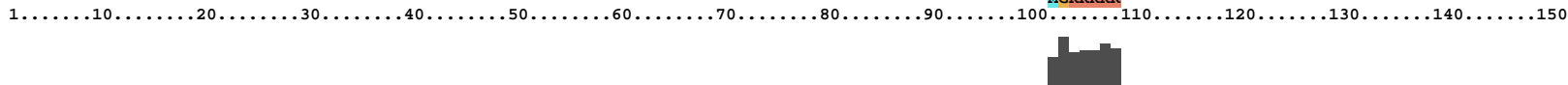


```

gi | 6756051 | ref | NP_035881.1 | -----MGRKKKK----- 150
gi | 84781684 | ref | NP_001034109.1 | -----MGRKKKK----- 150
gi | 114668206 | ref | XP_511402.2 | -----MGRKKKK----- 150
gi | 78369234 | ref | NP_001030345.1 | -----MGRKKKK----- 150
gi | 148612835 | ref | NP_001091977.1 | -----MGRKKKK----- 150
gi | 73967096 | ref | XP_537731.2 | MAAAPQRPVSTHSGRRPASCDPSRAWHRLRPQCLGAERRTRASAILCLFPVGRGRGRCRGRAGAPVGGGWDWEALLRPAEGVRDLGLEVGGLVARAGFGKTSOKREVPRARGSGSWGVSITQEVLASVLRWIPPPRTVSPKDVRE 150
gi | 118099726 | ref | XP_415665.2 | -----MGRKKKK----- 150
gi | 47085991 | ref | NP_998362.1 | -----MGRKKKK----- 150
gi | 17538210 | ref | NP_502124.1 | -----MGRKKKK----- 150
gi | 18397747 | ref | NP_564369.1 | -----MGRKKKRA----- 150
gi | 115480675 | ref | NP_001063931.1 | -----MGRKKKK----- 150

