

# AREBA RUFs Predicted Secondary Structures

June 2, 2014

Top50: the RUF is one of the most expressed RNAs. #AREBA, the total number of homologs among AREBA species.

RNAz predicts secondary structure potential of an RNA multiple sequence alignment. If RNAz p-value is higher than 0.5, it is classified as structured RNA. We set the threshold 0.7 to decrease false positive rate.

RNAcode predicts the coding potential of an RNA multiple sequence alignment. If p-value is lower than 0.05, it is classified as coding RNA.

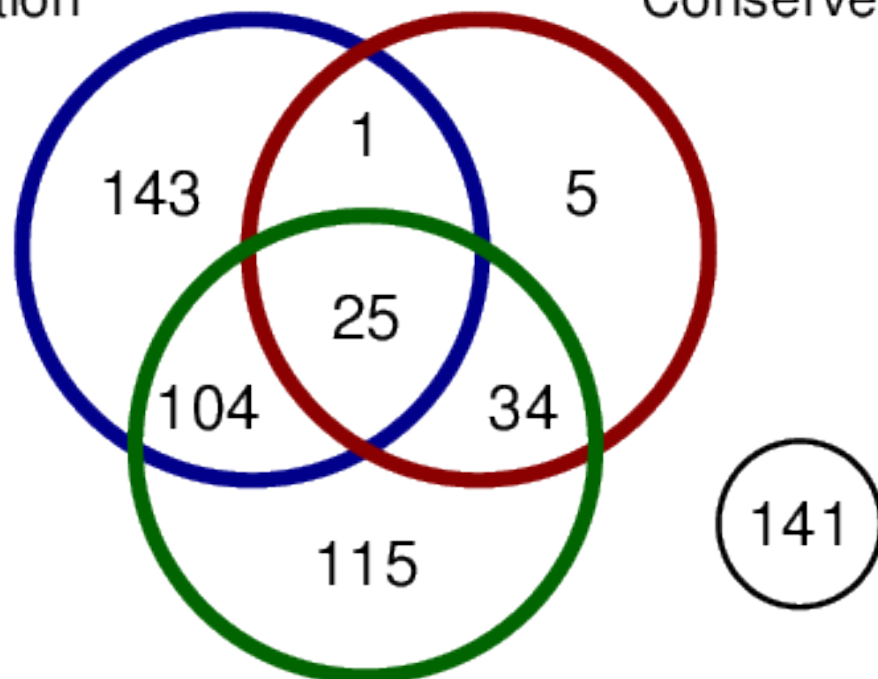
If RNALfold p-value is lower than 0.05, RNA has statistically significant secondary structure than dinucleotide shuffled random RNA sequences.

AlifoldZ predicts the z-score of native minimum free energy (MFE) of alignment by comparing MFE of shuffled multiple sequence alignments that shows structure potential of the alignment. We set the threshold of z-score to -2.5.

## Highly Expressed RUFs

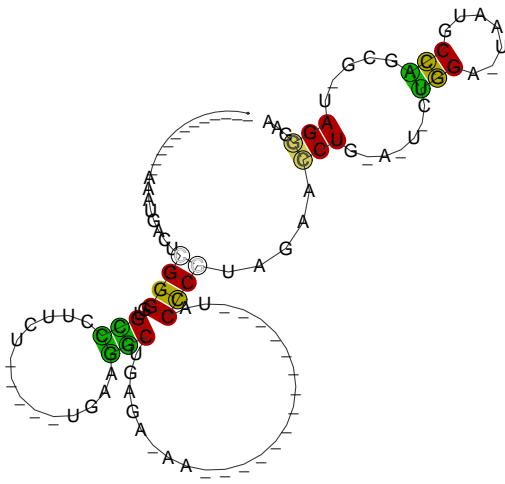
Secondary Structure  
Formation

Medium or Highly  
Conserved

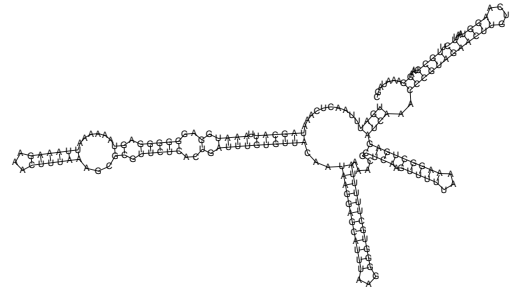


Expressed in other AREBA Species

Figure 1: Venn Diagram of Highly Expressed RUFs



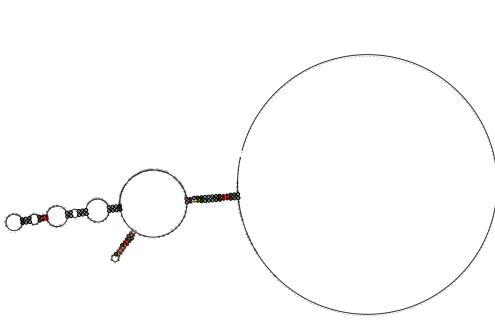
RNAalifold structure prediction



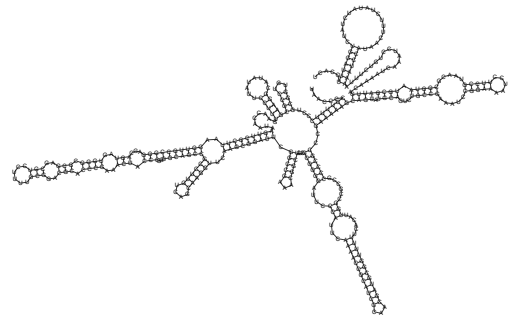
RNAfold structure prediction

Figure 2: Structure predictions of RUF: AE000511 1365213 1365400

RUF ID	Top50	#AREBA	
AE000511 1365213 1365400	No	23	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
0.440829	0.467	0.6304372	-3.2
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['HP_1289']	Forward	-2	
Closest downstream annotation	Strand	Distance to downstream element	
'locus_tag': ['HP_1290']	Forward	-1	



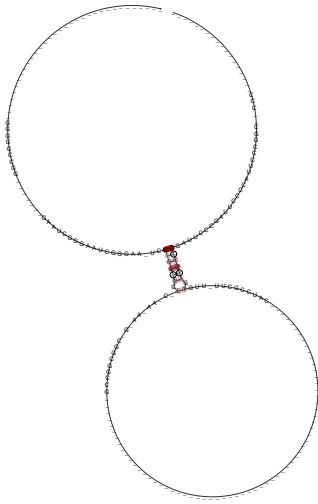
RNAalifold structure prediction



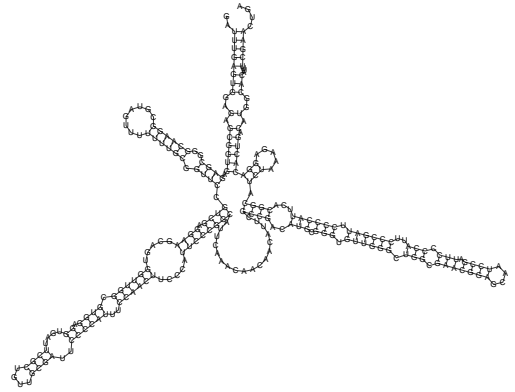
RNAfold structure prediction

Figure 3: Structure predictions of RUF: AE004969 1994807 1995171

RUF ID	Top50	#AREBA	
AE004969 1994807 1995171	Yes	12	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
0.999031	0.78	0.1191386	-4.1
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['NGO2023']	Forward	-2	
Closest downstream annotation	Strand	Distance to downstream element	
'locus_tag': ['NGO2024']	Forward	-1	



RNAalifold structure prediction



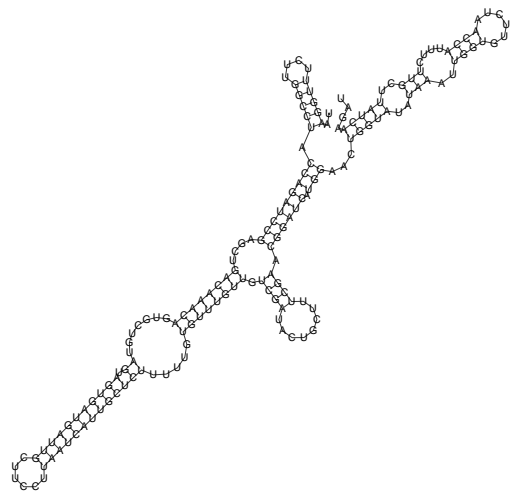
RNAfold structure prediction

Figure 4: Structure predictions of RUF: AE008923 929766 930017

RUF ID	Top50	#AREBA		
AE008923 929766 930017	Yes	1		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.998963	0.781	0.63482	-5.5	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['XAC0783'], 'gene': ['ftsA']		Forward	58	
Closest downstream annotation		Strand	Distance to downstream element	
'locus_tag': ['XAC0784'], 'gene': ['ftsZ']		Forward	-9	



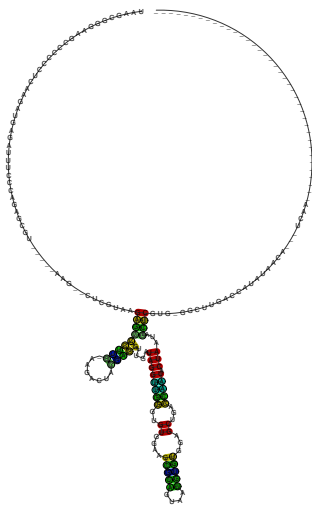
RNAalifold structure prediction



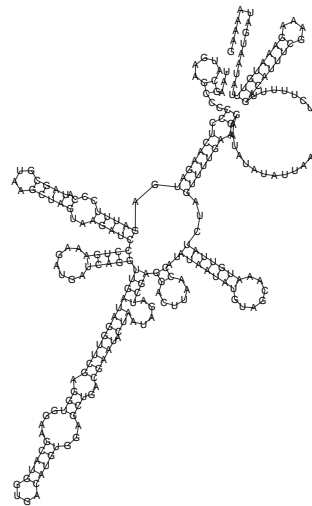
RNAfold structure prediction

Figure 5: Structure predictions of RUF: AE015924 422188 422353

RUF ID	Top50	#AREBA		
AE015924 422188 422353	Yes	16		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0	2.728e-13	0.5455509	-5.2	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['PG_t08']		Forward	72	
Closest downstream annotation		Strand	Distance to downstream element	
'old_locus_tag': ['PG0389'], 'locus_tag': ['PG_0389'], 'gene': ['nusG']		Forward	-1	



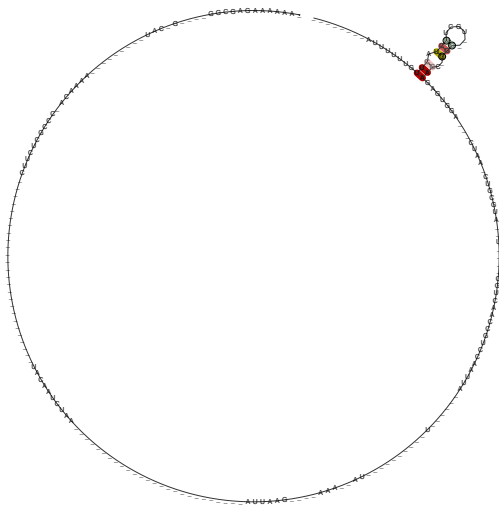
RNAalifold structure prediction



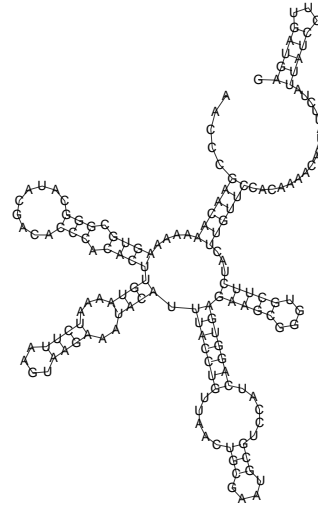
RNAfold structure prediction

Figure 6: Structure predictions of RUF: AE016877 155613 155847

RUF ID	Top50	#AREBA		
AE016877 155613 155847	No	29		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.99659	0.204	0.864027	-1.9	
Closest upstream annotation			Strand	Distance to upstream element
'old_locus_tag': ['BC0174'], 'operon': ['rRNA operon E'], 'locus_tag': ['BC_0174']			Forward	-2
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



