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                    ***:*******: **.*** *:**.** :. *.**.**.:**.**:** *.   ******.:********..********::**** .  *:**.* ..  *::**::***..:.* ** : ***.*.**:: *.* **.* *..:**.*
gi|24497501|ref|NP_004487.2|      MLGTVKMEGHETSDWNSYYADTQEAYSSVPVSNMNSGLGSMNSMNTYMTMNTMTTSGNMTPASFNMSYANPGLGAGLSPGAVAGMPGGSAGAMNSMTAAGVTAMGTALSPSGMGAMGAQQAASMNGLGPYAAAMNPCMSPMAYAPSNLGR   150
gi|114652732|ref|XP_001144389.1|  MLGTVKMEGHETSDWNSYYADTQEAYS-VPVSNMNSGLGSMNSMNTYMTMNTMTTSGNMTPASFNMSYANPGLGAGLSPGAVAGMPGGSAGAMNSMTAAGVTAMGTALSPSGMGAMGAQQAASMNGLGPYAAAMNPCMSPMAYAPSNLGR   150
gi|66793398|ref|NP_032285.2|      MLGTVKMEGHESNDWNSYYADTQEAYSSVPVSNMNSGLGSMNSMNTYMTMNTMTTSGNMTPASFNMSYANTGLGAGLSPGAVAGMPGASAGAMNSMTAAGVTAMGTALSPGGMGSMGAQPATSMNGLGPYAAAMNPCMSPMAYAPSNLGR   150
gi|6981034|ref|NP_036874.1|       MLGTVKMEGHESNDWNSYYADTQEAYSSVPVSNMNSGLGSMNSMNTYMTMNTMTTSGNMTPASFNMSYANPGLGAGLSPGAVAGMPGGSAGAMNSMTAAGVTAMGAALSPGGMGSMGAQPAASMNGLGPYAAAMNPCMSPMAYAPSNLGR   150
gi|73963239|ref|XP_852354.1|      MLGTVKMEGHESSDWNSYYADTQEAYSSVPVSNMNSGLGSMNSMNTYMTMNTMTTSGNMTPASFNMSYANPGLGAGLSPGAVAGMPGGSAGSMNSMTAAGVTAMGTALSPGGMGAMGAQPAASMNGLGPYAAAMNPCMSPMGYAPSNLGR   150
gi|61870516|ref|XP_613201.1|      MLGTVKMEGHESSDWNSYYADTQEAYSSVPVSNMNSGLGTMNSMNTYMTMNTMSTSGNMTPASFNMSYANPGLGAGLSPGAVAGMPGGSAGAMNSMTAG-VTAMGTTLSPGGMGAMGAQPAASMNGLGPYAAAMNPCMSPMAYAPSNLGR   150
gi|18858685|ref|NP_571359.1|      MLGAVKMEGHETPDWSSYYNDAQEVYSPMTNSSMNPGLSSMNNMNSYMGMS---TSGNMTSSSFNMSYANPALGAGLSPGTMAGMPTG--GAMNGMGGG-VSSMGTALSPSNLNAMTAQHS-SMNALNPYTS-MSPTMSSMTYVAANLNR   150
                    1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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gi|24497501|ref|NP_004487.2|      SR-AGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGGGG--------GSGSGGSGAKGGP   300
gi|114652732|ref|XP_001144389.1|  SR-AGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGGGG--------GSGSGGSGAKGGP   300
gi|66793398|ref|NP_032285.2|      SR-AGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGGG------------SGGGGSKGGP   300
gi|6981034|ref|NP_036874.1|       SR-AGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNACFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGGG------------SGGGGSKGVP   300
gi|73963239|ref|XP_852354.1|      SR-AGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGAGGGGGGGGGGGGGGGGAKGGP   300
gi|61870516|ref|XP_613201.1|      SRAAGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGP------------GGGGGGGGPKGGP   300
gi|18858685|ref|NP_571359.1|      AR------DNKTFRRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLSFNDCFVKVSRSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCDKKLPD----------------GKRSEGKR   300
                    .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                    *  :..: . .*:::.   * .**   **.                : *.    :*  * .* :.*  .:          .. *     * * **** :** ****************  :.****::*: . :****.**: : :
