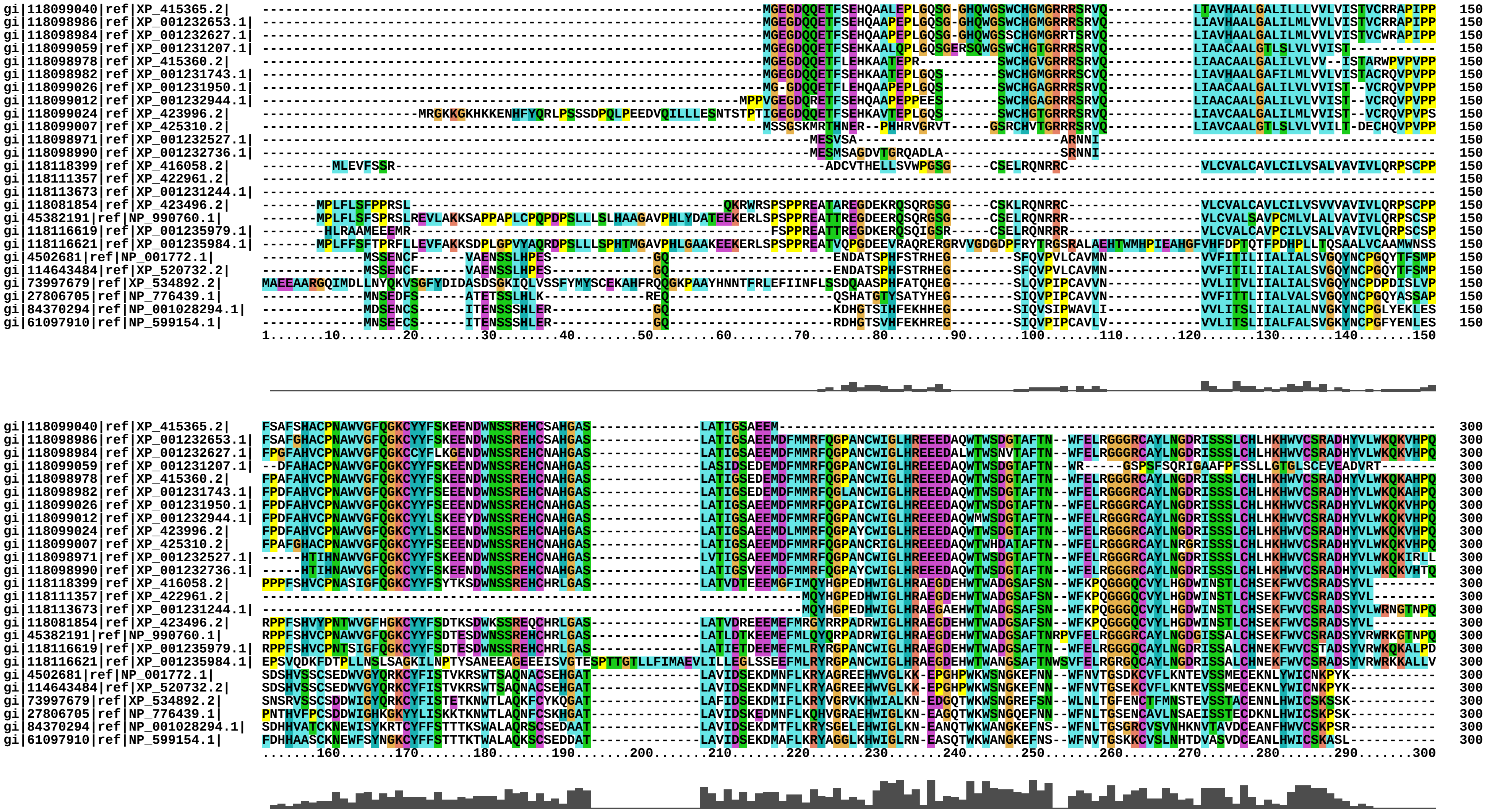

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gi|118099040|ref|XP_415365.2|     ----------------------------------------------------------------MGEGDQQETFSEHQAALEPLGQSG-GHQWGSWCHGMGRRRSRVQ-----------LTAVHAALGALILLLVVLVISTVCRRAPIPP   150
gi|118098986|ref|XP_001232653.1|  ----------------------------------------------------------------MGEGDQQETFSEHQAAPEPLGQSG-GHQWGSWCHGMGRRRSRVQ-----------LIAVHAALGALILMLVVLVISTVCRRAPIPP   150
gi|118098984|ref|XP_001232627.1|  ----------------------------------------------------------------MGEGDQQETFSEHQAAPEPLGQSG-GHQWGSSCHGMGRRTSRVQ-----------LIAVHAALGALILMLVVLVISTVCWRAPIPP   150
gi|118099059|ref|XP_001231207.1|  ----------------------------------------------------------------MGEGDQQETFSEHKAALQPLGQSGERSQWGSWCHGTGRRRSRVQ-----------LIAACAALGTLSLVLVVIST-----------   150
gi|118098978|ref|XP_415360.2|     ----------------------------------------------------------------MGEGDQQETFLEHKAATEPR----------SWCHGVGRRRSRVQ-----------LIAACAALGALILVLVV--ISTARWPVPVPP   150
gi|118098982|ref|XP_001231743.1|  ----------------------------------------------------------------MGEGDQQETFSEHKAATEPLGQS-------SWCHGMGRRRSCVQ-----------LIAVHAALGAFILMLVVLVISTACRQVPVPP   150
gi|118099026|ref|XP_001231950.1|  ----------------------------------------------------------------MG-GDQQETFLEHQAAPEPLGQS-------SWCHGAGRRRSRVQ-----------LIAACAALGALILVLVVIST--VCRQVPVPP   150
gi|118099012|ref|XP_001232944.1|  -------------------------------------------------------------MPPVGEGDQRETFSEHQAAPEPPEES-------SWCHGAGRRRSRVQ-----------LIAACAALGALILVLVVIST--VCRQVPVPP   150
gi|118099024|ref|XP_423996.2|     --------------------MRGKKGKHKKENHFYQRLPSSSDPQLPEEDVQILLLESNTSTPTIGEGDQQETFSEHKAVTEPLGQS-------SWCHGTGRRRSRVQ-----------LIAVCAALGALILMLVVIST--VCRQVPVPS   150
gi|118099007|ref|XP_425310.2|     ----------------------------------------------------------------MSSGSKMRTHNER--PHHRVGRVT-----GSRCHVTGRRRSRVQ-----------LIAVCAALGTLSLVLVVILT-DECHQVPVPP   150
gi|118098971|ref|XP_001232527.1|  ----------------------------------------------------------------------MESVSA--------------------------ARNNI-------------------------------------------   150