RNAalifold structure prediction

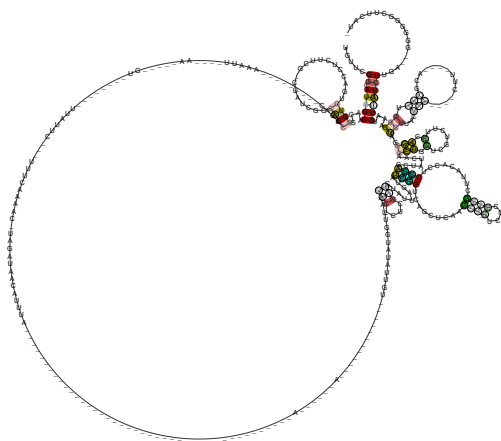


RNAfold structure prediction

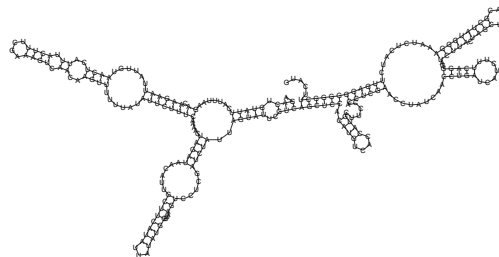
Figure 7: Structure predictions of RUF: AE016877 4519981 4520134

RUF ID	Top50	#AREBA		
AE016877 4519981 4520134	No	4		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.997285	0.641	0.3837924	-2.7	
Closest upstream annotation		Strand	Distance to upstream element	
NA		NA	NA	
Closest downstream annotation		Strand	Distance to downstream element	
'old_locus_tag': ['BC4575'], 'locus_tag': ['BC_4575']		Reverse	60	





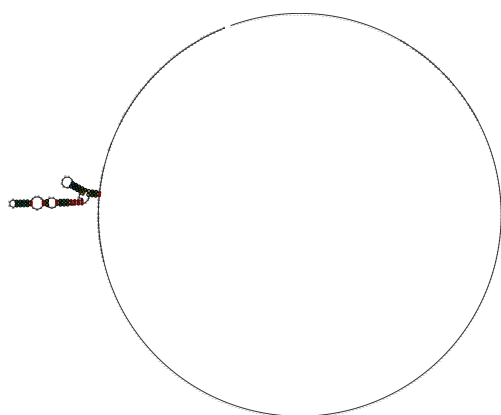
RNAalifold structure prediction



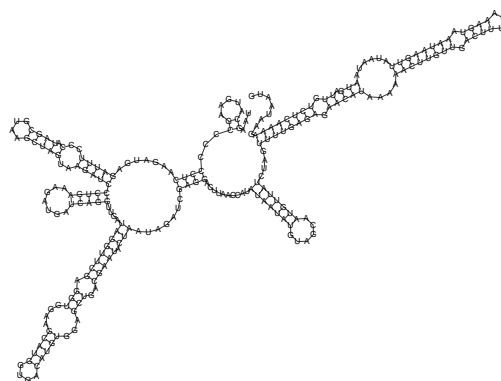
RNAfold structure prediction

Figure 8: Structure predictions of RUF: AE016877 4803926 4804169

RUF ID	Top50	#AREBA		
AE016877 4803926 4804169	No	29		
RNAz (prob)	RNAcode (prob)	RNAfold P-Value	Alifold Z-Score	
3e-06	0.021	0.6727253	-1.7	
Closest upstream annotation			Strand	Distance to upstream element
'old_locus_tag': ['BC4893'], 'operon': ['rRNA operon M'], 'locus_tag': ['BC_4893']			Reverse	-1
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



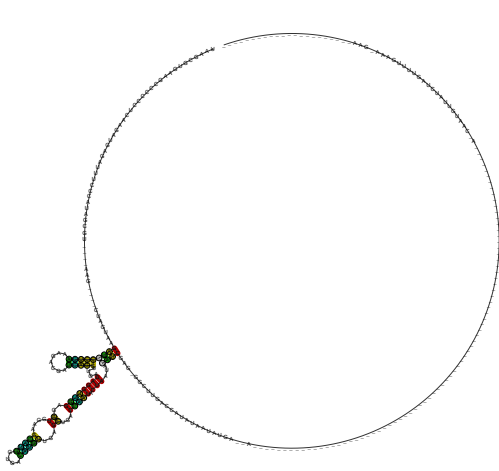
RNAalifold structure prediction



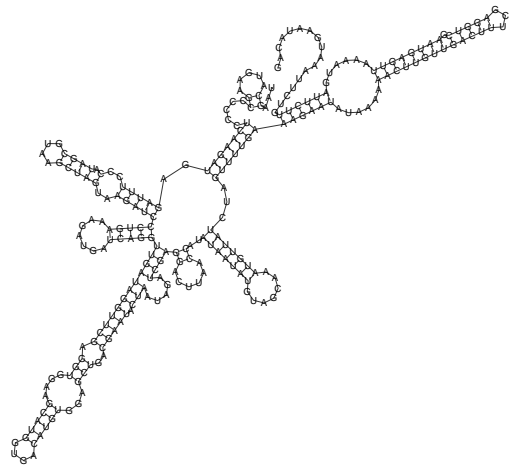
RNAfold structure prediction

Figure 9: Structure predictions of RUF: AE016877 514492 514735

RUF ID	Top50	#AREBA		
AE016877 514492 514735	No	29		
RNAz (prob)	RNAcode (prob)	RNAfold P-Value	Alifold Z-Score	
0.641288	3.111e-05	0.8535524	-3.1	
Closest upstream annotation			Strand	Distance to upstream element
'old_locus_tag': ['BC0522'], 'operon': ['rRNA operon K'], 'locus_tag': ['BC_0522']			Forward	-2
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



