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gi|6681099|ref|NP_031836.1|      ---MFLEMLNPMQYNVTIMVPETVTV----------------SAMPLLLIMGLLLLIWNCE-SSSSIPGPGYCLGIGPLISHGRFLWMGIGSACNYYNKMYGEFMRVWISGEETLIISKSSSMFHVMKHSHYISRFGSKRGLQCIGMHEN   150
gi|8393227|ref|NP_058781.1|      ---MFLEMLNPMHYNVTIMVPETVPV----------------SAMPLLLIMGLLLLIRNCE-SSSSIPGPGYCLGIGPLISHGRFLWMGIGSACNYYNKMYGEFMRVWISGEETLIISKSSSMVHVMKHSNYISRFGSKRGLQCIGMHEN   150
gi|13904858|ref|NP_000094.2|     ---MVLEMLNPIHYNITSIVPEAMPA----------------ATMPVLLLTGLFLLVWNYE-GTSSIPGPGYCMGIGPLISHGRFLWMGIGSACNYYNRVYGEFMRVWISGEETLIISKSSSMFHIMKHNHYSSRFGSKLGLQCIGMHEK   150
gi|114657058|ref|XP_001169384.1| ---MVLEMLNPIHYNITSIVPEAMPA----------------ATMPVLLLTGLFLLVWNYE-GTSSIPGPGYCMGIGPLISHGRFLWMGIGSACNYYNRVYGEFMRVWISGEETLIISKSSSMFHIMKHNHYSSRFGSKLGLQCIGMHEK   150
gi|56790279|ref|NP_001008715.1|  ---MLLEMLNPMHYNITSMMPEVMPV----------------ATMPILLLTGFLLLVWNYE-DTSSIPGPGYCMGIGPLISHCRFLWMGIGSACNYYNKMYGEFMRVWICGEETLIISKSSSMFHIMKHSHYSSRFGSKLGLQCIGMHEN   150
gi|27805827|ref|NP_776730.1|     ---MLLEVLNPRHYNVTSMVSEVVPI----------------ASIAILLLTGFLLLVWNYE-DTSSIPGPSYFLGIGPLISHCRFLWMGIGSACNYYNKMYGEFMRVWVCGEETLIISKSSSMFHVMKHSHYISRFGSKLGLQFIGMHEK   150
gi|48976119|ref|NP_001001761.1|  ---MIPETLNPLNY-FTSLVPDLMPV----------------ATVPIIILICFLFLIWNHE-ETSSIPGPGYCMGIGPLISHGRFLWMGVGNACNYYNKTYGEFVRVWISGEETFIISKSSSVFHVMKHWNYVSRFGSKLGLQCIGMYEN   150
gi|18858515|ref|NP_571717.1|     ----MMEHVVKDAVNIGAVVQGTLLL----------------LTGTLMLILLHRIFGVKNWR-NQSALPGPGWWLGLGPVLSYSRFLWMGIGTACNYYNEKYGSIARVWINGEETVILSKSSAVYHVLKSNNYTGRFASAKGLQCIGMFEQ   150
gi|183583540|ref|NP_571229.2|    MAGDLLQPCGMKPVRLGEAVVDLLIQRAHNGTERAQDNACGATATILLLLLCLLLAIRHHRPHKSHIPGPSFFFGLGPVVSYCRFIWSGIGTASNYYNSKYGDIVRVWINGEETLILSRSSAVYHVLRKSLYTSRFGSKLGLQCIGMHEQ   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|6681099|ref|NP_031836.1|      GIIFNNNPSLWRTIRPFFMKALTGPGLVRMVEVCVESIKQHLDRLGEVTDTSGYVDVLTLMRHIMLDTSNMLFLGIPLDESAIVKKIQGYFNAWQALLIKPNIFFKISWLYRKYERSVKDLKDEIAVLVEKKRHKVSTAEKLEDCMDFAT   300
gi|8393227|ref|NP_058781.1|      GIIFNNNPSLWRTVRPFFMKALTGPGLIRMVEVCVESIKQHLDRLGDVTDNSGYVDVVTLMRHIMLDTSNTLFLGIPLDESSIVKKIQGYFNAWQALLIKPNIFFKISWLYRKYERSVKDLKDEIEILVEKKRQKVSSAEKLEDCMDFAT   300
