

```

gi|70909322|ref|NP_034648.2|    -MVISVLLLLLAAYAVPAQGLGSEFVHCEPCDEKALSMCPPSPLGCELVKEPFGCCGCMTCALAEGQSCGVYTERCAOGLRCLPRDDEEKPLHALLHGRGVCLNEKSYGEQTKIERDSREHEEPTTSEMAEETYSPKVFRPKHTRISELKA 150
gi|6981088|ref|NP_036949.1|    -MVISVLLLLLAACAVPAQGLGSEFVHCEPCDEKALSMCPPSPLGCELVKEPFGCCGCMTCALAEGQSCGVYTERCAOGLRCLPRDDEEKPLHALLHGRGVCLNEKSYGEQTKIERDSREHEEPTTSEMAEETYSPKVFRPKHTRISELKA 150
gi|74005713|ref|XP_852885.1|    -MVLAVLLLLLACAGPAQGLGSEFVHCEPCDEKALSMCPPSPLGCELVKEPFGCCGCMTCALAEGQSCGVYTERCAOGLRCLPRDDEEKPLHALLHGRGVCLNEKSYREQAKIERDSREHEEPTTSEMAEETYSPKIFRPKHTRISELKA 150
gi|157427782|ref|NP_001098797.1| -MVLAVLLLLLACAGSAQGLGSEFVHCEPCDEKALSMCPPSPLGCELVKEPFGCCGCMTCALAEGQSCGVYTERCAOGLRCLPRDDEEKPLHALLHGRGVCLNEKSYREQAKIERDSREHEEPTTSEMAEETYSPKIFRPKHTRISELKA 150
gi|10834982|ref|NP_000590.1|    MVLAVLLLLLAAYAGPAQGLGSEFVHCEPCDEKALSMCPPSPLGCELVKEPFGCCGCMTCALAEGQSCGVYTERCAOGLRCLPRDDEEKPLHALLHGRGVCLNEKSYREQAKIERDSREHEEPTTSEMAEETYSPKIFRPKHTRISELKA 150
gi|118093780|ref|XP_422069.2|    -----MACLQVDAG-----LSRIK-----SERSWKKAFKEERESREHEEPTTSEMTEETYPKAVRPKHGRLSDLKA 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

*.***** :*** *****: **:* : *****:*** *****:*****:***** :*.:**:*:*****
gi|70909322|ref|NP_034648.2|    AVKDDRKKLQSKFVGGAEHTAHPRVIPAPEMRQESDQPCRRHMEASLQELKASPRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHAFDSSNVE 272
gi|6981088|ref|NP_036949.1|    AVKDDRKKLQSKFVGGAEHTAHPRVIPAPEMRQESDQPCRRHMEASLQELKASPRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHAFDSSNVE 272
gi|74005713|ref|XP_852885.1|    AVKDDRKKLQSKFVGGAEHTAHPRVIPAPEMRQESDQPCRRHMEASLQELKASPRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHAFDSSNVE 272
gi|157427782|ref|NP_001098797.1| AVKDDRKKLQSKFVGGAEHTAHPRVIPAPEMRQESDQPCRRHMEASLQELKASPRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHAFDSSNVE 272
gi|10834982|ref|NP_000590.1|    AVKDDRKKLQSKFVGGAEHTAHPRIIPAPEMRQESDQPCRRHMEASLQELKASPRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMEYVDGDFQCHAFDSSNVE 272
gi|118093780|ref|XP_422069.2|    ALKDDRKKLQAKFVGGAEHTAHPRVV-IPELRQEFELGPQRRHMEASLQELKSSQRMVPRAVYLPNCDRKGfyKRRKQCKPGRGRKRGICWCVDKYGMKLPGMDYLSGDLQCHAFDSSNVE 272
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270..

```

