

A**B**

TH1 1 M P T P D A T T P Q A K G F R R A V **S** E 60

TH4 1 ATGCCCAACCCCGACGCCACCACGCCACAGGCCAAGGGCTTCCGCAGGGCCGTGTCTGAG 60

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TH4 1 ATGCCCAACCCCGACGCCACCACGCCACAGGCCAAGGGCTTCCGCAGGGCCGTGTCTGAG 60

M P T P D A T T P Q A K G F R R A V S E

61 L D A K Q A E A I M 90

61 CTGGACGCCAAGCAGGCAGAGGCCATCATG----- 90

|||||

61 CTGGACGCCAAGCAGGCAGAGGCCATCATG**GGTAAGAGGGGCAGGGCGCCCCGGGGCCAGG** 120

L D A K Q A E A I M V R G Q G A P G P S

91 ----- 90

121 **CTCACAGGCTCTCCGTGGCCTGGAAGTGCAGCCCCAGCTGCATCCTACACCCCCACCCCA** 180

L T G S P W P G T A A P A A S Y T P T P

91 **S** P R F I G R R Q **S** L I E D A R K E R 147

---TCCCCGCGGTTTCATTGGGCGCAGGCAGAGCCTCATCGAGGACGCCCCGCAAGGAGCGG 147

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181 **AGG**TCCCCGCGGTTTCATTGGGCGCAGGCAGAGCCTCATCGAGGACGCCCCGCAAGGAGCGG 240

R S P R F I G R R Q S L I E D A R K E R