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gi |21687100|ref|NP_660303.1| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAMHLPRSSFQSKVPGTVSSLDARFOLPAFPWFPHVIOPKPEITAGGSEVP-ALKTTPRFDFANLALAAQTQEDPAK---LGRGEGPSPAGG 146
gi |114576304|ref|XP_001137836.1| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAMHLPRSSFQSKVPGTVSSLDARFOLPAFPWFPHVIOPKPEITAGGSEVP-ALKTTPRFDFANLALAAQTQEDPAK---LGRGEGPSPAGG 146
gi |57098461|ref|XP_540097.1| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAVHLPRSSFQSKMPGAVSSLDVTRFOLPAFPWFPHVIOPKPEITVGGSGPESLKTTPRFDFANLALAAQTQEDPSK---LGRGEGPSPAGG 147
gi |6754928|ref|NP_035989.1| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAMHLPRSSFQSKVPGAVSSLDARFOLPAFPWFPHVIOPKPEITAGGSG-AALKTKPRFDFANLALAAQTQEDPTK---LGRGEGPSPAGG 146
gi |109478045|ref|XP_233962.4| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAMHLPRSSFQSKVPGAVSSLDARFOLPAFPWFPHVIOPKPEITAGGSG-AALKTKPRFDFANLALAAQTQEDPTK---LGRGEGPSPAGG 146
gi |116004047|ref|NP_001070384.1| MGSKTLPAVPVPIHPSLQLTNYSLQAVNGLPVPVSDHLPNLYGFSALHAVHLHWLGLYPAMHLPRSSFQSKVPGAVSSLDARFOLPAFPWFPHVIOPKPEITAGGSGPAALKTKPRFDFANLALAAQTQEDPSK---LGRGEGPSPAGG 147
gi |54400660|ref|NP_001006079.1| MGSKTLPAVPVPLHPSLQLANYSFLQTSNGL-HLPADHMPSIYSFSALHAVHLHWLGLYPPFTLPRCIFSKLPG---LVDARFPLPSIPLFPFLVCPAKQESSGPGSGASSKSKPRFDFANLALAAQTQDALKAEGLSTNNG-HVRSFS 144
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |21687100|ref|NP_660303.1| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKTSKIKC----- 266
gi |114576304|ref|XP_001137836.1| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKTSKIKC----- 266
gi |57098461|ref|XP_540097.1| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKTSKIKC----- 267
gi |6754928|ref|NP_035989.1| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKTSKIKC----- 266
gi |109478045|ref|XP_233962.4| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKTSKIKC----- 266
gi |116004047|ref|NP_001070384.1| LGALLDVTKLS-PEKKPTRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKPPRSNAKQSLRVNRTLGHAAPSGGNRSPPRLWRA 296
gi |54400660|ref|NP_001006079.1| LGCLLDVAKLSSEPERRKPSRGRPLPSKTKKEFVCKFCGRHFTKSYNLLIHERHTHDERPYTCDICHKAFRRQDHLRDHRYIHSKEKPFKCECGKGFQSRITLAVHKTLSQVKELKPAKIK----- 264
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |21687100|ref|NP_660303.1| ----- 266
gi |114576304|ref|XP_001137836.1| ----- 266
gi |57098461|ref|XP_540097.1| ----- 267
gi |6754928|ref|NP_035989.1| ----- 266
gi |109478045|ref|XP_233962.4| ----- 266
gi |116004047|ref|NP_001070384.1| ARGAPGTFLHPKRVPVRVPGARGTSQPRPFG 326
gi |54400660|ref|NP_001006079.1| ----- 264
.....310.....320.....330

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