

MSDPTLFDYSMIKGTVEAILFQNSDNFYTVLKVDTIETNEDFD.TMPTTVVGFLPNIVEGDDVYTFKGGVVDPHRYGKQLKAE
MQQHMDLLKEDEPMTEAITFHNDNFYTTLKKVDTTETSEAFDDKAPSTTFFATQEEDTYFKGVTHPRYGLQLQAE

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

[illegible][illegible]

RLTEVYRQQEGSSVELAHQMKNGQLPNTLTQRTKDRSFRCQGSQIPTWEKWTSAVYNKGYTMDIQVLAPMYRGKAGINRNLN
 NLTEVYRQQDGSSIIELAHRMKLGKQKILDTITQRFHDRSFINCQANQIPTVVEKVVTSAYNKGYTMAIDIQVLAPMYKGNAGIKRNLN
 RLTDITYRQAEGSSVELAHQMKNGLLPNNLTAPT KD RSFIRCGSQIKEVVEKVVANALKKGYTAKIDIQVLAPMYRGKAGINELN

586
595

logo

NTDB id 136031 RM27 RS07990 WP 001283311.1
NTDB id 355 BSU 27480 NP 390625.1
consensus



671
680

logo

NTDB id 136031 RM27 RS07990 WP 001283311.1
NTDB id 355 BSU 27480 NP 390625.1
consensus



756
762

logo

NTDB id 136031 RM27 RS07990 WP 001283311.1
NTDB id 355 BSU 27480 NP 390625.1
consensus



825
798

☐ non conserved
☒ similar
☒ ≥ 50% conserved