

NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	MALSI ¹ GD ¹ RR ¹ LG ¹ AI ¹ LL ¹ DQ ¹ YL ¹ GD ¹ N ¹ DL ¹ QR ¹ AL ¹ ER ¹ H ¹ SE ¹ V ¹ GG ¹ RL ¹ AD ¹ VL ¹ ID ¹ SG ¹ MV ¹ GE ¹ K ¹ RI ¹ AR ¹ AI ¹ EE ¹ AL ¹ GI ¹ PL ¹ VN ¹ LL ¹ AV ¹ QP ¹ DP ¹ AA ¹ LR ¹	80
NTDB id 1168	A1552VC RS11070 WP 000957200.1	MALSI ¹ GD ¹ RR ¹ LG ¹ AI ¹ LL ¹ DQ ¹ YL ¹ GD ¹ N ¹ DL ¹ QR ¹ AL ¹ ER ¹ H ¹ SE ¹ V ¹ GG ¹ RL ¹ AD ¹ VL ¹ ID ¹ SG ¹ MV ¹ GE ¹ K ¹ RI ¹ AR ¹ AI ¹ EE ¹ AL ¹ GI ¹ PL ¹ VN ¹ LL ¹ AV ¹ QP ¹ DP ¹ AA ¹ LR 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 404707	IX0134 RS15760 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	Score
NTDB id 1306	DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	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 404707	IX0134 RS15760 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	Score
NTDB id 1306	DR RS10060 WP 027479822.1	GRTGGKLGRLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEEGTTFLPNPSGFHPGEEVLGSM	240
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 404707	IX0134 RS15760 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	Protein	Sequence	Score
NTDB id 1306	DR RS10060	WP 027479822.1	LRADALRLLAVPVDETEQGVTVLTSDFRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGLGEQLVQEGLTSRDQL	320
NTDB id 1168	A1552VC	RS11070 WP 000957200.1	MLTNLVAILRQAEILISATQ.	19
NTDB id 1293	VP RS12240	WP 005479695.1	MHSNLTILRQKGLLTFSQ.	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 404707	IX0134	RS15760 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			*** *!***** *	

logo

NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQAREGKVKPLGEVITELGFASPD	400
NTDB id 1168 A1552VC RS11070 WP 000957200.1	EQAVVTQVSASGTSVPEALL	69
NTDB id 1293 VP RS12240 WP 005479695.1	EESLIEQVKASGISMPEALLSSGFF	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	EESLIEQVKASGISMPEALLSSGFFQ	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	AEHYYNESQA..CKEVLPLMFLSDG	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	AIELHKLAAAEKISLLQYIVKNKIL	77
NTDB id 404707 IX0134 RS15760 WP 011408072.1	ARTAMEQAAAANKVPLPQWFAENRL	79
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MQTALDAAKRAKQDVTAYLIEEVHL	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MQQALEKAKKFQKDVPVYLLDNFNS	77
consensus	*****	

logo

NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPETARRVYVVPVRLQGN	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQQLGLRELITRYDALPIAKQCN	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQQLGLRELITRHNALPLHRTPT	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSST	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTETEHQMVETHCVPVFRG	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	CTIPVNLVNEKLIKRRHAMVPLFSRGT	157
NTDB id 404707 IX0134 RS15760 WP 011408072.1	NQNAVKLIVSEELIQKYHVLPLFKRCN	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLIKLRHRLPLLIQRGQ	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDKELIQKYRIMPLVHRGHV	157
consensus	*****	

logo

NTDB id 1306 DR RS10060 WP 027479822.1	ELA.....ERNKTQSQEADLSVADE	547
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKELISQDELANLVK...VSDDELQSI	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADEINIED	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIED	225
NTDB id 1110 NGFG RS09235 WP 003689817.1	GEGQ.E.....EESHTLYIDNEEAED	215
NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLETSADD...EDQDIDT	234
NTDB id 404707 IX0134 RS15760 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGGDSG	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EE.FDLVDN..LDGPTAQEDEE	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EE.LDLDVD..VDPHTTDDDED	229
consensus	*****	

