

gi | 157266317 | ref | NP_001175.2 | ...MGEHGLELASMPALRELQ-SATPEYNTVVKPROILCOFIDRILTDVNVVALELVKKTDSQPTSMVLLDFIQHIMKSSPLMFVN-VSGS---HEAGKSCIEFSNWIITRLLRIAAPSCHLLHKKICVICSLLFLFKSKSPAIFGV 144
gi | 114589666 | ref | XP_516792.2 | ...MQRBIKHSLEPPVGAYSLVAGNSATPEYNTVVKPROILCOFIDRILTDVNVVALELVKKTDSQPTSMVLLDFIQHIMKSSPLMFVN-VSGS---HEAGKSCIEFSNWIITRLLRIAAPSCHLLHKKICVICSLLFLFKSKSPAIFGV 146
gi | 73990328 | ref | XP_534295.2 | ...MGDRLGLELASMTPALRELQ-SASPEYNTVVKPROILCOFIDRILTDVNVVALELVKKTDSQPTSMVLLDFIQHIMKSSPLMFVN-VNGSQGNEAKGSCIEFSNWIITRLLRIAAPSCHLLHKKICVICSLLFLFKSKSPAIFGV 147
gi | 119885535 | ref | XP_581054.3 | ...MGEHGLELASMTPALRELQ-SASPEYNTVVKPROILCOFIDRILTDVNVVALELVKKTDSQPTSMVLLDFIQHIMKSSPLMFVN-VNGSHGNEAKGSCIEFSNWIITRLLRIAAPSCHMLHKKICVICALFLFKSKSPAIFGV 147
gi | 109483823 | ref | XP_001062084.1 | ...MGDRLGLELASMTPALRELQ-SATPEYNTVVKPROILCOFIDRILTDVNVVALELVKKTDSQPTSMVLLDFIQHIMKSSPLMFVN-VNGSQGNEAKGSCIEFSNWIITRLLRIAAPSCHMLHKKICVICSLLFLFKSKSPAIFGV 147
gi | 292610566 | ref | XP_696163.4 | ...MEOGLEMSAMIPALQELA-SASSVEYNQAVOKPROILCOFIDRILTDVNVVALELVKKTDSSEEPACVMLLDFVQIHKSSSLMFINPACGLDHFKNKENSCTDFTKWINRLLRIAACEPEDEHMKISVICSLLFLFRAPAVVFSL 147



gi | 157266317 | ref | NP_001175.2 | ...LTKKLLQLFEDLVYLHRRNVMHAVWEPVVMRSRFLSOLDEHMGVLCAPLQMLSMONLEFIEVLLMVLTRIIAIVFRRQELLWQIGCVLLEYGSPKIKSLAISFLTEFLGGLPAQPASTFFSFLKLLKHLVEMDADQLKYEEF 294
gi | 114589666 | ref | XP_516792.2 | ...LTKKLLQLFEDLVYLHRRNVMHAVWEPVVMRSRFLSOLDEHMGVLCAPLQMLSMONLEFIEVLLMVLTRIIAIVFRRQELLWQIGCVLLEYGSPKIKSLAISFLTEFLGGLPAQPASTFFSFLKLLKHLVEMDADQLKYEEF 296
gi | 73990328 | ref | XP_534295.2 | ...LTKKLLYLCEVDICLHRRNAVGHFVWEPVVMRSRFLSOLDEHMGVLCAPLQFMNMONLEFIEVLLMVLTRIIAIVFRRQELLWQIGCVLLEYGSPKIKSLAISFLTEFLGGLPAQPASTFFSFLGLLKHLVEMDADQLKYEEF 297
gi | 119885535 | ref | XP_581054.3 | ...LTKKLLHLFEDLIVFHRYAVEHFVWEPVVMRSRFLSOLDEHMGVLCAPLQMLSMONLEFIEVLLMVLTRIIAIVFRRQELLWQIGCVLLEYGSPKIKSLAISFLTEFLGGLPAQPASTFFSFLKLLKHLVEMDADQLKYEEF 297
gi | 109483823 | ref | XP_001062084.1 | ...LTKKLLYLFDLIVLHRRNAVGHFVWEPVVMRSRFLSOLDEHMGVLCAPLQFMNMONLEFIEVLLMVLTRIIAIVFRRQELLWQIGCVLLEYGSPKIKSLAISFLTEFLGGLPAQPASTFFSFLGGLKHLVEMDADQLKYEEF 297
gi | 292610566 | ref | XP_696163.4 | ...FSTELICLIQDLV--HKNLMTRSPQWVVERFVTKESGSAVYLTPTIQLSSLSSTQALLATSLRVLTDVIGLQFPPREVGIWDSICMLMSNGSPKIKAVEMVLLTRIVTLGGFPEDHQPFFSAFLHVLDSLPAPFESLGVFSRE 295



