

logo

NTDB id 1410 SGL RS13950 WP 010873519.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 139700 TE32 RS17795 WP 001274990.1		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	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	0
NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDTLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
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NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 139700 TE32 RS17795 WP 001274990.1		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	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVDPDPSAALLL	0
NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVDPDPSAALLL	240
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 139700 TE32 RS17795 WP 001274990.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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consensus

[illegible]

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consensus

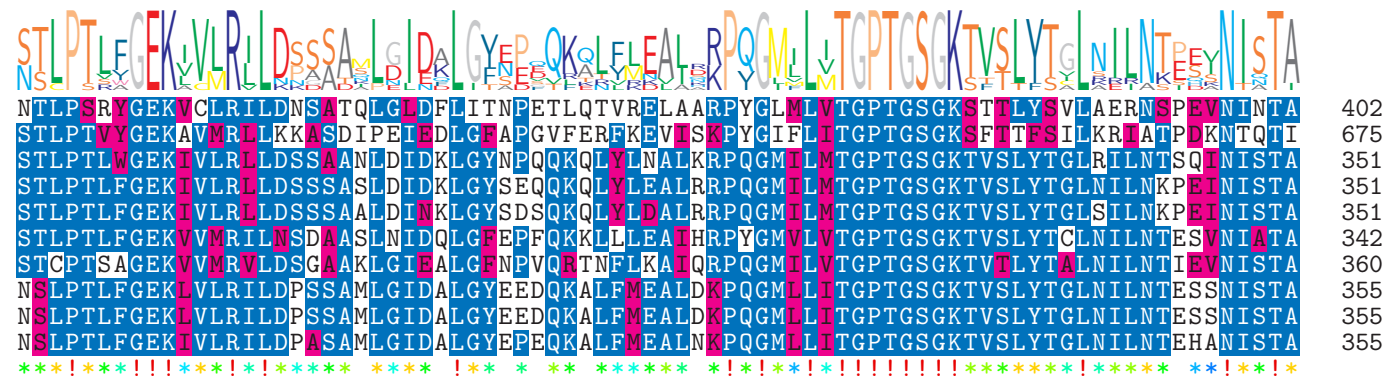
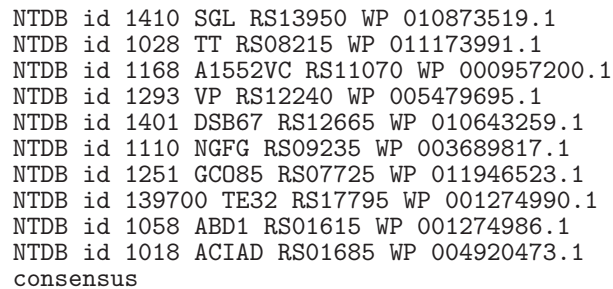
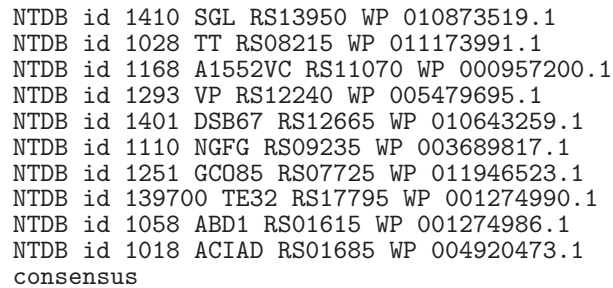
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MSA	TT	DM	ET	GL	Vo	G	Y	A	Q	AL	Q	V	K	A	G	S	P	E	X	L	T	SG	L	SP	EL	LA	E	T	TS	S	E	FG	P																										
SKKSRAVALRNYF	SPFGNK	LVAG	GH	VD	AEQ	RQ	ALV	Q	V	K	T	GRS	L	P	EL	KAV	TG	RE	L	S	P	EL	R	Q	Y	K	N	Q	L	F	E	L	K	V	L	G	V	D																					
KEA	EVQ	KGLP	RAK	P	GE	IL	VE	L	G	AR	P	DE	VE	EA	L	Q	K	R	R	G	G	R	E	D	T	L	V	Q	..	SG	K	R	PE	AL	QA	..	V	A	T	Q	L	G	Y	P															
.....	ML	TN	LV	AI	LR	QA	E	L	I	S	A	T	Q	E	A	V	T	Q	V	S	A	S	G	T	V	P	E	A	L	..	LS	I	F	H	A	E	L	T	E	Q	..	L	S	H	I	F	G	L	P										
.....	M	H	S	N	L	S	T	I	L	R	Q	K	L	T	F	S	Q	E	E	S	L	I	E	Q	V	K	A	S	G	I	S	M	P	E	A	L	L	S	..	SG	F	F	T	S	S	E	L	A	E	H									
.....	ML	TN	LV	AI	LR	QA	E	L	I	S	A	T	Q	E	A	V	T	Q	V	S	A	S	G	T	V	P	E	A	L	..	LS	I	F	H	A	E	L	T	E	Q	..	L	S	S	I	F	G	L	S										
.....	M	H	S	N	L	S	T	I	L	R	Q	K	L	T	F	S	Q	E	E	S	L	I	E	Q	V	K	A	S	G	I	S	M	P	E	A	L	L	S	..	SG	F	F	T	S	S	E	L	A	E	H									
.....	ML	TN	LV	AI	LR	QA	E	L	I	S	A	T	Q	E	A	V	T	Q	V	S	A	S	G	T	V	P	E	A	L	..	LS	I	F	H	A	E	L	T	E	Q	..	L	S	S	I	F	G	L	S										
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consensus

[illegible]

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consensus
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NTDB id 1293 VP RS12240 WP 005479695.1
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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
NTDB id 1028 TT RS08215 WP 011173991.1
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consensus



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NTDB id 1410 SGL RS13950 WP 010873519.1	KRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		561
NTDB id 1110 NGFG RS09235 WP 003689817.1		558
NTDB id 1251 GC085 RS07725 WP 011946523.1		574
NTDB id 139700 TE32 RS17795 WP 001274990.1		570
NTDB id 1058 ABD1 RS01615 WP 001274986.1		570
NTDB id 1018 ACIAD RS01685 WP 004920473.1		570
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved