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gi |9910482|ref|NP_064374.1| MEKPAASTEPQGRPALGRESVQVPDDODFRSFRSECEAEVGNWLTYSKAGVSVVWQAVEMDRTLHKIKCRMEECDVPAETLYDVLHDIYRKKWDSNVIEFDIARLTVNADVGYYSWRCPKPLKNRDVITLRSWLPMGADYIIMNYSV 150
gi |61556854|ref|NP_001013087.1| MEKPAASTEPQGRPALGRESVQVPDDODFRSFRSECEAEVGNWLTYSKAGVSVVWQAVEMDRTLHKIKCRMEECDVPAETLYDVLHDIYRKKWDSNVIEFDIARLTVNADVGYYSWRCPKPLKNRDVITLRSWLPMGADYIIMNYSV 150
gi |116812600|ref|NP_006636.2| MEKLAASTEPQGRPVLRGRESVQVPDDODFRSFRSECEAEVGNWLTYSRAGVSVVWQAVEMDRTLHKIKCRMEECDVPAETLYDVLHDIYRKKWDSNVIEFDIARLTVNADVGYYSWRCPKPLKNRDVITLRSWLPMGADYIIMNYSV 150
gi |194673360|ref|XP_592504.4| MEQSAVSPPEPPGPRPVLGRDSVQVPDDODFRSFRSECEAEAGWLTYSKAGVSVVWQAVEMDRTLHKIKCRMEECDVPAETLYDVLHDIYRKKWDSNVIEFDIARLTVNADVGYYSWRCPKPLKNRDVITLRSWLPMGADYIIMNYSV 150
gi |45387705|ref|NP_991209.1| MMMK-----GDDEVLIIPDRAFSRFKHECEAEAGWTYTHNKSNICVWIIQLLEDKSLHKIKRMTCKDIPAEIMYDVLHDIYRKKWDSNVIEFDIGKLTIVNADVGYYSWRCPKPLKNRDVITLRSWLPMGADYIIMNYSV 138
gi |118097207|ref|XP_425187.2| -----MVIYIPDSDPSSPRECEAEAGWHCRYNKAGVTVVWSQGEESCIVQKIKRISCKDVSAEITLYDVLHDIYRKKWDSHMIETVDIGRLTVNADVGYYSWKCPSPFKNRFVITLRSWLPGLNDYIILNYSV 130
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |9910482|ref|NP_064374.1| KHPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVITYLAQVDPKGS LPKWVVNKSSQFLAPKAMKKMYKACIKYPEWKQKHOPHFKPWLHPEQSPLPSLALSELVQHADSLENIDESAVTESREERAGGAGGESDDDTSLT 291
gi |61556854|ref|NP_001013087.1| KHPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVITYLAQVDPKGS LPKWVVNKSSQFLAPKAMKKMYKACIKYPEWKQKHOPHFKPWLHPEQSPLPSLALSELVQHADSLENIDESAVTESREERAGGAG-EGSDDDTSLT 290
gi |116812600|ref|NP_006636.2| KHPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVITYLAQVDPKGS LPKWVVNKSSQFLAPKAMKKMYKACLKYPEWKQKHOPHFKPWLHPEQSPLPSLALSELVQHADSLENIDESAVAESREERMGGAGGESDDDTSLT 291
gi |194673360|ref|XP_592504.4| KHPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVITYLAQVDPKGS LPKWVVNKSSQFLAPKAMKKMYKACVKKYPEWKQKHOPHFKPWLHPEQSPLPSLALSELVQHADSLENIDESAVAESRDRTGAGGAGGESDDDTSLT 291
gi |45387705|ref|NP_991209.1| KHSKYPPKDLVRAVSIQTGYLIQRTGPSCTLITYLAQVDPKGS LPKWVVNKSSQLLAPKAMKRISKACARYPEWKQKHSFGFKPWLFPQNPLSIPMSLSIQHAELENIDESALSERDRA-----EHSDEDNANN 274
gi |118097207|ref|XP_425187.2| KHPKYPPRKDFVRAVSLQTYLIKANGTSA CVLYYLTVQVDPKGS LPKWVVNRVQFVAPKAMKKIYKAGLKYPEWKRHRDPGYPWVYVPEQNTLPSLSLAE LSLQHADSLHIDE TGLSEH-----LSASDHEA--- 260
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290

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