

NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	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 1102117	Q9261 RS07770 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	Length
1306	DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	160
1168	A1552VC RS11070 WP 000957200.1		0
1293	VP RS12240 WP 005479695.1		0
1401	DSB67 RS12665 WP 010643259.1		0
1110	NGFG RS09235 WP 003689817.1		0
1251	GC085 RS07725 WP 011946523.1		0
1102117	Q9261 RS07770 WP 011408072.1		0
1058	ABD1 RS01615 WP 001274986.1		0
1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Sequence	Count
1306	DR RS10060 WP 027479822.1	GRTGGKLG ^{ER} LITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGGFHPGEEVLGSM	240
1168	A1552VC RS11070 WP 000957200.1	GRTGGKLG ^{ER} LITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGGFHPGEEVLGSM	0
1293	VP RS12240 WP 005479695.1		0
1401	DSB67 RS12665 WP 010643259.1		0
1110	NGFG RS09235 WP 003689817.1		0
1251	GC085 RS07725 WP 011946523.1		0
1102117	Q9261 RS07770 WP 011408072.1		0
1058	ABD1 RS01615 WP 001274986.1		0
1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Protein	Sequence	Score
NTDB id 1306	DR RS10060 WP 027479822.1	LRADALRL LAVPVD ETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGLGEQLVQEGLTSRDQL	320	
NTDB id 1168	A1552VC RS11070 WP 000957200.1	MLTNLVA TLRQAE LISATQ.	19	
NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLST ILRQKGLL TFSQ.	19	
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLST VLRQAGIL TFSQ.	19	
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLR ILVQNQVVTVEQ.	19	
NTDB id 1251	GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTK.	27	
NTDB id 1102117	Q9261 RS07770 WP 011408072.1	MNSVSTTNLVGITGIARRLVQDGALEETA.	29	
NTDB id 1058	ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFTGFFRR LVEEKH VSAAT.	27	
NTDB id 1018	ACIAD RS01685 WP 004920473.1	MS..AFTTPPKFSGFIRRLVEEGYVNAQN.	27	
consensus			*** *!***** *	

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NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQARECKVKPLGCEVITELGCFASPD	400
NTDB id 1168 A1552VC RS11070 WP 000957200.1	REALQVQAREGKVKPLGEVITELGFASPD	69
NTDB id 1293 VP RS12240 WP 005479695.1	EQAVVTQVSASGTSVPEALLSIFHAQELTEQLSHIFG	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EEELLHQVKASGISMPEALLSSGFFQSHELTEHSSVFC	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	EEELLHQVKASGISMPEALLSSGFFQSHELTEHSSVFC	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AEHYYNESQA.CKEVLPLMFLSDGVI.SPKSLAALIA	77
NTDB id 1102117 Q9261 RS07770 WP 011408072.1	AEHLHLKAAAEKISLLQYIVKNKILSAEQIALTA	79
NTDB id 1058 ABD1 RS01615 WP 001274986.1	ARTAMEQAAA.AKVPLPQWFAENRLVSASQLAA	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MQTALDAAKRAKQDVTAYLIEEVHLSPSLAE	77
consensus	MQALEKAKKFKQD.VPPLYIDNFS.SPLTTAEISLE	

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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPATARRVYVVPVRLQGNLSLVVAMKD	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQQLGLRELITRYDALPIAKQCNLLLLAVSD	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQQLGLRELITRHNALPLHRTPTSTLLLAV	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLLI	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTETHEQMVETHCVPVFRGDKVFF	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	CTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLAT	157
NTDB id 1102117 Q9261 RS07770 WP 011408072.1	NQNAVKLVSLELLQKYHVLPLFKRCNRLFVGV	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLLKHLRILPLIQRGQILYVAT	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDKLLIQKYRIMPLVHRGHVLYVAT	157
consensus	DPKVALMIPATARRVYVVPVRLQGNLSLVVAMKD	

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NTDB id 1306 DR RS10060 WP 027479822.1	ELA.....ERNKTQSSQEA.DLSVADESALVQV	547
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKELISQDELANLVK...VSDDELQSIEDLSQD	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADEINIEDLSQD	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIEDLSQD	225
NTDB id 1110 NGFG RS09235 WP 003689817.1	GEGQ.E.....EESHTLYIDNEEAEDGPVPR	215
NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLETSADD...EDQDIDTATSVT	234
NTDB id 1102117 Q9261 RS07770 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGGDSGVDAKG	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EE.FDLVDN..LDGPTAQEDEEAPQG	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EE.LDLDVD..VDPHTTDDDEDKCLK	229
consensus	ELA.....ERNKTQSSQEA.DLSVADESALVQV	

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NTDB id 1306 DR RS10060 WP 027479822.1	FPKGAAQQIMARLKIMGHLDIAERRVPQDGRVRF	625
NTDB id 1168 A1552VC RS11070 WP 000957200.1	PASHLSRRRLAARIKILSKLDIAERRVPQDGRIL	304
NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSRRLSARIKILSKLDIAERRVPQDGRIL	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERRVPQDGRIL	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDISEKRIPQDGRM	295
NTDB id 1251 GC085 RS07725 WP 011946523.1	PPASLSSRITARIKIVMSNLDISERRIPQDGGF	313
NTDB id 1102117 Q9261 RS07770 WP 011408072.1	APVKLSQRILARIKIVMSQLDIAEKRVPPQDGR	317
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PPLQLANRLASRIKIVMSQMDISEKRVPPQDGR	308
NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRIKIVMSQMDISEKRVPPQDGR	308
consensus	FPKGAAQQIMARLKIMGHLDIAERRVPQDGRVRF	

 non conserved
 similar
 $\geq 50\%$ conserved