

logo

```
NTDB id 32 MW RS07995 WP 000472256.1
NTDB id 16 SA RS07765 WP 000472256.1
NTDB id 1019855 AB0R64 RS11730 WP 003153087.1
NTDB id 98 BSU 24710 NP 390351.1
consensus
```

MFKFLKKTQGAFTLIEMLLVLLIISLLLILIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI 80
 MFKFLKKTQGAFTLIEMLLVLLIISLLLILIPNIAKQTAHIQSTGCNAQVKMVNSQIEAYALKHNRNPSSIEDLIADGFI 80
 .MLRLKNQDGFLLIEMLLVLLIISLLLITIPNVTKHNQSIQHKGCCEGLQNMVKAQVTAYEIDHEGKMPDNDLQSEGY 79
MNEKGFTLVEMLIVLLIISLLITIPNVTKHNQTIQKKGCEGLQNMVKAQMTAFELDHGQTPSLADLQSEGYV 75
 ***** **

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Sequence logo visualization showing conservation across four sequences. The y-axis represents information content in bits. The x-axis shows positions from 1 to 16. Conserved residues are highlighted in blue boxes.

Position	Sequence 1	Sequence 2	Sequence 3	Sequence 4
1	K	E	K	K
2	A	A	A	T
3	K	A	C	P
4	T	G	S	N
5	C	K	I	K
6	S	E	T	I
7	G	T	I	T
8	E	T	I	S
9	T	I	T	I
10	I	S	N	G
11	G	E	A	V
12	A	V	A	N
13	V	A	.	.
14	N	.	.	.
15	.	.	.	.
16	.	.	.	.

Sequence	Conservation Score
KEAQTCTCSGETITISNGEAVAN.	103
KEAQTCTCSGETITISNGEAVAN.	103
KKN.TACPNKGKQILISGGEVTVEQ	102
KKD.AVCPNKKRIITGGEVKVEH	98

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