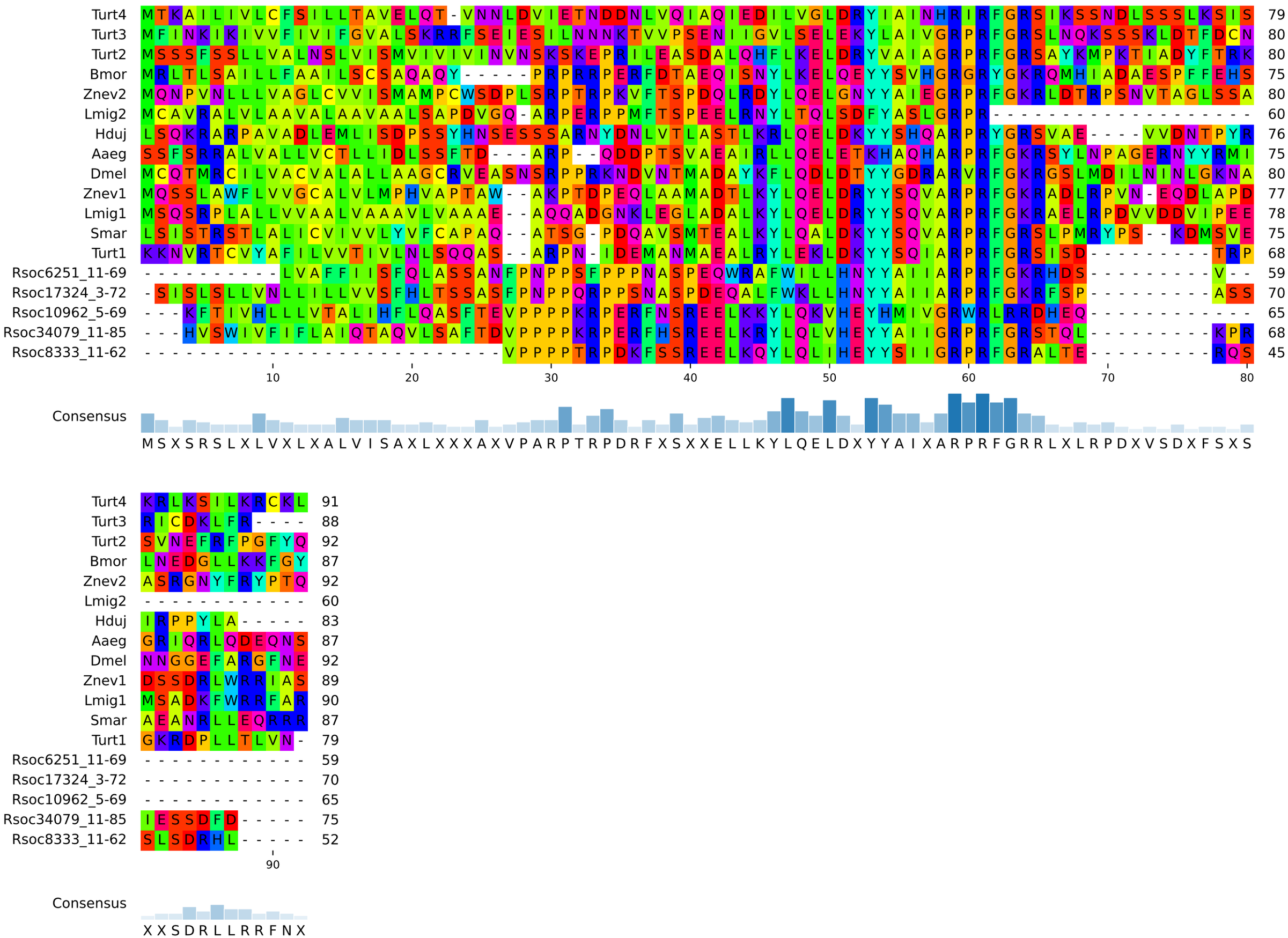
Turt4 MTKAILIVLCFSILLTAVELQT-VNNLDVIETNDDNLVQIAQIEDILVGLDRYIAINHRIRFGRSIKSSNDLSSSLKSIS 79
Turt3 MFINKIKIVVFIVIFGVALSKRRFSEIESILNNNKTVVPSENIIGVLSELEKYLAIVGRPRFGRSLNQKSSSKLDTFDCN 80
Turt2 MSSSFSSLLVALNSLVISMVIVIVINVNSKSKEPRILEASDALQHFLKELDRYVAIAGRPRFGRSAYKMPKTIADYFTRK 80
Bmor MRLTLSAILLFAAILSCSAQAQY-----PRPRRPERFDTAEQISNYLKELQEYYSVHGRGRYGKRQMHIADAESPFFEHS 75
Znev2 MQNPVNLLLVAGLCVVISMAMPCWSDPLSRPTRPKVFTSPDQLRDYLQELGNYYAIEGRPRFGKRLDTRPSNVTAGLSSA 80
Lmig2 MCAVRALVLAAVALAAVAALSAPDVGQ-ARPERPPMFTSPEELRNYLTQLSDFYASLGRPR---------- 60
Hduj LSQKRARPAVADLEMLISDPSSYHNSESSSARNYDNLVTLASTLKRLQELDKYYSHQARPRYGRSVAE----VVDNTPYR 76
Aaeg SSFSRRALVALLVCTLLIDLSSFTD---ARP--QDDPTSVAEAIRLLQELETKHAQHARPRFGKRSYLNPAGERNYYRMI 75
Dmel MCQTMRCILVACVALALLAAGCRVEASNSRPPRKNDVNTMADAYKFLQDLDTYYGDRARVRFGKRGSLMDILNINLGKNA 80
Znev1 MQSSLAWFLVVGCALVLMPHVAPTAW--AKPTDPEQLAAMADTLKYLQELDRYYSQVARPRFGKRADLRPVN-EQDLAPD 77
Lmig1 MSQSRPLALLVVAALVAAAVLVAAAE--AQQADGNKLEGLADALKYLQELDRYYSQVARPRFGKRAELRPDVVDDVIPEE 78
Smar LSISTRSTLALICVIVVLYVFCAPAQ--ATSG-PDQAVSMTEALKYLQALDKYYSQVARPRFGRSLPMRYPS--KDMSVE 75
Turt1 KKNVRTCVYAFILVVTIVLNLSQQAS--ARPN-IDEMANMAEALRYLEKLDKYYSQIARPRFGRSISD----------TRP 68