gi|24497501|ref|NP_004487.2|      ESRKDPSGASNPSADSPLHRGVHGKTGQLEGAPAPGPAAS------PQTLDHSGATATGGASELKTPASSTAPPISSGPGALASVPASHPAHGLAPHESQLHLKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGSTLPA   450
gi|114652732|ref|XP_001144389.1|  ESRKDPSGASNPSADSPLHRGVHGKTGQLEGAPAPGPAASPKTLDHPQTLDHSGATATGGASELKTPASSTAPPISSGPGALASVPASHPAHGLAPLESQLLLKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGSTLPA   450
gi|66793398|ref|NP_032285.2|      ESRKDPSGPGNPSAESPLHRGVHGKASQLEGAPAPGPAAS------PQTLDHSGATATGGASELKSPASSSAPPISSGPGALASVPPSHPAHGLAPHESQLHLKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGATLPA   450
gi|6981034|ref|NP_036874.1|       ENRKDPSGPVNPSAESPIHRGVHGKASQLEGAPAPGPAAS------PQTLDHSGATATGGGSELKSPASSSAPPISSGPGGWICTPLSP--TWLAPHESQLHLKGAPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGATLPA   450
gi|73963239|ref|XP_852354.1|      ESRKDPASAANPSANSPLHRGVHGKAGQLEGAPGPGPAAS------PQTLDHGGATATGGASELKTPPSSAAPPISSGPGALVSVPPSHPAHGLAPHESQLHLKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGAALKA   450
gi|61870516|ref|XP_613201.1|      ESRKDPSSAANPSADSPLHRGVHGKAGQLEGAPAPGPAAS------PQTLDHGGAAATGGASELKTPATSAAPPISSGPGALVSVPPSHPAHALAPHESQLHMKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGSALPA   450
gi|18858685|ref|NP_571359.1|      E--QSSARALRPATDQRQTR-AHG--LQLH----------------HLLKPVVQSAQFGPQEREPPKLGTEERWP----QVHPVSTSCSRCTLWPTESQLDLKGDPHYSFNHPFSINNLMS-LQSQHKLELKT-RTTLQYSSYGSGMSS   450
                    .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                    .**:..          :.  *                  :***..              :  .:. **  . :
gi|24497501|ref|NP_004487.2|      SLPLGSASVTTR------SPIEP------------------SALEPAY------------YQGVYSRPVLNTS----------------------------------------   566
gi|114652732|ref|XP_001144389.1|  SLPLGSASVTTR------SPIEP------------------SALEPAY------------YQGVYSRPVLNTS----------------------------------------   566
gi|66793398|ref|NP_032285.2|      SLPLGSASVATR------SPIEP------------------SALEPAY------------YQGVYSRPVLNTS----------------------------------------   566
gi|6981034|ref|NP_036874.1|       SLPLGGASVATR------SPIEP------------------SALEPAY------------YQGVYSRPVLNTS----------------------------------------   566
gi|73963239|ref|XP_852354.1|      SLPLGSASAETGPRSLSLSPHPPLAETFLGWWGARPRGLPAEAALEACLGSRSGGDARSWGFPRAFPPPVGSEACEHLARVRGVPGTCAPRLRMRVDPGRRVPGTGGQRRTAGILG   566
gi|61870516|ref|XP_613201.1|      SLPLGGASVATR------SPIEP------------------SALEPAY------------YQGVYSRPVLNTS----------------------------------------   566
gi|18858685|ref|NP_571359.1|      NLPMAGR-----------ASMDP------------------SAALEASY------------YQGVYSRPVLNTS----------------------------------------   566
                    .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560......
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