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                                                                                                                                                                          **:: *** * *:*******
gi|6678013|ref|NP_031880.1|        ----------------------------------------------------------------------------------------------------------------------------------MASVWFINSFCAVLQGSLFG   150
gi|13929038|ref|NP_113926.1|       MAHGNAPRDSYHLVGISFFILGLGTLLPWNFFITAIPYFQGRLAGT-NSSAETPSTNHTSPTDTFNFNNWVTLLSQLPLLLFTLLNSFLYQCIPESVRILGSLLAILLLFALTAALVKVDLSPGLFFSITMASVWFINSFCAVLQGSLFG   150
gi|38708299|ref|NP_001523.2|       MARGDAPRDSYHLVGISFFILGLGTLLPWNFFITAIPYFQARLAGAGNSTARILSTNHTGPEDAFNFNNWVTLLSQLPLLLFTLLNSFLYQCVPETVRILGSLLAILLLFALTAALVKVDMSPGPFFSITMASVCFINSFSAVLQGSLFG   150
gi|114638694|ref|XP_001171483.1|   MARGDAPRDSYHLVGISFFILGLGTLLPWNFFITAIPYFQVRLAGAGNSTARILSTNHTGSEDAFNFNNWVTLLSQLPLLLFTLLNSFLYQCVPEMVRILGSLLAILMLFALTAALVKVDMSPGPFFSITMASVCFINSFSAVLQGSLFG   150
gi|73983635|ref|XP_854729.1|       MARGDAPQDSYHLVGISFFILGLGTLLPWNFFITAIPYFQGRLAGA-NTTTGALDTNHTGLADTFNFNNWVTLLSQLPLLLFTLLNSLLYQCIPEMVRILGSLLVILLLFALTAALVKVDMSPGPFFSITMASVWFINSFCAVLQGSLFG   150
gi|157074056|ref|NP_001096739.1|   MARGDAPRDSYHLVGISFFILGLGTLLPWNFFITAIPYFQGRLAGA-NSTAETLGTNHTSSADTFNFNNWVTLLSQLPLLLFTLLNSFLYQCIPETVRILGSLLIILFLFTLTAVLVKVDMSPGLFFSITMASVWFINSFGAVLQGSLFG   150
gi|60279693|ref|NP_001012519.1|    -----------------------------------MTYFTDRLKNG---------TNSTQP-DTYMFSNNSVLLAQLPLLLFTLLNSFLYQHIAEKIRIAGSMVAILLLFILTAILVKVDMDRDSFFSITMATIWFINMFGAILQGSLFG   150
                                   1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                    :*.:** :*::*:***.:****:.**** *    .:.::**********.. .:::.*** ****.*** ** :   ::     *..*:   ::  :    .  :    :.     :    :: *.  *.:*  *::***: ***:.
gi|6678013|ref|NP_031880.1|        QLGTMPSTYSTLFLSGQGLAGIFAALAMLMSLASGVDAQTSALGYFITPCVGILLSIVCYLSLPHLKFARYYLTEKLSQAPTQELETKAELLQADEKNGVPISPQQASPTLDLDPEKEPEP--EEPQKPGKPSVFVVFRKIWLTALCLVL   300
gi|13929038|ref|NP_113926.1|       QLGTMPSTYSTLFLSGQGLAGIFAALAMLTSLASGVDPQTSALGYFITPCVGILLSIICYLSLPHLKFARYYLTKKP-QAPVQELETKAELLGADEKNGIPVSPQQAGPTLDLDPEKELELGLEEPQKPGKPSVFVVFRKIWLTALCLVL   300
gi|38708299|ref|NP_001523.2|       QLGTMPSTYSTLFLSGQGLAGIFAALAMLLSMASGVDAETSALGYFITPCVGILMSIVCYLSLPHLKFARYYLANKSSQAQAQELETKAELLQSDE-NGIPSSPQKVALTLDLDLEKEPESEPDEPQKPGKPSVFTVFQKIWLTALCLVL   300
gi|114638694|ref|XP_001171483.1|   QLGTMPSTYSTLFLSGQGLAGIFAALAMLLSMASGVDAETSALGYFITPCVGILMSIVCYLSLPHLKFARYYLANKSSQAQAQELETKAELLQSDE-NGIPSSPQKVALTLDLDLEKEPESEPDEPQKPGKPSVFTVFQKIWLTALCLVL   300
gi|73983635|ref|XP_854729.1|       QLGTMPSTYSTLFLSGQGLAGIFAALAMLMSMASGVDAQTSALGYFITPCVGIFVSIVCYLSLPHLEFARYYLAKKPSQAQGQELETKAELLQSDEKNGIPNSPQKVALTLDLDAEKDPELEPEEPQKPEKPSVFIVFQKIWLTALCLVL   300
