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gi|114596393|ref|XP_001153672.1|
gi|118089891|ref|XP_420447.2|
gi|73977942|ref|XP_867720.1|
gi|115495821|ref|NP_001069717.1|
gi|21218434|ref|NP_536353.2|
gi|292609708|ref|XP_693393.4|
gi|158294047|ref|XP_315369.4|
gi|17737533|ref|NP_523922.1|
gi|71995913|ref|NP_001023975.1|

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

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gi|16117781|ref|NP_361014.1| -----
gi|114596393|ref|XP_001153672.1| -----
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gi|73977942|ref|XP_867720.1| -----
gi|115495821|ref|NP_001069717.1| -----
gi|21218434|ref|NP_536353.2| -----
gi|292609708|ref|XP_693393.4| -----
gi|158294047|ref|XP_315369.4| ASVLRAAENTIEDDDNPLEQEGQGQHDAAAAVERDEEELLLDVQSMDAIERRDFEQEGGLIRNRNLISGDRNLNEFVINNTNARPAVNERRFAEQQPSAEAGLQAGLITATNAVSTNELLPAVEAAAAPTSQAQHTTPTSSRQKHDPH
gi|17737533|ref|NP_523922.1| QGFFN-EDNEDPPVVCLINDDDEEPPEEDEDDEELEDIEDEDAVDIVVGAISCPNISOLALADGTIMADGSKIFLETPVVEEAQPHPGCVITGOSQELKGPKRLSDEFLLGEEDQAENLALGRCIKSPEBVNPVDDNPSEGDDGA
gi|71995913|ref|NP_001023975.1| -----
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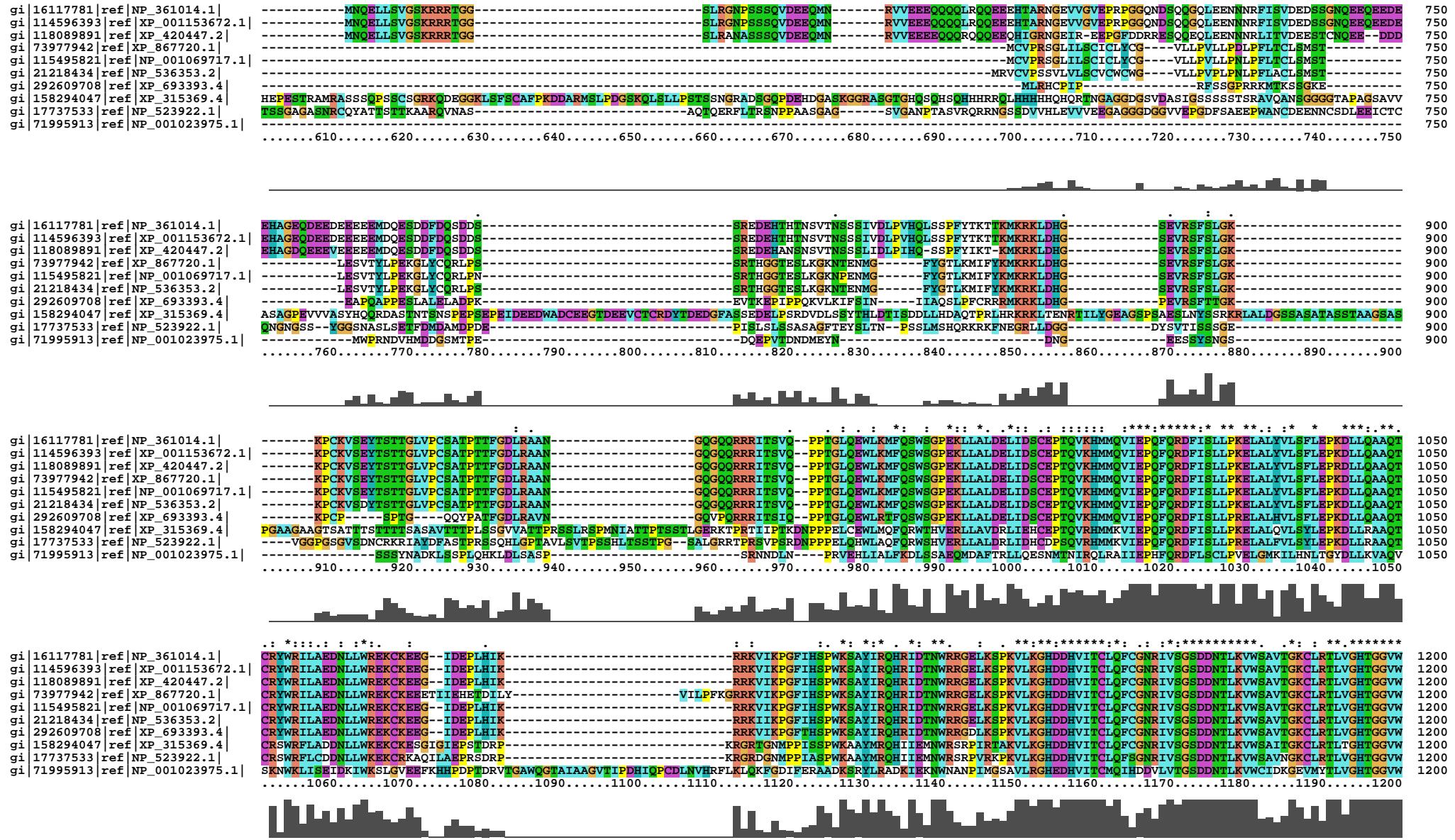
gi|16117781|ref|NP_361014.1| -----
gi|114596393|ref|XP_001153672.1| -----
gi|118089891|ref|XP_420447.2| -----
gi|73977942|ref|XP_867720.1| -----
gi|115495821|ref|NP_001069717.1| -----
gi|21218434|ref|NP_536353.2| -----
gi|292609708|ref|XP_693393.4| -----
gi|158294047|ref|XP_315369.4| -----
gi|17737533|ref|NP_539221.1| -----
gi|71995913|ref|NP_001023975.1| -----
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310 320 330 340 350 360 370 380 390 400 410 420 430 440 450

