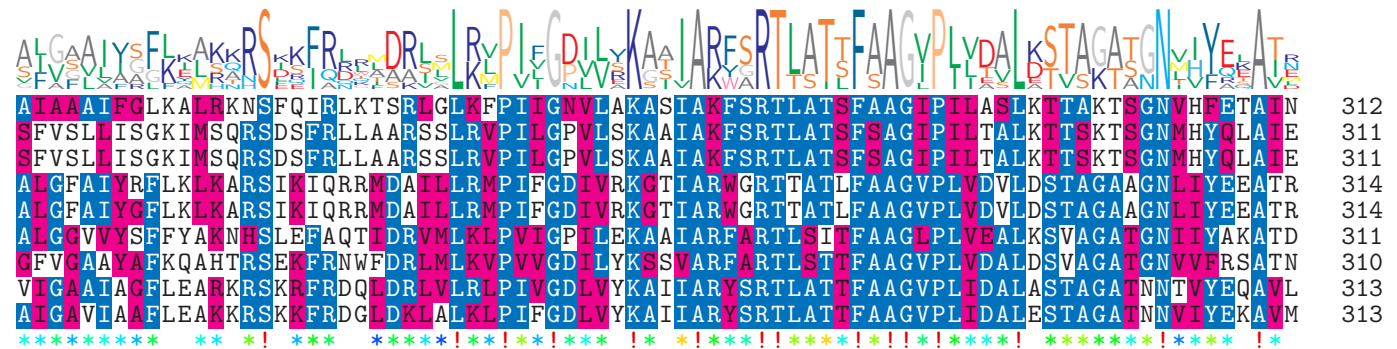
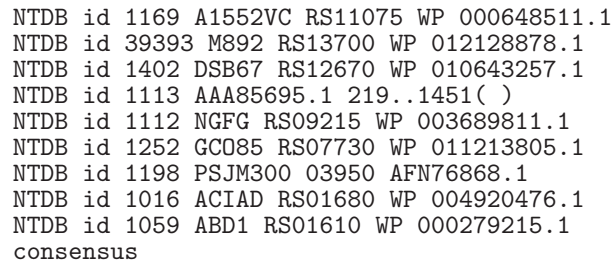
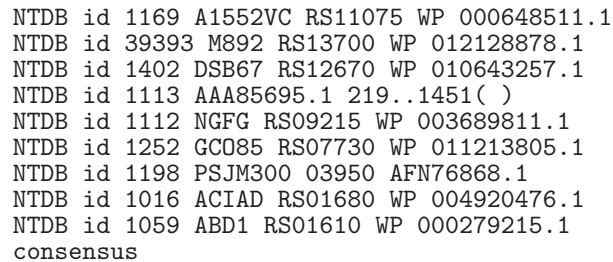
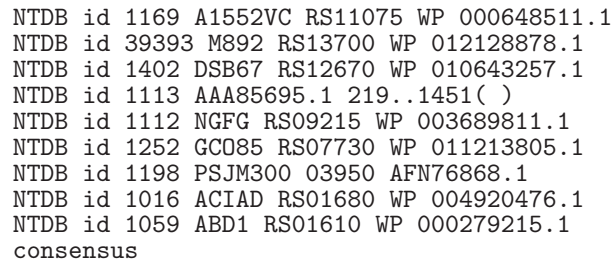


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NTDB id 39393 M892 RS13700 WP 012128878.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
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NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
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consensus

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logo

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NTDB id 1169 A1552VC RS11075 WP 000648511.1
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consensus

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E	I	R	R	D	V	A	G	M	L	A	M	R	T	N	F	L	F	P	M	L	Q	M	V	A	G	E	E	S	G	L	D	M	L	K	V	A	Y	E	V	D	N	V	D	L	S	S	M	E	P	L	I	V	L	G	W	G	L																				
K	V	K	E	R	T	T	G	L	S	L	N	S	E	S	E	S	R	F	L	A	V	S	S	N	E	A	R	E	E	L	S	L	V	A	T	E	F	E	F	E	V	D	N	V	D	L	S	S	M	E	P	L	I	V	L	G	W	G	L																		
E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	N	T	E	A	F	P	E	M	V	L	Q	M	V	M	I	G	E	E	S	G	R	L	D	D	M	L	N	K	V	A	I	Y	E	F	E	V	D	N	T	V	D	N	L	S	K	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	L
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E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	H	C	H	V	F	P	E	L	V	L	Q	M	V	M	I	G	E	E	S	G	R	L	D	D	M	L	N	K	I	A	I	Y	E	F	E	V	D	N	T	V	D	N	L	S	K	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	L
E	I	R	T	R	V	I	Q	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	R	L	D	D	M	L	N	K	A	A	F	Y	E	D	E	V	D	N	A	V	G	W	L	S	A	M	E	P	I	I	L	I	L	G	L	V	I	G	T	L			
E	I	R	T	R	V	I	Q	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	R	L	D	D	M	L	N	K	A	A	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	E	P	I	I	L	I	L	G	L	V	I	G	T	L			
K	I	R	E	V	A	T	G	Q	Q	L	N	F	I	A	M	E	N	T	H	L	F	P	N	M	V	I	Q	M	V	A	I	G	E	E	S	G	A	L	D	E	M	L	S	K	V	A	T	F	Y	E	E	V	E	V	N	A	V	D	L	S	S	L	E	P	I	I	M	S	I	G	L	V	G	L			
K	I	K	S	D	V	S	S	G	M	Q	L	N	F	S	M	R	T	T	G	T	F	P	S	M	A	V	Q	M	T	A	I	G	E	E	S	G	A	L	D	E	M	L	S	K	V	A	T	F	Y	E	D	E	V	D	N	M	V	D	G	L	T	A	L	M	E	P	M	I	M	A	V	L	G	V	L	G	L
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Sequence	Frequency
VVAMYLPiFNLMSVVG.	408
VTAMYLPiFNLMSVVG.	407
VTAMYLPiFNLMSVVG.	407
LVAMYLPiFNLGNVVA*	410
LVAMYLPiFNLGNVVA.	410
VVAMYLPiFKLGSAV..	406
IIAMYLPiFQMGSVV..	405
VIAMYLPiFQMGSVV..	408
VIAMYLPiFQMGSVV..	408

-  non conserved
-  similar
-  > 50% conserved