

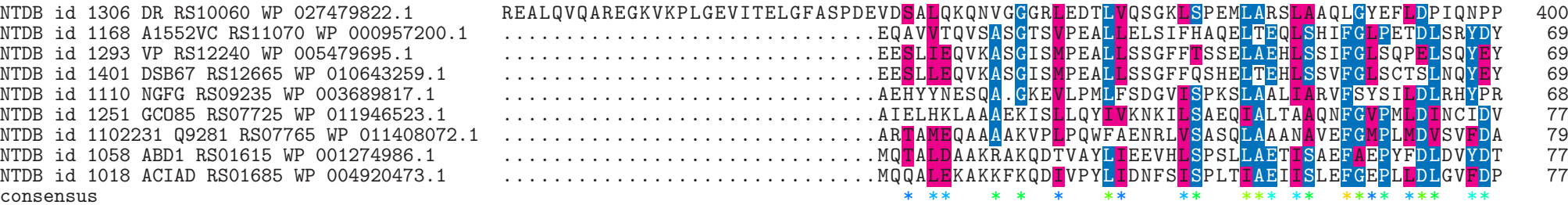
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NTDB id 1306	DR RS10060 WP 027479822.1	MALSIQDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
NTDB id 1293	VP RS12240 WP 005479695.1		0
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1102231	Q9281 RS07765 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	Length
NTDB id 1306	DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMMAIATHYPELGLEIVVPSGASDA	160
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NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1102231	Q9281 RS07765 WP 011408072.1		0
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NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM	240
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NTDB id 1102231	Q9281 RS07765 WP 011408072.1	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM	0
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consensus			

NTDB id	Accession	Protein	Sequence	Score
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NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLST	ILRQKGLLTF SQ	19
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLST	VL RQAGILTF SQ	19
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLR	ILVQNQVVTVEQ	19
NTDB id 1251	GC085 RS07725 WP 011946523.1	MALATEEYRLQ	GIGQLLVLEKLLDKTK	27
NTDB id 1102231	Q9281 RS07765 WP 011408072.1	MNSVSTTNLVGI	TGIARRLVQDGALEETA	29
NTDB id 1058	ABD1 RS01615 WP 001274986.1	MS..ALHTSPKFT	TGFFRRLVEEKHVSAAT	27
NTDB id 1018	ACIAD RS01685 WP 004920473.1	MS..AFTTPPKF	SGFIRRLVEEGYVNAQN	27
consensus			*** *!***** *	

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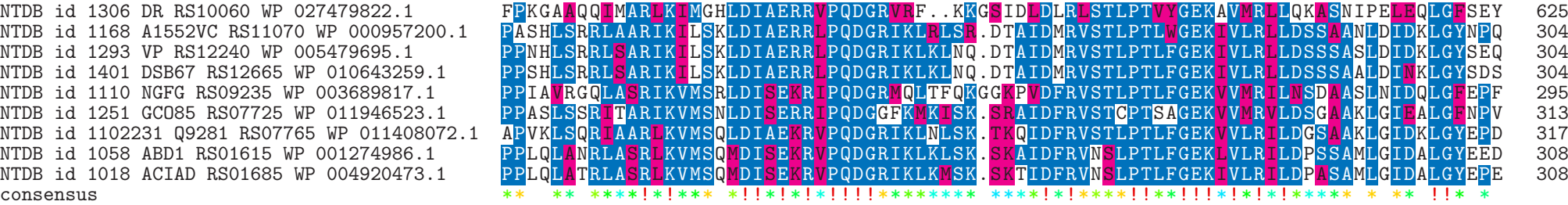
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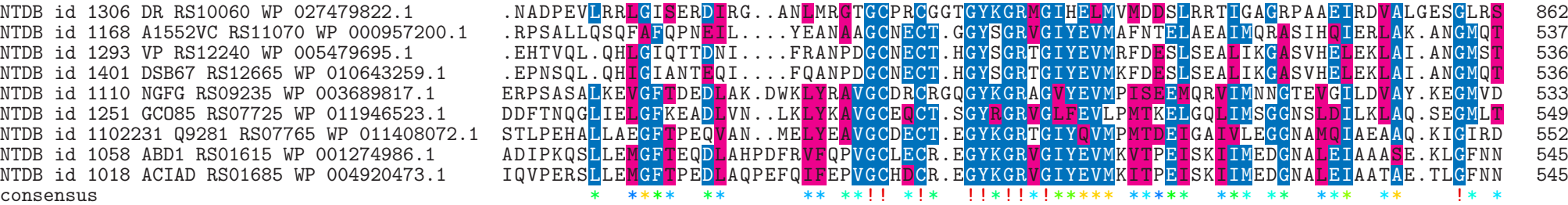
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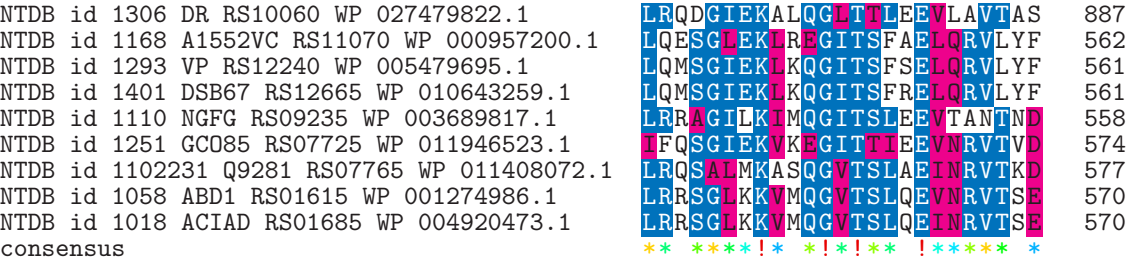
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 non conserved
 similar
 $\geq 50\%$ conserved