

logo

NTDB id 1402 DSB67 RS12670 WP 010643257.1	MAKNGGFMALPPKPKYFAWEKDSAGKKYKGEYSATEAFARATRKQGLPDKIRKKSKSFEERSKKKITCKDIT	70
NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKTIIAPQIKNYRWKGINSSG..KKTSGNVLAMTEIEVRERLDAQHIKIKKKLKKGSISFITKI..SHRVKGGKDIT	71
NTDB id 1112 NGFG RS09215 WP 003689811.1	MKATQTLPLKKNYRWKGINSG..KKVSGQMLAISEIEVRDKLKDQHIQIKKKLKKGSVSLLARL..THR.VKSKDIT	73
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGF..SLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQEDIT	73
NTDB id 69625 UNDYM RS04035 WP 162039885.1	MAKNGGF..SLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQEDIT	74
NTDB id 1252 GC085 RS07730 WP 011213805.1	MATNLAKSAKSGQPKEQLYAWEGKDKFG..KVVVRGETRAGGEATVNATLRRQGILVTKLKKKNYI....SGKAITDKDIT	70
NTDB id 1198 PSJM300 03950 AFN76868.1	MDKNSPPLLTFHYQGINKAG..QKMEGDIQARSLAIADLRKQGIVTNKVVKKRKPLFDR..KNKKITQADIT	69
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAQKAIKNSVFTWEGLDLRQG..AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIA	72
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAVKKAQMPMPTFAYEGVDRKG..VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDIT	72
consensus	MAAKKTQVMPVFAYEGVDRKG..IKLKGELPARNMALAKVTLRKQGIVTIRTIREKRKNIFEGLLKKKKVPLDIA	72

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	IFTRQIATMIMTGVPIVQALKLVSENHKKAEKMSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQV	150
NTDB id 1169 A1552VC RS11075 WP 000648511.1	ILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSIQAQITKSVEAGTPLSKAMRTASAHFDTLVLDLVETGEMSGNLPEV	151
NTDB id 1112 NGFG RS09215 WP 003689811.1	VFTRQLSTMIAKAGPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES	153
NTDB id 1113 AAA85695.1 219..1451()	VFTRQLSTMIAKAGPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES	153
NTDB id 69625 UNDYM RS04035 WP 162039885.1	LFTRQLATMMKAGVPLLQSFDIVSKGHSNPSVSKLLQDIRGDTVETGTSLNAAFRKFPLYFDPLFCNLVGAGEQAGILEDL	154
NTDB id 1252 GC085 RS07730 WP 011213805.1	VFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPPLYFNEFCNLVDAGEKSGSLDIM	150
NTDB id 1198 PSJM300 03950 AFN76868.1	LFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDLQKQEVAAAGNSFASSLRKKPKQYFDDLYCNLVDSGEQSGSLETL	149
NTDB id 1059 ABD1 RS01610 WP 000279215.1	IFTRQLATMMKAGVPLVQGFIEVAEGLENPAMREVVVLGKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETM	152
NTDB id 1016 ACIAD RS01680 WP 004920476.1	IFTRQLATMMKAGVPLVQGFIEVAEGLENPAMRDVVLGLKNEVEGGSTFAGALRKYPQYFDNLFCSLVESGEQSGSLEIM	152
consensus	IFTRQLATMMKAGVPLVQGFIEVAEGLENPAMRDVVLGLKNEVEGGSTFAGALRKYPQYFDNLFCSLVESGEQSGSLEIM	152

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	LDRLATYKKEKTEALKAKKIKKALYPAIAIYVAIGTAYMMIWPFAKDYASFEFGAELPAETQVVMMSQYWIYIF	230
NTDB id 1169 A1552VC RS11075 WP 000648511.1	FERLATYREKSEQLRKAKVIKALIIYPMVVLVALGVSYLMLTRVPIFEFEKMFTEGFGADLPFTQMVNLNSAWTQNGGPFIG	231
NTDB id 1112 NGFG RS09215 WP 003689811.1	FERLATYREKSEQLRKAKVIKALIIYPSMVVLVALGVSYLMLTMVPIFEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAF	233
NTDB id 1113 AAA85695.1 219..1451()	LDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMIMIFVLPAFKEVYANMGAELPPLTQTVMMDMSDFVSYGMMVL	233
NTDB id 69625 UNDYM RS04035 WP 162039885.1	LDKLAIYKEKTQAIRKKVKKTALTYPVSVIAVAIGLVFVMIMIFVLPAFKEVYANMGAELPALTQTVMMDMSDFVSYGMMVL	234
NTDB id 1252 GC085 RS07730 WP 011213805.1	LTRLAIYKEKTMAIKAKIKSALTYPYIAILGIAFIVTAVIMIWVVPFAFKQAFSSFGAELPAPTILVMNISDNFVKYWIIF	230
NTDB id 1198 PSJM300 03950 AFN76868.1	LDKVATYKEKIEIKKKIKKALTYPYIAVMVVALLVTAGLLIYVVPQFESLFKGFAGADLPAMTRAVITMSEFMQAYWYIIF	229
NTDB id 1059 ABD1 RS01610 WP 000279215.1	LDRVATYKEKTEALKAKIKKAMNYPYIAVVLVAVIVTATILLIKVVPQFQDVAFNFGAELPAFTLMVIGLSEALQAWWYVVL	232
NTDB id 1016 ACIAD RS01680 WP 004920476.1	LDRVATYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPFTQMVVNMSKWMQYWFIMI	232
consensus	LDRLATYKKEKTEALKAKKIKKALYPAIAIYVAIGTAYMMIWPFAKDYASFEFGAELPAETQVVMMSQYWIYIF	232

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NTDB id 1402 DSB67 RS12670 WP 010643257.1	LSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAAGIPILTALKTTSKTSGNMHYQLAI	310
NTDB id 1169 A1552VC RS11075 WP 000648511.1	IAIAAAIFGLKALKRNSFQIRLKTSRIGLKFPIIGNVLAKASIAKFSRTLATSFSAAGIPILASLKTITAKTSGNVHFFETAI	311
NTDB id 1112 NGFG RS09215 WP 003689811.1	IALGFAIYGFRLKLRKRSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT	313
NTDB id 1113 AAA85695.1 219..1451()	IALGFAIYGFRLKLRKRSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT	313
NTDB id 69625 UNDYM RS04035 WP 162039885.1	GGLFGSIYFFFTQWRRSLKMQIFGMDRALLQAPIFGDIVRKGTIARWRTLATLFAAGVPLVESLDSVGAAGNAYVYLDAT	314
NTDB id 1252 GC085 RS07730 WP 011213805.1	GALGGVVYSFFYAKNHSLEFAQTIIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKAT	310
NTDB id 1198 PSJM300 03950 AFN76868.1	AGFVGAAYAFKQAHTRSEKFRNWFDRMLMKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFERSAT	309
NTDB id 1059 ABD1 RS01610 WP 000279215.1	IAIGAVIAAFALEAKKRSKKFRDGLDKLALKLPVIGDLVYKAIIRYSRTLATTFAGVPLIDALESTAGATNNVIYEKAV	312
NTDB id 1016 ACIAD RS01680 WP 004920476.1	LVIGAAIAGFLEAKKRSKRFRDQLDRLVLRPLVIGDLVYKAIIRYSRTLATTFAGVPLIDALASTAGATNNTVYEQAV	312
consensus	LSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAAGIPILTALKTTSKTSGNMHYQLAI	312

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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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Position	390	391	392
Sequence	EEVYRD ¹ TAAG ² CM ³ PM ⁴ YI ⁵ AM ⁶ RH ⁷ CV ⁸ FP ⁹ EL ¹⁰ V ¹¹ LQ ¹² VM ¹³ IG ¹⁴ EE ¹⁵ SG ¹⁶ RL ¹⁷ D ¹⁸ ML ¹⁹ NK ²⁰ IA ²¹ AI ²² YF ²³ EV ²⁴ DN ²⁵ TV ²⁶ DN ²⁷ LS ²⁸ KI ²⁹ LE ³⁰ PL ³¹ II ³² VL ³³ FG ³⁴ VV ³⁵ GG ³⁶	NEVYRD ¹ TAAG ² CM ³ PM ⁴ YI ⁵ AM ⁶ RN ⁷ TE ⁸ AF ⁹ PE ¹⁰ VL ¹¹ QVM ¹² IG ¹³ EE ¹⁴ SG ¹⁵ GL ¹⁶ DD ¹⁷ ML ¹⁸ NK ¹⁹ VAT ²⁰ IY ²¹ EF ²² EV ²³ DN ²⁴ TV ²⁵ DN ²⁶ LK ²⁷ LE ²⁸ PL ²⁹ II ³⁰ VL ³¹ FG ³² VV ³³ GG ³⁴	REI ¹ TR ² RV ³ IQ ⁴ GL ⁵ SM ⁶ TS ⁷ G ⁸ MR ⁹ AT ¹⁰ EL ¹¹ FP ¹² NM ¹³ LQ ¹⁴ MS ¹⁵ S ¹⁶ IG ¹⁷ EE ¹⁸ SG ¹⁹ SL ²⁰ DD ²¹ ML ²² NK ²³ AA ²⁴ E ²⁵ F ²⁶ Y ²⁷ E ²⁸ VD ²⁹ NA ³⁰ VG ³¹ RL ³² SA ³³ ME ³⁴ PI ³⁵ II ³⁶ VL ³⁷ GL ³⁸ VI ³⁹ GT ⁴⁰
Conservation	***	***	***

Position	1	2	3	4	5	6	7	8	9	10
407	L	V	I	M	Y	P	F	N	L	M
408	L	V	I	M	Y	P	F	N	L	M
410	L	V	I	M	Y	P	F	N	L	M
410	L	V	I	M	Y	P	F	N	L	M
411	L	V	I	M	Y	P	F	N	L	M
406	L	V	I	M	Y	P	F	N	L	M
405	L	V	I	M	Y	P	F	N	L	M
408	L	V	I	M	Y	P	F	N	L	M
408	L	V	I	M	Y	P	F	N	L	M

! * * ! ! ! ! ! * ! * * * * * * *

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