

gi | 84370023 | ref | NP_001028400.1 | -----MVPRRPASLEVTACIWLILVILGVCISFNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRERMPCKVLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 133
gi | 13591884 | ref | NP_112256.1 | -----MVPRRPASLEVTACIWLILVILGFCVSNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRERAMPCKVLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 133
gi | 31657142 | ref | NP_852478.1 | -----MAPRRPRARPGVAVACWLLVILRCCISFNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRGELPCKVLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 133
gi | 114600333 | ref | XP_517769.2 | -----MAPRRPRARPGVAVACWLLVILRCCISFNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRGELPCKVLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 133
gi | 73954248 | ref | XP_546328.2 | -----MEIGDITDKEDYSIQSSLPSSGMGIVLGFVSNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRGKPLPCKIKLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 136
gi | 119913152 | ref | XP_616068.3 | -----MPERRGVYLDLWFLDILLMEVDILLYIISVERILNVLRFVCSFNVDVKNSMFSFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRSELPCKIKLDLVPVNTSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 149
gi | 45384200 | ref | NP_990400.1 | -----MAASYWMLHALPHLIGASNVDAAMFISFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRSDSQPCIKLNLDPATSIPNVTEIKENMTFGSTLVTNPKG--GFLACGPI 122
gi | 125827200 | ref | XP_699485.2 | -----MLSGVYQPTLAALALPWLSCFNVDKRNMFISFPVEDMFGYIVQOYENEEGKWWLIGSPLVGPARTGDVYKCPVGRSNSDSKCEKFLLENTIIPNTEIKENMTFGSTLVTNPKG--GFLACGPI 128



gi | 84370023 | ref | NP_001028400.1 | YAYRCGHLHYTTGICSDVSPPTFOVNSFAP-VQECSTQLDIVIVLDGNSIYPWESVTAFLNLLKRMIDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIGRRGGLQMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 282
gi | 13591884 | ref | NP_112256.1 | YAYRCGHLHYTTGICSDVSPPTFOVNSFAP-VQECSTQLDIVIVLDGNSIYPWESVTAFLNLLKRMIDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIGRRGGLQMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 282
gi | 31657142 | ref | NP_852478.1 | YAYRCGHLHYTTGICSDVSPPTFOVNSIAP-VQECSTQLDIVIVLDGNSIYPWDSVTAFLNLLERMDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIVORGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 282
gi | 114600333 | ref | XP_517769.2 | YAYRCGHLHYTTGICSDVSPPTFOVNSIAP-VQECSTQLDIVIVLDGNSIYPWDSVTAFLNLLERMDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIVORGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 282
gi | 73954248 | ref | XP_546328.2 | YAYRCGHLHYTTGICSDVSPPTFOVNSIAP-VQECSTQLDIVIVLDGNSIYPWDSVTAFLNLLERMDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIIRGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 285
gi | 119913152 | ref | XP_616068.3 | YAYRCGHLHYTTGICSDVSPPTFOVNSIAP-VQECSTQLDIVIVLDGNSIYPWESVTAFLNLLKRMIDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIVORGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 298
gi | 45384200 | ref | NP_990400.1 | YAYKCGRLHYTTGICSNVSSPFETKAVAPVQECSTQLDIVIVLDGNSIYPWESVTAFLNLLKRMIDIGPKOTQVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIIRORGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 272
gi | 125827200 | ref | XP_699485.2 | YAYKCGKQQYITGICSNVSSPFKVLNSIAPVRECSQDMDIVIVLDGNSIYPWDHITDFLVKFLNIIKIGP--ARVGIQVYGENVTHEFNLNKYSSTBEVLVAANKIIRORGGRTMTALGIDTARKEAFTARGARRGVKKVMVIVTDG 276



gi | 84370023 | ref | NP_001028400.1 | ESHDNYRLKQVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKANKVIPHNTTFQTEPKKMN 429
gi | 13591884 | ref | NP_112256.1 | ESHDNYRLKQVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKANKVIPHNTTFQTEPKKMN 429
gi | 31657142 | ref | NP_852478.1 | ESHDNRLLKVKVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKASQIIPRNTTFNVESTKKN 429
gi | 114600333 | ref | XP_517769.2 | ESHDNRLLKVKVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKASQIIPRNTTFNVESTKKN 429
gi | 73954248 | ref | XP_546328.2 | ESHDNRLLKVKVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKANKIIPRNTTFNVESTKKN 432
gi | 119913152 | ref | XP_616068.3 | ESHDNRLLKVKVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKADQVPIQNTTFNVESTKKN 445
gi | 45384200 | ref | NP_990400.1 | ESHDNYRLKQVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQKSDIIPRNTTFNVESTKKN 419
gi | 125827200 | ref | XP_699485.2 | ESHDNRLLKVKVIQDCEDENIQRFSAIILGHSYRGNLST---EKFVVEIKSIASEPTKHFVNSDELALVTVKALGERIFALEATADQSAASFEMEMSQTGFSAHYSQDWMVLGAVGAYDWNGTVMVQAGNEFVVPKKNTFNVESTKKN 426



