

NTDB id	1029	TT RS02230 WP 011228203.1	MPVYQYKARDRQGR.LVEATTEAEDLRTAARLLDRDGLFVAETKEPGKGLQAEVRIPALERGPGLKD	66
NTDB id	1169	A1552VC RS11075 WP 000648511.1	MKATQTLPLEKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLDDQHIIQIKLKKGGSVSLLARL.....THR.VKSKD	69
NTDB id	1402	DSB67 RS12670 WP 010643257.1	MKTIAPOQLKNYRWKGINSNGK.KTSGNVLMTEIEVRERLDAGHIKIKLKKGKSISFITKI.....SHRVKGGK	68
NTDB id	1113	AAA85695.1 219..1451()	MAKNGGFSLSFAKKEKR.FIFEGRHASADKL.VNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTS.....SKRKITQED	71
NTDB id	1112	NHGF RS09215 WP 003689811.1	MAKNGGFSLSFAKKEKR.FIFEGRHASADKL.VNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTS.....SKRKITQED	71
NTDB id	1252	GCO85 RS07730 WP 011213805.1	MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLATAKADLRKQGITVNKVVKRRKPLFDRK.....NKKITQAD	68
NTDB id	53695	AMEC673 RS14620 WP 014950403.1	MARAPVTFIWQQCKDRHGQ.SRKGEISAASLSEAKNLRLRQGGSANKVKKLAKPLFGGS.....PKITAAD	64
NTDB id	1198	PSJM300 03950 AFN76868.1	MAQAIAKNSVFTWEGLDRQGA.KTKGELSCVSPALVKAQLRKQGGINPOKVRKKSISIFS.....AGKKIKPMD	67
NTDB id	1016	ACIAD RS01680 WP 004920476.1	MAAKKTQVPVFAYEGVDKGI.KLKGELPARNMALAKVTLRKQGITTIRTIREKRKNIFEGL....LKKKVKPLD	70
NTDB id	1059	ABD1 RS01610 WP 000279215.1	MAVKKAQMMPTFAEGVDKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTLD	70
consensus			* * * * *	!

NTDB id	1029	TT RS02230 WP 011228203.1	LAI FSRQLATMIGAGLTLLQALATLERQTENRKFREILKQVRTDVEGGMAFSEALS KHK.IFSRLYVNLVRAGETSGGLD	145
NTDB id	1169	A1552VC RS11075 WP 000648511.1	ITITLTRLQLATMLITTGVPDIVQALKLVGDNRKAEMKSILAQTITSVEAGTPLSKAMRTASAHFDTLVVDLVETGEMSGNLP	149
NTDB id	1402	DSB67 RS12670 WP 010643257.1	ITIFTTRQIATMLMTGVPDIVQALKLVSENHKKAEKMSILMSVTRAVEAQTPMSKAMRTASTHFDPPLYTDLIATGEQSGSNLS	148
NTDB id	1113	AAA85695.1 219..1451()	ITVFTRQLSTMINAGELPLMQAFEIVARGHGPNPSMTEMLMEIRGGVEQGSSLSRAFSNHPPKYFDRFYCNLVAAAGETGGVLE	151
NTDB id	1112	NHGF RS09215 WP 003689811.1	ITVFTRQLSTMIKAGLPLMQAFEIVARGHGPNPSMTEMLMEIRGGVEQGSSLSRAFSNHPPKYFDRFYCNLVAAAGETGGVLE	151
NTDB id	1252	GCO85 RS07730 WP 011213805.1	ITVFSTRQLATMIESGIPLVQAFFDIVAKQQSNKRLLKDLETIKHDLETGLTIAESLIKHPLYFNELFCNLVDAGEKSGSLD	148
NTDB id	53695	AMEC673 RS14620 WP 014950403.1	ISVISRQIATMLAAGVTLLQSLEMISQGHANSSMRKLIGEITDEVKAGNP LSSALRKHPLYFDDLYCDLVYTGEQSGALE	144
NTDB id	1198	PSJM300 03950 AFN76868.1	IALLFTTRQMATTMMKAGVPLLQSFDIIGEGFDNPNMRKLVDLLKQEVAAGNSFASSLRKPKQYFDDL YCNLVDSGEQSGSLE	147
NTDB id	1016	ACIAD RS01680 WP 004920476.1	IAIFTRQLATMMKAGVPLVQAFFEIVAEGLENPAMRDVVVLGLKNEVEGGNIFAGALRKYPQYFDNFLFCSLIESGEQSGSLE	150
NTDB id	1059	ABD1 RS01610 WP 000279215.1	ITIFTTRQLATMMKAGVPLVQGFEEIVAEGLENPAMREVVVLGIKGEVEGGSTFASALRKYPQHFDNFLFCSLVESGEQSGALE	150
consensus			* * * * *	

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NTDB id 1029	TT RS02230 WP 011228203.1	LLILAVALLFFAYR.WYYGTPQGRRVTDRLKLRIPVFCNINRKTAVARFSRTLALLLSSGVMIVBALDITKGTAGNSVVEE	304
NTDB id 1169	A1552VC RS11075 WP 000648511.1	AFIATAAAIFGLKALRKNSFQIRLKTSRLGLKFPITGNVLAKASIAKFSRTLATSFAAGIPILASLKITAKTSGNVHFEET	309
NTDB id 1402	DSB67 RS12670 WP 010643257.1	TGLSFVSLIISGKIMSQRSDSFLLAARSSLRVPIIGPVLSKAAIAKFSRTLATSFSAGIPILTALKITSKTSGNMHYQL	308
NTDB id 1113	AAA85695.1 219..1451()	VLIALGFAIYRFIKLKLARSIKIQRMDATILLRMPIFGDIVRKGTIARWGRTTATILFAAGVPLVDVLDSTAGAAGNLIYEE	311
NTDB id 1112	NGFG RS09215 WP 003689811.1	VLIALGFAIYCFILKLARSIKIQRMDATILLRMPIFGDIVRKGTIARWGRTTATILFAAGVPLVDVLDSTAGAAGNLIYEE	311
NTDB id 1252	GCO85 RS07730 WP 011213805.1	IFGALCGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILKAAIARFARTLSITFAAGIPLVKALSVAGATGNIIYAK	308
NTDB id 53695	AMEC673 RS14620 WP 014950403.1	IAIGIGGAGFMFMRTYKRSQKLKRDVTDRNLIKIPVIGPILKKAIIARFRTTLATTTFAAGVPLIGALESAAGASGNAVYRE	304
NTDB id 1198	PSJM300 03950 AFN76868.1	VLAGFVCAAYAFKQAHTRSEKFRNWFDRMLKVPVVGDIYKSSVARFARTLSTTTFAAGVPLVDALDSVAGATGNVVERS	307
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LIIIVTGAATACFTEARKRSKRFRDQLDRLVLRPIVGDILVYKATIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ	310
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MIITAGAVTAAFLKAKRSKKFRDGLDKLALKLPIFGDLVYKATIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK	310
consensus		***** * * * * * ! * ! * ! * * ! * * ! * * ! * * * * * ! * * * * ! * * * * ! * * * *	

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NTDB id 1029	TT RS02230 WP 011228203.1	IVEAAKLKIQQCDPLNLTAAQHPFVFPPMVSSMVAIGEEIGALDMLSKVADFYBEREVDDEAVASLTAAIEPLMIIFLGVI	384
NTDB id 1169	A1552VC RS11075 WP 000648511.1	ATNEVYRDTAAGMPMYIAMR.NTEAFPEMVLQVMVIGEESGQLDDMLNKVATTIYEFVDNTVDNLGKILEPLIIVFLGTV	388
NTDB id 1402	DSB67 RS12670 WP 010643257.1	ATNEVYRDTAAGMPMYIAMR.HCHVPELVLMQVMIGEESGRLDDMLNKIAAIYEFVDNTVDNLGKILEPLIIVFLGTV	387
NTDB id 1113	AAA85695.1 219..1451()	ATREIRTRVIQCLSMTSCMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYDEVDNAVGVLSAMMEPTIILILGLV	390
NTDB id 1112	NGFG RS09215 WP 003689811.1	ATREIRTRVIQCLSMTSCMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYDEVDNAVGVLSAMMEPTIIVILGLV	390
NTDB id 1252	GCO85 RS07730 WP 011213805.1	ATDKIREEVATGQQMFTAME.NTHLFPNMVLMQVAIGEESGALDEKMLSKVADFYBEVNNAVDALSSILEPTIIMSILGIT	387
NTDB id 53695	AMEC673 RS14620 WP 014950403.1	ATILYRKKEVAGCMPMHVAMR.ATQVFPDMVTQMIAIGEESGAVDEMLSKTATTIYEAEVDDMVDGLTSILEPTIIMAVLGVI	383
NTDB id 1198	PSJM300 03950 AFN76868.1	ATNKKISDVSSGQMLNFSMR.TTGTFFSMAMVQMTAIGEESGALDEMLSKVATFYDEVDNMVDGLTALMEPTIIMAVLGVL	386
NTDB id 1016	ACIAD RS01680 WP 004920476.1	AVLKIREDDVSTGQQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHVDGLTSMMEPLIMAILGLV	389
NTDB id 1059	ABD1 RS01610 WP 000279215.1	AVMKIREDDVATGQQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVVDGLTSMMEPLIMAILGLV	389
consensus		* * * * * ! * * * * * * * ! ! * * * * ! * * ! ! ! * ! * * * ! ! ! * ! * ! ! ! * * * ! * * ! * * ! * * ! * * ! * *	

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NTDB id 1029	TT RS02230 WP 011228203.1	VGMIIVACMEPLPLFKIIGTISVQ	406
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VGGLVVAMYLPINFNLMSVLG..	408
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VGGLVTAMYLPINFNLMSVLG..	407
NTDB id 1113	AAA85695.1 219..1451()	IGTLLVAMYLPINFNLGNVVA*	410
NTDB id 1112	NGFG RS09215 WP 003689811.1	IGTLLVAMYLPINFNLGNVVA..	410
NTDB id 1252	GCO85 RS07730 WP 011213805.1	VGGLVVAMYLPINFNLGSAV...	406
NTDB id 53695	AMEC673 RS14620 WP 014950403.1	IGGLIVAMYLPINFNLGNVV...	402
NTDB id 1198	PSJM300 03950 AFN76868.1	VGGLIVAMYLPINFNLGSAV...	405
NTDB id 1016	ACIAD RS01680 WP 004920476.1	VGGLVIVAMYLPINFNLGSAV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	VGGLVIVAMYLPINFNLGSAV...	408
consensus		* ! * * * * ! * ! ! * ! * * * * *	

- ☐ non conserved
- ☒ similar
- ☒ ≥ 50% conserved