

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSXLSIGDRRLGAALLDQGYLDNLSLQRALERHREVGGLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVKV	80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1016157 ABRY27 RS07090 WP 003107297.1		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 1410 SGL RS13950 WP 010873519.1	RLPAEKAKELRAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLIEIVVPSGA	157
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1016157 ABRY27 RS07090 WP 003107297.1		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 1410 SGL RS13950 WP 010873519.1	SGEGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	0
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQGTTFLPNPSGFHPGEEVL	237
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1016157 ABRY27 RS07090 WP 003107297.1		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	1410	SGL	RS13950	WP	010873519.1
NTDB	id	1028	TT	RS08215	WP	011173991.1
NTDB	id	1306	DR	RS10060	WP	027479822.1
NTDB	id	1110	NGFG	RS09235	WP	003689817.1
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	1251	GC085	RS07725	WP	011946523.1
NTDB	id	1016157	ABRY27	RS07090	WP	003107297.1
NTDB	id	1058	ABD1	RS01615	WP	001274986.1
NTDB	id	1018	ACIAD	RS01685	WP	004920473.1
consensus						

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GSMRLRADALRLLAVPVDETEQGVTVLTS DPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGR LGEQLVQEGTLSR	317
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.....	0
.....	0
.....	0
.....	0

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NTDB	id	1293	VP	RS12240	WP	005479695.1
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NTDB	id	1251	GC085	RS07725	WP	011946523.1
NTDB	id	1016157	ABRY27	RS07090	WP	003107297.1
NTDB	id	1058	ABD1	RS01615	WP	001274986.1
NTDB	id	1018	ACIAD	RS01685	WP	004920473.1
consensus						

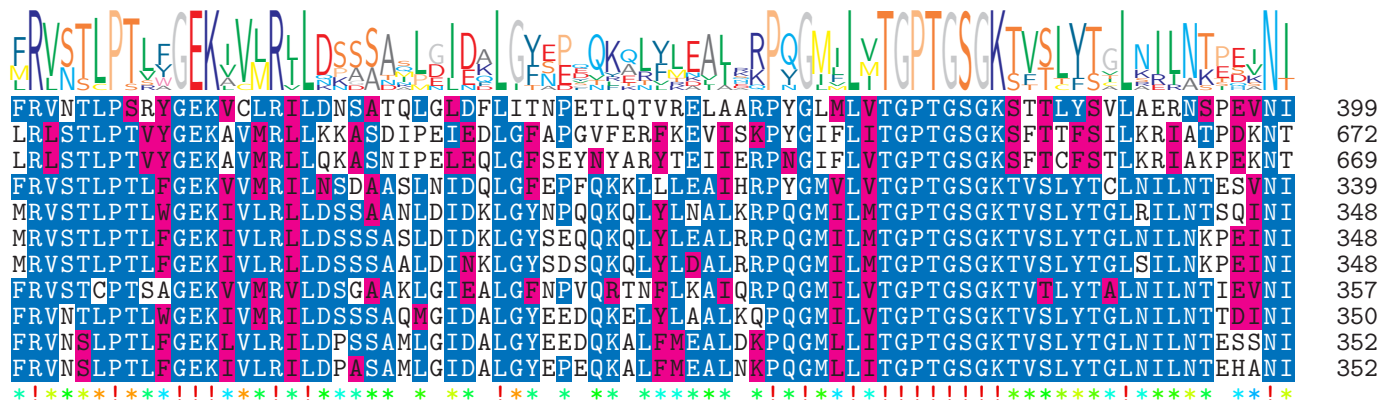
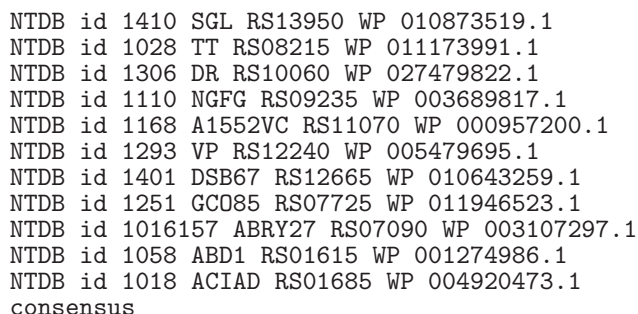
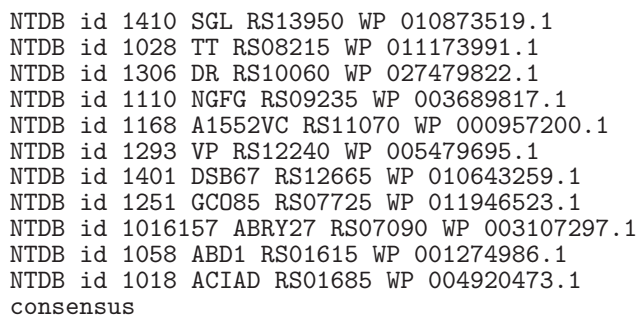
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EALKEALEVQKGLPRAKPLGETLVELGLARPEDVEEALQKQRRGGRIEDTLVQ..SGKIRPEALAQ A.....VATQL	388
DQLREALQVQAREGKVKPLGGEVITELGFASPDDEVDSALQKQNVGGRIEDTLVQ..SGKLSPEMLARS.....LAAQL	388
.....MSVGLLRILVQNQVVTVEQAEHYNE.SQACKEVLPMLFS..DGVISPKSLAAL.....IARVF	56
.....MLTNLVAILRQAEILSATQEAVVTQVSASGTSVPEALIE..LSIFHAQELTEQ.....LSHIF	57
.....MHSNLSLTLRQKGLTFSQEESLIEQVKASGISMPEALLS..SGFFTSSELAEH.....LSSIF	57
.....MLTNLSTVLRQAGILTFSQEESLIEQVKASGISMPEALLS..SGFFQSHELTEH.....LSSVF	57
.....MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVK..NKILSAEQIALT.....AAQNF	65
.....MNDSTPLSGLAKQLVLNELLDEKTARQAQVQAARNKQSLVSHLVQ..AKLVQSRA LVEV.....AAEQF	62
.....MSALHTSPKFTIGFFRRLVEEKHVSAATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAET.....TSAEF	65
.....MSAFTTPPKFTSGFIRR LVEEGYVNAQNMQQALEKAKKFKQDIPVYLID..NFSISPLTTAEI.....ISLEF	65
.....	65

