```
Lmig            -----VLLYLFSSIYIYIYRYFNCYTFSVTEFLKTLSL--------LNERLSEMQQ-STTYNDLVQ---FRVVRNLG---  60
Turt1           VSPSSSVLLNALIFFMSVSMVHSNSPYKSVETLSPLEL------SYNSNLEQSEVPPKRYSEFLGGPGKRVSEFLGGPG  73
Turt2           VSPSSSVLLNALIFFMSVSMVHSNSPYKSDVTADEMRLQYLKDASTFNERFRHSQCCPE-LGYYLNGQESRSASSL--PS  77
Vdes            -----MLDLSRALFAFGVAMTLLAVTY---TLASPIEFEVAGGQGSFGDGQGI----QKRYSEFLGGPGKRYSEFLGGPG  68
Isca            MSCLHLLALAVLATCGFVRLGHRCSTHSDGTLSRSLQQLYTGGSPFTNARQRVPSRENKRLSEFLGGPGKRYSEFLGGPG  80
Pcau17101_13-41 ----------------ERTHA-----------------------------------------RKRHIEFLGG--KRAVEFLGGKR  26
Pcau17101_142-193 ----------------SS-----------------------------------------TKRAIEFLGG--KRAVEFLGGRK  23
                                   10        20        30        40        50        60        70        80

Consensus       VSPSSSLLLNALIFFMSVSMXHSXSTYXSXXXXSPLELXYXGGXXSFNERXRXSQXXPKRYSEFLGGPGKRXXEFLGGPG
```

```
Lmig            ----------------SEFLGKRMGSEFLGKRMQNLKNILGVK---  87
Turt1           KRAPTYGYVSEQGKSEILRASNGPNLGPYRPG-GSEFLGGPGRR  116
Turt2           SSSPSLSALLFSGSSEFLGKRVGSEFLGKRVGSGSEFLGRRKRS  121
Vdes            KRY-------------SEFLGGP-GKRNRQENLRNLRMILSGRARR  100
Isca            KRY-------------SEFLGGP-GKRY--------SEFLGGPGKR  104
Pcau17101_13-41 ------------------------------------------SGY---  29
Pcau17101_142-193 RA-------------IEFLGGKRSARLLPYENKRGIEFLSGK---  52
                                  90       100       110       120

Consensus       KRYPXXXXXXXXXGXSEFLGGXXGXRXLXXRXGNGSEFLGGXGRR
```