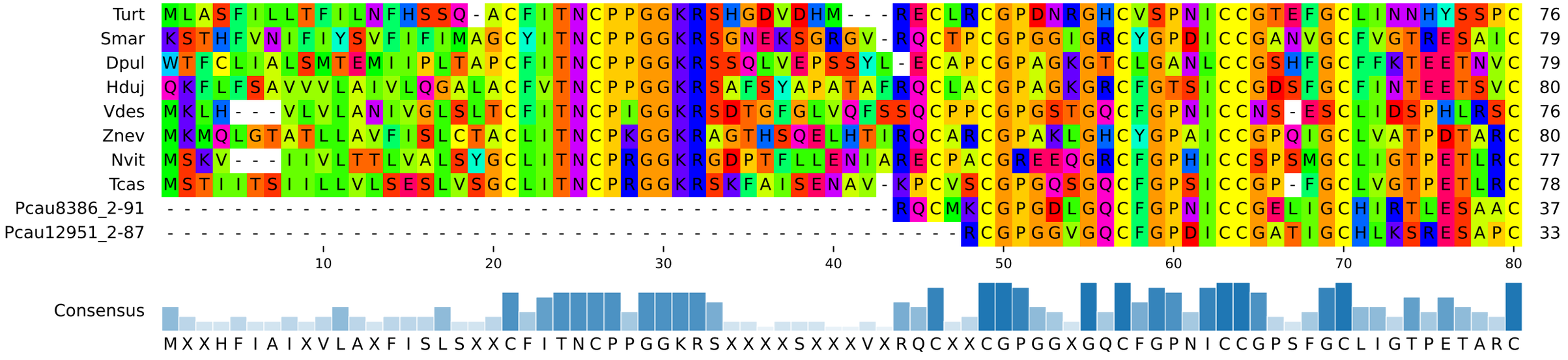
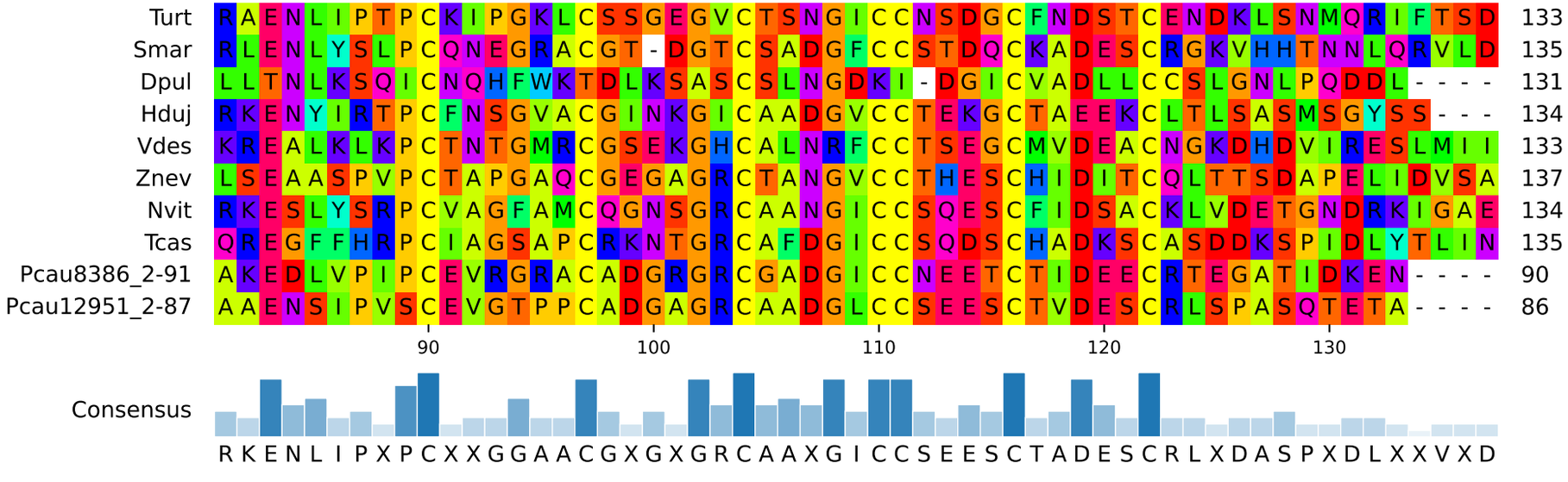

Turt MLASFILLTFILNFHSSQ-ACFITNCPPGGKRSHGDVDHM---RECLRCGPDNRGHCVSPNICCGTEFGCLINNHYSSPC 76
Smar KSTHFVNIFIYSVFIFIMAGCYITNCPPGGKRSGNEKSGRGV-RQCTPCGPGGIGRCYGPDICCGANVGCFVGTRESAIC 79
Dpul WTFCLIALSMTEMIIPLTAPCFITNCPPGGKRSSQLVEPSSYL-ECAPCGPAGKGTCLGANLCCGSHFGCFFKTEETNVC 79
Hduj QKFLFSAVVVLAIVLQGALACFVTNCPPGGKRSAFSYAPATAFRQCLACGPAGKGRCFGTSICCGDSFGCFINTEETSVC 80
Vdes MKLH---VLVLANIVGLSLTCFITNCPIGGKRSDTGFGLVQFSSQCPPCGPGSTGQCFGPNICCNS-ESCLIDSPHLRSC 76
Znev MKMQLGTATLLAVFISLCTACLITNCPKGGKRAGTHSQELHTIRQCARCGPAKLGHCYGPAICCGPQIGCLVATPDTARC 80
Nvit MSKV---IIVLTTLVALSYGCLITNCPRGGKRGDPTFLLENIARECPACGREEQGRCFGPHICCSPSMGCLIGTPETLRC 77
Tcas MSTIITSIILLVLSESLVSGCLITNCPRGGKRSKFAISENAV-KPCVSCGPGQSGQCFGPSICCGP-FGCLVGTPETLRC 78
Pcau8386_2-91 ----------RQCMKCGPGDLGQCFGPNICCGELIGCHIRTLESAAC 37
Pcau12951_2-87 ----------RCGPGGVGQCFGPDICCGATIGCHLKSRESAPC 33
10 20 30 40 50 60 70 80
Consensus
MXXHFIAIXVLAXFISLSXXCFITNCPPGGKRSXXXXSXXXVXRQCXXCGPGGXGQCFGPNICCGPSFGCLIGTPETARC


Turt RAENLIPTPCKIPGKLCSSGEGVCTSNGICCNSDGCFNDSTCENDKLSNMQRIFTSD 133
Smar RLENLYSLPCQNEGRACGT-DGTCSADGFCCSTDQCKADESCRGKVHHTNNLQRVLD 135
Dpul LLTNLKSQICNQHFWKTDLKSASCSLNGDKI-DGICVADLLCCSLGNLPQDDL---- 131
Hduj RKENYIRTPCFNSGVACGINKGICAADGVCCTEKGCTAEEKCLTLSASMSGYSS--- 134
Vdes KREALKLKPCTNTGMRCGSEKGHCALNRFCCTSEGCMVDEACNGKDHDVIRESLMII 133
Znev LSEAASPVPCTAPGAQCGEGAGRCTANGVCCTHESCHIDITCQLTTSDAPELIDVSA 137
Nvit RKESLYSRPCVAGFAMCQGNSGRCAANGICCSQESCFIDSACKLVDETGNDRKIGAE 134
Tcas QREGFFHRPCIAGSAPCRKNTGRCAFDGICCSQDSCHADKSCASDDKSPIDLYTLIN 135
Pcau8386_2-91 AKEDLVPIPCEVRGRACADGRGRCGADGICCNEETCTIDEECRTEGATIDKEN---- 90
Pcau12951_2-87 AAENSIPVSCEVGTPPCADGAGRCAADGLCCSEESCTVDESCRLSPASQTETA---- 86
90 100 110 120 130
Consensus
RKENLIPXPCXXGGAACGXGXGRCAAXGICCSEESCTADESCRLXDASPXDLXXVXD