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gi|115430223|ref|NP_002297.2|-----MADNFE--LHDALSGS-----GNPNPOGW-----PGAWG 27
gi|114653156|ref|XP_001148424.1|MTVLENAITGGGONMVDPGKSELTVGGDELPFRREGAAQPOLPRKDFPLSCKPAVWESNVHGSQADMVQMQPHIPTDSOSVRGPNSSFQVRETKYSAALGIPSDSCCRKMMADNFE--LHDALSGS-----GNPNPOGW-----PGAWG 134
gi|33859580|ref|NP_034835.1|-----MADNFE--LHDALSGS-----GNPNPOGW-----PGAWG 27
gi|13929190|ref|NP_114020.1|-----MADGFE--LNDALAGS-----GNPNPRGW-----PGAWG 27
gi|73963924|ref|XP_853675.1|-----MADNFE--LHDALSGS-----GNPNPOGW-----PGPWG 27
gi|156121327|ref|NP_001095811.1|-----MADGFE--LNDALAGS-----GNPNPRGW-----PGPWG 27
gi|47551305|ref|NP_999756.1|-----MADNFE--LHDALSGS-----GNPNPOGW-----PGAWG 27
gi|125833577|ref|XP_704272.2|-----MADGFE--LNDALAGS-----GNPNPRGW-----PGPWG 27
-----MQAMKARCWQPHWMLPLLPSSFLHPQLSDALPAHN-----PGAPPPQGNRFP-----GGGAPP 55
-----MADFLADAIPLDDVPEASEANKKHNPSAPGNAGPPTNFGWPGAPGGPHFFPGGGVQPFAGFPDITWPSARGSEF 75
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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gi|115430223|ref|NP_002297.2|NQPAGAGGYPGAS---YPGAY--PGQAPPGA-----YPGQAPPGAYPG-----APGAYPG-----APAGVYPGP-----PSGFGAYP-----SSGQPSATGAYPAT--GF 106
gi|114653156|ref|XP_001148424.1|NQPAGAGGYPGAS---YPGAY--PGQAPPGA-----YPRQAPPGAYPG-----APGAYPG-----APASGVYYPGP-----PSGFGAYP-----SSGQPSAPGAYPAT--GF 213
gi|33859580|ref|NP_034835.1|NQPAGAGGYPGAA---YPGAY--PGQAPPGA-----YPGQAPPGAYPG-----APGAYPG-----PTAPGAYPG-----STAPGAFPPQPGAPGAYPSAPGGYPAA--GF 120
gi|13929190|ref|NP_114020.1|NQPAGAGGYPGAS---YPGAY--PGQAPPGA-----YPGQAPPGAYPG-----APGAYPG-----PTAPGAYPG-----STAPGAFPPQPGAPGAYPSAPGGYPAA--GF 118
gi|73963924|ref|XP_853675.1|NQPAGAGGYPGAS---YPGAY--PGQAPPGA-----YPGQAPPGAYPG-----APGAYPG-----PTAPGAYPG-----STAPGAFPPQPGAPGAYPSAPGGYPAA--GF 143
gi|156121327|ref|NP_001095811.1|NQPAGAGGYPGAA---YPGAY--PGQAPPGA-----YPGQAPPGAYPG-----APGAYPG-----PTAPGAYPG-----STAPGAFPPQPGAPGAYPSAPGGYPAA--GF 121
gi|47551305|ref|NP_999756.1|AYPGYPGAYPGAPGF---YPGAPG-PHHGPPGP-----YPPG--PPGPYPG-----GPTAP--YSEA-----PAAPLVTLALSYFKGFCFS--SLCLAMG--GT 149
gi|125833577|ref|XP_704272.2|PFGPAGPQFPGAPAAPGFPGAPAAPGGYPPGGVPGQFPFPPNPGAPQFPSPMPQFPFPPGGAMPMPVVPVPGQFPSPPPGAPQGFENPNVYPPGPFSGPMYVGGFGAFPPDGGFGYGGMFPPVPPGFWGQFGGGFPAHPPGGYVGGFPMG 225
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300
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gi|115430223|ref|NP_002297.2|: * -----APAGP--LIVPYNLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--VFPFESGKPFKIQVLVEPDHFKVAVND 215
gi|114653156|ref|XP_001148424.1|YG-----APAGP--LIVPYNLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--VFPFESGKPFKIQVLVEPDHFKVAVND 322
gi|33859580|ref|NP_034835.1|YG-----VPAGP--LTVPYDLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--AFFPESGKPFKIQVLVEADHFKVAVND 229
gi|13929190|ref|NP_114020.1|FG-----APVGP--LTVPYDLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--AFFPESGKPFKIQVLVEADHFKVAVND 227
gi|73963924|ref|XP_853675.1|FG-----IPAGP--LTVPYDLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--AFFPESGKPFKIQVLVEADHFKVAVND 252
gi|156121327|ref|NP_001095811.1|YG-----IPSGP--LNVPYDLP LGGVVPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--VFPFESGKPFKIQVLVEPDHFKVAVND 230
gi|47551305|ref|NP_999756.1|WGCVSLGGCMSSHLAVMSLPSPLVVRPVLNLAVLFLCLLPNCPPL--QKVPYDLP LAGLMPRLMILTILGTVKPNANRIALDFORGNDAVAFHFNPRFNENNRVIVCNTKLDNNWGKEEROS--AFFPESGKPFKIQVLVEADHFKVAVND 297
gi|125833577|ref|XP_704272.2|YG-----GPAAPGGMLP YDLPLRAGIMPHELLITIVGEPILIGGDFRHFVDFMRGHEVVFHFNPRFHEN--TVVRSQGLGGLWGEERE--GFEEFVQGRQFELKILVEIDGKAVDGD 333
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450
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gi|115430223|ref|NP_002297.2|.***: : * : : : * * * * * * * : ** 250
gi|114653156|ref|XP_001148424.1|AHLLQYNHRVKKLNLEISKLGISGDIIDLTSASYTMI 357
gi|33859580|ref|NP_034835.1|AHLLQYNHRMKNLREISQLGISGDIILTASNHAMI 264
gi|13929190|ref|NP_114020.1|VHLLQYNHRMKNLREISQLGIIIDILTASNHAMI 262
gi|73963924|ref|XP_853675.1|AHLLQYNHRMKNLPEISKLGISGDIIDLTSASYAMI 287
gi|156121327|ref|NP_001095811.1|AHLLQYNHRVKNFGEISLTLGISGDIILTASHTMI 265
gi|47551305|ref|NP_999756.1|AHLLQYFNREKKNLEIITKLCIAGDIILTASVLTSMI 332
gi|125833577|ref|XP_704272.2|VHLLQYFNREKKNLEIITKLCIAGDIILTASVLTSMI 368
.....460.....470.....480.....
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