```



```

gi | 6756051 | ref | NP_035881.1 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 84781684 | ref | NP_001034109.1 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 114668206 | ref | XP_511402.2 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 78369234 | ref | NP_001030345.1 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 148612835 | ref | NP_001091977.1 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 73967096 | ref | XP_537731.2 | PAVVLLVQFNKGTSPVNTLLEYNDRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 118099726 | ref | XP_415665.2 | -----OLKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 47085991 | ref | NP_998362.1 | -----QMKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 17538210 | ref | NP_502124.1 | -----VDKPCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 18397747 | ref | NP_564369.1 | -----TEKVCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300
gi | 115480675 | ref | NP_001063931.1 | -----VEKVCWCYNRDFDDEKILLIQHAKHFKCHICHKKLYTGPGLAIHCMOVHKEITIDAVPNAIPGRDIELEIYGMGEGPEKMDERRRLLLEOKTC-ESQKKKQDDSDYEYDDESAASTSFQOP-VOPOOGYIYP 300

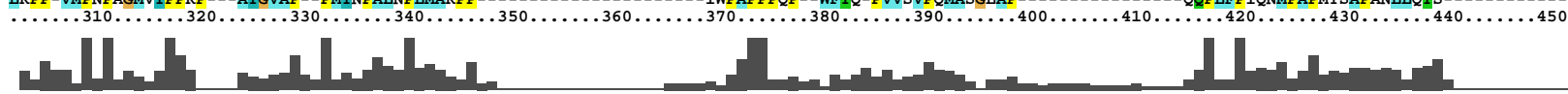
```



```

gi | 6756051 | ref | NP_035881.1 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAG----- 450
gi | 84781684 | ref | NP_001034109.1 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAG----- 450
gi | 114668206 | ref | XP_511402.2 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAGMGFPVTSST 450
gi | 78369234 | ref | NP_001030345.1 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAG----- 450
gi | 148612835 | ref | NP_001091977.1 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAGMGFPVTSST 450
gi | 73967096 | ref | XP_537731.2 | MAQPLPVPVPGAPGMPPG-----IPLMPGVPLMPGMPVMPGMPPLGHQRKYTQSFCEGIMMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAGMGFPVTSST 450
gi | 118099726 | ref | XP_415665.2 | MAQPLPVPVPGAPGMPPG-----IPLMAGVPLMPGMPVMPGMP-----MMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAGMGFPVTSST 450
gi | 47085991 | ref | NP_998362.1 | MTPCGMAPVVP-APGMPPGYSGMPPMMPGMPVMPGMP-----MMPMGMMPPGGIPLMPGMP-----PVP-RPGIPMTQAQAVSAPGILNRRPPATAVPAPOPVVKPLFPBAG----- 450
gi | 17538210 | ref | NP_502124.1 | MPFPQHFPPFGMPMPG-----PPPPSMAYGMPP-MP-----SGMPPR-----GMGAYPPPR-----YPPAPAGVYMPGMPGAYPPR----- 450
gi | 18397747 | ref | NP_564369.1 | APLGGVPRRYGMVYPPQ-----VPGAVPARMYYPG-PMRHPAP-----VWMPPPRQWYQNPALSVPPAAHLGYR-----PQPLFVQNMGMFTFETAPAPQSP----- 450
gi | 115480675 | ref | NP_001063931.1 | LRPP-VMPNFAGMVYPPR-----AVGVAP-----PMYNPALNLRAPP-----TWQAPPPQ-----WFTQ-PVVSVMQASGLAP-----QQLFETQNPAPMTPSAPANLQIS----- 450

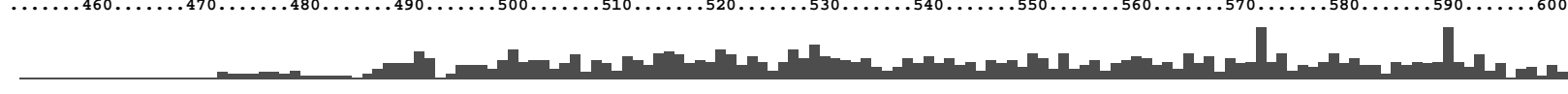
```



```

gi | 6756051 | ref | NP_035881.1 | -----QAQAAVQGVGDFKPLNSTPAATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQIPGNPVVPIGGMPPQFGLP-QQGM 600
gi | 84781684 | ref | NP_001034109.1 | -----QAQAAVQGVGDFKPLNSTPAATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQIPGNPVVPIGGMPPQFGLP-QQGM 600
gi | 114668206 | ref | XP_511402.2 | ASSNSELSASSKALFPSTQAQAAVQGVGDFKPLNSTP-ATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 78369234 | ref | NP_001030345.1 | -----QAQAAVQGVGDFKPLNSTP-ATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 148612835 | ref | NP_001091977.1 | ASSNSELSASSKALFPSTQAQAAVQGVGDFKPLNSTP-ATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 73967096 | ref | XP_537731.2 | ASSNSELSASSKALFPSTQAQAAVQGVGDFKPLNSTP-ATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 118099726 | ref | XP_415665.2 | ASSNSELSASSKALFPSTQAQAAVQGVGDFKPLNSTP-ATTEPPKPTFPAYTQSTASTTSTNSTAAKPAASITSKPATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 47085991 | ref | NP_998362.1 | -----QVQPAVSG-----VAASSP-----APSAAKPTFPAYTQSSAAPSSTNTVTKPTVTSKPAATLTTTSATSKLIHPDEDISLEERRAOLPKYQRLNRPFGQAPIGNPVVPIGGMPPQFGLP-QQGM 600
gi | 17538210 | ref | NP_502124.1 | -----MPIGHGP-----PGGPPMPGPPRRFRDQDGGDRGPPMRGVRTPR--YENEHEHDMQAPDDNQGGYDDRFRGDRGGF-PGGSRFDQKAEKKEIIEVFNNGP----- 600
gi | 18397747 | ref | NP_564369.1 | -----VTGVTPPGIPISSPAMP-VPOPLFFVNNH-IPQAPPPSAPLVGGAQQPSHADALGSADAYPPNNSIPGGTNAHSWASGENTSGPSIGPPPVIANKAPSNQF--NEVTLVWDD 600
gi | 115480675 | ref | NP_001063931.1 | -----FMAHVGVG-----SVTTPQVSGPLFPVSTAGNAVSPVAVAVAG-----SIPTSPPVAVAG-----VGYAATNOGTGGAAVPPASNNKAPAPQGANEVTLVWDD 600

```



```

gi|6756051|ref|NP_035881.1|      RPPMPPHGQYGGHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQGGRY- 661
gi|84781684|ref|NP_001034109.1| RPPMPPHGQYGGHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQGGRY- 661
gi|114668206|ref|XP_511402.2|    RPPMPPHGQYGGHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQALP- 661
gi|78369234|ref|NP_001030345.1|  RPPLTKVGLLDRWE----- 661
gi|148612835|ref|NP_001091977.1| RPPMPPHGQYGGHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQGGRY- 661
gi|73967096|ref|XP_537731.2|    RPPMPPHGQYGGHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQGGRY- 661
gi|118099726|ref|XP_415665.2|    RPPMPPHGQYGAHHGMPGYLPGAMPPYGGPPMVPPYGGGPPRPPMGMRPPVMSQGGRY- 661
gi|47085991|ref|NP_998362.1|    RRPQ--GFYGAFFQAVFGYVFGGMPFYGAAPPVPPYQAAPRPAIGMRPPVMSPGGRY- 661
gi|17538210|ref|NP_502124.1|    ---TSSGAAAASAAAIVASKLCSR-----TRIVYDDHSLSLEERRVKMLFEKRSNPPYH 661
gi|18397747|ref|NP_564369.1|    EAMSMEEERRSLPKYQVHDEISQMN-----SINAAIDRRISESLAGRMF----- 661
gi|115480675|ref|NP_001063931.1| EAMSMEEERRSLPKYQVHDEISQVSSDFYNFISVILMICEKNQVEVHGDAALNWNIV----- 661
.....610.....620.....630.....640.....650.....660.

```

