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                                 *********.*****:********************.*****:********:************** **.:*:*  .::    .  **:.:  :  :*  : :: *::*: : : :    .
gi|195972799|ref|NP_005578.2|    MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPDPDTSYVLTPHTEEKYKKINEEFDNMMRNHKIAPGLPPQN----------F   150
gi|114659136|ref|XP_001139415.1| MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPDPDTSYVLTPHTEEKYKKINEEFDNMMRNHKIAPGLPPQN----------F   150
gi|139949256|ref|NP_001077107.1| MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEALNKKEHRGCDSPDPDTSYVLTPHTEEKYKKINEEFDNMMRNHKIAPGLPPQN----------F   150
gi|73951070|ref|XP_857997.1|     ----------MDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPDADDYFEHSPLSEDRFSKLNEDSDFIFK--RGPPGLPPQN----------F   150
gi|76253934|ref|NP_001028885.1| MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPDADDYFEHSPLSEDRFSKLNEDSDFIFK--RGPPGLPPQN----------F   150
gi|45382367|ref|NP_990195.1|     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVETLRKKGLNGCESPDADDYFEHSPLSEDRFSKLNEDSDFIFK--RGPPGLPAQN----------F   150
gi|18859003|ref|NP_571376.1|     MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYNEPHESRTNSDIVEKLRNKGHNDCPSPDPDDCFGHSPLMDDRFGKLNEESDLMYKR-CGPTALPPQN----------F   150
gi|17136960|ref|NP_477018.1|     MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTEYNEPHESLTNKNIIEKENKNGVMSPDSPEAETDYTLTPRTEAKYNKIDEEFQNMMQRNQMAIGGAGAPRQLPNSS---Y   150
gi|158285355|ref|XP_564631.3|    MGRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDKVLLKYTEYNEPHESLTNKNIIEKENKNGTMSPDSPEPEDSYTLTPRTEAKYNKIDEDFQIMMQRNQQLTAGGARPMMATNSYSLPV   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|195972799|ref|NP_005578.2|    SMSVTVPVTSPNALSYTNPGSSLVSPSL--AASSTLTDS-----------SMLSPPQTTLHRN-VSPGAPQRPPSTGNAGGMLSTTDLTVPNGAGSSPVGNGFVNS----RASPNLIGATG-ANSLGKVMP----TKSPPPPGGGNLGMN   300
gi|114659136|ref|XP_001139415.1| SMSVTVPVTSPNALSYTNPGSSLVSPSL--AASSTLTDS-----------SMLSPPQTTLHRN-VSPGAPQRPPSTGNAGGMLSTTDLTVPNGAGSSPVGNGFVNS----RASPNLIGATG-ANSLGKVMP----TKSPPPPGGGNLGMN   300
gi|139949256|ref|NP_001077107.1| SMSVTVPVTSPSALSYTNPGSSLVSPSL--AASSALADT-----------SMLSPPQATLHRN-VSPGAPQRPPSTGSAGGMLSTSDLTVPNGAGSSPVGNGFVNS----RASPNLIGTTG-ANSLGKVMP----TKSPPPPGGGSLGMN   300
gi|73951070|ref|XP_857997.1|     SMSVTVPVTSPNALSYTNPGSSLVSPSL--AASSTLADS-----------SMLSPPQATLHRN-VSPGVPQRPPSTGSAG--------------------NGFVNS----RASPNLIGTTG-ANSLGKVMP----TKSPPPPGGGNLGMN   300
gi|76253934|ref|NP_001028885.1| SMSVTVPVTSPNALSYTNPGSSLVSPSL--AASSTLADS-----------SMLSPPPATLHRN-VSPGAPQRPPSTGSASGMLSTTDLTVPNGAGNSPVGNGFVNS----RASPNLIGNTG-ANSLGKVMP----TKSPPPPGGGSLGMN   300
gi|45382367|ref|NP_990195.1|     SMSVTVPVSNPNTLTYSNPGSSLVSPSL--AASSSLTST-----------TMLSPPQTTLHRN-VSPGAPQRPPSTGNAGGILGTTDLTVPNGAGTSPVGNGVWNS----RASPSLLGTAGGGNGLGKVMP----TKSPPPPGGGGLGMN   300
gi|18859003|ref|NP_571376.1|     SMHVAVPVTNPNAMSY-NPGASLSSQSLSAAAAASLSDG-----------AMLSPPQGSMHRS-VVP--PQRPPSTGSTG--------------------NGFVNP----RGSPGLLGTPS-GNGLGKVMP----AKSPPPPGG-NMGIG   300
gi|17136960|ref|NP_477018.1|     TLPVSVPVPGSYGDNLLQASPQMSHTNISPRPSSSETDSGGMSLIIYPSGSMLEMSNGYPHSHSPLVGSPSPGPSPGIAHHLSIK------------------------QQSP--GSQNGRASNLRVVIPPTIAPIPPNMSAPDDVGYA   300
gi|158285355|ref|XP_564631.3|    SVPVSVPVIGTYNDSMLQSSPQMAHNSISPRPSSSETDS------VYPSGGILEMSNGYPHSASPLGGSPSPGPSPGIGSHQAHNNNNNSHNTHNKSKHEFHFDNAVQTIKQSPSGGSGSSGSRSLRVVIP---APMNPTITA-DDISYV   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                 .:  .   : .*     *           .  :.. :.      :  :    : .*.:.   :: : ..:  .   . :   .   .    :::   .  .:  ...  . .:*   .:. .   .:   .   .:
gi|195972799|ref|NP_005578.2|    SRKPDLRVVIPPSSKGMMPPLN--------TQRISSSQATQPLATPVVSVTTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQHHLGQAALSSLVAGGQLSQGSNLSINTNQNISIKSEPISPPRDRMTPS   450
gi|114659136|ref|XP_001139415.1| SRKPDLRVVIPPSSKGMMPPLN--------TQRISSSQATQPLATPVVSVTTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQHHLGQAALSSLVAGGQLSQGSNLSINTNQNINIKSEPISPPRDRMTPS   450
gi|139949256|ref|NP_001077107.1| SRKPDLRVVIPPSSKGMMPPLN--------TQRISSSQATQPLATPVVSVTTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQHHLGQAALNSLVAGGQLSQGSNLSINTNQNINIKSEPISPPRDRMTPS   450
gi|73951070|ref|XP_857997.1|     SRKPDLRVVIPPTSKGMMPPLN--------TQRISSSQATQPLATPVVSVTTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQGFNSPGMLSLGQVSAWQQHHLGQAALSSLVAGGQLSQGSNLSINTNQNINIKSEPISPPRDRMTPS   450
gi|76253934|ref|NP_001028885.1| SRKPDLRVVIPPSSKGMMPPLSEEEEELELNAQRISSSQATQPLATPVVSVTTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQGFTSPGMLSLGQASAWQQHHLGQAALSSLVAGGQLSQGSNLSINTNQNINIKSEPISPPRDRMTPS   450
gi|45382367|ref|NP_990195.1|     NRKPDLRVVIPPSSKGMMPPLTEEDELELNTQRISSSQSTQPLATPVVSVTTPSFPPAGLVYSAMPTAYNTDYSLTSADLSAFEGFNSPGMLSLGQVSPWQQHHLGPATLSSLVSGSQLSQGSNLSINTNQNINIKSEPISPPRDRVNSS   450
gi|18859003|ref|NP_571376.1|     SRKPDLRVVIPPSSKGMMPPLN--------TQRISSSQSTQPLATPVVSVTTPSLAPQGLVYSGMPTAYNSEYSLSSAELSSLQGFGSPG-LSIGSVSAWQQHQLGQAALSSLVGGGHLPQGSNLSINTSQNVNIKSEPISPPRERVTPS   450
gi|17136960|ref|NP_477018.1|     DQRQSQTSLNTPVVTLQTPIPALTSY-----SFGAQDFSSSGVMNSADIMSLNTWHQGLVPHSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSASGHQQN--SNGSTGSGGSSSSTSSNASGGAGGGGAVSAANVITHLNNVSVL   450
gi|158285355|ref|XP_564631.3|    EHTRQQTNLNTPVVALQTPIPGLTNYTTTLGSFGAQDFSLNPDIMIGPWSAASSHSQNTILFSGLPHLAVSNSTPPPSTSPLSVKIKAEPISPPRDHHNTSHHHGGAPGGGSSSGASGSAPGANGVQSASGGGASSTATGLTAMGNVVVT   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                 .                                  .   *... ::.:          .      :    :.      : ::*.    ** *:.  * *
gi|195972799|ref|NP_005578.2|    GFQQQQQQQQQQQPPPPPQPQ--------PQPPQP-QPRQEMGRSPVDSLSSSSSSYD----GSDREDPRGDFHSPIVLGRPPN----TEDRESPS---VKRMRMDA-WVT   561
gi|114659136|ref|XP_001139415.1| GFQQQQQ----QQPPPPPQPQ--------PQPPQP-QPRQEMGRSPVDSLSSSSSSYD----GSDREDPRGDFHSPIVLGRPPN----TEDRESPS---VKRMRMDA-WVT   561
gi|139949256|ref|NP_001077107.1| GFQQQQQ----PQPPPPP-----------PQAPQP-QPRQEVGRSPVDSLSSSSSSYD----GSDREDPRGDFHSPVVLGRPPN----SEDRESPS---VKRMRMDA-WVT   561
gi|73951070|ref|XP_857997.1|     GFQQQQP----QQQQPPP-----------PQPSQPPQPRQEMGRSPVDSLSSSSSSYD----GSDREDPRGDFHSPIVLGRPPN----TEDRESPS---VKRMRMDA-WVT   561
gi|76253934|ref|NP_001028885.1| GFQQQQQ----PQQQQPP-----------PQPPQP-QPRQEMGRSPVDSLSSSSSSYD----GSDREDPRGDFHSPIVLGRPPN----TEDRESPS---VKRMRMDT-WVT   561
gi|45382367|ref|NP_990195.1|     GFPQQQP----PQQPQPP-----------QPPQQPPQRQEMGRSPVDSLSSSSSSYD----GSDREDPRSDFHSPVVLGRPPN----SEDRESPS---VKRMRMDT-WVT   561
gi|18859003|ref|NP_571376.1|     GFPPQQQ----------------------QPPSG---RPDMGRSPVDSLSSSCSSYD----GSDREDHRPDFHSPLGLGRPPAGG--ADERESPS---VKRMRMDT-WVT   561
gi|17136960|ref|NP_477018.1|     AGGPSGQGGGGGGGGGSNGNVEQATNLSVLSHAQQHHLGMPNSRPSSTGHITPTP------GAPSSDQDVRLAAVAVQQQQQQPHQQQQLGDYDAPN---HKRPRISGGWGT   561
gi|158285355|ref|XP_564631.3|    GGGGGGGSGGGGAGTSSLG-------------ANLNHSHLIHSRPSSTGHLTPTPDSYMPIGGHLAGSVTPTNAPSPVDIRHLSTGGSHLPEYDAPTAQAHKRPRISEGWAT   561
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.
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