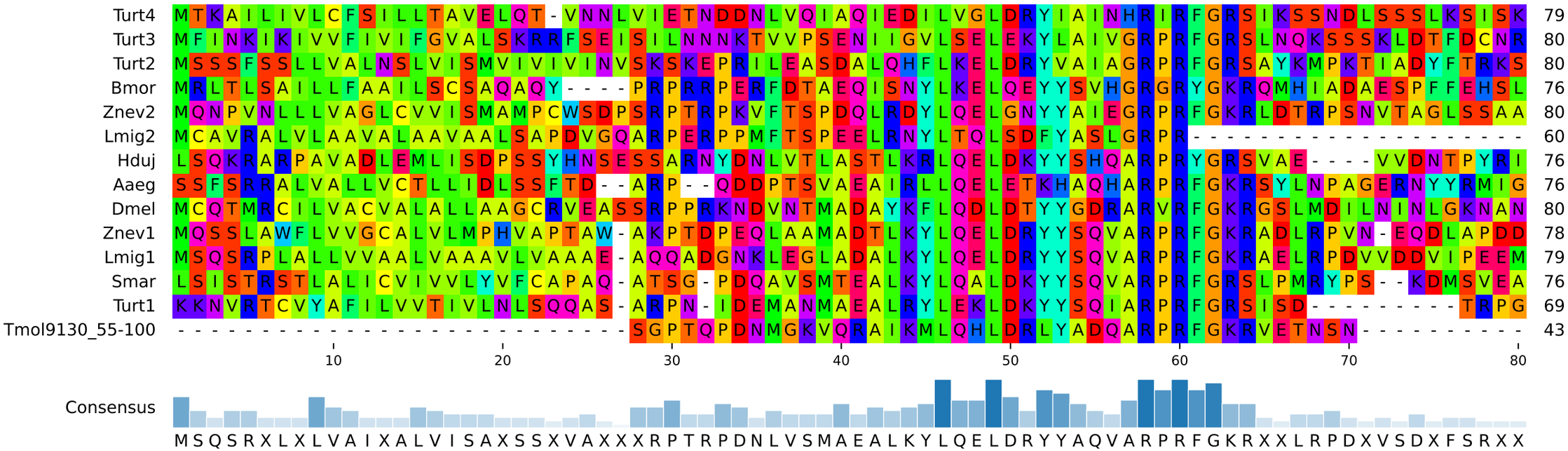
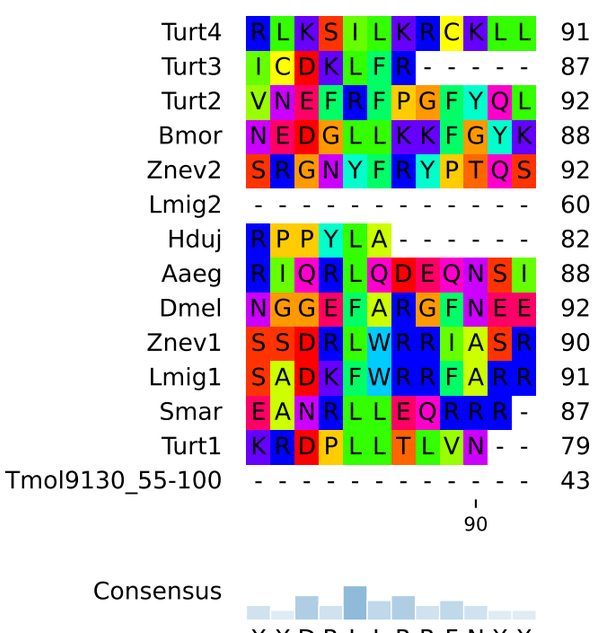

Turt4 MTKAILIVLCFSILLTAVELQT-VNNLVIETNDDNLVQIAQIEDILVGLDRYIAINHRIRFGRSIKSSNDLSSSLKSISK 79
Turt3 MFINKIKIVVFIVIFGVALSKRRFSEISILNNNKTVVPSENIIGVLSELEKYLAIVGRPRFGRSLNQKSSSKLDTFDCNR 80
Turt2 MSSSFSSLLVALNSLVISMVIVIVINVSKSKEPRILEASDALQHFLKELDRYVAIAGRPRFGRSAYKMPKTIADYFTRKS 80
Bmor MRLTLSAILLFAAILSCSAQAQY----PRPRRPERFDTAEQISNYLKELQEYYSVHGRGRYGKRQMHIADAESPFFEHSL 76
Znev2 MQNPVNLLLVAGLCVVISMAMPCWSDPSRPTRPKVFTSPDQLRDYLQELGNYYAIEGRPRFGKRLDTRPSNVTAGLSSAA 80
Lmig2 MCAVRALVLAAVALAAVAALSAPDVGQARPERPPMFTSPEELRNYLTQLSDFYASLGRPR---------- 60
Hduj LSQKRARPAVADLEMLISDPSSYHNSESSARNYDNLVTLASTLKRLQELDKYYSHQARPRYGRSVAE----VVDNTPYRI 76
Aaeg SSFSRRALVALLVCTLLIDLSSFTD--ARP--QDDPTSVAEAIRLLQELETKHAQHARPRFGKRSYLNPAGERNYYRMIG 76
Dmel MCQTMRCILVACVALALLAAGCRVEASSRPPRKNDVNTMADAYKFLQDLDTYYGDRARVRFGKRGSLMDILNINLGKNAN 80
Znev1 MQSSLAWFLVVGCALVLMPHVAPTAW-AKPTDPEQLAAMADTLKYLQELDRYYSQVARPRFGKRADLRPVN-EQDLAPDD 78
Lmig1 MSQSRPLALLVVAALVAAAVLVAAAE-AQQADGNKLEGLADALKYLQELDRYYSQVARPRFGKRAELRPDVVDDVIPEEM 79
Smar LSISTRSTLALICVIVVLYVFCAPAQ-ATSG-PDQAVSMTEALKYLQALDKYYSQVARPRFGRSLPMRYPS--KDMSVEA 76
Turt1 KKNVRTCVYAFILVVTIVLNLSQQAS-ARPN-IDEMANMAEALRYLEKLDKYYSQIARPRFGRSISD---------TRPG 69
Tmol9130_55-100 ----------SGPTQPDNMGKVQRAIKMLQHLDRLYADQARPRFGKRVETNSN---------- 43
10 20 30 40 50 60 70 80
Consensus
M S Q S R X L X L V A I X A L V I S A X S S X V A X X X R P T R P D N L V S M A E A L K Y L Q E L D R Y Y A Q V A R P R F G K R X X L R P D X V S D X F S R X X


Turt4 RLKSILKRCKLL 91
Turt3 ICDKLFR----- 87
Turt2 VNEFRFPGFYQL 92
Bmor NEDGLLKKFGYK 88
Znev2 SRGNYFRYPTQS 92
Lmig2 ---------- 60
Hduj RPPYLA------ 82
Aaeg RIQRLQDEQNSI 88
Dmel NGGEFARGFNEE 92
Znev1 SSDRLWRRIASR 90
Lmig1 SADKFWRRFARR 91
Smar EANRLLEQRRR- 87
Turt1 KRDPLLTLVN-- 79
Tmol9130_55-100 ---------- 43
90
Consensus
X X D R L L R R F N X X