

Tmol1014_24-164 SMCLDPRLTSNIAKATAASTTDECQVTPVIVHLQYPGCVPKPIPSFACIGRCASYIQVSGSKIWQMERSSCMCCQESGEREA 80
Tmol1685_57-131 - - - - - NKCE - - - - - GSCKSQVQPSVITPTGFLKECYCCRESFLRER 36

10 20 30 40 50 60 70 80

Consensus



Tmol1014_24-164 SVSLFCPKAKPGER - - - - - KFIKVTTKAPLECMCRPCTGVVEESAVIPQEIAGYADEGPLSNHFLKS 141
Tmol1685_57-131 TITLTHCYDPDGVRLTTENANSMDDVKLREPAECKCYKCG - - - - - 75

90 100 110 120 130 140

Consensus

