

Dmel6699_1-145 MKSMLVHIVLVIFI IAEFSTAE TDHDKNRRG ANMGLYAFPRVGRSDPSLANSLR DGLEAGVLDG IYGDASQEDY NEADFQ 80

10 20 30 40 50 60 70 80

Consensus



Dmel6699_1-145 KKASGLVAFPRVGRGDAELRKWAHL LALQQVLDKRTG P SASSGLWFGPR LGKR SVDAKSFADISK 145

90 100 110 120 130 140

Consensus