gi|13904858|ref|NP_000094.2|     GIIFNNNPELWKTTRPFFMKALSGPGLVRMVTVCAESLKTHLDRLEEVTNESGYVDVLTLLRRVMLDTSNTLFLRIPLDESAIVVKIQGYFDAWQALLIKPDIFFKISWLYKKYEKSVKDLKDAIEVLIAEKRRRISTEEKLEECMDFAT   300
gi|114657058|ref|XP_001169384.1| GIIFNNNPELWKTTRPFFMKALSGPGLVRMVTVCAESLKTHLDRLEEVTNESGYVDVLTLLRRVMLDTSNTLFLRIPLDESAIVVKIQGYFDAWQALLIKPDIFFKISWLYKKYEKSVKDLKDAMEVLIAEKRRRISTEEKLEECMDFAT   300
gi|56790279|ref|NP_001008715.1|  GIIFNNNPTLWKAIRPFFTKALSGPGLVRMVTVCVGSIITHLDRLEEVSNELGYVDVLTLMRRIMLDTSNILFLGIPLDESAIVVKIQGYFDAWQALLLKPDIFFKISWLYKKYEKSVKDLKDAMEILIEEKRHRISTAEKLEDHMDFAT   300
gi|27805827|ref|NP_776730.1|     GIIFNNNPALWKAVRPFFTKALSGPGLVRMVTICADSITKHLDRLEEVCNDLGYVDVLTLMRRIMLDTSNMLFLGIPLDESAIVVKIQGYFDAWQALLLKPDIFFKISWLCRKYEKSVKDLKDAMEILIEEKRHRISTAEKLEDSIDFAT   300
gi|48976119|ref|NP_001001761.1|  GIIFNNNPAHWKEIRPFFTKALSGPGLVRMIAICVESTIVHLDKLEEVTTEVGNVNVLNLMRRIMLDTSNKLFLGVPLDESAIVLKIQNYFDAWQALLLKPDIFFKISWLCKKYEEAAKDLKGAMEILIEQKRQKLSTVEKLDEHMDFAS   300
gi|18858515|ref|NP_571717.1|     GIIFNSNIAKWKKVRTYFTKALTGPGLQKSVEVCVSATNRQLDVLQEFTDASGHVDVLNLLRCIVVDVSNRLFLRIPLNEKELLIKIHRYFSTWQTVLIQPDIFFKLDFVYRKYHLAAKELQDEMGKLVEQKRQAINNTEKLDE-MDFAT   300
gi|183583540|ref|NP_571229.2|    GIIFNSNVALWKKVRAFYAKALTGPGLQRTMEICTTSTNSHLDDLSQLTDAQGQLDILNLLRCIVVDVSNRLFLGVPLNEHDLLQKIHKYFDTWQTVLIKPDVYFRLDWLHRKHKRDAQELQDAITALIEQKKVQLAHAEKLDH-LDFTA   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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gi|6681099|ref|NP_031836.1|      DLIFAERRGDLTKENVNQCILEMLIAAPDTMSVTLYFMLLLVAEYPEVEAAILKEIHTVVGDRDIKIEDIQNLKVVENFINESMRYQPVVDLVMRRALEDDVIDGYPVKKGTNIILNIGRMHRLEYFPKPNEFTLENFEKNVPYRYFQPF   450
gi|8393227|ref|NP_058781.1|      DLIFAERRGDLTKENVNQCILEMLIAAPDTMSVTLYVMLLLIAEYPEVETAILKEIHTVVGDRDIRIGDVQNLKVVENFINESLRYQPVVDLVMRRALEDDVIDGYPVKKGTNIILNIGRMHRLEYFPKPNEFTLENFEKNVPYRYFQPF   450
gi|13904858|ref|NP_000094.2|     ELILAEKRGDLTRENVNQCILEMLIAAPDTMSVSLFFMLFLIAKHPNVEEAIIKEIQTVIGERDIKIDDIQKLKVMENFIYESMRYQPVVDLVMRKALEDDVIDGYPVKKGTNIILNIGRMHRLEFFPKPNEFTLENFAKNVPYRYFQPF   450
gi|114657058|ref|XP_001169384.1| ELILAEKRGDLTRENVNQCILEMLIAAPDTMSVSLFFMLFLIAKHPNVEEAIIKEIQTVIGERDIKIDDIQKLKVMENFIYESMRYQPVVDLVMRKALEDDVIDGYPVKKGTNIILNIGRMHRLEFFPKPNEFTLENFAKNVPYRYFQPF   450
gi|56790279|ref|NP_001008715.1|  ELIFAEKRGELTRENVNQCILEMLIAAPDTMSVSVFFMLFLIAKHPKVEESIMKEIQAVVGERDIRIDDMQKLKVVENFIYESMRYQPVVNLVMRKALQDDIIDGYLVKKGTNIILNIGRMHRLEFFPKPNEFTLENFAKNVPYRYFQPF   450
