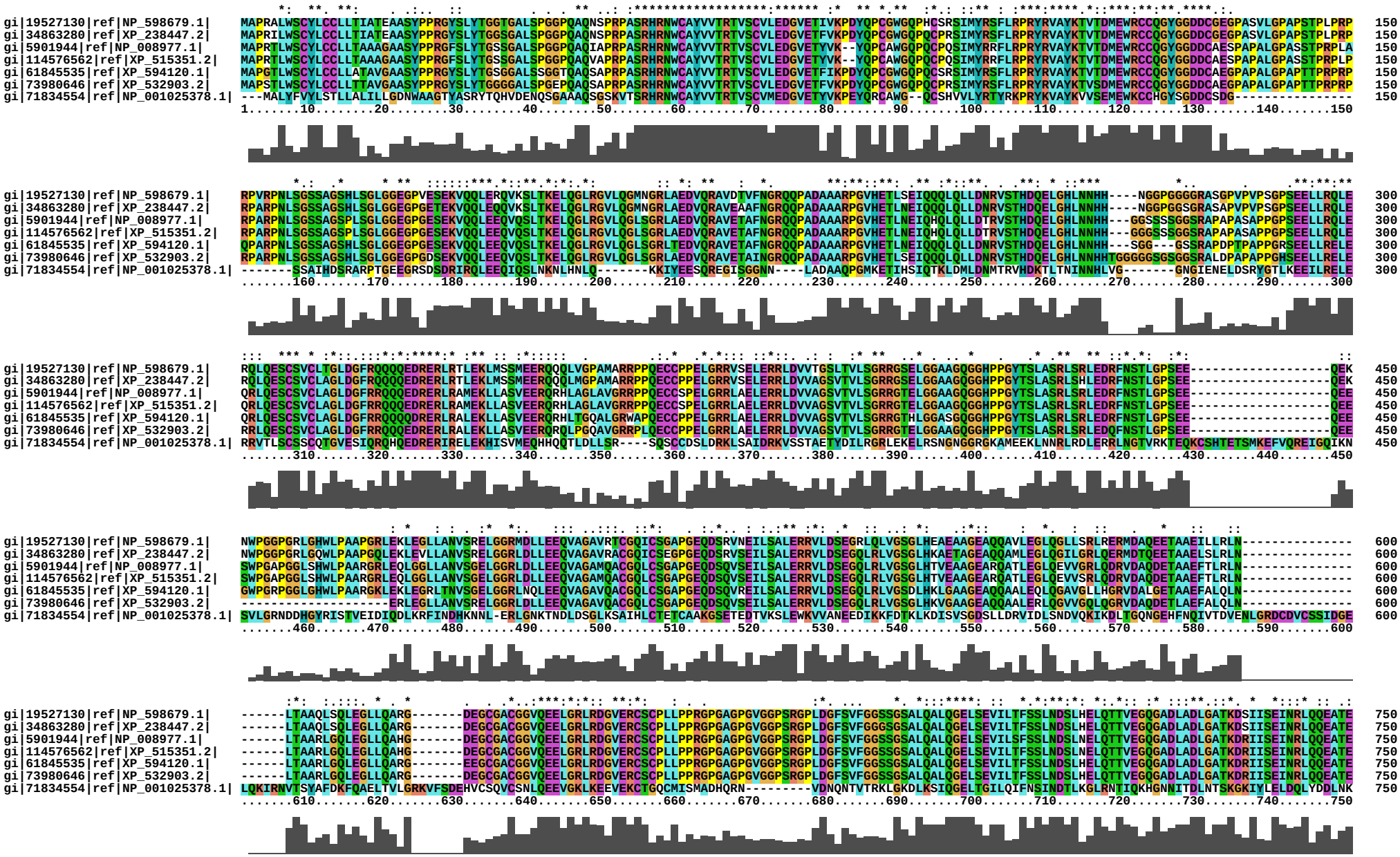
gi|19527130|ref|NP_598679.1|
gi|34863280|ref|XP_238447.2|
gi|5901944|ref|NP_008977.1|
gi|114576562|ref|XP_515351.2|
gi|61845535|ref|XP_594120.1|
gi|73980646|ref|XP_532903.2|
gi|71834554|ref|NP_001025378.1|

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gi|19527130|ref|NP_598679.1|     HVTESEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAAVRESNSTSLTQAALLEKLLGGQAG-LGRRLGALNNSLLLLEDRLQQLSLKDFTGPSGKAGPPGPPGLQGPSGPAGPPGP   900
gi|34863280|ref|XP_238447.2|     HITEIEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAAVRESNSTSLTQAALLEKLLGGQAG-LGRRLGALNSSLLLLEDRLQQLSLKDFTGPSGKAGPPGPPGLQGPPGPAGPPGP   900
gi|5901944|ref|NP_008977.1|      HATESEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAGLRETNTTSQMQAALLEKLVGGQAG-LGRRLGALNSSLQLLEDRLHQLSLKDLTGPAGEAGPPGPPGLQGPPGPAGPPGS   900
gi|114576562|ref|XP_515351.2|    HATESEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAGFRETNTTSQTQAALLEKLVGGQAG-LGRRLGALNSSLQLLEDRLHQLSLKDLTGPAGEAGPPGPPGLQGPPGPAGPPGS   900
gi|61845535|ref|XP_594120.1|     HATESEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAGLRETNSTSQTQAALLEKLLEGQAG-LGKRLGALNSSLLLLEDQLHQFSLKDLTGPAGEAGPPGPPGMQGPPGPAGPPGP   900
gi|73980646|ref|XP_532903.2|     HATESEERFRGLEEG----QAQAGQCPS----LEGRLGRLEGVCERLDTVAGGLQGLREGLSRHVAGLWAGLRETNSTSQTQAALLEKLLGGQAG-LGRRLSALNSSVLLLEDQLHQLSLKDLTG------------------------   900
gi|71834554|ref|NP_001025378.1|  HKVDSKGHFDSISSFNSNLMTEMGEGRLSREGLDKRLSKMEDVCGRLDTLSENLKTIKDGLSKHVSGLWTCVNDLNSTVISHSETISRIHNVHLENIQGRMNNLNSSIRNVLKEFQIFTEQDFTGPPGLPGPQGEKGSKGPPGPRGPLGK   900
                                 .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900
