

gi | 15232129 | ref | NP_189364.1 | -MGSQQVAISFLTNLAKAAPFLG--VAATALNSLIVDGGERRAVLFDLFRGVLDDQVGEETHFLIPILQPHIYDIRTKPHTFSKSGTKDLMQVNLTLRVLHRPEVSRPLPIYFQTLGLLEYDEKVLPSIGNEVLKAVVAQFNADQLLT 146
gi | 15237488 | ref | NP_198893.1 | -MGSQQAAVSVFLSNLAKAAPFLG--TAATVLTSLFVTDGGERAVLFDLFRGVMQTVGEGTHFLIPILORPHIFDIRTKPHTFSSTSGTKDLMQVNLTLRVLHRPEVSRPLPIYFQTLGLLEYDEKVLPSIGNEVLKAVVAQFNADQLLT 146
gi | 115446913 | ref | NP_001047236.1 | MAGGQQAASLLTKLAQAAAGL--IAASAASLALYVTDGGERAVLFDLFRGVLPEPTEGTHFLIPVWLOKPPFIDIRTRPHSFSSTSGTKDLMQVNLTLRVLHRPEVSRPLPIYFQTLGLLEYDEKVLPSIGNEVLKAVVAQFNADQLLT 147
gi | 115458812 | ref | NP_001053006.1 | MAGG-PAAVSVFLTNIAKAAAGL--AAASLLSASLYVTDGGERAVLFDLFRGVLPEPTEGTHFLIPVWLOKPPFIDIRTRPHSFSSTSGTKDLMQVNLTLRVLHRPEVSRPLPIYFQTLGLLEYDEKVLPSIGNEVLKAVVAQFNADQLLT 146
gi | 6321571 | ref | NP_011648.1 | ----MSN⁶AKLIDVITKVALPIG--IIASGIQYSMYDVGKGRVIFDRINGVKKQVVVGEETHFLVWPKAIIVDVRTPKPSIATNTGTKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 143
gi | 50307599 | ref | XP_453779.1 | ----MS--RVADVMARIAIPIG--LVYSALQYSMYDVRGGHRAVIFDRQVGVQAVIGEGTHFLVWPKSILFDIRTPKPNIAATNTGTKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 140
gi | 45198831 | ref | NP_985860.1 | ----MS--RLADSLVRLTLP¹LPIALAFSAVQFSMYDVRGGTRAIIFDRISGVKDDVVEGTHFLIPWLOKAIIFDVRTPKPNIAATNTGTKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 143
gi | 145603508 | ref | XP_369460.2 | ----MA--ASQFRLLP-FLAGAGA--LAFATAQASLYDKGGTRAVIFDRISGVKDDVVEGTHFLIPWLOKAIIFDVRTPKPNIAATNTGSKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 140
gi | 32421789 | ref | XP_331338.1 | ----MA--ARGLDMITKFAIPAT--VGVALLQNSIYDVRGGSRVIFDRVAGVKDITVNVNEGTHFLIPWLOKAIIFDVRTPKPIIPTT¹GSKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 19115625 | ref | NP_594713.1 | ----MA--VVLERVARVIAIPIG--IGFTLLQSSIYDVPGGKRAVIFDRISGVKQVVVGEETHFLIPWLOKAIIVDVRTPRPNIAATNTGSKDLMQVSLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 140
gi | 24585147 | ref | NP_476607.2 | ----MA--A¹QFFNRIQMGGLGVA--VLGGVNSALYNVGGHRAVIFDRFTGIKENNVVGEETHFFIPWVORPIIFDIRSQPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 158288134 | ref | XP_309992.2 | ----MA--TQFLNRIGQLGLGVA--VIGGVNSALYNVDGGHRAVIFDRFSGVKQVVVGEETHFFVWVORPIIFDIRSQPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 4505773 | ref | NP_002625.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 114666277 | ref | XP_001172487.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 77736091 | ref | NP_001029744.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 6679299 | ref | NP_032857.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 62664759 | ref | XP_579541.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAAT--DRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 136
gi | 57037802 | ref | XP_541546.1 | ----MA--TKVFSIDKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 50760715 | ref | XP_418103.1 | ----MA--AKVFSIGKFGGLALA--VAGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 141
gi | 41152028 | ref | NP_958454.1 | ----M--AKLFSIGKFGGLALA--IGGGVNSALYNVDAGHRAVIFDRFRGVQDIVVGEETHFLIPWVOKPIIFDCRSRPRNVVPIGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 140
gi | 17509869 | ref | NP_490929.1 | -MAASA-QKLLGRGLTVGVGLS--IAGGLIAQALYNVDGGQRAVIFDRFSGVKNEVVEGTHFLIPWVOKPIIFDIRTPKRAVITNTGSKDLMQVNLTLRVLHRPEVSLQPAIYNQNLGLDYDERVLPISIGNEVLKAVVAQFNADQLLT 144
