```
Hduj            MFATSSAVWVYLEPRFDGEFLSRNADVIDSISDEMYN-QQSAQPALG------SGIPIGGAASEMATLPRQMVRPLR-IP  72
Znev            --------MKQLGAVILFFYLLTTEFTSAAIQLEDNR---YLDKEFQTNAVNVRELATWIMQLLLHKGQQT-------IC  62
Lmig            ----MAVSGKLITVFVLSIYVLGLALTIHATQYDEEK-YQENEVRYG------RELATLLAQLAHKNEPA--------IC  61
Dmel            -----MARYTYLVALVLLAICCQWGYCGAMAMPDEER---YVRKEYN------RDLLDWFNNVGVGQFSPGQVATLCRYP  66
Aaed            --------MVNVQASFFVAICLCLSICASMPSYDDGI-VDVDNEPFI------RQLAELLAESDTNELSEIYSLPACRVC  65
Amel            --------MISRKCVIILIMMLGIAYQTFGTTEDSYRNLLALNFPYD------RGV-----NNDLQRIAKLLLLPPC-LC  60
Nvit            -----MRSWVSH--LIRAFFVFGAILCASASMEDTSH--MIMNNPYG------RSL-----DAEL--ITRLLLAPQR-LC  57
Dpul13704_147-169:. ----------------------------------------------------------------------------QP  2
                                10        20        30        40        50        60        70        80

Consensus
MFATXMASMVXLXAXILLXXXLGLAXCXXAXXXDXXRNXQYLNKPYGTNAVNVRXLATXLAXXXLXXXXRLLXXPLCRIC
```

```
Hduj            ---------TVP----MQKRNSEILNTLIGLPNKLKQRG--  98
Znev            ----------------THKRNSELINTLLGLPKILNEAGRK  87
Lmig            ----------------AHKRNSEIINSLLGLPKLLNDAGRK  86
Dmel            LILENSLGPSVP----IRKRNSELINSLLSLPKNMNDAGK-  102
Aaed            FYHLHNPYVNVVSNKRYGKRNSELINSLLSLPKKLNDAGK-  105
Amel            ----------------HSKRNSELINSLLGLPKNMNNAGK-  84
Nvit            ----------------HPKRNSELINSLLSLPKNMNNAGK-  81
Dpul13704_147-169:. ----------------YAKRNSELINSLLGLPRFMKV----  23
                          90        100       110       120

Consensus
XXXXXXXXXXVPSNKRXHKRNSELINSLLGLPKNXNDAGKK
```