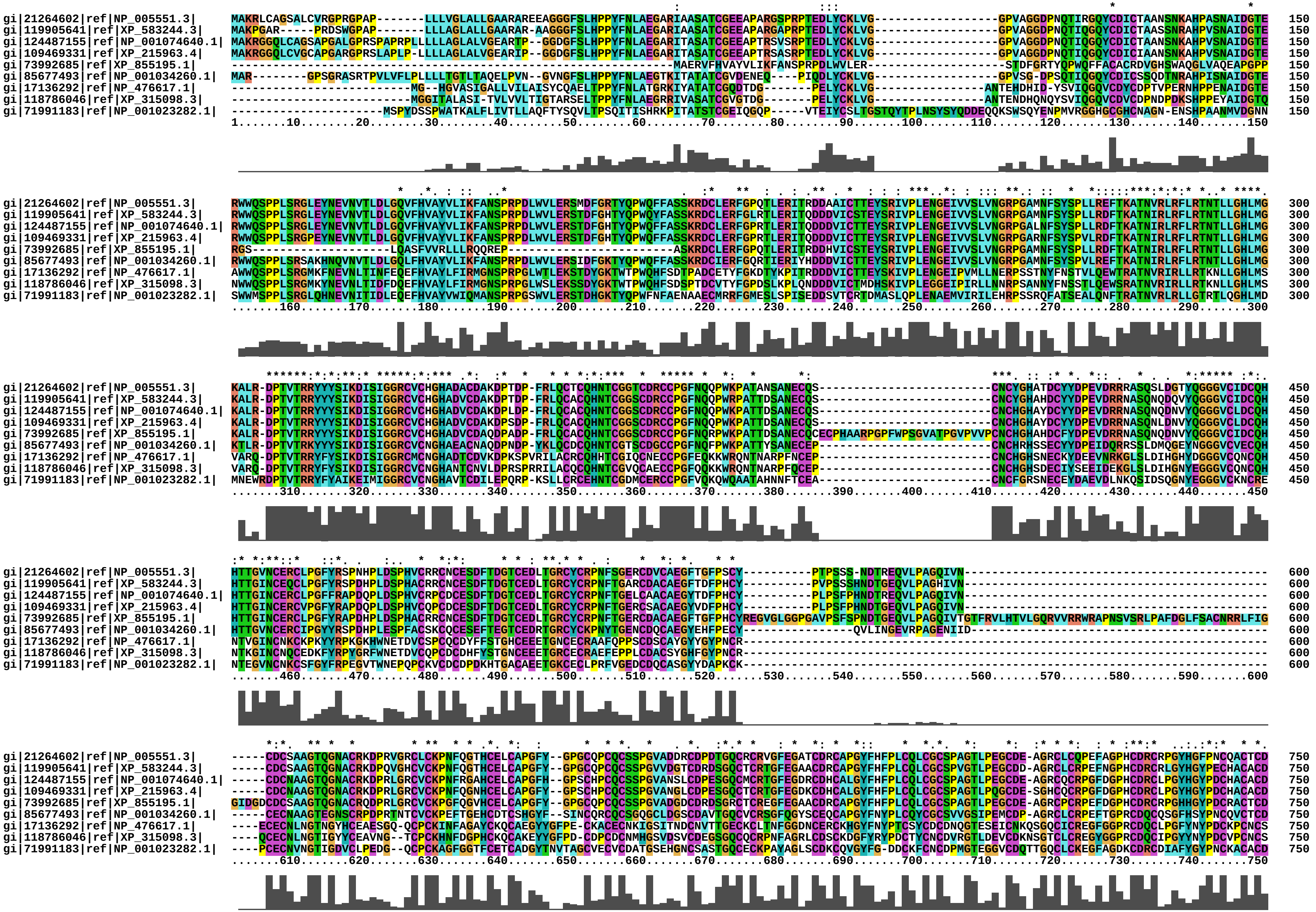

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                                                                                                  :                    :::                                         *                 *
gi|21264602|ref|NP_005551.3|      MAKRLCAGSALCVRGPRGPAP-------LLLVGLALLGAARAREEAGGGFSLHPPYFNLAEGARIAASATCGEEAPARGSPRPTEDLYCKLVG------------------GPVAGGDPNQTIRGQYCDICTAANSNKAHPASNAIDGTE   150
gi|119905641|ref|XP_583244.3|     MAKPGAR-----PRDSWGPAP-------LLLAGLALLGAARAR-AAGGGFSLHPPYFNLAEGARIAASATCGEEAPARGAPRPTEDLYCKLVG------------------GPVAGGDPNQTIQGQYCDICTAASSNRAHPVSNAIDGTE   150
gi|124487155|ref|NP_001074640.1|  MAKRGGQLCAGSAPGALGPRSPAPRPLLLLLAGLALVGEARTP--GGDGFSLHPPYFNLAEGARITASATCGEEAPTRSVSRPTEDLYCKLVG------------------GPVAGGDPNQTIQGQYCDICTAANSNKAHPVSNAIDGTE   150
gi|109469331|ref|XP_215963.4|     MAKRGGQLCVGCAPGARGPRSLAPLP-LLLLAGLALVGEARIP--GGDGFSLHPPYFNLAEGARITASATCGEEAPTRSASRPTEDLYCKLVG------------------GPVAGGDPNQTIQGQYCDICIAANSNKAHPVSNAIDGTE   150
gi|73992685|ref|XP_855195.1|      ----------------------------------------------------------------MAERVFHVAYVLIKFANSPRPDLWVLER--------------------STDFGRTYQPWQFFACACRDVGHSWAQGLVAQEAPGPP   150
gi|85677493|ref|NP_001034260.1|   MAR--------GPSGRASRTPVLVFLPLLLLTGTLTAQELPVN--GVNGFSLHPPYFNLAEGTKITATATCGVDENEQ----PIQDLYCKLVG------------------GPVSG-DPSQTIQGQYCDICSSQDTNRAHPISNAIDGTE   150
gi|17136292|ref|NP_476617.1|      --------------------------MG--HGVASIGALLVILAISYCQAELTPPYFNLATGRKIYATATCGQDTDG-------PELYCKLVG----------------ANTEHDHID-YSVIQGQVCDYCDPTVPERNHPPENAIDGTE   150
gi|118786046|ref|XP_315098.3|     --------------------------MGGITALASI-TVLVVLTIGTARSELTPPYFNLAEGRRIVASATCGVGTDG-------PELYCKLVG----------------ANTENDHQNQYSVIQGQVCDVCDPNDPDKSHPPEYAIDGTQ   150
gi|71991183|ref|NP_001023282.1|   ----------------------MSPYDSSPWATKALFLIVTLLAQFTYSQVLTPSQITISHRKPITATSTCGEIQGQP-----VTEIYCSLTGSTQYTPLNSYSYQDDEQQKSWSQYENPMVRGGHGCGHCNAGN-ENSHPAANMVDGNN   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                                          *  .*. : ::  ..*                         .  :*   **  : . : .** . *  : : : ***..*: : ::: **.: ::  *  *:::::***:*:*:* *..* ****.