gi | 84370023 | ref | NP_001028400.1 | EPLASVYLGTVNSAATIP-GDVLVIAGQPRYNHTGQVVIYKMGEDGNVILQILSGEQIGSYFGSVLTTIDIDKDSYIDLLLVGAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSLLKNSCTKENKNEPCGARFGATAAV 577
gi | 13591884 | ref | NP_112256.1 | EPLASVYLGTVNSAATIP-GDVLVIAGQPRYNHTGQVVIYKMGEDGNVILQILSGEQIGSYFGSVLTTIDIDKDSYIDLLLVGAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSLLKNSCTKENKNEPCGARFGATAAV 577
gi | 31657142 | ref | NP_852478.1 | EPLASVYLGTVNSAATASGDVLVIAGQPRYNHTGQVVIYRMBDGNIKILOQLSGEQIGSYFGSILTTIDIDKDSNTDILLVGAAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSRQHSCTKENKNEPCGARFGATAAV 578
gi | 114600333 | ref | XP_517769.2 | EPLASVYLGTVNSAATASGDVLVIAGQPRYNHTGQVVIYRMBDGNIKILOQLSGEQIGSYFGSILTTIDIDKDSNTDILLVGAAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSRQHSCTKENKNEPCGARFGATAAV 578
gi | 73954248 | ref | XP_546328.2 | EPLASVYLGTVNSAATVS-GAVLVIAGQPRYNHTGQVVIYRMBDGNIKILOQLSGEQIGSYFGSVLTTIDIDKDSNTDILLVGAAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSLLKNSCTKENKNEPCGARFGATAAV 580
gi | 119913152 | ref | XP_616068.3 | EPLASVYLGTVNSAATIP-GDVLVIAGQPRYNHTGQVVIYRMBDGNIKILOQLSGEQIGSYFGSVLTTIDIDKDSNTDILLVGAAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSLLKNSCTKENKNEPCGARFGATAAV 593
gi | 45384200 | ref | NP_990400.1 | EPLAALVYLGTVNSALIP-GDVLVIAGQPRYNHTGQVVIYKMEGRVQVLRQLKGEQIGSYFGGVVITIDINRDSFIDLLLVGAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSPLKHDIC-KVLKNEPCGARFGATAAV 566
gi | 125827200 | ref | XP_699485.2 | EGMAGVYGVYDQSAATIP-NGVLYITGAPRFNHSGRVTVVYRFDGQVTVIQLKGEQIGSYFGVLOPHIDGDNVYIDLLVVAAPMYMGTEKEBQKGVVYVALNQT-RFEYQMSLEPIKQTCSSGHSNNQKIVKNEPCGARFGATAAV 575



gi | 84370023 | ref | NP_001028400.1 | KDLNVDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWARDVAVVKTVMNFFPNKVNIOKKNCRVEGKETVCINAMCFHVKLSKEDSIYVADLQYRVILDS 727
gi | 13591884 | ref | NP_112256.1 | KDLNVDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWARDVAVVKTVMNFFPNKVNIOKKNCRVEGKETVCINAMCFHVKLSKEDSIYVADLQYRVILDS 727
gi | 31657142 | ref | NP_852478.1 | KDLNLDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 728
gi | 114600333 | ref | XP_517769.2 | KDLNLDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 728
gi | 73954248 | ref | XP_546328.2 | RDLNLDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 730
gi | 119913152 | ref | XP_616068.3 | KDLNLDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 743
gi | 45384200 | ref | NP_990400.1 | KDLNLDGFDVIVIGAPLEDDHAGAVIYHSGSKTIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 715
gi | 125827200 | ref | XP_699485.2 | PDLNLDKFSDIVIGSPLDDHAGAVIYHSGSKSIRKEAQAQRIIPSGDGGKILKFFGQSIHGEMDLNGDGLDVTITGGLGGAALFWRDVAVVKVMNFFPNKVNIOKKNCRVEGKETVCINAVCFDVKLSKEDSIYVADLQYRVILDS 724