RNAalifold structure prediction



RNAfold structure prediction

Figure 10: Structure predictions of RUF: AE016877 722915 723160

RUF ID	Top50	#AREBA		
AE016877 722915 723160	No	29		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
8e-06	0.634	0.04856569	-2.7	
Closest upstream annotation		Strand	Distance to upstream element	
'old_locus_tag': ['BC0716'], 'locus_tag': ['BC_0716']		Forward	-2	
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	

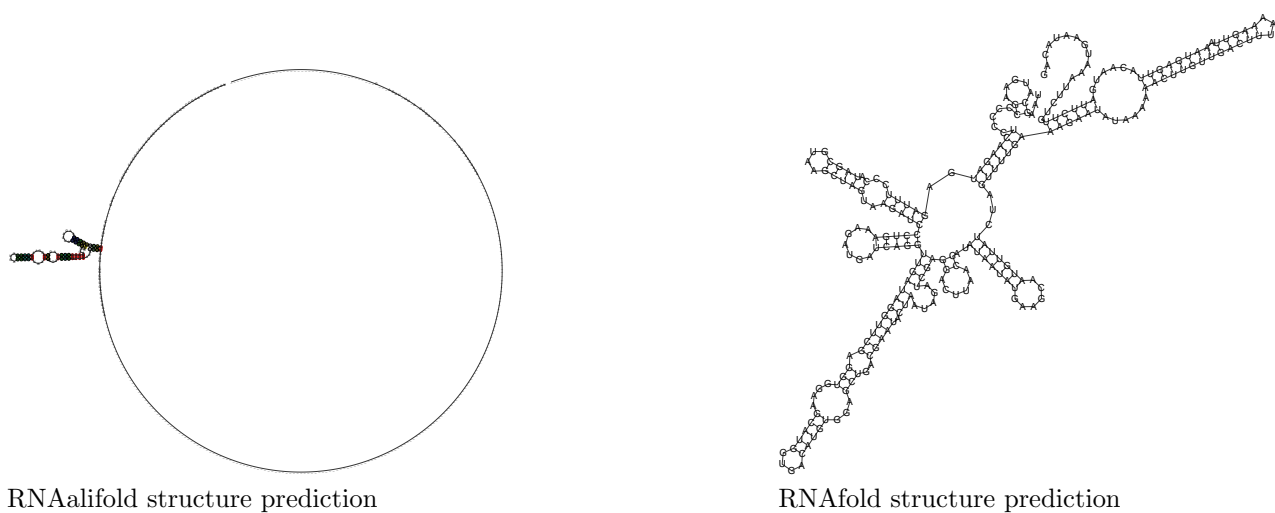
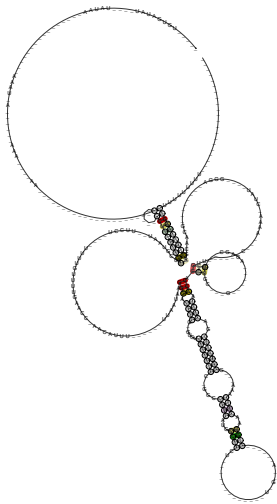
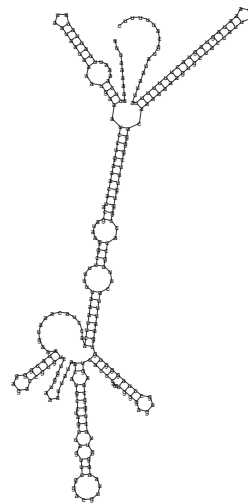


Figure 11: Structure predictions of RUF: AE016877 86691 86935

RUF ID		Top50	#AREBA		
AE016877 86691 86935		No	29		
RNAz (prob)		RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
2e-06		5.809e-05	0.3768843	-2.8	
Closest upstream annotation				Strand	Distance to upstream element
'old_locus_tag': ['BC0086'], 'operon': ['rRNA operon C'], 'locus_tag': ['BC_0086']				Forward	-2
Closest downstream annotation		Strand	Distance to downstream element		
NA		NA	NA		



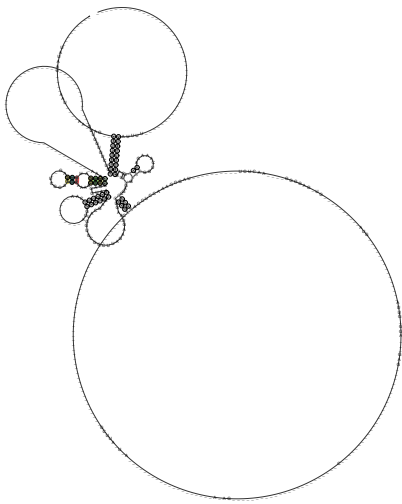
RNAalifold structure prediction



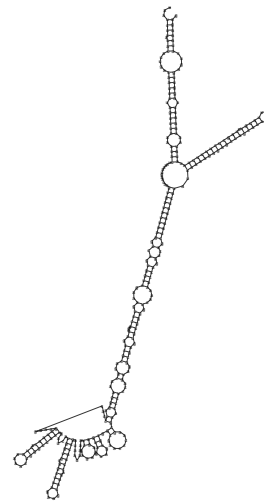
RNAfold structure prediction

Figure 12: Structure predictions of RUF: AM180355 1259865 1260134

RUF ID	Top50	#AREBA		
AM180355 1259865 1260134	Yes	6		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.999898	0.045	0.9153392	-3.2	
Closest upstream annotation		Strand	Distance to upstream element	
NA		NA	NA	
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



RNAalifold structure prediction



RNAfold structure prediction

Figure 13: Structure predictions of RUF: AM180355 180259 180592

RUF ID	Top50	#AREBA		
AM180355 180259 180592	No	2		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.842786	0.43	0.9445342	-1.2	
Closest upstream annotation		Strand	Distance to upstream element	
NA		NA	NA	
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	

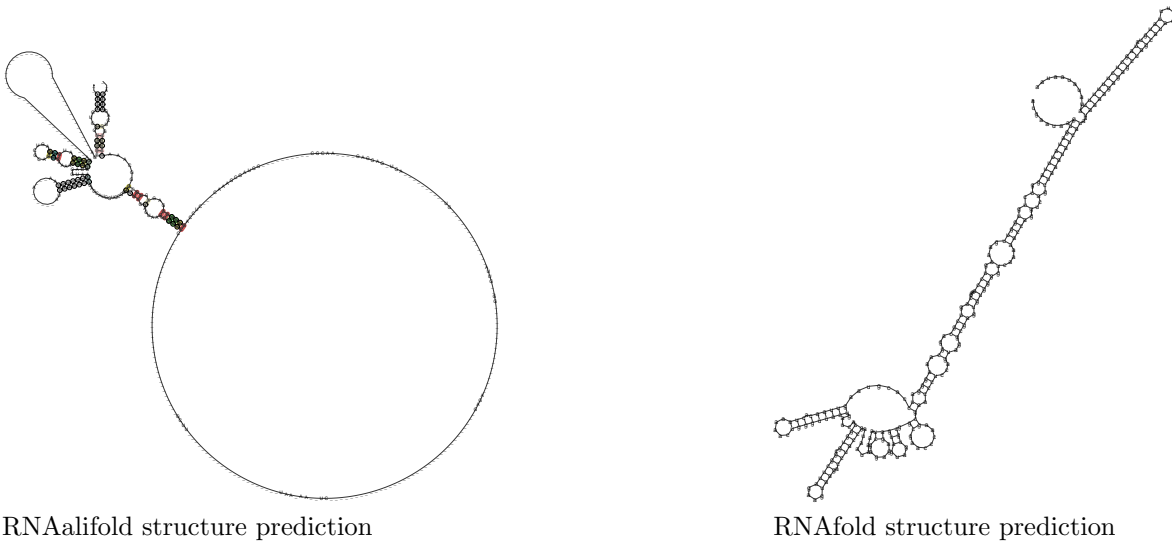
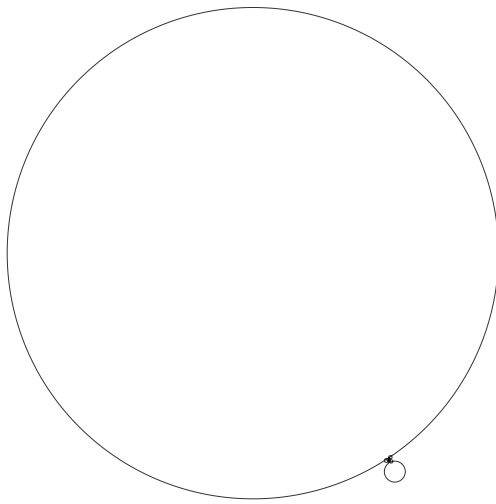
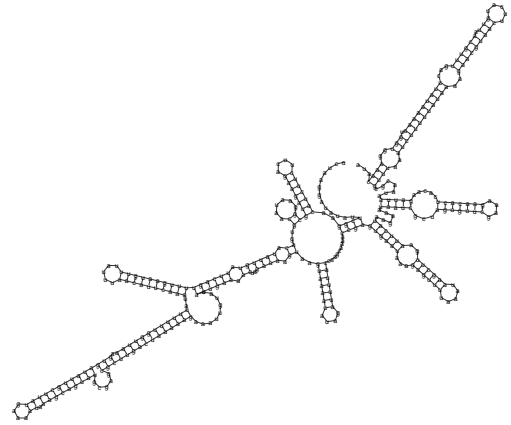


Figure 14: Structure predictions of RUF: AM180355 180298 180570

RUF ID	Top50	#AREBA		
AM180355 180298 180570	No	2		
RNAz (prob)	RNAcode (prob)	RNAfold P-Value	Alifold Z-Score	
0.133301	0.534	0.7989326	-3.1	
Closest upstream annotation	Strand	Distance to upstream element		
NA	NA	NA		
Closest downstream annotation	Strand	Distance to downstream element		
NA	NA	NA		



RNAalifold structure prediction

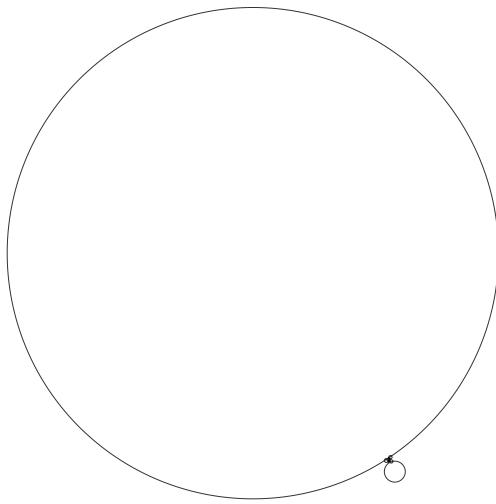


RNAfold structure prediction

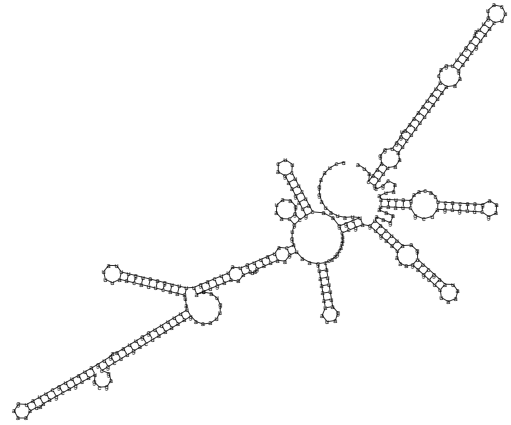
Figure 15: Structure predictions of RUF: CP000253 450372 450738

RUF ID	Top50	#AREBA		
CP000253 450372 450738	No	29		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
NA	NA	0.1234678	-4	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['SAOUHSC_R0001']		Forward	-2	
Closest downstream annotation		Strand	Distance to downstream element	
'locus_tag': ['SAOUHSC_R0006']		Forward	-1	





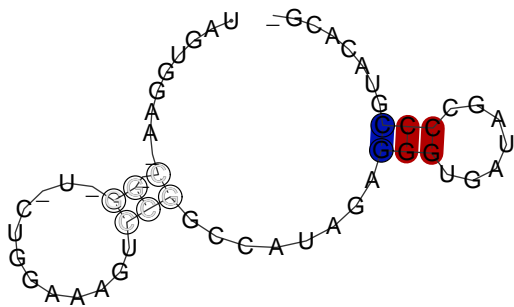
RNAalifold structure prediction



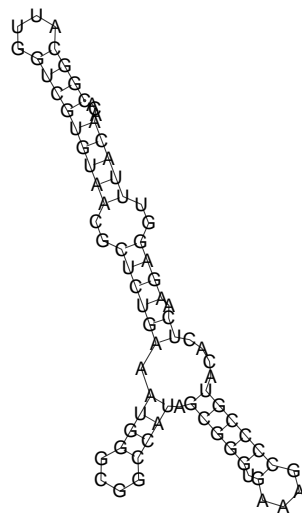
RNAfold structure prediction

Figure 16: Structure predictions of RUF: CP000253 494651 495017

RUF ID	Top50	#AREBA	
CP000253 494651 495017	No	29	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
NA	NA	0.1234678	-4.3
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['SAOUHSC_R0002']	Forward	-2	
Closest downstream annotation	Strand	Distance to downstream element	
'locus_tag': ['SAOUHSC_R0007']	Forward	-1	



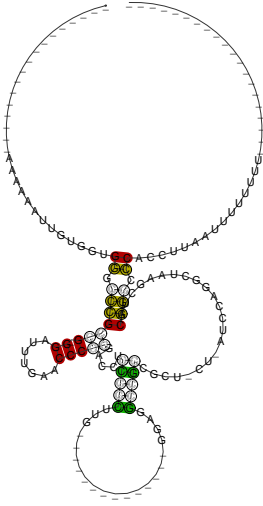
RNAalifold structure prediction



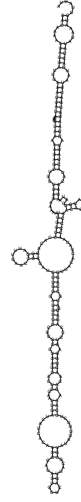
RNAfold structure prediction

Figure 17: Structure predictions of RUF: CP000438 759483 759559

RUF ID	Top50	#AREBA	
CP000438 759483 759559	No	12	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
8e-06	0.105	0.4611135	-4.9
Closest upstream annotation		Strand	Distance to upstream element
'locus_tag': ['PA14_08840'], 'gene': ['rpsJ']		Forward	7
Closest downstream annotation		Strand	Distance to downstream element
'locus_tag': ['PA14_08850'], 'gene': ['rplC']		Forward	0



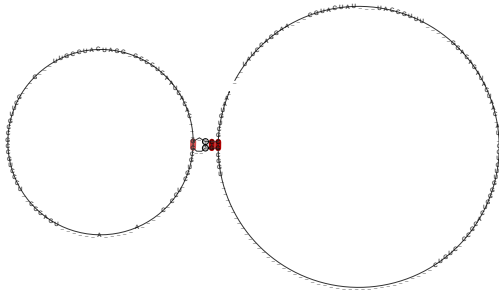
RNAalifold structure prediction



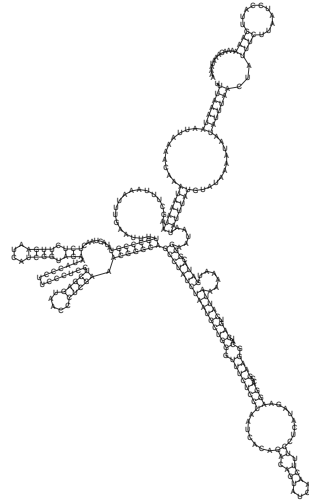
RNAfold structure prediction

Figure 18: Structure predictions of RUF: CP000678 1050048 1050310

RUF ID	Top50	#AREBA		
CP000678 1050048 1050310	No	5		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.9999	NA	0.2184433	-3.2	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['Msm_1098']		Reverse	-1	
Closest downstream annotation		Strand	Distance to downstream element	
'locus_tag': ['Msm_1097']		Reverse	-2	



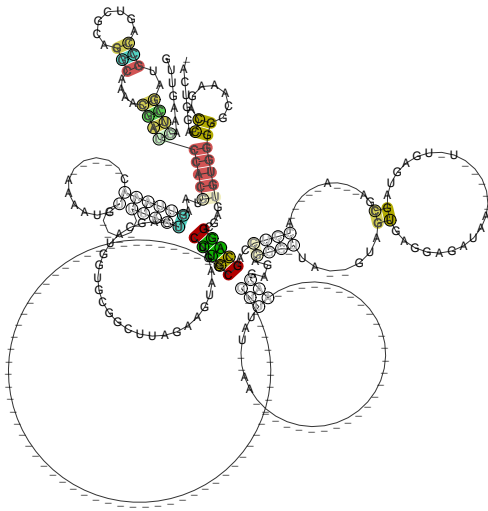
RNAalifold structure prediction



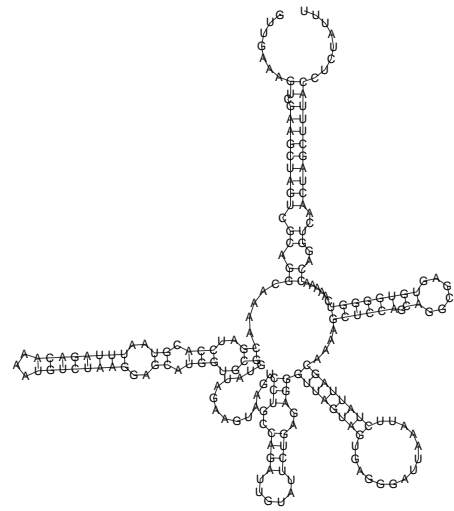
RNAfold structure prediction

Figure 19: Structure predictions of RUF: CP000678 515790 516060

RUF ID	Top50	#AREBA		
CP000678 515790 516060	Yes	2		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
1e-06	0.192	0.4804137	-3	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['Msm_1803']		Reverse	-51	
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



