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gi|31543960|ref|NP_033553.2| MTRKARRCLGHLFSLGIVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|62647835|ref|XP_342724.2| MTRKARRCLGHLFSLGIVYLRIGDFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|17505191|ref|NP_004616.2| MNRKARRCLGHLFSLGMVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|73984518|ref|XP_858028.1| MNRKARRCLGHLFSLGMVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|119914911|ref|XP_613296.3| MNRKARRCLGHLFSLGMVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|45383552|ref|NP_989623.1| MNRKTRRWIFHIFLCLGIIVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
gi|70887731|ref|NP_001020711.1| MSRKTTRRWIFHIFLCLGIIVYLRIGGFSSVVALGASIIICNKIPGLAPRQRAICQSRPDIIIVIGEGSQMGLDECQFQFRNGRWNCALGERTVFGKELKVGSRREAAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGOYHRDEGWKWG 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|31543960|ref|NP_033553.2| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKILEEN--MKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|62647835|ref|XP_342724.2| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKILEEN--MKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|17505191|ref|NP_004616.2| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKILEEN--MKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|73984518|ref|XP_858028.1| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKISLVGVRAIHLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|119914911|ref|XP_613296.3| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKILEEN--MKLECKCHGVSGSCTTKTCWTTLPQFRELGYVLKDKYNEAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|45383552|ref|NP_989623.1| GCSADIRYGIGFAKVFVDAREIKQARTLMNHLHNEAGRKILEEN--MKLECKCHGVSGSCTTKTCWTTLPKFRQLGYILKERYNHAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
gi|70887731|ref|NP_001020711.1| GCSADIRYGLSFSKVFVDAREIKQARTLMNHLHNEVGRKILEEN--MRLECKCHGVSGSCTTKTCWTTLPKFRQLGYILKERYNHAVHVEPVRASRNKRPTFLKIKKPLSYRKPMDIDLVIIEKSPNYCEDPVTGSGVGTQGRACNKTA 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|31543960|ref|NP_033553.2| PQASGCDLMCCGRGYNTHQYARVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|62647835|ref|XP_342724.2| PQASGCDLMCCGRGYNTHQYARVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|17505191|ref|NP_004616.2| PQASGCDLMCCGRGYNTHQYARVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|73984518|ref|XP_858028.1| PQASGCDLMCCGRGYNTHQYARVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|119914911|ref|XP_613296.3| PQASGCDLMCCGRGYNTHQYARVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|45383552|ref|NP_989623.1| QASNGCDLMCCGRGYNTHQYSRVWOCNCKFHWCCYVKCNTCSERTEMYTCK 351
gi|70887731|ref|NP_001020711.1| QHNGCDLMCCGRGYNTHQYSRVWOCNCKFLWCCYVKCNTCSERTEMYTCK 351
.....310.....320.....330.....340.....350.

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