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gi | 110815869 | ref | NP_084403.2 | MQARALLPATLAILATLAVLALAREPPAA--PCPARCDVSRCPSPRCPPGGYVPLDNCCLVCAASEGEPGGRPLDSPCGDSELEC-----VRGVCRCRWHTVCGTDGHTYADVCAALQASRRALQVSGTFVROLOKGCAP--SGLH 150
gi | 34878463 | ref | XP_341238.1 | MQARALLPATLAILATLAVLAREPPAA--PCPARCDVSRCPSPRCPPGGYVPLDNCCLVCAASEGEPGGRPLDSPCGDSELEC-----VRGVCRCRWHTVCGTDGHTYADVCAALQASRRALQISGTFVROLOKGCAP--SGLH 150
gi | 22129776 | ref | NP_444272.1 | MQARALL-----LAALALALAREPPAA--PCPARCDVSRCPSPRCPPGGYVPLDNCCLVCAASEGEPGGRPLDSPCGDSELEC-----VRGLCRCRWSHAVCGTDGHTYANVCAALQASRRALQLSGTFVROLOKGCAP--LGLH 150
gi | 118090706 | ref | XP_420813.2 | MRLSLLSP---LLLCLSRSRGSAELPAARAKCPTKCDVSKCPSPCSPSGYVPLDRCNCLVCSLGGEGAPCGRKEVDLGGDGLCKFPFGKRLSKGVCCCKTTHRVCGDGDGTYGVNVCCKMRWASRKAQQRRLEVVITRHKGSQAPSSSDPA 150
gi | 51011095 | ref | NP_001003502.1 | MGVILLAAATFIFTDLALAIKLSN-----CPSKCDVSKCPSPCSPSGYVPLDRCNCLVCSLGGEGAPCGRKEVDLGGDGLCKFPFGKRLSKGVCCCKTTHRVCGDGDGTYGVNVCCKMRWASRKAQQRRLEVVITRHKGSQAPSSSDPA 150

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gi | 110815869 | ref | NP_084403.2 | QLSPPRYKFNFIADVVEKIAPAVVHIELFLRHLPLFGRNVPLSSGSGFIMS EAGLIVTNAHVVSSTNAISGRQOLKVQLONGDAVEAIIQIDDKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVITGIVSTAQRDG 300
gi | 34878463 | ref | XP_341238.1 | QLSPPRYKFNFIADVVEKIAPAVVHIELFLRHLPLFGRNVPLSSGSGFIMS EAGLIVTNAHVVSSTNAISGRQOLKVQLONGDAVEAIIQIDDKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVITGIVSTAQRDG 300
gi | 22129776 | ref | NP_444272.1 | QLSPPRYKFNFIADVVEKIAPAVVHIELFLRHLPLFGRNVPLSSGSGFIMS EAGLIVTNAHVVSSTNAISGRQOLKVQLONGDYEATIKIDDKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVITGIVSTAQRDG 300
gi | 118090706 | ref | XP_420813.2 | QSSSPRYKFNFIADVVEKIAPAVVHIELFLRHLPLFGRNVPLSSGSGFIMS DSGLIVTNAHVVSSTNAISGRQOLKVQLONGDYEATIKIDDKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVITGIVSTAQRDG 300
gi | 51011095 | ref | NP_001003502.1 | HLNSPPRYKFNFIADVVEKIAPAVVHIELFLRHLPLFGRNVPLSSGSGFIMTQSLIVTNAHVVSSTNAISGRQHLRVQLHDGQTYEASIRDIIDDKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVITGIVSTQRDG 300

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gi | 110815869 | ref | NP_084403.2 | KELGLRDSMDYIQTDALINYGNSGGPLVNLGDEVIGINTLKVAAGISFAIPSDRIITRFLSEFONKHVKDWK-----KRFIGIRMRTITPVLVEELKAAANPDFPAVSSGIVVQEVVVPNSPSORGGIQDGDII 450
gi | 34878463 | ref | XP_341238.1 | KELGLRDSMDYIQTDALINYGNSGGPLVNLGDEVIGINTLKVAAGISFAIPSDRIITRFLSEFONKHVKDWK-----KRFIGIRMRTITPVLVEELKAAANPDFPAVSSGIVVQEVVVPNSPSORGGIQDGDII 450
gi | 22129776 | ref | NP_444272.1 | RELGLRDSMDYIQTDALINYGNSGGPLVNLGDEVIGINTLKVTAGISFAIPSDRIITRFLSEFONKHVKDWK-----KRFIGIRMRTITPVLVEELKAAANPDFPAVSSGIVVQEVVVPNSPSORGGIQDGDII 450
gi | 118090706 | ref | XP_420813.2 | KELGLRDSMDYIQTDALINYGNSGGPLVNLGDEVIGINTLKVTAGISFAIPSDRIITRFLSESLDKONKDK-----KRFIGIRMRTITPVLVEELKAAANPDFPAVSSGIVVQEVVVPNSPSORGGIQDGDII 450
gi | 51011095 | ref | NP_001003502.1 | KELGIRDSMDYIQTDALINYGNSGGPLVNLGDEVIGINTLKVTAGISFAIPSDRINKFLDSENDKQKVKQVVRVNTNYTQSQAMRTASDVNVPMKRFIGIKMVTITENLVHELKWHNPAFPDIGSGIIVHEVIADSPAKGGLSEGDII 450

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gi | 110815869 | ref | NP_084403.2 | VKVNGRPLADSSSELQEAVLNESLLELVRRGNDLLFSIPEVVM- 496
gi | 34878463 | ref | XP_341238.1 | VKVNGRPLVDSSELQEAVLNESLLELVRRGNDLLFSIPEVVM- 496
gi | 22129776 | ref | NP_444272.1 | VKVNGRPLVDSSELQEAVLTESPLLELVRRGNDLLFSIPEVVM- 496
gi | 118090706 | ref | XP_420813.2 | VKVNGRPLMTSSDLQEAVMNESPLLELVRRGNDLLFNIEPEVVM- 496
gi | 51011095 | ref | NP_001003502.1 | VKLNGHPLMNTGELQEAIQVDMPLLELVRRGNDLLFNIEPEVVM- 496

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