

gi	73972017	ref	XP_538813.2	-----MTAIFKRDVGKRR-----	17
gi	194669741	ref	XP_613511.4	---MRLWSWVLRG---LLSAALGCGLAERPRRARRDPRAGRPPRXXXKXXXXXXXXXXCLGAGGMVGGLEGVVQEPPLSWLRGRS---SREPHFAPSAR---WASEG---LYDK	109
gi	59676577	ref	NP_067337.1	---MRLWSWVLRG---LLSAALGCGLAERPRRARRDPRAVRPPRPAAGPATCAARAARGRRAPPPPP---GGAWAVRPPRRRQRAARGAE---PPPSRALYFSGRGEOLRLRADLELPDAFTLQVWLRABGGOKSPAVITGLYDK	140
gi	62649105	ref	XP_233037.3	---MRLWSWVLRG---LLSAALGCGLAERPRRARRDPRAVRPPRPAAGPATCAARAARGRRAPPPPP---GGAWAVRPPRRRQRAARGAE---PPPSRALYFSGRGEOLRLRADLELPDAFTLQVWLRABGGOKSPAVITGLYDK	140
gi	38045915	ref	NP_002572.2	---MRLWSWVLRG---LLSAALGCGLAERPRRARRDPRAGRPPRPAAGPATCAARAARGRRAPPPPPPPGGAWAVRPPRRRQRAARGAE---PPPSRALYFSGRGEOLRLRADLELPDAFTLQVWLRABGGOKSPAVITGLYDK	143
gi	118099221	ref	XP_415522.2	-----MDERSRRARRDTRHSR---OLLYTAPGTCARLARGRRS---TAGLEPG---HVPRRRQREVEDGEE---SLTPSRALYFSGGDLRLKADLELPDAFTLQVWLRABGGOKSPAVITGLYDK	113
gi	292614317	ref	XP_001919115.2	MKLLPICWLLCL---LFLVCLGSECGT---PRRIVRSKRDLDVIRREARS---PGACATRLPRGKRS---LPGIDR---RSPG---LQOAGES---PGRRRAYVFFGRGDQLRLKPNAEVPRANFTLEMMWIKPF---LYDK	122
gi	292629532	ref	XP_694455.3	MKLLPICWLLCL---LFLVCLGSECGT---PRRIVRSKRDLDVIRREARS---PGACATRLPRGKRS---LPGIDR---RSPG---LQOAGES---PGRRRAYVFFGRGDQLRLKPNAEVPRANFTLEMMWIKPF---LYDK	122
gi	292630193	ref	XP_002667774.1	---MKVWVFLQCLAILLVLLCVGSECGT---VLRNTRSKRELVKIREAKLVF---PGACGTRLPGRKRS---LPGMDR---RIPRRRRSSPTEDA---SRGKAVYFFGRGDQLRLKPGVEIPKGNFTLGMVWKAEG---LFDK	125



gi	73972017	ref	XP_538813.2	CSYTSRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	165
gi	194669741	ref	XP_613511.4	CSYASRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	257
gi	59676577	ref	NP_067337.1	CSYTSRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	288
gi	62649105	ref	XP_233037.3	CSYTSRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	288
gi	38045915	ref	NP_002572.2	CSYTSRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	291
gi	118099221	ref	XP_415522.2	CSYTSRDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	263
gi	292614317	ref	XP_001919115.2	CFYASDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	271
gi	292629532	ref	XP_694455.3	CFYASDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	271
gi	292630193	ref	XP_002667774.1	CFYASDRGWVVGIHTVSDQGNRDRPYFFSLKTDARARVTTINAHRSYVPGQVWHLAAIYDGRMLKLYMGAOVATSGEIVGGIFPLTKCKVLMGGSSALNFRGVIHLSLWKVARTOREVLLDME--HCLHAPLPOLLLOENWD	273



gi	73972017	ref	XP_538813.2	NVKRTWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	313
gi	194669741	ref	XP_613511.4	NVKRAWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	405
gi	59676577	ref	NP_067337.1	NVKRTWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	436
gi	62649105	ref	XP_233037.3	NVKRTWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	436
gi	38045915	ref	NP_002572.2	NVKRTWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	439
gi	118099221	ref	XP_415522.2	NVKRTWSPMKDGHMPHVEV---GAGFLLDTSLEPPLCGQTLCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	411
gi	292614317	ref	XP_001919115.2	NMSRRWLVTKDGSFPERLEHSDRSLASDLSLTKPPACGQTVCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	421
gi	292629532	ref	XP_694455.3	NMSRRWLVTKDGSFPERLEHSDRSLASDLSLTKPPACGQTVCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	421
gi	292630193	ref	XP_002667774.1	HPARKWLVTKDGSFPERLEHSDRSLASDLSLTKPPACGQTVCDNTEVIASYNQLPFRFRPKVRYRVVLLRDDRENPVSRQIDFOHROLADAFKHYNISWELQVLEVSNSSLRRLVLANCDISKIGDNCDEHCNHTLGHDDGD	422



