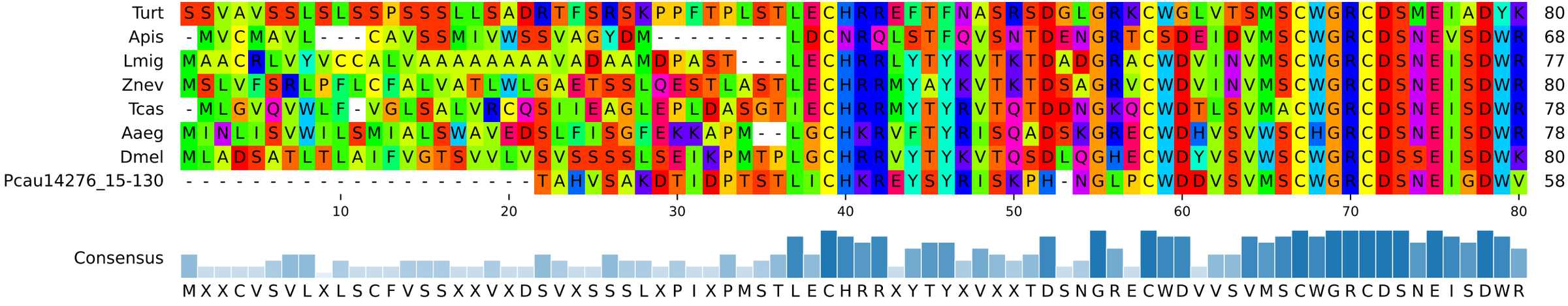
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Apis -MVCMAVL---CAVSSMIVWSSVAGYDM---------LDCNRQLSTFQVSNTDENGRTCSDEIDVMSCWGRCDSNEVSDWR 68
Lmig MAACRLVYVCCALVAAAAAAAAVADAAMDPAST---LECHRRLYTYKVTKTDADGRACWDVINVMSCWGRCDSNEISDWR 77
Znev MSLVFSRLPFLCFALVATLWLGAETSSLQESTLASTLECHRRMYAYKVTKTDSAGRVCWDVINVMSCWGRCDSNEISDWR 80
Tcas -MLGVQVWLF-VGLSALVRCQSIIEAGLEPLDASGTIECHRRMYTYRVTQTDDNGKQCWDTLSVMACWGRCDSNEISDWR 78
Aaeg MINLISVWILSMIALSWAVEDSLFISGFEKKAPM--LGCHKRVFTYRISQADSKGRECWDHVSVWSCHGRCDSNEISDWR 78
Dmel MLADSATLTLAIFVGTSVVLVSVSSSSLSEIKPMTPLGCHRRVYTYKVTQSDLQGHECWDYVSVWSCWGRCDSSEISDWK 80
Pcau14276_15-130 ----------TAHVSAKDTIDPTSTLICHKREYSYRISKPH-NGLPCWDDVSVMSCWGRCDSNEIGDWV 58
10 20 30 40 50 60 70 80
Consensus
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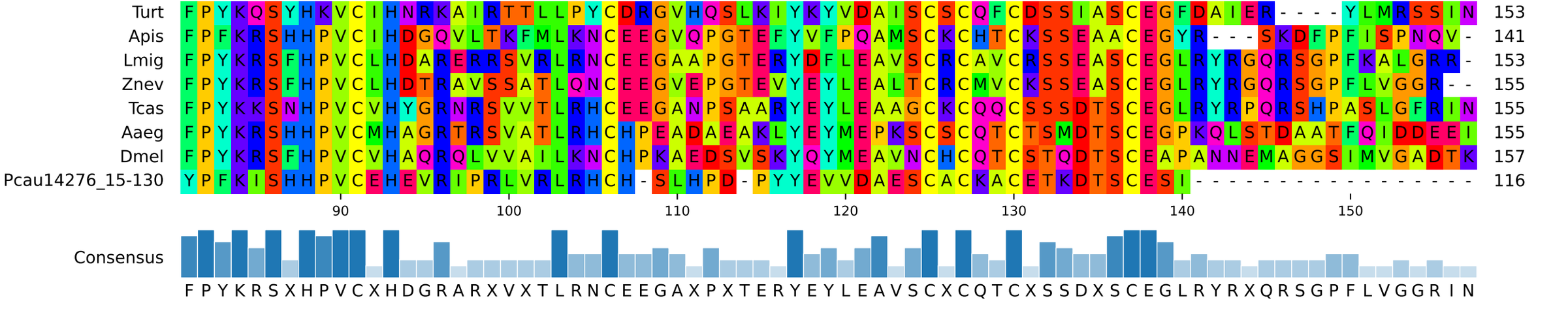
Turt FPYKQSYHKVCIHNRKAIRTTLLPYCDRGVHQSLKIYKYVDAISCSCQFCDSSIASCEGFDAIER----YLMRSSIN 153
Apis FPFKRSHHPVCIHDGQVLTKFMLKNCEEGVQPGTEFYVFPQAMSCKCHTCKSSEAACEGYR---SKDFPFISPNQV- 141
Lmig FPYKRSFHPVCLHDARERRSVRLRNCEEGAAPGTERYDFLEAVSCRCAVCRSSEASCEGLRYRGQRSGPFKALGRR- 153
Znev FPYKRSFHPVCLHDTRAVSSATLQNCEEGVEPGTEVYEYLEALTCRCMVCKSSEASCEGLRYRGQRSGPFLVGGR-- 155
Tcas FPYKKSNHPVCVHYGRNRSVVTLRHCEEGANPSAARYEYLEAAGCKCQQCSSSDTSCEGLRYRPQRSHPASLGFRIN 155
Aaeg FPYKRSHHPVCMHAGRTRSVATLRHCHPEADAEAKLYEYMEPKSCSCQTCTSMDTSCEGPKQLSTDAATFQIDDEEI 155
Dmel FPYKRSFHPVCVHAQRQLVVAILKNCHPKAEDSVSKYQYMEAVNCHCQTCSTQDTSCEAPANNEMAGGSIMVGADTK 157
Pcau14276_15-130 YPFKISHHPVCEHEVRIPRLVRLRHCH-SLHPD-PYYEVVDAESCACKACETKDTSCESI---------- 116
90 100 110 120 130 140 150
Consensus
FPYKRSXHPVCXHDGRARXVXTLRNCEEGAXPXTERYEYLEAVSCXCQTCXSSDXSCEGLRYRXQRSGPFLVGGRIN