

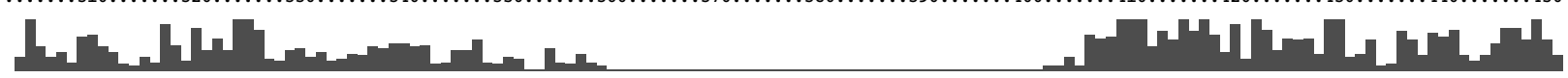
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gi 45187599 ref NP_983822.1 -----MEPTPGIITHDGNLNFKNTVNYLQELP-QPVQSRLYQSPATCLAIYR-LLSPMAKFFIMSMFQDEEVSRLRDLDRWVWPDA--KFLQHDIAIKSMKLLHLITTEGRS--GQPLMVQNSIFKESFKNALGG 125
gi 6325135 ref NP_015203.1 -----MSDYSLKHSVTQYLEETP-QQVQNRLYTSPATCLAIYR-ILPPLAKFFIMAMVFNENEVPLDLDKQWNSNG--KLFQFQNAIKSMKSLHLLTPNKKS--SGFLMNTNPTFKISLRNALGG 116
gi 19113355 ref NP_596563.1 -----MQAEFKSSINDFLQELP-N--HARLYQKPAACLAIFR-LLPILARQVVMMSLNFMPADSDDFDLWIKLSS--KVQSESFNKLVRMHIFQFDG--GYITLNSFBRKQFTTALTGG 109
gi 39974913 ref XP_368847.1 -----MSQGVVITLSDHLEKQN-GATFKKLYQQPAAFAIFRMLPPLAKFFVMVSLLYMPQPLPLAALDSVWVKEA--KKNKDQALSILRSMHITITPTVKHKPVOEMSLTFFNKFSRLRLALEGG 119
gi 32409795 ref XP_325378.1 -----MSLG-GQQLLEYLLEKLP-GTAFRRLYQSPATCLAIYR-LLSPMAKFFIMSMFQDEEVSRLRDLDRWVWPDA--KQPLLRLLNPIFKKSFKNVLGG 119
gi 21357821 ref NP_648780.1 -----MSEAKKSGSRHSAAAGSGNAVLNPLQGGPANLECKDFEYLRTQPL-PEVLEKLYNYPICLAIFR-ELPELARQFVIRILRFVDPVPOAVVTSWGAQRK--AKQABATSCLALNVRVTAIF--GGLSAWELSPFFKSVRQVLLGG 145
gi 31201525 ref XP_309710.1 -----MADKRSQSGSRTTSGKSSSSGSLIKPANLECKDFEYLRTQPL-PEVLEKLYNYPICLAIFR-ELPELARQFVIRILRFVDPVPOAVVTSWGAQRK--AKQABATSCLALNVRVTAIF--GGLSAWELSPFFKSVRQVLLGG 144
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gi 114606289 ref XP_518339.2 -----MESVPSRG-----LNRVHLOCRNLQEFGLGGLS-PGVLDRLYGHGPAICLAIFR-ELPPLAKNVMRMLFLEQPLPQAAVALWVKKKEF--SKAQEESTGLLSGLRIWHTQLLP--GGLOGLILNPIFRONLRIALGG 126
gi 6754094 ref NP_034494.1 -----MEITPARGG-----LNRVHLOCRNLQEFGLGGLS-PGVLDRLYGHGPAICLAIFR-ELPPLAKNVMRMLFLEQPLPQAAVALWVKKKEF--SKAQEESTGLLSGLRIWHTQLLP--GGLOGLILNPIFRONLRIALGG 127
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gi 73972150 ref XP_848919.1 -----MEITPARGG-----LNRVHLOCRNLQEFGLGGLS-PGVLDRLYGHGPAICLAIFR-ELPPLAKNVMRMLFLEQPLPQAAVALWVKKKEF--SKAQEESTGLLSGLRIWHTQLLP--GGLOGLILNPIFRONLRIALGG 127
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gi 42572935 ref NP_974564.1 -----MPQVKTIANKNFMMDVASLP-AIKLDKLYNNTVFCIAILLR-SLPPLAKKIVLQMLYIVDPVPAIMMEEWVLDG--TSKHRVAIDRLQLRIFSEISDR--KRGTSVSLNPTFONNLKHIISGG 118
gi 115461368 ref NP_001054284.1 -----MPQVMVVARNFMMDVAALP-AAKLDMLYDSAFICIAVLR-SLPPLAKKIVLQMLYIVDPVPAIMMEEWVLDG--AAKHRVAIDRLQLRIFSEISDR--KRGTSVSLNPTFONNLKHIISGG 118



gi 50310215 ref XP_455127.1 INNSFGD-VADDITNPFVSAITLDQVSAEKWEITILE-----YVVGTPNTN-----IPGGKVLDDLQHSGLMEE-AEYCG-E--LKIINOGFQFLLQDVNAQMWLTLLOYLKMAES--LQMDPVDVNLFIPLMGAQLG 235
gi 45187599 ref NP_983822.1 VKNSFGN-VVEENDPVTMAMLDVSAADKWEITILE-----FMVGPLTK-----SPGKNVLSLLRHSKLMVE-DESSKE--LKIINOGFQFLLQDANAIWTLLOYLTMABE--FQMDPVDVNLFIPLMGALELG 245
gi 6325135 ref NP_015203.1 VQNSFGV-VVEEN--VVSLLDLDVSAANKWEITILE-----FMVGPLAK-----IPSEKVLNLLKHSKLMVE-VNSTGE--FKIINOGFQFLLQDINSQWTLLOYLKMIET--SKMDLVDFVLFHFLMGALEVG 234
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gi 115461368 ref NP_001054284.1 -SLPREPISSVTRARLPTLAELSFALQEWVMTKAVVCIISYCLNATNVHSPSK-----GHSFLYKGLVLLAADDQLISSRERDKFQLIHDFNFAARSSSEFKLMEINAQLWYIMREYISAAE--RGVDPTEILSFLQFSFTLG 258



gi 50310215 ref XP_455127.1 KAYKCDQLSNQRTMLQDMRDYGLIYONSDYAKFYPTRLATLLTSDTKAFRSASVALDSVLNKA-----NETI-----AVEGDSGQDE--TTEERTDGLIIEINFKLYSYNSPLOIAIILSLFVHLKSRFANMVGQITRESVR 369
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gi 19113355 ref NP_596563.1 RAYSVDFTLTDIQQIMLEDLREYGLVQKRIITSKRFYPTRLATGLTIDYRSLSHGKQSEND-----DD-----KGFIVETNRYLYAYTSELOIATIALIFGFANLRFANLNVVGVITRDSIR 338
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gi 42572935 ref NP_974564.1 QANNLNTLTVQNNILKDLADLGLVKLOCRKDSWFIPTKLAITNLVSLADSSARKEG-----FVVVETNRYLYAYTSELOIATIALIFGFANLRFANLNVVGVITRDSIR 356
gi 115461368 ref NP_001054284.1 EAYSLLNTLTVQNNILKDLADLGLVKLOCRKDSWFIPTKLAITNLVSLADSSARKEG-----FVVVETNRYLYAYTSELOIATIALIFGFANLRFANLNVVGVITRDSIR 356



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gi | 45187599 | ref | NP_983822.1 | RALHNGITADQIIAYMETHAHPQMRRLAEDNLEKKLELDPNCRDPTLQVLPPTVVDQIKLWOLELDRIIISYDGYLFRDFDLQEQVLAQYARDIGVLLWSDDKKKMFVSKEGNAQVIDFFHKKRFRKK----- 514
gi | 6325135 | ref | NP_015203.1 | RALTNGITADQIIAYLETHAHPQMRRLAEELKLELDPNCKEPLQVLPPTVVDQIRLWOLELDRVIIEGSLYSDFEISQEYNLLSKYADIGVLLWQDDKKKFFIISKEGNSQVLDFAKRKLKQ----- 513
gi | 19113355 | ref | NP_596563.1 | RALMNGIAAEQIIITVLTTHAHPQMR-----SNVPLLPPTLVDDQIYLWELKRNLRATPGILFRDFLIDSGFDQAVEYAKELGVLVWSDSLKRMFFITTTGAQPMIAVLRRAVK----- 447
gi | 39974913 | ref | XP_368847.1 | RAISHGITADQIIIEYLASHAHEQMHRIAAIR-----NKPVLPPPTVVDQIRLWOLELTERMQVQRGYLFDKDFESQAEFKAIADYAEVGVLIWRSDARQLFFASKT--AEIANFIKSEKHKRKLAA----- 490
gi | 32409795 | ref | XP_325378.1 | QAIGFGITADQIIISYLAHAHQQMVREATVT-----GKPVLPPTVVDQIRLWOLENERMQTAGFLKDFESTEEYAALSRYAEEIGVLVWKNDRKQLFFASKH--EQLRDVLRKSRKGE----- 501
gi | 21357821 | ref | NP_648780.1 | QALRGGITAEQIIVSYLQYAHFNMRMVESAI-----HKSCLPPTVVDQIKLWELERNRFTYIEGVLYNQFLSHTDFVILRDYASISIHMLWQNERTRIMVQKNGHDDVKRFWKKYSKSGV----- 499
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gi | 4504201 | ref | NP_001508.1 | QAIASGITAEQIIHFLLRTRAHFVMLKOT-----PVLPPPTITDQIRLWELERDRLRFTIEGVLYNQFLSQVDFELLHAHARELGVLVFNESAKRLMVTTPAGHSDVKRFWKKRKHSE----- 462
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