

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MAKN	72
NTDB id 407614 GPY25 RS16220 WP 005493981.1	MAKNTQ.....TLPLKNYRWKGINNSGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLLKKGVSILLAR.LTHRVRKSKDITI	71
NTDB id 1402 DSB67 RS12670 WP 010643257.1	.MKTT.....TPQLKNFRWKGVNSSGKK.TSGQTLAMSETEVRERLDAQHIKIKKLLKKGSSISFLT.LSHRVKVKGDITV	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	.MKTI.....APQLKNYRWKGINNSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLLKKGSSISFITK.ISHRVKVKGDITI	74
NTDB id 1113 AAA85695.1 219..1451()	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	.MAKNGGFSLF AKKEKRFI FEGRHSASDKLVNVEVS AFTEEEARKKLA KRGI RPLQITRV.....KTSSKRKITQEDITV	71
NTDB id 1198 PSJM300 03950 AFN76868.1	.MDKN.....SPPLILTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGI VTNKV VVKRKP L FDR.KNKKITQADITV	70
NTDB id 1016 ACIAD RS01680 WP 004920476.1	.MAQK.....AIKNSVFTWEG LDRQGA K.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL	73
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAAKK.....TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI	73
consensus	MAVKK.....AQMMPTFA YEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVVTTLDITI	73

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	FTRQLATM	152
NTDB id 407614 GPY25 RS16220 WP 005493981.1	FTRQISTMLVTGVPLVQALKLVSDNHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASNHFDPPLYTDLIATGEQSGNLAIEVF	151
NTDB id 1402 DSB67 RS12670 WP 010643257.1	FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSI LMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1113 AAA85695.1 219..1451()	FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	FTRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHD IETGLTLAESLIKHPLYFNE LFCNLVDAGEKSGSLDIML	151
NTDB id 1198 PSJM300 03950 AFN76868.1	FTRQMATMMKAGVPLQSF DIIGEGFDNPNMRKLVDD LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL	150
NTDB id 1016 ACIAD RS01680 WP 004920476.1	FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML	153
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FTRQLATMMKAGVPLVQGF EIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML	153
consensus	FTRQLATM	153

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	DRLATYREKSEQLR	232
NTDB id 407614 GPY25 RS16220 WP 005493981.1	ERLATYREKNEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIP EFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI	231
NTDB id 1402 DSB67 RS12670 WP 010643257.1	ERLATYREKSEQLR	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1113 AAA85695.1 219..1451()	DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMIFVLPFAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	DKVATYKEKIEIKKKIKKALTYPPIAMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG	231
NTDB id 1198 PSJM300 03950 AFN76868.1	DRVATYKEKTEALKAKIKKAMNYPPIAVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTLMVIGLSEALQAWYVVLVLA	230
NTDB id 1016 ACIAD RS01680 WP 004920476.1	DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFTSFGADLP AFTQLVNMNSNMWQDYWFILIL	233
NTDB id 1059 ABD1 RS01610 WP 000279215.1	DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVVFQDLFASFGADLP AFTQMVMNSKWMQYWFIMII	233
consensus	ERLATYREKSEQLR	233

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	ATGAAIYSELK	312
NTDB id 407614 GPY25 RS16220 WP 005493981.1	GSISVFISARVLSKRSDSFRLLMNRSVLKFPVLGAVLSKAAIAKFSRTLATSFTAGIPILTSKLTTSKTS SGNMHYQLAIE	311
NTDB id 1402 DSB67 RS12670 WP 010643257.1	SFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS SGNMHYQLAIE	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	ALGFAIYGFLLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1113 AAA85695.1 219..1451()	ALGFAIYRFLKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEATR	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	ALGGVVSFFYAKNHSLEFAQTI DRVMLKLVPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD	311
NTDB id 1198 PSJM300 03950 AFN76868.1	FGVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSATN	310
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIGAATAGFLEARKRSKRFRDQLDRLVLRPIVGD LVYKAI IARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL	313
NTDB id 1059 ABD1 RS01610 WP 000279215.1	AIGAVIAAFLEARKRSKRFRDGLDKLALKLPIFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM	313
consensus	ATGAAIYSELK	313

```

NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 407614 GPY25 RS16220 WP 005493981.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

```

392
391
391
394
394
391
390
393
393

logo

```

NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 407614 GPY25 RS16220 WP 005493981.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

```

Position	V	A	M	Y	I	P	F	N	L	G	S	W
1	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
7	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
8	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0
9	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0
10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0

Sequence logo showing amino acid conservation across 10 positions. The y-axis represents information content in bits. Position 1 has a peak for V (~1.8 bits). Position 2 has peaks for A (~1.6 bits) and M (~1.4 bits). Position 3 has peaks for Y (~1.6 bits) and I (~1.4 bits). Position 4 has a peak for P (~1.8 bits). Position 5 has a peak for F (~1.8 bits). Position 6 has a peak for N (~1.8 bits). Position 7 has a peak for L (~1.8 bits). Position 8 has a peak for G (~1.8 bits). Position 9 has a peak for S (~1.8 bits). Position 10 has a peak for V (~1.8 bits).

Position	V	A	M	Y	I	P	F	N	L	G	S	W
1	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
7	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
8	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0
9	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0
10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0

Sequence logo showing amino acid conservation across 10 positions. The y-axis represents information content in bits. Position 1 has a peak for V (~1.8 bits). Position 2 has peaks for A (~1.6 bits) and M (~1.4 bits). Position 3 has peaks for Y (~1.6 bits) and I (~1.4 bits). Position 4 has a peak for P (~1.8 bits). Position 5 has a peak for F (~1.8 bits). Position 6 has a peak for N (~1.8 bits). Position 7 has a peak for L (~1.8 bits). Position 8 has a peak for G (~1.8 bits). Position 9 has a peak for S (~1.8 bits). Position 10 has a peak for V (~1.8 bits).

Position	V	A	M	Y	I	P	F	N	L	G	S	W
1	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
2	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
3	0.0	1.6	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
4	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
5	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
7	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0
8	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0	0.0
9	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0	0.0
10	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.0

Sequence logo showing amino acid conservation across 10 positions. The y-axis represents information content in bits. Position 1 has a peak for V (~1.8 bits). Position 2 has peaks for A (~1.6 bits) and M (~1.4 bits). Position 3 has peaks for Y (~1.6 bits) and I (~1.4 bits). Position 4 has a peak for P (~1.8 bits). Position 5 has a peak for F (~1.8 bits). Position

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