref | XP_416476.2 |
..... 310..... 320..... 330..... 340..... 350..... 360..... 370..... 380..... 390..... 400..... 410..... 420..... 430..... 440..... 450

gi | 189528839 | ref | XP_001923676.1 | 26
gi | 189528837 | ref | XP_001921577.1 | MALNVSC --- CWKGLLLIFLLVCVNGK
gi | 189528842 | ref | XP_001345438.2 | M 1
gi | 189528833 | ref | XP_001345556.2 | MAWTLVIMALNVSC --- CWKGLLNFFLFVCVNGQA 33
gi | 189528835 | ref | XP_001345541.2 | MALNVSC --- CWKGLLNFFLFVCVNGQA 26
gi | 189528831 | ref | XP_001345569.2 | MALIVSC --- CLRGFLLIFILFLCVNGK 26
gi | 189528829 | ref | XP_001921519.1 | MTGNKFC --- VWKGLILAILLE --- VNGQM 25
gi | 189528827 | ref | XP_697477.3 |
gi | 153945757 | ref | NP_001093623.1 |
gi | 167963454 | ref | NP_001108172.1 | MENI --- VWRLILLVLFPCFADGRSS --- ELFYVD 29
gi | 167621474 | ref | NP_001108028.1 | MAIMEIS --- VWKWINLVLFVCFVDGAM --- FALF 29
gi | 167963486 | ref | NP_001108188.1 | MAMMEIS --- VWKWINLVLFVCFVDGAM --- LALF 29
gi | 125816799 | ref | XP_001332356.1 | MAMMEIS --- VWKWINLVLFVCFVDGAM --- LALD 29
gi | 165972457 | ref | NP_001107101.1 | MAMMEIS --- VWKWINLVLFVCFVDGAK --- LIVE 29
gi | 189519439 | ref | XP_001922903.1 | MAVMGIS --- VWKWL --- IPALFVCFVDGIRRFEPITID 32
gi | 66932947 | ref | NP_000005.2 | MGKNKL --- LHPSLVLLLVLLEPDAVS 26
gi | 114643413 | ref | XP_001139819.1 | MGKNKL --- LHPSLVLLLVLLEPDAVS 26
gi | 73997689 | ref | XP_534893.2 | FNSMFCISGYQROLNPKHRDSSYSTFGEQYGRNODIMKYNIFPEEYVPFALKMOTVPHLCDGPKVHTSFCILNVRSCIKPSCPGELGSENQLGAGYNTVWSPGGPSSC MRKNKL --- LHPNFILLVFLPDAVS 587
gi | 157954061 | ref | NP_001103265.1 | MGKNKL --- LYPSTL LLLLLLPTDAVS 26
gi | 28274695 | ref | NP_783327.1 | MGKRWLSLALLPLPPLLLLLLLLPTNASAP 33
gi | 6978425 | ref | NP_036620.1 | MGKHLRS LALLPL --- LLRLLLLLPTDASAP 30
gi | 118083282 | ref | XP_416476.2 | MGKDG S --- SKLNIFILFFLLSDASPT 25
..... 460..... 470..... 480..... 490..... 500..... 510..... 520..... 530..... 540..... 550..... 560..... 570..... 580..... 590..... 600

gi	189528839	ref	XP_001923676.1	-----ARPSFMVFPVIVIESSGSEAKLCSALLNPNESLVMNIIYLNDG-NQSTLLLOEKAEQEFHRCFNFKAPL-AKAETVQKIKVLELOGKSFEMTERKVMFKSYDPLTFIOTDKPIYIP	138
gi	189528837	ref	XP_001921577.1	-----ARPSFMVFPVIVIESSGSEAKLCSALLNPNESLVMNIIYLNDG-NQSTLLLOEKAEQEFHRCFNFKAPL-AKAETVQKIKVLELOGKSFEMTERKVMFKSYDPLTFIOTDKPIYIP	
gi	189528842	ref	XP_001345438.2	-----AEPSPFMVIFPAVIESSGSEAKLCSALLNPNESLVMNIIYLVDHG-NQSTLLLOEKAEQEFHRCFNFKAPL-AVAESVQIMKVELOGESFKRTEERKVMFKSYHPLTFIOTDKPIYIP	113
gi	189528833	ref	XP_001345556.2	-----AEPSPFMVIFPAVIESSGSEAKLCSALLNPNESLVMNIIYLVDHG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIKVLELOGESFKMTEERKVMFKSYDPLTFIOTDKPIYIP	145
gi	189528835	ref	XP_001345541.2	-----AEPSPFMVIFPAVIESSGSEAKLCSALLNPNESLVMNIIYLVDHG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIKVLELOGESFKMTEERKVMFKSYDPLTFIOTDKPIYIP	138
gi	189528831	ref	XP_001345569.2	-----TRPIFMVIFPAVIESSGSEAKLCSALLNPNESLVMNIIYLVDHG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIKVLELOGESFKMTEERKVMFKSYHPLTFIOTDKPIYIP	138
gi	189528829	ref	XP_001921519.1	-----STPSPFMVIFPAVIESSGSEAKLCSALLNPNESLVMNIIYLNDG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIMKVELOGKSNFKMTEERKVMFKSYHPLTFIOTDKPIYIP	137
gi	189528827	ref	XP_697477.3	-----MVFPPAIRSGSEAKLCSALLNPNESLVMNIIYLNDG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIMKVELOGKSNFKMTEERKVMFKSYHPLTFIOTDKPIYIP	105
gi	153945757	ref	NP_001093623.1	-----MVFPPAIRSGSEAKLCSALLNPNESLVMNIIYLNDG-NQSTLLLOEKAEQEFHRCFNFKAPL-AEAEESVQIMKVELOGKSNFKMTEERKVMFKSYHPLTFIOTDKPIYIP	
gi	167963454	ref	NP_001108172.1	NPS-----HIGFVVDGRCPPGFPMVIFPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	155
gi	167621474	ref	NP_001108028.1	VPR-----PREPVVTADEQISGPLFMVIFPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	157
gi	167963486	ref	NP_001108188.1	APR-----PREPVVTADEQISGPLFMVIFPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	157
gi	125816799	ref	XP_001332356.1	APR-----PREPVVTADEQISGPLFMVIFPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	157
gi	165972457	ref	NP_001107101.1	APK-----PIEPLVNADEQISGPLFMVIFPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	157
gi	189519439	ref	XP_0019222903.1	DPSDPGPVIDRPFVILIEKSIIFRPIIPRPVLIIDPEVIVNGPIFMVMPPLIESSGDAKLCASLLNPNKDRFIMTISLDEKNIETRLVROASQRKLRHRCFKFQAPQ-VNGDSVQTVRVVVOGQSFKMTESKVMFRSYLPLTFIOTDKPLYNP	181
gi	66932947	ref	NP_000005.2	-----GKPOVMVLVPSLLHAEITEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	140