gi|157074056|ref|NP_001096739.1|   QLGTMPSKYSTIFLSGQGLAGIFAALAMLISMASGVDAQTSALGYFITPCVGTVMSIVCYLSLPHLKFARYYLAKKPSKAHGQELETKAELLQSDEKNGIPNSPQRAALTLDLDLEKETEVEPEEPQKPEKPSVFIVLRKIWLTALCLVL   300
gi|60279693|ref|NP_001012519.1|    LVGKLPSRFSSVFMSGQAVAGIFSGLAMLFSNIFETNPESSALGYFITPCAATLLTLFCYLLLPHLRFARTYLEKVSCETADAVKEPSAN--GSETVKVKLNDLGHEFNDIGETEACEKLNKFNDEQTEEKSTVPQVFRKIWVMALCVTC   300
                                   .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                   **:**********  ...*    **  . :* *:*.**:**:** :****** : **.  .*: *:*::*  *.:*:* :***:*  :  **::* :*  :* ** ***:****:  .*:*. **: * *:: *.:*:*********** **:
gi|6678013|ref|NP_031880.1|        VFTVTLSVFPAITAMVTTSSNSPGKWGLFFNPICCFLLFNVMDWLGRSLTSYFLWPDEDSQQLLPLLVCLRFLFVPLFMLCHVPQHARLPIIFRQDAYFITFMLLFAVSNGYLVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCGAS   450
gi|13929038|ref|NP_113926.1|       VFTVTLSVFPAITAMVTTSSNSPGKWSQFFNPICCFLLFNVMDWLGRSLTSYFLWPDEDSQ-LLPLLVCLRFLFVPLFMLCHVPQRARLPIIFWQDAYFITFMLLFAISNGYFVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCGAS   450
gi|38708299|ref|NP_001523.2|       VFTVTLSVFPAITAMVTSST-SPGKWSQFFNPICCFLLFNIMDWLGRSLTSYFLWPDEDSR-LLPLLVCLRFLFVPLFMLCHVPQRSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCGAS   450
gi|114638694|ref|XP_001171483.1|   VFTVTLSVFPAITAMVTSST-SPGKWSQFFNPICCFLLFNIMDWLGRSLTSYFLWPDEDSR-LLPLLVCLRFLFVPLFMLCHVPQRSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCLAPRQVLPHEREVAGALMTFFLALGLSCGAS   450
gi|73983635|ref|XP_854729.1|       VFTVTLSVFPAITAMVTSST-SPGKWSRFFNPICCFLLFNIMDWVGRSLTSYFLWPDEDSR-LLPLLVCLRVLFVPLFMLCHVPERSRLPILFPQDAYFITFMLLFAVSNGYLMSLTMCLAPRQVLPHEREVAGTLMTFFLALGLSCGAA   450
gi|157074056|ref|NP_001096739.1|   VFTVTLSVFPAITAMVTSST-GPGKWSQFFNPICCFLLFNVMDCLGRSLTSYFLWPDEDSR-LLPLLVCLRVLFVPLFMLCHVPERSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCLAPRQVLPQEREVTGTLMTFFLALGLSCGAS   450
gi|60279693|ref|NP_001012519.1|    VFAVTLSVFPAITINTKPSGFFEGK-DHIFVPLCSFLVFNVMDWIGRSLTSCLQWPSMKSR-LFPIFVLSRVVFIPALMLCNVQPRNYLPVVFNHDMAYIIFMSLFAISNGYLACLSMSYAPQLVRPKDAETAGALMTFFLALGLSLGAA   450
                                   .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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                                   :** :*:**
gi|6678013|ref|NP_031880.1|        LSFLFKALL-----   464
gi|13929038|ref|NP_113926.1|       LSFLFKALL-----   464
gi|38708299|ref|NP_001523.2|       LSFLFKALL-----   464
gi|114638694|ref|XP_001171483.1|   LSFLFKALL-----   464
gi|73983635|ref|XP_854729.1|       FSFLFKALL-----   464
gi|157074056|ref|NP_001096739.1|   LSFLFKALL-----   464
gi|60279693|ref|NP_001012519.1|    FSFGLKSLLSGKSN   464
                                   .......460....
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