Rsoc6251_11-69 ----------LVAFFIISFQLASSANFPNPPSFPPPNASPEQWRAFWILLHNYYAIIARPRFGKRHDS----------V-- 59
Rsoc17324_3-72 -SISLSLLVNLLILLVVSFHLTSSASFPNPPQRPPSNASPDEQALFWKLLHNYYAIIARPRFGKRFSP----------ASS 70
Rsoc10962_5-69 ---KFTIVHLLLVTALIHFLQASFTEVPPPPKRPERFNSREELKKYLQKVHEYHMIVGRWRLRRDHEQ---------- 65
Rsoc34079_11-85 ---HVSWIVFIFLAIQTAQVLSAFTDVPPPPKRPERFHSREELKRYLQLVHEYYAIIGRPRFGRSTQL---------KPR 68
Rsoc8333_11-62 ----------VPPPPTRPDKFSSREELKQYLQLIHEYYSIIGRPRFGRALTE----------RQS 45
10 20 30 40 50 60 70 80
Consensus
M S X S R S L X L V X L X A L V I S A X L X X X A X V P A R P T R P D R F X S X X E L L K Y L Q E L D X Y Y A I X A R P R F G R R L X L R P D X V S D X F S X S
Turt4 KRLKSILKRCKL 91
Turt3 RICDKLFR---- 88
Turt2 SVNEFRFPGFYQ 92
Bmor LNEDGLLKKFGY 87
Znev2 ASRGNYFRYPTQ 92
Lmig2 ---------- 60
Hduj IRPPYLA----- 83
Aaeg GRIQRLQDEQNS 87
Dmel NNGGEFARGFNE 92
Znev1 DSSDRLWRRIAS 89
Lmig1 MSADKFWRRFAR 90
Smar AEANRLLEQRRR 87
Turt1 GKRDPLLTLVN- 79
Rsoc6251_11-69 ---------- 59
Rsoc17324_3-72 ---------- 70
Rsoc10962_5-69 ---------- 65
Rsoc34079_11-85 IESSDFD----- 75
Rsoc8333_11-62 SLSDRHL----- 52
90
Consensus
X X S D R L L R R F N X