RNAalifold structure prediction



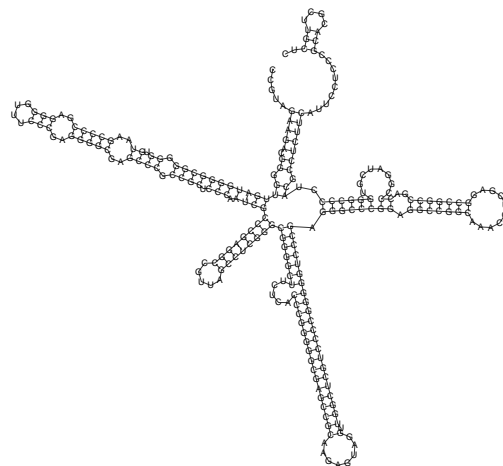
RNAfold structure prediction

Figure 20: Structure predictions of RUF: CP000721 522147 522347

RUF ID	Top50	#AREBA	
CP000721 522147 522347	Yes	2	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
0.012903	0.812	0.7684716	-2.5
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['Cbei_0431']	Forward	25	
Closest downstream annotation	Strand	Distance to downstream element	
NA	NA	NA	



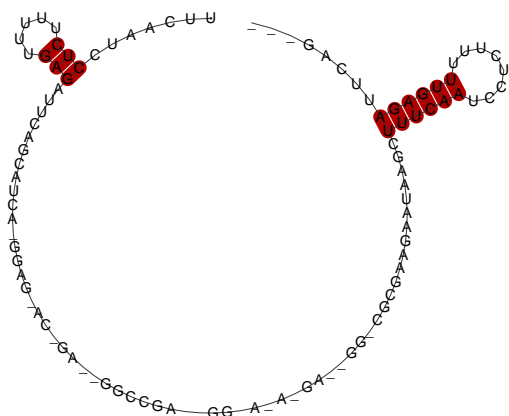
RNAalifold structure prediction



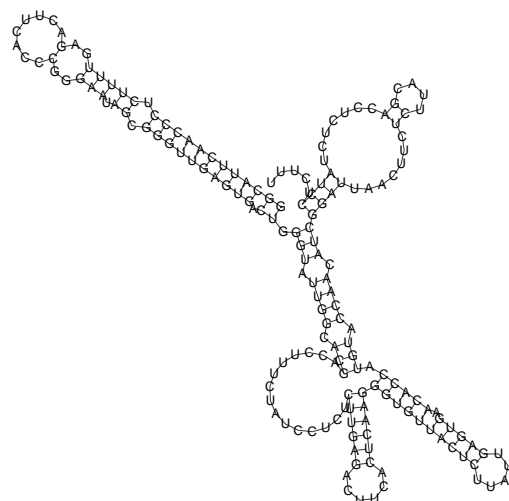
RNAfold structure prediction

Figure 21: Structure predictions of RUF: CP000816 734261 734505

RUF ID	Top50	#AREBA		
CP000816 734261 734505	No	5		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.999718	0.078	0.7541505	-2.7	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['Igni_0823']		Reverse	-1	
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



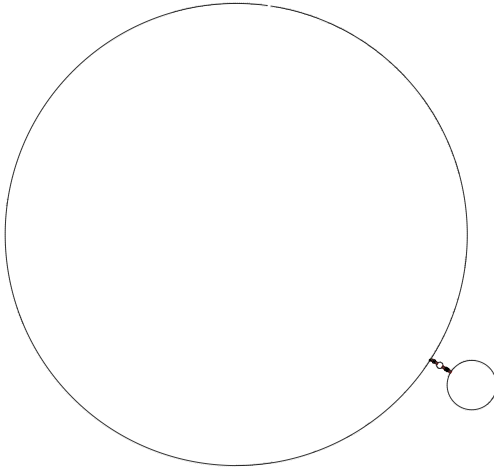
RNAalifold structure prediction



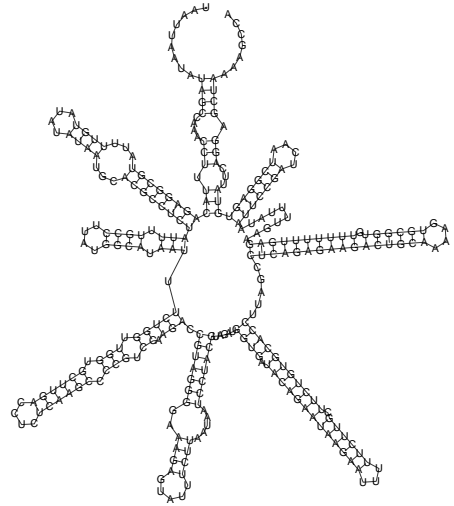
RNAfold structure prediction

Figure 22: Structure predictions of RUF: CP000816 795075 795246

RUF ID	Top50	#AREBA		
CP000816 795075 795246	Yes	1		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.014062	0.788	0.6266984	-4.2	
Closest upstream annotation				Strand
'locus_tag': ['Igni_0895'], 'pseudo': [''], 'product': ['putative cobalt transport system ATP-binding protein']				Forward
Closest downstream annotation		Strand	Distance to downstream element	
NA		NA	NA	



