

gi|292615272|ref|XP\_002662597.1|-----MAIFRFQGHIIKSSAVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVTDLFMTTQRVSSQIEKHFQA 150  
 gi|41152241|ref|NP\_957034.1|-----MAIFRFQGHIIKSSAVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVTDLFMTTQRVSSQIEKHFQA 150  
 gi|4503719|ref|NP\_002003.1|-----MSFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVADLFPQTQRVGTIVVEKHFHG 150  
 gi|114587495|ref|XP\_001156390.1|-----MSFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVADLFPQTQRVGTIVVEKHFHG 150  
 gi|6753862|ref|NP\_034340.1|-----MSFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVADLFPQTQRVGTIVVEKHFHG 150  
 gi|11120730|ref|NP\_068542.1|-----MSFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVADLFPQTQRVGTIVVEKHFHG 150  
 gi|99028931|ref|NP\_001035736.1|-----MSFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPPLRVVERFDLRPDEVADLFPQTQRVGTIVVEKHFHG 150  
 gi|118097032|ref|XP\_414409.2|-----MLRFGQNLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPVPRVVERFDLCPDEVADLFRFAQRVGNVAVKHFCA 150  
 gi|30697031|ref|NP\_200632.2|-----MLNLQVVG-----KTIILS--IIRCQRKMS-----FC-----FYAFGPKIDPREVFMAIPLSYAMVNLRLPLLPAHVLVCPRLVPRFTDLTADETSIDLWLTAKVGSKLETFHNA 150  
 gi|115483895|ref|NP\_001065609.1|MLPVLADLRRAPTPFELLPLALAPPPPPHLLRRRPLLLPRAISS-----STSPPPVQEMEAAYKGGPKIDAREVFHSTPLSYAMVNLRLPLL----VCPKREVKRFADLSNEISDLWLTAKVGSKLETFHNA 150  
 gi|19075336|ref|NP\_587836.1|-----MPKQLYFSKFPVVG--SQVVFYRTKLSAAFVNLKRPILPGHVLVLPQRAVPRKLDLTPSELDDLFTSRVKVQVIEKVFSA 150  
 gi|39951749|ref|XP\_363591.1|-----MPKIPAPSSITRLCTIKPISATWSYRQRVITPTSIITHTITAAAAAATIKNSITKTIIVPVRMA-----NSSSQTAPKTFGPEVET--IQVFHRTAHSFALVNLKRPILPGHVLVCPVPHRRLLDITAELEDDLFSAVRRIQHMLARFFS 150  
 gi|164423547|ref|XP\_962506.2|-----MSISSDP-----EGNIRPASTQKSHY-----IDS-----EIHFGPEKVT--NQVFLRTPHSFALVNLKRPILPGHVLVCPVPHKRLTDLSPAEVTDLFSIVVQVRLGRYYFH 150  
 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|292615272|ref|XP\_002662597.1|S-----SLTICVQDGEAGQTVKHHVHVHVLPRKAGDFEKN-----DSIYDELQKHDRESE----- 300  
 gi|41152241|ref|NP\_957034.1|S-----SLTICVQDGEAGQTVKHHVHVHVLPRKAGDFEKN-----DSIYDELQKHDRESE----- 300  
 gi|4503719|ref|NP\_002003.1|T-----SLTFSMQDGEAGQTVKHHVHVHVLPRKAGDFHRN-----DSIYEELQKHDKK----- 300  
 gi|114587495|ref|XP\_001156390.1|-----MODGPEAGQTVKHHVHVHVLPRKAGDFHRN-----DSIYEELQKHDKK----- 300  
 gi|6753862|ref|NP\_034340.1|T-----SITFSMDOGPEAGQTVKHHVHVHVLPRKAGDFHRN-----DNIYDELQKHDREE----- 300  
 gi|11120730|ref|NP\_068542.1|T-----SITFSMDOGPEAGQTVKHHVHVHILPRKSGDFRRN-----DNIYDELQKHDREE----- 300  
 gi|99028931|ref|NP\_001035736.1|T-----SITFSMDOGPEAGQTVKHHVHVHILPRKAGDFHRN-----DSIYDALEKHDREDK----- 300  
 gi|118097032|ref|XP\_414409.2|T-----SLTIAIQDGPQAGQTVKHHVHVHILPRRSGDFRRN-----DDVYKELQDHDKE----- 300  
 gi|30697031|ref|NP\_200632.2|T-----SLTIAIQDGPQAGQTVPHVHIHILPRKGGDFEKN-----DEIYDALDEKEKELK----- 300  
 gi|115483895|ref|NP\_001065609.1|S-----SLTFAIQDGPQAGQTVPHVHIHILPRKGGDFEKN-----DEIYDALDVKERELK----- 300  
 gi|19075336|ref|NP\_587836.1|S-----ASNIGIQDGVDAQQTVPHVHVHIIIPRKKADFSEN-----DLVYSLEKNEGNLASLYLTGN----- 300  
 gi|39951749|ref|XP\_363591.1|PSSSSSGAA-----ADAAAIVQGGSFNIAVQDGPQAGQTVPHVHVHIIIPRPGGEGAAARAGEFDLYVGMANEDGNVGGALWD----- 300  
 gi|164423547|ref|XP\_962506.2|PGTTTTTRPKQREKKEKEEKGVAEDKVMLETGGSFNIAVQDGPQAGQTVSHVHVHVIPRIIRNVSAKDTETPSDALYEWMAEKEKNGIGGAFWDRDYGHGCHGCHGCDGGPHHHHHHHLQHSSTFGQORERALGGQNLNGSGSDVQS 300  
 .....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|292615272|ref|XP\_002662597.1|DSSQ-----WRSEEMAKEEASELRSLSF----- 376  
 gi|41152241|ref|NP\_957034.1|DSSQ-----WRSEEMAKEEASELRSLSF----- 376  
 gi|4503719|ref|NP\_002003.1|DFPAS-----WRSEEMAAEAAALRVYF----- 376  
 gi|114587495|ref|XP\_001156390.1|DSPAS-----WRSEEMAAEAAALRVYF----- 376  
 gi|6753862|ref|NP\_034340.1|DSPAF-----WRSEEMAAEAEALRVYFQA----- 376  
 gi|11120730|ref|NP\_068542.1|DSPAF-----WRSEEMAAEAEVLRAYFQA----- 376  
 gi|99028931|ref|NP\_001035736.1|DSPAL-----WRSEEMAAEAAALRVYF----- 376  
 gi|118097032|ref|XP\_414409.2|DSPDK-----WRSEEMAAEAAVLKXVYFEN----- 376  
 gi|30697031|ref|NP\_200632.2|QLDLDKDRVDRSIQEMADEASQVRSLSFDC----- 376  
 gi|115483895|ref|NP\_001065609.1|KLDLDIERKDRITKEMAHEANEYRGLFS----- 376  
 gi|19075336|ref|NP\_587836.1|ERVAGDERPPTSMRQAIKDEDRKPRITLEEMKEEAQWLKGYFSEEDKE----- 376  
 gi|39951749|ref|XP\_363591.1|LHREAG-----RPLPGGFPIEDADR-----VARSMADMETEAAEFRLLRVMDEEKHRQG----- 376  
 gi|164423547|ref|XP\_962506.2|KECEALLREEEGEEEEGVAEMLARPKPGSFPSTIEDAAR-----TAREMEEMEREAGEYRRLVLEEMGILSV----- 376  
 .....310.....320.....330.....340.....350.....360.....370.....

