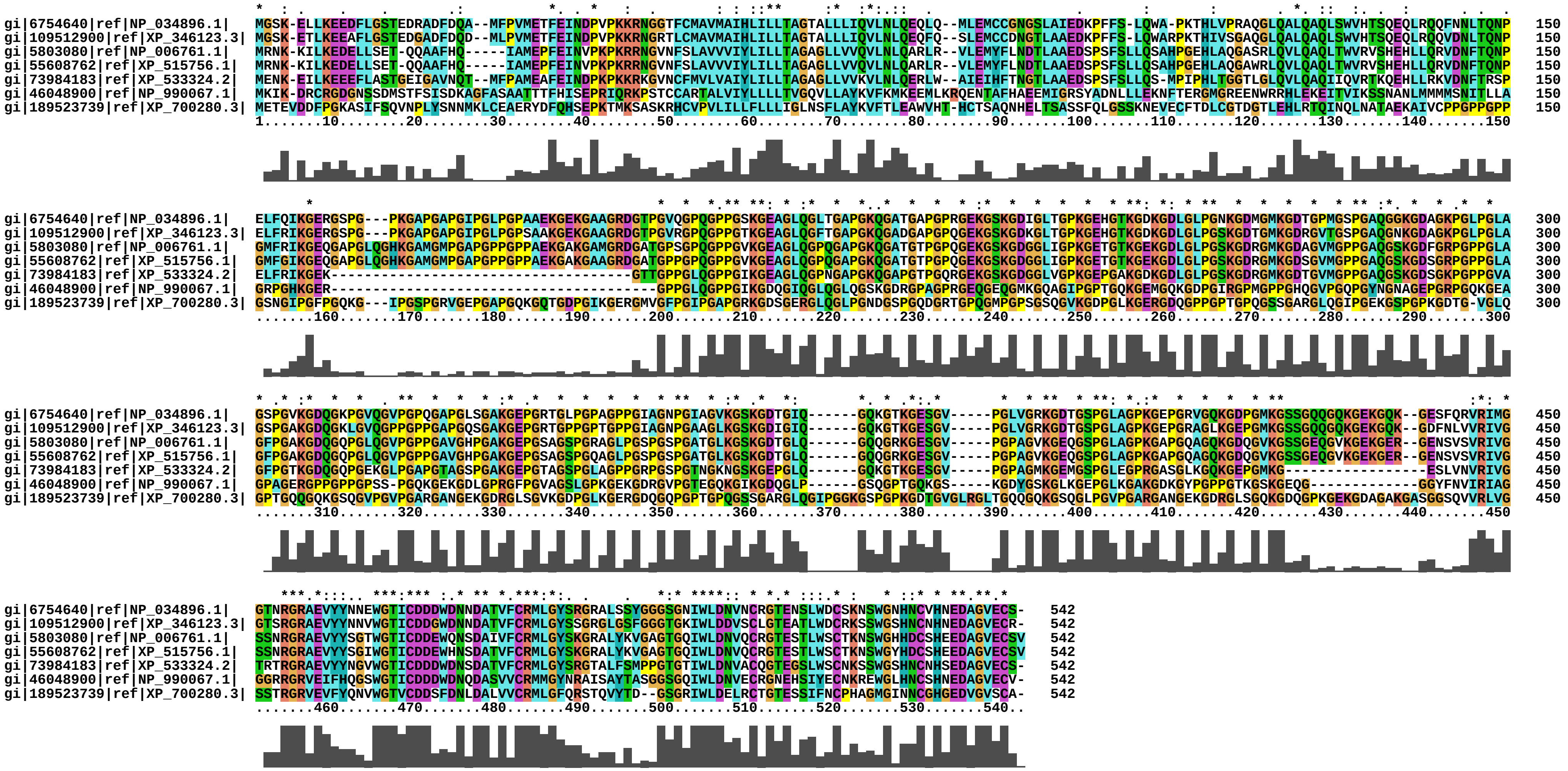

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                                 *  : .    .    .       .:          *. . *   :   .          : : ::**      :*  :*:.::  .              .          :          :          . *. ::  :. .  :          . .  .
gi|6754640|ref|NP_034896.1|      MGSK-ELLKEEDFLGSTEDRADFDQA--MFPVMETFEINDPVPKKRNGGTFCMAVMAIHLILLTAGTALLLIQVLNLQEQLQ--MLEMCCGNGSLAIEDKPFFS-LQWA-PKTHLVPRAQGLQALQAQLSWVHTSQEQLRQQFNNLTQNP   150
gi|109512900|ref|XP_346123.3|    MGSK-ETLKEEAFLGSTEDGADFDQD--MLPVMETFEINDPVPKKRNGRTLCMAVMAIHLILLTAGTALLLIQVLNLQEQFQ--SLEMCCDNGTLAAEDKPFFS-LQWARPKTHIVSGAQGLQALQAQLSWVHTSQEQLRQQVDNLTQNP   150
gi|5803080|ref|NP_006761.1|      MRNK-KILKEDELLSET-QQAAFHQ-----IAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLLVVQVLNLQARLR--VLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVSHEHLLQRVDNFTQNP   150
gi|55608762|ref|XP_515756.1|     MRNK-KILKEDELLSET-QQAAFHQ-----IAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLLVVQVLNLQARLR--VLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGAWRLQVLQAQLTWVRVSHEHLLQRVDNFTQNP   150
gi|73984183|ref|XP_533324.2|     MENK-EILKEEEFLASTGEIGAVNQT--MFPAMEAFEINDPKPKKRKGVNCFMVLVAIYLILLTAGAGLLVVKVLNLQERLW--AIEIHFTNGTLAAEDSPSFSLLQS-MPIPHLTGGTLGLQVLQAQIIQVRTKQEHLLRKVDNFTRSP   150
gi|46048900|ref|NP_990067.1|     MKIK-DRCRGDGNSSDMSTFSISDKAGFASAATTTFHISEPRIQRKPSTCCARTALVIYLLLLTVGQVLLAYKVFKMKEEMLKRQENTAFHAEEMIGRSYADNLLLEKNFTERGMGREENWRRHLEKEITVIKSSNANLMMMMSNITLLA   150
gi|189523739|ref|XP_700280.3|    METEVDDFPGKASIFSQVNPLYSNNMKLCEAERYDFQHSEPKTMKSASKRHCVPVLILLFLLLIGLNSFLAYKVFTLEAWVHT-HCTSAQNHELTSASSFQLGSSKNEVECFTDLCGTDGTLEHLRTQINQLNATAEKAIVCPPGPPGPP   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|6754640|ref|NP_034896.1|      ELFQIKGERGSPG---PKGAPGAPGIPGLPGPAAEKGEKGAAGRDGTPGVQGPQGPPGSKGEAGLQGLTGAPGKQGATGAPGPRGEKGSKGDIGLTGPKGEHGTKGDKGDLGLPGNKGDMGMKGDTGPMGSPGAQGGKGDAGKPGLPGLA   300
gi|109512900|ref|XP_346123.3|    ELFRIKGERGSPG---PKGAPGAPGIPGLPGPSAAKGEKGAAGRDGTPGVRGPQGPPGTKGEAGLQGFTGAPGKQGADGAPGPQGEKGSKGDKGLTGPKGEHGTKGDKGDLGLPGSKGDTGMKGDRGVTGSPGAQGNKGDAGKPGLPGLA   300
gi|5803080|ref|NP_006761.1|      GMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLA   300
gi|55608762|ref|XP_515756.1|     GMFGIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAAGRDGATGPPGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGMKGDSGVMGPPGAQGSKGDSGRPGPPGLA   300
gi|73984183|ref|XP_533324.2|     ELFRIKGEK---------------------------------GTTGPPGLQGPPGIKGEAGLQGPNGAPGKQGAPGTPGQRGEKGSKGDGGLVGPKGEPGAKGDKGDLGLPGSKGDRGMKGDTGVMGPPGAQGSKGDSGKPGPPGVA   300
gi|46048900|ref|NP_990067.1|     GRPGHKGER------------------------------------GPPGLQGPPGIKGDQGIQGLQGLQGSKGDRGPAGPRGEQGEQGMKGQAGIPGPTGQKGEMGQKGDPGIRGPMGPPGHQGVPGQPGYNGNAGEPGRPGQKGEA   300
