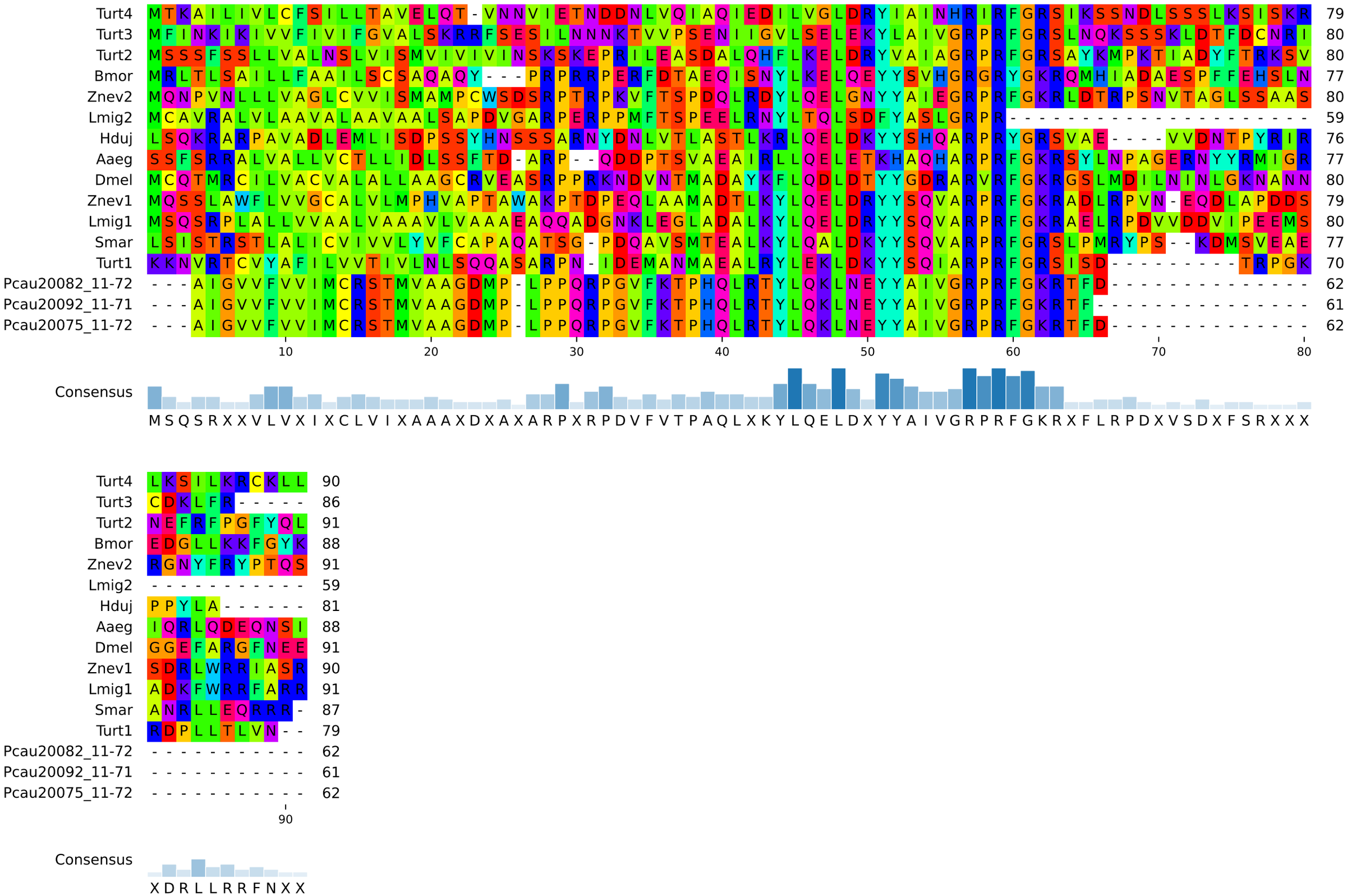
Turt4 MTKAILIVLCFSILLTAVELQT-VNNVIETNDDNLVQIAQIEDILVGLDRYIAINHRIRFGRSIKSSNDLSSSLKSISKR 79
Turt3 MFINKIKIVVFIVIFGVALSKRRFSESILNNNKTVVPSENIIGVLSELEKYLAIVGRPRFGRSLNQKSSSKLDTFDCNRI 80
Turt2 MSSSFSSLLVALNSLVISMVIVIVINSKSKEPRILEASDALQHFLKELDRYVAIAGRPRFGRSAYKMPKTIADYFTRKSV 80
Bmor MRLTLSAILLFAAILSCSAQAQY---PRPRRPERFDTAEQISNYLKELQEYYSVHGRGRYGKRQMHIADAESPFFEHSLN 77
Znev2 MQNPVNLLLVAGLCVVISMAMPCWSDSRPTRPKVFTSPDQLRDYLQELGNYYAIEGRPRFGKRLDTRPSNVTAGLSSAAS 80
Lmig2 MCAVRALVLAAVALAAVAALSAPDVGARPERPPMFTSPEELRNYLTQLSDFYASLGRPR---------- 59
Hduj LSQKRARPAVADLEMLISDPSSYHNSSSARNYDNLVTLASTLKRLQELDKYYSHQARPRYGRSVAE----VVDNTPYRIR 76
Aaeg SSFSRRALVALLVCTLLIDLSSFTD-ARP--QDDPTSVAEAIRLLQELETKHAQHARPRFGKRSYLNPAGERNYYRMIGR 77
Dmel MCQTMRCILVACVALALLAAGCRVEASRPPRKNDVNTMADAYKFLQDLDTYYGDRARVRFGKRGSLMDILNINLGKNANN 80
Znev1 MQSSLAWFLVVGCALVLMPHVAPTAWAKPTDPEQLAAMADTLKYLQELDRYYSQVARPRFGKRADLRPVN-EQDLAPDDS 79
Lmig1 MSQSRPLALLVVAALVAAAVLVAAAEAQQADGNKLEGLADALKYLQELDRYYSQVARPRFGKRAELRPDVVDDVIPEEMS 80
