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gi | 31982260 | ref | NP_032368.2 | -----MLPRLG-GPALPLLLP-----SLLLLLLL 150
gi | 6981082 | ref | NP_037254.1 | -----MLPRLG-GPALPLLLP-----SLLLLLLL 150
gi | 55925576 | ref | NP_000588.2 | -----MLPRVG-CPALPLPPPLPLPLPLLL 150
gi | 114583231 | ref | XP_516234.2 | MDGRREDSEKWSHSCARRVRRDGAEEQCTPRARSORGGGRAGVRALTCRREGVSGGKGVVSKRGRGEGRGRGEAGPLGPGCGGEGGGRSGGGGSRARRAVPPARPPARSLARRAALPTASMLPRVG-CPALPLPPP-----PLPLPLLLLL 150
gi | 74005711 | ref | XP_545637.2 | -----MOPRLG-GPALLLLP-----LLLLLLL 150
gi | 27807005 | ref | NP_776980.1 | -----MALGGVGRGGAARAAP-----RLLLAALA 150
gi | 45382495 | ref | NP_990690.1 | -----MLSVVS-----CGLL 150
gi | 18858891 | ref | NP_571533.1 | -----MS-----LALLC 150
gi | 189523776 | ref | XP_001335489.2 | ----- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 31982260 | ref | NP_032368.2 | GAGGCGPGVRAEVLFRCPPTPERLAACGPPDAP-----CAELVREPCCGCSVCARQEGEACGVYIPRCAQTLRCYPNPGSELPLKALVTGAGTCEKRR---VGTTPQVADSDDDHSEGLLVENHVDGTMNMLGGGS 300
gi | 6981082 | ref | NP_037254.1 | GAGGCGPGVRAEVLFRCPPTPERLAACGPPDAP-----CAELVREPCCGCSVCARQEGEACGVYIPRCAQTLRCYPNPGSELPLKALVTGAGTCEKRR---VGTTPQVADSEDDHSEGLLVENHVDGTMNMLGG-S 300
gi | 55925576 | ref | NP_000588.2 | GASGGGGGARA EVLFRCPPTPERLAACGPPVAPPAAVA AVAGGARMPCAELVREPCCGCSVCARLEGEACGVYIPRCAGTLRCYPNPGSELPLQALVMGEGTCEKRRDA-EYGASPEQVADNGDDHSEGLLVENHVDSTMNMLGGGG 300
gi | 114583231 | ref | XP_516234.2 | GASGGGGGARA EVLFRCPPTPERLAACGPPVAPPAAVA AVAGGARMPCAELVREPCCGCSVCARLEGEACGVYIPRCAGTLRCYPNPGSELPLQALVMGEGTCEKRRDA-EYGASPEQVADNGDDHSEGLLVENHVDSTMNMLGGGG 300
gi | 74005711 | ref | XP_545637.2 | -----MTISKNMDEFHQHDVEQ-----DKPE-TKRLP-----APGCGCSVCARLEGEACGVYIPRCAQTLRCYPNPGSELPLQALVLGEGTCEKRRDA-EYGASPEQVADNGDDHSEGLLVENHVDGTMNMLGGGG 300
gi | 27807005 | ref | NP_776980.1 | GAGGDCGARA EVLFRCPPTPESLAACKPPGAA-----AGPAGDARVPC-ELVREPCCGCSVCARLEGERCGVYIPRCAGTLRCYPNPGSELPLRALVHGEGETCEKHGDA-EYGASPEQVADNGEEHSEGLLVENHVDGNVLMGGGG 300
gi | 45382495 | ref | NP_990690.1 | PALALAGPALPEVLFRCPCTAERLAACSPAARP-----CPVLVREPCCGCPVCALEDACGVYIPRCAAGLRCYPDPGAEPLPQALVQGGTICARPPPTDEYGASTEPADNGDDHSEGLLVENHVDSTMNMLGGGG 300
gi | 18858891 | ref | NP_571533.1 | ALVTFHGTAAREMVFRCFPCTAERQAACPMLETTCG-----EIVREPCCGCPVCAREQELCGVYIPRCAGTLRCYPSANSELPLELIQGLRCCENKVDL-----EPIMTIQESAHSSEVQDPLDIGL 300
