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gi | 39946026 | ref | XP_362550.1 | LLSASFDPRMMLKLDIETGKCIKAFETGKPHVVRFNPTSELGHEFVAGMSDNKIVQFDTRAGNEIVQYDHLGPNVITLPCDDGRRFMTSDDRLRAWVEYGFVPIKYIAEYPLFAMTRAAHPGKVVAYOSSDNGIVVYSSN-DKFR 548
gi | 32413455 | ref | XP_327207.1 | LSGSFDPRWIKLWDIETGQCVNRFNTPKPHVIKFNPSVDOGHEFLAGLSNRRIVQYDSRAGADPVOEYDHLGAINILEFVDENRRFMSTSDRLRWVEYGIPIVEIKTISEPDMFALTKSTQHPSGKYVLYOCSDNSIVVYSSASDKFR 544
gi | 19112881 | ref | NP_596089.1 | LSTSFDKTIKLDWDELGKCLNCFNSDRLTNCVKFQVDPDKPNEFLAGTADKRILOFDIRS-PDIVOAVDHLGGINSITFLENGKRFVTSDDSRMRFWVEYGTIPVPIKFWADTAMHSMRVALRPNKSIACOSLDNCIVVYSSAY-EKYR 473
gi | 21355805 | ref | NP_651005.1 | LLSASVDRYIKLWDAETGDVVSREFTTRKMPFCVKFHPDNSKQHLFVAGTSDKKIICWDTRS-GDIVQYDRHLGVSITITFVDDNRRFVTSDDKSMRIWEWDIPVDMKYIADPTMHSMPAVTLAPNGKWMACOSLDNKIVIFSALN-RFK 492
gi | 58392861 | ref | XP_319677.2 | ISAGYDRYLKLDIETGDIVISRENSRKKIPFCVKFHPDNLQHLFVAGTSDKKIICWDTRS-GEVVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDMKYIADPTMHSMPAVTLAPNGKWLACOSLDNKIVIFSALN-RFK 503
gi | 73973753 | ref | XP_532261.2 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 495
gi | 115497198 | ref | NP_001069111.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 495
gi | 7706657 | ref | NP_056975.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 495
gi | 114608845 | ref | XP_518687.2 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 495
gi | 51765561 | ref | XP_483893.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 495
gi | 34852890 | ref | XP_342155.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 367
gi | 57530292 | ref | NP_001006407.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 496
gi | 58000457 | ref | NP_001009990.1 | LLSAAYDRYLKLDIETGQCISREFTNRKVPYCVKFNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEVVQYDRHLGAVNITFVDENRRFVTSDDKSLRWVEWDIPADFKYIAEPMHSMPAVTLSPNGKWLACOSMDNQLIFGAQN-RFR 494
gi | 17507469 | ref | NP_492851.1 | LLSASFDPRVVKLDIETGQVQRFHTGHVYPCLYKHPDDDKNHMFLVGMQNKLIQWDSRS-GEIVQYDRHLQAVNITFVDENRRFVTSDDKSVRIWEWDIPVDFKLIQVGLHAIPMKSNDKVVVGCMDNRIVLQVLDKLR 483
gi | 30681779 | ref | NP_172528.2 | LTAGYDNKIKYWDIETGOVISTFTGKIPYVVKLNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLQAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKLIQVGLHAIPMKSNDKVVVGCMDNRIVLQVLDKLR 489
gi | 115453403 | ref | NP_001050302.1 | LLSAGYDRNIQYWDIETGOVISTFTGKIPYVVKLNPDDEDKQNLVAVAGMSDKKIIVQWDIRS-GEIVQYDRHLQAVNITFVDENRRFVTSDDKSLRWVEWDIPVDFKLIQVGLHAIPMKSNDKVVVGCMDNRIVLQVLDKLR 489
gi | 124806005 | ref | XP_001350600.1 | LLSASFDPRVVKLDIETGQVQRFHTGHVYPCLYKHPDDDKNHMFLVGMQNKLIQWDSRS-GEIVQYDRHLQAVNITFVDENRRFVTSDDKSVRIWEWDIPVDFKLIQVGLHAIPMKSNDKVVVGCMDNRIVLQVLDKLR 534

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gi | 39946026 | ref | XP_362550.1 | QNRKKSVRGHNNAGSAIDIDISADGQFLASGDTGGYVAFVDWVKCKMFHKIQVED--GQVVCVKWHPQESSKVATGG-ASGIIKFDW 542
gi | 32413455 | ref | XP_327207.1 | QNRKKSVRGHNNAGSAIDIDISADGQFLASGDTGGYVAFVDWVKCKMFHKIHADTGGAINCVAVSEQETSQVFTAG-ARGEIRMDW 630
gi | 19112881 | ref | NP_596089.1 | QNRKKSVRGHNNAGSAIDIDISADGQFLASGDTGGYVAFVDWVKCKLMAKLPAAHS--GPVQSMAFHPQETSQVFTAG-ARGEIRMDW 558
gi | 21355805 | ref | NP_651005.1 | MNRKKTFTGHMVSYACQLDFSPDMSYVLSGDDGKCIYDWDKTKMKYKQWQAH--GVCISALWHPHEASKVITAG-WDGLIKLWD 576
gi | 58392861 | ref | XP_319677.2 | MNRKKTFTGHMVSYACQLDFSPDMSYVLSGDDGKCIYDWDKTKMKYKQWQAH--NVCIALWHPHEASKVITAG-WDGLIKLWD 587
gi | 73973753 | ref | XP_532261.2 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 579
gi | 115497198 | ref | NP_001069111.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 579
gi | 7706657 | ref | NP_056975.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 579
gi | 114608845 | ref | XP_518687.2 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 579
gi | 51765561 | ref | XP_483893.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 579
gi | 34852890 | ref | XP_342155.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 451
gi | 57530292 | ref | NP_001006407.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCIGAVWHPHETSQVITAG-WDGLIKLWD 580
gi | 58000457 | ref | NP_001009990.1 | LNKKKIFKGHMVAGYACQVDFSPDMSYVLSGDDGKCIYDWDKTKKLYSRFKAHD--KVCISALWHPHETSQVITAG-WDGLIKLWD 578
gi | 17507469 | ref | NP_492851.1 | FSKKKAFRGHNAAGYACNIDFSPDQSFLLISGDDGKCIYDWDKTKKLYSRFKAHD--SNCIALWHPHEASKVITAG-WDGLIKLWD 567
gi | 30681779 | ref | NP_172528.2 | LNKKKRFAGHIVAGYACQVDFSPDGRFVMSGDDGKCIYDWDKTKKLYSRFKAHD--GVCIGAVWHPHETSQVITAG-WDGLIKLWD 573
gi | 115453403 | ref | NP_001050302.1 | LNKKKRFAGHIVAGYACQVDFSPDGRFVMSGDDGKCIYDWDKTKKLYSRFKAHD--GVCIGAVWHPHETSQVITAG-WDGLIKLWD 573
gi | 124806005 | ref | XP_001350600.1 | LFSKKTFRGHNNIYGSINVSNDGKYVLSGDSNGGLFIWKKRMVFNKIKAHK--NVCIDCVWHPFKISMLATAS-WDGLIKLWD 618

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