

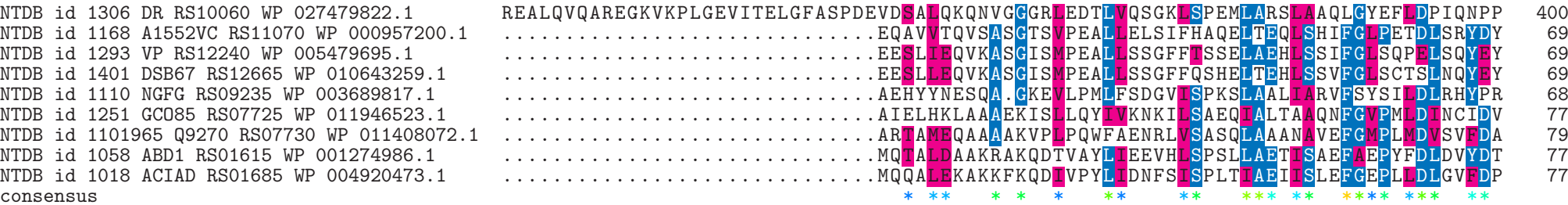
NTDB id	Accession	Protein	Sequence	Score
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80	
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0	
NTDB id 1293	VP RS12240 WP 005479695.1		0	
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0	
NTDB id 1110	NGFG RS09235 WP 003689817.1		0	
NTDB id 1251	GC085 RS07725 WP 011946523.1		0	
NTDB id 1101965	Q9270 RS07730 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 1101965	Q9270 RS07730 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
1101965	Q9270 RS07730 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	MHSNLSITILRQKGLLTFSQ.		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 1101965	Q9270 RS07730 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



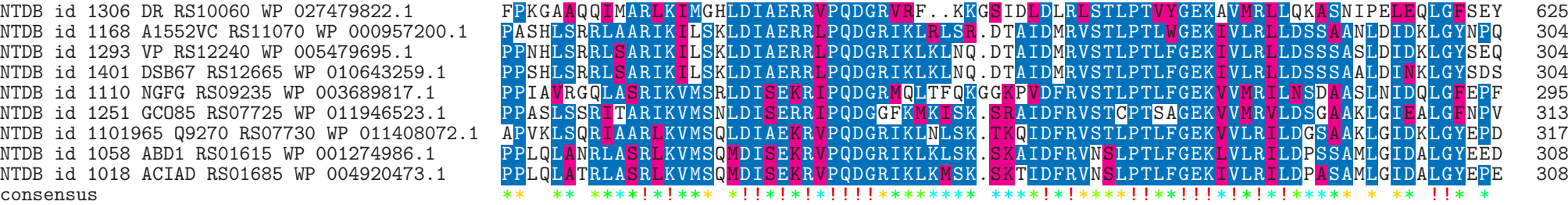
logo



logo



logo



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 1101965 Q9270 RS07730 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 1101965 Q9270 RS07730 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 1101965 Q9270 RS07730 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

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 1101965 Q9270 RS07730 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