gi | 189523776 | ref | XP_001335489.2 | SLLLVHGLSLEIVFRCPCTAERQAACPKLTTC-----EIVREPCCGCPVCAREQELCGVYIPRCAGTLRCYPSANSELPLELIQGLRCCENKVDL-----EPIMTIQESAHSSEVQDPLDIGL 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 31982260 | ref | NP_032368.2 | SAGRKPLKSGMKELAVFREKVNBOHROMGKGAK-HLSLEEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGRYLNKCKMSLNGORGEWCWVNPNTGKPIOGAPTIIRGDPECHLFYNEC-QETGGAHAGS 450
gi | 6981082 | ref | NP_037254.1 | SAGRKPPKSGMKELAVFREKVNBOHROMGKGAK-HLSLEEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSLNGORGEWCWVNPNTGKPIOGAPTIIRGDPECHLFYNEC-QENDGVHAOR 450
gi | 55925576 | ref | NP_000588.2 | SAGRKPLKSGMKELAVFREKVTBOHROMGKGGKHHLGLLEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSLNGORGEWCWVNPNTGKLI OGAPTIIRGDPECHLFYNEC-QEARGVHTOR 450
gi | 114583231 | ref | XP_516234.2 | SAGRKPLKSGMKELAVFREKVTBOHROMGKGGKHHLGLLEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSLNGORGEWCWVNPNTGKLI OGAPTIIRGDPECHLFYNEC-QEARGVHTOR 450
gi | 74005711 | ref | XP_545637.2 | GAGRKPLKSGMKELAVFREKVTBOHROMGKGGKHHLGLLEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSLNGORGEWCWVNPNTGKLI OGAPTIIRGDPECHLFYNEC-QEARGVHTOR 450
gi | 27807005 | ref | NP_776980.1 | GAGRKPLKSGMKELAVFREKVTBOHROMGKGGKHHLGLLEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSLNGORGEWCWVNPNTGKLI OGAPTIIRGDPECHLFYNEC-QEARGVHTOR 450
gi | 45382495 | ref | NP_990690.1 | ASSRKPLKSGMKEMPVREKVNBOHROMGKGGKHHLGLLEPKLRPPPARTPCQOELDQVLERISTMRLPDRGPLEHLYSLHIPNCDKHGLYLNKCKMSVNGORGEWCWVDPHKGVI OGAPTIIRGDPECHLFYTAHEQDRGAHALR 450
gi | 18858891 | ref | NP_571533.1 | -HEVPPIRKPKTDSP-WKESAVLQHRQQLKSKMKYKVEDPK--APHAKDSQOELDQVLERISKITFKDNRTPLEDLYSLHIPNCDKRGQYLNKCKMSVNGYRGEWCWVNPHTGRPMPTSPPLIRGDPNCQVLDGQ-EMDFSVDPNP 450
gi | 189523776 | ref | XP_001335489.2 | -RSPPMKPKGKDYQYIKETAVNKHHNNKTRM-NTQDDPK--TPHPKDSQOELDQVLENIIRMAFHNNKPLENLDLKFNP CDKTIQYLNKCKMSVNGYRGEWCWVNPYTGVOIPSSDKVRGDPNCQVYGGP-ELEPPLAQDK 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi | 31982260 | ref | NP_032368.2 | VQ 452
gi | 6981082 | ref | NP_037254.1 | VQ 452
gi | 55925576 | ref | NP_000588.2 | MQ 452
gi | 114583231 | ref | XP_516234.2 | MQ 452
gi | 74005711 | ref | XP_545637.2 | MQ 452
gi | 27807005 | ref | NP_776980.1 | MQ 452
gi | 45382495 | ref | NP_990690.1 | SQ 452
gi | 18858891 | ref | NP_571533.1 | -- 452
gi | 189523776 | ref | XP_001335489.2 | -- 452
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