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NTDB	id	1410	SGL	RS13950	WP	010873519.1
NTDB	id	1028	TT	RS08215	WP	011173991.1
NTDB	id	1306	DR	RS10060	WP	027479822.1
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NTDB	id	1058	ABD1	RS01615	WP	001274986.1
NTDB	id	1018	ACIAD	RS01685	WP	004920473.1
consensus						

GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPSSVLVAMVDPDNLA AQDELNRILRVKG..FELRRL	161
GYPYVDPEEDPPD....PGAPLLLPEDLCRRYGVPFHRLEG...NRLVLVLMKDPRNIALALDDVRLALKRKGLNIEVAPA	460
GYEFLDPIQNPPD....PKVALMIPEATARRYVVPVRLQG...NSLVVAMKDPRNVFALDDLKLITG.....KETLPA	455
SYSILDLRHYPRH....RVLIMGVLTEEQMVFEHCVVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG.....I AVELV	123
GLPETDLRSYDYA....NLCQQGLGLRELITRYDALPIAKQG...NLLLLAVSDPTLLQAEEFFRFATG.....LQVELA	124
GLSQPELSQYEYA....SLCQQGLGLRELITRHNA LPLHRT...STLLAVADPTNQQAEDDFRFATG.....LQVELV	124
GLSCTSLNQYEYA....SLCQTLGLRDLITRHNA LPLNRTS...STLILAVADPTNLQAEDDFRFATG.....LQVELV	124
GVPMLDINCIDVG....TIPVNLVN EKLKRHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAI	132
GIAYCDLNSLDRE....SIPKDVISERLVRQHRVPLWKR...NKLFIGLSDPTNHQAVTDIQFSTG.....LTTEAL	129
AEPYFDLDVYDTS....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFNSK.....LLVEPV	132
GEPLDLGVFDPA....LFLDKKID EKLIQKYRIMPLVHRG...HVLVATSNPTNIEAMDAIRFNSK.....LKVEPI	132
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NTDB id 1410 SGL RS13950 WP 010873519.1
NTDB id 1028 TT RS08215 WP 011173991.1
NTDB id 1306 DR RS10060 WP 027479822.1
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
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NTDB id 1410 SGL RS13950 WP 010873519.1	EMRAKRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
NTDB id 1028 TT RS08215 WP 011173991.1		889
NTDB id 1306 DR RS10060 WP 027479822.1		887
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1168 A1552VC RS11070 WP 000957200.1		562
NTDB id 1293 VP RS12240 WP 005479695.1		561
NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 1016157 ABRY27 RS07090 WP 003107297.1		566
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved