

logo

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NTDB id 32 MW RS07995 WP 000472256.1
NTDB id 16 SA RS07765 WP 000472256.1
NTDB id 1051875 ACE1EH RS11635 WP 003153087.1
NTDB id 98 BSU 24710 NP 390351.1
consensus
```

Sequence	Residues
MFKFLKKTQAF	1-10
FTLIEMLIVL	11-20
LIISLLILII	21-30
IPNIIAKQTA	31-40
HIQSTGCNA	41-50
AQVKMVNSQ	51-60
IEAYALKHNR	61-70
NPSSIEDLIA	71-80
DGFI	81-85
MLRLKKNQDG	1-10
FTLIEMLIVL	11-20
LIISLLILII	21-30
IPNIIAKQTA	31-40
HIQSTGCNA	41-50
AQVKMVNSQ	51-60
IEAYALKHNR	61-70
NPSSIEDLIA	71-80
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.MLRLKKNQDG	1-10
FTLIEMLIVL	11-20
LIISLLILII	21-30
IPNIIAKQTA	31-40
HIQSTGCNA	41-50
AQVKMVNSQ	51-60
IEAYALKHNR	61-70
NPSSIEDLIA	71-80
DGFI	81-85
.....MNEKG	1-10
FTLIEMLIVL	11-20
LIISLLILII	21-30
IPNIIAKQTA	31-40
HIQSTGCNA	41-50
AQVKMVNSQ	51-60
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Sequence logo for the 103 bp region. The logo shows the conservation of nucleotides across four sequences. The top sequence is KEAQKTCXSGETITISNGEAVAN. (103). The second sequence is KEAQKTCXSGETITISNGEAVAN. (103). The third sequence is KKN.TACPNKGKQILISGGEVTVEQ (102). The fourth sequence is KKD.AVCPNKGKRIITGGEVKVEH (98). The logo highlights the conserved regions in blue and the variable regions in red. The conservation is highest in the first 10 positions and the last 10 positions.

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