gi|27805827|ref|NP_776730.1|     ELIFAEKRGELTRENVNQCILEMLIAAPDTMSVSVFFMLFLIAKHPQVEEAIIREIQTVVGERDIRIDDMQKLKVVENFINESMRYQPVVDLVMRKALEDDVIDGYPVKKGTNIILNLGRMHRLEFFPKPNEFTLENFAKNVPYRYFQPF   450
gi|48976119|ref|NP_001001761.1|  QLIFAQNRGDLTAENVNQCVLEMMIAAPDTLSVTLFIMLILIADDPTVEEKMMREIETVMGDREVQSDDMPNLKIVENFIYESMRYQPVVDLIMRKALQDDVIDGYPVKKGTNIILNIGRMHKLEFFPKPNEFSLENFEKNVPSRYFQPF   450
gi|18858515|ref|NP_571717.1|     ELIFAQNHDELSVDDVRQCVLEMVIAAPDTLSISLFFMLLLLKQNSAVEEQIVQEIQSQIGSRDVESADLQKLNVLERFIKESLRYHPVVDFIMRQSLEDDYIDGYRVAKGTNLILNIGRMHKTEFFKKPNEFSLENFENTVPSRYFQPF   450
gi|183583540|ref|NP_571229.2|    ELIFAQSHGELSAENVRQCVLEMVIAAPDTLSISLFFMLLLLKQNPDVELKILQEMDSVLAGQSLQHSHLSKLQILESFINESLRFHPVVDFTMRRALDDDVIEGYNVKKGTNIILNVGRMHRSEFFSKPNQFSLDNFHKNVPSRFFQPF   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                 * ***.*.**.*:*** * :**::* *  *  . :   :..: :  .** :  *     : :
gi|6681099|ref|NP_031836.1|      GFGPRGCAGKYIAMVMMKVVLVTLLRRFQVKTLQKRCIENIPKKNDLSLHPNED-RHLVEIIFSPRNSDKYLQQ--------   532
gi|8393227|ref|NP_058781.1|      GFGPRSCAGKYIAMVMMKVVLVTLLKRFHVKTLQKRCIENMPKNNDLSLHLDED-SPIVEIIFRHIFNTPFLQCLYISL---   532
gi|13904858|ref|NP_000094.2|     GFGPRGCAGKYIAMVMMKAILVTLLRRFHVKTLQGQCVESIQKIHDLSLHPDET-KNMLEMIFTPRNSDRCLEH--------   532
gi|114657058|ref|XP_001169384.1| GFGPRGCAGKYIAMVMMKAILVTLLRRFHVKTLQGQCVESIQKIHDLSLHPDET-KNMLEMIFTPRNSDRCLEH--------   532
gi|56790279|ref|NP_001008715.1|  GFGPRSCAGKYIAMVMMKVVLVTLLRRFHVQTLQGECIENMQKKYGLSLHPDET-NNLLEMVFVPRNSEKCLER--------   532
gi|27805827|ref|NP_776730.1|     GFGPRACAGKYITMVMMKVVLVTLLRRFHVQTLQGRCVEKMQKKNDLSLHPDET-RDRLEMIFTPRNSDKCLER--------   532
gi|48976119|ref|NP_001001761.1|  GFGPRGCVGKFIAMVMMKAILVTLLRRCRVQTMKGRGLNNIQKNNDLSMHPIER-QPLLEMVFTQEAQTRIRVTKVDQH---   532
gi|18858515|ref|NP_571717.1|     GCGPRACVGKHIAMVMTKAILVTMLSRFTVCPRHGCTISTIKQTNNLSMQPVEEDPDCLAMRFIPRAQNSNGETADNRTSKE   532
gi|183583540|ref|NP_571229.2|    GSGPRSCVGKHIAMVMMKSILVALLSRFSVCPMKACTVENIPQTNNLSQQPVEE-PSSLSV--------------------   532
                                 .......460.......470.......480.......490.......500.......510.......520.......530..
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