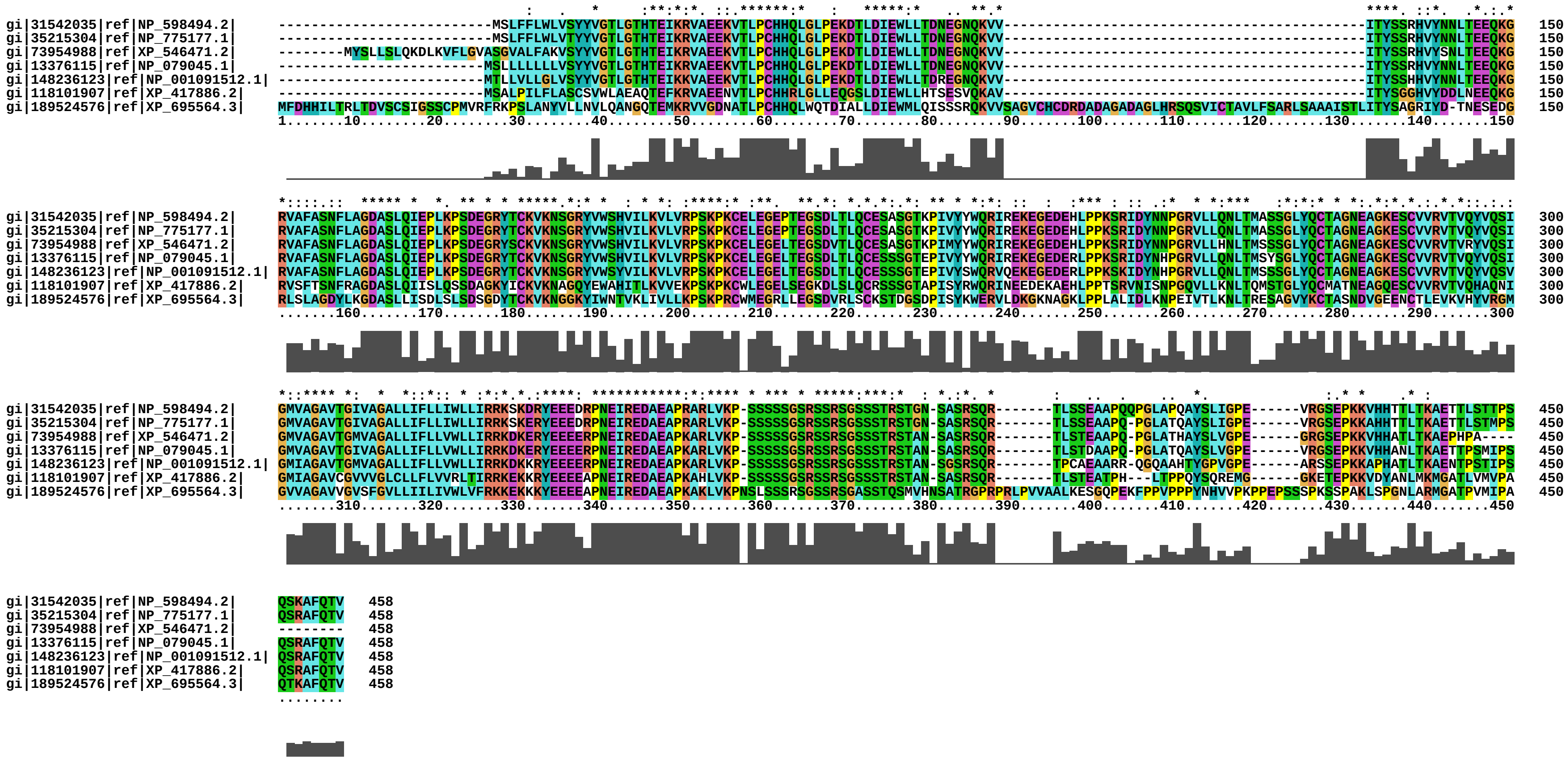

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                                                               :   .   *     :**:*:*. ::.******:*   :   *****:*   .. **.*                                            ****. ::*.  .*.:.*
gi|31542035|ref|NP_598494.2|     --------------------------MSLFFLWLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV--------------------------------------------ITYSSRHVYNNLTEEQKG   150
gi|35215304|ref|NP_775177.1|     --------------------------MSLFFLWLVTYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV--------------------------------------------ITYSSRHVYNNLTEEQKG   150
gi|73954988|ref|XP_546471.2|     --------MYSLLSLQKDLKVFLGVASGVALFAKVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV--------------------------------------------ITYSSRHVYSNLTEEQKG   150
gi|13376115|ref|NP_079045.1|     -------------------------MSLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV--------------------------------------------ITYSSRHVYNNLTEEQKG   150
gi|148236123|ref|NP_001091512.1| -------------------------MTLLVLLGLVSYYVGTLGTHTEIKKVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDREGNQKVV--------------------------------------------ITYSSHHVYNNLTEEQKG   150
gi|118101907|ref|XP_417886.2|    -------------------------MSALPILFLASCSVWLAEAQTEFKRVAEENVTLPCHHRLGLLEQGSLDIEWLLHTSESVQKAV--------------------------------------------ITYSGGHVYDDLNEEQKG   150
gi|189524576|ref|XP_695564.3|    MFDHHILTRLTDVSCSIGSSCPMVRFRKPSLANYVLLNVLQANGQTEMKRVVGDNATLPCHHQLWQTDIALLDIEWMLQISSSRQKVVSAGVCHCDRDADAGADAGLHRSQSVICTAVLFSARLSAAAISTLITYSAGRIYD-TNESEDG   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                 *::::.::  ***** *  *. ** * * *****.*:* *  : * *: :****:* :**.  **.*: *.*.*:.*: ** * *:*: ::  :  :*** : :: .:*  * *:***   :*:*:* * *:.*:*.*.:.*.*::.:.:
gi|31542035|ref|NP_598494.2|     RVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGEPTEGSDLTLQCESASGTKPIVYYWQRIREKEGEDEHLPPKSRIDYNNPGRVLLQNLTMASSGLYQCTAGNEAGKESCVVRVTVQYVQSI   300
gi|35215304|ref|NP_775177.1|     RVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGEPTEGSDLTLQCESASGTKPIVYYWQRIREKEGEDEHLPPKSRIDYNNPGRVLLQNLTMASSGLYQCTAGNEAGKESCVVRVTVQYVQSI   300
gi|73954988|ref|XP_546471.2|     RVAFASNFLAGDASLQIEPLKPSDEGRYSCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELTEGSDVTLQCESASGTKPIMYYWQRIREKEGEDEHLPPKSRIDYNNPGRVLLHNLTMSSSGLYQCTAGNEAGKESCVVRVTVRYVQSI   300
gi|13376115|ref|NP_079045.1|     RVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSI   300
