

logo

```
NTDB id 108 BSU 35470 NP 391427.1
NTDB id 615 LCA RS02545 WP 011374200.1
NTDB id 593 KW2 RS05130 WP 021037147.1
NTDB id 233129 CDH85 RS00695 WP 000432961.1
NTDB id 277 KZH43 RS10090 WP 000867601.1
NTDB id 236 SPD RS10765 WP 000867601.1
NTDB id 202 SPR RS10250 WP 000867601.1
NTDB id 167 SP RS11275 WP 000867616.1
NTDB id 507 SM12261 RS09240 WP 000867722.1
NTDB id 535 SMSK321 RS10515 WP 000867726.1
consensus
```

Sequence	Position
MNVLPVEKNSSFSKELQQTLSRHHLLRTELSFSDEMIEW...HINKGYITAENSISINRRYRCNRCGQTDRYFSFYHSSG	78
MGQQVIACGRQFTAAQLADTQNN...NYSLPQIKRRPAFLRVKHLIVCQRCQVVPPT...CLP	59
MNLILENLGHLLEKDISAFNNFTDQVNNENKLIKIGAMTSVNANKVRCNRCGTIHIKTNV...KLP	65
MENYLGRLWTKAQLSEQ...LRKIAISLPSFIKKGSDYICTRCSSVAKNC...QLP	51
MKVNLDYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54
MKVNLDYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54
MKVNLDYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54
MKVNLDYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54
MKVNPNYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54
MKVNPNYLGRLFTENELTEE...ERQLAEKLPA...MRKEGKGLFCQRCNST...ILEEW...YLP	54

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consensus
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[illegible]

