

gi|4504141|ref|NP_000832.1| ---MPGKRGLGWMMWARLPLCLLLSLYGPWVPSLGLKPKGHPHMNSIRIDGDIILGGLFPVHGRGS-EGKPCGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|114606763|ref|XP_527365.2| ---MPGKRGLGWMMWARLPLCLLLSLYGPWVPSLGLKPKGHPHMNSIRIDGDIILGGLFPVHGRGS-EGKPCGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|73972588|ref|XP_538870.2| ---MPGKRGWMMWARLPLCLLLSLYGPWVPSLGLKPKGHPHMNSIRIDGDIILGGLFPVHGRGS-EGKACGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|12083595|ref|NP_073157.1| ---MSGKGGWMMWARLPLCLLLSLYGPWVPSLGLKPKGHPHMNSIRIDGDIILGGLFPVHGRGS-EGKACGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|62945392|ref|NP_001013403.1| ---MSGKGGWMMWARLPLCLLLSLYGPWVPSLGLKPKGHPHMNSIRIDGDIILGGLFPVHGRGS-EGKACGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|189529171|ref|XP_695566.3| MSSAMGKMIGWSNHHCCGSAVLFLYLFMTALAAARKGP-GHTLNSIRIDGDIILGGLFPVHARGH-EGKACGELKKEKGIHRL EAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
gi|25149329|ref|NP_741400.1| ---MTCVSHFTPLRLRRYSIIQLNLFVFFLLHPIPSISIVKQLTVPGQIVLGLLFIHEAGRNASHQCGKTKADGGVORMVAMLFALDRINNDPDLNPIILGARILDTC SRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITII 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|4504141|ref|NP_000832.1| KPERVVGIVIGAGSSSVSMVANILRLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----ALKNWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|114606763|ref|XP_527365.2| CLPPGHLHPLRTPSVTAFQPSLAALISLPTGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|73972588|ref|XP_538870.2| KPERVVGIVIGAGSSSVSMVANILRLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----ALKNWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|12083595|ref|NP_073157.1| KPERVVGIVIGAGSSSVSMVANILRLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----ALKNWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|62945392|ref|NP_001013403.1| KPERVVGIVIGAGSSSVSMVANILRLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----ALKNWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|189529171|ref|XP_695566.3| KPERVVGIVIGAGSSSVSMVANILRLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----DMRWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
gi|25149329|ref|NP_741400.1| R-PPVVAVVGAAGSQVSMVAVMLQLFKIPQIISYASTAPDLSDNSRYDFFSRVVPDITYQAQAMVDIVR-----ALKNWYVSTLASEGSGYEGSVEAFIQKSRREDDGGVCIASVKIPREPKAGEFDKIIRRLLETSNAR 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|4504141|ref|NP_000832.1| AVIIFANEDDIRRVL EAARRANQTG-----HFFWMGSDSWGSKIAPVHLHLEEVAEAGAVIILPKRMSVVRGDFRYFSSRTLDNRRNINWFAEFWEDNFHCKLSRH-----ALKKGSHVKKCTNRERIGODSAYE OEGKVMFVIDAVYA 450
gi|114606763|ref|XP_527365.2| AVIIFANEDDIRRVL EAARRANQTG-----HFFWMGSDSWGSKIAPVHLHLEEVAEAGAVIILPKRMSVVRGDFRYFSSRTLDNRRNINWFAEFWEDNFHCKLSRH-----ALKKGSHVKKCTNRERIGODSAYE OEGKVMFVIDAVYA 450
gi|73972588|ref|XP_538870.2| AVIIFANEDDIRRVL EAARRANQTG-----HFFWMGSDSWGSKSTPVLHLEEVAEAGAVIILPKRMSVVR-----DRERIGODSAYE OEGKVMFVIDAVYA 450
gi|12083595|ref|NP_073157.1| GIIIFANEDDIRRVL EAARRANQTG-----HFFWMGSDSWGSKSAPVLRLEEVAEAGAVIILPKRMSVVRGDFRYFSSRTLDNRRNINWFAEFWEDNFHCKLSRH-----ALKKGSHVKKCTNRERIGODSAYE OEGKVMFVIDAVYA 450
gi|62945392|ref|NP_001013403.1| AVIIFANEDDIRRVL EAARRANQTG-----HFFWMGSDSWGSKSAPVLRLEEVAEAGAVIILPKRMSVVRGDFRYFSSRTLDNRRNINWFAEFWEDNFHCKLSRH-----ALKKGSHVKKCTNRERIGODSAYE OEGKVMFVIDAVYA 450
gi|189529171|ref|XP_695566.3| VVIIFANEDDIRRLLQAARKANQTG-----HFLWVGSWDSGSKISPVLNQEEAEAGAVIILPKRMSVVRGDFRYFSSRTLDNRRNINWFAEFWEDNFHCKLSRH-----ALKKGSHVKKCTNRERIGODSAYE OEGKVMFVIDAVYA 450
gi|25149329|ref|NP_741400.1| GVMVFVDEDLKRLKLTLDLVAEGHTLDRHFWFVASDSWGIKQSVVRLGHEHRTYGAIIAPMVRRETYGLEYFRLSPKGFVFLFEFFEYLGCSATVDVKTFGDCFDVNIILKQVYIHRRTIIFINVLKELQSYVFFVVDTWKI 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|4504141|ref|NP_000832.1| MGHALHAMHRDLCPGR--VGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|114606763|ref|XP_527365.2| MGHALHAMHRDLCPGR--VGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|73972588|ref|XP_538870.2| MGHALHAMHRDLCPGR--VGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|12083595|ref|NP_073157.1| MGHALHAMHRDLCPGR--VGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|62945392|ref|NP_001013403.1| MGHALHAMHRDLCPGR--VGLCPRMDPVDGTQLLKYIRNVNFSGIAGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|189529171|ref|XP_695566.3| MAHALHNMHKLCPGK--VGLCSKMDPVDGAGLLKIRVDVKTAGIGGNPVFNENGDAPGRYDIYQYQLRNDGSAEYKVGISWTDHLHLRIERMHWPGSGGQ--LPRSLCSLPCQGERKKIVKGMPCWCHCEPCTGYQYVDRYTCKTICP 600
gi|25149329|ref|NP_741400.1| IAKAISMYIEDDCGKI PFHCKTLAGSFGFRGERLQRYR--NMSLTKNEPALIDANGDIGRYDVFQLDNGVYQYVGVKWRSTDDFLVEVEKIRHAFKTAHERPMSVCSLDCPRG-HYRAYVDQCCWACIPCTDTSTSIHNEFSCRECA 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|4504141|ref|NP_000832.1| YDMRPTENRTGCRPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|114606763|ref|XP_527365.2| YDMRPTENRTGCRPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|73972588|ref|XP_538870.2| YDMRPTENRTGCRPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|12083595|ref|NP_073157.1| YDMRPTENRTGCRPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|62945392|ref|NP_001013403.1| YDMRPTENRTGCRPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|189529171|ref|XP_695566.3| FDLRPNKNIHGCQPIPIIKLEWGSPPWAVLPLFLAVVGI AATLFVVVITFVRVNDPIVKA SGR ELSYVLLAGIFLCYATFLMIAEPDLGTC SLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
gi|25149329|ref|NP_741400.1| VGMVDPRTLHFQVPIPIVSMQWDTWLSLIPAAFSILGIASITFVVSVFLKSNIPVIMASGR ELCVMSGIGMGTLLFFLVSQPTVITCSLRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPRFISPASQLAIFLISLQI 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi|4504141|ref|NP_000832.1| LGICVWFVVDPSHSVDFODRTLDPRFARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIVWLAFIGPFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPEONVPKRRSLK 900
gi|114606763|ref|XP_527365.2| LGICVWFVVDPSHSVDFODRTLDPRFARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIVWLAFIGPFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPEONVPKRRSLK 900
gi|73972588|ref|XP_538870.2| LGICVWFVVDPSHSVDFODRTLDPRFARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIVWLAFIGPFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPEONVPKRRSLK 900
gi|12083595|ref|NP_073157.1| LGICVWFVVDPSHSVDFODRTLDPRFARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIVWLAFIGPFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPEONVPKRRSLK 900
gi|62945392|ref|NP_001013403.1| LGICVWFVVDPSHSVDFODRTLDPRFARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIVWLAFIGPFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPEONVPKRRSLK 900
gi|189529171|ref|XP_695566.3| LGVCIWFAVDPSQALIDYEDQRTIDPEMARGVLKCDISDLSLICLLGYSMLLMVTCVVAIAKTRGVPETFNEAKPIGFTMYTTCIIWLAFIGPFFGTSQSTEK----- 900
gi|25149329|ref|NP_741400.1| IGTFFWILFDPPTMIVFPTK-----TEAVLTCKAATSHLLISLLNILLIVACTVVAFAKTRKTPENFNETHRIGFTMYSTCILWLAFIGPTVFATQS---DFRIQIISLCMCISLSGIVALICFFAPKVVIVLFOQYKNVTRKQSAVAG 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi|4504141|ref|NP_000832.1| AVVTAAT-----MSNKFQKGNFRPNGEAKSELCEALEAPALATKQTYVYTNHAI----- 1050
gi|114606763|ref|XP_527365.2| AVVTAAT-----MSNKFQKGNFRPNGEAKSELCEALEAPALATKQTYVYTNHAI----- 1050
gi|73972588|ref|XP_538870.2| AVVTAAT-----MSNKFQKGSFRPNGEAKSELCEALEAPALATKQTYVYTNHAI----- 1050
gi|12083595|ref|NP_073157.1| AVVTAAT-----MSNKFQKGNFRPNGEAKSELCEALEAPALATKQTYVYTNHAI----- 1050
gi|62945392|ref|NP_001013403.1| ----- 1050
gi|189529171|ref|XP_695566.3| ----- 1050
gi|25149329|ref|NP_741400.1| RLVNQOMRFMSQLTYNPDGCSNYQPMSSNQSYKPKSTESHSHTSNAQVQQPRAIPPHVIEQLAASLPIDDKNDLVKCLSLQDKFFNNNNNNENSEEIRRRRPPSSVHTVGVAVNGSSVAHIPPRSYTDKPKSEMIRQDAKSRISLAEASHG 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi|4504141|ref|NP_000832.1| ----- 1067
gi|114606763|ref|XP_527365.2| ----- 1067
gi|73972588|ref|XP_538870.2| ----- 1067
gi|12083595|ref|NP_073157.1| ----- 1067
gi|62945392|ref|NP_001013403.1| ----- 1067
gi|189529171|ref|XP_695566.3| ----- 1067
gi|25149329|ref|NP_741400.1| VDLTLEETAAADTNSIFL 1067
.....1060.....

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