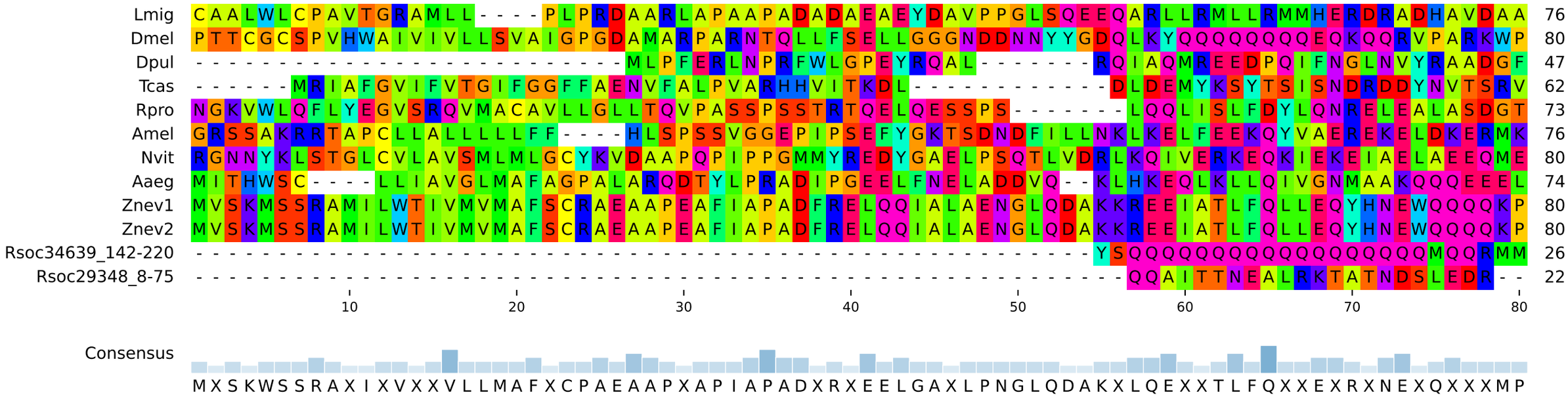
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Dpul ----------MLPFERLNPRFWLGPEYRQAL-------RQIAQMREEDPQIFNGLNVYRAADGF 47
Tcas ------MRIAFGVIFVTGIFGGFFAENVFALPVARHHVITKDL----------DLDEMYKSYTSISNDRDDYNVTSRV 62
Rpro NGKVWLQFLYEGVSRQVMACAVLLGLLTQVPASSPSSTRTQELQESSPS-------LQQLISLFDYLQNRELEALASDGT 73
Amel GRSSAKRRTAPCLLALLLLLFF----HLSPSSVGGEPIPSEFYGKTSDNDFILLNKLKELFEEKQYVAEREKELDKERMK 76
Nvit RGNNYKLSTGLCVLAVSMLMLGCYKVDAAPQPIPPGMMYREDYGAELPSQTLVDRLKQIVERKEQKIEKEIAELAEEQME 80
Aaeg MITHWSC----LLIAVGLMAFAGPALARQDTYLPRADIPGEELFNELADDVQ--KLHKEQLKLLQIVGNMAAKQQQEEEL 74
Znev1 MVSKMSSRAMILWTIVMVMAFSCRAEAAPEAFIAPADFRELQQIALAENGLQDAKKREEIATLFQLLEQYHNEWQQQQKP 80
Znev2 MVSKMSSRAMILWTIVMVMAFSCRAEAAPEAFIAPADFRELQQIALAENGLQDAKKREEIATLFQLLEQYHNEWQQQQKP 80
Rsoc34639_142-220 ----------YSQQQQQQQQQQQQQQQQQQMQQRMM 26
Rsoc29348_8-75 ----------QQAITTNEALRKTATNDSLEDR-- 22
10 20 30 40 50 60 70 80
Consensus
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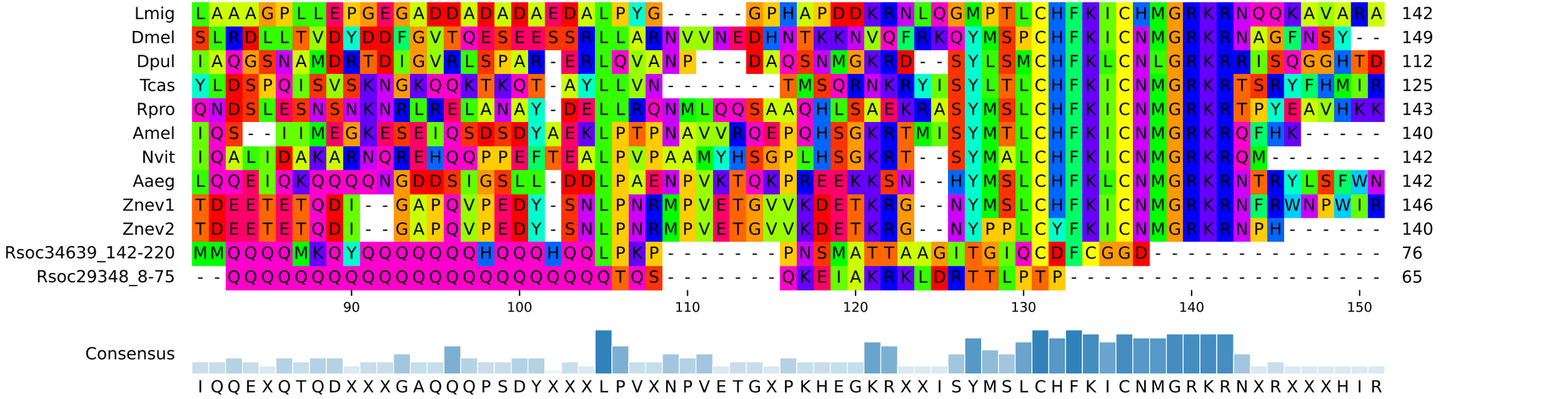
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Dpul IAQGSNAMDRTDIGVRLSPAR-ERLQVANP---DAQSNMGKRD--SYLSMCHFKLCNLGRKRRISQGGHTD 112
Tcas YLDSPQISVSKNGKQQKTKQT-AYLLVN-------TMSQRNKRYISYLTLCHFKICNMGRKRTSRYFHMIR 125
Rpro QNDSLESNSNKNRLRELANAY-DELLRQNMLQQSAAQHLSAEKRASYMSLCHFKICNMGRKRTPYEAVHKK 143
Amel IQS--IIMEGKESEIQSDSDYAEKLPTPNAVVRQEPQHSGKRTMISYMTLCHFKICNMGRKRQFHK----- 140
Nvit IQALIDAKARNQREHQQPPEFTEALPVPAAMYHSGPLHSGKRT--SYMALCHFKICNMGRKRQM------- 142
Aaeg LQQEIQKQQQQNGDDSIGSLL-DDLPAENPVKTQKPREEKKSN--HYMSLCHFKLCNMGRKRNTRYLSFWN 142
Znev1 TDEETETQDI--GAPQVPEDY-SNLPNRMPVETGVVKDETKRG--NYMSLCHFKICNMGRKRNFRWNPWIR 146
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90 100 110 120 130 140 150
Consensus
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