logo

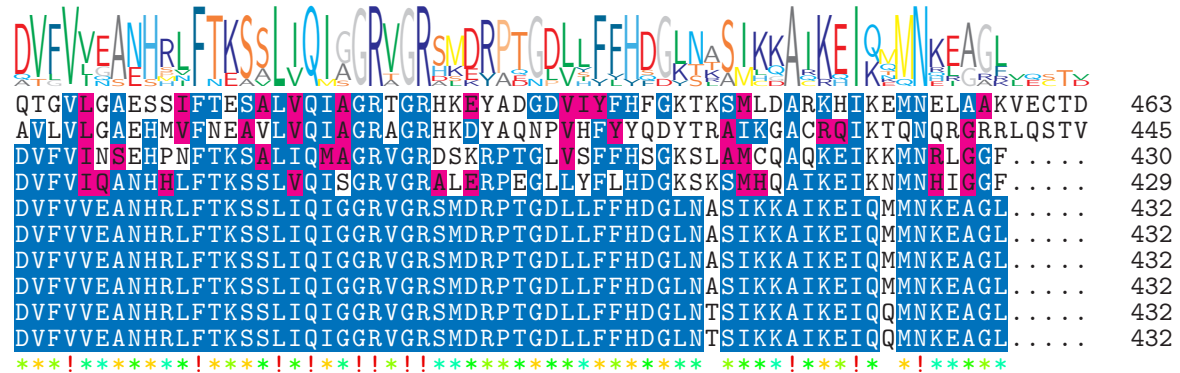
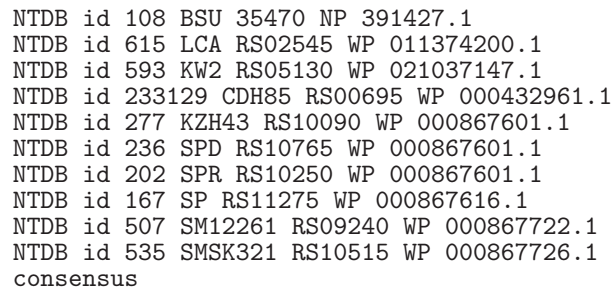
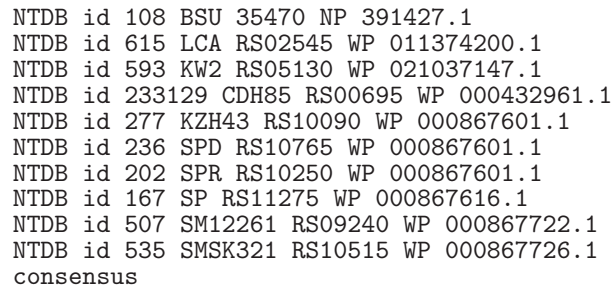
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V	V	A	K	V	I	N	G	A	V	C	L	S	P	R	I	D	V	C	E	L	y	k	R	L	Q	D	F	S		C		G	A		L	L	H	G	E	S	E	P	Y	E	R	T	P	L	V	W	A	T	T	H	Q	L	L	K	E	F	D	L	L	I	V	D	E	V	D	A	F											
E	E	S	A	L	S	P	R	I	D	V	C	E	L	y	k	R	L	Q	D	F	S		C		G	A		L	L	H	G	E	S	E	P	Y	E	R	T	P	L	V	W	A	T	T	H	Q	L	L	K	E	F	D	L	L	I	V	D	E	V	D	A	F																		
G	I	S	A	L	N	Q	G	L	R	V	C	I	A	P	R	T	D	V	L	E	L	A	P	R	L	K	A	A	F	Q	G	D	I	S	A	L	N	Q	G	S	D	D	K	G	R	L	S	P	M	I	S	T	T	H	Q	L	L	R	Y	K	D	A	I	D	V	M	I	D	E	V	D	A	F		238							
G	I	L	V	A	L	K	Q	G	R	V	C	L	A	P	R	T	D	V	L	E	L	A	P	R	L	K	A	A	F	A	T	S	I	M	L	M	H	G	E	Q	T	E	P	Y	R	T	P	L	V	I	C	T	T	H	Q	L	L	K	F	Y	H	A	F	D	L	L	I	V	D	E	V	D	A	F		219						
L	I	E	Q	I	L	S	H	G	S	V	G	L	A	S	P	R	I	D	V	C	E	L	H	Q	R	L	S	D	F	T	C	.	Q	I	P	L	L	Y	H	E	.	G	D	S	Y	F	R	S	P	L	V	M	T	S	H	Q	L	L	R	F	K	E	A	F	D	L	L	I	V	D	E	V	D	A	F		221					
S	V	A	K	V	I	D	T	G	S	S	V	C	I	A	S	P	R	I	D	V	C	E	L	E	L	y	K	R	L	S	N	D	F	R	C	.	A	I	T	L	M	H	G	E	.	S	P	S	Y	Q	R	S	P	L	T	I	A	T	T	H	Q	L	L	K	F	Y	H	A	F	D	L	L	I	V	D	E	V	D	A	F		207
V	V	A	K	V	I	N	A	G	G	A	V	C	L	A	S	P	R	I	D	V	C	E	L	E	L	y	K	R	L	Q	D	F	S	C	.	G	I	A	L	L	H	G	E	.	S	E	P	Y	F	R	T	P	L	V	V	A	T	T	H	Q	L	L	K	F	Y	Q	A	F	D	L	L	I	V	D	E	V	D	A	F		210	
V	V	A	K	V	I	N	A	G	G	A	V	C	L	A	S	P	R	I	D	V	C	E	L	E	L	y	K	R	L	Q	D	F	S	C	.	G	I	A	L	L	H	G	E	.	S	E	P	Y	F	R	T	P	L	V	V	A	T	T	H	Q	L	L	K	F	Y	Q	A	F	D	L	L	I	V	D	E	V	D	A	F		210	
V	V	A	K	V	I	N	A	G	G	A	V	C	L	A	S	P	R	I	D	V	C	E	L	E	L	y	K	R	L	Q	D	F	S	C	.	G	I	A	L	L	H	G	E	.	S	E	P	Y	F	R	T	P	L	V	V	A	T	T	H	Q	L	L	K	F	Y	Q	A	F	D	L	L	I	V	D	E	V	D	A	F		210	
V	V	A	K	V	I	N	A	G	G	A	V	C	L	A	S	P	R	I	D	V	C	E	L	E	L	y	K	R	L	Q	D	F	S	C	.	G	I	A	L	L	H	G	E	.	S	E	P	Y	F	R	T	P	L	V	V	A	T	T	H	Q	L	L	K	F	Y	Q	A	F	D	L	L	I	V	D	E	V	D	A	F		210	
V	V	A	K	V	I	N	A	G	G	A	V	C	L	A	S	P	R	I	D																																																															

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consensus

```



-  non conserved
-  similar
-  > 50% conserved