gi|118098990|ref|XP_001232736.1|  ----------------------------------------------------------------------MESMSAGDVTGRQADLA---------------SRNNI-------------------------------------------   150
gi|118118399|ref|XP_416058.2|     ---------MLEVFSSR-------------------------------------------------------ADCVTHELLSVWPGSG-----CSELRQNRRC-----------------VLCVALCAVLCILVSALVAVIVLQRPSCPP   150
gi|118111357|ref|XP_422961.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|118113673|ref|XP_001231244.1|  ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|118081854|ref|XP_423496.2|     -------MPLFLSFPPRSL----------------------------------------QKRWRSPSPPREATAREGDEKRQSQRGSG-----CSKLRQNRRC-----------------VLCVALCAVLCILVSVVVAVIVLQRPSCPP   150
gi|45382191|ref|NP_990760.1|      -------MPLFLSFSPRSLREVLAKKSAPPAPLCPQPDPSLLLSLHAAGAVPHLYDATEEKERLSPSPPREATTREGDEERQSQRGSG-----CSELRQNRRR-----------------VLCVALSAVPCMLVLALVAVIVLQRPSCSP   150
gi|118116619|ref|XP_001235979.1|  --------HLRAAMEEEMR----------------------------------------------FSPPREATTREGDKERQSQIGSR-----CSELRQNRRR-----------------VLCVALCAVPCILVSALVAVIVLQRPSCSP   150
gi|118116621|ref|XP_001235984.1|  -------MPLFFSFTPRFLLEVFAKKSDPLGPVYAQRDPSLLLSPHTMGAVPHLGAAKEEKERLSPSPPREATVQPGDEEVRAQRERGRVVGDGDPFRYTRGSRALAEHTWMHPIEAHGFVHFDPTQTFPDHPLLTQSAALVCAAMWNSS   150
gi|4502681|ref|NP_001772.1|       -------------MSSENCF------VAENSSLHPES-------------GQ---------------------ENDATSPHFSTRHEG--------SFQVPVLCAVMN------------VVFITILIIALIALSVGQYNCPGQYTFSMP   150
gi|114643484|ref|XP_520732.2|     -------------MSSENCF------VAENSSLHPES-------------GQ---------------------ENDATSPHFSTRHEG--------SFQVPVLCAVMN------------VVFITILIIALIALSVGQYNCPGQYTFSMP   150
gi|73997679|ref|XP_534892.2|      MAEEAARGQIMDLLNYQKVSGFYDIDASDSGKIQLVSSFYMYSCEKAHFRQQGKPAAYHNNTFRLEFIINFLSSDQAASPHFATQHEG--------SLQVPIPCAVVN------------VVLITVLIIALIALSVGQYNCPDPDISLVP   150
gi|27806705|ref|NP_776439.1|      -------------MNSEDFS------ATETSSLHLK-------------REQ---------------------QSHATGTYSATYHEG--------SIQVPIPCAVVN------------VVFITTLIIALVALSVGQYNCPGQYASSAP   150
