

```

* * * * * .:***: * :.***.***:*****: * :***:*****
gi | 188528609 | ref | NP_003006.2 | MRAAAAGGVRTAALALLLALGALHWAPARCCEYDYYGWAEP L-HGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWLP LLAKRCHSDTQVFLCSLFAPVCLDRPIYPCRSLCEAVRAGCAPLMEAVGFPWPEM 150
gi | 27806141 | ref | NP_776886.1 | MRAAAGG--ARA AVLALLLALGALGAPARGCEYDYYGWTEPL-HGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWLP LLAKRCHSDTQVFLCSLFAPVCLDRPIYPCRSLCEAVRAGCAPLMEAVGFPWPEM 150
gi | 31560421 | ref | NP_061250.2 | MWVAWSA--RTAALALLLALGALGAPTRGCEYDYYGWAEP L-HGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWLP LLAKRCHSDTQVFLCSLFAPVCLDRPIYPCRSLCEAVRAGCAPLMEAVGFPWPEM 150
gi | 62642337 | ref | XP_219887.3 | MRVAGGA--RTAALALLLALGALGAPARGCEYDYYGWTEPL-HGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWLP LLAKRCHSDTQVFLCSLFAPVCLDRPIYPCRSLCEAVRAGCAPLMEAVGFPWPEM 150
gi | 73998507 | ref | XP_543955.2 | -----MTRLGKAAA-----AHLLEHVLAEVKQOASSWLP LLAKRCHSDTQVFLCSLFAPVCLDRPIYPCRSLCEAVRAGCAPLMEAVGFPWPEM 150
gi | 50749675 | ref | XP_421707.1 | MPRASGP---FGTVL LALLALALPGECHYDYYGWAEPESVPRGRFYGREPCVDIPADMQLCHDVGYKRMRLPNLLEHESMAEAKQOASSWVPLLAQCHADTQLFLCSLFAPVCLDRPIYPCRSLCEVVRDSCAPVMESVGFWPEM 150
gi | 61097889 | ref | NP_571933.1 | MAELKRQV-LQAVL LALVLLLSASS-AEYDYYSWSDNFHSGRFYAKQPCVDIPADLRLCYNVGYKRMRLPNLLDHEIMPEVKQOAGSWVPLLAQCHADTQVFLCSLFAPVCLDRPIYPCRSLCEAVRSDCAPVMETVGFWPEM 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

*: * * * * * :***: * * * * * :***:*****
gi | 188528609 | ref | NP_003006.2 | LHCHKFPLDNDLCIAVQFGLPATAPPVTKICACEMEHSADGLMEQMCSSDFVVKMRIKEIKIENGDRKLI GAQKKKKLLKPGPLKRKDTKRLV LHMKNAGCCPQLDLS LAGSFLVMGRKVDGOLLMAVYRWDKKNKEMKFAVKFMF 300
gi | 27806141 | ref | NP_776886.1 | LHCHKFPLDNDLCIAVQFGLPATAPPVTKICACEMEHSADGLMEQMCSSDFVVKMRIKEIKIENGDRKLI GAQKKKKLLKSGPLKRKDTKRLV LHMKNAGCCPQLDLS LAGSFLVMGRKVDGOLLMAVYRWDKKNKEMKFAVKFMF 300
gi | 31560421 | ref | NP_061250.2 | LHCHKFPLDNDLCIAVQFGLPATAPPVTKICACEMEHSADGLMEQMCSSDFVVKMRIKEIKIENGDRKLI GAQKKKKLLKAGPLKRKDTKRLV LHMKNAGS CPCPQLDNL TGSFLVMGRKVEGOLL LTAVYRWDKKNKEMKFAVKFMF 300
gi | 62642337 | ref | XP_219887.3 | LHCHKFPLDNDLCIAVQFGLPATAPPVTKICACEIEHSADGLMEQMCSSDFVVKMRIKEIKIENGDRKLI GAQKKKKLLKAGPLKRKDTKRLV LHMKNAGS CPCPQLDNL TGSFLVMGRKVEGOLL LTAVYRWDKKNKEMKFAVKFMF 300
gi | 73998507 | ref | XP_543955.2 | LHCHKFPLDNDLCIAVQFGLPATAPPVTKICTCEMEHSADGLMEQMCSSDFVVKMRIKEIKIENGDRKLI GAQKKKKLLKPGPLKRKDTKRLV LHMKNAGS CPCPQLDLS LAGSFLVMGRKVDGOLLMAVYRWDKKNKEMKFAVKFMF 300
gi | 50749675 | ref | XP_421707.1 | LHCGKFPDHDLCIAVQFGNNQATPPPVPKICTCEMEHRADGMQMCSSDFVVKMRIKEIVIEENGKRLVAAQKKK-VLKLGPLKRKDTKKMVLHMRNTGS CPCPOLANL SGSFLVLGRKVGSRLL LLAIFWQKHKEMKFAVKFMF 300
gi | 61097889 | ref | NP_571933.1 | LQCEKFPDNDLCIPMFSAGHATQTPVSKVCPDCNELKADTIMEHYCASDFALKMKIKEARKEKGRKLI AAKKKKVLKMGILRKKDLKKLTLYIKNGANCPQLDNL GSNFLMGRKVDGOLL LMSIHKWDKSKELKFAIKYIK 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



```

* * * * *
gi | 188528609 | ref | NP_003006.2 | SYPCSLYYPFFYGAAEPH 318
gi | 27806141 | ref | NP_776886.1 | SYPCSLYYPFFYGAAEPH 318
gi | 31560421 | ref | NP_061250.2 | SYPCSLYYPFFYGAAEPH 318
gi | 62642337 | ref | XP_219887.3 | SYPCSLYYPFFYGAAEPH 318
gi | 73998507 | ref | XP_543955.2 | SYPCSLYYPFFYGAAEPH 318
gi | 50749675 | ref | XP_421707.1 | SYPCSLYHPLL YGAGQH 318
gi | 61097889 | ref | NP_571933.1 | SQQCPYHSVFEQ----- 318
.....310.....

```

