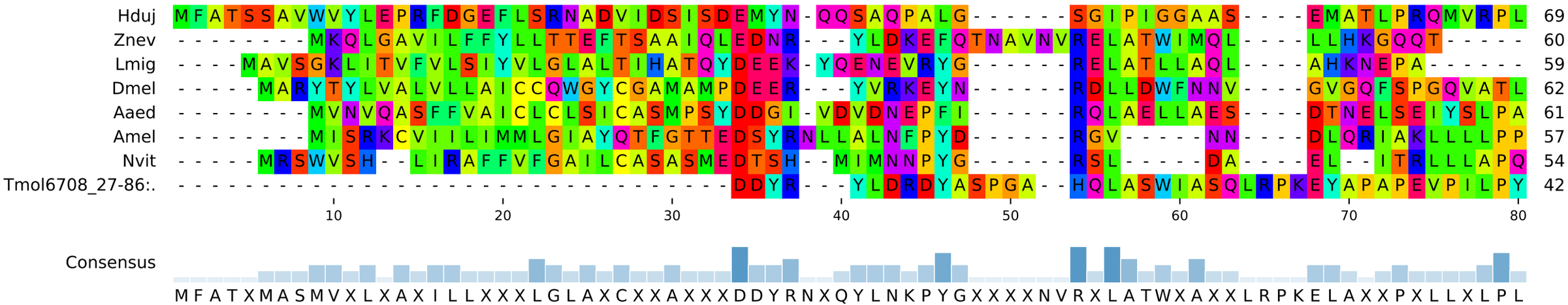
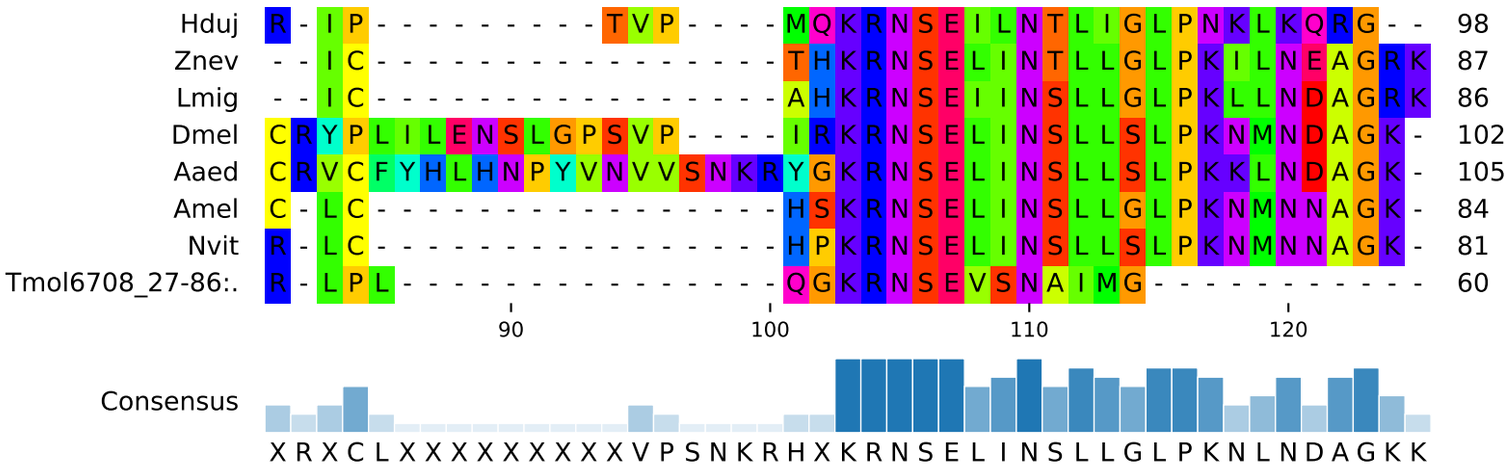

Hduj MFATSSAVWVYLEPRFDGEFLSRNADVIDSISDEMYN-QQSAQPALG------SGIPIGGAAS----EMATLPRQMVRPL 69
Znev ---------MKQLGAVILFFYLLTTEFTSAAIQLEDNR---YLDKEFQTNAVNVRELATWIMQL----LLHKGQQT----- 60
Lmig ----MAVSGKLITVFVLSIYVLGLALTIHATQYDEEK-YQENEVRYG------RELATLLAQL----AHKNEPA------ 59
Dmel -----MARYTYLVALVLLAICCQWGYCGAMAMPDEER---YVRKEYN------RDLLDWFNNV----GVGQFSPGQVATL 62
Aaed ---------MVNVQASFFVAICLCLSICASMPSYDDGI-VDVDNEPFI------RQLAELLAES----DTNELSEIYSLPA 61
Amel ---------MISRKCVIILIMMLGIAYQTFGTTEDSYRNLLALNFPYD------RGV-----NN----DLQRIAKLLLLPP 57
Nvit -----MRSWVSH--LIRAFFVFGAILCASASMEDTSH--MIMNNPYG------RSL-----DA----EL--ITRLLLAPQ 54
Tmol6708_27-86:. ----------DDYR---YLDRDYASPGA--HQLASWIASQLRPKEYAPAPEVPILPY 42
10 20 30 40 50 60 70 80
Consensus
MFATXMASMVXLXAXILLXXXLGLAXCXXAXXXDDYRNXQYLNKPYGXXXXNVRXLATWXAXXLRPKELAXXPXLLXLPL


Hduj R-IP---------TVP----MQKRNSEILNTLIGLPNKLKQRG-- 98
Znev --IC----------THKRNSELINTLLGLPKILNEAGRK 87
Lmig --IC----------AHKRNSEIINSLLGLPKLLNDAGRK 86
Dmel CRYPLILENSLGPSVP----IRKRNSELINSLLSLPKNMNDAGK- 102
Aaed CRVCFYHLHNPYVNVVSNKRYGKRNSELINSLLSLPKKLNDAGK- 105
Amel C-LC----------HSKRNSELINSLLGLPKNMNNAGK- 84
Nvit R-LC----------HPKRNSELINSLLSLPKNMNNAGK- 81
Tmol6708_27-86:. R-LPL----------QGKRNSEVSNAIMG---------- 60
90 100 110 120
Consensus
XRXCLXXXXXXXXXXVPSNKRHXKRNSELINSLLGLPKNLNDAGKK