gi | 124512202 | ref | XP_001349234.1 | ----MERILLSSIGKLSVAG--GLSLIPIYTFIVDVGGERVCMFNRFGGVSENT¹FGEGSHFVVPWF¹TPVIYDIKMKPKVINIT¹GT¹RDLD¹IV¹TS¹LRLLFRPH¹QHL¹PLYLHST¹LG¹PDY¹DERVLPISIGNEVLKAVVAQFNADQLLT 140
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 15232129 | ref | NP_189364.1 | ERFPQVSALVRDALIKRAREFNIELDDIAITHLSYGAEFSRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFNLPGR--- 279
gi | 15237488 | ref | NP_198893.1 | ERPHVVALVRSLITRAKDFNIVLDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 277
gi | 115446913 | ref | NP_001047236.1 | ERPHVVALVRSLITRAKDFNIVLDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 282
gi | 115458812 | ref | NP_001053006.1 | ERPHVVALVRDALIRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 284
gi | 6321571 | ref | NP_011648.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 287
gi | 50307599 | ref | XP_453779.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 226
gi | 45198831 | ref | NP_985860.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 283
gi | 145603508 | ref | XP_369460.2 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 275
gi | 32421789 | ref | XP_331338.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 276
gi | 19115625 | ref | NP_594713.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 282
gi | 24585147 | ref | NP_476607.2 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 276
gi | 158288134 | ref | XP_309992.2 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 4505773 | ref | NP_002625.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 114666277 | ref | XP_001172487.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 77736091 | ref | NP_001029744.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 6679299 | ref | NP_032857.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 62664759 | ref | XP_579541.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 253
gi | 57037802 | ref | XP_541546.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 50760715 | ref | XP_418103.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
gi | 41152028 | ref | NP_958454.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 271
gi | 17509869 | ref | NP_490929.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 275
gi | 124512202 | ref | XP_001349234.1 | QREIVSQIRIRAE¹LKRAREFNIELDDVAITHLSYGVFESRAVEAKQVAQ¹EAERSK¹VFVMKAD¹ERRAAVIRAE¹GESEAAQLISDA¹AKAGMGLIELRRIEASREVAATLARS-PNVAVLPGGQ-----MLFALNR--- 272
160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi		15232129		ref		NP_189364.1		-----	279
gi		15237488		ref		NP_198893.1		-----	277
gi		115446913		ref		NP_001047236.1		-----	282
gi		115458812		ref		NP_001053006.1		-----	293
gi		6321571		ref		NP_011648.1		-----	287
gi		50307599		ref		XP_453779.1		-----	226
gi		45198831		ref		NP_985860.1		-----	283
gi		145603508		ref		XP_369460.2		-----	275
gi		32421789		ref		XP_331338.1		-----	276
gi		19115625		ref		NP_594713.1		-----	282
gi		24585147		ref		NP_476607.2		-----	276
gi		158288134		ref		XP_309992.2		-----	272
gi		4505773		ref		NP_002625.1		-----	272
gi		114666277		ref		XP_001172487.1		-----	272
gi		77736091		ref		NP_001029744.1		-----	272
gi		6679299		ref		NP_032857.1		-----	272
gi		62664759		ref		XP_579541.1		-----	253
gi		57037802		ref		XP_541546.1		-----	272
gi		50760715		ref		XP_418103.1		-----	272
gi		41152028		ref		NP_958454.1		-----	271
gi		17509869		ref		NP_490929.1		-----	275
gi		124512202		ref		XP_001349234.1		-----	272
								