gi | 157266317 | ref | NP_001175.2 | ...LSKLIKTLFPFEAEAYRNIEPVVNLMLLEKLCVMEFEDVLMRLKSDLLKAALCHLLOVFLKFPVAGYESALQVRKVVYVNRICKALLDVLG-----IEVDAEYLLGPLYAALKMESMEIEEIOCOTQC-ENLSSNSDGIKSPKRRRLSS 436
gi | 114589666 | ref | XP_516792.2 | ...LSKLIKTLFPFEAEAYRNIEPVVNLMLLEKLCVMEFEDVLMRLKSDLLKAALCHLLOVFLKFPVAGYESALQVRKVVYVNRICKALLDVLG-----IQVDAEYLLGPLYAALKMESMEIEEIOCOTQC-ENLSSNSDGIKSPKRRRLSS 438
gi | 73990328 | ref | XP_534295.2 | ...LSKLIKTLFPFEAEAYRNIEPVVNLMLLEKLCVMEFEDVLMRLKSDLLKAALCHLLOVFLKFPVAGYESALQVRKVVYVNRICKVLDVLG-----IQVDAEYLLGPLYAALKMESMEIEEIOCOTQC-ENLSSNSDGIKSAKRRRLSS 439
gi | 119885535 | ref | XP_581054.3 | ...LSKLIKTLFSEAEAYRNIEPVVNLMLLEKLCVMEFEDVLLQKSDLLKAALCHLLOVFLKFPVAGYESALQVRKVVYVNRICKALLDVLG-----IQVDAEYLLGPLYAALKMESMEIEEIOCOTQC-EDLSSNSDGIKSPKRRRLSS 439
gi | 109483823 | ref | XP_001062084.1 | ...LSKLVKTLFPFEAEAYRNIEPVVNLMLLEKLRVMEFEDVLMRLKSDLLKAALCHLLOVFLKFPVAGYESALQVRKVVYVNTICRALVDVLG-----VQTHVYLLGFFVYALKMESTEIERICQCAQC-ENLRGNSDGIKSPKRRRLSS 439
gi | 292610566 | ref | XP_696163.4 | ...FOGLERCIFQHEEGASRRFERVHLLMMLERLEKLVVIGALEHLKVKVEKVAALCEVFCFLLGFPVPGYCALQIRKERVAAICAKLIKTLGTDKQDHEQAIQDQSLLEGVLYAALKTDATAAMQDVQASVSDPADPRMYEELPAKRNPLSL 445



gi | 157266317 | ref | NP_001175.2 | ...SLNPSKRAPKQTEIEIKHVDNMQSILWSALKQKAEISLQISLEYSGLKNPVIEMLEGIAVVLQTLTALCVHCHSHNMNCRFTKDCQHKSKKPPSVVITWMSLDFYTKVLSKRSLLS-VQKPDLEATIDKVKVIYDALIYMC-----VNS 580
gi | 114589666 | ref | XP_516792.2 | ...SLNPSKRAPKQTEIEIKHVDNMQSILWSALKQKAEISLQISLEYSGLKNPVIEMLEGIAVVLQTLTALCVHCHSHNMNCRFTKDCQHKSKKPPSVVITWMSLDFYTKVLSKRSLLS-VQKPDLEATIDKVKVIYDALIYMC-----VNS 582
gi | 73990328 | ref | XP_534295.2 | ...SLNSKRPPKQTEIEIKHVDNMQSILWSALKQKAEISLQIFLEYNGLNPNVIALEGITIVLQTLTALCVHCHSHNMNCRFRDCHQCKKKPSVETITWMSLDFYTKVLSKRSLLS-VQKPDLEAVIDKVKVIYDALIYH-----MKT 583
gi | 119885535 | ref | XP_581054.3 | ...SLNASKRAPKQTEIEIKHVDINKKSILWSALKQKAEISLQIFLESNNVKNPIIELEGIATVILQTLTALCVHCHSHNMNCRFRDCHQCKKKPSVETITWMSLDFYTKVLSKRSLLS-VQKPDLEAVIDKVKVIYDALIYH-----VNT 583
gi | 109483823 | ref | XP_001062084.1 | ...SLSSYKPRSRQSEIEINVDMDKKSILWNLVKQKAEISLQISLEGTLNQVAALEGITIVLQTLTALCVHCHSHNMNCRFRDCHQCKKKPSVETITWMSLDFYTKVLSKRSLLS-VQKHELELVIDSVVRVYDALMVIC-----VKS 583
gi | 292610566 | ref | XP_696163.4 | ...PQLRSRDKTQP---MQVDMKSRSEVWAADVCRLEELLQMRNHTVS-QCVSAVQGLAVIFHLAALCESHSLKGPQRG-----EKSSESSVVAQLIWLKPKQLAQVVEKCRVPLANNNEEHLEHLVEGIVRILDAVLYLSNNLFAANS 585



gi | 157266317 | ref | NP_001175.2 | ...SFEDHILEDLCMGLSLPWIYSHSDDGCKLITFAANLLLSCRISDSYSPQAQSRVCFLLLFPRRIFLWRITAVYNWALQSSHEVIRASCVSGFFILLQQQ--NSCNRVPKILIDKVKDSDIVKKEFASILGQLVCTLHGMYFLTSSL 728
gi | 114589666 | ref | XP_516792.2 | ...SFEDHILEDLCMGLSLPWIYSHSDDGCKLITFAANLLLSCRISDSYSPQAQSRVCFLLLFPRRIFLWRITAVYNWALQSSHEVIRASCVSGFFILLQQQ--NSCNRVPRILIDKVKDSDIVKKEFASILGQLVCTLHGMYFLTSSL 730
gi | 73990328 | ref | XP_534295.2 | ...SFEDHILEDLCMGLSLPWIYSHSDDGCKLITFAANLLLSQRISDSYSPQAQSRVCFLLLFPRRIFLWRITAVYNWALQSSHEVIRASCVSGFFILLQQQ--NSCNRVPKILIDKVKDSDIVKKEFASILGQLVCTLHGMYFLTSSL 731
gi | 119885535 | ref | XP_581054.3 | ...SFEDHILEDLCMGLSLPWIYSHSDDGCKLITFAANLLLSQRISDSYSPQAQSRVCFLLLFPRRIHLEWRITAVYNWALQSSHEVIRASCVSGFFILLQQQ--NPNRNVPKILIDKVKDSDIVKKEFASILGQLVCTLHGMYFLTSSL 731
gi | 109483823 | ref | XP_001062084.1 | ...SFQDHVLEELCMGLSLPWIYSHSDDNSLKMITFAANLLRLSRVWESYSPPAQSCVCFLLLFPRRIFLWRITAVYNWALQSSHEVIRASCVSGFFILLQQQ--NSCNRVPMKILIDKVKDSDIVKKEFASILGQLVCTLHGMYFLTSSL 731
gi | 292610566 | ref | XP_696163.4 | ...EEDKSFHRNIGALLSVPWLEHSQSQSVYQTAFFPASPALIALSOKLAPVYNAQTRAHCVFLLALPSKSVCGDWRSSVYRWALQSRSEAEERASAVRGFPILLHGLGKNSLTHEALLNRLQDSDEVKTELAGITGQLACLS-----ESSQL 731