RNAalifold structure prediction

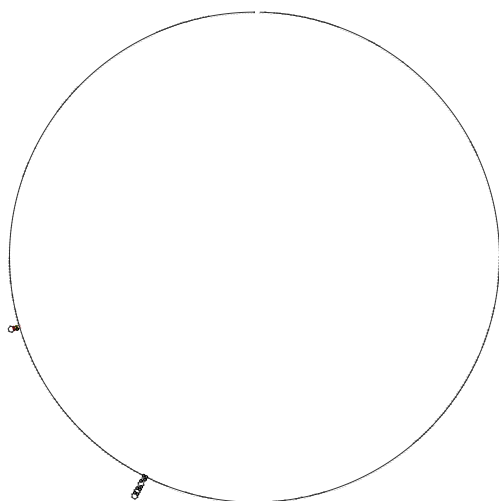


RNAfold structure prediction

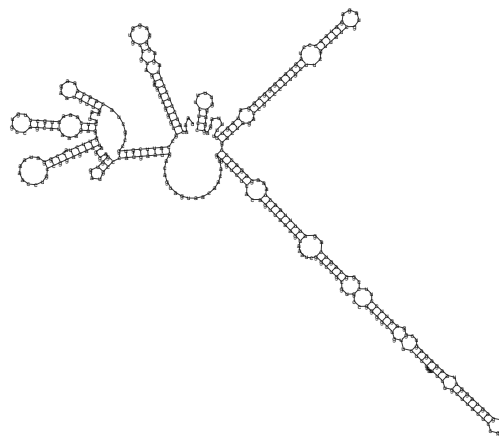
Figure 23: Structure predictions of RUF: CP000947 29447 29732

RUF ID	Top50	#AREBA		
CP000947 29447 29732	No	8		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.999398	0.479	0.3058769	-5.8	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['HSM_0037']		Forward	-2	
Closest downstream annotation		Strand	Distance to downstream element	
'locus_tag': ['HSM_0038']		Forward	-1	





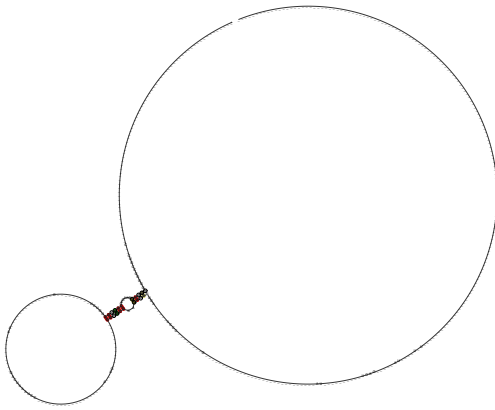
RNAalifold structure prediction



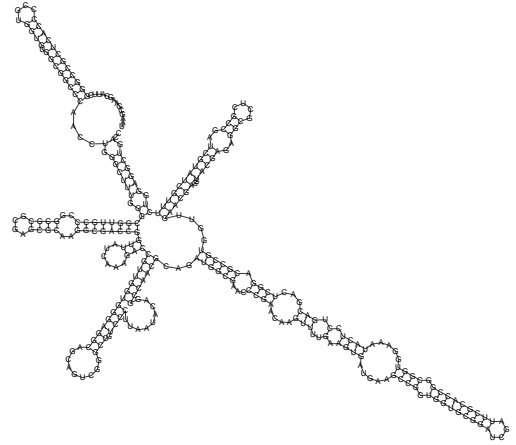
RNAfold structure prediction

Figure 24: Structure predictions of RUF: CP000951 2935512 2935882

RUF ID	Top50	#AREBA		
CP000951 2935512 2935882	Yes	2		
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score	
0.996547	0.944	0.9150239	0	
Closest upstream annotation		Strand	Distance to upstream element	
'locus_tag': ['SYNPCC7002_A2811']		Forward	-2	
Closest downstream annotation		Strand	Distance to downstream element	
'locus_tag': ['SYNPCC7002_A2812'], 'gene': ['phhB']		Forward	-1	



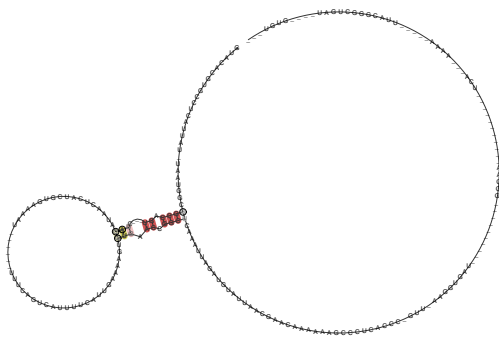
RNAalifold structure prediction



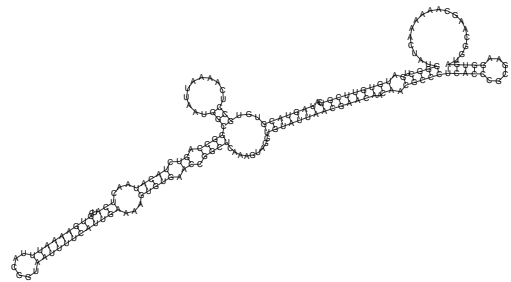
RNAfold structure prediction

Figure 25: Structure predictions of RUF: CP001503 267086 267386

RUF ID	Top50	#AREBA	
CP001503 267086 267386	Yes	7	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
8e-06	0.103	0.2966998	-5.2
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['bglu_1g02470']	Forward	-2	
Closest downstream annotation	Strand	Distance to downstream element	
'locus_tag': ['bglu_1g02480']	Forward	-1	



RNAalifold structure prediction



RNAfold structure prediction

Figure 26: Structure predictions of RUF: CP003200 4726877 4727051

RUF ID	Top50	#AREBA	
CP003200 4726877 4727051	No	5	
RNAz (prob)	RNAcode (prob)	RNALfold P-Value	Alifold Z-Score
0.185037	0.859	0.8007048	-2.8
Closest upstream annotation	Strand	Distance to upstream element	
'locus_tag': ['KPHS_47080']	Reverse	-2	
Closest downstream annotation	Strand	Distance to downstream element	
'locus_tag': ['KPHS_47070']	Reverse	2	