

Dpul10065\_1-145 MKGKGAF LMVLAGWGLIGLMILT TAVEEAAPH PADY TSSSVNNQRDFRSRRGF KTVGLATARGFGKRAPSL SNFNSFQDAA 80

10 20 30 40 50 60 70 80

Consensus



Dpul10065\_1-145 EQMMQQQEENPN SDPDVFPVDWLVN YLQNKPDVIRYMVEHLLDHNGDGQVTSQEMMTSLQQQRED 145

90 100 110 120 130 140

Consensus