gi	114643413	ref	XP_001139819.1	-----GKPOVMVLVPSLLHAEITEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	140
gi	73997689	ref	XP_534893.2	-----GKPOVMVLVPSLLHAEITEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	701
gi	157954061	ref	NP_001103265.1	-----GKPOVMVLVPSLLHAEITEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	140
gi	28274695	ref	NP_783327.1	-----GKPIVMVPSLLHAGTEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	146
gi	6978425	ref	NP_036620.1	-----QKPIVMVPSLLHAGTEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	143
gi	118083282	ref	XP_416476.2	-----TKPOVMVLVPSLLHAEITEKGCVLLSYLNETVTVASLESVGRNRSFLDLEAENDVLVHCVAFVPKSSNEEVMFLTVQVKGPTQEFKRRITVMVKNEDSLIVFVOTDKSIYK	139



gi	189528839	ref	XP_001923676.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	282
gi	189528837	ref	XP_001921577.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	
gi	189528842	ref	XP_001345438.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	257
gi	189528833	ref	XP_001345556.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	286
gi	189528835	ref	XP_001345541.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	279
gi	189528831	ref	XP_001345569.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	277
gi	189528829	ref	XP_001921519.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	260
gi	189528827	ref	XP_697477.3	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	227
gi	153945757	ref	NP_001093623.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	9
gi	167963454	ref	NP_001108172.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	278
gi	167621474	ref	NP_001108028.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	301
gi	167963486	ref	NP_001108188.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	301
gi	125816799	ref	XP_001332356.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	301
gi	165972457	ref	NP_001107101.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	301
gi	189519439	ref	XP_0019222903.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	325
gi	66932947	ref	NP_000005.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	287
gi	114643413	ref	XP_001139819.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	287
gi	73997689	ref	XP_534893.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	848
gi	157954061	ref	NP_001103265.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	287
gi	28274695	ref	NP_783327.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	293
gi	6978425	ref	NP_036620.1	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	290
gi	118083282	ref	XP_416476.2	GQTVNFRIVLIDKIFAPLDQYSVVLEDSQDNRIQOWNVSS-TR-WILQRSYELNPECREGAYKLFKAFIGERMISHY-FQVKKYVLPKFEVAVKPKNKVSVDEEELSLIEVCA-KYTYGQPVPGKSWKVCNRNSVPIF---HTKDFNPLC	287



gi | 189528839 | ref | XP_001923676.1 | SEEITETIKGCAIHNFGVSVFLN-STLKERLKDHLHVEAVVT EEGEITMAKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 430
gi | 189528837 | ref | XP_001921577.1 | ---MTKITKGCIAHNFGVSVFLN-STLKERLKDHLHVEAVVT EEGEITMAKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 145
gi | 189528842 | ref | XP_001345438.2 | SEEITETIKGCAIHNFGVSVFLN-STLKERLMDHLHVEAVVT EEGEITMTKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 405
gi | 189528833 | ref | XP_001345556.2 | LEEITLKITKGCIAHNFGVSVFLN-STLKDNLKDLHVEAVVT EEGEITMTKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 434
gi | 189528835 | ref | XP_001345541.2 | LGEITLKITKGCIAHNFGVSVFLN-STLKNLKDHLHVEAVVT EEGEITRTKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 427
gi | 189528831 | ref | XP_001345569.2 | VKESITLKITKGCIAHNFGVSVFLN-STLKNLKDHLHVEAVVT EEGEITMTKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 424
gi | 189528829 | ref | XP_001921519.1 | LNKAACMNELGCASFIFNTSAFLN-STFENLQNLNLLVNVTE EEGDIVMTKSEVPLTYEIGKVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 408
gi | 189528827 | ref | XP_697477.3 | ----RLNKGCAEFEMFPLSFTQKSVFYVYLSQSLKLEFASIT EEGEGITEGGTEKVTIYIIGTVKVIDLPNIEHGVS-IEGKIKLDFDKDAPIPNKEVYLLEGENWSSKLLLNLTDSGLASFSLNTSSLSKDDISLIANVYDPDR 366
gi | 153945757 | ref | NP_001093623.1 | FPKNVIQGSARCSVSVIG--DIMG-RALK-NLANLQMPYCGEONMIIIGPNYIIRLKVTAQLTPAIQDTAMTQLQSGYQGLNRYHRSDGS 99
gi | 167963454 | ref | NP_001108172.1 | FPNVVKGSARCSVSVIG--DIMG-RSLR-NLANLQMPYCGEONMIIIGPNYIIRLKVTAQLTPAIQDTAMTQLQSGYQGLNRYHRSDGS 368
gi | 167621474 | ref | NP_001108028.1 | LNKSITKNNTCGASLTLSTSSFFG-TSFEENLQNSFVNVNLT EEGGVVMSKSTVSIITFEVGVKTFVLDLPKPFYNYGST-VNGKISVSDFNNGPIYKAVYLLDSSIWPNKLLFNLTNNYGFAKFSLDITSPFPQADLNLVASATPQSY 449
gi | 167963486 | ref | NP_001108188.1 | LNKSITKNNTCGASLTLSTSSFFG-TSFEENLQNSFVNVNLT EEGGVVMSKSTVSIITFEVGVKTFVLDLPKPFYNYGST-VNGKISVSDFNNGPIYKAVYLLDSSIWPNKLLFNLTNNYGFAKFSLDITSPFPQADLNLVASATPQSY 401
gi | 125816799 | ref | XP_001332356.1 | LKKSITKNNTCGASLTLSTSSFFG-TSFEENLQNSFVNVNLT EEGGVVMSKSTVSIITFEVGVKTFVLDLPKPFYNYGST-VNGKISVSDFNNGPIYKAVYLLDSSIWPNKLLFNLTNNYGFAKFSLDITSPFPQADLNLVASATPQSY 449
gi | 165972457 | ref | NP_001107101.1 | LNKSITKNNTCGASLTLSTSSFFG-TSFEENLQNSFVNVNLT EEGGVVMSKSTVSIITFEVGVKTFVLDLPKPFYNYGST-VNGKISVSDFNNGPIYKAVYLLDSSIWPNKLLFNLTNNYGFAKFSLDITSPFPQADLNLVASATPQSY 449
gi | 189519439 | ref | XP_001922903.1 | LKKSITKNNTCGASLTLSTSSFFG-TSFEENLQNSFVNVNLT EEGGVVMSKSTVSIITFEVGVKTFVLDLPKPFYNYGST-VNGKISVSDFNNGPIYKAVYLLDSSIWPNKLLFNLTNNYGFAKFSLDITSPFPQADLNLVASATPQSY 473
gi | 66932947 | ref | NP_000005.2 | EKFSQGLNSHCFFVQVVKIKVFLQ----KRKEVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 430
gi | 114643413 | ref | XP_001139819.1 | EKFSQGLNSHCFFVQVVKIKVFLQ----KRKEVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 430
gi | 73997689 | ref | XP_534893.2 | EKFSQGLNSHCFFVQVVKIKVFLQ----KRQGVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 991
gi | 157954061 | ref | NP_001103265.1 | EKFSQGLNSHCFFVQVVKIKVFLQ----KRQGVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 430
gi | 28274695 | ref | NP_783327.1 | EKFSQGLNSHCFFVQVVKIKVFLQ----KRQGVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 436
gi | 6978425 | ref | NP_036620.1 | EKLSQGLNSHCFFVQVVKIKVFLQ----KRQGVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 433
gi | 118083282 | ref | XP_416476.2 | DEFSQGLNSHCFFVQVVKIKVFLQ----KRQGVEMKLEHTEAQIQEEGVVELTGRQSEITRTITKLSFVKVDSHFROGIP-FFGVRLVDGKGVPIPNKVFIRGNEANYYS--NATIDEHGLVQFISINTINMGTSLIVRVNKKDRSP 429
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 189528839 | ref | XP_001923676.1 | FRQYKIPVFSRDKKTKVLF-QTATPYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 577
gi | 189528837 | ref | XP_001921577.1 | FRQYKIPVFSRDKKTKVLF-QTATPYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 292
gi | 189528842 | ref | XP_001345438.2 | FREYKIPVFSRDKKTKVLF-QTADPYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 553
gi | 189528833 | ref | XP_001345556.2 | YGYKIPVFSRDKKTKVLF-RIATVYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 582
gi | 189528835 | ref | XP_001345541.2 | YGYKIPVFSRDKKTKVLF-RIATVYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 575
gi | 189528831 | ref | XP_001345569.2 | SYFQKSPVFNTEKTVQVFPKPAASYTPFSELIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 572
gi | 189528829 | ref | XP_001921519.1 | YG-YKIPVFSRDKKTKVLF-RIATVYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 555
gi | 189528827 | ref | XP_697477.3 | LSTPEFVFSRDKKTKVLF-RIATVYSPFSLKLIENIEQPIKCGTEITATVKYVYFVGETVEDFN-ADIVMVLRSKGVIVHHEGYEKVEVKS-NGVASGTMSEFSLVGDVAPVVRILAYCVLPSENIIAASKSLDIEKCFGNKVSLOFS 511
gi | 153945757 | ref | NP_001093623.1 | ----LVPSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 99
gi | 167963454 | ref | NP_001108172.1 | ----LVPSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 368
gi | 167621474 | ref | NP_001108028.1 | FSSNSPYFTLDSQVVQLS---QDDPTPFFSFLSIVKLEQPLKCGTYSVTVKYLTVGVE-IGDYS-ADIIYVMVSRGVIVLHGFKTVQARAF-NLTLRGTVTFDLSILAKMAPVQILVYVSLPQTVVTGSAFDTIEKCFNSQVLSLOFS 593
gi | 167963486 | ref | NP_001108188.1 | FSSNSPYFTLDSQVVQLS---QDDPTPFFSFLSIVKLEQPLKCGTYSVTVKYLTVGVE-IGDYS-ADIIYVMVSRGVIVLHGFKTVQARAF-NLTLRGTVTFDLSILAKMAPVQILVYVSLPQTVVTGSAFDTIEKCFNSQVLSLOFS 401
gi | 125816799 | ref | XP_001332356.1 | FSSNSPYFTLDSQVVQLS---QDDPTPFFSFLSIVKLEQPLKCGTYSVTVKYLTVGVE-IGDYS-ADIIYVMVSRGVIVLHGFKTVQARAF-NLTLRGTVTFDLSILAKMAPVQILVYVSLPQTVVTGSAFDTIEKCFNSQVLSLOFS 593
gi | 165972457 | ref | NP_001107101.1 | FSYNSPYFTLDSQVVQLS---QDDPTPFFSFLSIVKLEQPLKCGTYSVTVKYLTVGVE-IGDYS-ADIIYVMVSRGVIVLHGFKTVQARAF-NLTLRGTVTFDLSILAKMAPVQILVYVSLPQTVVTGSAFDTIEKCFNSQVLSLOFS 593
gi | 189519439 | ref | XP_001922903.1 | YGYNQVWSEEHAAHTAY----LVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 618
gi | 66932947 | ref | NP_000005.2 | CYGYQVWSEEHAAHTAY----LVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 573
gi | 114643413 | ref | XP_001139819.1 | CYGYQVWSEEHAAHTAY----LVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 573
gi | 73997689 | ref | XP_534893.2 | CYGYQVWSEEHAAHTAY----LVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 1134
gi | 157954061 | ref | NP_001103265.1 | CYGYQVWSEEHAAHTAY----LVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 573
gi | 28274695 | ref | NP_783327.1 | CYGFRWLTEENVAAHTAY----AVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 579
gi | 6978425 | ref | NP_036620.1 | CYGFRWLTEENVAAHTAY----AVFSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 576
gi | 118083282 | ref | XP_416476.2 | CDFHSWVNPYEDGYLHVK----RFYSPKSFVHLEPMSHELPCGHQITVQAHYILNNGGVLGKLLKLSFYFLIMAKGGIVRKTHTLVPVEQG---DMRGHFSISIPVKSADIAPVARLLIYAVLPTGDVIGDSAKVDVENCLANKVLDLSPF 572
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 189528839 | ref | XP_001923676.1 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPQYV-YYPY---SAEDEOPCLVPRRRSVLADN-VYNLSKSVGLKMASNLA-VRVPECLSRGLTYHR-----FRDIVMHTSGRVGLGSSIE 709
gi | 189528837 | ref | XP_001921577.1 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPQYV-YYPY---SAEDEOPCLVPRRRSVLADN-VYNLSKSVGLKMASNLA-VRVPECLSRGLTYHR-----FRDIVMHTSGRVGLGSSIE 424
gi | 189528842 | ref | XP_001345438.2 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPVQSVSYYPY---SVDEOPCLVPRRRSVLADN-VYNLSKSVGLKMASNLA-VRVPECLSRGLTYHRKIGTCTATYVPRIGVNYHARSRMGFRSPES 696
gi | 189528833 | ref | XP_001345556.2 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPVQSVSYYPY---SVDEOACLVPRRRSVLADN-TYETLKS SVGLKMATNLA-VRVPDCLSYRGLTYHKNL-----VMYDPDRFPVPMFALGMAGV 717
gi | 189528835 | ref | XP_001345541.2 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPVHVSVDYYPY---SVDEGACLVPRRRSVLADN-TYETLKS SVGLKMATNLA-VRVPECLLYKGLAYHKNF GK-----LMYRQNAFAPGMPAQGMAGV 712
gi | 189528831 | ref | XP_001345569.2 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPVKYSGSYPS---SLPDEKCFYVMA--VPIEN-IFKSKRIGLKMATNLAGVQEAENTAPGTSVDEDCQG-RVHKQSHSLCVFVQVRLSSVQDLS 712
gi | 189528829 | ref | XP_001921519.1 | PAKAVPGEKNTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFSLLPVQYMSDYLK---SVDEOACLVPRRRSVLADN-TYETLKS SVGLKMATNLA-VRVPECLTYRGLTYHR-----SFADYSEDFVVKMAMNYE-E 687
gi | 189528827 | ref | XP_697477.3 | PTTAVPGEENTLQLSAQPGSLCGLSAVDQSVLILESGKRLDADKIFVFKMLP---TMTFTY---DVEDQMECLKFRSKRSLRGLDAVFEFKNMGLKVALNLV-IRIPHCIKFRDVLFR-----AYGKLSVCIYSLALHTYT 643
gi | 153945757 | ref | NP_001093623.1 | ----- 99
gi | 167963454 | ref | NP_001108172.1 | ----- 368
gi | 167621474 | ref | NP_001108028.1 | PSTAVPGEISILTYSAGAGSLCGLSAIDQSVLIMOSGGRLSAEAVFNMLPLQSLSDYYPY---GAEDQOCLNVRPRRAVPTDQ-AYNFKSVGMKIATNLP-VREPECLKFKDLYRNFHWG---VRDAVFAMA EKA-----PVSLAMA 729
gi | 167963486 | ref | NP_001108188.1 | ----- 401
gi | 125816799 | ref | XP_001332356.1 | PASAVPGEISILTYSAGAGSLCGLSAIDQSVLIMOSGGRLSAEAVFNMLPLQSLSDYYPY---GAEDQOCLNVRPRRAVPTDQ-AYNFKSVGMKIATNLP-VREPECLKFKDLYRNFHWG---VFP LREVAFAVSGKAPAPLAMAEM 734
gi | 165972457 | ref | NP_001107101.1 | PATAVPGEISILTYSAGAGSLCGLSAIDQSVLIMOSGGRLSAEAVFNMLPLQSLSDYYPY---GAEDQOCLNVRPRRAVPTDQ-AYNFKSVGMKIATNLP-VREPECLKFKDLYRNFHR---VIPFRGTGFAMAEMAPLAMA EI 734
gi | 189519439 | ref | XP_0019222903.1 | PATAVPGEISILTYSAGAGSLCGLSAIDQSVLIMOSGGRLSAEAVFNMLPLQSLSNYPP---GAEDQOCLNVRPRRAVPTDQ-AYNFKSVGMKIATNLP-VREPECLKFKDLYRNFHWG---VVP LQEVAFAMAREAPAIKAEV 759
gi | 66932947 | ref | NP_000005.2 | PSQSLPASHAHLRVTAAQFVICALRAVDQSVLLMKPDAELSAASVYNLLPEKDLTGFPK-PLNDQ--DDEDICINRHNVIYNGITYPVSSINTEKMDYSFLEDMLKFAFTNSKIRKPKMCPQLQQVEMHGPEGLRVGFYESDVMG-RGHAR 719
gi | 114643413 | ref | XP_001139819.1 | PSQSLPASHAHLRVTAAQFVICALRAVDQSVLLMKPDAELSAASVYNLLPEKDLTGFPK-PLNDQ--DDEDICINRHNVIYNGITYPVSSINTEKMDYSFLEDMLKFAFTNSKIRKPKMCPQLQQVEMHGPEGLRVGFYESDVMG-RGHAR 719
gi | 73997689 | ref | XP_534893.2 | PTQSLPASQAHLQISAPQSLCALRAVDQSVLLAKPEAEASAASVYNLLPVKDLGFPK-SLNQOQEDDRCCVHHNIYINGVKYPSVNTNEKMDYSFLKDMGLKVFNTNKRHKPKVCEQPEHVAHSSRLRFPASVVSKEALQSHLTD 1283
gi | 157954061 | ref | NP_001103265.1 | PQQSPASQAHLRVTAAQFVICALRAVDQSVLLMKPDAELSAATVYNLLPVKDLGFPK-SVNOQOEDNECISHDNVIYNGITYPVSSINTEKMDYSFLEDMLKFAFTNSKIRKPKMCPQLQQVEMHGPEGLRVGFYESDVMG-RGHAR 721
gi | 28274695 | ref | NP_783327.1 | PNIGLPATRAFLSVMASPOSLCGLRAVDQSVLLMKPEADLSHSSVYNLLPVKDLGFPK-GVNOQOEDTNGCLKQNDTYIR-NPVLPRQNTNEEDMYGFLKDMGLKVFNTNLRKPKVCEQPEHVAHSSRLRFPASVVSKEALQSHLTD 718
gi | 6978425 | ref | NP_036620.1 | PNSGLPATRALLSVMASPOSLCGLRAVDQSVLLMKPEADLSHSSVYNLLPVKDLGFPK-GADQOEDTNGCLKQNDTYINGILYPSVNTNEEDMYGFLKDMGLKVFNTNLRKPKVCEQPEHVAHSSRLRFPASVVSKEALQSHLTD 717
gi | 118083282 | ref | XP_416476.2 | SSEGLPSSDTHLLFRASPKSLCAVRAVDSVLLMKPEADLSHSSVYNLLPVKDLGFPK-DMLLEELPDCVPLKKIILNGITYPVVEMNEDDYSFLKDMGLKVFNTNLRKPKVCEQPEHVAHSSRLRFPASVVSKEALQSHLTD 711
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 189528839 | ref | XP_001923676.1 | SSTFDNS-AVIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 857
gi | 189528837 | ref | XP_001921577.1 | SSTFDNS-AVIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 572
gi | 189528842 | ref | XP_001345438.2 | SILVNRDSEFVIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGMN 845
gi | 189528833 | ref | XP_001345556.2 | DGPVGNPSVIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 866
gi | 189528835 | ref | XP_001345541.2 | DGLVGNPSVIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 861
gi | 189528831 | ref | XP_001345569.2 | LATGVAVDENVRVFPKTLWQLIEISDGSAAEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 861
gi | 189528829 | ref | XP_001921519.1 | DSFVAVSPDAIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 836
gi | 189528827 | ref | XP_697477.3 | DQKIKGILEEIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-STGLGLAPPAQLVFPFFLELSLPYSIIRGEIFELKATVFNYSKICIMVKVSPAPSSDYTLKASSDDQYSSCLCANGRQTFKWLITPSVGLGVN 792
gi | 153945757 | ref | NP_001093623.1 | ----- 99
gi | 167963454 | ref | NP_001108172.1 | ----- 368
gi | 167621474 | ref | NP_001108028.1 | G-TGGSSVDMIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 876
gi | 167963486 | ref | NP_001108188.1 | ----- 401
gi | 125816799 | ref | XP_001332356.1 | A-GTGGSSVDMIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 881
gi | 165972457 | ref | NP_001107101.1 | GSTRGSSVDMIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 882
gi | 189519439 | ref | XP_0019222903.1 | A--GSSVDMIRIRIFPETWIWDLAEVGDGSGTEVPVIVPDIITTWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 905
gi | 66932947 | ref | NP_000005.2 | LVHVEEPTETVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 869
gi | 114643413 | ref | XP_001139819.1 | MVHFSEPLTEVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 869
gi | 73997689 | ref | XP_534893.2 | FDDTSEPPTEVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 1431
gi | 157954061 | ref | NP_001103265.1 | FDDTSEPPTEVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 870
gi | 28274695 | ref | NP_783327.1 | FLESSESPTEVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 868
gi | 6978425 | ref | NP_036620.1 | FLESSESPTEVRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 867
gi | 118083282 | ref | XP_416476.2 | TPTTPEEVTETIRKYFPETWIWDLVVDVNSAGVAEVGIVPDIITWTEAFCLS-SNGFGLAPPALLSFQFFLELTLPSYIIRGEAFELVATVFNYSKICIQVTPPSSNYTLTPI-NDLSSSTLSINWRKTIKVALTASVIGTVN 861
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi | 189528839 | ref | XP_001923676.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSENVDLIVPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 971
gi | 189528837 | ref | XP_001921577.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSENVDLIVPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 686
gi | 189528842 | ref | XP_001345438.2 | IIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSENMNLLPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 959
gi | 189528833 | ref | XP_001345556.2 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSEKVDLILPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 980
gi | 189528835 | ref | XP_001345541.2 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSEKVDLILPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 975
gi | 189528831 | ref | XP_001345569.2 | IIVRAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSEKVDLILPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 975
gi | 189528829 | ref | XP_001921519.1 | IIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GSRVDEVTLLPDSVVIKGSVRSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 950
gi | 189528827 | ref | XP_697477.3 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GQNHLEVEVLAFFQNVIEGSGRAIVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 906
gi | 153945757 | ref | NP_001093623.1 | -----
gi | 167963454 | ref | NP_001108172.1 | -----
gi | 167621474 | ref | NP_001108028.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GDSLSENVDLIVPKDVIIEGSAKSSVSVIGDILGRALONLHGLLRMPYCGGEONMVLSPN 990
gi | 167963486 | ref | NP_001108188.1 | -----
gi | 125816799 | ref | XP_001332356.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GSMLESSEVKIILPNTNVIQGSASCSVSVIGDIMGRALNLANLLQMPSCCGEONMILLAPN 401
gi | 165972457 | ref | NP_001107101.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GSMLESSEVKIILPKSVIQGSASCSVSVIGDIMGRALNLANLLQMPSCCGEONMILLAPN 996
gi | 189519439 | ref | XP_001922903.1 | VIVSAAEAASQTVCDNEIVSVPERGRIDIVTRSLRVLAEGVETFRSLLCPK-----GTTLSEVVKIIFPNTNVIQGSASCSVSVIGDIMGRALNLANLLQMPSCCGEONMILLAPN 1019
gi | 66932947 | ref | NP_000005.2 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----SGGEVSEELSLKLPNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 983
gi | 114643413 | ref | XP_001139819.1 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----SGGEVSEELSLKLPNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 983
gi | 73997689 | ref | XP_534893.2 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----SDAEVSEQLSLKLPKNVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 1545
gi | 157954061 | ref | NP_001103265.1 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----GAKVSEELSLKLPNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 1020
gi | 28274695 | ref | NP_783327.1 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----TGAEVSEQLSLKLPNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 982
gi | 6978425 | ref | NP_036620.1 | FIVSAAEALESQELCGTEVPPVPEHGKRDIVIKPLLVPEEGLEKETFRNSLLCPK-----MGAEVSEELSLKLPNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 981
gi | 118083282 | ref | XP_416476.2 | FLVSTEALQNPQCRNTIVETPEKGRKDIVIKPLLVPEEGLEKETFRNSLLCPK-----GESVSEKLSLKLPSNVVVEEARSASVSVIGDILGSAMONTQNLQMPYCGGEONMVLFPAN 975
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi | 189528839 | ref | XP_001923676.1 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GYDGNITWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1117
gi | 189528837 | ref | XP_001921577.1 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GYDGNITWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 832
gi | 189528842 | ref | XP_001345438.2 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GYDGNITWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1105
gi | 189528833 | ref | XP_001345556.2 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GYDGNITWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1126
gi | 189528835 | ref | XP_001345541.2 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GYDGNITWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1121
gi | 189528831 | ref | XP_001345569.2 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GNGKGNLWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1121
gi | 189528829 | ref | XP_001921519.1 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GNGKGNLWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1096
gi | 189528827 | ref | XP_697477.3 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GNGKGNLWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1052
gi | 153945757 | ref | NP_001093623.1 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GNGKGNLWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 204
gi | 167963454 | ref | NP_001108172.1 | IYILQYLENTKQLSAIREKASFLKSGYORQLNYKHFDGAYSTF---GNGKGNLWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 473
gi | 167621474 | ref | NP_001108028.1 | VYILRYLTVTAQLTPAIDTATSYLLTGYOGLNYRHSDDGFSFTF---GYDASNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1136
gi | 167963486 | ref | NP_001108188.1 | -----
gi | 125816799 | ref | XP_001332356.1 | VYILRYLTVTAQLTPAIDTATSYLLTGYOGLNYRHSDDGFSFTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1141
gi | 165972457 | ref | NP_001107101.1 | VYILRYLTVTAQLTPAIDTATSYLLTGYOGLNYRHSDDGFSFTF---GYDASNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1142
gi | 189519439 | ref | XP_001922903.1 | IYILRYLTVTAQLTPAIDTATSYLLTGYOGLNYRHSDDGFSFTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1165
gi | 66932947 | ref | NP_000005.2 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1133
gi | 114643413 | ref | XP_001139819.1 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1133
gi | 73997689 | ref | XP_534893.2 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1695
gi | 157954061 | ref | NP_001103265.1 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1170
gi | 28274695 | ref | NP_783327.1 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1132
gi | 6978425 | ref | NP_036620.1 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1131
gi | 118083282 | ref | XP_416476.2 | IYVLDYLNQQLPEIKSKAIGYLNIGYORQLNYKHFDGAYSTF---GYDPSNTWLAFLVRSFGKAQKTYFIDPQIIQSADWLIERRDSGCFIQOGRLFNRMKGGVTDNVTMTAYITASLLELEFPVDPVITKGLSCLRSVIE 1124
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



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gi | 189528839 | ref | XP_001923676.1 | DVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1249
gi | 189528837 | ref | XP_001921577.1 | DVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 964
gi | 189528842 | ref | XP_001345438.2 | DVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1237
gi | 189528833 | ref | XP_001345556.2 | EVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSRASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1258
gi | 189528835 | ref | XP_001345561.2 | EVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1253
gi | 189528831 | ref | XP_001345569.2 | DVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1253
gi | 189528829 | ref | XP_001921519.1 | DVK-----NTYTTALLAYTFSLARDTNRQQLFNKLEDLAI SDGPLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1228
gi | 189528827 | ref | XP_697477.3 | DIR-----NLTYTALLAYSITFSLAKIKVEVRDSSLNKLNIASIEGFLVHWSQASADD-----SASLDVEISSYVLLAVLTADSLTT--ADLGFANRIVSWLVKQONAYGGFSSSTODTVVALQALSLYATKVF--SDGSSTVTVOS- 1184
gi | 153945757 | ref | NP_001093623.1 | NLG-----NTYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 334
gi | 167963454 | ref | NP_001108172.1 | NLG-----NTYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 603
gi | 167621474 | ref | NP_001108028.1 | YLG-----NTYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVSWIVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 1266
gi | 167963486 | ref | NP_001108188.1 | -----NTYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVSWIVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 419
gi | 125816799 | ref | XP_001332356.1 | NLG-----NTYVVALLAHTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 1271
gi | 165972457 | ref | NP_001107101.1 | NLG-----NAYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVSWIVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 1272
gi | 189519439 | ref | XP_001922903.1 | NLG-----NTYVVALLAYTFSLAGETSRAQLLSLRNTAIS EGTLLHWSQTSGD-----TLAVEISAYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALQALALYAAQVTF--PGSSSTVTVOSS 1295
gi | 66932947 | ref | NP_000005.2 | TAQEGDGHSHVYTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALHALSKYGAATFRTKGAQAQVTIQSS 1283
gi | 114643413 | ref | XP_001139819.1 | TAQEGDGHSHVYTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALHALSKYGAATFRTKGAQAQVTIQSS 1283
gi | 73997689 | ref | XP_534893.2 | SAKEGSPGHKHYVTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALGSLRYGAATFRTKGPQOVTIQSS 1845
gi | 157954061 | ref | NP_001103265.1 | SAKEGSQGSHVYTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALHALSKYGAATFRTKGAQAQVTIQSS 1320
gi | 28274695 | ref | NP_783327.1 | SARRGASGNHYVTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALHALSKYGAATFRTKGAQAQVTIQSS 1282
gi | 6978425 | ref | NP_036620.1 | SARGGAGSHVYTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALHALSKYGAATFRTKGAQAQVTIQSS 1281
gi | 118083282 | ref | XP_416476.2 | SKE-----NHVYTKALLAYAFALAGNQDRKRKVEVLKSLNBEAVKKNDSVHWERPQKPKAPVGFHYEFPAPSAEVEVMTSYVLLAVLTADSLTT--ANLGYANRIVNWLVAQONPYGGFSTODTVVALQALSLYATKVF--SDGSSTVTVOS 1269
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950

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gi | 189528839 | ref | XP_001923676.1 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNIPTP--TEAKT--LSIDAEEVGGCKKTFQONLMLNVTYTDGPG--NRTNMVIVDIKLLSGFTAD--TSMLKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1392
gi | 189528837 | ref | XP_001921577.1 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNIPTP--TEAKT--LSIDAEEVGGCKKTFQONLMLNVTYTDGPG--NRTNMVIVDIKLLSGFTAD--TSMLKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1107
gi | 189528842 | ref | XP_001345438.2 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNILPTP--TEAKT--LSIDAEEVGGCKKTFQKSLNFTYTDGPG--AKTNMIVDIKLLSGFTAD--TSMLKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1373
gi | 189528833 | ref | XP_001345556.2 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNIPTP--TEAKT--LSIDAKIEGDC--EALQNFIFDFTVKIDGPE--EKTNMAIVDIKLLSGFTAD--TSALGTSSTGTVS-----LVERVDSKDDHVLVYL 1393
gi | 189528835 | ref | XP_001345561.2 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNIPTP--TEAKT--LSIDAKIEGDC--EALQNFIFDFTVKIDGPE--EKTNMAIVDIKLLSGFTAD--TSALGTSSTGTVS-----LVERVDSKDDHVLVYL 1388
gi | 189528831 | ref | XP_001345569.2 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMAQFYNIPTP--TEAKT--LSIDVKEGCKKTFQONLMLNVTYTDGPH--ETTNMIVDIKLLSGFTAD--TSMFKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1390
