```
Nvit            -MGRRLSIGLAAAAIL-FSCMLHF-ALAQVTFSKGWGP-GKRSALYET----DCSRVNYKSLALLFHTLLAEVKHLMACD 72
Smar            --MKWIAVYLLLTIIV-LTIVAPV--EGQVTFSRDWTPAGKRGM--------DCGFVKTKLLRDIAVLLQMEANSLKSCG 67
Aaeg            --MRNSIYKLIMFAVLCMVLTSSL-SYAQVTFSRDWNA-GKRSLAEAAQSTGDCAAI-WRSVTNLCAAVTKNIQHLTMCE 75
Lmig            -----MIARLLLTLTV-TAWCCYL-VASQVTFSRDWSP-GKRSP--EP----ACA----KHAATICQLLLNELRQLAACE 62
Tcas            MALKFRIFALVAVLVL-MAWMFTG-TQAQVTFSRDWNP-GKRTENTDL----HNT---LKTASAVCHLLMNQVRQLASCD 70
Znev            MTSRRLCGRALLLVAV-LNCLHFR-TWGQVTFSRDWNA-GKRSPA-DL----QCSAI-IKSADEFCRVLIEEFRQLAACE 71
Tcas12692_4-82:. ---KFRIFALVAVLVL-MAWMFTG-TQAQVTFSRDWNP-GKR------TENTDLHNT-LKTASAVCHLLMNQVRQLASCD 67
Tcas15624_5-68:. ----FLIVVLIA----------FVGVCTAQLNFSTDW---GKRSGSSAGSDANNCKEP-VETIMLIYKIIQNEAQKIIECE 63
                 10        20        30        40        50        60        70        80
Consensus
                 MXMXFLIXXLLAXLVLCMAWMFTGVTQAQVTFSRDWNPAGKRSPAXXLXXXXDCXAXXLKXAXXICHLLXNEVRQLAXCE
```

```
Nvit            HQATVNYLQSVERQ-------------------------------------- 86
Smar            LPVMEPFHDNK----------------------------------------- 78
Aaeg            ARALMKNLQSEDAS-------MENNGGGGLPLFSNGHL-- 106
Lmig            VKSLLRYHAEEVNVPVPQEIYIDGNGGR------------- 90
Tcas            NNNELEPGATIFSGRR------------------------------------ 86
Znev            TKSLLRFLKDYDDSQA--DIFMESQNGRQTPTNDLHQRNF 109
Tcas12692_4-82:. NNNELEPGATIF----------------------------------------- 79
Tcas15624_5-68:. K---------------------------------------------------- 64
                 90        100       110       120
Consensus
                 NXXLLXXLAXXXXSXXPQXIXMEXNGGRXXPXXXXXXXNF
```