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                                 * *::       . **:::*****: *:::.**: *::*::*:   *:*:*******: ***::*******:: *:*****:** *:** **.**:*****: *:**:: :**:* :*.::**** ***:*:***
gi|19527130|ref|NP_598679.1|     PGKDGQQGAIGPPGPQGEQGAEGAPAAPVPRVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNLGVARIDSGGYEPEGLENKPVAESQPSPGALGVFSLILPLQVGDTVCIDLVM  1050
gi|34863280|ref|XP_238447.2|     PGKDGQRGAIGPPGPQGEQGVEGAPAAPVPRVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNLGVARIDSGGYEPEGLENKPVAESQPSPGALGVFSLILPLQVGDTVCIDLVM  1050
gi|5901944|ref|NP_008977.1|      PGKDGQEGPIGPPGPQGEQGVEGAPAAPVPQVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLENKPVAESQPSPGTLGVFSLILPLQAGDTVCVDLVM  1050
gi|114576562|ref|XP_515351.2|    PGKDGQEGPIGPPGPQGEQGVEGAPAAPVPRVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNQGVARVDSGGYEPEGLENKPVAESQPSPGTLGVFSLILPLQAGDTVCVDLVM  1050
gi|61845535|ref|XP_594120.1|     PGKDGQKGPMGPPGPQGEQGPEGAPAASVPRVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNLGVARIDSGGYEPEGLENKPVAESQPSPGALGVFSLILPLQVGDTVCIDLVM  1050
gi|73980646|ref|XP_532903.2|     --------------PQGEQGVEGAPAPFVPRVAFSAALSLPRSEPGTVPFDRVLLNDGGYYDPETGVFTAPLAGRYLLSAVLTGHRHEKVEAVLSRSNLGVARIDSGGYEPEGLENKPIAESQPSPGALGVFSLILPLQAGDTVCIDLVM  1050
gi|71834554|ref|NP_001025378.1|  EGPQGRVGPVGPPGPPGKD-------ANVPRLSFSAALTRPQASSGTIIFNKVFINERKAYNPKTGVFTAPVRGRYFFSAVLTGHKNVKIEAVLSKSNFGIARGDSAGYQPEGLEK-PMAEARHTPGSLVIFNIVLPLQEGDTICIDLVT  1050
                                 .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050
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                                 *:**** ******                *   :   .