gi|84370294|ref|NP_001028294.1|   -------------MDSENCS------ITENSSSHLER-------------GQ---------------------KDHGTSIHFEKHHEG--------SIQVSIPWAVLI------------VVLITSLIIALIALNVGKYNCPGLYEKLES   150
gi|61097910|ref|NP_599154.1|      -------------MNSEECS------ITENSSSHLER-------------GQ---------------------RDHGTSVHFEKHREG--------SIQVPIPCAVLV------------VVLITSLIIALFALSVGKYNCPGFYENLES   150
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gi|118099040|ref|XP_415365.2|     FSAFSHACPNAWVGFQGKCYYFSKEENDWNSSREHCSAHGAS--------------LATIGSAEEM------------------------------------------------------------------------------------   300
gi|118098986|ref|XP_001232653.1|  FSAFGHACPNAWVGFQGKCYYFSKEENDWNSSREHCSAHGAS--------------LATIGSAEEMDFMMRFQGPANCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118098984|ref|XP_001232627.1|  FPGFAHVCPNAWVGFQGKCCYFLKGENDWNSSREHCNAHGAS--------------LATIGSAEEMDFMMRFQGPANCWIGLHREEEDALWTWSNVTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118099059|ref|XP_001231207.1|  --DFAHACPNAWVGFQGKCYYFSKEENDWNSSREHCNAHGAS--------------LASIDSEDEMDFMMRFQGPANCWIGLHREEEDAQWTWSDGTAFTN--WR-----GSPSFSQRIGAAFPFSSLLGTGLSCEVEADVRT-------   300
gi|118098978|ref|XP_415360.2|     FPAFAHVCPNAWVGFQGKCYYFSKEENDWNSSREHCNAHGAS--------------LATIGSEDEMDFMMRFQGPANCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKAHPQ   300
gi|118098982|ref|XP_001231743.1|  FPDFAHVCPNAWVGFQGKCYYFSEEENDWNSSREHCNAHGAS--------------LATIGSEDEMDFMMRFQGLANCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKAHPQ   300
gi|118099026|ref|XP_001231950.1|  FPDFAHVCPNAWVGFQGKCYYFSEEENDWNSSREHCNAHGAS--------------LATIGSAEEMDFMMRFQGPAICWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118099012|ref|XP_001232944.1|  FPDFAHVCPNAWVGFQGKCYYLSKEEYDWNSSREHCNAHGAS--------------LATIGSAEEMDFMMRFQGPANCWIGLHREEEDAQWMWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118099024|ref|XP_423996.2|     FPDFAHVCPNAWVGFQGKCYYLSKEENDWNSSREHCNAHGAS--------------LATIGSAEEMDLMMRFQGPAYCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118099007|ref|XP_425310.2|     FPAFGHACPNAWVGFQGKCYYFSEEENDWNSSREHCNAHGAS--------------LATIGSAEEMDFMMRFQGPANCRIGLHREEEDAQWTWHDATAFTN--WFELRGGGRCAYLNRGRISSSLCHLHKHWVCSRADHYVLWKQKVHPQ   300
