

NTDB id	Accession	Protein	Sequence	Score
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	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 1102211	Q9285 RS06770 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		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 1102211	Q9285 RS06770 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
1306	DR RS10060 WP 027479822.1	GRTGGKLG ^{ER} LITHGYITDAQLQVALDAQQQTGEALGATLISQRAIT ^{ED} QLYEVLAEQEGTTFLPNPSGGFHPGEEVLGSM	240
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
1102211	Q9285 RS06770 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	LRADALRLLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGR	LGEQLVQEGLSRDQL	320
NTDB id 1168	A1552VC RS11070 WP 000957200.1	MLTNLVAIILRQAELISATQ.		19
NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTF SQ.		19
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQ.		19
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQ.		19
NTDB id 1251	GC085 RS07725 WP 011946523.1	MALATEEYRLQGIGQLLVLEKLLDKTK.		27
NTDB id 1102211	Q9285 RS06770 WP 011408072.1	MNSVSTTNLVGITGIARRLVQDGALEETA.		29
NTDB id 1058	ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFTGFFRRLVEEKHVSAAAT.		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	REALQVQARECKVKPLGCEVITELGCFASPDEVD	400
NTDB id 1168 A1552VC RS11070 WP 000957200.1	EQAVVTQVSASGTSVPEALLSLSIFHAQELTEQLSHIFGPETDLSRYDY	69
NTDB id 1293 VP RS12240 WP 005479695.1	EESLIEQVKKASGISMPEALLSSGFFTSSELAEHLSSIFGTSQPELSQVEY	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EESLIEQVKKASGISMPEALLSSGFFQSHELTEHSSVFCISCTSLNQVEY	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	AEHYYNESQA..CKEVLPLMLFSDGVI..SPKSLAALIARVFSYSILDLRHYP	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQAQNFVPMIDINCIDV	77
NTDB id 1102211 Q9285 RS06770 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	MQQALEKAKKFQKDVPVYLLIDNFS..SPLTTIAETISLEFGPEPLDLGVFDP	77
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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPETARRVYVVPVRLQGNLSLVVAMKDPRNVFALDDLKLTGKEILPAVMAEKDITIRITERYFGGKGFELKLNK	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQQLGLRELITRYDALPIAKQCENLLLLAVSDPTLLQAEEEFRRFATGLQVELALADHRAALQAATIRRLYGRSISQGAANQ	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQQLGLRELITRHNALPLHRTPTSTLLLAVADPTNQQAEDDFRFATGLQVELVLADFRELSTAIRRLYGRSLSHEKSG	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLLIIVADPTNIQAEDDFRFATGLQVELVLADFRELTAATIRRLYGRSLGQKEKSG	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTIEHQMVFEHCVVFFRRGDKVFFAVSDPTQMPQI..QKTVSAACTAVELVIVEDDQLAGLLDWVGRSSTLLQEL	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSE	157
NTDB id 1102211 Q9285 RS06770 WP 011408072.1	NQNAVKLIVSEELIQKYHVLPPLFKRCNRLFVGVSNPTQTRALDDIKFHTNLVVEPTILVDEDQIRRTLEQWQASNAFSGSSL	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLLKHRILPLIQRGQILYVATSNPSNTEADDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFDFND	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDKELIQKYRIMPLVHRGHVLYVATSNPTNTEADDAIRFNSKLLVEPTIIVHDKLERLLSEHVEETHFNFD	157
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NTDB id 1306 DR RS10060 WP 027479822.1	ELA.....ERNKTQQSQEADLSVADESALVQVVDSTIREAALQDASDIHETTEDAVKVRVRLDGALREQNS	547
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKELISQDELANLVK...VSDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRRCDCGLVETQQ	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADEINIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYKMYRVRRLRCDCGLIETQQ	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYKMYRVRRLRCDCGLIETQQ	225
NTDB id 1110 NGFG RS09235 WP 003689817.1	GEGQ.E.....EESHTLYIDNEEAEDGPVPRFIHKTLSDALRSASDIHFEPYEHMARTFRVDCGLREVQ	215
NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLETSADD...EDQDIDTATSVTDAPITVKFVNKLLDAIRQGASDIHFEPYEREYRIRVRCDCGLHEVAT	234
NTDB id 1102211 Q9285 RS06770 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGGDSGVDAKGDDTPVVVKFVNKVLVDAIRRGASDIHFEPYEDDYRVRIRIDGILLKNVAK	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EE..FDLDVN..LDGPTAQEDEE..EAPQGDEAPITVKYINKLLDAIRMGASDIHFEPYEKSYRVRVYRDCGLRQIAN	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EE..LDLDVE..VDPHTTDDDEDKCLKDEAPITVKYINKLLDAIRMSASDIHFEPYEKSYRVRVYRDCGLRLIAT	229
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	FPKGAAQQIMARLIKIMGHLDIAERRVPQDGRVRF..KKSIDLDLRLSTLPTVYGEKAVMRLLQKASNIPELEQLCFSEY	625
NTDB id 1168 A1552VC RS11070 WP 000957200.1	PASHLSRRRLAARIKILSKLDIAERRVPQDGRILKLSH..DTAIDMRVSTLPTLWGEKIVLRILDSSAANLIDTKLGYNPQ	304
NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSRRLSARIKILSKLDIAERRVPQDGRILKLNQ..DTAIDMRVSTLPTLTFGEKIVLRILDSSASLIDIDKLGYSEQ	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERRVPQDGRILKLNQ..DTAIDMRVSTLPTLTFGEKIVLRILDSSAALDINKLGYSDS	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDISEKRIPQDGRMQLTFQKGGKPVDFRVSTLPTLFGKIVMRILNSDAASLNDIQLGHEPF	295
NTDB id 1251 GC085 RS07725 WP 011946523.1	PPASLSSRITARIKIVMSNLDISERRIPQDGGFKMKISK..SRAIDFRVSTCPTSAGEKVMVRVLDSGAAKLGIEALGFNPV	313
NTDB id 1102211 Q9285 RS06770 WP 011408072.1	APVKLSQRITARIKIVMSQLDIAEKRVPPQDGRILKLSK..TKQIDFRVSTLPTLFGKIVLRILDGSAAKLGIDKLGYEPD	317
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PPLQLANRLASRIKIVMSQMDISEKRVPPQDGRILKLSK..SKAIDFRVNSLPTLFGKIVLRILDPSSAMLGIDALGYEED	308
NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRIKIVMSQMDISEKRVPPQDGRILKLSK..SKTIDFRVNSLPTLFGKIVLRILDPASAMLGIDALGYEPE	308
consensus	*****	

 non conserved
 similar
 $\geq 50\%$ conserved