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gi|197304670|ref|NP_002403.2|-----MLGQPAPLERFASRR-----PQVLAVRTVCDLVLGKMDKDCMKRRTILDSPLGKLELSGCCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPE----PLMOCTAWLNAYFHC 150
gi|114633356|ref|XP_001142341.1|-----MLGQPAPLERFASRR-----PQVLAVRTVCDLVLGKMDKDCMKRRTILDSPLGKLELSGCCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGLE----PLMOCTAWLNAYFHC 150
gi|6678878|ref|NP_032624.1|-----MAETCKMKYSVLDSPGLKMEISGCERGLHGIRLLSGKTPNTDPEAPATPEVLGGPEGVPEPLVOC TAWLEAYFHE 150
gi|6981202|ref|NP_036993.1|-----MAETCKMKYSVLDSPGLKMEISGCERGLHGIRLLSGKTPNTDPEAPATPEVLGGPEGVPEPLVOC TAWLEAYFHE 150
gi|50979242|ref|NP_001003376.1|-----MDKACKMRYKIMDSPLGKIEISGCAQGLHEIRLHDKRTPDPGPAEAPAPPELLGCPPEMTEPLVOC VAWLDAYFHE 150
gi|119917939|ref|XP_001249418.1|-----MDETCEMKYKVVDSPLGKLEISGCERGLHGIRLLSGKTPDTPGPAEAAAPAEOLGGSGAVLEPLLOCAAWLDAYFHE 150
gi|118093188|ref|XP_421823.2|MF TKRPRRALEQLSADAI SARPSVSPPPPIPPPIPEHAGGARKASRRRGEVVLPGGRQASPSIMASRRVPKMM SKEGTSQCQEKHAVLLSPVGLKLEISGCETGVHEIKLFR LSVLPNGTEAAMRCELSGSVTSMPEPLQCCAAWLNAYFCE 150
gi|125841844|ref|XP_684479.2|-----MSASGACVLCVLTLSVVGTEILLRGCCKGKVHTIDIK----LNTDKESVHFVVLSEMS-----ELQRCVDWLQCYFMN 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|197304670|ref|NP_002403.2|PEAIEEFVVPALHHPVFQESFTRQVLWKLLKVVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|114633356|ref|XP_001142341.1|PEAIEEFVVPALHHPVFQESFTRQVLWKLLKVVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|6678878|ref|NP_032624.1|PAAIEGLPLPALHHPVFQDSFTRQVLWKLLKVVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|6981202|ref|NP_036993.1|PAAIEGLPLPALHHPVFQDSFTRQVLWKLLKVVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|50979242|ref|NP_001003376.1|PSVLPGLPLPAIHHPIFORGSFTARVLRKLLLELVKFGDVTYSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAMGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|119917939|ref|XP_001249418.1|PAVLEGLVVPALHHPVFQESFTRQVLWKLLKVVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAMGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|118093188|ref|XP_421823.2|PSRTEQLPLPFHHPMLQDSFTEKLVLTLLREVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
gi|125841844|ref|XP_684479.2|PESISALPLPALHHPMLQDSFTEKLVLTLLREVKFGFVTSYQOLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGG--LAVKEWLLAHEGHRLLGKPLGGSGLAGAWLKGAGATSGSPAGRN----- 292
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290..

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