gi	73972017	ref	XP_538813.2	CR---NLRHPAFVKKQHNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	459
gi	194669741	ref	XP_613511.4	CR---HLRHPAFVKKQHNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	551
gi	59676577	ref	NP_067337.1	CR---QLRYPAFMKKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	582
gi	62649105	ref	XP_233037.3	CR---QLRYPAFMKKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	582
gi	38045915	ref	NP_002572.2	CR---HLRHPAFVKKQHNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	585
gi	118099221	ref	XP_415522.2	CR---HVRHTLFNKKKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	557
gi	292614317	ref	XP_001919115.2	CR---RQIARCPENKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	567
gi	292629532	ref	XP_694455.3	CR---RQIARCPENKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	567
gi	292630193	ref	XP_002667774.1	CKPRPEKREKCPENKQNGVCDMDCNERYFNDFDGGECCEPPIIDVTKTCFDPDSPHRAYLDVNEKLNILRLDGSHTLNIFFANSSDEELAGVAWPDWKEALMHLGGIVLNPFSFYGPHTHTMIHEIGHSLGLYHIFRGISEIQCSD	572



gi	73972017	ref	XP_538813.2	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	609
gi	194669741	ref	XP_613511.4	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	701
gi	59676577	ref	NP_067337.1	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	732
gi	62649105	ref	XP_233037.3	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	732
gi	38045915	ref	NP_002572.2	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	717
gi	118099221	ref	XP_415522.2	PCMETEPSFETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	707
gi	292614317	ref	XP_001919115.2	ACLETEPSLETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	717
gi	292629532	ref	XP_694455.3	ACLETEPSLETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	717
gi	292630193	ref	XP_002667774.1	ACLETEPSLETGDLCSDTNPAKHKFCGDPGGNDTCGFHSFFNTPNYNNFMSYADDDCDSFTPNQVARMHCYLLDLYQGWOPSRKPAVALAPQVGHITNSVLEWFPFNILWDRLEGSACELCEGRILVQYAFNASSPMPGCPG	710



gi | 73972017 | ref | XP\_538813.2 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 757  
gi | 194669741 | ref | XP\_613511.4 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCHLDLRFYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 849  
gi | 59676577 | ref | NP\_067337.1 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 880  
gi | 62649105 | ref | XP\_233037.3 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 880  
gi | 38045915 | ref | NP\_002572.2 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 883  
gi | 118099221 | ref | XP\_415522.2 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 857  
gi | 292614317 | ref | XP\_001919115.2 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 864  
gi | 292629532 | ref | XP\_694455.3 | GHWSPREAEAGHPDVEQPCCKSSVRTWSPNSAVNPHIVPPACPEPGCCYLELEFRYPLVPEESLIWVTFVSTDWDSSGAVNDIKLLTVSGKNIISLGPONVFCVDPVPLTIKLRD--VGEVSVGCIQIYTLDEHLEIDAAMLTSIADSPCLCECKP 864  
gi | 292630193 | ref | XP\_002667774.1 | -----EFRGPPDVEQACEPSEVHWSPHNGMDLGLVPP-PPCPLGCMLOLEFAYAVVPPDLSLWVWVFFSSQDETVLPAIHNIILLVGGNNLSLGPNSLFCIDPLTIKLRD--QEKVYGVQFYTMEOHLEIDAALLTSKPKDCLCGDCEP 850  
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



gi | 73972017 | ref | XP\_538813.2 | LQYKVVDRDPPPLH-VDVASLLH-LHRRFTDIDLSTGTYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 905  
gi | 194669741 | ref | XP\_613511.4 | LQYKVVDRDPPPLQ-VDVASLLH-FSRRFTDIDLSTGTYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 997  
gi | 59676577 | ref | NP\_067337.1 | LQYKVVDRDPPPLH-EDVASLLH-LNRRFMDIDLSTGTYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1028  
gi | 62649105 | ref | XP\_233037.3 | LQYKVVDRDPPPLH-DDVGSLLH-LNRRFMDIDLSTGTYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1028  
gi | 38045915 | ref | NP\_002572.2 | LQYKVVDRDPPPLQ-MDVASLLH-LNRRFMDIDLSTGTYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1031  
gi | 118099221 | ref | XP\_415522.2 | LQYKVVDRDPPFQ-SGSPVILSNLRRFIDMELSDSITTYVQVIVVSGAESESPSPALVLIHSGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1006  
gi | 292614317 | ref | XP\_001919115.2 | LRYRLLRQPPFTSHPGIIITQEPFLRYERDRDINDETYYHVLVSRRAESESPPLVQLGSPYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1014  
gi | 292629532 | ref | XP\_694455.3 | LRYRLLRQPPFTSHPGIIITQEPFLRYERDRDINDETYYHVLVSRRAESESPPLVQLGSPYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1014  
gi | 292630193 | ref | XP\_002667774.1 | LHFRLLRQPPFSNSKQGIIMLSDSTRYTRDRDVEYGGIITTYVQVIVVSRSESESPSPALVLIHSGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1000  
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi | 73972017 | ref | XP\_538813.2 | C-DQCCPGWVIGGPAASQVCRITKVIDLSEGISQHWAYPCTIISYPYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1054  
gi | 194669741 | ref | XP\_613511.4 | C-DQCCPGWVIGGPAASQVCRITKVIDLSEGISQHWAYPCTIISYPYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1145  
gi | 59676577 | ref | NP\_067337.1 | C-DQCCPGWVIGGPAASQVCRITKVIDLSEGISQHWAYPCTIISYPYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1176  
gi | 62649105 | ref | XP\_233037.3 | C-DQCCPGWVIGGPAASQVCRITKVIDLSEGISQHWAYPCTIISYPYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1176  
gi | 38045915 | ref | NP\_002572.2 | C-DQCCPGWVIGGPAASQVCRITKVIDLSEGISQHWAYPCTIISYPYVYVWVITISGSESESPSPAAIYIHGSGYCGDGIIOKSGEECDMMKNGDGCISLFCROEDSFNCIDEPSCRYFHDGDGVCCEFEQKTSIKDCGVYTPQGFLDQWASNAVS 1179  
gi | 118099221 | ref | XP\_415522.2 | HSDQCCPGWVIGGPAATQCRITKVIDLNDGVSQYAWPFCESQ--SWT--YWLKAYAHPMVAAAVIHLAADGTADMDTCHNITVHLVDIKDTHPLGDSRLSCRNNPLVIVPVDLVAFAVYRTKAIIVSFSPLVAISGVGLR 1155  
gi | 292614317 | ref | XP\_001919115.2 | EBAIHCPAEVAAGYPAVTKSCQSKVFDLHSGVSQYAWPFCESQ--SWT--YWLKAYAHPMVAAAVIHLAADGTADMDTCHNITVHLVDIKDTHPLGDSRLSCRNNPLVIVPVDLVAFAVYRTKAIIVSFSPLVAISGVGLR 1159  
gi | 292629532 | ref | XP\_694455.3 | EBAIHCPAEVAAGYPAVTKSCQSKVFDLHSGVSQYAWPFCESQ--SWT--YWLKAYAHPMVAAAVIHLAADGTADMDTCHNITVHLVDIKDTHPLGDSRLSCRNNPLVIVPVDLVAFAVYRTKAIIVSFSPLVAISGVGLR 1159  
gi | 292630193 | ref | XP\_002667774.1 | EERLYCPADVAAGYPATIKSCSNVVDLADGVSQYAWPFCESQ--SWT--YWLKAYAHPMVAAAVIHLAADGTADMDTCHNITVHLVDIKDTHPLGDSRLSCRNNPLVIVPVDLVAFAVYRTKAIIVSFSPLVAISGVGLR 1147  
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 73972017 | ref | XP\_538813.2 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1204  
gi | 194669741 | ref | XP\_613511.4 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1295  
gi | 59676577 | ref | NP\_067337.1 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1326  
gi | 62649105 | ref | XP\_233037.3 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1326  
gi | 38045915 | ref | NP\_002572.2 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1329  
gi | 118099221 | ref | XP\_415522.2 | SFDNFDPTLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1305  
