

[illegible]

Sequence logos for the 100 amino acid residues of the protein. The top sequence is the consensus sequence: P R I E T L Q D D L A Q L G T L S Q H R E S W T S V Y K R V Q N V S W Q T L K R V K K S E Y N P D L V K Q V T S L R N K A K K L V K K L Q T E Y F T R S P E S H L R S L. The bottom sequence is the average sequence: P R A D N F L D L A Q I D L I Q H Q D D F S S E L Y K R V P A V S F K R A K A V K G D E F D P A L L D E A T D L R N G A K K L L E K L K T D Y F T R S P E Q H L S L. Asterisks are placed below the average sequence at positions 1, 4, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100.

[illegible]

QLVTSGSESTGNLFMVGDVKQSIYRFLAEPGLFLSKYKRFTQSGEGTGRKIDLNKNFRSRHEYLDSTNFTFKQIMGKYGEYDY
 KFTVTKDSESEGNLFMVGDVKQSIYRFLAEPGLFLGKYKRFTQEGLGGMKIDLAKNFRSRHEVLAGTNFTFKQIMGEEVGEIDY
 QLVTSGPSETGNLFMVGDVKQSIYRFLAEPGLFLSKYKRFTESGEGTGRKIDLNKNFRSRADILDSNFTLFKQLMGKIGEVVDY

[illegible]594
589

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



679
674

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

764
757

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

849
842

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus

934
927

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



1017
1009

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



1100
1094

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



1185
1178

logo

NTDB id 113734 MI63 RS05870 WP 000970459.1
NTDB id 119 BSU 10630 NP 388944.2
consensus



 non conserved
 similar
 ≥ 50% conserved