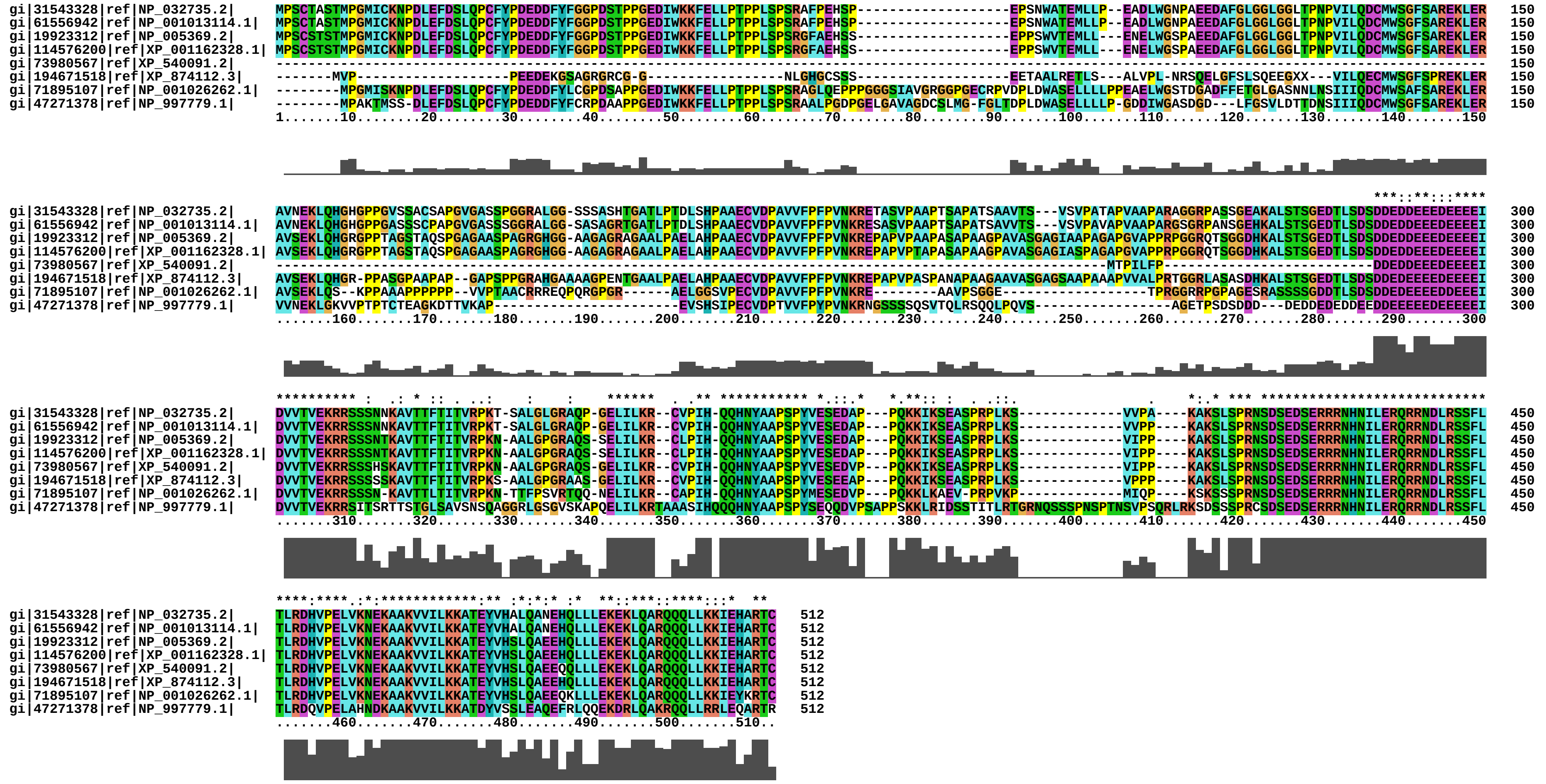

```
                                                                                                                                                                                                    
gi|31543328|ref|NP_032735.2|     MPSCTASTMPGMICKNPDLEFDSLQPCFYPDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRAFPEHSP-------------------EPSNWATEMLLP--EADLWGNPAEEDAFGLGGLGGLTPNPVILQDCMWSGFSAREKLER   150
gi|61556942|ref|NP_001013114.1|  MPSCTASTMPGMICKNPDLEFDSLQPCFYPDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRAFPEHSP-------------------EPSNWATEMLLP--EADLWGNPAEEDAFGLGGLGGLTPNPVILQDCMWSGFSAREKLER   150
gi|19923312|ref|NP_005369.2|     MPSCSTSTMPGMICKNPDLEFDSLQPCFYPDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRGFAEHSS-------------------EPPSWVTEMLL---ENELWGSPAEEDAFGLGGLGGLTPNPVILQDCMWSGFSAREKLER   150
gi|114576200|ref|XP_001162328.1| MPSCSTSTMPGMICKNPDLEFDSLQPCFYPDEDDFYFGGPDSTPPGEDIWKKFELLPTPPLSPSRGFAEHSS-------------------EPPSWVTEMLL---ENELWGSPAEEDAFGLGGLGGLTPNPVILQDCMWSGFSAREKLER   150
gi|73980567|ref|XP_540091.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|194671518|ref|XP_874112.3|    -------MVP-------------------PEEDEKGSAGRGRCG-G-----------------NLGHGCSSS-------------------EETAALRETLS---ALVPL-NRSQELGFSLSQEEGXX---VILQECMWSGFSPREKLER   150
gi|71895107|ref|NP_001026262.1|  --------MPGMISKNPDLEFDSLQPCFYPDEDDFYLCGPDSAPPGEDIWKKFELLPTPPLSPSRAGLQEPPPGGGSIAVGRGGPGECRPVDPLDWASELLLLPPEAELWGSTDGADFFETGLGASNNLNSIIIQDCMWSAFSAREKLER   150
gi|47271378|ref|NP_997779.1|     --------MPAKTMSS-DLEFDSLQPCFYPDEDDFYFCRPDAAPPGEDIWKKFELLPTPPLSPSRAALPGDPGELGAVAGDCSLMG-FGLTDPLDWASELLLLP-GDDIWGASDGD---LFGSVLDTTDNSIIIQDCMWSGFSAREKLER   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                                                                                                                                                        ***::**:::****
gi|31543328|ref|NP_032735.2|     AVNEKLQHGHGPPGVSSACSAPGVGASSPGGRALGG-SSSASHTGATLPTDLSHPAAECVDPAVVFPFPVNKRETASVPAAPTSAPATSAAVTS---VSVPATAPVAAPARAGGRPASSGEAKALSTSGEDTLSDSDDEDDEEEDEEEEI   300
gi|61556942|ref|NP_001013114.1|  AVNEKLQHGHGPPGASSSCPAPGVGASSSGGRALGG-SASAGRTGATLPTDLSHPAAECVDPAVVFPFPVNKRESASVPAAPTSAPATSAVVTS---VSVPAVAPVAAPARGSGRPANSGEHKALSTSGEDTLSDSDDEDDEEEDEEEEI   300
gi|19923312|ref|NP_005369.2|     AVSEKLQHGRGPPTAGSTAQSPGAGAASPAGRGHGG-AAGAGRAGAALPAELAHPAAECVDPAVVFPFPVNKREPAPVPAAPASAPAAGPAVASGAGIAAPAGAPGVAPPRPGGRQTSGGDHKALSTSGEDTLSDSDDEDDEEEDEEEEI   300
gi|114576200|ref|XP_001162328.1| AVSEKLQHGRGPPTAGSTAQSPGAGAASPAGRGHGG-AAGAGRAGAALPAELAHPAAECVDPAVVFPFPVNKREPAPVPTAPASAPAAGPAVASGAGIASPAGAPGVAPPRPGGRQTSGGDHKALSTSGEDTLSDSDDEDDEEEDEEEEI   300
gi|73980567|ref|XP_540091.2|     -------------------------------------------------------------------------------------------------------MTPILFP--------------------------DDEDDEEEDEEEEI   300
gi|194671518|ref|XP_874112.3|    AVSEKLQHGR-PPASGPAAPAP--GAPSPPGRAHGAAAAGPENTGAALPAELAHPAAECVDPAVVFPFPVNKREPAPVPASPANAPAAGAAVASGAGSAAPAAAPVVALPRTGGRLASASDHKALSTSGEDTLSDSDDEDEEEEDEEEEI   300
gi|71895107|ref|NP_001026262.1|  AVSEKLQS--KPPAAAPPPPPP--VVPTAACRRREQPQRGPGR------AELGGSVPECVDPAVVFPFPVNKRE--------AAVPSGGE------------------TPRGGRRPGPAGESRASSSSGDDTLSDSDDEDEEEEDDEEEI   300
gi|47271378|ref|NP_997779.1|     VVNEKLGKVVPTPTCTEAGKDTTVKAP-----------------------EVSHSIPECVDPTVVFPYPVNKRNGSSSSQSVTQLRSQQLPQVS-----------------AGETPSDSDDD---DEDDEDEDDEEDDEEEEEDEEEEEI   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                 ********** :  .: * :: . ..:    :    :    ******  . .** *********** *.::.*   *.**:: :  . .::.                .    *:.* *** ****************************
gi|31543328|ref|NP_032735.2|     DVVTVEKRRSSSNNKAVTTFTITVRPKT-SALGLGRAQP-GELILKR--CVPIH-QQHNYAAPSPYVESEDAP---PQKKIKSEASPRPLKS-------------VVPA----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|61556942|ref|NP_001013114.1|  DVVTVEKRRSSSNNKAVTTFTITVRPKT-SALGLGRAQP-GELILKR--CVPIH-QQHNYAAPSPYVESEDAP---PQKKIKSEASPRPLKS-------------VVPP----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|19923312|ref|NP_005369.2|     DVVTVEKRRSSSNTKAVTTFTITVRPKN-AALGPGRAQS-SELILKR--CLPIH-QQHNYAAPSPYVESEDAP---PQKKIKSEASPRPLKS-------------VIPP----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|114576200|ref|XP_001162328.1| DVVTVEKRRSSSNTKAVTTFTITVRPKN-AALGPGRAQS-SELILKR--CLPIH-QQHNYAAPSPYVESEDAP---PQKKIKSEASPRPLKS-------------VIPP----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|73980567|ref|XP_540091.2|     