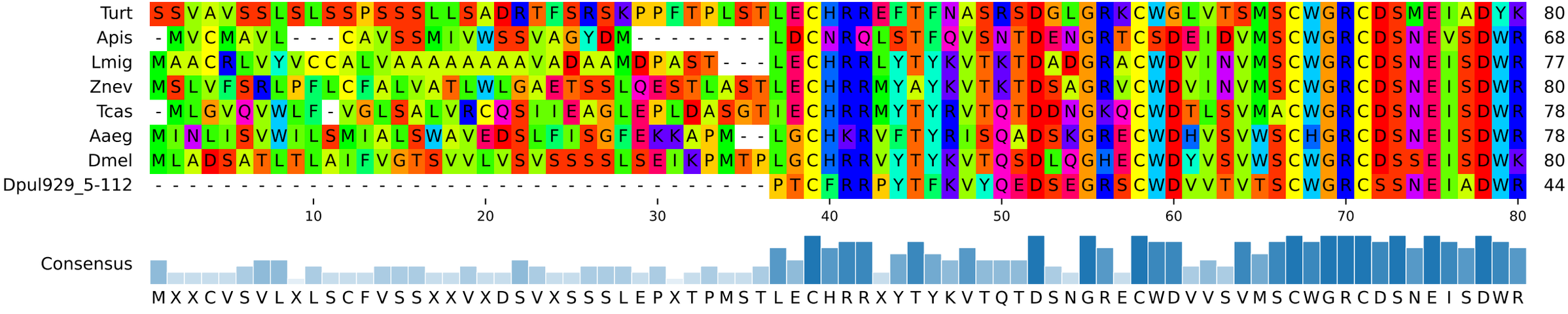
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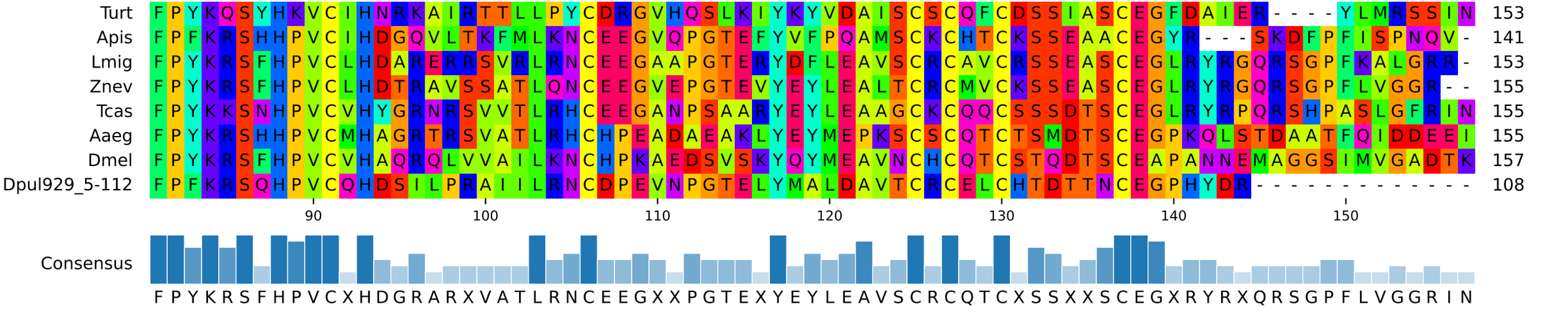
Apis -MVCMAVL---CAVSSMIVWSSVAGYDM---------LDCNRQLSTFQVSNTDENGRTCSDEIDVMSCWGRCDSNEVSDWR 68
Lmig MAACRLVYVCCALVAAAAAAAAVADAAMDPAST---LECHRRLYTYKVTKTDADGRACWDVINVMSCWGRCDSNEISDWR 77
Znev MSLVFSRLPFLCFALVATLWLGAETSSLQESTLASTLECHRRMYAYKVTKTDSAGRVCWDVINVMSCWGRCDSNEISDWR 80
Tcas -MLGVQVWLF-VGLSALVRCQSIIEAGLEPLDASGTIECHRRMYTYRVTQTDDNGKQCWDTLSVMACWGRCDSNEISDWR 78
Aaeg MINLISVWILSMIALSWAVEDSLFISGFEKKAPM--LGCHKRVFTYRISQADSKGRECWDHVSVWSCHGRCDSNEISDWR 78
Dmel MLADSATLTLAIFVGTSVVLVSVSSSSLSEIKPMTPLGCHRRVYTYKVTQSDLQGHECWDYVSVWSCWGRCDSSEISDWK 80
Dpul929_5-112 ----------PTCFRRPYTFKVYQEDSEGRSCWDVVTVTSCWGRCSSNEIADWR 44
10 20 30 40 50 60 70 80
Consensus
MXXCVSVLXLSCFVSSXXVXDSVXSSSLEPXTPMSTLECHRRXYTYKVTQTDSNGRECWDVVSVMSCWGRCDSNEISDWR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Apis FPFKRSHHPVCIHDGQVLTKFMLKNCEEGVQPGTEFYVFPQAMSCKCHTCKSSEAACEGYR---SKDFPFISPNQV- 141
Lmig FPYKRSFHPVCLHDARERRSVRLRNCEEGAAPGTERYDFLEAVSCRCAVCRSSEASCEGLRYRGQRSGPFKALGRR- 153
Znev FPYKRSFHPVCLHDTRAVSSATLQNCEEGVEPGTEVYEYLEALTCRCMVCKSSEASCEGLRYRGQRSGPFLVGGR-- 155
Tcas FPYKKSNHPVCVHYGRNRSVVTLRHCEEGANPSAARYEYLEAAGCKCQQCSSSDTSCEGLRYRPQRSHPASLGFRIN 155
Aaeg FPYKRSHHPVCMHAGRTRSVATLRHCHPEADAEAKLYEYMEPKSCSCQTCTSMDTSCEGPKQLSTDAATFQIDDEEI 155
Dmel FPYKRSFHPVCVHAQRQLVVAILKNCHPKAEDSVSKYQYMEAVNCHCQTCSTQDTSCEAPANNEMAGGSIMVGADTK 157
Dpul929_5-112 FPFKRSQHPVCQHDSILPRAIILRNCDPEVNPGTELYMALDAVTCRCELCHTDTTNCEGPHYDR---------- 108
90 100 110 120 130 140 150
Consensus
FPYKRSFHPVCXHDGRARXVATLRNCEEGXXPGTEXYEYLEAVSCRCQTCXSSXXSCEGXRYRXQRSGPFLVGGRIN