

NTDB id	Accession	Species	Protein	Sequence	Score
NTDB id 1306	DR RS10060	WP 027479822.1	MALSI	CDRRRLCAIILLDQGYLGNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	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	GCO85	RS07725	WP 011946523.1		0
NTDB id 163852	ATY45	RS15765	WP 011408072.1		0
NTDB id 1058	ABD1	RS01615	WP 001274986.1		0
NTDB id 1018	ACIAD	RS01685	WP 004920473.1		0
consensus					0

NTDB id	Accession	Length	Consensus
1306	DR RS10060 WP 027479822.1	160	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA
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	
163852	ATY45 RS15765 WP 011408072.1	0	
1058	ABD1 RS01615 WP 001274986.1	0	
1018	ACIAD RS01685 WP 004920473.1	0	
consensus			

NTDB id	Accession	Species	Gene	Protein	Consensus
1306	DR	RS10060	WP_027479822.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVLGSM	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
163852	ATY45	RS15765	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	LRADALRLLAVPVDETEQGVTVLTS	320
NTDB id 1168	A1552VC	RS11070	WP_000957200.1	LRADALRLLAVPVDETEQGVTVLTS	19
NTDB id 1293	VP	RS12240	WP_005479695.1	MLTNLVA	19
NTDB id 1401	DSB67	RS12665	WP_010643259.1	MHSNLSTILRQKGLTFSQ	19
NTDB id 1110	NGFG	RS09235	WP_003689817.1	MLTNLSTVLRQAGILTFSQ	19
NTDB id 1251	GCO85	RS07725	WP_011946523.1	MSVGLLRILVQNQVVTVEQ	19
NTDB id 163852	ATY45	RS15765	WP_011408072.1	MALATEEYRLQGIGQLLVLEKLLDKTK	27
NTDB id 1058	ABD1	RS01615	WP_001274986.1	MNSVSTTNLVGITGIARRLVQDGALEETIA	29
NTDB id 1018	ACIAD	RS01685	WP_004920473.1	MS..ALHTSPKFTGFFRRLVEEKHVSAAAT	27
consensus				MS..AFTTPPKFSGFIRRLVEEGYVNAQN	27

logo

NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQAREGKVKPLGEVITELGFASPD	400
NTDB id 1168 A1552VC RS11070 WP 000957200.1	REALQVQAREGKVKPLGEVITELGFASPD	69
NTDB id 1293 VP RS12240 WP 005479695.1	EQAVVTQVSASGTSVPEALL	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EESLIEQVKASGISMPEALL	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	AEHYYNESQA.GKEVLPM	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AIELHKLAAAEKISLLQY	77
NTDB id 163852 ATY45 RS15765 WP 011408072.1	ARTAMEQAAAAKVPLPQWFAENRLVSASQLAAANAVEFGMPLMDVSVF	79
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MQTALDAAKRAKQDVTAYLIEEVHLSPLSLAEETISAEFAEYPFDLDVYDT	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MQQALEKAKKFKQDITVPVLI	77
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIP	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQLGLRELITRYDALPIAKQGNLL	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQLGLRELITRHNALPLHRT	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTGLGLRDLITRHNALPLNRTSST	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTEEQMV	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFS	157
NTDB id 163852 ATY45 RS15765 WP 011408072.1	NQNAVKLVSEELIKKYHVLPLFK	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLILK	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKYRIMPLVHR	157
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	ELA.....ERNKTQSSQ	547
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKEISQDELANLVK...VSDDELQSI	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADENI	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGADEI	225
NTDB id 1110 NGFG RS09235 WP 003689817.1	GEGQ.E.....EESHTLYI	215
NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLEISADD...EDQDIDTATS	234
NTDB id 163852 ATY45 RS15765 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGG	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EE.FDLDVN...LDGPTAQE	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EE.LDLDVE...VDPHTTDD	229
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	FPGKAAQQIMARLKT	625
NTDB id 1168 A1552VC RS11070 WP 000957200.1	PASHLSRRLAARIKILSKLDIAERRLPQDGR	304
NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSSRLSARIKILSKLDIAERRLPQDGR	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERRLPQDGR	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDIS	295
NTDB id 1251 GC085 RS07725 WP 011946523.1	PPASLSSRITARIKIVMSNLDISERRIPQDGG	313
NTDB id 163852 ATY45 RS15765 WP 011408072.1	APVKLSQRIAAARIKIVMSQLDIAEKRV	317
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PPLQLANRLASRLKVMSQMDISEKRV	308
NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRLKVMSQMDISEKRV	308
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1
NTDB id 1168 A1552VC RS11070 WP 000957200.1
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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