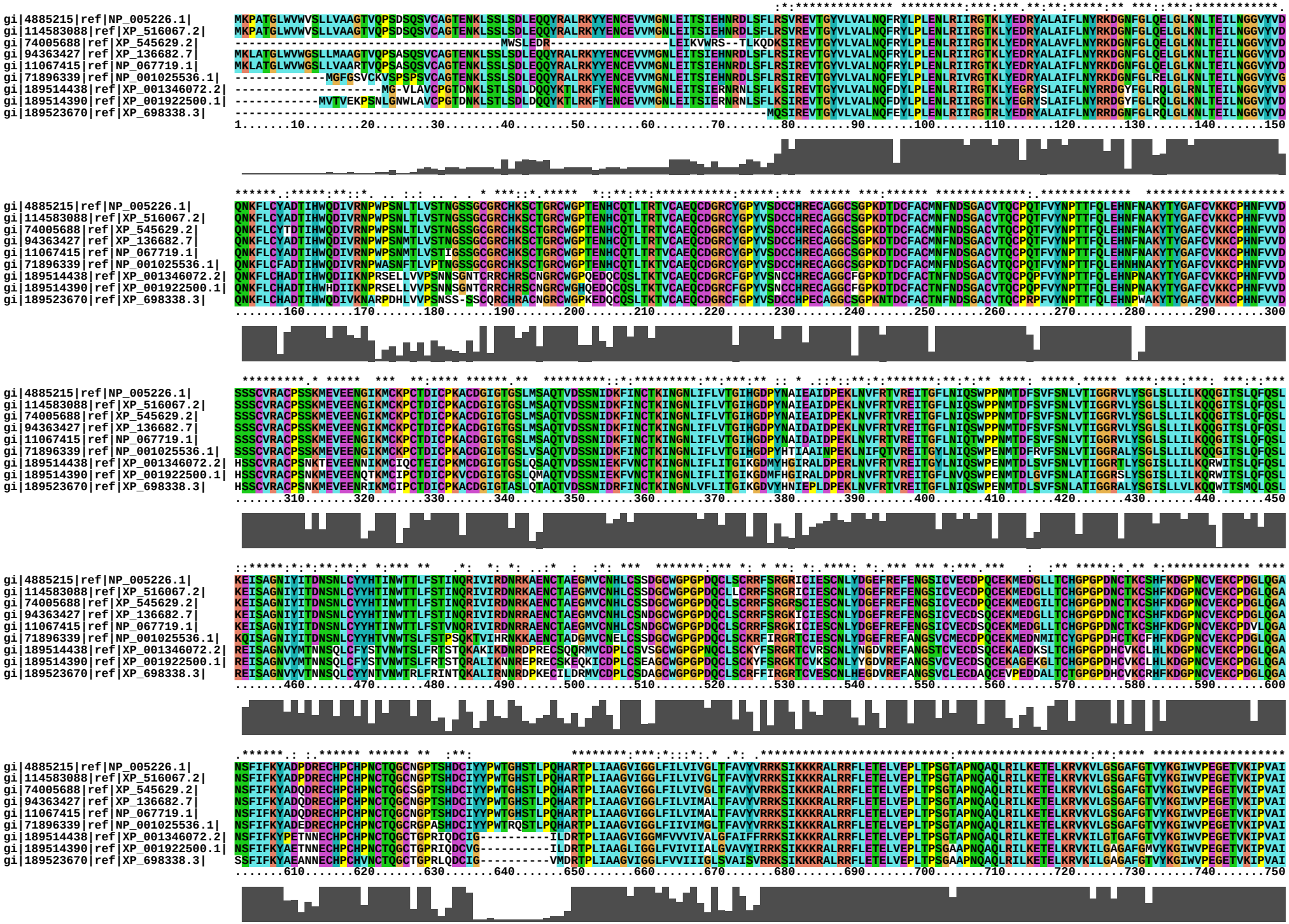
gi|4885215|ref|NP_005226.1|
gi|114583088|ref|XP_516067.2|
gi|74005688|ref|XP_545629.2|
gi|94363427|ref|XP_136682.7|
gi|11067415|ref|NP_067719.1|
gi|71896339|ref|NP_001025536.1|
gi|189514438|ref|XP_001346072.2|
gi|189514390|ref|XP_001922500.1|
gi|189523670|ref|XP_698338.3|

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gi|4885215|ref|NP_005226.1|      KILNETTGPKANVEFMD-----EALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|114583088|ref|XP_516067.2|    KILNETTGPKANVEFMD-----EALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|74005688|ref|XP_545629.2|     KILNETTGPKANVEFMD-----EALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|94363427|ref|XP_136682.7|     KILNETTGPKANVEFMD-----EALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|11067415|ref|NP_067719.1|     KILNETTGPKANVEFMD-----EALIMASVDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLEYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|71896339|ref|NP_001025536.1|  KILNETTGPKANVEFMD-----EALIMASMDHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHVKITDFGLARLLEGDEKEYNADGGKMPIKWMALECIHYR   900
gi|189514438|ref|XP_001346072.2| KILNESTGPKANVEFMD-----EALIMASMEHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHQDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHIKITDFGLARLLETNEKEYSADEGKMPIKWMALECIHYR   900
gi|189514390|ref|XP_001922500.1| KILNESTGPKANVEFMD-----EALIMASMEHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHQDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHIKITDFGLARLLDTDEKEYNSDGGKMPIKWMALECIHYR   900
gi|189523670|ref|XP_698338.3|    KILNEATGPKANVEFMDVSVTLRALIMASMEHPHLVRLLGVCLSPTIQLVTQLMPHGCLLDYVHEHKDNIGSQLLLNWCVQIAKGMMYLEERRLVHRDLAARNVLVKSPNHIKITDFGLARLLDANEKEYNADGGKMPIKWMALECIHYR   900
                                 .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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gi|4885215|ref|NP_005226.1|      KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRARIDSNR  1050
gi|114583088|ref|XP_516067.2|    KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRARIDSNR  1050
gi|74005688|ref|XP_545629.2|     KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRARIDSNR  1050
gi|94363427|ref|XP_136682.7|     KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRTRIDSNR  1050
