

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKATQTLP..LKNYRWKGINNSGK..KVSQGLMAISEIEVRDKLKDQHIQIKLKKKGSVSLILAR.LTHR	65
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKTIIAPQLKNYRWKGINSSGK..KTSGNVLAMTEIEVRERLDAQHIKIKLKKKGSISFITK.ISHRV	64
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRV....KTSSKRKI	67
NTDB id 1112 NGFG RS09215 WP 003689811.1	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSATFEEEARKKLAKRGIRPLQITRV....KTSSKRKI	67
NTDB id 26351 SFRI RS19430 WP 011639198.1	MATITAKKKPKAKKKTKHQPKVFTYQWKGVNRDQ..RTSGELKGSTIAEIRSVLKAQGVTPKGVRRKKSAPLWK..TEKSI	77
NTDB id 1252 GC085 RS07730 WP 011213805.1	MDKNSPPLLTFHYQGINKAGQ..KMEGDIQARSLAIKADLRKQGIVTNKVVKKRKPLFDR.KNKKI	64
NTDB id 1198 PSJM300 03950 AFN76868.1	MAQKAIKNSVFTWEGLDLRQGA..KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKI	63
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKKTQVMPVFAYEGVDRKGI..KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKV	66
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKKAKQMPFTFAYEGVDRKGV..KIKGELPAKNMALAKVTLRKQGVTVNRNIREKRKNILEGLFKKKV	66
consensus	* * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	KSKDITILTRQLATMITTGVPVIVQALKLVGDNHRKAEMKKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMS	145
NTDB id 1402 DSB67 RS12670 WP 010643257.1	KGKDITIFTRQIATMLMTGVPVIVQALKLVSENHKAEMKKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQS	144
NTDB id 1113 AAA85695.1 219..1451()	TQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG	147
NTDB id 1112 NGFG RS09215 WP 003689811.1	TQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG	147
NTDB id 26351 SFRI RS19430 WP 011639198.1	TAMDIAMITRQIATMLAAGVPLVTITIELLGRGHEKAKVRELLGTILSDVQSGIPLSDALRPHRRYFDDLYVDLVAAAGEHS	157
NTDB id 1252 GC085 RS07730 WP 011213805.1	TQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKS	144
NTDB id 1198 PSJM300 03950 AFN76868.1	KPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDLLKQEVAAAGNSFASSLRKKPQYFDDLYCNLVDSGEQS	143
NTDB id 1016 ACIAD RS01680 WP 004920476.1	KPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLNPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQS	146
NTDB id 1059 ABD1 RS01610 WP 000279215.1	TTLDITIFTRQLATMMKAGVPLVQAFEIVAEGLNPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQS	146
consensus	* ! ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	GNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIFEPEFESMFKGFGAELPWFTTQQVLKLSHWVQA	225
NTDB id 1402 DSB67 RS12670 WP 010643257.1	GNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIFEPEKMFMTGFGADLPFTQMVLNLSAWTQN	224
NTDB id 1113 AAA85695.1 219..1451()	GVLESLLDKLAIYKEKTQAIRKKVKLTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDSDFVVS	227
NTDB id 1112 NGFG RS09215 WP 003689811.1	GVLESLLDKLAIYKEKTQAIRKKVKLTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDSDFVVS	227
NTDB id 26351 SFRI RS19430 WP 011639198.1	GS�DAVFDRIATYREKAEQLKSKIKKAMFYPAAVVVVAIAVTSLLLLFVVPQFEDIFNGFGAELPAFTQMIIGISRWLQS	237
NTDB id 1252 GC085 RS07730 WP 011213805.1	GS�DIMLDKVATYKEKIEITIKKKIKKALTPIAVMVVALLVTAGLLIYVVPQFESLFKGFADLPAMTRAVITMSEFMQA	224
NTDB id 1198 PSJM300 03950 AFN76868.1	GSLETLLDRVATYKEKTEALKAKIKKAMNYPVIAVVLVAVIVTALLIKVVPQFQDVAFANFGAELPAFTLMVIGLSEALQA	223
NTDB id 1016 ACIAD RS01680 WP 004920476.1	GSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPFTQLVVNMNSNMQD	226
NTDB id 1059 ABD1 RS01610 WP 000279215.1	GALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVQDLFASFGADLPFTQMNVNMMSKWMQ	226
consensus	! ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1	YSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPITGNVLAKASIAKFSRTLATSFAGIPILASLKTAKTSGNV	305
NTDB id 1402 DSB67 RS12670 WP 010643257.1	WGPFIIGLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFAGIPILTALKTTSTSGNM	304
NTDB id 1113 AAA85695.1 219..1451()	YGWMVLIAGLFAIYRFLKLKARSIKIQRMDAAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL	307
NTDB id 1112 NGFG RS09215 WP 003689811.1	YGWMVLIAGLFAIYGLFLKLKARSIKIQRMDAAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL	307
NTDB id 26351 SFRI RS19430 WP 011639198.1	SWYFFVIAIVIGIWLFRRTHRNSQSFRDRIDQMVLLKIPVIGDILHKASMSRFARTLSTTFAAGVPLVDGLESAAGSGNY	317
NTDB id 1252 GC085 RS07730 WP 011213805.1	YWYIIFGALGGVVYSFFYAKNHSLEFAQTIIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNT	304
NTDB id 1198 PSJM300 03950 AFN76868.1	WWYVVLIAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNV	303
NTDB id 1016 ACIAD RS01680 WP 004920476.1	YWFILILVIGAATAGFLEARKRSKRFRDQLDRLVLRPLVIGDLVYKAIITARYSRTLATTTFAAGVPLIDALASTAGATNNT	306
NTDB id 1059 ABD1 RS01610 WP 000279215.1	YWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPVIGDLVYKAIITARYSRTLATTTFAAGVPLIDALESTAGATNNV	306
consensus	* * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 26351 SFRI RS19430 WP 011639198.1
NTDB id 1252 GC085 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
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NTDB id 1169	A1552VC RS11075 WP 000648511.1	GTVVGGGLVVMYLPPIFNLMSVLG.	408
NTDB id 1402	DSB67 RS12670 WP 010643257.1	GVVVGGLVTAMYLPPIFNLMSVLG.	407
NTDB id 1113	AAA85695.1 219..1451()	GLVIGTLLVAMYLPLFNLGNVVA*	410
NTDB id 1112	NGFG RS09215 WP 003689811.1	GLVIGITLLVAMYLPLFNLGNVVA.	410
NTDB id 26351	SFRI RS19430 WP 011639198.1	GTLVGGLIVGMYPPIFEMGNVV..	419
NTDB id 1252	GCO85 RS07730 WP 011213805.1	GTLVGGGLVVMYLPPIFKLGSAAV.	406
NTDB id 1198	PSJM300 03950 AFN76868.1	GVLVGGLIIAMYLPPIFQMGSVV..	405
NTDB id 1016	ACTAD RS01680 WP 004920476.1	GILVGGGLVIAMYLPIFQMGSVV..	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	GLVVGGLVIAMYLPIFQMGSVV..	408
consensus		!***!!**!*!!!!!!	

	385
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	397
	394
	383
	386
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- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved