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gi | 118129742 | ref | XP_424434.2 | -----MPVHVVTYKGIKFPFAVNVHLSFAHNEFLVRDDDFVNIITYPKSGTVWMTIELSLIRSHGHPVWNOIVLNSDRMPWFSIRLGLA-ALSYF 91
gi | 118105213 | ref | XP_001236918.1 | -----TVWMTIELSLIRSHGHPVWNOIVLNSDRMPWFSIRLGLA-ALSYF 45
gi | 118129738 | ref | XP_001233158.1 | -----MPVHVVTYKGIKFPFAVNVHLSFAHNEFLVRDDDFVNIITYPKSGTVWMTIELSLIRSHGHPVWNOIVLNSDRMPWFSIRLGLA-ALSYF 91
gi | 8567408 | ref | NP_059493.1 | -----MDGPPQR--ALWSSSEK-----NVSEMSWNFG-----GEYFRYKGIPTFPVGMYSPELSLAENTSNVRDDDFIVITYPKSGTNWMIIEIVCLILKDGDPWIRSEPIWQAPWCEIISAFN-VLDRP 114
gi | 89145411 | ref | NP_001034754.1 | MSPPWRNTCYSSPEMRLDRSCARNIARWGHWKEGKPHGGLTGETEAGSSWNGGSESQKLGQGEYFRYKGIPTFPVGMYSPELSLAENTSNVRDDDFIVITYPKSGTNWMIIEIVCLILKDGDPWIRSEPIWQAPWCEIISAFN-LPERF 149
gi | 31563388 | ref | NP_004596.2 | -----MASPPPFHSQLKPGYFRYKGVPPFVGLYSLEISLAENTQDVRDDDFIITYPKSGTWMIEIICLILKDGDPWIRSEPIWQAPWCEIIVGAFS-LPDQM 102
gi | 114678251 | ref | XP_001171127.1 | -----MASPPPFHSQLKPGYFRYKGVPPFVGLYSLEISLAENTQDVRDDDFIITYPKSGTWMIEIICLILKDGDPWIRSEPIWQAPWCEIIVGAFS-LPDQM 102
gi | 73948049 | ref | XP_541518.2 | -----MQGLLKR-----WGLRMA-----VLIVSPPHSYSQKLSGEYFRYKGIPTFPVGIYSPERIRMEN-ADVQDDDFIITYPKSGTNWMIIEIICLILKDGDPWIRSEPIWQAPWCEIIMGAFS-LSDDQ 116
gi | 47271433 | ref | NP_944596.2 | -----MTEAELYSYKGVLPVSVYVHFAESLKYED-FTFRPDDILIIITPKSGTWMQEIIVPLVSEGDLLPVLIVPNWDRVPWLEHRAILLSELQRA 93
gi | 118197267 | ref | NP_001071637.1 | -----MTESELYVHKGVFVPHLHFAESLKYED-FTFRPDDILIIITPKSGTWMQEIIVPLVSEGDLLPVLIVPNWDRVPWLEHRAILLSELQRA 93
gi | 145279639 | ref | NP_001071636.2 | -----MEVSEFNLLYKGLLPLKLAHTEESLQYLEN-FKVKDDDFVAVITYPKSGTWMQENLPPLLNGDLPVQIVPNWDRVPWLEHRAAAV-LEERF 92
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 118129742 | ref | XP_424434.2 | SPLLTCHELPRHIFPKSFSHSTAKVIYTLRDRPRDVVVSYFYFCMKMNSYEDPVSFEQFLRDFLSGELPHGSWFHEHVRGWMQMKDRENFFFIITYEELKQDLQGSVRRRLCHFLGQNLDDDAISVAVQNASFMAMRQNPMSILLPTDMDQ 241
gi | 118105213 | ref | XP_001236918.1 | SPLLTCHELPRHIFPKSFSHSTAKVIYTLRDRPRDVVVSYFYFCMKMNSYEDPVSFEQFLRDFLSGELPHGSWFHEHVRGWMQMKDRENFFFIITYEELKQDLQGSVRRRLCHFLGQNLDDDAISVAVQNASFMAMRQNPMSILLPTDMDQ 166
gi | 118129738 | ref | XP_001233158.1 | SPLLTCHELPRHIFPKSFSHSTAK-----DEBAALSQQHLVQGN-----IMPHGSWFHEHVRGWMQMKDRENFFFIITYEELKQDLQGSVRRRLCHFLGQNLDDDAISVAVQNASFMAMRQNPMSILLPTDMDQ 216
gi | 8567408 | ref | NP_059493.1 | SPRIMSSHLPIELFTKAFFSSKAKVIYVGRNPRDVVVSLYYSKIAQOLKDPGTPDQFLQNLKGEVQFGSDFDHKIGWIRMRQENFLFIITYEELQDLRGSVQICEFLGRPLGEEALSSVVAHSAFAAMKANMNSNYLLPASLLDH 264
gi | 89145411 | ref | NP_001034754.1 | SPRLMCSHLPIELFTKAFFSSKAKVIYVGRNPRDVVVSLYYSKIAQOLKDPGTPDQFLQNLKGEVQFGSDFDHKIGWIRMRQENFLFIITYEELQDLRGSVQICEFLGRPLGEEALSSVVAHSAFAAMKANMNSNYLLPASLLDH 299
gi | 31563388 | ref | NP_004596.2 | SPRLMSSHLPIQIFTKAFFSSKAKVIYVGRNPRDVVVSLYHYSKIAGQLKDPGTPDQFLRDFLKGGEVQFGSDFDHKIGWLRMKGKDNFLFIITYEELQDLQGSVERICGFLGRPLGKEALGSVVAHSTFGAMKANMNSNYLLPPSLLDH 252
gi | 114678251 | ref | XP_001171127.1 | SPRLMSSHLPIQLFTKAFFNSKAKVIYVGRNPRDVVVSLYHYSKIAGQLKDPGTPDQFLQNLKGEVQFGSDFDHKIGWLRMRQENFLFIITYEELQDLHGSVQICEFLGRPLGEEALGSVVAHSAFGAMKANMNSNYLLPPSLLDQ 266
gi | 73948049 | ref | XP_541518.2 | SPRIFATHFHOMMNPSTYFKIEPRVLYVMRNPKDVFISYHFHMASFLVSPGTQDEFMEKFLNGIMFGSDFDHVKGWLNAAEAEHILYIYSYEMINDLRASVEKIATFLGKSLSSVEVVEKIADHCVFKNMKNKMSNLSLVPPEEFMDQ 243
gi | 118197267 | ref | NP_001071637.1 | SPRIFATHFHOMMNPSTYFKIEPRVLYVMRNPKDVFISYHFHMASFLVSPGTQDEFMEKFLNGIMFGSDFDHVKGWLNAAEAEHILYIYSYEMINDLRASVEKIATFLGKSLSSVEVVEKIADHCVFKNMKNKMSNLSLVPPEEFMDQ 243
gi | 145279639 | ref | NP_001071636.2 | SPRAIVSHPVRLMPSSTYFKSIAKVIYVARNPKDVFISYHFHMASFLVSPGTQDEFVFNKFLSGEIVFGKWSHDKSRNPELKDRIIVITYEEMLDLRGVLCRMKFLGRELSTEALDRVNSSTFKNMKNKMSNYIMVPEIMDN 242
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 118129742 | ref | XP_424434.2 | TKGQFLRKGICGDWKNHFTVAQTEFNRIYLEKMRGLNVAFPWDRDQ-----PDLTEQ----- 295
gi | 118105213 | ref | XP_001236918.1 | -----PDLTEQ----- 166
gi | 118129738 | ref | XP_001233158.1 | TKGQFLRKGICGDWKNHFTVAQTEFNRIYLEKMRGLNVAFPWDRDQ-----PDLTEQ----- 270
gi | 8567408 | ref | NP_059493.1 | RQGEFLRKGICGDWKNHFTVAQSEAFDSVYREOMHGVLQ-RFPWDTSEI-DSPDQPDPEP-----SPSP-----AFDDFNPSSG 338
gi | 89145411 | ref | NP_001034754.1 | RQGAFLRKGICGDWKNHFTVAQSEAFDQVYREOMHGVLQ-RFPWDRSAE-DGSPDGETESP-----SPSP-----LASDDFNPSSG 375
gi | 31563388 | ref | NP_004596.2 | RRGAFRLKGVCGDWKNHFTVAQSEAFDRAYRKQMRGMP-TFPWDEDPEEDGSPDPEPSPPEPKPSLEPNTSLEREPNNSPSPSPG-QASETPHPRP----- 350
gi | 114678251 | ref | XP_001171127.1 | RRGAFRLKGVCGDWKNHFTVAQSEAFDRVYRKQMRGMP-TFPWDEDPE-DGSPDPAPSPEPEPKPSLEPNTSLEREPNNSPSPSPGPGQASEPPHPRP----- 350
gi | 73948049 | ref | XP_541518.2 | RRGAFRLKGVCGDWKNHFTVAQSEAFDRVYRKQMRGMP-TFPWD-VPE-DTSPDPDPSPE-----PQAG-----SEPLHE----- 334
gi | 47271433 | ref | NP_944596.2 | KKSEFLRKGIVGDWKNHFTVAQSEAFKFNAYQEKMRDVKFSPWD----- 287
gi | 118197267 | ref | NP_001071637.1 | KKSEFLRKGIVGDWKNHFTVAQSEAFKFNAYQEKMRDVKFSPWD----- 287
gi | 145279639 | ref | NP_001071636.2 | NKSAFLRKGIVGDWKNHFTVAQSEAFKFNAYQEKMRDVKFSPWD----- 288
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400..

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