DVVTVEKRRSSSHSKAVTTFTITVRPKN-AALGPGRAQS-GELILKR--CVPIH-QQHNYAAPSPYVESEDVP---PQKKIKSEASPRPLKS-------------VIPP----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|194671518|ref|XP_874112.3|    DVVTVEKRRSSSSSKAVTTFTITVRPKS-AALGPGRAAS-GELILKR--CVPIH-QQHNYAAPSPYVESEEAP---PQKKIKSEASPRPLKS-------------VPPP----KAKSLSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|71895107|ref|NP_001026262.1|  DVVTVEKRRSSSN-KAVTTLTITVRPKN-TTFPSVRTQQ-NELILKR--CAPIH-QQHNYAAPSPYMESEDVP---PQKKLKAEV-PRPVKP-------------MIQP----KSKSSSPRNSDSEDSERRRNHNILERQRRNDLRSSFL   450
gi|47271378|ref|NP_997779.1|     DVVTVEKRRSITSRTTSTGLSAVSNSQAGGRLGSGVSKAPQELILKRTAAASIHQQQHNYAAPSPYSEQQDVPSAPPSKKLRIDSSTITLRTGRNQSSSPNSPTNSVPSQRLRKSDSSSPRCSDSEDSERRRNHNILERQRRNDLRSSFL   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                 ****:****.:*:************:** :*:*:* :*  **::***::****:::*  **
gi|31543328|ref|NP_032735.2|     TLRDHVPELVKNEKAAKVVILKKATEYVHALQANEHQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|61556942|ref|NP_001013114.1|  TLRDHVPELVKNEKAAKVVILKKATEYVHALQANEHQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|19923312|ref|NP_005369.2|     TLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEHQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|114576200|ref|XP_001162328.1| TLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEHQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|73980567|ref|XP_540091.2|     TLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEQQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|194671518|ref|XP_874112.3|    TLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEHQLLLEKEKLQARQQQLLKKIEHARTC   512
gi|71895107|ref|NP_001026262.1|  TLRDHVPELVKNEKAAKVVILKKATEYVHSLQAEEQKLLLEKEKLQARQQQLLKKIEYKRTC   512
gi|47271378|ref|NP_997779.1|     TLRDQVPELAHNDKAAKVVILKKATDYVSSLEAQEFRLQQEKDRLQAKRQQLLRRLEQARTR   512
                                 .......460.......470.......480.......490.......500.......510..
```