gi|118098971|ref|XP_001232527.1|  -----HTIHNAWVGFQGKCYYFSKEENDWNSSREHCNAHGAS--------------LVTIGSAEEMDFMMRFQGPANCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKIRLL   300
gi|118098990|ref|XP_001232736.1|  -----HTIHNAWVGFQGKCYYFSKEENDWNSSREHCNAHGAS--------------LATIGSVEEMDFMMRFQGPAYCWIGLHREEEDAQWTWSDGTAFTN--WFELRGGGRCAYLNGDRISSSLCHLHKHWVCSRADHYVLWKQKVHTQ   300
gi|118118399|ref|XP_416058.2|     PPPFSHVCPNASIGFQGKCYYFSYTKSDWNSSREHCHRLGAS--------------LATVDTEEEMGFIMQYHGPEDHWIGLHRAEGDEHWTWADGSAFSN--WFKPQGGGQCVYLHGDWINSTLCHSEKFWVCSRADSYVL--------   300
gi|118111357|ref|XP_422961.2|     ---------------------------------------------------------------------MQYHGPEDHWIGLHRAEGDEHWTWADGSAFSN--WFKPQGGGQCVYLHGDWINSTLCHSEKFWVCSRADSYVL--------   300
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gi|118081854|ref|XP_423496.2|     RPPFSHVYPNTWVGFHGKCYYFSDTKSDWKSSREQCHRLGAS--------------LATVDREEEMEFMRGYRRPADRWIGLHRAEGDEHWTWADGSAFSN--WFKPQGGGQCVYLHGDWINSTLCHSEKFWVCSRADSYVL--------   300
gi|45382191|ref|NP_990760.1|      RPPFSHVCPNAWVGFQGKCYYFSDTESDWNSSREHCHRLGAS--------------LATLDTKEEMEFMLQYQRPADRWIGLHRAEGDEHWTWADGSAFTNRPVFELRGGGRCAYLNGDGISSALCHSEKFWVCSRADSYVRWRKGTNPQ   300
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gi|118116621|ref|XP_001235984.1|  EPSVQDKFDTPLLNSLSAGKILNPTYSANEEAGEEEISVGTESPTTGTLLFIMAEVLILLEGLSSEEFMLRYRGPANCWIGLHRAEGDEHWTWANGSAFTNWSVFELRGRGQCAYLNGDRISSALCHNEKFWVCSRADSYVRWRKKALLV   300
gi|4502681|ref|NP_001772.1|       SDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGAT--------------LAVIDSEKDMNFLKRYAGREEHWVGLKK-EPGHPWKWSNGKEFNN--WFNVTGSDKCVFLKNTEVSSMECEKNLYWICNKPYK-----------   300
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gi|61097910|ref|NP_599154.1|      FDHHAASCKNEWFSYNGKCYFFSTTTKTWALAQKSCSEDDAT--------------LAVIDSEKDMAFLKRYAGGLKHWIGLRN-EASQTWKWANGKEFNS--WFNVTGSKKCVSLNHTDVASVDCEANLHWICSKASL-----------   300
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