```
Lmig            -----VLLYLFSSIYIYIYRYFNCYTFSVTEFLKTLSL--------LNERLSEMQQ-STTYNDLVQ---FRVVRNLG---  60
Turt1           VSPSSSVLLNALIFFMSVSMVHSNSPYKSVETLSPLEL------SYNSNLEQSEVPPKRYSEFLGGPGKRVSEFLGGPG  73
Turt2           VSPSSSVLLNALIFFMSVSMVHSNSPYKSDVTADEMRLQYLKDASTFNERFRHSQCCPE-LGYYLNGQESRSASSL--PS  77
Vdes            -----MLDLSRALFAFGVAMTLLAVTY---TLASPIEFEVAGGQGSFGDGQGI----QKRYSEFLGGPGKRYSEFLGGPG  68
Isca            MSCLHLLALAVLATCGFVRLGHRCSTHSDGTLSRSLQQLYTGGSPFTNARQRVPSRENKRLSEFLGGPGKRYSEFLGGPG  80
Pcau17101_76-128 ----------------------------------------Q-------------------------TKRAIEFLGG--KRATSSVVADA  22
Pcau17101_13-41  ----------------------------------ERTHA-------------------------RKRHIEFLGG--K----------  16
Pcau17101_142-193 ----------------------------------------SS-------------------------TKRAIEFLGG--KRAVEFL--GG  21
                                  10        20        30        40        50        60        70        80

Consensus
VSPSSSLLLNALIFFMSVSMVHSXSTYXSXXXXSPLXLXYXGGXXSFNERXRXSQXXXKRYXEFLGGPGKRXSEFLGGPG

Lmig            ----------SEFLGKRMGSEFLGKRMQNLKNILGVK---  87
Turt1           KRAPTYGYVSEQGKSEILRASNGPNLGPYRPG-GSEFLGGPGRR  116
Turt2           SSSPSLSALLFSGSSEFLGKRVGSEFLGKRVGSGSEFLGRRKRS  121
Vdes            KRY----------SEFLGGP-GKRNRQENLRNLRMILSGRARR  100
Isca            KRY----------SEFLGGP-GKRY--------SEFLGGPGKR  104
Pcau17101_76-128 DKRA----------IEFLSGKRSTTSDIADAKRAIEFLGGK---  53
Pcau17101_13-41  --RA----------VEFLGGKRS----------GY---  29
Pcau17101_142-193 RKRA----------IEFLGGKRSARLLPYENKRGIEFLSGK---  52
                            90        100       110       120

Consensus
KRRAXXXXXXXXGXSEFLGGKRGXRXLXXRXXXGSEFLGGKGRR
```