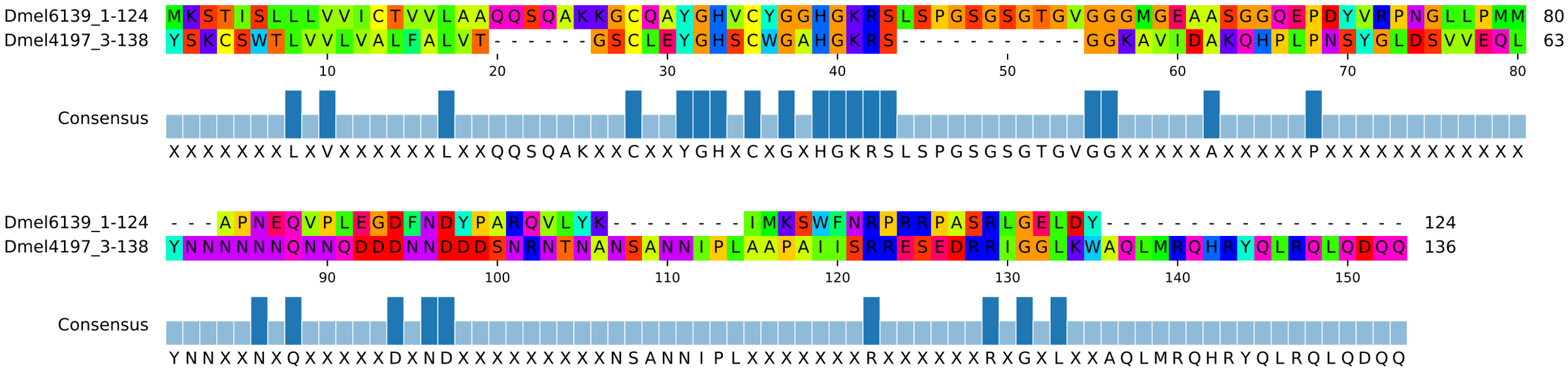
Dmel6139_1-124 MKSTISLLLVVICTVVLAAQQSQAKKGCQAYGHVCYGGHGKRSLSPGSGSGTGVGGGMGEAASGGQEPDYVRPNGLLPMM 80
Dmel4197_3-138 YSKCSWTLVVLVALFALVT------GSCLEYGHSCWGAHGKRS----------GGKAVIDAKQHPLPNSYGLDSVVEQL 63
10 20 30 40 50 60 70 80
Consensus
XXXXXXXLXVXXXXXXLXXQQSQAKXXCXXYGHXCXGXHGKRSLSPGSGSGTGVGGXXXXXAXXXXXPXXXXXXXXXXX
Dmel6139_1-124 ---APNEQVPLEGDFNDYPARQVLYK-------IMKSWFNRPRRPASRLGELDY---------- 124
Dmel4197_3-138 YNNNNNNQNNQDDDNNDDDSNRNTNANSANNIPLAAPAIISRRESEDRRIGGLKWAQLMRQHRYQLRQLQDQQ 136
90 100 110 120 130 140 150
Consensus
YNNXXNXQXXXXXDXNDXXXXXXXXXXNSANNIPLXXXXXXXRXXXXXXXRXGXLXXAQLMRQHRYQLRQLQDQQ