

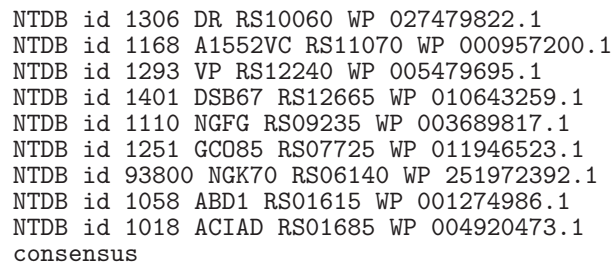
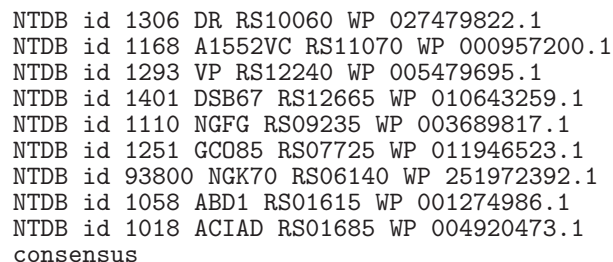
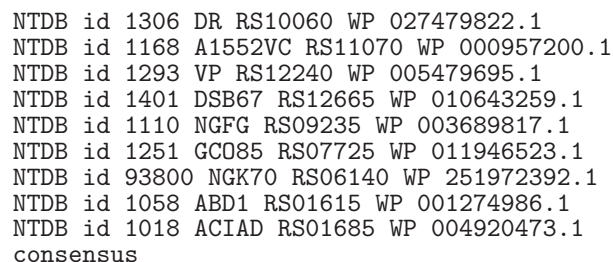
NTDB id	Accession	Sequence	Count
NTDB id 1306	DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
NTDB id 1293	VP RS12240 WP 005479695.1		0
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1110	NGFG RS09235 WP 003689817.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 93800	NGK70 RS06140 WP 251972392.1		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	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	160
NTDB id 1168	A1552VC RS11070 WP 000957200.1	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGASDA	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 93800	NGK70 RS06140 WP 251972392.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
consensus			

NTDB id	Accession	Length	Consensus
1306	DR RS10060 WP 027479822.1	240	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1168	A1552VC RS11070 WP 000957200.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1293	VP RS12240 WP 005479695.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1401	DSB67 RS12665 WP 010643259.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1110	NGFG RS09235 WP 003689817.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1251	GC085 RS07725 WP 011946523.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
93800	NGK70 RS06140 WP 251972392.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1058	ABD1 RS01615 WP 001274986.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
1018	ACIAD RS01685 WP 004920473.1	0	GRTGGKLG ER LITHGYITDAQLQVALDAQQTGEALGATLISQRAIT ED QLYEVLA AE QEGTTFLPNPSGGFHPGEEVLGSM
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NTDB id	Accession	Sequence	Score
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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
93800	NGK70 RS06140 WP 251972392.1	M	1
1058	ABD1 RS01615 WP 001274986.1		0
1018	ACIAD RS01685 WP 004920473.1		0
consensus			

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 93800 NGK70 RS06140 WP 251972392.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
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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
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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus



 non conserved
 similar
 $\geq 50\%$ conserved