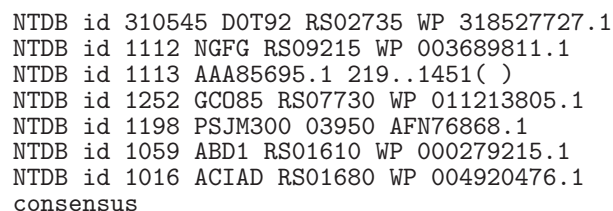
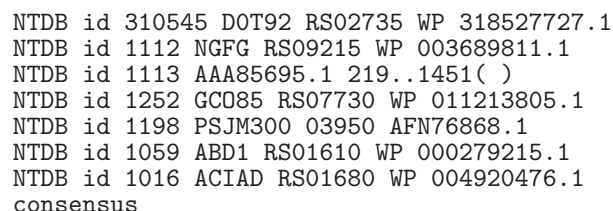
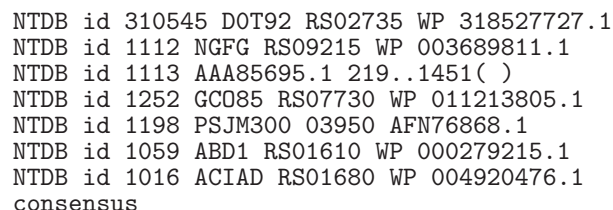


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NTDB id 310545 DOT92 RS02735 WP 318527727.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA5695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

```



```
NTDB id 310545 DOT92 RS02735 WP 318527727.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus
```

395
390
390
387
386
389
389

logo

```
NTDB id 310545 DOT92 RS02735 WP 318527727.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus
```

Sequence	Position 1	Position 2	Position 3	Position 4	Position 5	Position 6	Position 7	Position 8	Position 9	Position 10	Score
IGVITLVAMYLPIFNLGNVVG.	I	G	V	I	T	L	V	A	M	Y	415
IGTLLVAMYLPIFNLGNVVA.	I	G	T	L	L	V	A	M	Y	410	
IGTLLVAMYLPIFNLGNVVA*	I	G	T	L	L	V	A	M	Y	410	
VGGLVVAMYLPIFKLGSAAV..	V	G	G	L	V	V	A	M	Y	406	
VGGLITAMYLPIFQMGSVV..	V	G	G	L	I	T	A	M	Y	405	
VGGLVITAMYLPIFQMGSVV..	V	G	G	L	V	I	T	A	M	408	
VGGLVITAMYLPIFQMGSVV..	V	G	G	L	V	I	T	A	M	408	

-  non conserved
-  similar
-  > 50% conserved