```
gi|19923590|ref|NP_071928.2|      ----------------------------------------------------------------------------------------------------MASETEKTHALLQT   14
gi|114600402|ref|XP_001135483.1|  ----------------------------------------------------------------------------------------------------MASETEKTHALLQT   14
gi|119331222|ref|NP_001073263.1|  ----------------------------------------------------------------------------------------------------MASETEKTHALLQS   14
gi|85986653|ref|NP_001034333.1|   ----------------------------------------------------------------------------------------------------MASKVEKTHALPPC   14
gi|109464421|ref|XP_574856.2|     MGKNSQQPSAHPVKDQRCFERIPRLCVCGDSEDSAALASQHSSLYGAAKGRSPVGSPADREARWERLSCSKRGAQGPMDRGASRGKPEQGKDIKCIIMQAFAIVQHAETKTRKMQGMQTRIACWFLMSFTLVTQFMMASKVEKTHALPPC  150
gi|50761615|ref|XP_424781.1|      ----------------------------------------------------------------------------------------------------MASETEKAHALLQT   14
gi|52218892|ref|NP_001004514.1|   ------------------------------------------------------------------------------------------MRGFYSKLDS---SSIGMAVPLNLAVETEKAQALLQT   34
gi|24657049|ref|NP_647838.1|      ----------------------------------------------------------------------------------------------------------------MPHCHT    6
gi|158294087|ref|XP_315389.3|     ------------------------------------------------------------------------------------------------------------------------MN    2
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

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                                      :.    :   *  .*.:       :   ::*  ** .*  :*            : .       :    .::* **:***  : *: :: * .* :** ** *::     :              .       : :  :** **
gi|19923590|ref|NP_071928.2|      CSTESLISSLGLGAFCLVADRLLQFSTIQQNDWLRALSDNAVHCVIGMWS---WAVVTGIKKKTDFGEIILAG--FLASVIDVDHFFLAGSMSLKAALTLPRRPFLHCSTVIPVVVLTLKFTMHLFKLKDSWCFLPWMLFISWTSHHIRD  159
gi|114600402|ref|XP_001135483.1|  CSTESLISSLGLGAFCLVADRLLQFSTIQQNDWLRALSDNAVHCVIGMWS---WAVVIGIKKKTDFGEIILAG--FLASVIDVDHFFLAGSMSLKAALTLPRRPFLHCSTVIPVVVLTLKFTMHLFKLKDSWCFLPWMLFISWTSHHIRD  159
gi|119331222|ref|NP_001073263.1|  CSTESLLSSLGLGLFCTVADRLLQFPIIQQNAWLRALSDNSVHCVIGMWS---WAIVIGIRKKTDFGEIILAG--FLASVIDIDHFLLSGSLSLKAALSLPRRPFLHCSTVIPTVVLTLKFTMHFFKLKDSWCFLPWMLFISWTSHHIRD  159
gi|85986653|ref|NP_001034333.1|   CSTESLISSIGLGIFCLVADRLLRFPIIQHNDWLRAISDNIVHGVIGMWS---WAVVTGIRKKSDFGEVLLAG--FLASVIDVDHFFQARSLSLQAALTLPRRPFLHCSTVIPIAVLSVKLAVHLFKLRDSWRFLPWMILVSWTSHHIRD  159
gi|109464421|ref|XP_574856.2|     YSTESLISSLGLGIFCLIADRLLRFSIIQQSDWLRALSDNVVHGVIGMWS---WAVVIGIRKKSDFAEVLLAG--FLASVIDVDHFFMARSLSLQAALTLQRRPFLHCSTVIPITVLSVKLAMHLFKLRDSWRFLPWMIFISWTSHHIRD  295
gi|50761615|ref|XP_424781.1|      FSAASVISSLGLGIFCFAADRLLQVSFVQQNDWLRAFSDNAVHGILGMWS---WAIVIGLRKKSDFTEVTLAG--FLASVIDLDHFLLAGSLSLKAALSLPRRPLLHCSTVIPVVALTLKLIMHLFRLKDSWCFLPWMLFISWTSHHIRD  159
gi|52218892|ref|NP_001004514.1|   FSTASLFASAGLGAFCFVADHFLTLPFIQHHLWLRALFDNTVHAIIGLWS---WAIVIGLRKKSDFYEVILAG--FLASVIDLDHFYMAGSLSIKAAVNLPHRPPLHCSTLIPALCFSLRLLMWACRLKDSWCSLPWMLFISLTSHHIRD  179
gi|24657049|ref|NP_647838.1|      MVYMRIVLTTLVTITCLLGDNFVEL---TQHPLLKALADNATHAAIGALTGITFATQFYERTSQLFGWILIFTCFVVSSFIDLDHFVEARSLYLEDATNLSKRPFLHCSSIIVVMLLFYMCTACLNYFRTSLMLG--SLLCAFITHHTRD  151
gi|158294087|ref|XP_315389.3|     WNLLLVLKHVILCCVCVIGDKLGES--AQKPALVRACIDNATHAFIGCIVAELVLFNFKHQLTRHEYCWLLFVATIISSCIDLDHFIEAKSFRLQDATNLDRRPFLHNSTICVVIFILFILTKRAS---NQLRMLIAMAFVAFSTHHLRD  147
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                  . *:* *.  .   :     .   *:          . :  .                          :     ::*
gi|19923590|ref|NP_071928.2|      GIRHGLWICPFGKTSPLPFWLYVIITSSLPHICSFVMYLT-----------------GTRQMMSSKHGVRIDV-   215
gi|114600402|ref|XP_001135483.1|  GIRHGLWICPFGKTSPLPFWLYVIITSSLPHICSFVMYLT-----------------GTRQMMSSKHGVRIDV-   215
gi|119331222|ref|NP_001073263.1|  GIRHGLWMCPFGKTSPLPFWLYVIITSSLPHICSFVMYFT-----------------GTRQMMSSKHGIHIDV-   215
gi|85986653|ref|NP_001034333.1|   GIRHGLWICPFGKTPPLPSSFYVISTLSLPHLCSFLMYLT-----------------GTRQTVSSKYGMRIDV-   215
gi|109464421|ref|XP_574856.2|     GIRHGLWICPFGKTPPLPFWFYVISTLSLPHTCSFLMYLT-----------------GTRETMSSKHEMRIDV-   351
gi|50761615|ref|XP_424781.1|      GIRHGLWICPFGKTPPLPYWLYVAITASLPHLCSFIMYLT-----------------GTRELMSIKHGIHIDV-   215
gi|52218892|ref|NP_001004514.1|   GVRHGLWVCPFGNTAPISYWLYVTITATLPHLCSVLMYLT-----------------GTRDMISTKHGVAIDV-   235
gi|24657049|ref|NP_647838.1|      AVRRGYWLCPLGHTDRMPQLAYILTTILTPHLLGCLHNVCRSATVLNFLGQYVKLSEGQYRSGSTANYRYMQV-   224
gi|158294087|ref|XP_315389.3|     ATRRGIWFKSPFQDSSSPAVPYVLYIAYVNIIPSVIVYLL-----------------QTTGSSTVPKMKLVEVV   204
                                  .......310.......320.......330.......340.......350.......360.......370....
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