

gi | 28872778 | ref | NP_037501.2 |MAAIPALDPEAEPEMDVILVGSSELSSVSPGTGRDLIAYEVKANQRNIEDICICCGSLQVHTQHPLEGGGICAPCKDKFLDALFLYDDDGYSYCSICCGSETLLICGNP 111
gi | 114684638 | ref | XP_525483.2 |MAAIPALDPEAEPEMDVILVGSSELSSISPRIGRDLIAYEVKANQRNIEDICICCGSLQVHTQHPLEGGGICAPCKDKSILDALFLYDDDGYSYCSICCGSETLLICGNP 111
gi | 74001340 | ref | XP_849972.1 |MAHSSLGTLNLETMDGSDPPDPPALPPDREQWPPCEILLDPEPEHSLDIILVGSSELSSPPSPGPRRDFIAYEVKNQRDIEDVCIICCGSLQVHTQHPLEGGGICAPCKDKFLDCLFLYDDDGYSYCSICCGRDLLICENP 60
gi | 119887082 | ref | XP_869990.2 |MGSRETPSSCKTLETLDLETSDSSSPDA---DPLLEEQLKSSPALKE-DVVDVLEDCKEPLSPSSPPTGEMIRYEVKVNRRSIEDICLCCGTLOVYTRHPLEGGGICAPCKDKFLESLFLYDDDGYSYCTICCGGTLFICENP 142
gi | 126158899 | ref | NP_001075164.1 |MGSRETPSSCKTLETLDLETSDSSSPDA---DPLLEEQLKSSPALKE-DVVDVLEDCKEPLSPSSPPTGEMIRYEVKVNRRSIEDICLCCGTLOVYTRHPLEGGGICAPCKDKFLESLFLYDDDGYSYCTICCGGTLFICENP 145
gi | 51556269 | ref | NP_001003964.1 |MGSRETPSSCKTLETLDLETSDSSSPDA---DPLLEEQLKSSPALKE-DVVDVLEDCKEPLSPSSPPTGEMIRYEVKVNRRSIEDICLCCGTLOVYTRHPLEGGGICAPCKDKFLESLFLYDDDGYSYCTICCGGTLFICENP 146
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



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gi | 28872778 | ref | NP_037501.2 | DCTRCYCFEVDILVGPSTSGKVHAMSNNVFCVLCPLPSRSGLLQRRRKRWSQKAFYDRESENPLEMFETVPVWRROPVVRVLSLFEDIKKEKLSLGFLES--GSDPGQLKVVVDVDTVRKDVVEEWGPFDLVYGATPPLGHTCDRPPSWY 259
gi | 114684638 | ref | XP_525483.2 | DCTRCYCFEVDILVGPSTSGKVHAMSNNVFCVLCPLPSRSGLLQRRRKRWSQKAFYDRESENPLEMFETVPVWRROPVVRVLSLFEDIKKEKLSLGFLES--GSDPGQLKVVVDVDTVRKDVVEEWGPFDLVYGATPPLGHTCDRPPSWY 259
gi | 74001340 | ref | XP_849972.1 | DCTRCYCFKCVDTLVAPGTSGRVQAATSNVVCFLCRFPFRSGLLQRRRKRWGLKAFCDREKSEPLETVEYVPPVWRREPVRVLSLFEDIKKEKLSLGFLES--GNPAGLKHLDVVDTVRRDVEEWGPFNLYVGTPLGHTCDRPPSWY 208
gi | 119887082 | ref | XP_869990.2 | DCTRCYCFEVDILVGPSTSGKVHAMSNNVFCVLCPLPSRSGLLQRRRKRWTWKAFYDREASEPLVMYKIVPVWRREPVRVLSLFEDIKKEKLSLGFLES--GKPGRLKHLDDVTNIVRRDVEEWGPFDLVYGTPLGHTCDRPPSWY 290
gi | 126158899 | ref | NP_001075164.1 | DCTRCYCFEVDILVGPSTSERINAMACVVCFLCLPFPSRSGLLQRRRKRWHQKAFHDREGASPVETVYKIVPVWRREPVRVLSLFERNIDKVLKSLGFLES--GGGGTLKYVEDVTVVRRDVEEWGPFDLVYGTPLGSSCDRCPGWY 295
gi | 51556269 | ref | NP_001003964.1 | DCTRCYCFEVDILVGPSTSERINAMACVVCFLCLPFPSRSGLLQRRRKRWHQKAFHDREGASPVETVYKIVPVWRREPVRVLSLFERNIDKVLKSLGFLES--GGGGTLKYVEDVTVVRRDVEEWGPFDLVYGTPLGYSCDRCPGWY 296
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



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gi | 28872778 | ref | NP_037501.2 | LFCFHRLLOYARPKPGSPRPFWMFVDNLVLNKEEDLVASRFLMEPVITPDVHGSLQNAVVRVSNIPAIRSSRHWALVSEELSLLAONKQSSKLAAKWPTKLVKNCPLPREYFKYFSTELTSSL 387
gi | 114684638 | ref | XP_525483.2 | LFCFHRLLOYARPKPGSPRPFWMFVDNLVLNKEEDLVASRFLMEPVITPDVHGSLQNAVVRVSNIPAIRSSRHWALVSEELSLLAONKQSSKLAAKWPTKLVKNCPLPREYFKYFSTELTSSL 387
gi | 74001340 | ref | XP_849972.1 | LFCYHRVLOYARPRKPGSPRPFWMFVDNLVLNKEEDLVATRFLEADPVITPDVCGQAVRDVAVHVSNIIPAVKSSRSALASREELSLLAHRNQRTPKPLGPAKLKNCPLPREYFKYFSTELTSSL 336
gi | 119887082 | ref | XP_869990.2 | VFCFHRLLOYARLPKPGSPRPFWMFVDNLVLNKEEDLVATRFLEADPVITPDVCGQAVRDVAVHVSNIIPAVKSSRSALASREELSLLAHRNQRTPKPLGPAKLKNCPLPREYFKYFSTELTSSL 417
gi | 126158899 | ref | NP_001075164.1 | MFCFHRLLOYALPRKPGSPRPFWIFVMDNLVLEEDDQETVTRFLOTEAVTLDVGRGRVQNAVVRVSNIPGLKSKHAPLNFKEEYLQAVRVRSLKLAAPKVDSLKVKYCLLPLREYFKYFSONSLPL- 421
gi | 51556269 | ref | NP_001003964.1 | MFCFHRLLOYARPRQDQSPRPFWIFVMDNLVLEEDDQETVTRFLOTEAVTLDVGRGRVQNAVVRVSNIPGLKSKHAPLNFKEEYLQAVRVRSLKLAAPKVDSLKVKYCLLPLREYFKYFSONSLPL- 422
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....