gi|148236123|ref|NP_001091512.1| RVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSYVILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYSWQRVQEKEGEDERLPPKSKIDYNHPGRVLLQNLTMSSSGLYQCTAGNEAGKESCVVRVTVQYVQSV   300
gi|118101907|ref|XP_417886.2|    RVSFTSNFRAGDASLQIISLQSSDAGKYICKVKNAGQYEWAHITLKVVEKPSKPKCWLEGELSEGKDLSLQCRSSSGTAPISYRWQRINEEDEKAEHLPPTSRVNISNPGQVLLKNLTQMSTGLYQCMATNEAGQESCVVRVTVQHAQNI   300
gi|189524576|ref|XP_695564.3|    RLSLAGDYLKGDASLLISDLSLSDSGDYTCKVKNGGKYIWNTVKLIVLLKPSKPRCWMEGRLLEGSDVRLSCKSTDGSDPISYKWERVLDKGKNAGKLPPLALIDLKNPEIVTLKNLTRESAGVYKCTASNDVGEENCTLEVKVHYVRGM   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                 *::**** *:  *  *::*:: * :*:*.*.:****: ***********:*:**** * *** * *****:***:*  : *.:*. *       :   ..  .    ..  *.              :.* *    .* :
gi|31542035|ref|NP_598494.2|     GMVAGAVTGIVAGALLIFLLIWLLIRRKSKDRYEEEDRPNEIREDAEAPRARLVKP-SSSSSGSRSSRSGSSSTRSTGN-SASRSQR-------TLSSEAAPQQPGLAPQAYSLIGPE------VRGSEPKKVHHTTLTKAETTLSTTPS   450
gi|35215304|ref|NP_775177.1|     GMVAGAVTGIVAGALLIFLLIWLLIRRKSKERYEEEDRPNEIREDAEAPRARLVKP-SSSSSGSRSSRSGSSSTRSTGN-SASRSQR-------TLSSEAAPQ-PGLATQAYSLIGPE------VRGSEPKKAHHTTLTKAETTLSTMPS   450
gi|73954988|ref|XP_546471.2|     GMVAGAVTGMVAGALLIFLLVWLLIRRKDKERYEEEERPNEIREDAEAPKARLVKP-SSSSSGSRSSRSGSSSTRSTAN-SASRSQR-------TLSTEAAPQ-PGLATHAYSLVGPE------GRGSEPKKVHHATLTKAEPHPA----   450
gi|13376115|ref|NP_079045.1|     GMVAGAVTGIVAGALLIFLLVWLLIRRKDKERYEEEERPNEIREDAEAPKARLVKP-SSSSSGSRSSRSGSSSTRSTAN-SASRSQR-------TLSTDAAPQ-PGLATQAYSLVGPE------VRGSEPKKVHHANLTKAETTPSMIPS   450
gi|148236123|ref|NP_001091512.1| GMIAGAVTGMVAGALLIFLLVWLLIRRKDKKRYEEEERPNEIREDAEAPKARLVKP-SSSSSGSRSSRSGSSSTRSTAN-SGSRSQR-------TPCAEAARR-QGQAAHTYGPVGPE------ARSSEPKKAPHATLTKAENTPSTIPS   450
gi|118101907|ref|XP_417886.2|    GMIAGAVCGVVVGLCLLFLVVRLTIRRKEKKRYEEEEAPNEIREDAEAPKAHLVKP-SSSSSGSRSSRSGSSSTRSTAN-SASRSQR-------TLSTEATPH---LTPPQYSQREMG------GKETEPKKVDYANLMKMGATLVMVPA   450
gi|189524576|ref|XP_695564.3|    GVVAGAVVGVSFGVLLIILIVWLVFRKKEKKKYEEEEAPNEIREDAEAPKAKLVKPNSLSSSRSGSSRSGASSTQSMVHNSATRGPRPRLPVVAALKESGQPEKFPPVPPPYNHVVPKPPEPSSSPKSSPAKLSPGNLARMGATPVMIPA   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

gi|31542035|ref|NP_598494.2|     QSKAFQTV   458
gi|35215304|ref|NP_775177.1|     QSRAFQTV   458
gi|73954988|ref|XP_546471.2|     --------   458
gi|13376115|ref|NP_079045.1|     QSRAFQTV   458
gi|148236123|ref|NP_001091512.1| QSRAFQTV   458
gi|118101907|ref|XP_417886.2|    QSRAFQTV   458
gi|189524576|ref|XP_695564.3|    QTKAFQTV   458
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