Smar LSISTRSTLALICVIVVLYVFCAPAQATSG-PDQAVSMTEALKYLQALDKYYSQVARPRFGRSLPMRYPS--KDMSVEAE 77
Turt1 KKNVRTCVYAFILVVTIVLNLSQQASARPN-IDEMANMAEALRYLEKLDKYYSQIARPRFGRSISD----------TRPGK 70
Pcau20082_11-72 ---AIGVVFVVIMCRSTMVAAGDMP-LPPQRPGVFKTPHQLRTYLQKLNEYYAIVGRPRFGKRTFD---------- 62
Pcau20092_11-71 ---AIGVVFVVIMCRSTMVAAGDMP-LPPQRPGVFKTPHQLRTYLQKLNEYYAIVGRPRFGKRTF---------- 61
Pcau20075_11-72 ---AIGVVFVVIMCRSTMVAAGDMP-LPPQRPGVFKTPHQLRTYLQKLNEYYAIVGRPRFGKRTFD---------- 62
10 20 30 40 50 60 70 80
Consensus
MSQSRXXVLVXIXCLVIXAAAXDXAXARPXRPDVFVTPAQLXKYLQELDXYYAIVGRPRFGKRXFLRPDXVSDXFSRXXX
Turt4 LKSILKRCKLL 90
Turt3 CDKLFR----- 86
Turt2 NEFRFPGFYQL 91
Bmor EDGLLKKFGYK 88
Znev2 RGNYFRYPTQS 91
Lmig2 ---------- 59
Hduj PPYLA----- 81
Aaeg IQRLQDEQNSI 88
Dmel GGEFARGFNEE 91
Znev1 SDRLWRRIASR 90
Lmig1 ADKFWRRFARR 91
Smar ANRLLEQRRR- 87
Turt1 RDPLLTLVN-- 79
Pcau20082_11-72 ---------- 62
Pcau20092_11-71 ---------- 61
Pcau20075_11-72 ---------- 62
90
Consensus
XDRLLRRFNXX