gi | 189528829 | ref | XP_001921519.1 | --AGDSQHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQIPLFYNIPTPPPTTIKT--LSVEASVTGDCCLASTAKNMLNFTIKYSGTG--TRTNMIVDIKLLSGFTAD--TSMFKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1365
gi | 189528827 | ref | XP_697477.3 | --AGDSHFHDVNDQNKLLYQEKQLANVPGKYSIEVKGACVSVQMSLFYNIPTP--KKSINK--LEFSVKEGTCQNTDQIILNVLVYKGI--YIETSNMIVDMKLLSGFTAD--TSMFKIQRQSFDSLDFGHAFVERIDSKDDHVLVYL 1318
gi | 153945757 | ref | NP_001093623.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 471
gi | 167963454 | ref | NP_001108172.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 741
gi | 167621474 | ref | NP_001108028.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 1403
gi | 167963486 | ref | NP_001108188.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 556
gi | 125816799 | ref | XP_001332356.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 1408
gi | 165972457 | ref | NP_001107101.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 1409
gi | 189519439 | ref | XP_001922903.1 | VPAGDVNFVAVTPNRRLLYQESPLNFPFGTYSVVARGSACASVQVACFYNIPTP--VTVARILSVVAKVTGDCQAAAPVN--LMLTFTVKYNGRK--PTTNMVLVDIKVLSGFTAD--TSLGSPPNFAP-----LVRVDSNGDHVLVYL 1432
gi | 66932947 | ref | NP_000005.2 | --GTFSSKFQVDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSN-----HVSRTVSSNHVLIYL 1419
gi | 114643413 | ref | XP_001139819.1 | --GTFSSKFQVDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSN-----HVSRTVSSNHVLIYL 1419
gi | 73997689 | ref | XP_534893.2 | --GTFSSKFQVDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSN-----HVSRTVSSNHVLIYL 1981
gi | 157954061 | ref | NP_001103265.1 | --GTFSSKFQVDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSN-----HVSRTVSSNHVLIYL 1455
gi | 28274695 | ref | NP_783327.1 | --CAFYTKFQVNDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSV-----HVSRTVSSNHVLIYL 1418
gi | 6978425 | ref | NP_036620.1 | --GTFSSKFQVNDNRRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSV-----HVSRTVSSNHVLIYL 1417
gi | 118083282 | ref | XP_416476.2 | --GDFQDFHVDPSNRLLQLCVLPELPEVPEYEMSVTGGCCVYLOTSILKYNILPEKEEFPFALGVQ--LPGTCDEPKAHTSFQISLSVSYTGSR--SASNMAIVDKMVSGFIPKPTVKMLERSV-----HVSRTVSSNHVLIYL 1405
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100

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gi |189528839|ref |XP_001923676.1| EEVLKEDPVNLQIGLNGIIQVKNLKPAVIKVVDYYQTSDQSEMEYSSHCE----- 1442
gi |189528837|ref |XP_001921577.1| EEVLKEDPVNLQIGLNGIIQVKNLKPAVIKVVDYYQTSDQSEMEYSSHCE----- 1157
gi |189528842|ref |XP_001345438.2| KEVPKADPVNLQIGLNGIIQVKNLKPAVIKVVDYYQTSDQSEMEYSSHCE----- 1423
gi |189528833|ref |XP_001345556.2| KEISKNVAMNYQIQMKQVLQVKNLKPAVVKVVDYYQTSDQSEIEYSFHCEALKNIN--- 1449
gi |189528835|ref |XP_001345541.2| KEIPKNVAMNYQIQMKQVLQVKNLKPAVVKVVDYYQTSDQSEIEYSFHCEALKNIN--- 1444
gi |189528831|ref |XP_001345569.2| KEVPKHFPVNNYQIQMKQVLHVMNLKPAVIKVVDYYQTSDQSETEYYFHC----- 1439
gi |189528829|ref |XP_001921519.1| KEVPKNSPQLYTIQMKQAFVVRSLRPAVVKVVDYYQTSDQSETLYSSPCA----- 1415
gi |189528827|ref |XP_697477.3| NRIRNNINRILPFRIKRIEIVKLNKPAVVKVVDYYQTSERAEAEYTNHCA----- 1368
gi |153945757|ref |NP_001093623.1| QEVPKGVVPTYSIQLTQTVAVKNLKPAVINVDYYQREESFETTYTSVCS----- 521
gi |167963454|ref |NP_001108172.1| QEVPKGVVPTFSIQLTQAVAVKNLKPAVINVDYYQREDRFETKYTSR----- 790
gi |167621474|ref |NP_001108028.1| QEVPKGIPVTFFSIQLTQTVAVQNLKPAVINVDYYQRNDKFETTYKSPCP----- 1453
gi |167963486|ref |NP_001108188.1| QEVPKGVVPTFSIQLTQAVAVQNLKPAVINVDYYQRNDKFETTYKSPCP----- 606
gi |125816799|ref |XP_001332356.1| QEVPKGVVPTFSIQLTQTVAVQNLKPAVINVDYYQRNDKFETTYKSPCP----- 1458
gi |165972457|ref |NP_001107101.1| QEVPKGVVPTFSIQLTQTVAVQNLKPAVINVDYYQRNDKFETTYKSPCP----- 1459
gi |189519439|ref |XP_001922903.1| QEVPKGVVPTFSIQLTQAVAVQNLKPAVIYIYDYYQRNDKFETTYKSPCP----- 1482
gi |66932947|ref |NP_000005.2| DKVSN-QTLSLFFTVLQDVPVRDLKPAIVKVDYYEDEFVAIAEYNAPCS---KDLGNA 1474
gi |114643413|ref |XP_001139819.1| DKVSN-QTLSLFFTVLQDVPVRDLKPAIVKVDYYEDEFVAIAEYNAPCS---KDLGNA 1474
gi |73997689|ref |XP_534893.2| DKVTN-QTLSLRFVVLQDVPVRDLKPAIVKVDYYEDEFVAIAEYNAPCS---KDHGNA 2036
gi |157954061|ref |NP_001103265.1| DKVTN-ETLTLRFVVLQDIPVRDLKPAIVKVDYYEDEFVAIAEYSAPCS---KDIGNA 1510
gi |28274695|ref |NP_783327.1| DKVSN-QMLTLRFVVLQDIPVRDLKPAIVKVDYYEKDEFVAIAEYSAPCS---AGYGNA 1473
gi |6978425|ref |NP_036620.1| DKVSN-QTVNLSFTVQDIPVRDLKPAVVKVVDYYEKDEFVAIAEYSAPCS---TDYGNA 1472
gi |118083282|ref |XP_416476.2| EKLSN-VTLRFSTVVEQDIPVQGLKPAQVKVDYYEDEFVAIQEYSAPCTAKAEQGNA 1463
.....2110.....2120.....2130.....2140.....2150.....

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