gi | 292614317 | ref | XP\_001919115.2 | SFQYFDPITLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1309  
gi | 292629532 | ref | XP\_694455.3 | SFQYFDPITLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1183  
gi | 292630193 | ref | XP\_002667774.1 | SFQYFDPITLSSCORGETYSABEQSCVHFACAAADCPCLAVENASLNCSSSDRYHGAOCTVSCRYGVVLOIQRDDELIKSQVGPSTVIVCTEGKWNKQVACEPDCGIPDQHHVYAAFSCLKGTTFGSKCSFCRHPAOLKGNNSLLTC 1297  
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 73972017 | ref | XP\_538813.2 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1346  
gi | 194669741 | ref | XP\_613511.4 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1437  
gi | 59676577 | ref | NP\_067337.1 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1468  
gi | 62649105 | ref | XP\_233037.3 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1468  
gi | 38045915 | ref | NP\_002572.2 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1471  
gi | 118099221 | ref | XP\_415522.2 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1447  
gi | 292614317 | ref | XP\_001919115.2 | MEDGMWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1449  
gi | 292629532 | ref | XP\_694455.3 | MEDGMWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1183  
gi | 292630193 | ref | XP\_002667774.1 | MEDGLWSPPEALCELMCLAPPPVPAADLQATRCRENKHKVGSFCKYKCKPGYHVPVGSRRKSKRAFKTQCTODGSWEGACVPTCDPPPKFHLGYCTNGFQNSFCRIKCEDSD-----AAGRGSNIHCRKDGTVSGSFHLC 1444  
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi		73972017		ref		XP_538813.2		QEMGGCCSAPDQNSNLKLLQCPGEGAIGSECVTISCLDHNSEIILPVNVIVRDIP--HWLNPTRVERVVC TAGLKWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCASTVKTKKVI PFPMSCDLQGDCA CRDPQAQEHSRK	1494
gi		194669741		ref		XP_613511.4		QEMGGCCSAPDQNSNLKLLQCPGEGAIGSECVTISCLDHNSEIILPVNVIVRDIP--HWLNPTRVORVVC TAGLKWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCASTVKTKKVI PFPMSCDLQGDCA CRDPQAQEHSRK	1585
gi		59676577		ref		NP_067337.1		REMGGCCSAPNQLNSHLKLLQCPDGYAIGSECAISCLDHNSEIILPVNLIVRDIP--HWMNPTRVORIVC TAGLQWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCSTVKTKKVI PFPMSCDLQDDCA CRDPQAQEHNRK	1616
gi		62649105		ref		XP_233037.3		REMGGCCSAPNQLNSHLKLLQCPDGYAIGSECAISCLDHNSEIILPVNLIVRDIP--HWMNPTRVORIVC TAGLQWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCSTVKTKKVI PFPMSCDLQDDCA CRDPQAQEHNRK	1616
gi		38045915		ref		NP_002572.2		QEMGGCCSVPNELNSHLKLLQCPDGYAIGSECATSCLDHNSEIILPMNVIVRDIP--HWLNPTRVERVVC TAGLKWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCSTVKTKKVI PFPMSCDLQGDCA CRDPQAQEHSRK	1619
gi		118099221		ref		XP_415522.2		REMGGCCALPTQLNSHLKLLQCSGGYGIGAECTISCLDHSHPEILLRNEIVODIQ--HWMNPQRVKSVC TAGLKWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCASTVKTKKVI PFPMSCDLQGECA CRDPQAQEHNRK	1595
gi		292614317		ref		XP_001919115.2		PNLTGCCSLPQNLSPNIHLSCKDGHGIGKEEVS CRDASSVVLVPSNMSVAAVMKDHWNPVKVIVC IMGLKWYHPALIHCVKGCPEPFMGDNYCDAINNRAFCNYDGGDCCSTVKTKKVI PFPMSCDLREDCACRDPQAQENK	1599
gi		292629532		ref		XP_694455.3		-----	1183
gi		292630193		ref		XP_002667774.1		PQLKGGCSLPPQNLHPSTIRISCKKGGHIGEECELS CRDSSNDVVILPGNMTTSSIMRHHWMPKVK-----	1510
								.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650	



gi		73972017		ref		XP_538813.2		DLRGYSHG	1502
gi		194669741		ref		XP_613511.4		DLRGYSHG	1593
gi		59676577		ref		NP_067337.1		DLRGYSHG	1624
gi		62649105		ref		XP_233037.3		DLRGYSHG	1624
gi		38045915		ref		NP_002572.2		DLRGYSHG	1627
gi		118099221		ref		XP_415522.2		DLRGFSLG	1603
gi		292614317		ref		XP_001919115.2		ARHRIG-	1606
gi		292629532		ref		XP_694455.3		-----	1183
gi		292630193		ref		XP_002667774.1		-----	1510
								.....	