gi | 157266317 | ref | NP_001175.2 | ...TEPFSSEHGHVDFCRNLKATSOHECSSSOLKASVCKPFLFLLKKKIPSPVKLAFIDNHLHCKHLDFREDETDVKAVALGILLNLMEDPKDVRVAFSGNIKIHILESLDSDGFIKELFVLRMKEAYTHAISRNNELKDILILTTGDIGR 878
gi | 114589666 | ref | XP_516792.2 | ...TEPFSSEHGHVDFCRNLKATSOHECSSSOLKASVCKPFLFLLKKKIPSPVKLAFIDNHLHCKHLDFREDETDVKAVALGILLNLMEDPKDVRVAFSGNIKIHILESLDSDGFIKELFVLRMKEAYTHAISRNNELKDILILTTGDIGR 880
gi | 73990328 | ref | XP_534295.2 | ...TEPFSSEHGHVDFCRNLKATSOHECSSSOLKASVCKPFLFLLKKKIPSPVKLAFIDNHLHCKHLDFREDETDVKTIVLGTLLNLMEDPKDVRVAFSGNIKIHILESLDSDGFIKELFVLRMKEAYTHAISRNNELKDILILTTGDIGR 881
gi | 119885535 | ref | XP_581054.3 | ...TEPFSSEHGHVDFCRNLKATSOHECSSSOLKASVCKPFLFLLKKKIPSPVKLAFIDNHLHCKHLDFREDETDVKTIVLGTLLNLMEDPKDVRVAFSGNIKIHILESLDSDGFIKELFVLRMKEAYTHAISRNNELKDILILTTGDIGR 881
gi | 109483823 | ref | XP_001062084.1 | ...VEPFE--FGPVDLFCRNLKATSOHECSSSOLKASVCKPFLFLLKNTSPVKLAFIDNHLHCKHLDFREDETDVKAVALGILLNLMEDPKDVRVAFSGNIKIHILESLDSDGFIKELFVLRMKEAYTHAISRNNELKDILILTTGDIGR 879
gi | 292610566 | ref | XP_696163.4 | ...QFPQETMPSHQLLCSGLSISDFHSSQSSIGFSILTPTLQLLKVPEDMKVQAFIKNIRHLFKHVDLQNTDPPDKALVALNALVLIEDPQDEVIRIMFGQNIKNLLEFNG--NGFLKELLYSRKKEAYTHAISRNNELKDILILTTGEBIGR 880



gi | 157266317 | ref | NP_001175.2 | AAKGDLVFPALLHLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1028
gi | 114589666 | ref | XP_516792.2 | AAKGDLVFPALLHLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1030
gi | 73990328 | ref | XP_534295.2 | AAKGDLVFPALLHLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1031
gi | 119885535 | ref | XP_581054.3 | AAKGDLVFPALLHLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1031
gi | 109483823 | ref | XP_001062084.1 | AAKGDLVFPALLHLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1029
gi | 292610566 | ref | XP_696163.4 | AEGNLVSPALLRLLHLLSASVSGAAYTEIRALVAAKSVKLNQFFSQYKKPICQFLVESHSSQMTALPNPCONADVRRQDVAHOREMALNTLSEIANVDFDFDLNRFLLRTRLOVLLPDLAAKASPAASALIRITLQKQLNVNRRREI 1030



gi | 157266317 | ref | NP_001175.2 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1177
gi | 114589666 | ref | XP_516792.2 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1179
gi | 73990328 | ref | XP_534295.2 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1180
gi | 119885535 | ref | XP_581054.3 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1180
gi | 109483823 | ref | XP_001062084.1 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1178
gi | 292610566 | ref | XP_696163.4 | LINNFKYIFSHLVCSCKDELERALHYLKNETIEELGSLLRQDFQGLHNEILLRIGEHYQVFNGLSILASFASDDDPYQGPRIISPELMADYLQPKLLGILAFFNMQLLSSVSGIEDKKMALNSLMSLMKLMGPKHVSVRVKMMTT 1180



gi | 157266317 | ref | NP_001175.2 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1327
gi | 114589666 | ref | XP_516792.2 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1329
gi | 73990328 | ref | XP_534295.2 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1330
gi | 119885535 | ref | XP_581054.3 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1330
gi | 109483823 | ref | XP_001062084.1 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1328
gi | 292610566 | ref | XP_696163.4 | LRTGLRFKDDFPELCCRAWDCFVRCLDHAYLGSLLSHVIVALLPLIHIOPKETAALFHYLIENRDAVQDFLHEIYFPLDPHPELKKIKAVLQYRKETSESTDLQTLQLSMKAIQHENVDVRIHALTSLKETLYKNQEKLIKVAIDSET 1330



