Tmol16094_24-179   MKNRNYRLLDYDEMNNSEESKCVDNDLCRNTFGEQVKKEVQEDEESIFASDEDKKKTTRLAPHYHSTRPMPCSCGIDFRL   80
Tmol3288_95-210   - - - - - - - - - - - - - NHVEAAK - - - - - - RKHMSRRSERGVD - LVEQWQ - - - - - - CKSKIEW - -   33

Consensus

MKNRNYRLLDYDEMNXXEXXKCVDNDLCRXXXXXXXXXXVXEDEESIFASDEDKKKTTRLXXXXXSTRPMPCXXXIXXRL

Tmol16094_24-179   LDLGHHYFPRYLHTGVCKSEICR-GLYRCVERHYKVRVLKQRDPRSPEIKTTMT- - - - - - LPDTLKGMWQPELVTVTVAC   153
Tmol3288_95-210   VDLGPDYFPRYLRKVVCQNQNCWFGLFRCKAKAFNVKLLRRKKEYCTNGEGNNTKVGFVGLPKELTELWVWEERAVTFCC   113

Consensus

XDLGXXYFPRYLXXXVCXXXXCXFGLXRCXXXXXXXXVXXLXXXXXXXXXXXXTKVGFVGLPXXLXXXWXEXXXVTXXC

Tmol16094_24-179   ECS   156
Tmol3288_95-210   ECG   116

Consensus

ECX