gi|19527130|ref|NP_598679.1|     GQLAHSEEPLTIFSG--------------ALLYEDTELEQV------------------------------------------------------------------------------------------------  1200
gi|34863280|ref|XP_238447.2|     GQLAHSEEPLTIFSG--------------ALLYEDTDLEQV------------------------------------------------------------------------------------------------  1200
gi|5901944|ref|NP_008977.1|      GQLAHSEEPLTIFSG--------------ALLYGDPELEHA------------------------------------------------------------------------------------------------  1200
gi|114576562|ref|XP_515351.2|    GQLAHSEEPLTIFSG--------------ALLYGDPELEHA------------------------------------------------------------------------------------------------  1200
gi|61845535|ref|XP_594120.1|     GQLAHSEEPLTIFSG--------------ALLYGDLELEQA------------------------------------------------------------------------------------------------  1200
gi|73980646|ref|XP_532903.2|     GQLAHSEEPLTIFRVSLGEELGTQRRSQISLWRGDPILRDKRQSPGGAQSARRAEGSGSSPMEDKQILCVGLVVLDIISVVDKYPEEDTDSRCLSQRWQRGGNASNSCTVLSLLGAPCAFMGSMAPGHVADFLVADFRQRGVDVSQVAWQ  1200
gi|71834554|ref|NP_001025378.1|  GKLAHSVEPLTIFSG--------------MLLYEESEDRL------------------------------------------------------------------------------------------------  1200
                                 ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200
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gi|19527130|ref|NP_598679.1|     ------------------------------------------------------------------------------------------------------------------------------------------  1350
gi|34863280|ref|XP_238447.2|     ------------------------------------------------------------------------------------------------------------------------------------------  1350
gi|5901944|ref|NP_008977.1|      ------------------------------------------------------------------------------------------------------------------------------------------  1350
gi|114576562|ref|XP_515351.2|    ------------------------------------------------------------------------------------------------------------------------------------------  1350
gi|61845535|ref|XP_594120.1|     ------------------------------------------------------------------------------------------------------------------------------------------  1350
gi|73980646|ref|XP_532903.2|     GKGETPCSCCIVNNSNGSRTIVLYDTNLPDVSATDFDNVDLTRFKWIHIEGRNASEQVKMLQRIERHNATQPPGQKIQVSVEVEKPREELFSCLPPFHCPQVFVSKDVARHLGYRSAVEALRGLYGRVRKGATLICAWAEEGADALGPDG  1350
gi|71834554|ref|NP_001025378.1|  ------------------------------------------------------------------------------------------------------------------------------------------  1350
                                 ......1210......1220......1230......1240......1250......1260......1270......1280......1290......1300......1310......1320......1330......1340......1350
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gi|19527130|ref|NP_598679.1|     ------------------------------------------------------------  1411
gi|34863280|ref|XP_238447.2|     ------------------------------------------------------------  1411
gi|5901944|ref|NP_008977.1|      ------------------------------------------------------------  1411
gi|114576562|ref|XP_515351.2|    ------------------------------------------------------------  1411
gi|61845535|ref|XP_594120.1|     ------------------------------------------------------------  1411
gi|73980646|ref|XP_532903.2|     RLLHSDAFPPPRVVDTLGAGDTFNASVIFSLSQGKTMQEALRFGCQVAGKKCGLQGFEGIV  1411
gi|71834554|ref|NP_001025378.1|  ------------------------------------------------------------  1411
                                 ......1360......1370......1380......1390......1400......1410.
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