

logo

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NTDB id 32 MW RS07995 WP 000472256.1
NTDB id 16 SA RS07765 WP 000472256.1
NTDB id 1019471 AB0R90 RS12845 WP 003153087.1
NTDB id 98 BSU 24710 NP 390351.1
consensus
```

Sequence	Score
MFKFLKKTQGAFTLIEMLLVLLIISLLLILIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI	80
MFKFLKKTQGAFTLIEMLLVLLIISLLLILIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI	80
.MLRLKNQDGFLLIEMLLVLLIISLLLITIPNVTKHNQSIQHKGCCEGLQNMVKAQVTAYEIDHEGKMPDNDLQSEGY	79
....MNEKGFTLVEMLIVLLIISLLLITIPNVTKHNQTIQKKGCEGLQNMVKAQMTAFELDHGQTPSLADLQSEGYV	75

logo

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Sequence logo for the 103 bp region. The logo shows the conservation of nucleotides at each position. The top part shows the consensus sequence: KKAQKTCPSGKETITISNGEAVAN. The bottom part shows the sequence logo with nucleotide counts. The positions are numbered 1 to 103. The logo indicates that positions 1-10 are highly conserved, with K and A being the most frequent nucleotides. Positions 11-20 are also conserved, with G and T being the most frequent. Positions 21-30 are less conserved, with A and T being the most frequent. Positions 31-40 are highly conserved, with G and T being the most frequent. Positions 41-50 are also conserved, with G and T being the most frequent. Positions 51-60 are less conserved, with A and T being the most frequent. Positions 61-70 are highly conserved, with G and T being the most frequent. Positions 71-80 are also conserved, with G and T being the most frequent. Positions 81-90 are less conserved, with A and T being the most frequent. Positions 91-100 are highly conserved, with G and T being the most frequent. Positions 101-103 are also conserved, with G and T being the most frequent.

-  non conserved
-  similar
-  $\geq 50\%$ conserved