

Sequence logos for the 85 amino acid protein. The top logo shows the full sequence with varying heights indicating conservation. The bottom logo shows the same sequence with asterisks (*) below certain residues (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85) indicating positions of interest. The sequence is: M K K L F K R L T G K E N G M Y L L T V L F T C F S V Y L E L V P T Y I S E I T E L I G T P G T E L G L W S P A A K M M G L S L L A F L S S V T V G F F A S R V A A S. The bottom logo shows the same sequence with asterisks (*) below certain residues (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85) indicating positions of interest.

Y T R L R S D I F N R V M D Y S Q E I K R F S I P S L L T R T T N D I T Q V Q M L F T M G L Q V V T R G P I M A W A L T K I W G K S E Y H T W A V W A V L W W L
F T T H L R R S D I F N R V L D F S Q T E I K R F S I P S L L T R T T N D I T Q V Q M L F T M G L Q V V T R G P I M A W A L T K I L G K S E Y H T W A V W A V L W W L

170 170

* *

IYWGAYTTNDISKIPMTSVTAAKGATLAERLSYFSDMVVFSSYANQWVGMFLLMGALFIVLPRTLVSAGKRLNQVLDELHSSVHNPSY 328
 IYWGAYLLNDIKIPMTSVTAAKGAIADRISVFSDMVVFSYANQVVVGMFMMAIFILPLRALVSAKRINEVLALHSSVHFKEY 340

R N K V G Y I P Q R A V L F S G D T Y R S N L D F G K S K E T P L G E A K M W Q A L E L A Q S K N F Y E D K E K G L D T E V A Q G G T N F S G G Q R Q R L A I A R A L A R K
 R N K V G Y I P Q K A V L F S G D V K D N L D F G K S K E T P L G E A M W Q A L E L A Q S K N F I E D K E A G L A S E V A Q G G T N F S G G Q R Q R L A I A R A L A R K 498
 N N K V G Y I P Q R A V L F S G T I R S N I A F G Q S D Q A P L D A K I W E A L E L A Q A K N F V E E K E K G L D T E V A Q G G T N F S G G Q R Q R L A I A R A L A R K 509

PEILIFDDSF⁵⁸³SALDYKTDRILR⁵⁹⁴ELAE⁵⁸³KT⁵⁹⁴KS⁵⁸³MTKLIV⁵⁹⁴AQRISTIM⁵⁸³DAD⁵⁹⁴HLVLDQ⁵⁸³GK⁵⁹⁴VVG⁵⁸³QG⁵⁹⁴THKELLAT⁵⁸³N⁵⁹⁴EV⁵⁸³YQ⁵⁹⁴EIA⁵⁸³YS⁵⁹⁴QL⁵⁸³SK⁵⁹⁴E

logo

NTDB id 69039 ST01 RS01435 WP 096421641.1	ELHGGK	589
NTDB id 369 SMU RS04255 WP 002263293.1	ELHGGK	600
consensus	!!!*!!	

-  non conserved
-  similar
-  ≥ 50% conserved