gi|189523739|ref|XP_700280.3|    GSNGIPGFPGQKG---IPGSPGRVGEPGAPGQKGQTGDPGIKGERGMVGFPGIPGAPGRKGDSGERGLQGLPGNDGSPGQDGRTGPQGMPGPSGSQGVKGDPGLKGERGDQGPPGPTGPQGSSGARGLQGIPGEKGSPGPKGDTG-VGLQ   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|6754640|ref|NP_034896.1|      GSPGVKGDQGKPGVQGVPGPQGAPGLSGAKGEPGRTGLPGPAGPPGIAGNPGIAGVKGSKGDTGIQ------GQKGTKGESGV-----PGLVGRKGDTGSPGLAGPKGEPGRVGQKGDPGMKGSSGQQGQKGEKGQK--GESFQRVRIMG   450
gi|109512900|ref|XP_346123.3|    GSPGAKGDQGKLGVQGPPGPPGAPGQSGAKGEPGRTGPPGPTGPPGIAGNPGAAGLKGSKGDIGIQ------GQKGTKGESGV-----PGLVGRKGDTGSPGLAGPKGEPGRAGLKGEPGMKGSSGQQGQKGEKGQK--GDFNLVVRIVG   450
gi|5803080|ref|NP_006761.1|      GFPGAKGDQGQPGLQGVPGPPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDTGLQ------GQQGRKGESGV-----PGPAGVKGEQGSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGER--GENSVSVRIVG   450
gi|55608762|ref|XP_515756.1|     GFPGAKGDQGQPGLQGVPGPPGAVGHPGAKGEPGSAGSPGQAGLPGSPGSPGATGLKGSKGDTGLQ------GQQGRKGESGV-----PGPAGVKGEQGSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGER--GENSVSVRIVG   450
gi|73984183|ref|XP_533324.2|     GFPGTKGDQGQPGEKGLPGAPGTAGSPGAKGEPGTAGSPGLAGPPGRPGSPGTNGKNGSKGEPGLQ------GQKGTKGESGV-----PGPAGMKGEMGSPGLEGPRGASGLKGQKGEPGMKG-----------------ESLVNVRIVG   450
gi|46048900|ref|NP_990067.1|     GPAGERGPPGPPGPSS-PGQKGEKGDLGPRGFPGVAGSLGPKGEKGDRGVPGTEGQKGIKGDQGLP------GSQGPTGQKGS-----KGDYGSKGLKGEPGLKGAKGDKGYPGPPGTKGSKGEQG-------------GGYFNVIRIAG   450
gi|189523739|ref|XP_700280.3|    GPTGQQGQKGSQGVPGVPGARGANGEKGDRGLSGVKGDPGLKGERGDQGQPGPTGPQGSSGARGLQGIPGGKGSPGPKGDTGVGLRGLTGQQGQKGSQGLPGVPGARGANGEKGDRGLSGQKGDQGPKGEKGDAGAKGASGGSQVVRLVG   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                    ***.*:::.. ***:*** :.* ** *.***:*:.  .    .   *:* ****:: * *.* :::.* :   * ::* * **.**.*
gi|6754640|ref|NP_034896.1|      GTNRGRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYSRGRALSSYGGGSGNIWLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVECS-   542
gi|109512900|ref|XP_346123.3|    GTSRGRAEVYYNNVWGTICDDGWDNNDATVFCRMLGYSSGRGLGSFGGGTGKIWLDDVSCLGTEATLWDCRKSSWGSHNCNHNEDAGVECR-   542
gi|5803080|ref|NP_006761.1|      SSNRGRAEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVECSV   542
gi|55608762|ref|XP_515756.1|     SSNRGRAEVYYSGIWGTICDDEWHNSDATVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWGYHDCSHEEDAGVECSV   542
gi|73984183|ref|XP_533324.2|     TRTRGRAEVYYNGVWGTICDDDWDNSDATVFCRMLGYSRGTALFSMPPGTGTIWLDNVACQGTEGSLWSCNKSSWGSHNCNHSEDAGVECS-   542
gi|46048900|ref|NP_990067.1|     GGRRGRVEIFHQGSWGTICDDDWDNQDASVVCRMMGYNRAISAYTASGGSGQIWLDNVECRGNEHSIYECNKREWGLHNCSHNEDAGVECV-   542
gi|189523739|ref|XP_700280.3|    SSTRGRVEVFYQNVWGTVCDDSFDNLDALVVCRMLGFQRSTQVYTD--GSGRIWLDELRCTGTESSIFNCPHAGMGINNCGHGEDVGVSCA-   542
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540..
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