gi|11067415|ref|NP_067719.1|     KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYIVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRTRIDSNR  1050
gi|71896339|ref|NP_001025536.1|  KFTHQSDVWSYGVTIWELMTFGGKPYDGIPIREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPKFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQNLLDEEDLEDMMDAEEYLVPQAFNIPPPIYTSRTRIDSNR  1050
gi|189514438|ref|XP_001346072.2| KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDILEKGERLPQPPICTIDVYMVMVKCWMIDADSRPRFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNHSKFFQSLLDEEELDDLMDADEYLVPHSLNAPPTSHIPHPHVDS--  1050
gi|189514390|ref|XP_001922500.1| KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTRDIPDILEKGERLPQPPICTIDVYMVMVKCWMIDADSRPRFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNHSTFFKSLLDEEELDDLMDADEYLVPQTCNISTSTYTSRTTMDA--  1050
gi|189523670|ref|XP_698338.3|    KFTHQSDVWSYGVTIWELMTFGGKPYDGIPTREIPDLLEKGERLPQPPICTIDVYMVMVKCWMIDADSRPRFKELAAEFSRMARDPQRYLVIQGDDRMKLPSPNDSKFFQSLLDEEELEDLMDAEEYLVPQAYSIPPLAYTTRSRMDPNR  1050
                                 .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050
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gi|4885215|ref|NP_005226.1|      SEIG---HSPPPAYTPMSGNQFVYRDGGFAAEQGVS-----VPYRAPTSTIPEAPVAQG-----ATAEIFDDSCCNGTLRKPV--APHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVEENPFVSRRKNGDL  1200
gi|114583088|ref|XP_516067.2|    SEIG---HSPPPAYTPMSGNQFVYRDGGFAAEQGVS-----VPYRAPTSTIPEAPVAQG-----ATAEIFDDSCCNGTLRKPV--APHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVEENPFVSRRKNGDL  1200
gi|74005688|ref|XP_545629.2|     SEIG---HSPPPAYTPMSGNQFVYRDGGFAAEQGVP-----VPYRATTSTIPEAPVAQG-----ATAEIFDDSCCNGTLRKPV--APHVQEDSSTQRYSADPTVFAPERSPRGELDEEGYMTPMRDKPKQEYLNPVEENPFVSRRKNGDL  1200
gi|94363427|ref|XP_136682.7|     SEIG---HSPPPAYTPMSGNQFVYQDGGFATQQGMP-----MPYRATTSTIPEAPVAQG-----ATAEMFDDSCCNGTLRKPV--APHVQEDSSTQRYSADPTVFAPERNPRGELDEEGYMTPMHDKPKQEYLNPVEENPFVSRRKNGDL  1200
gi|11067415|ref|NP_067719.1|     SEIG---HSPPPAYTPMSGSQFVYQDGGFATQQGMP-----MPYTATTSTIPEAPVAQG-----ATAEMFDDSCCNGTLRKPV--VPHVQEDSSTQRYSADPTVFAPERNPRAELDEEGYMTPMHDKPKQEYLNPVEENPFVSRRKNGDL  1200
gi|71896339|ref|NP_001025536.1|  ------------------NQFVYRDGGYAAEQGVP-----MPYRAPGCIIPEAPVAQG-----ATAEIFEDTCCIGTLRKQV--ATLAKEDSSTQRYSADPTVFIPERVIRGELDEDGYMTPMRDKPKTDYLNPVEENPFVSRRKNGDL  1200