gi | 157266317 | ref | NP_001175.2 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1477
gi | 114589666 | ref | XP_516792.2 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1479
gi | 73990328 | ref | XP_534295.2 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1480
gi | 119885535 | ref | XP_581054.3 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1480
gi | 109483823 | ref | XP_001062084.1 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1478
gi | 292610566 | ref | XP_696163.4 | VEPVTSQLVTVLLKGCQDANSQARLLCGECLGELGAIIDPGRLLDFSTTETQKDFTFVTVGVEDSSFAFGLLMELTRAVLAYADNSRAQDSAAAYAIQELLSIYDCREMTNGPGHQLWRRFFPEHVREILEPHLNTRYKSSQKSTDWSGVKPF 1480



gi | 157266317 | ref | NP_001175.2 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIMMKHDFKVTIYLLPHILVYVLLGCNGEDQEVYAEIMAVLKHDDQHTINTQDIASDLCLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1627
gi | 114589666 | ref | XP_516792.2 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIMMKHDFKVTIYLLPHILVYVLLGCNGEDQEVYAEIMAVLKHDDQHTINTQDIASDLCLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1629
gi | 73990328 | ref | XP_534295.2 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIMMKHDFKVTIYLLPHILVYVLLGCNGEDQEVYAEIMAVLKHDDQHTINTQDIASDLCLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1630
gi | 119885535 | ref | XP_581054.3 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIMMKHDFKVTIYLLPHILVYVLLGCNGEDQEVYAEIMAVLKHDDQHTINTQDIASDLCLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1630
gi | 109483823 | ref | XP_001062084.1 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIMMKHDFKVTIYLLPHILVYVLLGCNGEDQEVYAEIMAVLKHDDQHTINTQDIASDLCLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1622
gi | 292610566 | ref | XP_696163.4 | IYLSKLGSNFAEWSASWAGYLIITKVRHDLASKIFCCSIFIKHDKYVTIYLLPHILVYVLLGCTEGRVETIEIMAVLKEGPRIVRLQENASSLSLSLSTQTVFSMLDHLTQWARHKFQALNAEKCPHSKSNRNKVDMSVSTVDYEDYQ 1626



gi | 157266317 | ref | NP_001175.2 | SVTRFLDLIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1777
gi | 114589666 | ref | XP_516792.2 | SVTRFLDLIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1779
gi | 73990328 | ref | XP_534295.2 | SVTRFLDLIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1780
gi | 119885535 | ref | XP_581054.3 | SVTRFLDLIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1780
gi | 109483823 | ref | XP_001062084.1 | SVTRFLDLIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1772
gi | 292610566 | ref | XP_696163.4 | SVVAFNLNIPQDITLAVASFRSKAYTRAVMHFESFITEKKONIQEHGFLQKLYAAMHEPDGVAGVSAIRKAEPKSLKEQILEHESIGLLRDATAACYDRAIQLEPDIHYHGTVKSMGLGOLSTVITQVGVHANRSEWDELNTYRVEA 1776



gi | 157266317 | ref | NP_001175.2 | *****:*****:***: * **:*:*****:***:***: * **:*:***: * **:*:*****:*****:*****:*****: * .. * ***** 1924
gi | 114589666 | ref | XP_516792.2 | AWKLSQWDLVENVYLAADGKSTTWSVRLGQLLSAKKRDIITAFYDITLKLVRAEQIVPLSAASFERGSGYRGVEYIVRHLMLCELEHSIKPLFQHSPPGDSGC --EDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGEWC 1926
gi | 73990328 | ref | XP_534295.2 | AWKLSQWDLVENVYLAADGKSTTWSVRLGQLLSAKKRDIITAFYDITLKLVRAEQIVPLSAASFERGSGYRGVEYIVRHLMLCELEHSIKPLFQHSPPGDSGC --EDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGEWC 1927
gi | 119885535 | ref | XP_581054.3 | AWKLSQWDLVENVYLAADGKSTTWSVRLGQLLSAKKRDIITAFYDITLKLVRAEQIVPLSAASFERGSGYRGVEYIVRHLMLCELEHSIKPLFQHSPPGDSGC --EDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGEWC 1929
gi | 109483823 | ref | XP_001062084.1 | AWKLSQWDLVENVYLAADGKSTTWSVRLGQLLSAKKRDIITAFYDITLKLVRAEQIVPLSAASFERGSGYRGVEYIVRHLMLCELEHSIKPLFQHSPPGDSGC --EDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGEWC 1919
gi | 292610566 | ref | XP_696163.4 | AWKLSQWDLVENVYLAADGKSTTWSVRLGQLLSAKKRDIITAFYDITLKLVRAEQIVPLSAASFERGSGYRGVEYIVRHLMLCELEHSIKPLFQHSPPGDSGC --EDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGEWC 1926
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950