gi|21264602|ref|NP_005551.3|      RWWQSPPLSRGLEYNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWVLERSMDFGRTYQPWQFFASSKRDCLERFGPQTLERITRDDAAICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLREFTKATNVRLRFLRTNTLLGHLMG   300
gi|119905641|ref|XP_583244.3|     RWWQSPPLSRGLEYNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWVLERSTDFGHTYQPWQYFASSKRDCLERFGLRTLERITQDDDVICSTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDFTKATNIRLRFLRTNTLLGHLMG   300
gi|124487155|ref|NP_001074640.1|  RWWQSPPLSRGLEYNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWVLERSTDFGHTYQPWQFFASSKRDCLERFGPRTLERITQDDDVICTTEYSRIVPLENGEIVVSLVNGRPGALNFSYSPLLRDFTKATNIRLRFLRTNTLLGHLMG   300
gi|109469331|ref|XP_215963.4|     RWWQSPPLSRGPEYNEVNVTLDLGQVFHVAYVLIKFANSPRPDLWVLERSTDFGHTYQPWQFFASSKRDCLERFGPRTLERITQDDDVICTTEYSRIVPLENGEIVVSLVNGRPGARNFSYSPVLRDFTKATNIRLRFLRTNTLLGHLMG   300
gi|73992685|ref|XP_855195.1|      RGS--------------------LQASFVVRLLLRQQREP------------------------ASKRDCLERFGPQTLERITRDDHVICSTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPLLRDFTKATNIRLRFLRTNTLLGHLMG   300
gi|85677493|ref|NP_001034260.1|   RWWQSPPLSRSAKHNQVNVTLDLGQLFHVAYVLIKFANSPRPDLWVLERSIDFGKTYQPWQFFASSKRDCIERFGQRTIERIYHDDDVICTTEYSRIVPLENGEIVVSLVNGRPGAMNFSYSPVLREFTKATNIRLRFLRTNTLLGHLMG   300
gi|17136292|ref|NP_476617.1|      AWWQSPPLSRGMKFNEVNLTINFEQEFHVAYLFIRMGNSPRPGLWTLEKSTDYGKTWTPWQHFSDTPADCETYFGKDTYKPITRDDDVICTTEYSKIVPLENGEIPVMLLNERPSSTNYFNSTVLQEWTRATNVRIRLLRTKNLLGHLMS   300
gi|118786046|ref|XP_315098.3|     NWWQSPPLSRGMKYNEVNLTIDFDQEFHVAYLFIRMGNSPRPGLWSLEKSSDYGKTWTPWQHFSDSPTDCVTYFGPDSLKPLQNDDDVICTMDHSKIVPLEGGEIPIRLLNNRPSANNYFNSSTLQEWSRATNVRIRLLRTKNLLGHLMS   300
gi|71991183|ref|NP_001023282.1|   SWWMSPPLSRGLQHNEVNITIDLEQEFHVAYVWIQMANSPRPGSWVLERSTDHGKTYQPWFNFAENAAECMRRFGMESLSPISEDDSVTCRTDMASLQPLENAEMVIRILEHRPSSRQFATSEALQNFTRATNVRLRLLGTRTLQGHLMD   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|21264602|ref|NP_005551.3|      KALR-DPTVTRRYYYSIKDISIGGRCVCHGHADACDAKDPTDP-FRLQCTCQHNTCGGTCDRCCPGFNQQPWKPATANSANECQS-------------------------CNCYGHATDCYYDPEVDRRRASQSLDGTYQGGGVCIDCQH   450
gi|119905641|ref|XP_583244.3|     KALR-DPTVTRRYYYSIKDISIGGRCVCHGHADVCDAKDPTDP-FRLQCACQHNTCGGSCDRCCPGFNQQPWRPATTDSANECQS-------------------------CNCYGHAHDCYYDPEVDRRNASQNQDQVYQGGGVCIDCQH   450
gi|124487155|ref|NP_001074640.1|  KALR-DPTVTRRYYYSIKDISIGGRCVCHGHADVCDAKDPLDP-FRLQCACQHNTCGGSCDRCCPGFNQQPWKPATTDSANECQS-------------------------CNCHGHAYDCYYDPEVDRRNASQNQDNVYQGGGVCLDCQH   450
gi|109469331|ref|XP_215963.4|     KALR-DPTVTRRYYYSIKDISIGGRCVCHGHADVCDAKDPSDP-FRLQCACQHNTCGGSCDRCCPGFNQQPWKPATTDSANECQS-------------------------CNCHGHAYDCYYDPEVDRRNASQNLDNVYQGGGVCLDCQH   450
gi|73992685|ref|XP_855195.1|      KALR-DPTVTRRYYYSIKDISIGGRCVCHGHADVCDAQDPADP-FRLQCACQHNTCGGSCDRCCPGFNQRPWKPATTDSANECQCECPHAARPGPFWPSGVATPGVPVVPCNCHGHAHDCFYDPEVDRRNASQNQDNVYQGGGVCIDCQH   450
gi|85677493|ref|NP_001034260.1|   KTLR-DPTVTRKYYYSIKDISIGGRCVCNGHAEACNAQDPNDP-YKLQCDCQHNTCGTSCDGCCPGFNQFPWKPATTYSANECEP-------------------------CNCHRHSSECYYDPEIDQRRSSLDMQGEYNGGGVCVECQH   450
gi|17136292|ref|NP_476617.1|      VARQ-DPTVTRRYFYSIKDISIGGRCMCNGHADTCDVKDPKSPVRILACRCQHHTCGIQCNECCPGFEQKKWRQNTNARPFNCEP-------------------------CNCHGHSNECKYDEEVNRKGLSLDIHGHYDGGGVCQNCQH   450
gi|118786046|ref|XP_315098.3|     VARQ-DPTVTRRYFYSIKDISIGGRCVCNGHANTCNVLDPRSPRRILACQCQHNTCGVQCAECCPGFQQKKWRQNTNARPFQCEP-------------------------CNCHGHSDECIYSEEIDEKGLSLDIHGNYEGGGVCQNCQH   450
gi|71991183|ref|NP_001023282.1|   MNEWRDPTVTRRYFYAIKEIMIGGRCVCNGHAVTCDILEPQRP-KSLLCRCEHNTCGDMCERCCPGFVQKQWQAATAHNNFTCEA-------------------------CNCFGRSNECEYDAEVDLNKQSIDSQGNYEGGGVCKNCRE   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

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gi|21264602|ref|NP_005551.3|      HTTGVNCERCLPGFYRSPNHPLDSPHVCRRCNCESDFTDGTCEDLTGRCYCRPNFSGERCDVCAEGFTGFPSCY----------PTPSSS-NDTREQVLPAGQIVN--------------------------------------------   600
gi|119905641|ref|XP_583244.3|     HTTGINCEQCLPGFYRSPDHPLDSPHACRRCNCESDFTDGTCEDLTGRCYCRPNFTGARCDACAEGFTDFPHCY----------PVPSSSHNDTGEQVLPAGHIVN--------------------------------------------   600
gi|124487155|ref|NP_001074640.1|  HTTGINCERCLPGFFRAPDQPLDSPHVCRPCDCESDFTDGTCEDLTGRCYCRPNFTGELCAACAEGYTDFPHCY----------PLPSFPHNDTREQVLPAGQIVN--------------------------------------------   600
gi|109469331|ref|XP_215963.4|     HTTGINCERCVPGFYRAPDQPLDSPHVCQPCDCESDFTDGTCEDLTGRCYCRPNFTGERCSACAEGYVDFPHCY----------PLPSFPHNDTGEQVLPAGQIVN--------------------------------------------   600
gi|73992685|ref|XP_855195.1|      HTTGINCERCLPGFYRAPDHPLDSPHACRRCNCESDFTDGTCEDLTGRCYCRPNFTGERCDACAEGFTGFPHCYREGVGLGGPGAVPSFSPNDTGEQVLPAGQIVTGTFRVLHTVLGQRVVRRWRAPNSVSRLPAFDGLFSACNRRLFIG   600
gi|85677493|ref|NP_001034260.1|   HTTGVNCERCIPGYYRSPDHPLESPFACSKCQCESEFTEGTCEDRTGRCYCKPNYTGENCDQCAEGYEHFPECY----------------QVLINGEVRPAGENIID-------------------------------------------   600
gi|17136292|ref|NP_476617.1|      NTVGINCNKCKPKYYRPKGKHWNETDVCSPCQCDYFFSTGHCEEETGNCECRAAFQPPSCDSCAYGYYGYPNCR----------------------------------------------------------------------------   600
gi|118786046|ref|XP_315098.3|     NTKGINCNQCEDKFYRPYGRFWNETDVCQPCDCDHFYSTGNCEEETGRCECRAEFEPPLCDACSYGHFGYPNCR----------------------------------------------------------------------------   600
gi|71991183|ref|NP_001023282.1|   NTEGVNCNKCSFGYFRPEGVTWNEPQPCKVCDCDPDKHTGACAEETGKCECLPRFVGEDCDQCASGYYDAPKCK----------------------------------------------------------------------------   600
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                                       *:*.  ** *  *        * **  * * .*. *:  :      *  * *.  *   . *.  :*.* *   : *  *: *  *::    *  *.*.  *:    *:  :* * *:  : * :**:*  ..:.:*:*  * *.
gi|21264602|ref|NP_005551.3|      -----CDCSAAGTQGNACRKDPRVGRCLCKPNFQGTHCELCAPGFY--GPGCQPCQCSSPGVADDRCDPDTGQCRCRVGFEGATCDRCAPGYFHFPLCQLCGCSPAGTLPEGCDE-AGRCLCQPEFAGPHCDRCRPGYHGFPNCQACTCD   750
gi|119905641|ref|XP_583244.3|     -----CDCSAAGTQGNACRKDPQVGHCVCKPNFQGTHCELCAPGFY--GPGCQPCQCSSPGVVDGTCDRDSGQCTCRTGFEGAACDRCAPGYFHFPLCQLCGCSPVGTLPEGCDD-AGRCLCRPEFNGPHCDRCRLGYHGYPECHACACD   750
gi|124487155|ref|NP_001074640.1|  -----CDCNAAGTQGNACRKDPRLGRCVCKPNFRGAHCELCAPGFH--GPSCHPCQCSSPGVANSLCDPESGQCMCRTGFEGDRCDHCALGYFHFPLCQLCGCSPAGTLPEGCDE-AGRCQCRPGFDGPHCDRCLPGYHGYPDCHACACD   750
gi|109469331|ref|XP_215963.4|     -----CDCNAAGTQGNACRKDPRLGRCVCKPNFQGNHCELCAPGFY--GPSCHPCQCSSPGVANGLCDPESGQCTCRTGFEGDKCDHCALGYFHFPLCQLCGCSPAGTLPQGCDE-SGHCQCRPGFDGPHCDRCLPGYHGYPDCHACACD   750
gi|73992685|ref|XP_855195.1|      GIDGDCDCSAAGTQGNACRQDPRLGRCVCKPGFQGVHCELCAPGFY--GPGCQPCQCSSPGVADGDCDRDSGRCTCREGFEGAACDRCAPGYFHFPLCQLCGCSPAGTLPEGCDE-AGRCPCRPEFDGPHCDRCRPGHHGYPDCRACTCD   750
gi|85677493|ref|NP_001034260.1|   -----CECNAAGTEGNSCRPDPRTNTCVCKPEFTGEHCDTCSHGYF--SINCQRCQCSGQGCLDGSCDAVTGQCVCRSGFQGYSCEQCAPGYFNYPLCQYCGCSVVGSIPEMCDP-AGRCLCRPEFTGPRCDQCQSGFHSYPNCQVCTCD   750
gi|17136292|ref|NP_476617.1|      ----ECECNLNGTNGYHCEAESGQ-QCPCKINFAGAYCKQCAEGYYGFPE-CKACECNKIGSITNDCNVTTGECKCLTNFGGDNCERCKHGYFNYPTCSYCDCDNQGTESEICNKQSGQCICREGFGGPRCDQCLPGFYNYPDCKPCNCS   750
gi|118786046|ref|XP_315098.3|     ----QCECNLNGTIGYYCEAVNG--TCPCKHNFDGPHCKQCAKEYYGFPD-CDPCDCNMHGSVDSVCDEGSGQCQCRPNFAGRLCDSCKDGFYRYPDCTYCNCDVRGTLDEVCDKNSGTCLCREGYGGPRCDQCIPGYYNYPDCVPCNCS   750
gi|71991183|ref|NP_001023282.1|   ----PCECNVNGTIGDVCLPEDG--QCPCKAGFGGTFCETCADGYTNVTAGCVECVCDATGSEHGNCSASTGQCECKPAYAGLSCDKCQVGYFG-DDCKFCNCDPMGTEGGVCDQTTGQCLCKEGFAGDKCDRCDIAFYGYPNCKACACD   750
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
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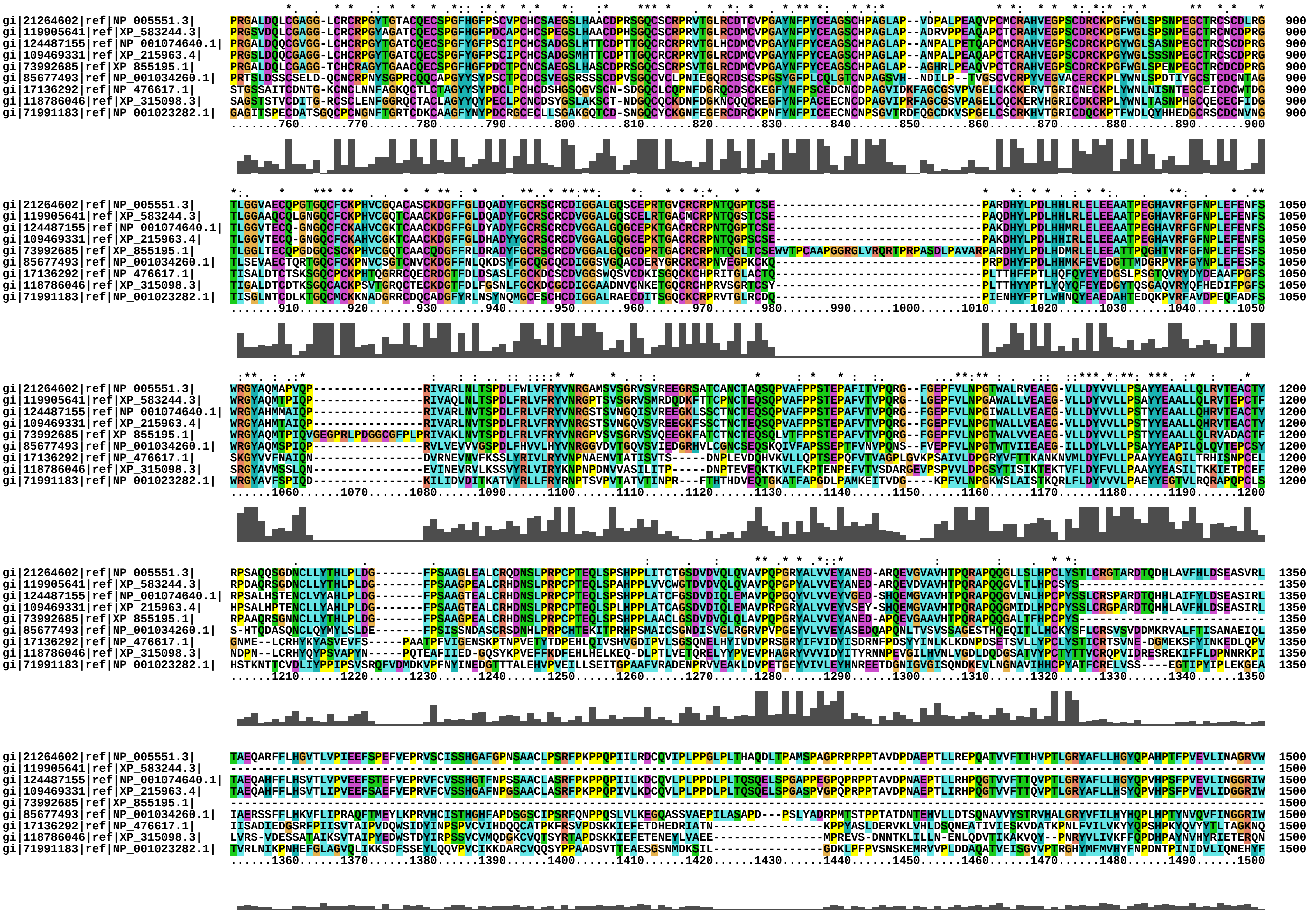

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                                        *.   .  * *   .: *   *   *  .*::  :*.*   *.*    *:    :*     *** *    .  * .*: *   . *.** *:   .*.*:*               .               * *:   * *   *:.*:* :*.*         **   *.*    *
gi|21264602|ref|NP_005551.3|       PRGALDQLCGAGG-LCRCRPGYTGTACQECSPGFHGFPSCVPCHCSAEGSLHAACDPRSGQCSCRPRVTGLRCDTCVPGAYNFPYCEAGSCHPAGLAP--VDPALPEAQVPCMCRAHVEGPSCDRCKPGFWGLSPSNPEGCTRCSCDLRG   900
gi|119905641|ref|XP_583244.3|      PRGSVDQLCGAGG-LCRCRPGYAGATCQECSPGFHGFPDCAPCHCSPEGSLHAACDPHSGQCSCRPRVTGLRCDMCVPGAYNFPYCEAGSCHPAGLAP--ADRVPPEAQAPCTCRAHVEGPSCDRCKPGFWGLSPSNPEGCTRCNCDPRG   900
gi|124487155|ref|NP_001074640.1|   PRGALDQQCGVGG-LCHCRPGYTGATCQECSPGFYGFPSCIPCHCSADGSLHTTCDPTTGQCRCRPRVTGLHCDMCVPGAYNFPYCEAGSCHPAGLAP--ANPALPETQAPCMCRAHVEGPSCDRCKPGYWGLSASNPEGCTRCSCDPRG   900
gi|109469331|ref|XP_215963.4|      PRGSLDQQCGAGG-LCHCRPGYTGATCQECSPGFYGFPSCIPCHCSADGSMHTTCDPTTGQCRCRPRVTGLRCDMCVPGAYNFPYCEAGSCHPAGLAP--ANPALPEAQAPCTCRAHVEGPSCDRCKPGYWGLSSSNPEGCTRCSCDPRG   900
gi|73992685|ref|XP_855195.1|       PRGALDQLCGAGG-TCHCRAGYTGAACQECSPGFHGFPDCTPCNCSAEGSLHASCDPRSGQCSCRPSVTGLRCDMCVPGAYNFPYCEAGSCHPAGLAP--AGHRLPEAQVPCTCRAHVEGPSCDRCKPGFWGLSPENPEGCTRCDCDPRG   900
gi|85677493|ref|NP_001034260.1|    PRTSLDSSCSELD-QCNCRPNYSGPRCQQCAPGYYSYPSCTPCDCSVEGSRSSSCDPVSGQCVCLPNIEGQRCDSCSPGSYGFPLCQLGTCNPAGSVH--NDILP--TVGSCVCRPYVEGVACERCKPLYWNLSPDTIYGCSTCDCNTAG   900
gi|17136292|ref|NP_476617.1|       STGSSAITCDNTG-KCNCLNNFAGKQCTLCTAGYYSYPDCLPCHCDSHGSQGVSCN-SDGQCLCQPNFDGRQCDSCKEGFYNFPSCEDCNCDPAGVIDKFAGCGSVPVGELCKCKERVTGRICNECKPLYWNLNISNTEGCEICDCWTDG   900
gi|118786046|ref|XP_315098.3|      SAGSTSTVCDITG-RCSCLENFGGRQCTACLAGYYQYPECLPCNCDSYGSLAKSCT-NDGQCQCKDNFDGKNCQQCREGFYNFPACEECNCDPAGVIPRFAGCGSVPAGELCQCKERVHGRICDKCRPLYWNLTASNPHGCQECECFIDG   900
gi|71991183|ref|NP_001023282.1|    GAGITSPECDATSGQCPCNGNFTGRTCDKCAAGFYNYPDCRGCECLLSGAKGQTCD-SNGQCYCKGNFEGERCDRCKPNFYNFPICEECNCNPSGVTRDFQGCDKVSPGELCSCRKHVTGRICDQCKPTFWDLQYHHEDGCRSCDCNVNG   900
                                   .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900

                                   *:.     *    *** **   . .   *   * ** : *    .   **..* **:**:     *:    * * *:*.  *  *                              *    *: * *  . : * *:.    .    **:  .    * .**
gi|21264602|ref|NP_005551.3|       TLGGVAECQPGTGQCFCKPHVCGQACASCKDGFFGLDQADYFGCRSCRCDIGGALGQSCEPRTGVCRCRPNTQGPTCSE-------------------------------PARDHYLPDLHHLRLELEEAATPEGHAVRFGFNPLEFENFS  1050
gi|119905641|ref|XP_583244.3|      TLGGAAQCQLGNGQCFCKPHVCGQTCAACKDGFFGLDQADYFGCRSCRCDVGGALGQSCELRTGACMCRPNTQGSTCSE-------------------------------PAQDHYLPDLHHLRLELEEAATPEGHAVRFGFNPLEFENFS  1050
gi|124487155|ref|NP_001074640.1|   TLGGVTECQ-GNGQCFCKAHVCGKTCAACKDGFFGLDYADYFGCRSCRCDVGGALGQGCEPKTGACRCRPNTQGPTCSE-------------------------------PAKDHYLPDLHHMRLELEEAATPEGHAVRFGFNPLEFENFS  1050
gi|109469331|ref|XP_215963.4|      TLGGVTECQ-GNGQCFCKAHVCGKTCAACKDGFFGLDHADYYGCRSCRCDVGGALGQGCEPKTGACRCRPNTQGPSCSE-------------------------------PAKDHYLPDLHHIRLELEEAATPEGHAVRFGFNPLEFENFS  1050
gi|73992685|ref|XP_855195.1|       TLGGLTECQPGDGQCSCKPHVCGQTCAACQDGFFRLDRADYFGCRSCRCDVGGALGQGCDPRTGACRCRPNTQGLTCSEWVTPCAAPGGRGLVRQRTPRPASDLPAVARPARDHYLPDLHDMRLELEEATTPQGHTVRFGFNPLEFESFS  1050
gi|85677493|ref|NP_001034260.1|    TLSEVAECTQRTGQCFCKPNVCSGTCNVCKDGFFNLQKDSYFGCQGCQCDIGGSVGQACDERYGRCRCRPNVEGPKCKQ-------------------------------PRPDHYFPDLHHMKFEVEDGTTMDGRPVRFGYNPLEFESFS  1050
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gi|118786046|ref|XP_315098.3|      TIGALDTCDTKSGQCACKPSVTGRQCTECKDGTFDLFGSNLFGCKDCGCDIGGAADNVCNKETGQCRCHPRVSGRTCSY-------------------------------PLTTHYYPTLYQYQFEYEDGYTQSGAQVRYQFHEDIFPGFS  1050
gi|71991183|ref|NP_001023282.1|    TISGLNTCDLKTGQCMCKKNADGRRCDQCADGFYRLNSYNQMGCESCHCDIGGALRAECDITSGQCKCRPRVTGLRCDQ-------------------------------PIENHYFPTLWHNQYEAEDAHTEDQKPVRFAVDPEQFADFS  1050
                                   .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050

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gi|21264602|ref|NP_005551.3|       WRGYAQMAPVQP----------------RIVARLNLTSPDLFWLVFRYVNRGAMSVSGRVSVREEGRSATCANCTAQSQPVAFPPSTEPAFITVPQRG--FGEPFVLNPGTWALRVEAEG-VLLDYVVLLPSAYYEAALLQLRVTEACTY  1200
gi|119905641|ref|XP_583244.3|      WRGYAQMTPIQP----------------RIVAQLNLTSPDLFRLVFRYVNRGPTSVSGRVSMRDQDKFTTCPNCTEQSQPVAFPPSTEPAFVTVPQRG--LGEPFVLNPGAWALLVEAEG-VLLDYVVLLPSAYYEAALLQLRVTEPCTF  1200
gi|124487155|ref|NP_001074640.1|   WRGYAHMMAIQP----------------RIVARLNVTSPDLFRLVFRYVNRGSTSVNGQISVREEGKLSSCTNCTEQSQPVAFPPSTEPAFVTVPQRG--FGEPFVLNPGIWALLVEAEG-VLLDYVVLLPSTYYEAALLQHRVTEACTY  1200
gi|109469331|ref|XP_215963.4|      WRGYAHMTAIQP----------------RIVARLNVTSPDLFRLVFRYVNRGSTSVNGQVSVREEGKFSSCTNCTEQSQPVAFPPSTEPAFVTVPQRG--FGEPFVLNPGTWALLVEAEG-VLLDYVVLLPSTYYEAALLQHRVTEACTY  1200
gi|73992685|ref|XP_855195.1|       WRGYAQMTPIQVGEGPRLPDGGCGFPLPRIVAKLNVTSPDLFRLVFRYVNRGPVSVSGRVSVQEEGKFATCTNCTEQSQLVTFPPSTEPAFVTVPQRG--FGEPFVLNPGTWALVVEAEG-VLLDYVVLLPSTYYEAALLQLRVADACTF  1200
gi|85677493|ref|NP_001034260.1|    WRGYAQMSPIQP----------------RVLVEVVVGSPDLFHVVLHYVNRGGVDVTGQVSVIEDGRHVLCGNCSEQSKQIVFAPSSEPTFVNVPQNS--FVEPFVLNPGTWTVIIEAEG-ILLDYLVLLPSAYYEAPILQLQVTEPCSY  1200
gi|17136292|ref|NP_476617.1|       SKGYVVFNAIQN----------------DVRNEVNVFKSSLYRIVLRYVNPNAENVTATISVTS-----DNPLEVDQHVKVLLQPTSEPQFVTVAGPLGVKPSAIVLDPGRYVFTTKANKNVMLDYFVLLPAAYYEAGILTRHISNPCEL  1200
gi|118786046|ref|XP_315098.3|      SRGYAVMSSLQN----------------EVINEVRVLKSSVYRLVIRYKNPNPDNVVASILITP-----DNPTEVEQKTKVLFKPTENPEFVTVSDARGEVPSPVVLDPGSYTISIKTEKTVFLDYFVLLPAAYYEASILTKKIETPCEF  1200
gi|71991183|ref|NP_001023282.1|    WRGYAVFSPIQD----------------KILIDVDITKATVYRLLFRYRNPTSVPVTATVTINPR---FTHTHDVEQTGKATFAPGDLPAMKEITVDG----KPFVLNPGKWSLAISTKQRLFLDYVVVLPAEYYEGTVLRQRAPQPCLS  1200
                                   ......1060......1070......1080......1090......1100......1110......1120......1130......1140......1150......1160......1170......1180......1190......1200

                                             .         .         .                                    :     .    :      ** .* *  .*::*              :          :      .   * *:
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gi|71991183|ref|NP_001023282.1|    HSTKNTTCVDLIYPPIPSVSRQFVDMDKVPFNYINEDGTTTALEHVPVEILLSEITGPAAFVRADENPRVVEAKLDVPETGEYVIVLEYHNREETDGNIGVGISQNDKEVLNGNAVIHHCPYATFCRELVSS----EGTIPYIPLEKGEA  1350
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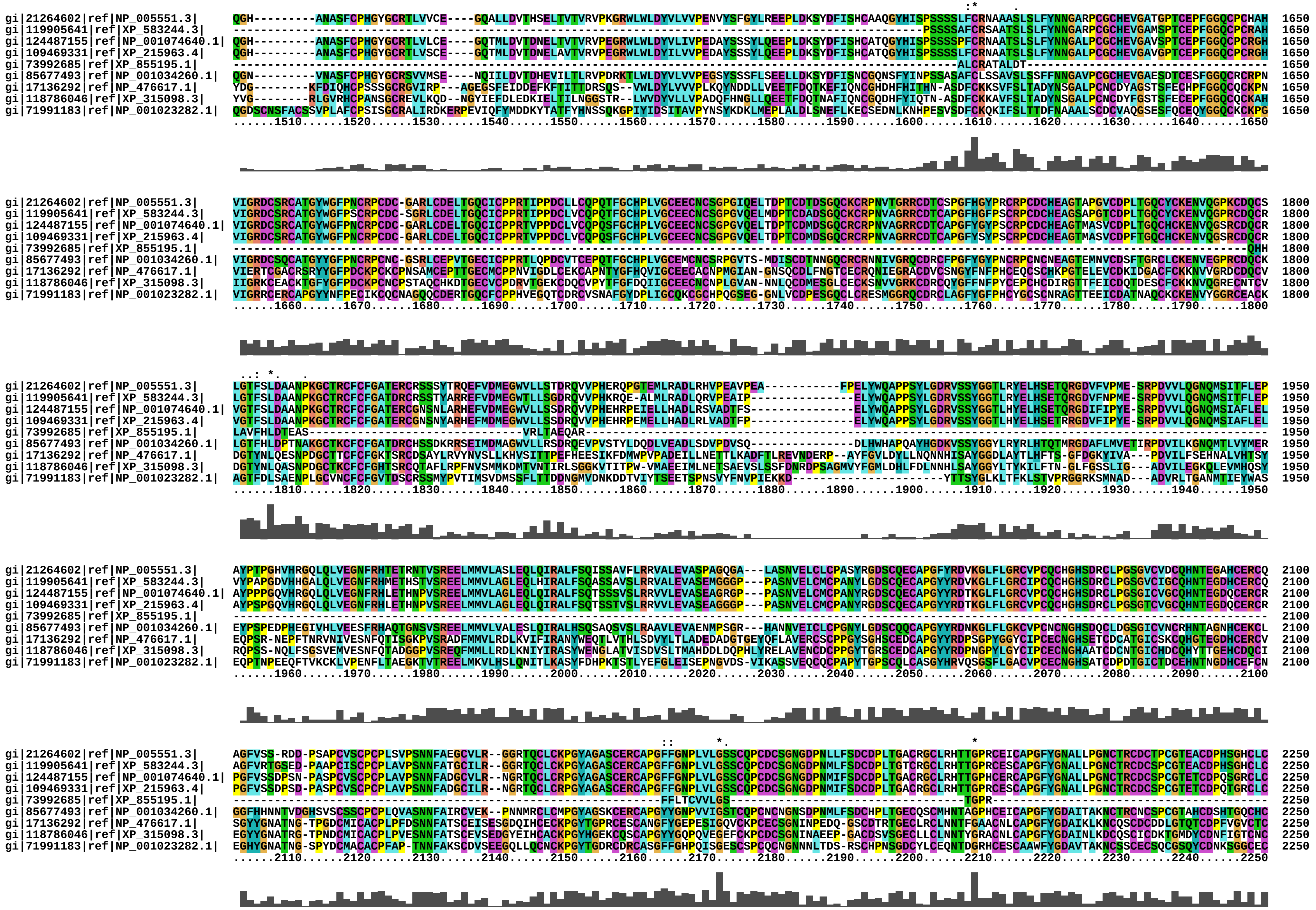

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gi|73992685|ref|XP_855195.1|     LAVFHLDTEAS-------------------------------VRLTAEQAR---------------------------------------------------------------------------------------------------  1950
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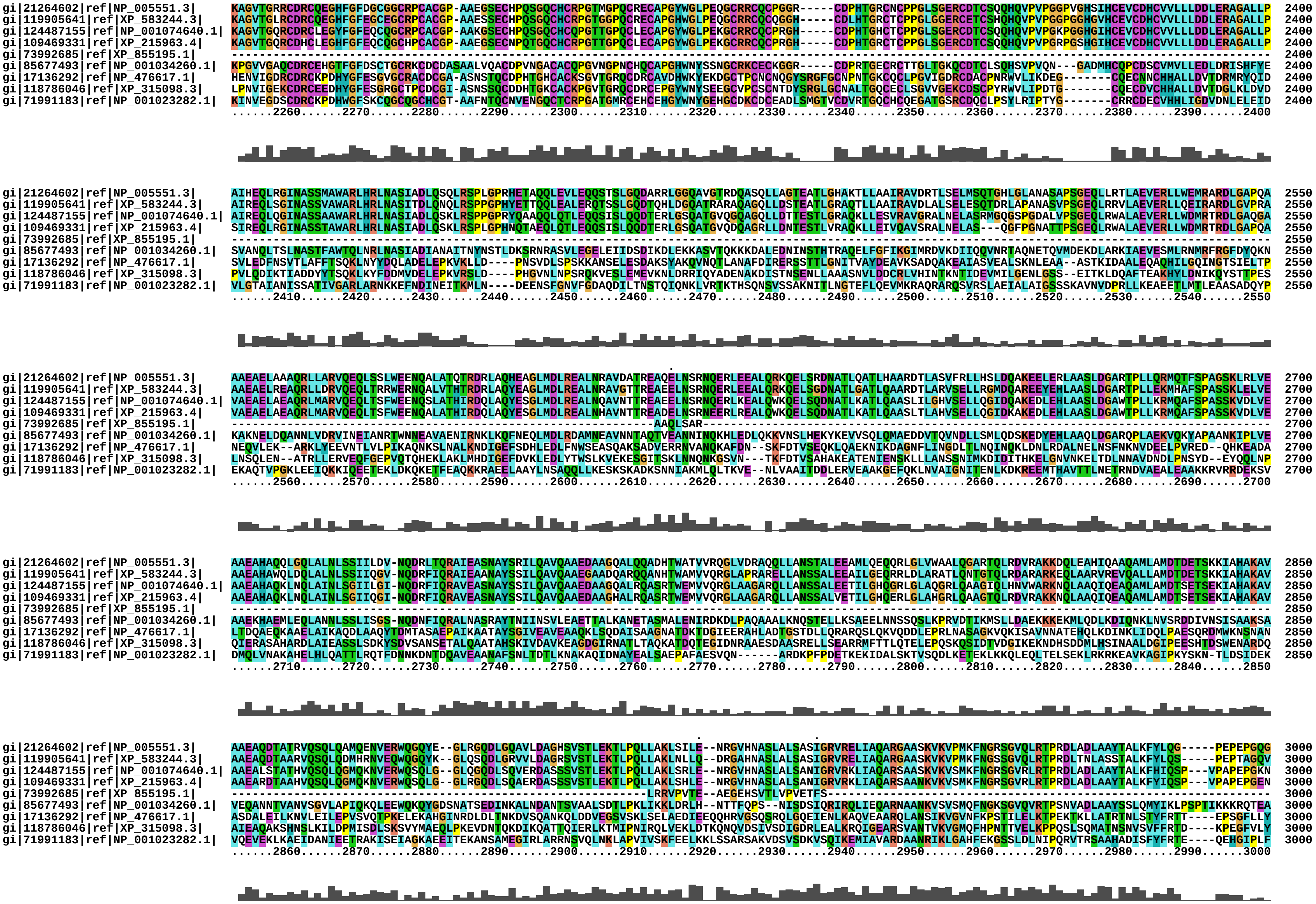

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gi|119905641|ref|XP_583244.3|     AAEAELREAQRLLDRVQEQLTRRWERNQALVTHTRDRLAQYEAGLMDLREALNRAVGTTREAEELNSRNQERLEEALQRKQELSGDNATLGATLQAARDTLARVSELLRGMDQAREEYEHLAASLDGARTPLLEKMHAFSPASSKLELVE  2700
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gi|109469331|ref|XP_215963.4|     VAEAELAEAQRLMARVQEQLTSFWEENQALATHIRDQLAQYESGLMDLREALNHAVNTTREADELNSRNEERLREALQWKQELSQDNATLKATLQAASLTLAHVSELLQGIDKAKEDLEHLAASLDGAWTPLLKRMQAFSPASSKVDLVE  2700
gi|73992685|ref|XP_855195.1|      -------------------------------------------------------------AAQLSAR----------------------------------------------------------------------------------  2700
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gi|71991183|ref|NP_001023282.1|   EKAQTVPGKLEEIQKKIQEETEKLDKQKETFEAQKKRAEELAAYLNSAQQLLKESKSKADKSNNIAKMLQLTKVE--NLVAAITDDLERVEAAKGEFQKLNVAIGNITENLKDKREEMTHAVTTLNETRNDVAEALEAAKKRVRRDEKSV  2700
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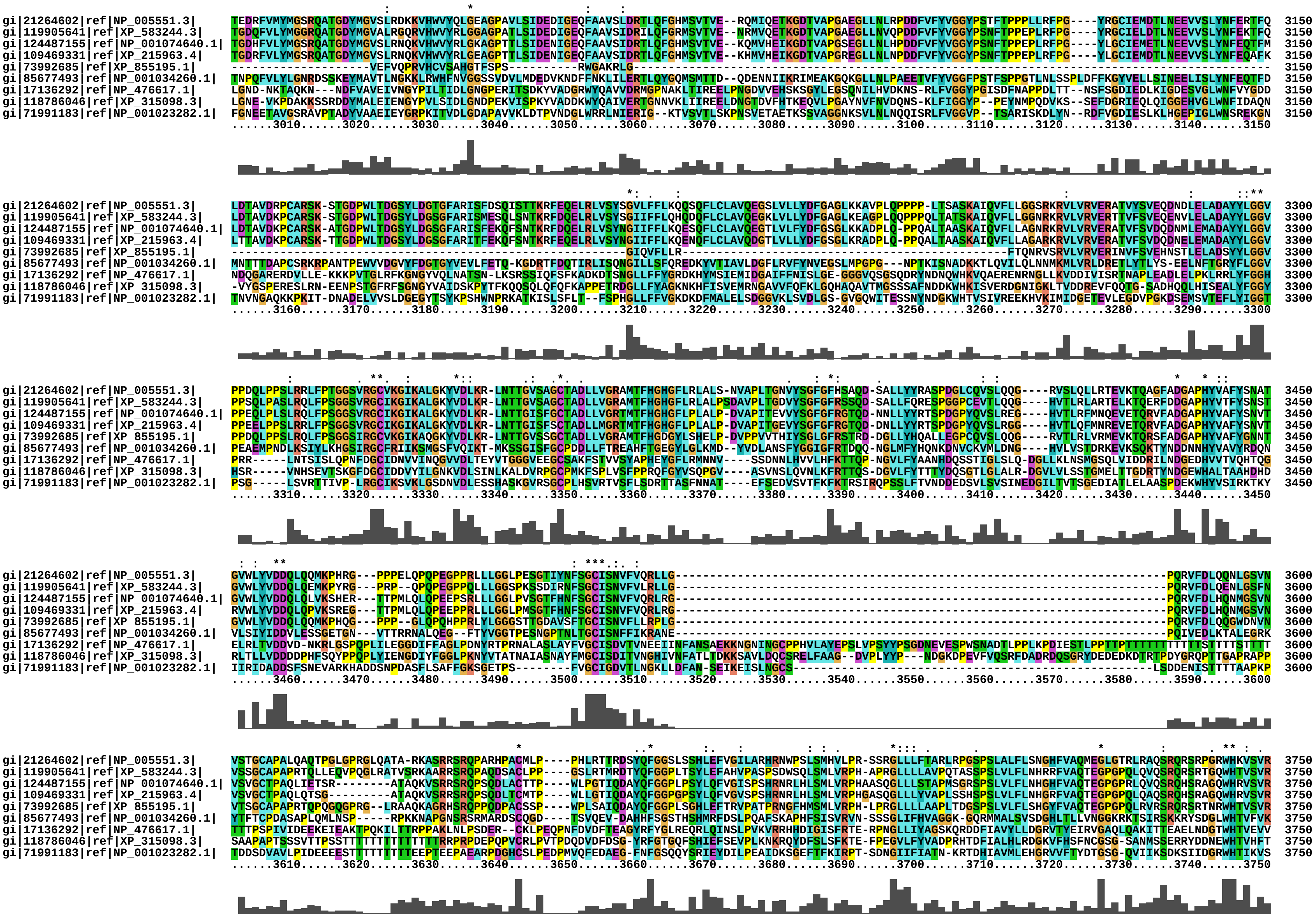

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gi|119905641|ref|XP_583244.3|     TGDQFVLYMGGRQATGDYMGVALRGQRVHWVYRLGGAGPATLSIDEDIGEQFAAVSIDRILQFGRMSVTVE--NRMVQETKGDTVAPGAEGLLNVQPDDFVFYVGGYPSNFTPPEPLRFPG----YRGCIELDTLNEEVVSLYNFEKTFQ  3150
gi|124487155|ref|NP_001074640.1|  TGDHFVLYMGSRQATGDYMGVSLRNQKVHWVYRLGKAGPTTLSIDENIGEQFAAVSIDRTLQFGHMSVTVE--KQMVHEIKGDTVAPGSEGLLNLHPDDFVFYVGGYPSNFTPPEPLRFPG----YLGCIEMETLNEEVVSLYNFEQTFM  3150
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                                                                                           *: .   :                                                       :                 :      ::**
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gi|73992685|ref|XP_855195.1|      ---------------------------------------------------------GIQVFLLR-----------------------------------------------FTQNRVSRVLVRVERINVFSVEHNSTLELADSYYLGGV  3300
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                                          :         . **.  :      *::       .:  .*. .                             .   : *:     .              : :                         *   * ::
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gi|119905641|ref|XP_583244.3|     PPSQLPASLRQLFPSGGSVRGCIKGIKALGKYVDLKR-LNTTGVSAGCTADLLVGRAMTFHGHGFLRLALPSDAVPLTGDVYSGFGFRSSQD-SALLFQRESPGGPCEVTLQQG----HVTLRLARTELKTQERFDDGAPHYVTFYSNST  3450
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                                   : :  **                                         : ***.:. :
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                                                                           *                ..*       :.   :         : : .       *::: .      .                 *        :      . ** : .
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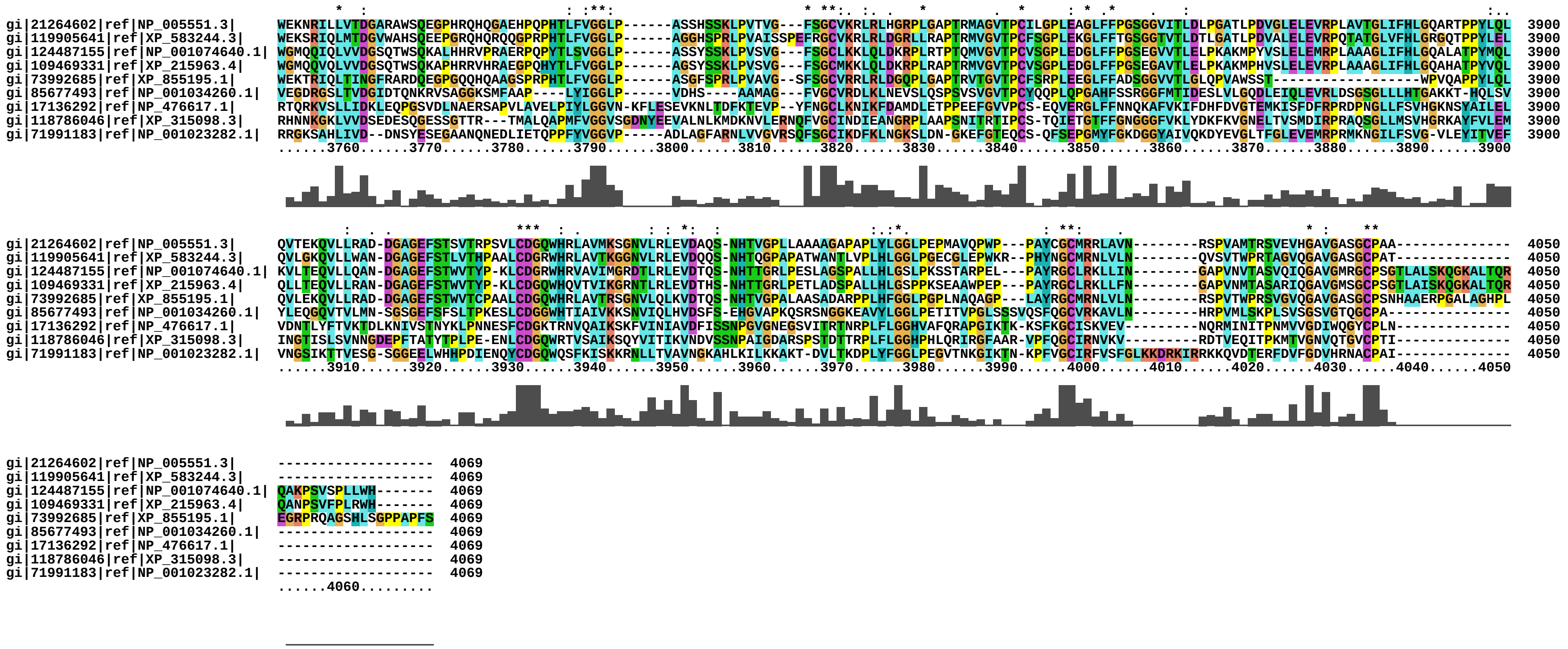
gi|118786046|ref|XP_315098.3|     SAAPAPTSSSVTTPSSTTTTTTTTTTTTTTRRPRPDEPQPVCRLPVTPDQDVDFDSG-YRFGTGQFSHIEFSEVPLKNKRQYDFSLSFKTE-FPEGVLFYVADPRHTDFIALHLRDGKVFHSFNCGSG-SANMSSERRYDDNEWHTVHFT  3750
gi|71991183|ref|NP_001023282.1|   TDDSDVAVLPIDEEEESTTTTTTTTTEEPTEEPAEARPDGHCSLPEDPMVQFEDAEG-FNFGSQQYSRIEYDILPEAIDKSGEFTFKIRPT-SDNGIIFIATN-KRTDHIAVMLEHGRVVFTYDTGSG-QVIIKSDKSIIDGRWHTIKVS  3750
                                  ......3610......3620......3630......3640......3650......3660......3670......3680......3690......3700......3710......3720......3730......3740......3750
```



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                                        *  :                        : :**:                       * **:. :. .   *        .  *     : * .*    .   :                                    :..
gi|21264602|ref|NP_005551.3|     WEKNRILLVTDGARAWSQEGPHRQHQGAEHPQPHTLFVGGLP------ASSHSSKLPVTVG---FSGCVKRLRLHGRPLGAPTRMAGVTPCILGPLEAGLFFPGSGGVITLDLPGATLPDVGLELEVRPLAVTGLIFHLGQARTPPYLQL  3900
gi|119905641|ref|XP_583244.3|    WEKSRIQLMTDGVWAHSQEEPGRQHQRQQGPRPHTLFVGGLP------AGGHSPRLPVAISSPEFRGCVKRLRLDGRLLRAPTRMVGVTPCFSGPLEKGLFFTGSGGTVTLDTLGATLPDVALELEVRPQTATGLVFHLGRGQTPPYLEL  3900
gi|124487155|ref|NP_001074640.1| WGMQQIQLVVDGSQTWSQKALHHRVPRAERPQPYTLSVGGLP------ASSYSSKLPVSVG---FSGCLKKLQLDKRPLRTPTQMVGVTPCVSGPLEDGLFFPGSEGVVTLELPKAKMPYVSLELEMRPLAAAGLIFHLGQALATPYMQL  3900
gi|109469331|ref|XP_215963.4|    WGMQQVQLVVDGSQTWSQKAPHRRVHRAEGPQHYTLFVGGLP------AGSYSSKLPVSVG---FSGCMKKLQLDKRPLRAPTRMVGVTPCVSGPLEDGLFFPGSEGAVTLELPKAKMPHVSLELEVRPLAAAGLIFHLGQAHATPYVQL  3900
gi|73992685|ref|XP_855195.1|     WEKTRIQLTINGFRARDQEGPGQQHQAAGSPRPHTLFVGGLP------ASGFSPRLPVAVG--SFSGCVRRLRLDGQPLGAPTRVTGVTPCFSRPLEEGLFFADSGGVVTLGLQPVAWSST------------------WPVQAPPYLQL  3900
gi|85677493|ref|NP_001034260.1|  VEGDRGSLTVDGIDTQNKRVSAGGKSMFAAP----LYIGGLP------VDHS----AAMAG---FVGCVRDLKLNEVSLQSPSVSVGVTPCYQQPLQPGAHFSSRGGFMTIDESLVLGQDLEIQLEVRLDSGSGLLLHTGAKKT-HQLSV  3900
gi|17136292|ref|NP_476617.1|     RTQRKVSLLIDKLEQPGSVDLNAERSAPVLAVELPIYLGGVN-KFLESEVKNLTDFKTEVP--YFNGCLKNIKFDAMDLETPPEEFGVVPCS-EQVERGLFFNNQKAFVKIFDHFDVGTEMKISFDFRPRDPNGLLFSVHGKNSYAILEL  3900
gi|118786046|ref|XP_315098.3|    RHNNKGKLVVDSEDESQGESSGTTR---TMALQAPMFVGGVSGDNYEEVALNLKMDKNVLERNQFVGCINDIEANGRPLAAPSNITRTIPCS-TQIETGTFFGNGGGFVKLYDKFKVGNELTVSMDIRPRAQSGLLMSVHGRKAYFVLEM  3900
gi|71991183|ref|NP_001023282.1|  RRGKSAHLIVD--DNSYESEGAANQNEDLIETQPPFYVGGVP-----ADLAGFARNLVVGVRSQFSGCIKDFKLNGKSLDN-GKEFGTEQCS-QFSEPGMYFGKDGGYAIVQKDYEVGLTFGLEVEMRPRMKNGILFSVG-VLEYITVEF  3900
                                 ......3760......3770......3780......3790......3800......3810......3820......3830......3840......3850......3860......3870......3880......3890......3900

                                         :  . .               ***  : .        : : *:  :                  :.:*.                : **:    .                      * :    **
gi|21264602|ref|NP_005551.3|     QVTEKQVLLRAD-DGAGEFSTSVTRPSVLCDGQWHRLAVMKSGNVLRLEVDAQS-NHTVGPLLAAAAGAPAPLYLGGLPEPMAVQPWP---PAYCGCMRRLAVN--------RSPVAMTRSVEVHGAVGASGCPAA--------------  4050
gi|119905641|ref|XP_583244.3|    QVLGKQVLLWAN-DGAGEFSTLVTHPAALCDGRWHRLAVTKGGNVLRLEVDQQS-NHTQGPAPATWANTLVPLHLGGLPGECGLEPWKR--PHYNGCMRNLVLN--------QVSVTWPRTAGVQGAVGASGCPAT--------------  4050
gi|124487155|ref|NP_001074640.1| KVLTEQVLLQAN-DGAGEFSTWVTYP-KLCDGRWHRVAVIMGRDTLRLEVDTQS-NHTTGRLPESLAGSPALLHLGSLPKSSTARPEL---PAYRGCLRKLLIN--------GAPVNVTASVQIQGAVGMRGCPSGTLALSKQGKALTQR  4050
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gi|73992685|ref|XP_855195.1|     QVLEKQVLLRAD-DGAGEFSTWVTCPAALCDGQWHRLAVTRSGNVLQLKVDTQS-NHTVGPALAASADARPPLHFGGLPGPLNAQAGP---LAYRGCMRNLVLN--------RSPVTWPRSVGVQGAVGASGCPSNHAAERPGALAGHPL  4050
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gi|17136292|ref|NP_476617.1|     VDNTLYFTVKTDLKNIVSTNYKLPNNESFCDGKTRNVQAIKSKFVINIAVDFISSNPGVGNEGSVITRTNRPLFLGGHVAFQRAPGIKTK-KSFKGCISKVEV---------NQRMINITPNMVVGDIWQGYCPLN--------------  4050
gi|118786046|ref|XP_315098.3|    INGTISLSVNNGDEPFTATYTPLPE-ENLCDGQWRTVSAIKSQYVITIKVNDVSSNPAIGDARSPSTDTTRPLFLGGHPHLQRIRGFAAR-VPFQGCIRNVKV---------RDTVEQITPKMTVGNVQTGVCPTI--------------  4050
gi|71991183|ref|NP_001023282.1|  VNGSIKTTVESG-SGGEELWHHPDIENQYCDGQWQSFKISKKRNLLTVAVNGKAHLKILKKAKT-DVLTKDPLYFGGLPEGVTNKGIKTN-KPFVGCIRFVSFGLKKDRKIRRKKQVDTERFDVFGDVHRNACPAI--------------  4050
                                 ......3910......3920......3930......3940......3950......3960......3970......3980......3990......4000......4010......4020......4030......4040......4050

gi|21264602|ref|NP_005551.3|     -------------------  4069
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gi|109469331|ref|XP_215963.4|    QANPSVFPLRWH-------  4069
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gi|85677493|ref|NP_001034260.1|  -------------------  4069
gi|17136292|ref|NP_476617.1|     -------------------  4069
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gi|71991183|ref|NP_001023282.1|  -------------------  4069
                                 ......4060.........
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