gi|189514438|ref|XP_001346072.2| -----------------NQNQFGYHDGSRCPEDVT--RFHEVAAAGNAPSALGSAQRAG-------LDLVEEQHCNGSLKKQA-TVH-SVEDSSGQRYSADPTVLLGEKTQREDTDEDGYMSPMKDKISTNHLNPVEENPFVTRRKSKDV  1200
gi|189514390|ref|XP_001922500.1| -----------------SWT-LRCRDRVFSPEDGMGACSRDVPASASAVFVPVSTQAAG-------LNVLEEQHCNGSLKKQQ-PMSGSGDDCDGQRYSADPTVFLGERSLKN-TDEDGYMSPMN-KSTSDHLSPVEENPFVNHRKNGNI  1200
gi|189523670|ref|XP_698338.3|    VSASARSHTPIQCLPVFLQNQFAYQDGSFGMEDMMATIPRVVAVSAVSPGCSTQKQSKGQQGASGSSEAFEDSRCNGTLRKKASPRASTGDDSSGQRYSADPTVILCEHGARAETDQDGYMSAMQDKKPSDFLNPVEENPFVTHRRNGEV  1200
                                 ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200
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gi|4885215|ref|NP_005226.1|      QALDNPEYHNASNGPPKA-EDEYVNEPLYLNTFANTLG-KAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTVLPPPPYRHRNTVV  1331
gi|114583088|ref|XP_516067.2|    QALDNPEYHNASNGPPKA-EDEYVNEPLYLNTFANTLG-KAEYLKNNILSMPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTVLPPPPYRHRNTVV  1331
gi|74005688|ref|XP_545629.2|     QALDNPEYHNASNGPPKA-EDEYVNEPLYLNTFANALG-NAEYLKNNVLSVPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTVLPPPPYRHRNTVV  1331
gi|94363427|ref|XP_136682.7|     QALDNPEYHSASSGPPKA-EDEYVNEPLYLNTFANALG-SAEYMKNSVLSVPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTMLPPPPYRHRNTVV  1331
gi|11067415|ref|NP_067719.1|     QALDNPEYHSASSGPPKA-EDEYVNEPLYLNTFTNALG-NAEYMKNSLLSVPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTMLPPPPYRHRNTVV  1331
gi|71896339|ref|NP_001025536.1|  QAVDNPEYHNAPNGQPKA-EDEYVNEPLYLNTFASTLE-NAEYLKN---NLPEKAKKAFDNPDYWNHSLPPRSTLQHP-DYLQEYSTKYFYKQNGRIRPIVAENPEYLSEFSLKPGTVLPPPPYRHRNTVV  1331
gi|189514438|ref|XP_001346072.2| HALDNPGYHNTPDGKPKC-EDEYINEPLYLNTFNNTSDIHQEMLRKNGVSIPEMYKNSFDNPEYWQHSLPP--PQISQDSSSAVCNNKFLYKQNGRVQPPAAENPEYLSGVK--PGMVLPPPPYRQRNTVV  1331
gi|189514390|ref|XP_001922500.1| TALDNPGYHSTPDKKSKAEEDEYINEPLYLNAYNTTGGTNLEIMRRNGSSIPRKSKKNFDNPDYWQHSLPPKVTQANPQDPTQTCKSKHLYRHSIRSRLAVADNPEFVSEFNKRPGPVLPPPPYRHRNTVV  1331
gi|189523670|ref|XP_698338.3|    HTLER-GYHSTSNGQPKL-EDEYVNDPLYLNTFHNTGEKSHDALRKNGVPADLKAKKTFDSPEYWQHSLPPKATLHNP-EYLQDCSTRFFYRQNGRIRPAVAENQEYLSDYALKPGTVLPPPPYRQRNTVV  1331
                                 ......1210......1220......1230......1240......1250......1260......1270......1280......1290......1300......1310......1320......1330.
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