

logo

NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKTIIAPQIKNYRWKGINSSG..KKTSGNVLAMTEIEVRRERLDAQHIKIKKKLKKGSISFITK..	59
NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKATQTLPLKNYRWKGINSG..KKVSGQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLAR..	60
NTDB id 1112 NGFG RS09215 WP 003689811.1	MAKNG...GFSLF AKKEKRFIEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVKT.....S	62
NTDB id 1113 AAA85695.1 219..1451()	MAKNG...GFSLF AKKEKRFIEGRHSASDKLVNGEVS AFTEEEARKKLAKRGIRPLQITRVKT.....S	62
NTDB id 193676 BC350 RS10300 WP 011002732.1	MATRAPTANRSAAASARKTAATKAPTQYIFEWEGKDRKG..KIFKGEMRAESITEVNAVLRKQGLSITKSKRRRA.....A	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	MDKNSPPLILTFHYQGINKAG..QKMEGDIQARSLAIADLRKQGI VTNKVVKKKRKP L FDR..	59
NTDB id 1198 PSJM300 03950 AFN76868.1	MAQKAIKNSVFTWEGLD RQG..AKIKGELSGVSPALVKAQLRKQGINPQKVRKKKSISLFS..	58
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKK AQMMP TFAYEGVDRKG..VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL	61
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKTKQVMPVFAYEGVDRKG..IKLKGELPARNMALAKVTLRKQGITRTIREKRKNIFEGL	61
consensus	* * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	ISHRVKGK DITIFTRQIATMIMTGVPVIVQALKLVSENHKKAE MKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIA	139
NTDB id 1169 A1552VC RS11075 WP 000648511.1	LTHRVKSKDITILTRQLATMLTTGVPVIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVE	140
NTDB id 1112 NGFG RS09215 WP 003689811.1	SKRKITQEDITVFRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKQYFDRFYCNLVA	142
NTDB id 1113 AAA85695.1 219..1451()	SKRKITQEDITVFRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKQYFDRFYCNLVA	142
NTDB id 193676 BC350 RS10300 WP 011002732.1	RGKKIVPKDIAYFTRQLSTMKAGVPLLSVDITARGHANPNFTQLLTEIRVDIESGSSMAQAFRRHPQHFDLSLYCNLID	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVD	139
NTDB id 1198 PSJM300 03950 AFN76868.1	AGKKIKPMDIALFTRQMATMMKAGVPLLSFDITIGEGFDNPNMRKLVDL LKQEVAAAGNSFASSLRKKPQYFDDLYCNLVD	138
NTDB id 1059 ABD1 RS01610 WP 000279215.1	FKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLG IKGEVEGGSTFASALRKYYPQHFDNLFCSLVE	141
NTDB id 1016 ACIAD RS01680 WP 004920476.1	LKKVKVPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYYPQYFNDLFCSLIE	141
consensus	*** ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * *	

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	TGEQSGNLSQVFERLATYREKSEQLR AKVIKALIYPAMVVLVALGVSYLMLTRVPIFEFEKMF TGF GADLP AFTQMVLNLS	219
NTDB id 1169 A1552VC RS11075 WP 000648511.1	TGEMSGNLP EVFERLATYREKSEQLR AKVIKALIYPSMVVLVALGVSYLMLTMVPIFEFESMFKGFGAELPWFTQQVLKLS	220
NTDB id 1112 NGFG RS09215 WP 003689811.1	AGETGGVLESLLDKLAIYKEKTQAIRKKVK TALTYPVSVIAVAIGLVFVMIFVLP AFKEVYANMGAELP LTTQTVM DMS	222
NTDB id 1113 AAA85695.1 219..1451()	AGETGGVLESLLDKLAIYKEKTQAIRKKVK TALTYPVSVIAVAIGLVFVMIFVLP AFKEVYANMGAELP LTTQTVM DMS	222
NTDB id 193676 BC350 RS10300 WP 011002732.1	AGEQG GILDALLERLSMYMEKSIALKAQIKSAMIYPI SVLTVAFLVTVLMIFVVP AFKNVFASFGATLPAPT LTVMGIS	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	AGEKSGSLDIMLDKVATYKEKIEI IKKKIKKALTYP IAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMS	219
NTDB id 1198 PSJM300 03950 AFN76868.1	SGEQSGSLETLLDRVATYKEKTEALKA KIKKAMNYP IAVVVLVAVIVTATILLIKVVPQFQDV FANFGAELPAFTL MVI GLS	218
NTDB id 1059 ABD1 RS01610 WP 000279215.1	SGEQSGALETMLDRVAIYKEKSELKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLP AFTQM VVNMS	221
NTDB id 1016 ACIAD RS01680 WP 004920476.1	SGEQSGSLEIMLDRAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFTSFGADLP AFTQL VVNMS	221
consensus	* ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * * ! ! * * * * *	

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	AMTQN WGPFI GLSFVSL LISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSK	299
NTDB id 1169 A1552VC RS11075 WP 000648511.1	HWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKT SRIGLKFP IIGNVLAKASIAKFSRTLATSFAAGIPILASLKT TAK	300
NTDB id 1112 NGFG RS09215 WP 003689811.1	DDFFVSYGWMVLIALGFAIYGFLK LKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG	302
NTDB id 1113 AAA85695.1 219..1451()	DDFFVSYGWMVLIALGFAIYRFLK LKARSIKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG	302
NTDB id 193676 BC350 RS10300 WP 011002732.1	DDFFV K WYIIIFTPIVGIFLYVRAFKRSEK VQRNTHKAILKMPIFGSIIRKAT IARWTRTLATMFSAGT PLVESMESVAG	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	EFMQAYWYIIIFGALGGVVSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAG	299
NTDB id 1198 PSJM300 03950 AFN76868.1	EALQAWYVVL IAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVG DILYKSSVARFARTLSTTFAAGVPLVDALDSVAG	298
NTDB id 1059 ABD1 RS01610 WP 000279215.1	KWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLP IFGDLVYKAI IARYSRTLATTFAAGVPLIDALESTAG	301
NTDB id 1016 ACIAD RS01680 WP 004920476.1	NWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLLVRLPIVGDLVYKAI IARYSRTLATTFAAGVPLIDALASTAG	301
consensus	***** ***** * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * *	

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NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

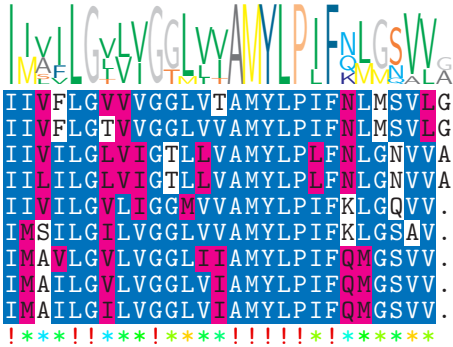


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NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus



407
408
410
410
421
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405
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 non conserved
 similar
 ≥ 50% conserved