

NTDB id	Accession	Protein	Sequence	Score
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIIGDRRLGAILLDQGYLGDN	LDQLRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1168	A1552VC RS11070 WP 000957200.1			0
NTDB id 1293	VP RS12240 WP 005479695.1			0
NTDB id 1401	DSB67 RS12665 WP 010643259.1			0
NTDB id 1110	NGFG RS09235 WP 003689817.1			0
NTDB id 1251	GC085 RS07725 WP 011946523.1			0
NTDB id 1102174	Q9274 RS07745 WP 011408072.1			0
NTDB id 1058	ABD1 RS01615 WP 001274986.1			0
NTDB id 1018	ACIAD RS01685 WP 004920473.1			0
consensus				

NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	160
NTDB id 1168	A1552VC RS11070 WP 000957200.1	SIRPQTALNLQAFPPFALEGGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	0
NTDB id 1293	VP RS12240 WP 005479695.1		0
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NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1102174	Q9274 RS07745 WP 011408072.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Length	Consensus
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1168	A1552VC RS11070 WP 000957200.1	0	0
1293	VP RS12240 WP 005479695.1	0	0
1401	DSB67 RS12665 WP 010643259.1	0	0
1110	NGFG RS09235 WP 003689817.1	0	0
1251	GC085 RS07725 WP 011946523.1	0	0
1102174	Q9274 RS07745 WP 011408072.1	0	0
1058	ABD1 RS01615 WP 001274986.1	0	0
1018	ACIAD RS01685 WP 004920473.1	0	0
consensus			

[illegible]

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NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQARECKVKPLGCEVITELGCFASPDEVD	400
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NTDB id 1293 VP RS12240 WP 005479695.1	EESLIEQVKKASGISMPEALLSSGFFTSSELAEHLSSIFGTSQPELSQVEY	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EESLIEQVKKASGISMPEALLSSGFFQSHELTEHTSSVFCISCTSLNQVEY	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	AEHYYNESQA..CKEVLPLMFLSDGVI..SPKSLAALIARVFSYSILDLRHYP	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFVPMIDINCIDV	77
NTDB id 1102174 Q9274 RS07745 WP 011408072.1	ARTAMEQAAA..AKVPLPQWFAENRLVSASQLAAANA..VEFCMPLMDVSVFDA	79
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MQTALDAAKRAKQDVTAYLIEEVHLSPSLAEETISAEFAEPYFDLDVYDT	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MQQALEKAKKFKQDVPVYLLIDNFS..SPLTTIAETISLEFGPEPLDLGVFDP	77
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPETARRVYVVPVRLQGNLSLVVAMKDPPNVFALDDLKLTGKEILPAVMAEKDITIRLTERYFGEKGFEKLNK	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQQLGLRELITRYDALPIAKQCENLLLLAVSDPTLLQAEEEFRRFATGLQVELALADHRAALQAATIRRLYGRSISQGAANQ	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQQAEDDFRFATGLQVELVLADFRELSTAIRRLYGRSLSHEKSG	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLLAVADPTNQAEDDFRFATGLQVELVLADFRELTAATIRRLYGRSLGQKEKSG	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTETEQMVETHCVPVFRGDKVFFAVSDPTQMPQITQKTVSAACTAVELVIVEDDQLAGLLDWVGRSSTSLQLQEL	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEITQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSE	157
NTDB id 1102174 Q9274 RS07745 WP 011408072.1	NQNAVKLIVSEELIQKYHVLPLFKRCNRLFVGVSNPTQTRALDDIKFHTNLVVEPTILVDEDQIRRTLEQWQASNAFSGSSL	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLIKLRHRLPLIQRGQILYVATSNPSNTEADDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFDFND	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDKELIQKYRIMPLVHRGHVLYVATSNPTNTEADDAIRFNSKLLVEPTIIVHDKLERLLSEHVEETHFNFD	157
consensus	*****	

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NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKELISQDELANLVK...VSDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRRCDCGTLVETQQ	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADEINIEDLSQDESPPVSRYINQILLDAVRKGASDIHFEPYEKMYRVRRLRCDCGILLIETQQ	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIEDLSQDESPPVSRYINQILLDAVRKGASDIHFEPYENMYRVRRLRCDCGILLIETQQ	225
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NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLETSADD...EDQDIDTATSVTDAPITVKFVNKILLDAIRQGASDIHFEPYEREYRIRVRQDCGILHEVAT	234
NTDB id 1102174 Q9274 RS07745 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGGDSGVDAKGDDTPVVVKFVNKVLVDAIRRGASDIHFEPYEDDYRVRIRIDGILLKNVAK	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EEFDLDVN..LDGPTAQEDEEAPQGDAPITVKYINKLLDATERMGASDIHFEPYEKSYRVRVYRVDGVLRLQIAN	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EEFDLDVVE..VDPHTTDDDEDKCLKDEAPITVKYINKLLDATERMSASDIHFEPYEKSYRVRVYRVDGVLRLIAT	229
consensus	*****	

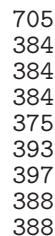
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NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSRRLSARIKILSKLDIAERRVPQDGRILKLNLQ.DTAIDMRVSTLPTLFGEKIVLRILDSSASLIDIDKLGYSEQ	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERRVPQDGRILKLNLQ.DTAIDMRVSTLPTLFGEKIVLRILDSSAALDINKLGYSDS	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDISEKRIPQDGRMLTFQKGGKPYDFRVSTLPTLFGEKIVMRILNSDAASLNDIQLGHEPF	295
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NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRIKIVMSQMDISEKRVPPQDGRILKLNLQSK.SKTIDFRVNSLPTLFGEKIVLRILDPASAMLGIDALGYEPE	308
consensus	*****	

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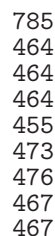
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consensus

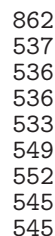
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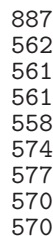
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NTDB id 1401 DSB67 RS12665 WP 010643259.1
NTDB id 1110 NGFG RS09235 WP 003689817.1
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NTDB id 1102174 Q9274 RS07745 WP 011408072.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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 non conserved
 similar
 $\geq 50\%$ conserved