

logo

NTDB id 1029	TT RS02230 WP 011228203.1	MAKN	65
NTDB id 1169	A1552VC RS11075 WP 000648511.1	MAKNGGFSLEF	68
NTDB id 1402	DSB67 RS12670 WP 010643257.1	MAKNGGFSLEF	67
NTDB id 1112	NGFG RS09215 WP 003689811.1	MAKNGGFSLEF	70
NTDB id 1113	AAA85695.1 219..1451()	MAKNGGFSLEF	70
NTDB id 1252	GC085 RS07730 WP 011213805.1	MAKNGGFSLEF	67
NTDB id 1198	PSJM300 03950 AFN76868.1	MAKNGGFSLEF	66
NTDB id 1016	ACIAD RS01680 WP 004920476.1	MAKNGGFSLEF	69
NTDB id 1059	ABD1 RS01610 WP 000279215.1	MAKNGGFSLEF	69
consensus		MAKNGGFSLEF	

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NTDB id 1029	TT RS02230 WP 011228203.1	DITIFTRQLATM	144
NTDB id 1169	A1552VC RS11075 WP 000648511.1	DITIFTRQLATM	148
NTDB id 1402	DSB67 RS12670 WP 010643257.1	DITIFTRQLATM	147
NTDB id 1112	NGFG RS09215 WP 003689811.1	DITIFTRQLATM	150
NTDB id 1113	AAA85695.1 219..1451()	DITIFTRQLATM	150
NTDB id 1252	GC085 RS07730 WP 011213805.1	DITIFTRQLATM	147
NTDB id 1198	PSJM300 03950 AFN76868.1	DITIFTRQLATM	146
NTDB id 1016	ACIAD RS01680 WP 004920476.1	DITIFTRQLATM	149
NTDB id 1059	ABD1 RS01610 WP 000279215.1	DITIFTRQLATM	149
consensus		DITIFTRQLATM	

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NTDB id 1029	TT RS02230 WP 011228203.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	224
NTDB id 1169	A1552VC RS11075 WP 000648511.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	228
NTDB id 1402	DSB67 RS12670 WP 010643257.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1112	NGFG RS09215 WP 003689811.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	230
NTDB id 1113	AAA85695.1 219..1451()	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	230
NTDB id 1252	GC085 RS07730 WP 011213805.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	227
NTDB id 1198	PSJM300 03950 AFN76868.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	226
NTDB id 1016	ACIAD RS01680 WP 004920476.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	229
NTDB id 1059	ABD1 RS01610 WP 000279215.1	DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	229
consensus		DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL	

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NTDB id 1029	TT RS02230 WP 011228203.1	PLLLLAVALFFAYRW.YYGTPQGRRV	303
NTDB id 1169	A1552VC RS11075 WP 000648511.1	PLLLLAVALFFAYRW.YYGTPQGRRV	308
NTDB id 1402	DSB67 RS12670 WP 010643257.1	PLLLLAVALFFAYRW.YYGTPQGRRV	307
NTDB id 1112	NGFG RS09215 WP 003689811.1	PLLLLAVALFFAYRW.YYGTPQGRRV	310
NTDB id 1113	AAA85695.1 219..1451()	PLLLLAVALFFAYRW.YYGTPQGRRV	310
NTDB id 1252	GC085 RS07730 WP 011213805.1	PLLLLAVALFFAYRW.YYGTPQGRRV	307
NTDB id 1198	PSJM300 03950 AFN76868.1	PLLLLAVALFFAYRW.YYGTPQGRRV	306
NTDB id 1016	ACIAD RS01680 WP 004920476.1	PLLLLAVALFFAYRW.YYGTPQGRRV	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	PLLLLAVALFFAYRW.YYGTPQGRRV	309
consensus		PLLLLAVALFFAYRW.YYGTPQGRRV	

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NTDB id 1029 TT RS02230 WP 011228203.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GCO85 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 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGT	LSVQ	406
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVWAMYLPPIFNLMSV	LG..	408
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VVGGLVTAMYLPPIFNLMSV	LG..	407
NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGNV	VA..	410
NTDB id 1113	AAA85695.1 219..1451()	VIGTLLVAMYLPLFNLGNV	VA..	410
NTDB id 1252	GCO85 RS07730 WP 011213805.1	LVGGLVWAMYLPPIFKLGS	AV...	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLIIAMYLPIFQMG	SVV...	405
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVIAMYLPIFQMG	SVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVIAMYLPIFQMG	SVV...	408
consensus		***!***!!*!*	*****	

[illegible]

Sequence logo for the 100 best hits. The logo shows the conservation of amino acids at each position. The top sequence is YVGGGLVYAMLPFNLGWSV. Below it are 100 hits, mostly starting with TVGGGLVYAMLPFNLGWSV, with some variations in the first few positions. The bottom row shows the conservation score for each position, with a color scale from green (low) to red (high).

-  non conserved
-  similar
-  $\geq 50\%$ conserved