gi | 157266317 | ref | NP_001175.2 | *****:*****:***** :*:*:***:*****:*****:*****:*****: * **:*:***: * **:*:*****:*****:*****:*****: * **:*:***: 2074
gi | 114589666 | ref | XP_516792.2 | LOSARVARKAGHHQTAYNALLNAGESRLAELVVERAKWLWSKGDVHQALIVLQKGVLCFPENETPPEGKNMLIHGRAMLLVGRFMEEETANFESNAIMKKYKDVITACLPEWEDGHFYLAKYDKLMPMVTDNKMEKQGDRLIRYIVLHFGK 2076
gi | 73990328 | ref | XP_534295.2 | LOSARVARKAGHHQTAYNALLNAGESRLAELVVERAKWLWSKGDVHQALIVLQKGVLCFPENETPPEGKNMLIHGRAMLLVGRFMEEETANFESNAIMKKYKDVITACLPEWEDGHFYLAKYDKLMPMVTDNKMEKQGDRLIRYIVLHFGK 2077
gi | 119885535 | ref | XP_581054.3 | LOSARVARKAGHHQTAYNALLNAGESRLAELVVERAKWLWSKGDVHQALIVLQKGVLCFPENETPPEGKNMLIHGRAMLLVGRFMEEETANFESNAIMKKYKDVITACLPEWEDGHFYLAKYDKLMPMVTDNKMEKQGDRLIRYIVLHFGK 2077
gi | 109483823 | ref | XP_001062084.1 | LOSARVARKAGHHQTAYNALLNAGESRLAELVVERAKWLWSKGDVHQALIVLQKGVLCFPENETPPEGKNMLIHGRAMLLVGRFMEEETANFESNAIMKKYKDVITACLPEWEDGHFYLAKYDKLMPMVTDNKMEKQGDRLIRYIVLHFGK 2021
gi | 292610566 | ref | XP_696163.4 | LOSARVARKAGHHQTAYNALLNAGESRLAELVVERAKWLWSKGDVHQALIVLQKGVLCFPENETPPEGKNMLIHGRAMLLVGRFMEEETANFESNAIMKKYKDVITACLPEWEDGHFYLAKYDKLMPMVTDNKMEKQGDRLIRYIVLHFGK 2076
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100



gi | 157266317 | ref | NP_001175.2 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2224
gi | 114589666 | ref | XP_516792.2 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2226
gi | 73990328 | ref | XP_534295.2 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2227
gi | 119885535 | ref | XP_581054.3 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2227
gi | 109483823 | ref | XP_001062084.1 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2021
gi | 292610566 | ref | XP_696163.4 | SLOYGNQFIYQSMRMLTLWLDYGTAKAYEWEKAGRSRDRVOMRNDLGKINKVITTEHTNYLAPYQFLTAFSOLISRICSHSDEVFVLMETIAKVFVFLAYPQOAMWMMTAVSKSSYPMRVRNCKEILNKAIHMKKSLKPFVGDATRLTDKLLK 2226
.....2110.....2120.....2130.....2140.....2150.....2160.....2170.....2180.....2190.....2200.....2210.....2220.....2230.....2240.....2250



gi | 157266317 | ref | NP_001175.2 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2374
gi | 114589666 | ref | XP_516792.2 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2376
gi | 73990328 | ref | XP_534295.2 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2374
gi | 119885535 | ref | XP_581054.3 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2374
gi | 109483823 | ref | XP_001062084.1 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2021
gi | 292610566 | ref | XP_696163.4 | LCNKPVDGSSSTLSMSTHFKMLKLVVEEATFSEIILIPLOSVMIPITLPSILGTHANHASHEPPFGHWAYIAGFDDMVEILASLQPKPKISLKGSDGKGYIMMCKPKDDLKDKRDLMEFNSLINKCLRKDAESRRRELHIRTAVIPLNDEC 2373
.....2260.....2270.....2280.....2290.....2300.....2310.....2320.....2330.....2340.....2350.....2360.....2370.....2380.....2390.....2400



