```
Turt          SSVAVSSLSLSSPSSSLLSADRTFSRSKPPFTPLSTLECHRREFTFNASRSDGLGRKCWGLVTSMSCWGRCDSMEIADYK  80
Apis          -MVCMAVL---CAVSSMIVWSSVAGYDM---------LDCNRQLSTFQVSNTDENGRTCSDEIDVMSCWGRCDSNEVSDWR  68
Lmig          MAACRLVYVCCALVAAAAAAAAVADAAMDPAST---LECHRRLYTYKVTKTDADGRACWDVINVMSCWGRCDSNEISDWR  77
Znev          MSLVFSRLPFLCFALVATLWLGAETSSLQESTLASTLECHRRMYAYKVTKTDSAGRVCWDVINVMSCWGRCDSNEISDWR  80
Tcas          -MLGVQVWLF-VGLSALVRCQSIIEAGLEPLDASGTIECHRRMYTYRVTQTDDNGKQCWDTLSVMACWGRCDSNEISDWR  78
Aaeg          MINLISVWILSMIALSWAVEDSLFISGFEKKAPM--LGCHKRVFTYRISQADSKGRECWDHVSVWSCHGRCDSNEISDWR  78
Dmel          MLADSATLTLAIFVGTSVVLVSVSSSSLSEIKPMTPLGCHRRVYTYKVTQSDLQGHECWDYVSVWSCWGRCDSSEISDWK  80
Rsoc26209_25-122 ----------------------------------------KHHCQVEPYTETIYLQNCRSQPI--KIDTTRCRGQCYSEDIYDWQ  43
                                10        20        30        40        50        60        70        80

Consensus
MXXCVSVLXLSCFVSSXXVXDSVXSSSLEPXTPMSTLECHRRXYTYKVTQTDSNGRECWDVISVMSCWGRCDSNEISDWR

Turt          FPYKQSYHKVCIHNRKAIRTTLLPYCDRGVHQSLKIYKYVDAISCSCQFCDSSIASCEGFDAIER----YLMRSSIN  153
Apis          FPFKRSHHPVCIHDGQVLTKFMLKNCEEGVQPGTEFYVFPQAMSCKCHTCKSSEAACEGYR---SKDFPFISPNQV-  141
Lmig          FPYKRSFHPVCLHDARERRSVRLRNCEEGAAPGTERYDFLEAVSCRCAVCRSSEASCEGLRYRGQRSGPFKALGRR-  153
Znev          FPYKRSFHPVCLHDTRAVSSATLQNCEEGVEPGTEVYEYLEALTCRCMVCKSSEASCEGLRYRGQRSGPFLVGGR--  155
Tcas          FPYKKSNHPVCVHYGRNRSVVTLRHCEEGANPSAARYEYLEAAGCKCQQCSSSDTSCEGLRYRPQRSHPASLGFRIN  155
Aaeg          FPYKRSHHPVCMHAGRTRSVATLRHCHPEADAEAKLYEYMEPKSCSCQTCTSMDTSCEGPKQLSTDAATFQIDDEEI  155
Dmel          FPYKRSFHPVCVHAQRQLVVAILKNCHPKAEDSVSKYQYMEAVNCHCQTCSTQDTSCEAPANNEMAGGSIMVGADTK  157
Rsoc26209_25-122 NAYRHKRHLFCCSPTNTEAQEIRVTCENENEPQTVKYRFV--ISCECKPCND----------------------  93
                                90       100       110       120       130       140       150

Consensus
FPYKRSFHPVCXHDGRXRSVATLRNCEEGAEPXTEXYEYLEAXSCXCQTCXSSXASCEGLRYRXQRSGPFLVGGRIN
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