

```

gi|25777684|ref|NP_733832.1|-----MSGEPELIELRELPAGRAGKGR-----TRLERANALRIARCTACNPTR- 150
gi|114587016|ref|XP_001168270.1|-----MSGEPELIELRELPAGRAGQGR-----TRLERANALRIARCTACNPTR- 150
gi|73985427|ref|XP_850255.1|-----MSTPELIELRELEFPARRGGPGR-----SRLERANALRIAPGTARNPAR- 150
gi|83025054|ref|NP_001032644.1|-----MSAEPELIELRELPASGRIGPGR-----TRLERANALRIAPGTTRNPSQ- 150
gi|50763950|ref|XP_422923.1|-----MAKCELLIELDLTPNDRIELAPPVPPVPPVVPVTLDRWSRGKVVVMVGERVRLDDPD 150
gi|52218954|ref|NP_001004550.1|-----MLRSVVNNNDKAKESEQSVRVAIDDPVYQSYAFQPTSSSSNISWFGGLRKLKLSQLSLFDDMWSQLGKIDDEKMETSSSTSSPQSEQSIGEYDESLVFRFPVQLDHFGGAGEDDGEQVDLWDFGATFLADLDSNHVWNDLIERQHFGLK 150
gi|71996187|ref|NP_001022361.1|-----1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

gi|25777684|ref|NP_733832.1|---OLVPG---RGHRFQAGPAPATHWCDLCGDFIWGVVRKGLQCARLSADCKFTCHYRCRALVCLDCGPRDLGWEP---AVERDINVDEP--VEWET 300
gi|114587016|ref|XP_001168270.1|---OLVPG---RGHRFQAGPAPATHWCDLCGDFIWGVVRKGLQCARLSADCKFTCHYRCRALVCLDCGPRDLGWEP---AVERDINVDEP--VEWET 300
gi|73985427|ref|XP_850255.1|---OLVAG---RGHRFQAGPAPATHWCDLCGDFIWGVVRKGLQCA---HCKFTCHYRCRALVCLDCGPRDLGWEP---ALERDINVDEP--AEWEI 300
gi|83025054|ref|NP_001032644.1|---OLVPG---RGHRFQAGPAPATHWCDLCGDFIWGVVRKGLQCA---HCKFTCHYRCRALVCLDCGPRDLGWDP---ALERDINVDEA--VERET 300
gi|50763950|ref|XP_422923.1|---WLTCKPG---RGHDFQPCSQQLSWCDLCGDFIWGLYRQSLRCL---HCNYTCHYRCQPFQIDGSSNTDITICEQSNYS---EDTLETDINVDEQSEVDWRK 300
gi|52218954|ref|NP_001004550.1|---DLITGGGANKLNNSFKTHSLHPHWCDKCGDFIWGLKALRCE---HCNYTCHARCRDLVLDGRSPGSSLASSTEFDLIVPQLDGLGTIPKGLILPPAMSSSTGSKENGNNSAGISAEPIFVKNSEFLLPKSFPVDSLRI 300
gi|71996187|ref|NP_001022361.1|-----.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



```

gi|25777684|ref|NP_733832.1|-----PDLQAETEQKIKEYNAQINSNLFMSLNKDGSYTGFIKVLKLVKLRPVSVPS---SKKPPSLQDARRGPGRGTSVRRRTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|114587016|ref|XP_001168270.1|-----PDLQAETEQKIKEYNAQINSNLFMSLNKDGSYTGFIKVLKLVKLRPVSVPS---SKKPPSLQDARRGPGRGTSVRRRTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|73985427|ref|XP_850255.1|-----PDLQAETEQKIKEYNAQINSNLFMSLNKDGSYTGFIKVLKLVKLRPVSVPS---SKKPPSLQDARRGPGRGTAVKRRTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|83025054|ref|NP_001032644.1|-----PDLQAETEQKIKEYNAQINSNLFMSLNKDGSYTGFIKVLKLVKLRPVSVPS---SKKPPSLQDARRGPGRGSIAVKRRTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|50763950|ref|XP_422923.1|-----AELDPAQVEQRIKEYNSQINSNLFMSLNKDGSYTGFIKVLKLVKLRPVSVPA---AKRGP---GGRPGQ-RTAGVKRRTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|52218954|ref|NP_001004550.1|-----QDLVTLTQQKVEYNAQVNSNLFMVLNRDGSYTGFIKVLKLVKLRPVSLPP---PRSVSSSISSSCLGWDGGCOERTSFYLPKDAVKHLHLVLSRTRAREVIEALLRKFVVDPRKFKAL 450
gi|71996187|ref|NP_001022361.1|-----KEPSAPPESRYATLRRVVERVYKEDTPEFWEIDYKEMDLERKIHSYNSLAKGMEITLHEDGVNFGGHIHVNMNLSRPISSVVGQVIPPVTVVAVNTAKSTAKTISLRTTISFFLRNTAKVINIDSKITARKMIVTLKLFKRVADNPRKFKAL 450

```



```

gi|25777684|ref|NP_733832.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|114587016|ref|XP_001168270.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|73985427|ref|XP_850255.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|83025054|ref|NP_001032644.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|50763950|ref|XP_422923.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|52218954|ref|NP_001004550.1|FERRERHGOV---YLRKLLDDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
gi|71996187|ref|NP_001022361.1|YERSEK---DEG---YLRKLLADDEQPLRLRLLAGPSDKALSFVLKENDSGEVNWDAFSMPPELHNFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600
YECEIIDEAICLNRKLRISDDACPLKVVLNWQSPHCGRALVQENDIGDILWDAFEIPELENFLRILQREEEHRLQILQKYSYCRQKIQEALHACPLG 600

```



```

gi|25777684|ref|NP_733832.1|----- 619
gi|114587016|ref|XP_001168270.1|----- 619
gi|73985427|ref|XP_850255.1|----- 619
gi|83025054|ref|NP_001032644.1|----- 619
gi|50763950|ref|XP_422923.1|----- 619
gi|52218954|ref|NP_001004550.1|----- 619
gi|71996187|ref|NP_001022361.1|DVTNLEVLKKNMDDQSNL 619
-----610-----

```