gi | 157266317 | ref | NP_001175.2 | *****:***:*****:***:..** 2524
gi | 114589666 | ref | XP_516792.2 | GIIEVWNTAGLRPILTKLYKEKGVYMTGKELRQCMLPKSAALSEKLVKVFREFLLPRHPPVFHEWFLRTPDPDTSWYSSRSAYCRSTAVMSMVGYLGLGDRHGENILFDSLIGECVHVDVDFNCLFNKGETFEVPEIVPFRLTHNMVNGMG 2526
gi | 73990328 | ref | XP_534295.2 | GIIEVWNTAGLRPILTKLYKEKGVYMTGKELRQCMLPKSAALSEKLVKVFREFLLPRHPPVFHEWFLRTPDPDTSWYSSRSAYCRSTAVMSMVGYLGLGDRHGENILFDSLIGECVHVDVDFNCLFNKGETFEVPEIVPFRLTHNMVNGMG 2524
gi | 119885535 | ref | XP_581054.3 | GIIEVWNTAGLRPILTKLYKEKGVYMTGKELRQCMLPKSAALSEKLVKVFREFLLPRHPPVFHEWFLRTPDPDTSWYSSRSAYCRSTAVMSMVGYLGLGDRHGENILFDSLIGECVHVDVDFNCLFNKGETFEVPEIVPFRLTHNMVNGMG 2524
gi | 109483823 | ref | XP_001062084.1 | GIIEVWNTAGLRPILTKLYKEKGVYMTGKELRQCMLPKSAALSEKLVKVFREFLLPRHPPVFHEWFLRTPDPDTSWYSSRSAYCRSTAVMSMVGYLGLGDRHGENILFDSLIGECVHVDVDFNCLFNKGETFEVPEIVPFRLTHNMVNGMG 2046
gi | 292610566 | ref | XP_696163.4 | GIIEVWNTAGLRPILTKLYKEKGVYMTGKELRQCMLPKSAALSEKLVKVFREFLLPRHPPVFHEWFLRTPDPDTSWYSSRSAYCRSTAVMSMVGYLGLGDRHGENILFDSLIGECVHVDVDFNCLFNKGETFEVPEIVPFRLTHNMVNGMG 2523
.....2410.....2420.....2430.....2440.....2450.....2460.....2470.....2480.....2490.....2500.....2510.....2520.....2530.....2540.....2550



gi | 157266317 | ref | NP_001175.2 | *****:***:*****:*****:*****:*****:*****:*****: * **:*:***: * **:*:*****:*****:*****:*****: * **:*:***: 2644
gi | 114589666 | ref | XP_516792.2 | PMGTEGLFRACEVIMRLMRDQREPLMSVLKIFLHDPVLEWSPKPVKGSKAPLNETGEVVEKAKTHVLDIEORLQGVIKTRNRVTGLPLSIEGHVHYLIQEAIDENLLCOMVIGWTPYM 2646
gi | 73990328 | ref | XP_534295.2 | PMGTEGLFRACEVIMRLMRDQREPLMSVLKIFLHDPVLEWSPKPVKGSKAPLNETGEVVEKAKTHVLDIEORLQGVIKTRNRVTGLPLSIEGHVHYLIQEAIDENLLCOMVIGWTPYM 2644
gi | 119885535 | ref | XP_581054.3 | PMGTEGLFRACEVIMRLMRDQREPLMSVLKIFLHDPVLEWSPKPVKGSKAPLNETGEVVEKAKTHVLDIEORLQGVIKTRNRVTGLPLSIEGHVHYLIQEAIDENLLCOMVIGWTPYM 2644
gi | 109483823 | ref | XP_001062084.1 | PMGTEGLFRACEVIMRLMRDQREPLMSVLKIFLHDPVLEWSPKPVKGSKAPLNETGEVVEKAKTHVLDIEORLQGVIKTRNRVTGLPLSIEGHVHYLIQEAIDENLLCOMVIGWTPYM 2166
gi | 292610566 | ref | XP_696163.4 | PMGTEGLFRACEVIMRLMRDQREPLMSVLKIFLHDPVLEWSPKPVKGSKAPLNETGEVVEKAKTHVLDIEORLQGVIKTRNRVTGLPLSIEGHVHYLIQEAIDENLLCOMVIGWTPYM 2643
.....2560.....2570.....2580.....2590.....2600.....2610.....2620.....2630.....2640.....2650.....2660.....2670

