

logo

NTDB id 1306 DR RS10060 WP 027479822.1	MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAALR	80
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
NTDB id 1468 ASU2 RS05090 WP 014991734.1		0
NTDB id 34257 D7S RS08000 WP 005540457.1		0
NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	SIRPQTALNLQAFPPFALEGDRRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIWPVSGASDA	160
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
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NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	GRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVLGSM	240
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NTDB id 1366 NTHI RS01950 WP 011271972.1		0
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	LRADALRLLAVPVDETEQGVTVLTS DPRKRPDI DAL I GRPVQLMLTRPRDIERLIEQFYPPQRGRLGEQLVQEGTLSRDQL	320
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NTDB id 1355 HI 0298 AAC21962.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
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NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1306 DR RS10060 WP 027479822.1	REALQVQAREGKVKPLGEVITELGFASPDEVDSALQKQNVGGGRLEDTLVQSGKLSPEMLARSLAAQLGYEFLDPIQNP	400
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NTDB id 1468 ASU2 RS05090 WP 014991734.1	MQY.....SV.....CDMNSQQVVF.....DISE	18
NTDB id 34257 D7S RS08000 WP 005540457.1	MQNLMAGKYL.....THSQNHGDF.....TIAP	23
NTDB id 1366 NTHI RS01950 WP 011271972.1	MTSYALLHTQR.....VTAQNGEIF.....TISP	24
NTDB id 1355 HI 0298 AAC21962.1	MTSYALLHTQR.....VTAKNGEVF.....TISP	24
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVAIIRQAELISATQEQAVVTQVSASGTSVPEALLELSIFHAQELTEQLSHIFGLPETDLSRYDY	69
NTDB id 1401 DSB67 RS12665 WP 010643259.1	MLTNLSTVIRQAGILTFSQEESSLLEQVKASGISMPEALLSSGFFQSHELTEHLSSVFGLSCTSLNQY	69
NTDB id 1293 VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSQEESSLIEQVKASGISMPEALLSSGFFTSSSLAEHLSSIFGLSQPELSQY	69
NTDB id 1110 NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMFLSDGVTISPKSALAALIARVFSYSILDLRHYPR	68
NTDB id 1251 GC085 RS07725 WP 011946523.1	...MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNF	77
NTDB id 1018 ACIAD RS01685 WP 004920473.1	...MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGVFDP	77
NTDB id 1058 ABD1 RS01615 WP 001274986.1	...MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAKRAKQDTVAYLIEEVHLSPSLLAETISAEFAEPYFDLDVYDT	77
consensus		

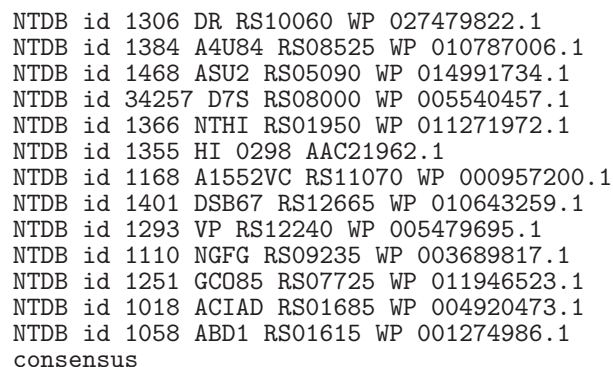
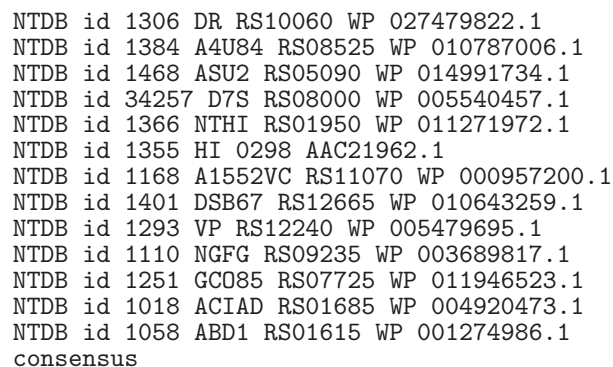
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NTDB id 1306 DR RS10060 WP 027479822.1	DPKVALMIPEATARRVYVVPVRLQGNLSLVVAMKDPNRVFDLDDLKLITGKETLPVAVMAEKDIIRLIERYFGEKGFEKLNK	480
NTDB id 1384 A4U84 RS08525 WP 010787006.1	SRWQKNCEEKQLILRYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTHKQIEPVVVIASDELKYLLNALSPEQQPIYEE	99
NTDB id 1468 ASU2 RS05090 WP 014991734.1	SLWQKNCDEKHLILRYLAIPIQENDDTLWLAIDDMNNLSACEIFAFIAHKTIEPVLISSDELKYLLNQLSPEQQSLYEET	98
NTDB id 34257 D7S RS08000 WP 005540457.1	ELWLKNQQQQTIVLLRYLALPLAENGQTLWLGLDSLTLNSACEAFSFLTGTKTIEPVLIESQTLKTALQDLSRPRVEKVEENQ	103
NTDB id 1366 NTHI RS01950 WP 011271972.1	DLWERNQQQQSLILRYFALPLKEENNRLWLGVDSLNLNSACETIAFITGKPVPEPILLESSQLKELLQQLTPHQMVEEQV	104
NTDB id 1355 HI 0298 AAC21962.1	DLWERNQQQQSLILRYFALPLKEENNRLWLGVDSLNLNSACETIAFITGKPVPEPILLESSQLKELLQQLTPNQMQVEEQV	104
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ANLCQQLGLRELITRYDALPIAKQGNLILLAVSDPTLLQAEFEFRFATGLQVELALADHRAALQAATIRRLYGRSLIQGAANQ	149
NTDB id 1401 DSB67 RS12665 WP 010643259.1	ASLCQTLGLRDLITRHNALPLNRTSSTLILAVADPTNLQAEDDFRATGLQVELVLADFRELTAATIRRLYGRSLGQEKSG	149
NTDB id 1293 VP RS12240 WP 005479695.1	ASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQQAEDDFRATGLQVELVLADFRELSTAATIRRLYGRSLSHEKSG	149
NTDB id 1110 NGFG RS09235 WP 003689817.1	HRVLMGVLTEEQMVVEHCVPVFRRGDKVFFAVSDPTQMPQIQKTVSAAGIAVELVIVEDDQLAGLLDWVGSRSSTSL..LQ	146
NTDB id 1251 GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFRSGTNLYLATDPSKQASLKEIHFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSE	157
NTDB id 1018 ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKVRIMPLVHRGHVLYVATSNPTNIEAMDIAIRFNSKLLKVEPIIVEHDKLIERLSEHVFTEETHFNFD	157
NTDB id 1058 ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLLIKHRIPLLIQRGQILYVATSNPSNIEAIDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFDFND	157
consensus		

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NTDB id 1018 ACIAD RS01685 WP 004920473.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
consensus

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 non conserved
 similar
 $\geq 50\%$ conserved