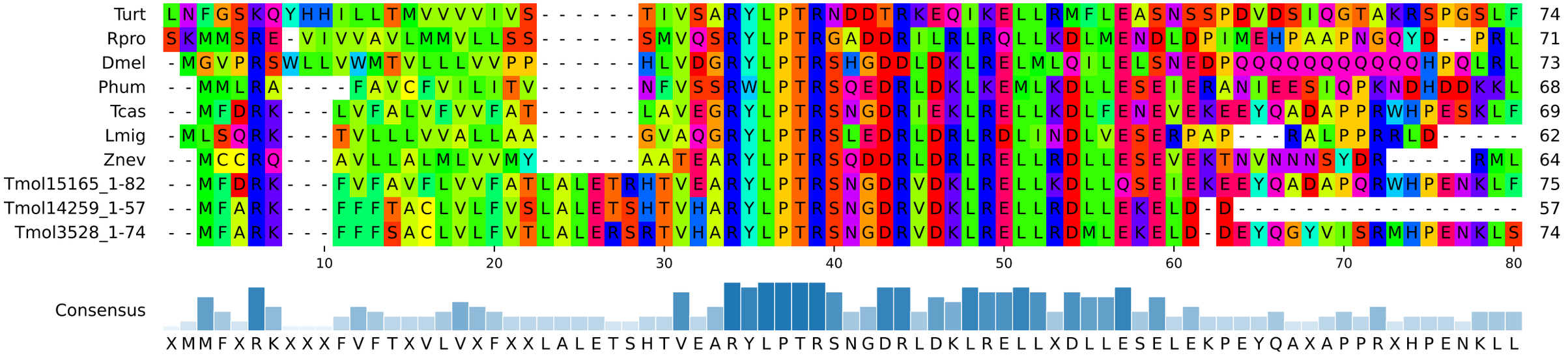
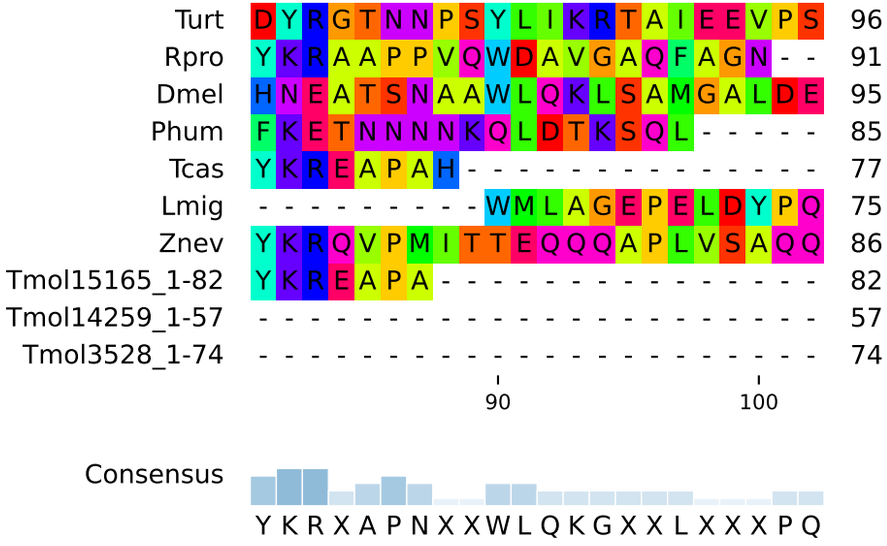

Turt LNFGSKQYHHILLTMVVVVIVS------TIVSARYLPTRNDDTRKEQIKELLRMFLEASNSSPDVDSIQGTAKRSPGSLF 74
Rpro SKMMSRE-VIVVAVLMMVLLSS------SMVQSRYLPTRGADDRILRLRQLLKDLMENDLDPIMEHPAAPNGQYD--PRL 71
Dmel -MGVPRSWLLVWMTVLLLVVPP------HLVDGRYLPTRSHGDDLDKLRELMLQILELSNEDPQQQQQQQQQQQHPQLRL 73
Phum --MMLRA----FAVCFVILITV------NFVSSRWLPTRSQEDRLDKLKEMLKDLLESEIERANIEESIQPKNDHDDKKL 68
Tcas --MFDRK---LVFALVFVVFAT------LAVEGRYLPTRSNGDRIEKLRELLKDLFENEVEKEEYQADAPPRWHPESKLF 69
Lmig -MLSQRK---TVLLLVVALLAA------GVAQGRYLPTRSLEDRLDRLRDLINDLVESERPAP---RALPPRRLD-----
Znev --MCCRQ---AVLLALMLVVMY------AATEARYLPTRSQDDRLDRLRELLRDLLESEVEKTNVNNNSYDR-----RML 64
Tmol15165_1-82 --MFDRK---FVFAVFLVVFATLALETRHTVEARYLPTRSNGDRVDKLRELLKDLLQSEIEKEEYQADAPQRWHPENKLF 75
Tmol14259_1-57 --MFARK---FFFTACLVLFVSLALETSHTVHARYLPTRSNGDRVDKLRELLRDLLEKELD-D----------- 57
Tmol3528_1-74 --MFARK---FFFSACLVLFVTLALERSRTVHARYLPTRSNGDRVDKLRELLRDMLEKELD-DEYQGYVISRMHPENKLS 74
10 20 30 40 50 60 70 80
Consensus
XMMFXRKXXXFVFTXVLVXFXXLALETSHTVEARYLPTRSNGDRLDKLRELLXDLLESELEKPEYQAXAPPRXHPENKLL


Turt DYRGTNNPSYLIKRTAIEEVPS 96
Rpro YKRAAPPVQWDAVGAQFAGN-- 91
Dmel HNEATSNAAWLQKLSAMGALDE 95
Phum FKETNNNNKQLDTKSQL----- 85
Tcas YKREAPAH---------- 77
Lmig ---------WMLAGEPELDYPQ 75
Znev YKRQVPMITTEQQQAPLVSAQQ 86
Tmol15165_1-82 YKREAPA---------- 82
Tmol14259_1-57 ---------- 57
Tmol3528_1-74 ---------- 74
90 100
Consensus
YKRXAPNXXWLQKGXXLXXXPQ