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gi|16117781|ref|NP_361014.1| -----
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gi|115495821|ref|NP_001069717.1| -----
gi|21218434|ref|NP_536353.2| -----
gi|292609708|ref|XP_693393.4| -----
gi|158294047|ref|XP_315369.4| -----
gi|17737533|ref|NP_529221.1| -----
gi|71995913|ref|NP_001023975.1| -----
ALPEECKPAAELAEAFNLANNSNDEV--SSGRSLFVGVHTEVEEAAI|AVDVKTEEEEHHI|HHDDPCCSSSTSASYESSSSPLPSQTATAQHAEDVMSICSSAALPTTAHSASSVSAHDESTLTSAAHNDGKPLCDGEADEGDD
PTSSRKYINSLRSKSIAKLNLGSSILGASSCSQHRSGSTSKMSESTCTGAARIDVVTNTNSNDYPSLATTSGSSSTGGCQODI-----ENVVASVSYSVSGQTOSQSGCRTTAIN----PTAACSTGSACLGDQSASTSAS

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gi	16117781   ref   NP_361014.1	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPNKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTKTGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
gi	114596393   ref   XP_001153672.1	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPNKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTKTGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
gi	118089891   ref   XP_420447.2	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPNKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTKTGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
gi	73977942   ref   XP_867720.1	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPNKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTKTGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
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gi	21218434   ref   NP_536353.2	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPNKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTKTGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
gi	292609708   ref   XP_693393.4	---	NCIHTLGHQSLSGMELKDNLILVSGNADSTVKIWDIKTGOCLOTLGPHQKHOQSAVTCLQFN--	KNFVITSSDDGTVKLWDLTRIGEFIRNLVLIESGGSGGVWRIRASNLKLCVAVSRNGEETKLVLVDFDVDMK--	1495
gi	158294047   ref   XP_315369.4	---	SCKHALMGHQSLTSGMELRQLILVSGNADSTVKVWDITTGOCLOTLGSPNKHQSAVTCLQFN--	SRFVITSSDDGTVKLWDLVKTGOCLOTLGSPNKHQSAVTCLQFN--	1495
gi	17737533   ref   NP_532922.1	---	NCKHTLMGHQSLTSGMELRQLILVSGNADSTVKVWDITTGOCLOTLGSPNKHQSAVTCLQFN--	SRFVITSSDDGTVKLWDLVKTGDFIRNLVALDSGGSGGVWRIRANDEKLCIACVSRNGEETKLMLVDFDVGAVCAVCKS	1495
gi	71995913   ref   NP_001023975.1	EGGECVALLOGTSLSGMQLRGNLILVSGNADSHVRVWDLTHEGTCVHMLSG--	HRSAITSLQWFGRNMVATSSDDGTVKLWDLIERGALIRDVLTDGGNGGCIWRLCSISMLACAVSRNGEETKLVLFFDADYLP--	1495	

