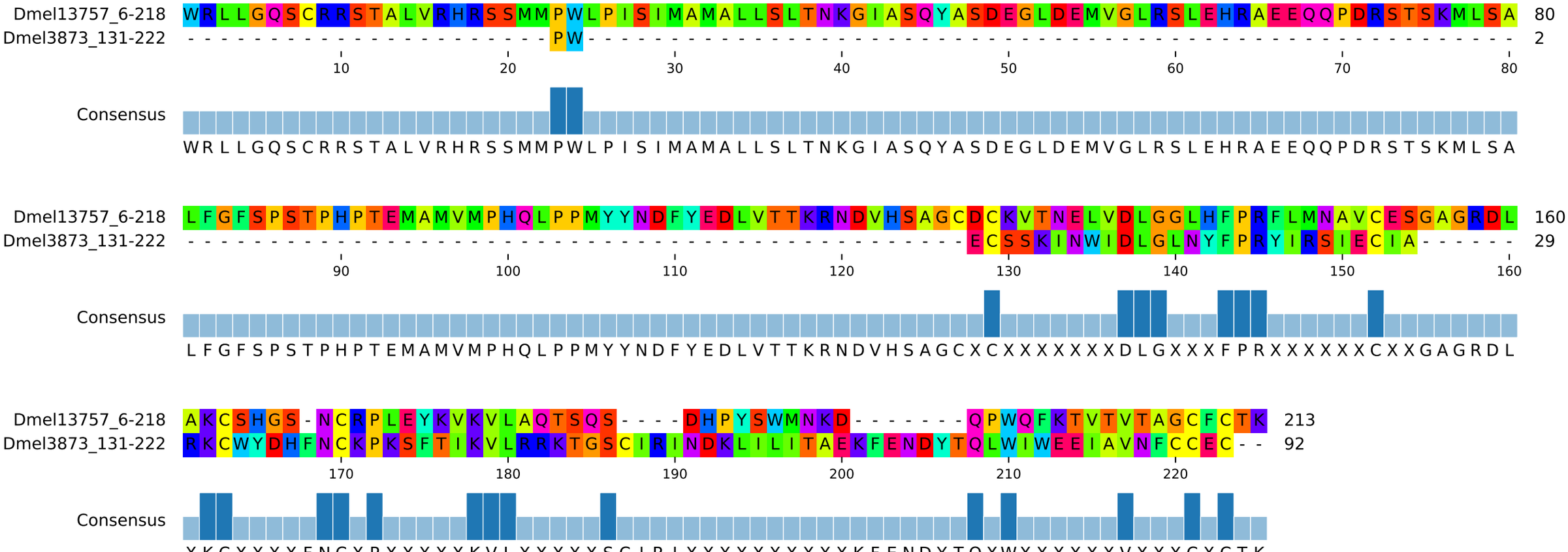
Dmel13757_6-218 WRLLGQSCRRSTALVRHRSSMMPWLPISIMAMALLSLTNKGIASQYASDEGLDEMVGLRSLEHRAEEQQPDRSTSKMLSA 80
Dmel3873_131-222 ----------PW---------- 2
10 20 30 40 50 60 70 80
Consensus
WRLLGQSCRRSTALVRHRSSMMPWLPISIMAMALLSLTNKGIASQYASDEGLDEMVGLRSLEHRAEEQQPDRSTSKMLSA
Dmel13757_6-218 LFGFSPSTPHPTEMAMVMPHQLPPMYYNDFYEDLVTTKRNDVHSAGCDCKVTNELVDLGGLHFPRFLMNAVCESGAGRDL 160
Dmel3873_131-222 ----------ECSSKINWIDLGLNYFPRYIRSIECIA------ 29
90 100 110 120 130 140 150 160
Consensus
LFGFSPSTPHPTEMAMVMPHQLPPMYYNDFYEDLVTTKRNDVHSAGCXCXXXXXXXDLGXXXFPRXXXXXXCXXGAGRDL
Dmel13757_6-218 AKCSHGS-NCRPLEYKVKVLAQTSQS----DHPYSWMNKD-------QPWQFKTVTVTAGCFCTK 213
Dmel3873_131-222 RKCWYDHFNCKPKSFTIKVLRRKTGSCIRINDKLILITAEKFENDYTQLWIWEEIAVNFCCEC-- 92
170 180 190 200 210 220
Consensus
XKCXXXXFNCXPXXXXXKVLXXXXXSCIRIXXXXXXXXXXKFENDYTQXWXXXXXXVXXXCXCTK