```
Dmel9254_6-139   LLFVAAILVPQCLRALRYSQGTGDENCETLKSEIHLIKEEFDELGRMQRTCNADVIVNKCEGLCNSQVQPSVITPTGFLK  80
Dmel7883_75-143  ------------------------------------------------------------ACVGRCASYIQVSGSKIWQMER  22
                                  10        20        30        40        50        60        70        80

Consensus
                 LLFVAAILVPQCLRALRYSQGTGDENCETLKSEIHLIKEEFDELGRMQRTCNADVIVNXCXGXCXSXXQXSXXXXXXXXXX

Dmel9254_6-139   ECYCCRESFLKEKVITLTHCYDPDGTRLTSPEMGSMDIRLREPTECKCFKCGDF  134
Dmel7883_75-143  SCMCCQESGEREAAVSL-FC-----PKVKPGERKFKKVLTKAPLECMCRPCTS-  69
                                  90       100       110       120       130

Consensus
                 XCXCCXESXXXEXXXXLTXCYDPDGXXXXXXEXXXXXXXXXXXXPXECXCXXCXXF
```