logo

NTDB id 1306 DR RS10060 WP 027479822.1	FPKGAAQQIMARLIKIMGHLDIAERR	625
NTDB id 1168 A1552VC RS11070 WP 000957200.1	PASHLSRRRLAARIKILSKLDIAERR	304
NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSRRLSARIKILSKLDIAERR	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERR	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDISEKR	295
NTDB id 1251 GC085 RS07725 WP 011946523.1	PPASLSSRITARIKIVMSNLDISERR	313
NTDB id 404707 IX0134 RS15760 WP 011408072.1	APVKLSQRITARIKIVMSQLDIAEKRV	317
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PPLQLANRLASRIKIVMSQMDISEKR	308
NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRIKIVMSQMDISEKR	308
consensus	*****	

logo

NTDB id 1306 DR RS10060 WP 027479822.1

NTDB id 1168 A1552VC RS11070 WP 000957200.1

NTDB id 1293 VP RS12240 WP 005479695.1

NTDB id 1401 DSB67 RS12665 WP 010643259.1

NTDB id 1110 NGFG RS09235 WP 003689817.1

NTDB id 1251 GC085 RS07725 WP 011946523.1

NTDB id 404707 IX0134 RS15760 WP 011408072.1

NTDB id 1058 ABD1 RS01615 WP 001274986.1

NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

Sequence logo for the first motif. The logo shows the conservation of amino acids across 10 sequences. The consensus sequence is highlighted in red at the bottom.

705

384

384

384

375

393

397

388

388

logo

NTDB id 1306 DR RS10060 WP 027479822.1

NTDB id 1168 A1552VC RS11070 WP 000957200.1

NTDB id 1293 VP RS12240 WP 005479695.1

NTDB id 1401 DSB67 RS12665 WP 010643259.1

NTDB id 1110 NGFG RS09235 WP 003689817.1

NTDB id 1251 GC085 RS07725 WP 011946523.1

NTDB id 404707 IX0134 RS15760 WP 011408072.1

NTDB id 1058 ABD1 RS01615 WP 001274986.1

NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

Sequence logo for the second motif. The logo shows the conservation of amino acids across 10 sequences. The consensus sequence is highlighted in red at the bottom.

785

464

464

464

455

473

476

467

467

logo

NTDB id 1306 DR RS10060 WP 027479822.1

NTDB id 1168 A1552VC RS11070 WP 000957200.1

NTDB id 1293 VP RS12240 WP 005479695.1

NTDB id 1401 DSB67 RS12665 WP 010643259.1

NTDB id 1110 NGFG RS09235 WP 003689817.1

NTDB id 1251 GC085 RS07725 WP 011946523.1

NTDB id 404707 IX0134 RS15760 WP 011408072.1

NTDB id 1058 ABD1 RS01615 WP 001274986.1

NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

Sequence logo for the third motif. The logo shows the conservation of amino acids across 10 sequences. The consensus sequence is highlighted in red at the bottom.

862

537

536

536

533

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552

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545

logo

NTDB id 1306 DR RS10060 WP 027479822.1

NTDB id 1168 A1552VC RS11070 WP 000957200.1

NTDB id 1293 VP RS12240 WP 005479695.1

NTDB id 1401 DSB67 RS12665 WP 010643259.1

NTDB id 1110 NGFG RS09235 WP 003689817.1

NTDB id 1251 GC085 RS07725 WP 011946523.1

NTDB id 404707 IX0134 RS15760 WP 011408072.1

NTDB id 1058 ABD1 RS01615 WP 001274986.1

NTDB id 1018 ACIAD RS01685 WP 004920473.1

consensus

Sequence logo for the fourth motif. The logo shows the conservation of amino acids across 10 sequences. The consensus sequence is highlighted in red at the bottom.

887

562

561

561

558

574

577

570

570

 non conserved
 similar
 $\geq 50\%$ conserved