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                                  *  .         :                    :    .     :    .*    *  ::****:************** **:*****************************************:*.******************:
gi|223718064|ref|NP_001138773.1| -MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTTLQHQLPVSGYSTPSPATIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCF   149
gi|194676103|ref|XP_001790364.1| -MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTTLQHQLPVSGYSTPSPATIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCF   149
gi|60460883|ref|NP_001012663.1|  -MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTTLQHQLPVSGYSTPSPATIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCF   149
gi|116734873|ref|NP_033050.2|    -MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGALTSLQHQLPVSGYSTPSPATIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCF   149
gi|13928712|ref|NP_113716.1|     MYESVEVGGLTPAPNPFLVVDFYNQNRACLLQEKGLPAPGPYSTPLRTPLWNG----SNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCF   146
gi|110626153|ref|NP_571474.1|    MYESVDVVGLTPSPNPFLSMDYYHQNRGCLIPDKGLVSGAARG--FRNPHWSG----SNHSVETQSTSSEEIVPSPPSPPPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHREKSCIINKVTRNRCQYCRLQKCL   144
gi|62990125|ref|NP_571481.2|     MYESVDVN-------PFLMMDYYNQSRGCLIPDK-MPHPFSSS--IRHQHWSG----SNHSIETQSTSSEEIVPSPPSPPPPPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHREKNCIINKVTRNRCQYCRLQKCL   136
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 :***************:**:  * ** *.*.*:*:. ::*::****:*****:*********.**:::**:**:*************************************************************:*******:**********:
gi|223718064|ref|NP_001138773.1| EVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN   299
gi|194676103|ref|XP_001790364.1| EVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN   299
gi|60460883|ref|NP_001012663.1|  EVGMSKESVRNDRNKKKKEAPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSEGLTLNRTQMHK   299
gi|116734873|ref|NP_033050.2|    DVGMSKESVRNDRNKKKKEAPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN   299
gi|13928712|ref|NP_113716.1|     EVGMSKESVRNDRNKKKKETPKPECSESYTLTPEVGELIEKVRKANQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN   296
gi|110626153|ref|NP_571474.1|    EVGMSKESVRNDRNKRKKDDKKQECLENYVLSPDTEKMIEQVRKAHQETFPSLCQLGKYTTNNSADHRVALDVDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPDQDTMTFSDGLTLNRTQMHN   294
gi|62990125|ref|NP_571481.2|     EVGMSKESVRNDRNKKKKEEKKPECTENYTLSPDTEQMIDRVRKAHQETFPSLCQLGKYTTSNSSERRVALDVDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN   286
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gi|223718064|ref|NP_001138773.1| AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQ-PGGGGRDGGGLAPPPGSCSPSL   448
gi|194676103|ref|XP_001790364.1| AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQ-AGSGGRDGGGLAPPPGSCSPSL   448
gi|60460883|ref|NP_001012663.1|  AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQ-PGGGGRDGGGLAPPPGSCSPSL   448
gi|116734873|ref|NP_033050.2|    AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDKVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQ-SGGGTRDGGGLAPPPGSCSPSL   448
gi|13928712|ref|NP_113716.1|     AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDKVDMLQEPLLEALKVYVRKRRPSQPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQ-SGGGTRDGGGLAPPPGSCSPSL   445
gi|110626153|ref|NP_571474.1|    AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLLCGDRQDLEQSDKVDELQEPLLEALKIYVRNRRPHKPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLEGGGSKGAGGGGGGGGKGAPPGSCSPSL   444
gi|62990125|ref|NP_571481.2|     AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLLCGDRQDLEQADKVDVLQEPLLEALKIYVRNRRPHKPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLE------SSSGAQGSRASATTPGSCSPSL   430
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|223718064|ref|NP_001138773.1| SPSSNRSSPATHSP   462
gi|194676103|ref|XP_001790364.1| SPSSNRSSPATHSP   462
gi|60460883|ref|NP_001012663.1|  SPSSNRSSPATHSP   462
gi|116734873|ref|NP_033050.2|    SPSSHRSSPATQSP   462
gi|13928712|ref|NP_113716.1|     SPSSHRSSPATQSP   459
gi|110626153|ref|NP_571474.1|    SPSSAHSSPSAHSP   458
gi|62990125|ref|NP_571481.2|     SPNSAQSSPPTQSP   444
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