

logo

NTDB id 32 MW RS07995 WP 000472256.1
NTDB id 16 SA RS07765 WP 000472256.1
NTDB id 1002098 ABFY42 RS13120 WP 014418376.1
NTDB id 98 BSU 24710 NP 390351.1
consensus

MFKFLKKTQGAFTLIEMLVLLIISLLILLIIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI 80
 MFKFLKKTQGAFTLIEMLVLLIISLLILLIIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI 80
 .MLRLKNQDGFLLIEMLVLLIISLLILLITIPNVTKHNQSIQRKGCEGLQNMVKAQVTAYEIDHEGKMPDNDLQSEGY 79
MNEKGFTLVEMLIVLFIISILLITIPNVTKHNQTIQKKGCEGLQNMVKAQTAFELDHGQTPSLADLQSEGYV 75
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logo

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Sequence logo for the 103 bp region. The logo shows the conservation of amino acids at each position. The top row shows the most conserved residues: K, A, Q, T, C, S, G, E, T, I, T, I, S, N, G, E, A, V, A, N. The bottom row shows the least conserved residues: E, D, A, A, K, N, E, S, T, T, G, G, L, A, K, A, E, Q. The sequence is: KEAQKTCXSGETITISNGEAVAN. 103, KEAQKTCXSGETITISNGEAVAN. 103, KKN.TACPNKGKQILISGGEVTVEQ 102, KKD.AVCPNKGKRIITGGEVKVEH 98. The positions are numbered 103, 103, 102, 98 from left to right.

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