```
Amel        MATTVIFIQRCMIIVAILLC--YFHAQSESVNCELYPFHHTCRGTMSRKRFPIAYGSECEESKGNINCVKEEKNRIAYIP  78
Turt2       MVKSGIEIQV---ISYIMMFWFILHGQVNSLDCRRHVFAPGCRGIVAKRTHQNSIKFEDPSKKLTASSDEMVNRKPNVIN  77
Isca        MKRTCIQA-----LVGVLFFAALVHQLHAELDCRKYPFYYRCRGISAKRSFAPITKMEAMSLKELYEDDDGWKNRRRPVD  75
Znev        MSRGCARLLPLLLSTGMLLYIAMTEAVPGPLDCRRFVYAPKCRGVAAKRGFLPGYLLDTDRKVDGLEEVLGLYATPQPIA  80
Dpul        FNSMSSSSTILLLFAGIVIF-AAVHVHSRDLDCRRFVFAPMCRGATIKRSFIPNIGVNQDDVHELLLD----YPKQQVMD  75
Lmig        MTKTHVLSLLMIVLCALCLA-IGSAKGQKRVDCRMYPFAPICRGIMTKKRDLDSTGVASSAIQKSAD-----YPDARQWS  74
Turt1       MVSSVNQLTVLVTLLSIVLFNLIVVSTAYPVDCSKFVFAPTCRGVIAKRINSNGFKTNSKSTQNDLTDRSDPWPEMNPSS  80
Tcas7641_38-58 ----------------------------------KKNHCRTHIFSPVCRG-QQKRD-----------------------  21
                                  10        20        30        40        50        60        70        80

Consensus   MVXTXIQXXVLLLLVGILLFXAIVHAQSKXLDCRRXVFAPTCRGIMAKRXFLPXXXVESDSKKELLEDXXGXYPXPXPIX
```

```
Amel        LSKSKLLIALLDDDLRKDIKLRNDEMIKQNSALMENFLSQLDSSD  123
Turt2       SPDYNNNNNLNNNNINPSASLTGSNNNRNSNPLTTIINSSNQNND  122
Isca        AVLGWVRNKYGDDIFDPDEPLDATRGSFERKELY-------------  109
Znev        VPQQSDSRGQVQGFATRGHSAAGDQQGLKTDTFYDWYLSNRKRSR  125
Dpul        AETQPLLIPILID-----------RRIFEARSAANRHQPQLDAED  109
Lmig        APEQVAMFPWLLN-----------NWPKRTAADYDY---------  99
Turt1       SSYKNIISKLFPSMVKEMHPSNTNSGWDRFDSLYQGNDGLLFGS-  124
Tcas7641_38-58 ----------------------------------------------  21
                    90        100       110       120

Consensus   APXQNLLXXLLDDXXXPDHXLXGDRXXFXRDXLYXXYLSQLDXSD
```