

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	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 1101980 Q9278 RS15170 WP 011408072.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

logo

NTDB id 1306 DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIIVVPSGASDA	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 GCO85 RS07725 WP 011946523.1		0
NTDB id 1101980 Q9278 RS15170 WP 011408072.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	GRTGGKLGGERLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSCGFHPGEEVLGSM	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 GCO85 RS07725 WP 011946523.1		0
NTDB id 1101980 Q9278 RS15170 WP 011408072.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

logo

NTDB id 1306 DR RS10060 WP 027479822.1	LRADALRLLAVPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPQGRIGEQLVQECTLSRDQL	320
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLINLVALRQAEILSATQ.	19
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTLRQKGLTFSQ.	19
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQ.	19
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLRLVLQNQVITVEQ.	19
NTDB id 1251 GCO85 RS07725 WP 011946523.1	MALATEEYRLQCTGQLLVLEKLLDKTK.	27
NTDB id 1101980 Q9278 RS15170 WP 011408072.1	MNSVSTTNLVGITCIARRLVQDGALEETA.	29
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFTGFFRRLVEEKHVSAAAT.	27
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MS..AFTTPPKFSCFIRRLVEECYVNAQN.	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	EESLIEQVKKASGISMPEALLSSGFFTSSELAEHLSSIFGSLSQPEYSQVEY	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 1101980 Q9278 RS15170 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	MQQALEKAKKFKQDVPVYLIDNFS..SPLTTIAETISLEFGPEPLDLGVFDP	77
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPETARRVYVVPVRLQGNLSLVVAMKDPRNVFALDDLKLTGKEILPAVMAEKDITIRITERYFGKGFKEKLNK	480
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQQLGLRELITRYDALPIAKQCENLALLAVSDPTLLQAEEEFRRFATGLQVELALADHRAALQAATIRRLYGRSISQGAANQ	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQQLGLRELITRHNALPLHRTPTSTLLLAVADPTNQQAEDDFRFATGLQVELVLADFRELSTAIRRLYGRSLSHEKSG	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLLIIVADPTNIIQAEDDFRFATGLQVELVLADFRELTAATIRRLYGRSLGQKEKSG	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTETEQMVETHCVPVFRGDKVFFAVSDPTQMPQI..QKTVSAACTAVELVIVEDDQLAGLLDWVGRSSTLLQEL	148
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSE	157
NTDB id 1101980 Q9278 RS15170 WP 011408072.1	NQNAVKLIVSEELIQKYHVLPPLFKRCNRLFVGVSNPTQTRALDDIKFHTNLVVEPTILVDEDQIRRTLEQWQASNA..SFGSSL	159
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLIKLRHRLPLIQRGQILYVATSNPSNTEADDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESS..SDFDND	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDKELIQKYRIMPLVHRGHVLYVATSNPTNTEADDAIRFNSKLLVEPTIIVHDKLERLLSEHVEETHFNFD	157
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	ELA.....ERNKTQQSQEADLSVADESALVQVVDSTIREAALQDASDIHETTEDAVKVRVRLDGALREQNS	547
NTDB id 1168 A1552VC RS11070 WP 000957200.1	GKELISQDELANLVK...VSDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRRCDCGILVETQQ	225
NTDB id 1293 VP RS12240 WP 005479695.1	LKEINQEELASLVD...VGADEINIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYEKMYRVRRLRCDCGILVETQQ	225
NTDB id 1401 DSB67 RS12665 WP 010643259.1	LKEINQDELAGLVD...IGDEIENIEDLSQDESPPVSRFINQVLLDAVRKGASDIHFEPYENMYRVRRLRCDCGILVETQQ	225
NTDB id 1110 NGFG RS09235 WP 003689817.1	GEGQ.E.....EESHTLYIDNEEAEDGPVPRFIHKTLSDALRSASDIHFEPYEHMARIRFRVDCGQLEVVQ	215
NTDB id 1251 GC085 RS07725 WP 011946523.1	YVEDSGDLEGLETSADD...EDQDIDTATSVTDAPITVKFVNKLLDAIRQGASDIHFEPYEREYRIRVRQDCGILHEVAT	234
NTDB id 1101980 Q9278 RS15170 WP 011408072.1	GNDD.EEMGDLDVSTGDEDMGAGGDSGVDAKGDDTPVVVKFVNKVLVDAIRRGASDIHFEPYEDDYRVRIRIDGILKNVAK	238
NTDB id 1058 ABD1 RS01615 WP 001274986.1	EE..FDLDVN..LDGPTAQEDEE..EAPQGDEAPITVKYINKLLDAIRMGASDIHFEPYEKSYRVRVYRVDGVLRLQIAN	229
NTDB id 1018 ACIAD RS01685 WP 004920473.1	EE..LDLDVE..VDPHTTDDDED..DKLKDAPITVKYINKLLDAIRMSASDIHFEPYEKSYRVRVYRVDGVLRLIAT	229
consensus	*****	

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NTDB id 1306 DR RS10060 WP 027479822.1	FPKGAAQQIMARLIKIMGHLDIAERRVPQDGRVRF..KKGSIDLRLSTLPTVYGEKAVMRLLQKASNIPELEQLCFSEY	625
NTDB id 1168 A1552VC RS11070 WP 000957200.1	PASHLSRRRLAARIKILSKLDIAERRVPQDGRILKLSH..DTAIDMRVSTLPTLWGEKIVLRILDSSAANLIDTKLGYNPQ	304
NTDB id 1293 VP RS12240 WP 005479695.1	PPNHLSRRLSARIKILSKLDIAERRVPQDGRILKLNQ..DTAIDMRVSTLPTLFGEKIVLRILDSSASLIDIDKLGyseQ	304
NTDB id 1401 DSB67 RS12665 WP 010643259.1	PPSHLSRRLSARIKILSKLDIAERRVPQDGRILKLNQ..DTAIDMRVSTLPTLFGEKIVLRILDSSAALDINKLGYSDS	304
NTDB id 1110 NGFG RS09235 WP 003689817.1	PPIAVRGQLASRIKIVMSRLDISEKRIPQDGRMQLTFQKGGKIPVDFRVSTLPTLFGEKIVMRILNSDAASLNDIQLGHEPF	295
NTDB id 1251 GC085 RS07725 WP 011946523.1	PPASLSSRITARIKIVMSNLDISERRIPQDGGFKMKISK..SRAIDFRVSTCPTSAGEKVMVRVLDSGAAKLGIEALGFNPV	313
NTDB id 1101980 Q9278 RS15170 WP 011408072.1	APVKLSQRITARIKIVMSQLDIAEKRVPPQDGRILKLSK..TKQIDFRVSTLPTLFGEKIVLRILDGSAAKLGIDKLGYPEP	317
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PPLQLANRLASRIKIVMSQMDISEKRVPPQDGRILKLSK..SKAIDFRVNSLPTLFGEKIVLRILDPSSAMLGIDALGYEED	308
NTDB id 1018 ACIAD RS01685 WP 004920473.1	PPLQLATRLASRIKIVMSQMDISEKRVPPQDGRILKLSK..SKTIDFRVNSLPTLFGEKIVLRILDPASAMLGIDALGYEPE	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 1101980 Q9278 RS15170 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 indicated 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 1101980 Q9278 RS15170 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 indicated 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 1101980 Q9278 RS15170 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 indicated at the bottom.

862

537

536

536

533

549

552

545

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 1101980 Q9278 RS15170 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 indicated at the bottom.

887

562

561

561

558

574

577

570

570

 non conserved
 similar
 $\geq 50\%$ conserved