SUPPLEMENTARY DATA

Automated 3D structure composition for large RNAs

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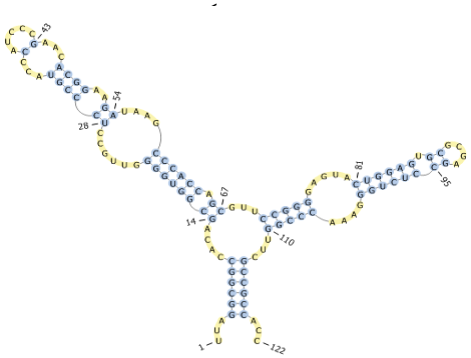
Supplementary Data are available at NAR online:

Supplementary tables S1-S9

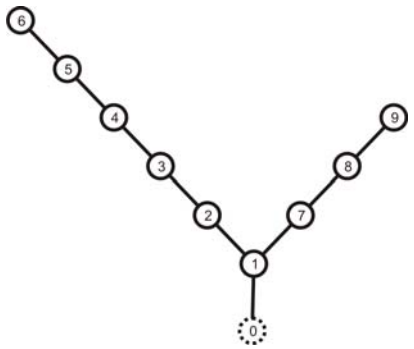
Supplementary figures S1-S3

Supplementary dataset S1

TABLE S1. The RNA secondary structure fragmentation based on its tree graph representation. The 5S rRNA secondary structure as an example



5S rRNA *H. Marismortui* secondary structure derived from the X-ray structure (PDB ID 1FFK)



5S rRNA tree graph representation (numbered)

Graph element	Structure element		Size [nt]	In-secondary structure localization		RNA FRABASE dictionary input pattern [a]		
				first residue	last residue	strand name	secondary structure	
							sequence	topology
vertices								
0	single strands	5' end	4	1	4	strand1	^UUAG	^...(
		3' end	4	119	122	strand2	CACC$	)...$
1	3-way junction loop		16	9 67 110	14 71 114	strand1 strand2 strand3	CCACAG CGUUC GUUCG	(....( )...( )...)
2	bulge		5	15 64	16 66	strand1 strand2	CG CAG	(( ).)
3	internal loop		14	21 54	29 59	strand1 strand2	GGUUGCCU AUAAGC	(......( )....)
4	bulge		6	29 50	30 53	strand1 strand2	CC GAAG	(( )..)
5	internal loop		10	33 43	37 47	strand1 strand2	UACCC GAACA	(...( )...)
6	hairpin loop		7	37	43	strand1	CAUCCCG	(.....)
7	internal loop		13	75 101	81 106	strand1 strand2	GGAGUAC GGAAAC	(.....( )....)
8	bulge		5	86 95	88 96	strand1 strand2	GUG CC	(.( ))
9	hairpin		6	89	94	strand1	CGCGAG	(....)
edges								
1	stem		12	4 114	9 119	strand1 strand2	GGCGGC GCCGCC	(((((( ))))))
2	stem		4	14 66	15 67	strand1 strand2	GC GC	(( ))
3	stem		12	16 59	21 64	strand1 strand2	GGUGGG CCCACC	(((((( ))))))
4	stem		4	28 53	29 54	strand1 strand2	UC GA	(( ))
5	stem		8	30 47	33 50	strand1 strand2	CCGU ACGG	(((( ))))
6	single base pair		2	37 43	37 43	strand1 strand2	C G	( )
7	stem		10	71 106	75 110	strand1 strand2	CCGGG CCCGG	((((( )))))
8	stem		12	81 96	86 101	strand1 strand2	CUGGAG CUCUGG	(((((( ))))))
9	stem		4	88 94	89 95	strand1 strand2	GC GC	(( ))

[a] notation as reported in the RNA FRABASE (25)

TABLE S2. The RNA FRABASE dictionary statistics of secondary structure and tertiary structure elements

Structure element	Number of elements [a)]		
	secondary structure elements		tertiary structure elements
	sequence not specified	sequence specified	
Loops:			
hairpin	35	1,525	21,869
bulge and internal	338	5,458	70,604
3-way junction	889	1,874	13,740
4-way	928	1,422	8,584
5-way	720	910	6,580
6-way	174	210	1,164
7-way	336	392	1,680
8-way	112	128	200
9-way	27	27	27
10-way	40	50	50
11-way	217	230	231
12-way	48	58	60
14-way	14	14	14
Stems	17	1,828	63,417
Single strands:			
5'-end	10	38	155
3'-end	30	187	1,387
linking domains	21	113	1,166
All	**3,956**	**14,464**	**190,928**

[a)] In order to increase the number of items in the dictionary, strand shift operation (25) was applied for such elements like bulges, internal and n-way junction loops.

TABLE S3. Statistical analysis of machine translation steps and properties of the 3D models predicted for a set of 95 RNAs with randomized sequence

No.	Strand length [nt]	Fragmentation number of secondary structure elements				In-dictionary search number of secondary structure elements			Refinement number of final 3D models			Secondary structure conservation [MCC] [a]	Precision r.m.s.d. [Å] [b]
						found with sequence similarity		missing	refined with energy		not refined		
		total	single strands	loops	stems	complete	not complete		low	high			
1	30	4	2	1	1	0	4	0	10	0	0	1.00	1.9
2	35	5	1	2	2	1	4	0	10	0	0	1.00	2.0
3	40	3	1	1	1	1	2	0	10	0	0	1.00	1.4
4	45	8	2	3	3	3	5	0	10	0	0	1.00	2.0
5	50	6	2	2	2	1	5	0	10	0	0	0.96	5.3
6	55	9	3	4	2	3	6	0	10	0	0	0.98	4.0
7	60	6	2	2	2	1	5	0	10	0	0	1.00	1.7
8	65	12	2	5	5	5	7	0	10	0	0	0.99	3.9
9	70	8	2	3	3	1	6	1	10	0	0	1.00	2.5
10	75	14	3	6	5	8	6	0	10	0	0	0.96	6.0
11	80	15	2	7	6	9	6	0	10	0	0	1.00	5.5
12	85	18	2	8	8	10	8	0	10	0	0	1.00	7.8
13	90	16	1	8	7	9	6	1	8	0	2	0.99	4.9
14	95	12	2	5	5	2	10	0	10	0	0	0.99	2.9
15	100	16	2	7	7	6	10	0	10	0	0	1.00	7.4
16	105	23	5	9	9	11	12	0	9	0	1	0.99	6.9
17	110	16	4	6	6	3	13	0	10	0	0	1.00	13.2
18	115	20	3	9	8	8	12	0	9	0	1	0.98	9.7
19	120	15	2	7	6	2	12	1	10	0	0	0.98	11.6
20	125	18	3	8	7	6	11	1	10	0	0	0.99	3.6
21	130	15	3	6	6	4	10	1	10	0	0	1.00	9.0
22	135	24	2	11	11	14	9	1	9	0	1	0.98	6.5
23	140	22	1	11	10	14	7	1	8	0	2	0.98	7.4
24	145	26	0	13	13	16	9	1	7	0	3	0.99	4.5
25	150	28	1	14	13	17	11	0	10	0	0	1.00	8.8
26	155	21	3	9	9	6	15	0	10	0	0	0.99	7.1
27	160	22	2	10	10	5	16	1	6	0	4	0.98	7.0
28	165	27	3	12	12	11	16	0	10	0	0	1.00	6.8
29	170	28	2	14	12	11	17	0	9	0	1	0.98	10.5
30	175	26	2	12	12	12	12	2	10	0	0	1.00	17.1
31	180	29	1	14	14	14	13	2	10	0	0	1.00	9.5
32	185	28	3	13	12	7	21	0	8	0	2	0.98	19.4
33	190	24	1	12	11	8	15	1	7	1	2	0.98	12.7
34	195	24	2	11	11	10	12	2	9	0	1	0.99	7.3
35	200	31	3	14	14	13	18	0	8	0	2	0.99	13.1
36	205	31	2	15	14	11	18	2	9	1	0	0.98	4.9
37	210	39	2	19	18	22	16	1	9	0	1	0.99	8.2
38	215	32	3	15	14	16	15	1	9	0	1	0.98	18.3
39	220	36	4	17	15	10	26	0	5	2	3	0.96	11.0
40	225	35	1	17	17	12	21	2	10	0	0	0.99	11.1
41	230	36	4	16	16	11	24	1	9	0	1	0.99	8.1
42	235	33	3	15	15	10	21	2	7	0	3	0.99	20.1
43	240	36	3	17	16	13	23	0	10	0	0	0.99	8.6
44	245	40	1	20	19	22	17	1	9	1	0	1.00	8.2
45	250	41	2	21	18	18	22	1	6	0	4	0.96	12.2
46	255	38	3	18	17	13	24	1	9	1	0	1.00	8.4
47	260	41	2	20	19	14	24	3	7	1	2	0.99	8.3
48	265	50	3	25	22	25	25	0	9	0	1	0.99	11.6
49	270	35	1	18	16	9	24	2	9	0	1	1.00	8.5
50	275	37	2	18	17	8	28	1	9	1	0	0.99	17.8
51	280	33	1	16	16	12	18	3	6	1	3	0.99	18.3
52	285	48	4	22	22	24	23	1	6	3	1	0.99	10.5
53	290	43	3	21	19	15	25	3	9	0	1	0.99	10.5
54	295	41	2	20	19	9	30	2	4	3	3	0.98	10.7
55	300	39	1	20	18	10	25	4	9	0	1	0.99	6.5
56	305	49	5	23	21	20	27	2	8	0	2	0.98	15.2
57	310	39	2	19	18	13	24	2	9	0	1	0.99	15.1
58	315	47	1	23	23	19	25	3	8	1	1	0.99	9.2
59	320	46	2	23	21	20	24	2	10	0	0	0.99	10.3
60	325	46	2	22	22	19	26	1	7	0	3	0.98	8.4
61	330	52	3	26	23	26	23	3	6	1	3	0.99	15.8
62	335	45	2	22	21	15	27	3	8	1	1	1.00	22.1

63	340	48	3	23	22	16	30	2	9	1	0	0.99	9.7
64	345	53	2	27	24	15	35	3	9	1	0	0.98	17.6
65	350	50	1	25	24	20	29	1	8	0	2	0.99	25.0
66	355	56	2	28	26	20	36	0	3	1	6	0.97	15.0
67	360	45	1	23	21	15	28	2	10	0	0	0.99	10.1
68	365	53	3	26	24	16	35	2	9	0	1	0.99	11.9
69	370	53	4	26	23	18	34	1	6	0	4	0.99	13.5
70	375	52	3	26	23	17	31	4	9	1	0	1.00	17.3
71	380	55	3	26	26	19	32	4	9	1	0	0.99	19.3
72	385	59	2	31	26	20	39	0	8	1	1	0.98	12.7
73	390	63	2	32	29	31	31	1	7	0	3	0.98	11.7
74	395	54	2	28	24	23	29	2	5	3	2	0.99	13.6
75	400	52	3	25	24	19	30	3	3	4	3	0.98	13.1
76	405	55	3	27	25	19	33	3	10	0	0	1.00	18.7
77	410	55	2	27	26	14	40	1	7	2	1	0.97	16.2
78	415	65	2	32	31	24	40	1	3	5	2	0.98	13.5
79	420	71	1	38	32	34	36	1	8	0	2	0.98	14.7
80	425	52	2	26	24	14	34	4	4	1	5	0.98	18.5
81	430	57	4	27	26	16	38	3	3	5	2	0.98	12.5
82	435	69	3	35	31	29	37	3	8	0	2	0.99	11.6
83	440	72	5	34	33	27	42	3	4	3	3	0.98	17.8
84	445	52	2	25	25	16	32	4	5	2	3	0.98	14.6
85	450	67	1	35	31	32	34	1	7	1	2	0.98	11.1
86	455	68	3	33	32	28	36	4	6	3	1	0.98	17.5
87	460	62	2	31	29	23	35	4	5	4	1	0.99	11.9
88	465	59	3	28	28	18	37	4	3	3	4	0.98	22.4
89	470	59	3	29	27	19	35	5	3	4	3	0.99	16.1
90	475	61	3	29	29	26	31	4	8	1	1	0.99	21.0
91	480	74	2	37	35	33	37	4	3	2	5	0.96	29.1
92	485	71	4	35	32	31	36	4	8	1	1	0.99	27.2
93	490	75	4	38	33	32	40	3	2	4	4	0.97	21.1
94	495	74	3	39	32	31	40	3	2	6	2	0.97	25.2
95	500	70	2	34	34	24	41	5	4	4	2	0.98	27.9
								sum	741	82	127		

[a)] Average of Matthews correlation coefficient (41) between the input and recovered secondary structures derived from the 10 final 3D models.
[b)] Average heavy-atom r.m.s.d. between the 10 final RNA 3D models and their mean coordinates structure.

Table S4. 3D structure prediction details for the 500-mer RNA with randomized sequence

No.	Size [nt]	Target secondary structure element				Source tertiary structure element					Selection criteria				
		localization		secondary structure		localization			secondary structure		secondary structure topology[a)]	sequence similarity [%] [b)]	pyrimidines / purines compatibility [%] [c)]	source structure resolution [Å]	energy [kcal/mol]
		residues				PDB ID	residues								
		first	last	sequence	topology		first	last	sequence	topology					
Single strands															
0	5	1	5	GUACU	....(	3I21 A	1	5	UGAAG	....(	identical	20.0	20.0	3.7	-30.4
	6	495	500	AUUCAU	).....	1F7U B	71	76	AAGCCA	).....	identical	33.3	33.3	2.2	-47.6
Loops															
1	5	6	7	GA	((	3I55 0	2279	2280	GA	((	identical	100.0	100.0	3.1	-17.7
		492	494	UAC	).)		2290	2292	UAC	).)					
2	12	11	19	GACUAAUCU	(.......(	1AUD B	18	26	CAUUGCACC	(.......(	identical	33.3	58.3	- [d)]	-157.6
		486	488	GCC	).)		5	7	GAG	).)					
3	6	23	25	UAA	(.(	1JZX A	1680	1682	UAA	(.(	identical	100.0	100.0	3.1	-29.6
		480	482	UCA	).)		1978	1980	UCA	).)					
4	5	27	29	GUC	(.(	1F7H A	5	7	GUC	(.(	identical	100.0	100.0	- [d)]	-128.3
		477	478	GC	))		22	23	GC	))					
5	9	32	37	CGAAGC	(....(	3E5C A	27	32	AGAUGC	(....(	identical	66.7	66.7	2.2	-119.5
		472	474	GAG	).)		12	14	GAU	).)					
6	5	41	42	CC	((	2ZJR X	863	864	CC	((	identical	100.0	100.0	2.9	-75.9
		466	468	GCG	).)		938	940	GCG	).)					
7	8	47	48	CC	((	1C2W B	2512	2513	CA	((	identical	50.0	75.0	7.5	-105.2
		456	461	GAUACG	)....)		2571	2576	UACGCG	)....)					
8	12	55	58	UACU	(..(	1NWX 0	2489	2492	CUCG	(..(	identical	33.3	75.0	3.5	-174.1
		442	449	AACGUAGA	)......)		2550	2557	CACGCGAG	)......)					
9	6	60	62	UCU	(.(	2GY9 A	80	82	UCU	(.(	identical	83.3	100.0	15.0	-96.7
		438	440	AAA	).)		72	74	AGA	).)					
10	21	66	81	ACAUAUAUGUAAACAG	(.....(	missing in dictionary					tertiary structure element is generated				
		127	129	CAA	).(										
		433	434	UU	))										
11	14	84	90	AAAAAAG	(.....(	2AAR 0	2540	2546	AUUAAAG	(.....(	identical	64.3	71.4	3.5	-113.0
		97	100	CCAC	)..(		2496	2499	CAUC	)..(					
		122	124	GCU	).)		2524	2526	GUU	).)					
12	6	91	96	GUCGUC	(....)	3JYX 5	1022	1027	GUCUUC	(....)	identical	83.3	83.3	8.9	-110.4
13	7	108	114	UCUCUUG	(.....)	2GYB A	803	809	UGUCUCG	(.....)	identical	71.4	85.7	15.0	-90.6
14	9	134	135	CG	((	1NTB B	35	36	CG	((	identical	77.8	77.8	2.9	-146.1
		422	428	CCUUUCG	).....)		7	13	CAUUUGG	).....)					
15	5	137	139	CAC	(.(	1YL4 A	1242	1244	CAC	(.(	identical	100.0	100.0	5.5	-91.0
		419	420	GG	))		1255	1256	GG	))					
16	6	143	144	AU	((	1R2P A	8	9	AU	((	identical	83.3	100.0	- [d)]	-70.2

		412	415	AUGU	)..)		24	27	ACGU	)..)					
17	9	146 154 407	147 156 410	GG CAG UAAC	(( ).( )..)	2UUC A	738 570 635	739 572 638	CG CGG CUAG	(( ).( )..)	identical	44.4	66.7	3.1	-55.7
18	6	148	153	UUUAAG	(....)	3CMA 0	732	737	UUCAAG	(....)	identical	83.3	100.0	2.8	-54.6
19	19	163 307 388	164 310 400	GG CAGU AAAAACGGCAAGC	(( )..( ).....)	missing in dictionary					tertiary structure element is generated				
20	6	170 299	172 301	GCG CAC	(.( ).)	1U9S A	103 117	105 119	GCG CAC	(.( ).)	identical	100.0	100.0	2.9	-63.8
21	19	173 191 290	177 195 298	CGGCU ACUGA UAUAUUAAG	(...( )...( ).....)	missing in dictionary					tertiary structure element is generated				
22	7	181	187	CCGUCUG	(.....)	3JYX 5	400	406	CCUUCGG	(.....)	identical	71.4	71.4	8.9	-77.1
23	8	198 284	201 287	UCUU AUCA	(..( )..)	3I8G 1	1755 1505	1758 1508	UUUU AUCA	(..( )..)	identical	87.5	100.0	3.1	-54.4
24	14	205 269	206 280	CG UCCACCCAAAGG	(( ).....)	missing in dictionary					tertiary structure element is generated				
25	12	210 260	215 265	CAUUUU AUCCCG	(....( )....)	2WR Q 2WR A	1285 1311	1290 1316	CGGAUU AUGAAG	(....( )....)	identical	50.0	58.3	3.6	-4.3
26	10	220 252	225 255	GGUCGU AAAC	(....( )..)	2OGO 0	1503 1514	1508 1517	GGUCAG CUAC	(....( )..)	identical	60.0	70.0	3.7	-94.3
27	5	227 249	229 250	ACG CU	(.( ))	1BVJ A	5 18	7 19	ACG CU	(.( ))	identical	100.0	100.0	- [d]	-72.0
28	9	231 246	237 247	UUCUCUG CA	(.....( ))	1NTA A 1NTA B	7 35	13 36	CAUUUGG CG	(.....( ))	identical	33.3	77.8	2.9	-155.0
29	6	239	244	GCACAC	(....)	2WH4 A	681	686	GCACGC	(....)	identical	83.3	100.0	3.5	-47.8
30	22	313 364 379	325 365 385	GAACCUAAAUAAG CC GAAACCC	(.....( )( ).....)	missing in dictionary					tertiary structure element is generated				
31	6	328 359	330 361	UAA UAG	(.( ).)	2QBA B	2446 2507	2448 2509	CAA UAG	(.( ).)	identical	83.3	100.0	3.5	-43.9
32	16	332 350	339 357	AGUUCUAC GGCACAAU	(.....( ).....)	2VHP A	673 710	680 717	AGAAUUCC GGAGGAAU	(.....( ).....)	identical	56.2	68.8	3.7	-151.5
33	10	340	349	CGAGACUAAG	(........)	1P9X 0	2383	2392	CGUGUGGAAG	(........)	identical	60.0	60.0	3.4	-99.2
34	7	369	375	GUAGCGC	(.....)	1U9S A	10	16	GUAACGC	(.....)	identical	85.7	100.0	2.9	-58.3
Stems															
1	4	5 494	6 495	UG CA	(( ))	3MS0 A	894 1373	895 1374	UG CA	(( ))	identical	100.0	100.0	3.6	-38.4
2	10	7 488	11 492	AGCGG CCGCU	((((( ))))))	2VHM B	1396 1410	1400 1414	AGCGG CCGCU	((((( ))))))	identical	100.0	100.0	3.7	-206.3
3	10	19 482	23 486	UGUAU AUACG	((((( ))))))	3CF5 X	835 844	839 848	UGUAU GUACA	((((( ))))))	identical	80.0	100.0	3.3	-178.4
4	6	25 478	27 480	AUG CGU	((( )))	1VOZ A	595 627	597 629	AUG CGU	((( )))	identical	100.0	100.0	11.5	-93.9
5	8	29 474	32 477	CGAC GUUG	(((( ))))	1J5A A	1178 1193	1181 1196	CAAC GUUG	(((( ))))	identical	87.5	100.0	3.5	-144.3

6	10	37 468	41 472	CCGGC GCCGG	((((( )))))	1P9X 0	589 1269	593 1273	CCGGC GCCGG	((((( )))))	identical	100.0	100.0	3.4	-104.8
7	12	42 461	47 466	CUUCGC GCGAAG	(((((( ))))))	1QVF 0	930 1033	935 1038	CUCCGC GCGGGG	(((((( ))))))	identical	75.0	100.0	3.1	-111.2
8	16	48 449	55 456	CGUUAACU AGUUAACG	((((((( )))))))	3E1B B	268 285	275 292	CAUUAACU GGUUAAUG	((((((( )))))))	identical	81.2	100.0	9.0	-227.7
9	6	58 440	60 442	UCU AGA	((( )))	2FRL A	7 15	9 17	UCU AGA	((( )))	identical	100.0	100.0	- [d]	-100.0
10	10	62 434	66 438	UCAUA UGUGA	((((( )))))	2OGO 0	2827 2836	2831 2840	GCAUA UGUGU	((((( )))))	identical	80.0	80.0	3.7	-12.8
11	8	81 124	84 127	GGAA UUCC	(((( ))))	1W2B 0	1408 1696	1411 1699	GGAU GUCC	(((( ))))	identical	75.0	75.0	3.5	-118.2
12	4	90 96	91 97	GG CC	(( ))	3BBX B	1593 1600	1594 1601	GG CC	(( ))	identical	100.0	100.0	10.0	-69.9
13	18	100 114	108 122	CUGAGUGCU GGUAUUCAG	((((((((( )))))))))	1YJ9 0	2381 2399	2389 2407	CAGUGUUCU GGAACGCUG	((((((((( )))))))))	identical	61.1	66.7	2.9	-340.3
14	12	129 428	134 433	AGUGGC GCCAUU	(((((( ))))))	3CUL C	2 12	7 17	GAUGGC GCCAUU	(((((( ))))))	identical	83.3	100.0	2.8	-93.7
15	6	135 420	137 422	GGC GCC	((( )))	1HNX A	489 508	491 510	GGC GCC	((( )))	identical	100.0	100.0	3.4	-117.6
16	10	139 415	143 419	CCGUA UACGG	((((( )))))	1JGQ D	178 190	182 194	CCGGA UCCGG	((((( )))))	identical	80.0	80.0	5.0	-188.5
17	6	144 410	146 412	UCG CGA	((( )))	3EPJ F	71 135	73 137	UCG CGA	((( )))	identical	100.0	100.0	3.1	-58.3
18	4	147 153	148 154	GU GC	(( ))	1PNY 0	1865 1871	1866 1872	GU GC	(( ))	identical	100.0	100.0	9.5	-97.6
19	16	156 400	163 407	GAUAGACG CGUCUAUU	((((((( )))))))	1VS6 B	1284 1298	1291 1305	CAGCGACG CGUUGUUG	((((((( )))))))	identical	56.2	62.5	3.5	-270.5
20	14	164 301	170 307	GAAGGAG CUCCUUC	((((((( )))))))	3JYV A	1432 1485	1438 1491	GACGGAG CUCCGUC	((((((( )))))))	identical	85.7	85.7	8.9	-298.8
21	4	172 298	173 299	GC GC	(( ))	3D5B A	1116 1124	1117 1125	GC GC	(( ))	identical	100.0	100.0	3.2	-103.0
22	10	177 187	181 191	UGCGC GCGUA	((((( )))))	2HEM A	6 15	10 19	GGCGC GCGUC	((((( )))))	identical	80.0	80.0	- [d]	-259.9
23	8	195 287	198 290	AUAU AUGU	(((( ))))	2BYT E	110 125	113 128	GCAU AUGU	(((( ))))	identical	75.0	100.0	3.3	-104.9
24	10	201 280	205 284	UCUCC GGAGA	((((( )))))	1YL3 A	2595 2621	2599 2625	UCUCC GGAGG	((((( )))))	identical	90.0	100.0	5.5	-160.3
25	10	206 265	210 269	GGAGC GCUCU	((((( )))))	3BBO A	2647 2802	2651 2806	AGAGC GCUCU	((((( )))))	identical	90.0	100.0	9.4	-183.4
26	12	215 255	220 260	UGUAGG CCUAUA	(((((( ))))))	3A3A A	28 41	33 46	UGCAGG CCUGUA	(((((( ))))))	identical	83.3	100.0	3.1	-159.9
27	6	225 250	227 252	UGA UCA	((( )))	3CCU 0	560 595	562 597	UGA UCA	((( )))	identical	100.0	100.0	2.8	-69.2
28	6	229 247	231 249	GCU AGC	((( )))	2WRR A	325 338	327 340	GCU AGC	((( )))	identical	100.0	100.0	3.6	-34.5
29	6	237	239	GAG	(((	1PNX A	402	404	GAG	(((	identical	100.0	100.0	9.5	-89.8

		244	246	CUC	)))		428	430	CUC	)))					
30	8	310 385	313 388	UCGG CCGA	(((( ))))	2QBG B	992 1022	995 1025	UCGG CCGA	(((( ))))	identical	100.0	100.0	3.3	-96.7
31	8	325 361	328 364	GUAU GUAC	(((( ))))	2QAL A	406 433	409 436	GUAU GUAC	(((( ))))	identical	100.0	100.0	3.2	-69.9
32	6	330 357	332 359	ACA UGU	((( )))	1JGO D	162 174	164 176	ACA UGU	((( )))	identical	100.0	100.0	5.6	-108.5
33	4	339 349	340 350	CC GG	(( ))	3MRZ A	1026 1155	1027 1156	CC GG	(( ))	identical	100.0	100.0	3.6	-73.4
34	10	365 375	369 379	CGUUG CAACG	((((( )))))	2QAO B	2935 2947	2939 2951	CGUUG CGACG	((((( )))))	identical	90.0	100.0	3.2	-178.4

[a] encompassing the secondary structure element size, number and length of RNA strands
[b] between the target and source RNA sequence
[c] shows matching of the purine / pyrimidine residues for the target and source RNA of given sequence
[d] the NMR structure as a source

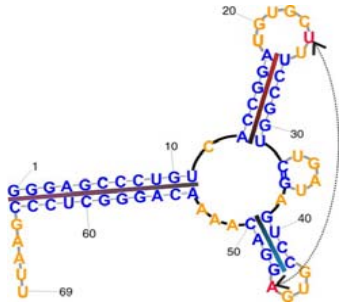
Table S5. MolProbity RNA structure stereochemical quality assessment for the 3D models predicted by RNAComposer for set of 40 benchmark structures described in the Table 1. An assessment includes respective high-resolution X-ray structures.

PDB code and chain	RNA strand length [nt]	clash-score, all atoms		nucleic acid geometry							
				potentially incorrect				outlier bonds [%]		outlier angles [%]	
				sugar puckers		backbone conformations					
		RNA Composer	X-ray	RNA Composer	X-ray	RNA Composer	X-ray	RNA Composer	X-ray	RNA Composer	X-ray
hairpin											
2DR8 B	33	17.92	33.87	1	3	7	6	0.00	0.00	0.00	0.00
3OVA C	34	16.64	6.45	2	2	6	3	0.00	0.00	0.00	17.65
hairpin internal loop											
1JBR D	31	16.93	6.95	0	1	3	7	0.00	6.45	0.00	3.23
2HW8 B	36	12.90	4.28	1	1	3	4	0.00	0.00	0.00	11.11
1ZHO B	38	12.23	12.21	1	1	5	3	0.00	2.63	0.00	13.16
3IAB R	46	16.90	13.50	2	3	11	12	0.00	2.17	0.00	17.39
hairpin internal loops											
1I6U C	37	14.31	9.20	1	4	4	7	0.00	0.00	0.00	8.11
2PXL B	47	15.79	11.47	0	0	5	1	0.00	0.00	0.00	0.00
2VPL B	48	12.24	3.22	2	3	10	8	0.00	0.00	0.00	27.08
2PXB B	49	11.46	11.58	0	0	5	2	0.00	0.00	0.00	0.00
1MZP B	55	13.48	14.00	4	7	10	9	0.00	0.00	0.00	7.27
1KXK A	70	19.07	27.47	1	4	16	15	0.00	0.00	0.00	1.43
three-way junction											
1DK1 B	57	19.57	37.28	3	3	9	13	0.00	3.51	0.00	8.77
1MMS C	58	15.56	14.41	0	0	7	3	0.00	0.00	0.00	0.00
1UN6 E	61	14.23	26.40	1	0	9	6	0.00	0.00	0.00	0.00
three-way junction (hammerhead)											
2QUS A	69	12.63	8.5	0	5	11	19	0.00	1.47	0.00	41.18
three-way junction (riboswitch)											
3LA5 A	71	18.57	6.13	1	2	8	1	0.00	0.00	0.00	7.04
3D2V A	77	18.51	11.03	1	1	11	10	0.00	0.00	0.00	2.60
three-way junction (GMP riboswitch)											
3IWN A	93	7.99	38.36	0	11	13	25	0.00	0.00	0.00	10.75
three-way junction (SRP)											
2V3C M	96	17.70	65.64	2	16	19	52	0.00	56.25	0.00	98.96
1LNG B	97	15.95	41.76	1	10	26	39	0.00	6.19	0.00	49.48
1Z43 A	101	14.38	76.81	1	14	25	54	0.00	35.64	0.00	87.13
3NDB M	136	13.87	31.14	2	14	28	68	0.00	8.09	0.00	74.26
three-way junction (5S rRNA)											
3OFQ B	117	17.48	64.06	2	16	24	44	0.00	0.00	0.00	22.22
3OFR B	118	14.44	33.82	3	17	19	34	0.00	0.00	0.00	36.44
3KIR B	119	15.56	22.34	1	1	23	18	0.00	0.00	0.00	0.84
3I9E B	120	13.92	35.83	0	6	18	21	0.00	0.00	0.00	5.00
1VQO 9	122	14.01	15.01	1	2	24	16	0.00	0.00	0.00	0.82
four-way junction (tRNA)											
1EXD B	73	8.10	46.77	2	12	16	19	0.00	0.00	0.00	12.33
1U0B A	74	16.44	22.74	7	8	15	15	0.00	1.35	0.00	1.35
1FFY T	75	19.47	26.39	6	12	18	25	0.00	0.00	0.00	5.33
2J00 W	76	18.44	40.92	2	3	18	15	0.00	0.00	0.00	6.58
four-way junction (riboswitch)											
3IQP A	94	13.12	35.29	5	10	17	27	0.00	2.13	0.00	11.70
five-way junction (tRNA)											
3AM1 B	81	16.08	42.46	4	6	14	22	0.00	0.00	0.00	30.86
1WZ2 C	88	13.06	32.09	4	7	26	24	0.00	0.00	0.00	6.82
3ADB C	92	17.18	21.20	1	1	16	13	0.00	1.09	0.00	4.35
pseudoknot											
2QWY A	52	22.67	39.77	2	3	13	15	0.00	0.00	0.00	1.92
pseudoknot (HDV ribozyme)											
1CX0 B	72	12.96	24.09	3	8	16	16	0.00	0.00	0.00	9.72
P4-P6 ribozyme domain											
2R8S R	159	12.89	2.34	10	5	21	14	10.06	0.00	10.06	8.81
M-box riboswitch											
3PDR A	161	17.83	8.11	1	2	30	17	0.00	0.00	0.00	11.80
average		**15.31**	**25.62**	**2.03**	**5.60**	**14.47**	**18.05**	**0.25**	**3.17**	**0.25**	**16.59**

Table S6. RNA 3D structure prediction details for the n-way junctions

PDB code 2QUS; three-way junction (hammerhead)
GGGAGCCCUGUCACCGGAUGUGCUUUCCGGUCUGAUGAGUCCGUGAGGACAAAACAGGGCUCCCGAAUU
((((((((((.((((((.....[.))))))(....).((((...]))))...)))))))))).....

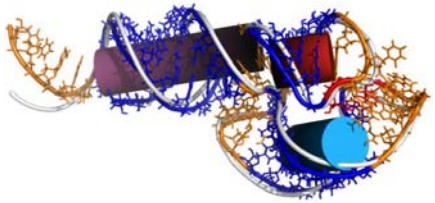
Input data
Secondary structure derived from the RNA FRABASE
Note the square bracket for **U24-A46** loop-loop interaction



Secondary structure visualization

10 superimposed 3D models

Model No.	Energy [kcal/mol]	r.m.s.d. [Å]
1	-1622	3.7
2	-1637	3.4
3	-1585	3.8
4	-1598	3.7
5	-1555	4.3
6	-1622	3.6
7	-1584	3.8
8	-1620	4.1
9	-1601	3.8
10	-1580	3.9



Lowest r.m.s.d. 3D model (No. 2)

Details of the model No. 2 prediction [a)]

No.	Size [nt]	Target secondary structure element				Source tertiary structure element					Selection criteria				
		localization		secondary structure		localization			secondary structure		secondary structure topology b)	sequence similarity [%] c)	pyrimidines / purines compatibility [%] d)	source structure resolution [Å]	energy [kcal/mol]
		residues		sequence	topology	PDB ID	residues		sequence	topology					
		first	last				first	last							
Single strands															
0	6	64	69	CGAAUU	).....	2QUW D	133	138	CGAAUU	).....	identical	100.0	100.0	2.2	-78.8
Loops															
1	13	11 31 37 50	13 32 39 54	UCA UC GAG CAAAA	(.( )( ).( )...)	2GOZ B 2GOZ A	48 14 20 35	50 15 22 39	UCC GC GAG CGAAA	(.( )( ).( )...)	identical	76.9	84.6	2.2	-267.9
2	9	18	26	AUGUGCUUU	(.....[.)	2QUW B	18	26	AUGUGCUUU	(.....[.)	identical	100.0	100.0	2.2	-98.7
3	6	32	37	CUGAUG	(....)	2GOZ A	15	20	CUGAUG	(....)	identical	100.0	100.0	2.2	-127.2
4	6	42	47	CGUGAG	(...])	2QUW D	111	116	CGUGAG	(...])	identical	100.0	100.0	2.2	-87.4
Stems															
1	22	1 54	11 64	GGGAGCCCUGU ACAGGGCUCCC	(((((((((( ))))))))))	2HGQ A	15 541	25 551	GGGCCCACGGU ACCGUGGGCUU	(((((((((( ))))))))))	identical	54.5	63.6	5.5	-493.5
2	12	13 26	18 31	ACCGGA UCCGGU	(((((( ))))))	2G5K A 2G5K B	10 33	15 38	UCCGGA UCCGGA	(((((( ))))))	identical	83.3	83.3	2.8	-200.6
3	2	32 37	32 37	C G	( )	single base pair - not used					single base pair - not used				
4	8	39 47	42 50	GUCC GGAC	(((( ))))	2GOZ A 2GOZ A	22 32	25 35	GUCC GGAC	(((( ))))	identical	100.0	100.0	2.2	-171.5

PDB code 2QUS; three-way junction (hammerhead)

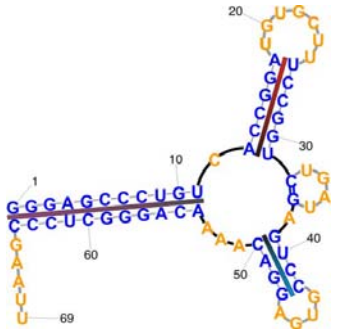
GGGAGCCCUGUCACCGGAUGUGCUUUCCGGUCUGAUGAGUCCGUGAGGACAAAACAGGGCUCCCGAAUU

((((((((((.((((((.......))))))(....).((((....))))...))))))))))).....

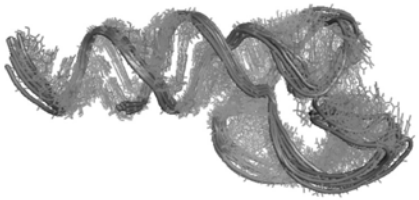
Input data

Secondary structure derived from the RNA FRABASE

A square bracket to note **U24-A46** interaction was purposefully removed.

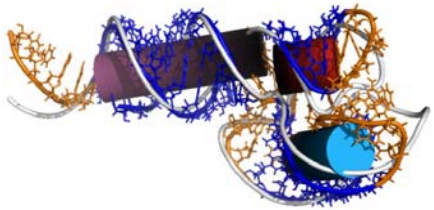


Secondary structure visualization



10 superimposed 3D models

Model No.	Energy [kcal/mol]	r.m.s.d. [Å]
1	-1670	6.4
2	-1620	6.0
3	-1646	6.6
4	-1611	5.9
5	-1664	6.0
6	-1615	7.2
7	-1647	5.9
8	-1643	7.3
9	-1631	7.0
10	-1642	6.5



Lowest r.m.s.d. 3D model (No. 4)

Details of the model No. 4 prediction [a)]

No.	Size [nt]	Target secondary structure element				Source tertiary structure element					Selection criteria				
		localization		secondary structure		localization			secondary structure		secondary structure topology b)	sequence similarity [%] c)	pyrimidines / purines compatibility [%] d)	source structure resolution [Å]	energy [kcal/mol]
		residues		sequence	topology	PDB ID	residues		sequence	topology					
		first	last				first	last							
Single strands															
0	6	64	69	CGAAUU	).....	2QUW D	133	138	CGAAUU	).....	identica1	100.0	100.0	2.2	-78.8
Loops															
1	13	11 31 37 50	13 32 39 54	UCA UC GAG CAAAA	(.( )( ).( )...)	2GOZ B 2GOZ A	48 14 20 35	50 15 22 39	UCC GC GAG CGAAA	(.( )( ).( )...)	identical	76.9	84.6	2.2	-267.9
2	9	18	26	AUGUGCUUU	(.....)	3JYX 5	1691	1699	AUGAGAACU	(.....)	identical	55.6	66.7	8.9	-82.2
3	6	32	37	CUGAUG	(....)	2QUW D	101	106	CUGAUG	(....)	identical	100.0	100.0	2.2	-125.4
4	6	42	47	CGUGAG	(....)	2VQF A	1059	1064	CGUGAG	(....)	identical	100.0	100.0	2.9	-51.7
Stems															
1	22	1 54	11 64	GGGAGCCCUGU ACAGGGCUCCC	(((((((((( ))))))))))	2HGU A	15 541	25 551	GGGCCCACGGU ACCGUGGGCUU	(((((((((( ))))))))))	identical	54.5	63.6	4.5	-464.9
2	12	13 26	18 31	ACCGGA UCCGGU	(((((( ))))))	3ADB D	120 133	125 138	GCCGGA UCCGGC	(((((( ))))))	identical	83.3	100.0	2.8	-230.7
3	2	32 37	32 37	C G	( )						single base pair - not used				
4	8	39 47	42 50	GUCC GGAC	(((( ))))	3JYX 5	458 470	461 473	GUCC GGAC	(((( ))))	identical	100.0	100.0	8.9	-135.5

PDB code 3ADB; five-way-junction (tRNA)

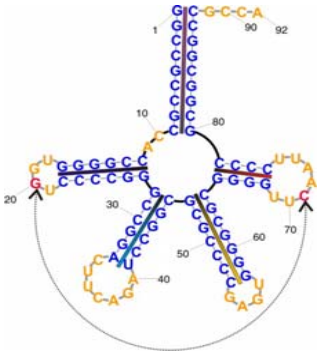
GGCCGCCGCCACCGGGGUGGUCCCCGGGCCGGACUUCAGAUCCGGCGCGCCCCGAGUGGGGCGCGGGGUUCAAUUCCCCGCGGCGGCCGCCA

((((((((((..((((((..[.))))))((((((.....))))))((((((....))))))((((..].....))))))))))))).....

Input data

Secondary structure derived from the RNA FRABASE

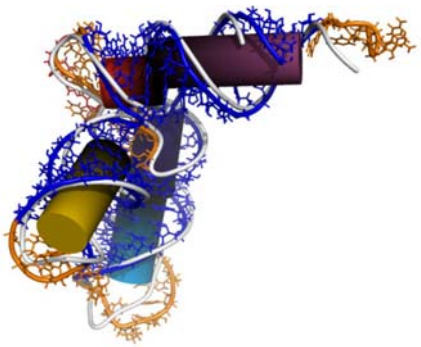
Note the square bracket for **G20-C71** loop-loop interaction



Secondary structure visualization

10 superimposed 3D models

Model No.	Energy [kcal/mol]	r.m.s.d. [Å]
1	-2457	3.9
2	-2446	5.7
3	-2349	6.4
4	-2403	3.6
5	-2365	3.6
6	-2379	5.0
7	-2434	4.4
8	-2408	5.9
9	-2457	3.6
10	-2414	4.9



Lowest r.m.s.d. 3D model (No. 4)

Details of the model No. 4 prediction [a)]

No.	Size [nt]	Target secondary structure element				Source tertiary structure element					Selection criteria				
		localization		secondary structure		localization			secondary structure		secondary structure topology b)	sequence similarity [%] c)	pyrimidines / purines compatibility [%] d)	source structure resolution [Å]	energy [kcal/mol]
		residues		sequence	topology	PDB ID	residues		sequence	topology					
		first	last				first	last							
Single strands															
0	5	88	92	CGCCA	))....	3ADC D	180	184	CGCCA	))....	identical	100.0	100.0	2.9	-47.9
Loops															
1	12	9	12	CCAC	(..(	3ADD C	9	12	CCAC	(..(	identical	100.0	100.0	2.4	-9.2
		27	28	GG	)(		27	28	GG	)(					
		46	47	CG	)(		46	47	CG	)(					
		64	65	CG	)(		64	65	CG	)(					
		79	80	CG	))		79	80	CG	))					
2	6	17	22	GUGGUC	(..[.)	3ADD C	17	22	GUGGUC	(..[.)	identical	100.0	100.0	2.4	-111.3
3	9	33	41	ACUUCAGAU	(.......)	3ADC D	125	133	ACUUCAGAU	(.......)	identical	100.0	100.0	2.9	-67.1
4	6	53	58	CGAGUG	(....)	3ADD D	145	150	CGAGUG	(....)	identical	100.0	100.0	2.4	-98.3
5	9	68	76	GUUCAAUUC	(..]....)	1ASZ R	52	60	GUUCAAUUC	(..]....)	identical	100.0	100.0	3.0	-165.8
Stems															
1	18	1	9	GGCCGCCGC	(((((((((	3ADC C	1	9	GGCCGCCGC	(((((((((	identical	100.0	100.0	2.9	-349.3
		80	88	GCGGCGGCC	)))))))))		80	88	GCGGCGGCC	)))))))))					
2	12	12	17	CCGGGG	((((((	3ADC D	104	109	CCGGGG	((((((	identical	100.0	100.0	2.9	-240.5
		22	27	CCCCGG	))))))		114	119	CCCCGG	))))))					
3	12	28	33	GCCGGA	((((((	3ADC C	28	33	GCCGGA	((((((	identical	100.0	100.0	2.9	-220.5
		41	46	UCCGGC	))))))		41	46	UCCGGC	))))))					
4	14	47	53	GCGCCCC	(((((((	3ADC D	139	145	GCGCCCC	(((((((	identical	100.0	100.0	2.9	-279.7
		58	64	GGGGCGC	)))))))		150	156	GGGGCGC	)))))))					
5	8	65	68	GGGG	((((	3FIN A	2598	2601	GGGG	((((	identical	100.0	100.0	6.4	-40.7
		76	79	CCCC	))))		2730	2733	CCCC	))))					

PDB code 3ADB; five-way-junction (tRNA)

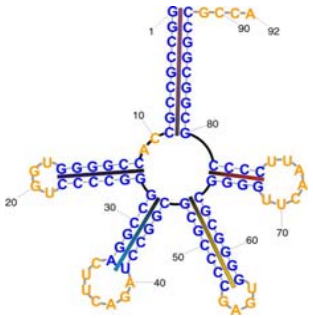
GGCCGCCGCCACCGGGGUGGUCCCCGGGCCGGACUUCAGAUCCGGCGCGCCCCGAGUGGGGCGCGGGGUUCAAUUCCCCGCGGCGGCCGCCA

(((((((((..(((((((....)))))))(((((.......)))))(((((((....)))))))(((.......)))))))))))....

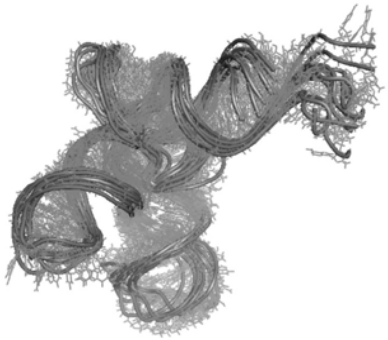
Input data

Secondary structure derived from the RNA FRABASE

The square bracket to note G20-C71 interaction was removed.

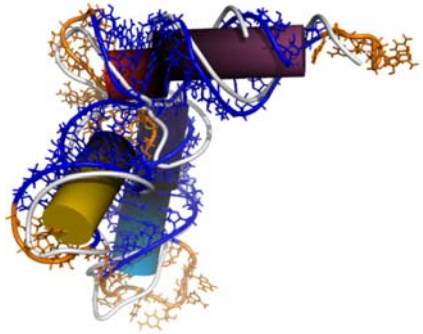


Secondary structure visualization



10 superimposed 3D models

Model No.	Energy [kcal/mol]	r.m.s.d. [Å]
1	-2388	5.1
2	-2333	5.1
3	-2361	6.7
4	-2319	6.3
5	-2393	4.8
6	-2350	4.8
7	-2322	6.3
8	-2372	6.2
9	-2334	5.7
10	-2389	6.7



Lowest r.m.s.d. 3D model (No. 5)

Details of the model No. 5 prediction [a)]

No.	Size [nt]	Target secondary structure element				Source tertiary structure element					Selection criteria				
		localization		secondary structure		localization			secondary structure		secondary structure topology b)	sequence similarity [%] c)	pyrimidines / purines compatibility [%] d)	source structure resolution [Å]	energy [kcal/mol]
		residues		sequence	topology	PDB ID	residues		sequence	topology					
		first	last				first	last							
Single strands															
0	5	88	92	CGCCA	))....	1FIR A	72	76	CGCCA	))....	identical	100.0	100.0	3.3	-46.1
Loops															
1	12	9 27 46 64 79	12 28 47 65 80	CCAC GG CG CG CG	(..( )( )( )( ))	3ADD C	9 27 46 64 79	12 28 47 65 80	CCAC GG CG CG CG	(..( )( )( )( ))	identical	100.0	100.0	2.4	-9.2
2	6	17	22	GUGGUC	(..[.)	3JYX 5	1022	1027	GUCUUC	(....)	identical	66.7	66.7	8.9	-110.4
3	9	33	41	ACUUCAGAU	(.......)	3ADC D	125	133	ACUUCAGAU	(.......)	identical	100.0	100.0	2.9	-67.1
4	6	53	58	CGAGUG	(....)	3ADD C	53	58	CGAGUG	(....)	identical	100.0	100.0	2.4	-13.7
5	9	68	76	GUUCAAUUC	(..]....)	486D A	52	60	GUUCAAUUC	(.......)	identical	100.0	100.0	7.5	-2.9
Stems															
1	18	1 80	9 88	GGCCGCCGC GCGGCGGCC	((((((((( )))))))))	3ADD D	93 172	101 180	GGCCGCCGC GCGGCGGCC	((((((((( )))))))))	identical	100.0	100.0	2.4	-231.7
2	12	12 22	17 27	CCGGGG CCCCGG	(((((( ))))))	3ADD D	104 114	109 119	CCGGGG CCCCGG	(((((( ))))))	identical	100.0	100.0	2.4	-252.4
3	12	28 41	33 46	GCCGGA UCCGGC	(((((( ))))))	3ADC D	120 133	125 138	GCCGGA UCCGGC	(((((( ))))))	identical	100.0	100.0	2.9	-242.1
4	14	47 58	53 64	GCGCCCC GGGGCGC	((((((( )))))))	3ADC D	139 150	145 156	GCGCCCC GGGGCGC	((((((( )))))))	identical	100.0	100.0	2.9	-279.7
5	8	65 76	68 79	GGGG CCCC	(((( ))))	3I8F A	2650 2782	2653 2785	GGGG CCCC	(((( ))))	identical	100.0	100.0	3.1	-171.6

[a] all the 3D structure elements comprised by the respective crystal PDB structure were excluded from the dictionary
[b] encompassing the structure element size, number and length of RNA strands
[c] similarity between the target and source RNA sequence
[d] shows matching of the purine / pyrimidine residues for the target and source RNA of given sequence

TABLE S7. The quality of 3D models predicted[a)] for the 5S rRNA *H. Marismortui* (PDB code 1FFK)

Sequence:
UUAGGCGGCCACAGCGGUGGGGUUGCCUCCCGUACCCAUCCCGAACACGGAAGAUAAGCCCACCAGCGUUCCGGGGAGUAC
UGGAGUGCGCGAGCCUCUGGGAAACCCGGUUCGCCGCCACC

Input reference secondary structure
(RNA FRABASE database):
...((((((....((((((((.....((((((...(..
...)...))))..))....))))))..))...((((((...
..((((((.((....))))))))....))))))...))))
))...

Prediction output – 10 models.

Structure models energy [c)] and selected parameters defining models quality [d), e)]

Model	energy [kcal/mol]	r.m.s.d. [Å]	INF^{cbp}	INF^{all}
1	-2952	3.3	1.00	0.83
2	n.a.	3.6	1.00	0.83
3	-2920	5.6	1.00	0.81
4	-2902	4.0	1.00	0.82
5	-2960	3.8	1.00	0.83
6	-2903	3.9	1.00	0.81
7	-2871	4.5	1.00	0.79
8	-2881	3.8	1.00	0.82
9	-2865	3.6	1.00	0.81
10	-2925	3.5	1.00	0.83
mean		4.0	1.00	0.82
st. dev.		0.6	0.00	0.02

Time elapsed to generate 10 models**: 3 min. 49 sec.**

Input determined in this work secondary structure
RNAstructure & SHAPE ; MCC [b)] = 0.99):
...((((((....((((((((.....(((((...(..
...)...))))..)....))))))..))...((((((...
..((((((.((....))))))))....))))))...))))
))...

Prediction output – 10 models.

Structure models energy [c)] and selected parameters defining models quality [d), e)]

Model	energy [kcal/mol]	r.m.s.d. [Å]	INF^{cbp}	INF^{all}
1	-2846	11.4	0.94	0.81
2	-2905	10.9	1.00	0.79
3	-2790	15.1	0.94	0.77
4	-2872	13.2	0.97	0.78
5	-2749	9.4	0.97	0.74
6	-2888	13.1	1.00	0.77
7	-2854	13.7	0.94	0.80
8	-2873	9.5	0.97	0.76
9	-2837	14.1	0.95	0.75
10	-2853	10.6	0.94	0.77
mean		12.1	0.96	0.77
st. dev.		1.9	0.03	0.03

Time elapsed to generate 10 models**: 4 min. 15 sec.**

[a)] upon validation all the 3D structure elements comprised by the respective crystal PDB structure were excluded from the dictionary
[b)] Matthews correlation coefficient (41) corresponds to the RNA FRABASE secondary structure parsed from the tertiary PDB structure
[c)] potential energy of the final 3D structures were calculated with XPLOR-NIH ver. 2.2 program (26) using parameters from the "dna-rna allatom.param" file
[d)] r.m.s.d. values for all heavy atoms were calculated with XPLOR ver. 2.2 program (26)
[e)] INF^{cbp} describes the interaction network fidelity (33) values over canonical base paring only; the INF^{all} describes all the base pairing interactions and base stacking . Base pair interactions and base stacking network from tertiary PDB structure were obtained using the RNAView (34) and MC-Annotate (35) programs, respectively.

Table S8. Accuracy of RNA 3D models predicted by RNAComposer, MC-Fold/MC-Sym (21) and iFoldRNA servers (15).

PDB code and chain	Strand length [nt]	RNAComposer			MC-Sym module			iFoldRNA		
		global r.m.s.d. [Å]	INF^{all}	INF^{cbp}	global r.m.s.d. [Å]	INF^{all}	INF^{cbp}	global r.m.s.d. [Å]	INF^{all}	INF^{cbp}
2HW8 B	36	1.7	0.89	1.00	10.8	0.68	1.00	9.5	0.48	0.59
1I6U C	37	2.1	0.90	1.00	2.6	0.83	1.00	4.1	0.62	0.61
1ZHO B	38	1.1	0.83	1.00	10.6	0.76	1.00	11.4	0.58	0.62
2VPL B	48	4.9	0.79	1.00	10.9	0.74	1.00	11.0	0.67	0.78
2PXB B	49	2.5	0.91	1.00	11.1	0.70	1.00	16.2	0.31	0.18
1DK1 B	57	2.4	0.52	0.98	13.2	0.51	1.00	12.5	0.34	0.80
1KXK A	70	9.3	0.74	0.98	10.1	0.69	1.00	10.0	0.58	0.68
3AM1 B	81	5.7	0.78	1.00	12.3	0.76	0.99	21.5	0.54	0.86
Average		**3.7**	**0.80**	**1.00**	**10.2**	**0.71**	**1.00**	**12.0**	**0.52**	**0.64**

Table S9. MolProbity RNA structure stereochemical quality assessment for the 3D models predicted by RNAComposer, MC-Fold/MC-Sym (21) and iFoldRNA (15) servers

PDB code and chain	RNAComposer			MC-Sym module			iFoldRNA		
	clash-score, all atoms	outlier bonds [%]	outlier angles [%]	clash-score, all atoms	outlier bonds [%]	outlier angles [%]	clash-score, all atoms	outlier bonds [%]	outlier angles [%]
2HW8 B	12.90	0.00	0.00	92.78	66.67	91.67	105.74	13.89	77.78
1I6U C	14.31	0.00	0.00	72.33	43.24	97.30	104.86	21.62	72.97
1ZHO B	12.23	0.00	0.00	110.84	71.05	92.11	103.63	21.05	71.05
2VPL B	12.24	0.00	0.00	172.57	79.17	100.00	99.60	22.92	66.67
2PXB B	11.36	0.00	0.00	117.91	71.43	93.88	106.52	22.45	89.80
1DK1 B	19.57	0.00	0.00	125.48	66.67	85.96	109.30	26.32	71.93
1KXK A	19.07	0.00	0.00	95.74	71.43	95.71	110.59	22.86	72.86
3AM1 B	16.08	0.00	0.00	123.61	65.43	90.12	106.55	25.93	71.60
Average	**14.72**	**0.00**	**0.00**	**113.91**	**66.89**	**93.34**	**105.85**	**22.13**	**74.33**

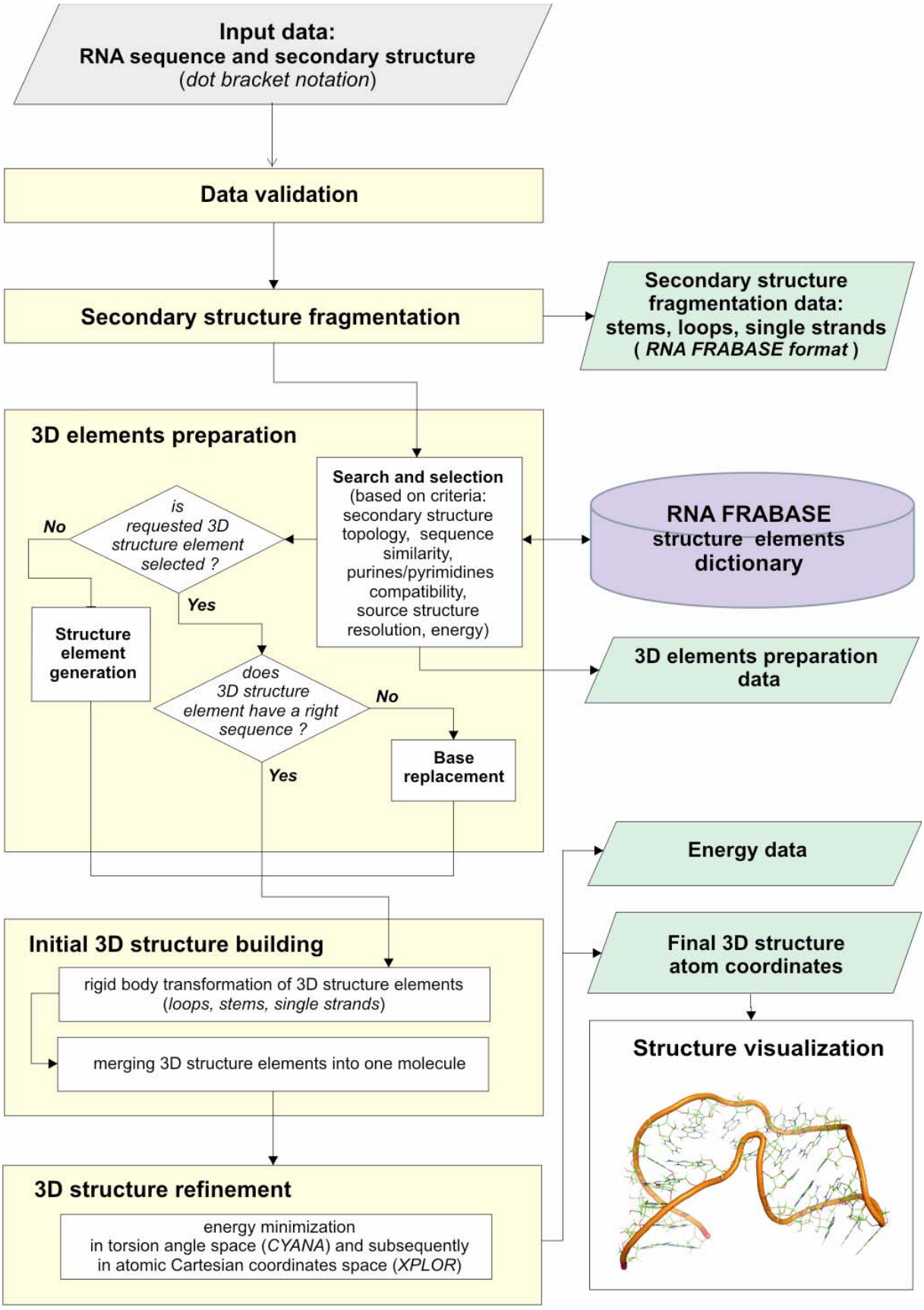


FIGURE S1. Detailed flowchart of the machine translation method to predict RNA 3D structures from secondary structure. User-accessible output files are shown as the rhombohedras (*in green*)

A

```
>Randomized_500
GUACUGAGCGGACUAAUCUGUAUAAUGUCGACGAAGCCGGCCUUCGCCGUUAACUACUCUCUCAUACAUAUAUGUAAACAGGAAAAAAAGGUCG
UCCCACUGAGUGCUCUCUUGGUAUUCAGCUUCCAAGUGGCGGCACCGUAUCGGUUUAAGCAGAUAGACGGAAGGAGCGCGGCUGCGCCGUCUGC
GUACUGAUAUCUUCUCCGGAGCAUUUUGUAGGGUCGUGACGCUUCUCUGAGCACACUCAGCUCAAACCUAUAUCCCGCUCUCCACCCAAAGGGA
GAUCAUGUAUAUUAAGCACUCCUUCAGUCGGAACCUAAAUAAGUAUAACAGUUCUACCGAGACUAAGGGCACAAUGUAGUACCGUUGUAGCGCA
ACGAAACCCCGAAAAACGGCAAGCGUCUAUUAACGAUGUACGGGCCCUUUCGCCAUUUGUGAAAGAACGUAGAGUUAACGAUACGCGAAGCGCC
GGAGUUGCGUCAUACGCCCGCUACAUUCAU
....(((((((.......(((((.(((.((((....(((((((((((((((((((..(((.(((((.............((((.....((...
.))..(((((((((.....)))))))))).))))).(((((((((.((((((((((....)).(((((((((((((((.((...(((((.....))
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))..))))).......)).)))))))..((((...........((((.(((......((........)).....))).))))(((((.....))
)))).....))))...........)))))))..)))..)))))))).....))))))))))).)))......)))))))....))))))).)))
)).)))))))).)))))..)))))..)).....
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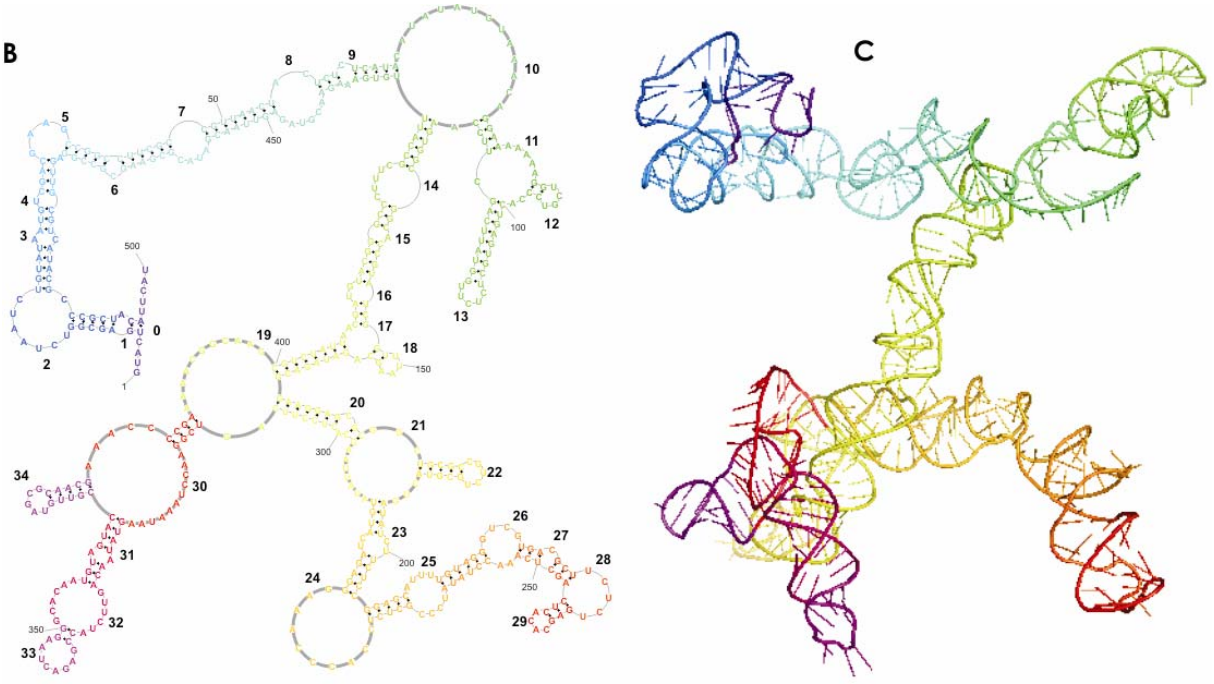

FIGURE S2. 3D structure prediction for the 500-mer RNA with randomized sequence. (**A**) Input data. Secondary structure generated with the arbitrary chosen RNAfold program (39). (**B**) 500-mer RNA secondary structure visualized with Pseudoviewer (43) and loops numbered. Marked with the thicker line loops (10, 19, 21, 24, 30) are missing in the RNA FRABASE dictionary and therefore are subjected to a generation procedure. (**C**) Visualized with PYMOL (44) final RNA 3D structure (best of ten models, energy -9832 kcal/mol; MMC=0.98)

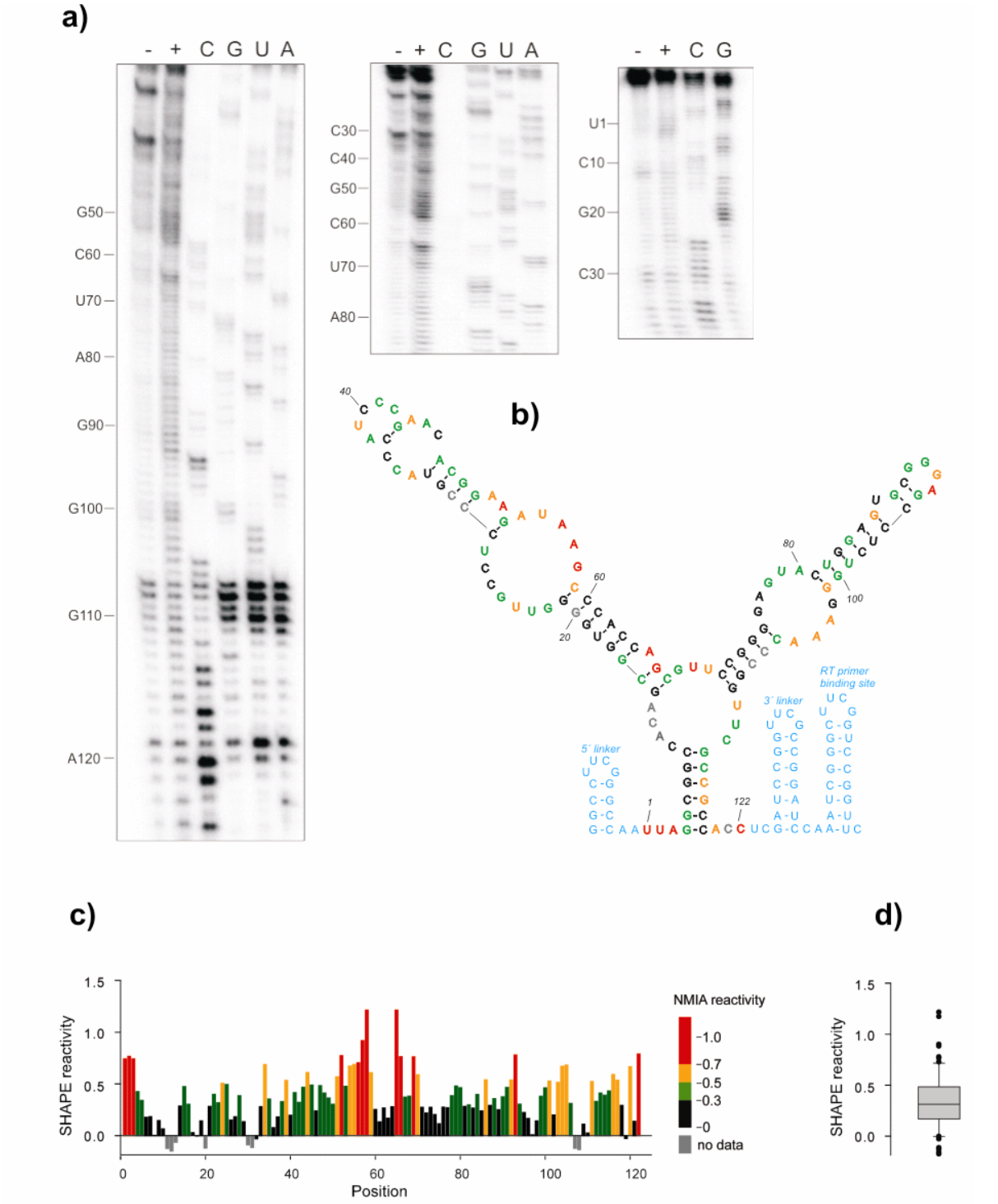

FIGURE S3. Determination of the 5S rRNA H. Marismortui secondary structure. (**a**) Typical gel electrophoresis patterns for SHAPE analysis of the 5S rRNA. Lanes (-) represent control sample with untreated RNA; lanes (+) NMIA modification, A, C, G and U are sequencing lanes. (**b**) Secondary structure of the 122-mer 5S rRNA containing 3' structure cassette and 5' flanking sequence to facilitate the analysis of entire RNA by primer extension (36). Nucleotide residues accessibilities to NMIA are given in colours and according to scale. (**c**) Processed SHAPE reactivities as a function of nucleotide position. Red and orange bars reflect reactive positions in the RNA. (**d**) Box plot analysis of distinct reactivity distributions for the 5S rRNA. Box outline middle 50% of dataset; the median is shown with heavy line. Circles indicate extreme values: 1.5 times the interquartile range (boxed). Horizontal lines above and below the box are the largest or smallest non-outlier values.

DATASET S1. Input secondary structures for the 3D structure prediction of 95 RNAs with randomized sequence

No.	Strand length [nt]	The lowest energy secondary structure predicted with RNAfold program (39)
1	30	GAGACCGUUGUUCUUCAUAGGUGAAGGAGA ..........(((((((....)))))))..
2	35	CGUUGUUCUUCAUAGGUGAAGGAGACGCACAAACG ((((.(((((((....)))))))))))..........
3	40	GGCCCCUACUUAAAUCUUCUUUUGGCCUAUGCAAACCACG ((((...................)))).............
4	45	GUCUUGGUGACUACUCCUUUAGAUCGACUUUCCACCGCUGGUUGC ((((.((........))...))))(((((..........))))).
5	50	CAGUCCCAUCGUUCGGAUCAGGGAUUCGUUUAUCGGGGGCCCGCGAAUUA ..(((((......((((((...)))))).......)))))..........
6	55	GUACACCUCCAUCUUCCGUCGGAGGCGAUAUACAGACCCGCCAUUUAUCAGCGAC ...(.(((((..(....)..))))).)...........(((.........)))..
7	60	ACAACAACUGUACGAAGUAACAUCGCAGAGGCUAUAAAUAGGACUACAGUUGCCCCUUCG ....((((((((............((....))............))))))))........
8	65	ACGGAACGUUAUGCGUGGGCACCGUUAGUAGUCACCGCGGGGUCUACCGAAGGCAGUAGCAGACU .......(((((((((((((.((((..((....)).)))).)))))).....))).))))....
9	70	CUUACAUUUUGAGGCUGUAGUGGCCAACAUCCUAGAGAUCCGCCUCUUAGCGGAUAUAAUACAGCCGAAA ............((((((((((.....)))......((((((......))))))....)))))))....
10	75	UUGCCAGUUGGUCCUGUCGGAAACGGUGGCGCUAUAGGAUGGCGCUAACAACAAGUCUCUUAAUUGUAAUGGAUG ..((((..((((.(..(((....)))..).)))).....))))...........((((.(((....))).)))).
11	80	ACCUUAGCGGUAUCAGCUCUUAUAUGGGCAGCGGUUACCUUAGGUUCAAACCAGCGUGCUAAGUAGCACACAUGGCUAUA ((((....((((...((((((....))).)))...))))..)))).....((((.(((((....))))).).))).....
12	85	ACCACCCCAGCGGACAGCCGUAUUUGAAACGUUAGGAGCAGUUUAGGGAGUAAGGCAGAUAUAAGUACUAGGCGCUAGUCUCUGU ...(((((.((((....)))).....((((((.....)).)))).))).))...(((((.((.(((.......))).)).)))))
13	90	GGGACCGUGCCGAGUGUUCCAAAUCACAUUAUGAAGUGGGGGCACUGUCACACCGCAGGUGAUGCUUCUCCUCGAAUGAAUCUACCCUAG (((...(((.(.((((((((...(((.....)))....))))))))).)))..((.(((.((....)).))))).........)))...
14	95	GCCCCUUAGCAUCUGUACAUGAACGUCUAAUCAUUUGUUUAUCGGUGGUGCGGGAUACUCACUCUAGUUUUGUAUCAUGUACAUUUAGGUUACAC ......((((...((((((((..((((.((((((..........))))))...))))....((....))......))))))))).....))))...
15	100	GCCAUUGCGCUCUUCAAGAUCACCCGGUACAGCCAUGCAUGUUACAUGUACAUGUGAAAACCUCGUAUUGUGAUAAACGGCGCUUAGUGAUUCGAGUUUG ........((((.....((((((..(((...(((.....(((((((.((((..((....))...)))))))))))...))))))..)))))).))))...
16	105	ACAUGCGUAAGCGUUUCCUAAACGUUAGCGGCUUCCCCGGAUCUCGGCGAAGUGGUGGAAAAGGUUGCUCACCUCAUUGACCCGUAUUGGCGCUCAAGUAGCUAU .....(((.((((((.....)))))).)))(((((.(((.....))).)))))(((.((..((((.....))))..)).))).....((((((....)).)))).
17	110	AAGCUAUACUGCAAGACGUUCAAAUAUACGUUCCCCACUAGCACAAGACAGCGUUCCGCGCCACGACACCCUGCUUUCGAGGCUAAAAAAAGCAAGUCUUAUAGUAGGUC ..((((...((...(((((........)))))...)).))))........(((.....)))........((((((...((((((..........))))))..))))))..
18	115	GACUAUGCUAUAGUCGAGGAAGUCAUAUUGAGGCUCCCGUUUACUACGAACAACACAUAGCAGAACACAGAAAAAGGAGUCAACUGUAUUUGCCAUAAGUCUGCCGUGUAGGUAC ((((((...))))))..((.((((.......)))).))...........((...(((..(((((.......(((.(.((....)).).)))........)))))..)))..))..
19	120	GUACCCGCGUCCGAAGGCCGUUUGCCAUCCGUUGGGCAAUAGGGGUGCGGCUAGGAUAGCACUCCCUCUCUCCGAUUAGACUCCAAGUCGCUCUUGAUCGGUGUGCUGCUCAUAUAUCGC ((((((..((((((.(((.....))).....)))))).....)))))).....(..((((((.........((((((((((.....))).....))))))).)))))))..).........
20	125	GAGGAUCGAUCCGGUCACAUAGGAAGUAAGGAGAUAAUGUGUCAUGGAGCAGGUAUUUUGAGAGGCAAACAAAGUGAACCGGGUCACCAAAAUCCAAAAAAGGAUCCCAGUGUAGAAAUUGCAAU ..((...(((((((((((...........((((((.(((.........)))..))))))....(.....)...))).))))))))......((((......)))).))..(((((...)))))..
21	130	UCACCGGAAACUGAAAGUGCAUAACUUAAAUCUAACCGUCUAACGAAUUCCCUAAAAUCUACAUCCUCUCCGUAUGUAAUGCGGCGGAAAAACCUGUUAGCAGGUUAUUAUUACUUUUUAUCCCGUUAGC ....(((.......((((.....))))........))).((((((..................(((...((((((...)))))).)))..((((((....)))))).................)))))).
22	135	GGACAUUUGCCGCACUGAGCCGGGUAGCAUUAUACAUGCGCCCCACUGCCAAAACGAUGGGAGCUUCCAAUCGAGUACCAAGUCUCAUAGUAUGUGGACAGAGUCGACUGCUAACCCUGGGCUGUCGGCGAAAAC .....(((((((.((..((((((((((((...(((((((((((((.((......)).)))).))........(((........)))...)))))))(((...)))...)))).))))..)))))))))))))...
23	140	AAUUUCUUUGCUGACACUUUUCAUGGUAGUCCGCGAUGUGGUCUAAGCACAUGAUCGCCGUUCGGGCAGCAAGUUCGUAG

		CCAUCGCAGGGCAGAUCAAAGCAGGUUAAUAAGUGCCACACUGCCGAUCGUCUUUCCAGC .........((((.......(((((.(((.((((...)))).)))....)))))..(((.(.(((((.((......)).)))..)).).))).((((...((((................)))).)))).......))))
24	145	CGAGUAAGCGGCAGUAUUUAACCUAAUGGCCGCGUCAUACGUUCCUCGACCUGCUUGGAGGCGAGGAAAAUAUGUUGGGG CACGUAAACCAGAGACAUACACGAAAGUGAGUCGCUCCAUCGAUCUUGACCGUGGCUUGAUCUCG ((((((((.((.((..........((((((.((.((((..(((((((.(((......))))))))))..)))).)).))).)))......(((..((.(((....))).))..)))..........)).)).)))))..))))
25	150	AGCGGUCGUGGAAGGCGUACACCGAUGGCACACCUACAGCGCGGGACUCUUCUCAUGUGAAGAAUAGCACAUCAACAGAG GUACGAGUUGAGGAAGUUACGCUCGCUGGAUAAUCCGUUGCACCUACACACGUAUCCGUUGGCAUUAUUG (((((.(((((.(((.(((...(((((..((.(((.((((.((...((((....(((((........)))))....)))) ...)).))))))))..))..)).)))..((.....))..))).))).).))))...))))).........
26	155	CAGUCAAAUGCGUGAUAUAAGCCCGGGUAUGCUCGUAACGUAAGAAAACUCCCUGAAUUAUGCGGCACGGUGCUCCAAUU GUUCGACUGAACAGAACUUAAGAUACUAACCGGUCGGACCCAAAUAGCGGAUCCACCGAAAAUGCCGCCUUCGGA ........(((((..((..(((.........)))..)))))))..........(((((....(((((((((((.(((.((((((((((((.....................)))))))))...)))...)))..)))))....)))))).))))).
27	160	AUUUCCAACUAAAGCGGUCAGGUCUACUACCGCGAGAUAUCGUACAACCCCAGUGUCAUCUGGGCCAGUUAGCCCGAGAU UACUCAGGUCAAGAGAGUCGCGGUGCGACGUAGAAGGAUACCGCUGAGUAGGGGAGAGACUAAAACCGUGAACCGAAUUC .(((((..(((.((((((....((((((((((((....((.....(((..((((..((((((((......)))).))))))))..))).....)).))))))))....)))))......))))))...))).)))))).....................
28	165	ACAGAUGCUGUAGCGCCGAGGGUCGAGGACUUUGAGCGAAGUAACCCGACAAGUUAGCGGGCGUCCUUUCUUGCCUCACU CCAUGCUCCAGGUUGGACUCUACAUACGUAUUACCUUGUGUGCUAUGUCAAUCCAGUCAGGAUAGUGCUGUCCUGGCUGG UUCAC ...(((...((((((((((((((((.(((((((....)))))..))))))..((.....((.((((..(((.((...... ....))...)))..)))).))....))......))))).))))))))))...((((((((((((....)))))))))))) .....
29	170	GGGUAGGGCCGUCCAUGCCUAAAAGGUAAACGUGGUAGCCACAUGUGAUCGGCUAAUCCCGUCUGCACAGCUAGGUAAUG ACCCGGGCAAACGUGGAGGGAGUAGGCUGCCCGCACACGCUCUGGUUCUACCACACUGCCGGCCGAGAGCUAACUCCAGU GAGUCCGCUC ......(((((....((((.....))))...(((((((((((.((((..(((((..((((.((..(...(((.(((....)))..)))....)..))))))...)))))....)))).)...)))..)))))))).....))))).((((..((((....))))..))))
30	175	CACGUGUUCCUGAACCUCCAGCGUCCUACCUAGAUACAAGGCUGGUAACUUGCUAGGACACCGUUCUUCAACUUCGGACC UACUCUUAGGGUAAAUAUUAACUGUUCAUAAGCCUCCCAGGAAGUGGCUGGUAACCACAGUAGCGUGAUUAUCUUAACAA AUACGGAAUCCCCGA ((((....(((.....(((((((((..(((((...((((........)))))))))).....(((....)))...)))). ((((((.(((......(((.........)))....)))))).))))))))).......)))..)))))............ ...(((.....))).
31	180	GUUCGUAGCCGAAGAGCAGCGGACCUUGCGACUUGGGCGCGGCGGACGGCGUCACCCGACUCGAAACUUUGUAUUAGUCU UCUCAAGAUUGAGGAAUCUGUCUCAGAUUCUCUCCGUACUGGAUCUACCGGGCUUAUGUCAGCAGCUUUGGCCAAGCCCC GGAAGCGUCCCCGGAUCGCA ((((((.((.......)).)))))))..(((((((.((((((.((((((((.(((....))))))))..........(((((((......))))))).(((((((...))))))))..)))))..........((((((((..(((((.....))))).))).)))))..))).))).)).)))))
32	185	AGGAUUUAACGAGCUCCAAAUGUAUACUAUUUCUCUUUGUCGAGACCUAUGUCUAUCCCUGACGCUUGGCGUAUUGUUAG UAAUCCGCCGCGGCAGCUGCCUGUGGCGUAUAUGGAUUUAGUUGGUCGGCAUCAUAUGAAUAGGGGGUCUAGAGCUCGAC AUAGCUUGAGAUUUAAGCCAAUAGG .........(((((((...((.(...((((((.....((((..((((.((....((((...(((((.((((.((((....)))).)))))..((....)))...)))))....))))...)).))))))))).....)))))).).))...)))))))).. ...((((((...))))))).......
33	190	GAGGAUCUAUCCACAGUUUUGAUCUUAUAGUCGGUCCUAUAUAAUCGACAAAAAUACGUUUGCUAUCGCUGUGUACGUGC CAAGUGAAUAAAUGUGAAGAAAACACCCUGUACCGGUUUCAUGCACCCCGAGCUGCCGAGCUCGGGCAUUUUUACAGGCG GCCCGUCGUCGGAUUAGAUUGGUUUCUUCG (((((.....(((....((((((((....(.(((.((................((((((((...(((((..((....)) ..))))).))))))))).........((((((...((.....))..((((((((....)))))))).......)))))).)).))).)...))))))))).)))..))))).
34	195	ACACUAAUCGCCUCCGCAUACAAAUUUAAUGUCACUAUUAGGUGAAUUAUAAUGAAAUAAUAUAGUAACCCGCGUGACAG GCCUUAAAUUACAGGUUCACAUAUCCUAAAACACCCACCGGUUGUGUCACCGACACUGCCUAGACUGGGUUUGUAAUCCA GGUAACAGAAACCGUACUAACUCUGGAUGGUACUC .........((((((...((((((((((..(((.......((((.((((((.........)))))).......((((.... ((((.........)))))))).........))))....(((.(((((...))))).)))..)))))))))))))))..... (((.......)))...........))).)))....
35	200	GUUAUGUAUAGGAUGAUUUGCAACAGUAGCCCGUUGGGGUCUUUAAACUGAAUCGGCUGUAUCUUUUUCACCCUGGCUAA UGCGUACGAUAGACGAUUCAGCAGGCACCGUUCGGGUGACAUGUUAAAUUUCCUACCUCUUUAAGAUGGUCGGGCCGCCC CUUGUAGACGAGAAUCUGAAGUAAAUGGUUUGGCGAUAGU ........(((((.((((((..(((((.(((((.(((.((((.....((((((((.((((................((... .)).....)))).)))))))).)))).)))..))))).)).))))))))))))))).........((.(((((((((.... (((.((((......))))))))....))))))))).))...
36	205	UAAUUUUGGCAGGAGCUACACUCGCCUGUCGAUUCGUUAAUAAUGUAAUGAUUGCACUAUUGGCGGGCCCUGAAUGGCGC GAAGCGCUAAUGAGUGGAGGCGUGGUUCAACAUUGCAGGUUUUUCUAGCUAGUUCGGGAUAGAUUAGAUAAACAUAUGAU UGAGAUGAUUACGACAUGAAUCCAAUGUUAUAACUGGAGCUAUUG ......((((..(((((((.((((((((((((((((((((......))))))........)))))))))).((.(.(((((((...))))))).).))..)))..)))))))..((((.((.((((.((((((((.........))).))))).))))...)).. ...)))).(((..((((.......))))..)))......))))...
37	210	UGGGCCCCCGACAAUGUGCUAGUUCCCACUCCUUGCCGCUAACAUUGGGGUAUGAAUAAAUGCAGAUAGUAGCCGUUUCC UCCCAUGUCUUCAGAUGCGAGAUUACGCAUGAUGGGCGUGUUUGCGUCGCGAUAUAGAUUUCGGUACGCAAGCCGUCGCA CACAAAUAGACGCUAUCAUAGCAUGCAGCAGCUCCCGGGCCCCACAGCCU

		.((((((..((...(((((..((((..(((((.((.......))..)))))..))))..((((.((((((.((.((...(((.(((.........))).)))...)))).((.((((((.(((((((((.(((.........)))).)))))))))))).))))..........))))))...))))))).))..))..))))))........
38	215	GUACUCGCAGAGGACGGUUUUCGAGAAAUCGCCAGGCAGUCUUGUGUCUGAUAGUACUAGAGGAAAGCUGUAUAGCCGCU UUGCUCGACCCCGAGUAGCUUCAGCCUUCCUUCGCCUUACCCAAGCCCGAGCUUAAAUACACCAUGAUCUACUACACUUU GAUUCGAGUUGAGGCUCGAAUUCUCCGCGUAUUCUUUUACAAGUACGGCCCGGUC (((((..((((((((.((((.(((....)))..)))).))))....))))..)))))..((((((.((((...(((.... .((((((....))))))))).)))).)))))).(((.(((..((((....))))..................(((.(... (((((((((....)))))))))....).)))...........))).)))......
39	220	ACUACAUUGGGCGACUUGACUCGGUGUUGGAUCGACAUAUGAAUGGGAACAUACAUACGCAACGAUUCCCAGCUAUUCAU CGUUAUGGAAUGCCCGACUUUUUGUUGAUGGUACACUUUUCAGUUCUAAACUAAUCACCCGGGAUGGGGAGUUUCGACUA GGGCCAGCCUAAGCACGUAUUGGACUGGUUUUUCAACCGUCGUGAUUGCUGCGCAAUCAA ......(((((((.(.((((..((.(((((((((.(.((((.(((....))).)))).)...))))..)))))...)).. .)))).)...)))))))........((((((..((((..((.((((..............))))))..))))...((..((((((((.((((.......)))).)))))))))).)))))).(((((((...))))))).
40	225	CCGCUCUACAGUGUUCGUAUUUUUGCCGGCUGCCCCGUUCGCCUCCUAAUGUUGUGUUAACCCUCUCAGCGUUCAUGCUC CCCAAUGACUGAGCACUACAUGAUCGCUCCGGGAAAGGAAAAAGUCAGCUAGAUGCUUUCGCUAGUUUUGUCAUAGUUCA CGUGCCACAGGACAGCCGGCACCCCGAACGAGCCACAGAAAUAUCCCAAAAUGCGUGGCAACGUG .(((........(((((.....(((((((((.((.((..((.((((......((....))..((((((((.((((((((..........))))).....))).)))).))))).))))....((.(((((((((((......)))...))).))))).))..)).)).)).))))))))...)))))..(((((.....................)))))...)))
41	230	CACGUCCAGUCCACUGAGGACGAGUUAGUCGAAGGCGGGCCCGUCGGGGGACAUGCGUUCUUCUUAUGACGCACUACCUA UGGUCGAAUAGGUGGUCACUGAGACUUAGCUGAAGUUCUGCACCAGGGUGCGAGUAGGGAGCGCUCAGCGGCCAGGAUGA AGGCCAAGGCGACCUACUUGAUCUAGUAUCAUGAGGAACAGACUCUAACGCGAUAGUGACAUACUGUCCG ..(((((((....))..))))).(((((..(((.(((..(((.....)))...))).)))((((((((...((((.... .((((((.(((((.(((...........(((((.((((((((....))))......)))))..)))))((((....... .))))..))).)))))).)))))))))).))))))))).......)))))..(((((((...)))))))..
42	235	AGUGGACCCGGCAAAGCCUUAUCCCUAGCGGAAUUCAGCGGAUCUAACUUCGUAUACCAUCUCGAAGCGACUCAGUUAGU CCCCACUAAAUAGCCGCCGUCUCACACCGGUUGUGCCCCUAAACCGCGUGUGGUGACAUUUCCUCGUUCCGGUGGCGAGA CAACCGUAAGUCUUGAAGUCUCACCGACACUUCCUCAUAGGCCAGAUAUGGACUGGAUCUAUUCCGUCUUUAGGU .........(((...))).....((((((((((.....((((((..(((((((.((....(((.(((.((...(((((....)))))..)).))).((((((((((((((.........))))).)))))).)))......)))...((((((((((((........))))))).....)))))).............))....))))))).))))))))))))))...))))).
43	240	UGAACUUCAGGACAACGUUUACAGUGUCUCUUGGCGCAGUAAUCGGUUUGGUCUUAAUUUGAAUGGUAAUACUGGAACUC CCACGUCAGGUUCAAGAGCGUGCGGGAUCCAAUCCUGGGUUGGAAAAGCACCCGAUGCCGAUCUCGUCAGGCUUGACCUA UAUGACAGCGCGUAAUCUGCUGCCUGGUACUACGACAAAUAGCCCUUAGCUAGCGGCACGUUAUAUGUCCAGACUUUAAG ........(((((..((.((((.(((((....))))).)))).)).....))))).................(((((.... ....((((((((...((((.(((((((((..(((..((((.(......))))))))...))))))).)).)))))))).. ..)))).....(((((.((((((...((......))...((((.....)))))))))).)))))...)))))).......
44	245	CUCAGACCUGGGUUUCUAGGUUGGCGUCAUAGAACACUGUACUUUUUUGCUACUUAAAUAAGAACCAAGUUCUGCCACC GAUGCAUAGGACACACCGUAAGGGAAUUGGGCAGCGUUUAAAACCAAAGUUAGGCGGAGUAGUGGCUCCCCAUACGUUAG CACCAGCGGGCUGACCACAAUGGUACGAACGAAUAGCGCUAUGUCCUCUUAGUCGGGAGGGGCGUAGGCGAUCGGAAGAA GGGCA (((.(((((((....)))))))..((((..(((((...((.(((.(((........))).))).))...)))))(((.(((((....((((((..((....)).....(.((..(((((...((((......((.(((((....)))))))....((((((.((...)))))))))).....))))..))))).....)).)..)))))).....)))))....)))...)))).((....)).)))..
45	250	UGUAGGUAUUAAAUAGUUAUGCGAUCCAAUUCUGCCAGAUAUUAGCGCGCGCUUAGGGAUCUAUGCCUGCGCCCCCCCUU UUUCUGGGACCGCACCUCGUCGCGGGGACACUAUCAAAUGCCCGGGGACGGCGCGACUCGUUUGGGUUCUCCUAGUACGG AUGAGAUGAGUCCGCGGUUACAUAGUCAGACGCACACACGGUCAAUGAUGGUGAGCGAAACAUUUCCACCUUGCGUGUGA AAAGUGGAUC .((((.(((...))).)))).((((((......(((((.....(((((.((.(((....))).)).)))))........ ..)))))((((((...(((((.(.(((.((.........))))).).)))))...((((((((.(.....(((......))))).))))))))).))))))......(((.(((((..(((.(((...))).))).(.(((....)))).....))))).))) ....))))))
46	255	CACGCGGAAGUAGCACGGCUAUGAUGUGAGGUUCGGCCGAAGUGGAGCCUUGGGUUCCUCCAGAACACUGUUGCCACCUC UAAAAGUUCCUUCAUUAUCUAGUUGCAGUGUCAAGCAUUCGCGACUUAGGAUGCCUCGUAGCGGGUAAUGCUAAUCGGGG CUGGCAAGAAUGAACGUGUUUGUCGCCUUGUCAAAGACCGCAAUAUCAUUAUGUUAAAGAUCAGCUCGGUCCCAUACUGC UUUGAACAGAUGCAG ...((((...((((((.(((((((.(((((((..(((......((((((...))))))..(((....)))..)))))))) .......((((.........((((((((((.....)))).)))))).)))).)).))))))).)....)))))..((((((.((((((.((....)).)))))))))))).......))))..................((((.....)))).....(((((((....))).))))
47	260	GGGACUAUAACACACGCCCCUUGGGUCCCGUCUGAUGCGAGUGUAAGAUGCAACGUCCCUCCUGAGUAUAUAAGGAAGAG AGUUGCUGCGAGCAGCUAUGUGGAAGGUUCCCAGGUAUGACUGAGGAAGGGGGGGUCAAAUAUUGGCUCAUCACUAAUAA AAGGAUAAUCAUCUAAUCCCAUUCAUAGAACUGCUGCUUACCGGGCCUCUUACAGGUGUAUAACCAGUGGUGUAAGCCGG UAGUGGAAAAGUUAAGUUGU ..((((.((((..(((((.((((.(((......))).)))).((((((.(((((.(((.((((.........)))).).)))))))...((((((((..((((((...(((((((......))).))))(((.((((((.....)))))).......... ..((((....))))...))).)))))))......))))))).........))))))).)))))....(((.((.((.....)).)).)))....)))))))))..
48	265	UGUCUCAGAGCUGCCGUCAAUGGGGGUCGAUGCAGGUUCUCUCCGAUGAACCGCAAACAAAGGCAACAGUCGAGCACUGG UAAUCAGCUUCUAAGAAUCCAGCGGAGAAUCGGAGACGGUCCGGAUACCUAUGAGUCUAGCUCCGGGUAUAAACCGGCCG CUACACAGUCCGGAGCCUAGAUUAGAGUGUCGGGGAAUGAAAGAAGAGAGGUGUUACUCACUGUUACCUUGCUCUCCACU UAGUUGGACAUGGUGAUCCGCUACC ..(((.(((((((......((.(((.(((((((.(((((.........))))))).......(....).))))).).)).)

		)...)))).))).)))....((((((..(((..((.(((.((((((((((..(((.....))).)))))...))))))))).....((((((...(((....(((.(.((((((..(((....((.(((......))).)).)))))))).)))...)))))))))).))..))))))..
49	270	AACUUCGCAUGCCCUUACUGAAUUCGGCAGCGCUCCUUUUGCCUGUAAAUCCUUUCGCGGUACGUAUUAUAAAUCGAAUA CAUACCCGCUCCUAUCCGAAUGGAGUUCACGGGUAAAUAUAUGCCUCACAUAUACGCGCCCCCUAUACGUGUUACCGCUA GGGGCUAGGCGUAUGAACCCCGCGGACUGAACGGUUUCUCUAGACUGGGGAGGCAAAGAGUGGCAUCGGGCUCUUAUCCG UAGUCUGACGCAACGCAUGGUUAACUACAU ((((..((.((((.............)))).(((((..(((((((.(...((..(((((((...(((((........))))).((((((((((.........))))....))))))..............(((((((..((((((...(((....)))))))))....)))))))....)))))))..)).(((((.....))))).).)))))))))))))((.(((((((.....) .)))))))..))...))..))))........
50	275	CUGGCACGGUCCAUGCUUGAGCAGCUUGUGAGAUAGCUUCGUCUAACACGCAGGGGUAAAGGCUUCACGUCAUAGGGCGG CAAUACUCAUCCUAGGGGAGGCGAUCCCCUUCUCCAGAUGUUAGCUGCUUCUGAAUAGCUCAGUUUUUCACGCUAAAGCA GUCUCUAUCUAGGGUUCGUCGCAUUAUAUGAUGAUCCGCCAGCUUCCAAAUCCUCGGGGUCUUGGUUAAAAGCGCUCCCG CAGAGGGGUGGGAAAUUGAGACUAGAUGUCGGGGU (((((.........((((..((..((((((.(.(((.......))).).)))))).))..))))....(((((((..(((((...((((.....((((((.....))))))).....((((((...(((((((.....(((.............)))))))))))...)))))..))))..)))))....)))))))....)))))).........((((((.((((.((((..((....((((((......))))))..))..))))))))).)))))).
51	280	CACAGCUGAAAUCCACGGUCGAGCUAGAGUCGAUGCAGAUAACAUGGACUGGAAUGGUCAUGCUUCCACCACCGCUACUC UGUGUCUGUCGAACACCUACUAUUAGGGCAAGCUGUUUCAUACAGAUUAGGUCCGAGAUACACCAAGGUUCAGACCUUCG CGUUUUUUCAUAACACCUUUGAAACGGAAAUUCAACGCCACCCUUCUUUGAAUACAAGUGGUCUCCAAUGGACACGAACU UGCUACCGAUUAAUUCCCGCGACUCGGGUUGCUUUUUCCG ..............(((..((((..((((((.....((((((((((.(((..((((.........))))...))).)))))))).))))..............((((((((((.....)))))).....(((((((((.(((....(((((((.....(((((.((((....((....)).....))))...)))))........)))))))....)))))))....))))).....))))))..............)))))).....
52	285	AAUCCUGAGGGGAGUAAGACCUGCACCCUCAAAAACCACGAGAGUCCGCUCCAUAAAAUUAGCGGCUCAUUCAUCCAUUA GUAGCACCUAGGUUAAACGUACAAUUGGUAUAUCUAUAAACAUAUAGCUUACAAGGCUCCCCCAAAGAAGAUAUCAUAAA GAAAGUUUGAGGUGGGAUAUUACGUGUGGCUGGGAACUGAUAGUCUUUAUAAUUUAUACCCCGACCGAUUGCGAUUCAUU UAUUUCAUCAUCUGCUGGUAUGGGUCCGCCCGCCGCCCCGUACU .....((((((..(((.....))).))))))..((((....(((.(((((.........))))))))).........(((.....)))))))....(((.....(((...(((((....)))))..)))..(((....(((.(((.(((...((((((((.((....((((((.(((....(((((((.........)))))...)))....))).))).)))....)).)))))))...))).)))..)))...(((....)))...)))).....
53	290	GUAGAAAAGAGUGCUAUUUUUGGAAUCGCUUCGGAGCGGAUCAGUGACUCGAUAGAGUCCCUUCCCUAACCACUGCUGGG CCAAUCGGGUGUUGUGCCUCUCGCGUCAUUAACAAUAUUCCUAGGCUAGGGUAGUAUGUGCUGACGGCUCAGCUUGCAUA GGUUAGUGCGUGCGGAAAACAAGUUUCACCCAGAUAGGGGAAUAAGGAGCGGAAGAAAUACACUCCACAAGAUGCGCAAA CCUAAUUGCUUCUCCUAUUGAUCGUGGUGACUAUGGGCCGGCCGUCCGAA ....((...(((....)))..))...((((((..(((..((.(((((....)))))).)))))).........(((((. (((...((((((((((...(((((((.(((((((.....(((((...)))))...((((((((((....)))))..))))) .)))))))))).))))..))))....)))))).((((((((((....(((((.(.........).))))).........((((. .....))))).)))))))))......(....)..)))..)))))..)))))).
54	295	CCCAAAGAUAACCUCAACAAGAAACCGUUUUGCGGUGCAUGACGGGGAGCGAUCUCAUCGCCGAGAACCAAUACGAUACC UUUGGGUCGAAUGGCGCUUCUAUGUAUCAUUGUGUGUUAAAGAGUGGACCUCGUUUCAAACGAUUUCAUGUGGGGCUAUA UGAAAAGCGCUUGGAAUGAAUACCUAGGAUACGGAGCAACCGGAGUGGCUUGCCUCAUAUUGUGCGUAAGAGAUUGACGC ACGCGUAACUGGGGUGAAUACGUCUGUCAUCGGCAGUGACAAAUGGAGCAAAUAU (((((((....((((..((....(((((.....))))...))..))))).(((((...)))))).................)))))))..........(((.((((...(((((((((((((..((.(((....(((((((((.((.(((((((((....))))))))))..)).)))))))))..)))))..)))))........(((((((..(..(((((((((((((((.........))))))).)))..)))))..).)))..))))......)))))))...))))))).....
55	300	UUGACGCUUCUCUGUACCUGAGCUAAUAGAACCAUCGCUGACGAUGGAAAAAUCGCGGGUUUGGCUACACCCGCGCAAAG UGACUAAAAACAACGAAACUCAUUCUAAGCCCGUAAGAGAGCCAAUGUUACGACGAGAGUUAGCACGCCCCGUACCGCGU UCAGUGCUGUUCUAGAACCUAGUGUCGUGUCCAAGCCUCGACAUUUCGUAGUCUCAUACUGAGCCGUCAUAAUGCUGGCGG ACCGAAGCUCAUACGUGUAUCUAGGCCACAUUCCUGAAAAGCAAUAGAAGGGUUGAGCAU (..((.(((((.(((...((((((..(((..(((((((....))))))......(((((((........))))))))..... ...)))).......((...((((.........(((((.(.......).)))))..((((..((((((....((.....)). ...))))))).......((..(((((((.((...)).)).))))))).))..))))....))))((((((.....)))))) ..)).))))))..........(((.......))))....)))..)))))..))..))....
56	305	AGCCGAGUUCUGAAACUCCUGUUAAAGCUAACGCAGAUCGGUUGAACACUACUGAUGCCAGGCGACGCCAUUCAUACCGC UAUGCAACCACCCCUCGUGGCUGAUUGGUCCUGUCAGUGCGACUCUCCUGUCCCCGUUUAGAGGGGAGGUAGUCGUAACA UGCGGACCCUGGUAUGGUAGGCGCGUUAACUUCAGACGCAAUAGUGAUGGAUGGCACUUAACGGACAUACUAUGAUAAGC AAUGUGAGGCGGAUUACUUCACGGGUCCUAUCACAGCGUCAAAAGAUUCCCCUGGGCCCCCACGU ....(((((....)))))........((....)).(((((((........)))))).(((((((.((((..(((((((.. ....((.((((.....)))).)).)...(((((.(.((.(((((((..((..(((((.......)))))))..)))))))...))))))))..)))))))..))))))....(((..(((((.(((((((.((..((........)).))))))))(((((.(. ..(((((((.......)))))))...).))))...)))))..)))).....))))).....
57	310	UCCUUGCUCAAAUUAAUACGCAUGACAAACGUUGAUGUACCGCGCAGUCGCAUGUCGAGGAUUGAGCCACAGGGUGGUUG UAUCCCUUACGGAUGGCCAUUACGCGACGAACAGGCAUAUUCACAUGUCGAAGGCUGCAGGCAACCGACAAAGAUAUCAC GUUGGUGUCCUCCGUUGAGUGUGGAACGGAUCAACUGUUCUAGCGGUACUUACCGACCCACGUCCAGCAUGAGCGAUGGA CAUGCAUUAGAGUUAACGCAAUCAAUAUGCCUGGUAGACUACCUCAGAAUACAUUCGCGCAGUCGCACGC ....(((.............(((((((....))).))))...((((.(((((.......((((..((((((...)))))))..))))).....((....)).....)))))...((((((((((..((((((.(..(((..(((..((((((...........))))))..))))..((((..((((((..(((....(((((....)))))).....)))..)))))..)))))...)))..).))))))).......((....)).....))))))))))..................))))....))))...
58	315	CCUUGCACCUCUUUUAACCCAUAGCAGGGCCUGGACCUAGGUGUACAUAUCACCAAGAGGAUCGUGGAGUAGCUGGGCCG

		ACUAUUCGGCUGUCCUGGAGCCAUGCAAGGCGGAACUACUAGCGCGAAGCCAUUCUGAUCGAGGAUUGGUGCUGCCUAUG ACUACCCUACCUGAUCCCUUUCACUCUCACCACUUUGAAGUGAGUGCCAAGCAUAAGACAAAGUAUAGACACGAAGUGUC UUGGUACCGGAACUUCAAUGUUCCAAUGCGUAAUACCGGACGUUAUGUGUCCGUAUAAUGCCGGCAGGGACAUUU ((((((..........(((....((..(((......((.((((.......)))).)).(((((((((.((((...((((((....))))))).(((....(((......))))))).....(((.(((..((((.(((......))).)))).)))))).. .)))).))))..))))))..((((((.(((.....))))))))).)))..)).............((((((...)))))).)))...(((((......))))).....((((.((((.(((((.....)))))))).))))..)))))).....
59	320	CCCGGUGAUUCGUUUCGCACGCGACUCGUGCCGCUGCAGUCACCCCCACGCACGCUGGAAAUUCGUCAUGUUGUGCCAGC GUAGAUACCGCAUAGACCUCGAUCGACGAGGAUCCUCGGCAACCAACAUCGGAAUGCAGUAGAGGUGGGGACUCCCCUAC UUAUUUAUUAUAGCGCGAUAUGUUUCUAACCCUCUAAUCUAGGGCCAGCUGAUUCCGACGGUAUUUGGCGCCGCGAGAGA AAAAGCCAGCCGUCUGUUUAUCCCAGACUUCUGCGCCGUCCGCAUAAUUCACACUCUCGACUUACCGCGAAUCGCCGGAA .((((((((((((...(((.(((.(....).))))))).(((.......(((.(((..((...(((((.(((((((((.(((.......))).((((((((.....)))))).))...))))..)))))..(((((.((((..(((((((((....)))))))).....................(((.......))))...)))))))))))))..))..))))..))).(((. ....((((((..(((((.......)))))..)))).)).(....).........)))..))).....)))))))))))..
60	325	UUUUCGAAGUAAUCAUAGACAACUGAAAACAUCCUUCAGCUGGAUUACUCGCCGGUGUAUCCCCAAUAUUUCACCCGUGU CCUAAGCAACCGUAAGAUUACAGCUGGCCCGCGCUCUGCUGGCGAGACCCCAUUACUCGCAUGAGCCGACGGACAACCUU UUACGACCAGACGCGCGGUUCGGAUCAAUUACUACCACUUAUCGCAAGAGAAGCUAGGUACCCCAAGAACUUGGAUAGAU CCAGCUUUAACAUAGCGUCGAUUUUAGACCACUACACCCAGGGUCGAAAUUUCCAGCGCCAAUCGGCGCCACCGUGUCGA ACAAA ..(((((.((((((.(((....(((((.......)))))))))))))....(((((..........((((((((((. .(((((....(((((((.......(((...((.((((.....(((((.........)))))..)))))).))).......)))))))....(((((..((((.(((((.......((((.(((.((....)).)))...)))).)..((((....)))))...)))))))))........))))))...))))))..)))........))))).)))))).....(((((....)))))))))..))))))....
61	330	UUGUGGUCGUUAGGAGAAUCUUCAAACAAUCGUGUCUACCCGAUAGUCCGAUGCAGCCGAAAAAUCAUCCUGGGGCAAUU UUAAACCGGACCCUCCUUCCGUCUCGCGCCGAUUUCUAGUCAAACCCAGUGAGGAGAUAACAUUGUAAGAGCCGACAGUU UCGCAGCUCUGUAUUGGCUGUGGAAACGACGCCUAGACUAAACGGGCAAACUUGUCUUCCUUUGAUACUCAGGAAAUUCU CAUGCUUAACAAGCGUUAGUCCCCGUCAGAAACGCCAUAAACUGGCAAAAGGUAGACCGGCUUAAUGUUGUUCCGACAAA AGGUAGAGGA ....(((.(((.((((...)))).))).))).(.((((((.(((..(.((.......)).)..))))....(((((((((. ((((.((((..(..((((..((((.(((.((.((((((((((...(((((.........)))))..(((((((((.....)))..)))))...)))))))).))))..)).))))...(((((.........(((((.........)))))...((.(((((.....)))))..))..)))))..(((((.....)))))..)))))..).))))..))))..))))))))))..... .)))))).).
62	335	AUUUACUCUAUACGUGCUACGGUCUUUCGAGAUCAUUAAGGCAUUAGCCUAACCAUGUGGCAACAUUUCCUGUUUCUUCU GUAGCCUUGCUGGACCGUGGGUCUCCAACUCUGUACGUGAAUCUUACCAUUACAUGCCUGCUGAAAUCGCAGAAGCCUAU GCAUGUUAGUUAACAUUUCAUCGUGAUUUCGUUGGAAAGAGCUCAGUUAACUCGCCCACUUAUGUUGAAACUUUUAGUUG GUAUAUGAAAAUCUUGAUUUUGUCGGAAUGCGGUUCUAGAAGGCCAGGCACGGUUUGGGAUUCAUAUAUGUUAAACCAGU GCCCUUAUGGUGAGA .........(((((((.(((((((..((((.......((((....)))).....(((....)))............. .....)))))..)))))))(((.....)))).)))))))..(((((((((.....((((.(((.(((((((....((... (((.((.(((((((.(((((.((......)).)))))).(....).)))))))..))....((((((...(((.....))). ..)))))).............)))..))..)))))))..)))..))))..(((((((((((.((......)).)))))))..)))))...))))))))
63	340	GGCGGUCGUCUAGGCUCCUCAAUUCUGGGCUUUUUUUUCAAACCGUUGCUCGUGGUGCUGCCAAUCGCAUAUGUUAGAGCU CACGGGCGGAUGAUUUUGGGACCGUAUGGCGGUCAUGCUCCACGGUGUGAAACAGGCCUAGAUAAGAUCGCUAUCCCAAA GCAACUCCGCAUAUGGUAAGUUACCUCAAGCAACCGGCUACCCUUGUUGUGUCUGGGUACGUUGUUACAGAGAAACCUCC GUCCCCUCAGUUCUUACUGCGCGACGGCAUUGCUUCAUGAUAGCAUCCCCUAGGCCGGACCGAGGUCGAACGAUGAUUUC CUAUCUACAGACCCUCAUAC ..((((((((((((.........(((((((((..(((((.(((((.(((((((((.(((.((........)).))).)).)))))))).............(((((.....)))))).......)))))..)))))..)))))))))...(((.((((((...(((((((((.((....((((...)))).....))...(((((((((...........)))))..))))).....))).....(((((..(.((((....)))))..).)))))..)))))))...)))))))))..)))))))..)))))..((((....((((..... .))))....)))).....).
64	345	AGGGUCGUGAGUCAAUGUCUGGACAAUCCUCGGUGGGCCCAAGUUAUCACGUGGAGUUACCGUUGCUUAUUGGAACGUGA ACCAUUCCGGAGCUCUUCAGACUUAUGGGGUACAUCAAGGGGACUUUGUUGUUGAUAAGAUGGUCUUGGUCAGGCGCUUG ACAAGCACAUCAGGGUUUAAAUGAUUCCAAGCAUGGACAAAGUGAUUAUUGAAGGAUAUAAUGUAAAGACGUGAAGAUUG CGGUUCGCACGUUCUAUGACGUUAUUCGGCGGCAACUGUGUGUUUCACCGCCGCAUUUGUGCAGAUGCUCUAGCAAGGGG ACGCAACCAGAUAUCUUACCUUCCA .(((..((((((...(((((((((....(((((..(((((((...(((((((..((((..((...((((...((((.(... .)..)))))..))))..((((((.....))))).......))..))))..).).)))))))((((..((((.((((....))))))))..)))).)))))).....)))))))))..((((((.(((((.............((.(((((((..(((((((..(((.. ..)))..)))))..)))...)))))))))).((((((....(((.....))).)))))..)))))..))..))))).......))))).....)))))))))))))..))).
65	350	UUGACGUGACAGGGCCUUCUAGUGAGGUUUCGUAGAUCGUGACCUAAGUGUGAUUUCUUGACCCCACGAAGUCCAUCGUU GAUAGGACAGGCAGCAAUAUAGGCGUCAACAAUGCCCAAGCCUACUCUUAGUUGCGAAUAUUGAAAAUCGAAGCGUCGUA UUGUGCGCACGUACCAUAGUACUCGGGAUCAACAUGCGACCCGCAUUAACACAAAUAGGUGCCCAUGCGCGUAUGGAGGG GCCCGGUCUCGGUAACCCUAUACUCUCGCCCGUUCCGGCGCUUCUACGCACACAUAUCAAGCUGACGCUUCAGCUGGUCU AACACGGUUCAGUCAAACUCAGAGCAGCCU (((((...((..((((((.....))))))..)).(((((((......(((.((((((.((....)).))))))))).... ....((((.(((..((((((.(((((.....)))))...((..((.....)).))..))))))......(((((((((((((((((....((((..((.((.((((..(..((((((...(((((...(((.....)))...)))))))))))...). .)))))))).))))............(((.....))))......))))))..))))......)))))))..)))..)))) ..)))))))..))))).....
66	355	CUACGUUUUGUUAGAAGUAGAAUCGCGCUGGUUAAGUAUGCCUUCCUAAAGGUAGUCGUCGAACCCUCCCAUCAAAUUUG

		CCACCCUCGACAUCCCCGAAAAGAGCCUCACCGAGGUCAGCAGCGGACUGACGGCUAACAUUGAGGAGAUAGGUAAGUAG ACGGUCCUCGCGUAGACAUGACUACUCUCGAUGGUGCGGGUACCAUUCAAGUGGCUUACUUAGUCUGCGAAGAGCACUAG GGACGCGUUAUCUUUCUUGUGAUUUCGUGGUACAUCUAAACGCAAUGUGCGCCGACUACGGUCAUACUCUGCCCGGCAGG CUGACAUUAUGCUUACCACCGUACUCGGGAAUAGU (((((....((((.(((.(((..((((..((((.....((((((....))))))).......)))).((((.....(((((((.(((((((.............((((((((((..(....)..)))..)))..))))....)))))).)...))))))).. ..(((.(((.(((((((.(((((((((...(((((((....)))))))..)))))..)))....)))))))..)))..))).))))))))...)))..))))..))))..)))))).....(((..(((.....)))(((((.((((((((((.((.(((.....))).))...))))......))))))..))))...))).
67	360	CACGGUAUGGACAAGGUGCUCGCAGUCUAAUACCCCGCACCCCUACUCUUUAAGAUCGUGUCCUUAUCCCCAGUAACAGC AGCGCGGAUCACGCCGAGUCUUCUAGCGAUAAUGUAGGCUCAUGAGCCGGUCUACAUACGUCUAGUCUCACCGUAGACAC UGAUGAUAUAUUUUUGCCCAGAAGUGCCUCUGAACACGUUUAUGAUUGCUGACUAUGUGGACGCUAUGUGUGGGGCAAUC GAAGUUCCUAGCUGCCCUUAUUGGUGCGGGACCACGCGCAUCACGACCGCAUGCUGAUACCCGAAAUGGACCCUCCACGA UUAAUGAUGAGAGGAGGUGUGUUUCCUCCUCUCCCUAUCG ..(((((.((....(((((.................)))))...........((((((((((...((....(((.(((((..(((((..(((((.(((((((.(.........).)))))).)))(((..(((((((((.(((.(((.....(((((((.. ....((..(((((((....)))))))..)).......)))))))...)))))))))))))))))))..)))))(((((... ....)))))....(((((((.(....).)))))))...)))).)))))..)))..))...))))).....)))))).....((((((((((.......)))))))))))))))
68	365	CCUCGAACCCAGUCGAACUUAGUUGGGGACAUUCCAUUCAUGGAUUGACCGAAGGUCUGGGAGUCCGAACGACCAUAUUU CAUUGGCUGAGUACAACUAUGAAAGACAAUUCGACCUCCUGAUGGCCUAGUACUACGUGUGGCUUUGCACAGUGGGAACG GGCACGGCGUACAUAGUAGGAGCUAAUCUAUUGGGUUUCAUGCAUCAUGCUUCGCAUCUAACAUCUACUGAUGUAAAAUU AGCCUCCCGCUGUGGCUCCCCGGCACGCGGGCUUGAGUAUAAACUAUAAAGGAAAUGUAACCACACUUACUCUUGCUGUU AGUCUGAAGAGCAUAAUGGAAAUAACGCCCGGUGAACCAUGUUCG ....(..(((((.(.......))))))..).........(((((.((.((((.(((((.(((((..((((........((((((.((.((....)).)))))))).....)))))..)))))...)))))....(((.((((((.....((((((((((... (((...(((.....((((.((((.(((.....)))).....)).)).)))).)))).....(((((....)))))..... .)))))))))))))(((((((((.....)))).)...))))..................))))))).......((((.((......)).))))...)))..........))))..))))))))....
69	370	UAACCAAGCUGGAGGAAUUGGUGCCCAAUCCACCCUGUUUUUUCUCUAGAAGGUCUUUGCACAUUUCGUUCUGCUAGAAA UUCUGCGUCCGGUCCUCGGAAUUGGCUGUUUCGUCAUAUUUCGUCCAUUCUGGAUCGGGAAACAACCUCUUCUGAUAGGU GACCCAUCUGAAUUAUGUUUAAAUAUGUACAACCAUUGAUCUAACGUUCGCUGGAUCCCGCUUCGAGUAUCAGUAAUUGC AAAACCACAGGGAACUACAUGUGUUUACAUUAGAUGCCAGUCACCAGACUGUGUAGGGGCCACGGUUCGUACUGCCGUGU ACAUGAAAAAGGGCGACAUACGAAGGACCUACAUGCAAUGAUCGUAGCAA ........(((((((((..((((.......)))).....)))))))).(((((((((.(..((.(((((((......... ..(((((..(((((.((((((..((.((((((........((((((.....))).)))))))))).))..)))))))..((((((.(((((((....(((....(((((((...(((.(((.(....).))).))).((((.......(((........))) ....))))..)))))))....))))))))))...)))))).)))))))))).(..((((((.......)))))). .)........)))))))..))..)))))))))...(((.((....)).))).
70	375	CAUACCUAGAAGGUACAUAACGUCAUCUACCCCUCGGCUUAGGUACCUCGUGACACAUAUCGUACCCGAACUUUGCACGU GGUCUGACACCCGACUGAUCGGCGCUGUCGGUCAUACGAAACCGAUACUAUUACCAAUCGUGCAUUAAUUACUAGCGAUG UGAUCUCGGCAGAUUCCCCUCCGUACAAACUGGGGGUACGGUGCUCGGCGGGCGAUAUAGGGAAGGGUUCAGUAGUGGUC GAUCGCCCUACCUGAGAGCACUGCCUAAGAUAGCUCAAACAAUCUAAUGAAUAAUUUGCAGGUCGCGCUAGGGUCAUUCG CGUCCUACCCGACAAUCCUUUACCGCUUUAUCGGCGUGGGAGUGAUCUAUCAAUC ....(((((.((((((.(((.(((...........))))))).)))))))(((((.(((((((((.........(((((((((((((((((((....)))).).)))))).....((....)).....)))).))))))..........)))))))).....(((((((.(((((.((....)).)))))..(((((((..(((((.....(((((...(((((.........))))).)))))))).)))))))....((((.(......).)))).......)))))))..))))))))))).....((((.((((((((((.((..(......)..)).)))))..))))))))).....
71	380	UUCGCAGCGCCGUUAGUCUUACCCUAUUUUAGACAUUUUCUCUCCAGAAUGAAACAAACCGCGGGAUACAGCGUGGCGAA CAUACUCACCAUGUCCUUUGGCGGAUCUUCCGCAACGUUAAGAGAUGACACUUGUCCUGUGGUAAAAGCGUACCAUUAGC AUGAGCUAACCACUCGGUCUGGUUGGCCAGUCCUGGAUCGGCCUGCCCGGCGCAAGUAAUAGUUUGGCGGGGACCUGUGC AGCAUGGAUAGGCCGAAGCCCUCACGGACUAUCUGUACUUUAUUCCAAGCGAGAUUAGCUGACGAGUGCUAUUCAGAUAA GAGUGACUGACGCGCUGAAAGCAAAAAGUAAUAGUGGGCGACAUAGACAUGUUUGGACAA ....((((((.(((((((.(((.((........((((((......))))))......(((((((((((..(((((((.(.....)).))))))......(((.....)))))...(((.....))))...)))))))))))...)).)))...(((((....)))))..((((.(((((..((((.(((((.((.(((((((((.((.((....)).)))).(((..((((....)))).)))..)).)))))))).)))...))....)))))...........((((..(((........)))...)))))))).)))))..))))))))))))))))....((((..((....(((.....)))..))...)))).....)
72	385	AAAUAGGACUGCGUGUGAAUAACUCGUUAAUGGUUUGCUGAGAACGCGACGUUGCCAUGGAACCGUUUCUACCUCUGCCU AAUAAGGAGCCCGGAUUGGAGGACUAAGAGAACAAUCUACCUGGGACAUGCGGGACCGGCGUGUUUUAUCCAGUCAGUUG CUUGACGGGUCGAACGUUUAUACGGAGCGAAUGUGCUUCGCUAGCAUGGCGCGACUUCGCAUGUGGACGCAUGAGGUAUG GCGCGAUCCAGACCCUUGUGGUGUGUCGGGAUCUAUACCCUGUUUGCAUACACCCUUCAUUGCAGAGAAUCGUGUACUGG AUGCAUGCAGAUCGGUGGGGUCUGAAUUGUAAAGGUCGGCUUGGCUUGGAACCGCCUGUAUGACA ..(((((...(((.((.....)).)))....(((((((..((....((((...(((..(....).....((((((.((((..((((.(((...(((((((.....(((.....)))...(((((((((((....).)))))))))))))))).))).))))..))))....(((((((((((((((..((((((.....))))))...)).)))))..)))))))...)))))).)))((((((.(((((((..((((.(((..(.((((((((.(.((((((.............)))))).)...).))).))))).)..))).))))..)))))))).))))).....))))..))...))))).....
73	390	UACAUACUAACAGCAUCUUCAUUUUUCCGGGAGGAUCUGGCACCCUCGUAGAGUUGCGGACUAUUACACUGUUACAGGCG CCGGCCCCCGAGAGUGACACAUGUACGUUAGCGACAAUGAGACUGGGCGAAGCAUGUCCUGUGUCUGAGACGCCUUGGAC GGACCUUUCUUGUGAGUCCCCAAUUCCAGCGCCGAGGGAACUUCAGGAAGUGGUGUCAAUCGUCACGUUGGUUGCCUAUG UCUACCAAGAAUAUAGACUGACGAUUACAUUUGGAUGCCGGUGAGGAAGAAUGAUGCUAACAGGUGUCGUAUUUGGCGAC UGCCUCGGCCUUGCCAGUGCGUCAUGGCUUAGGUGCCCACCGUAAUCCAACAAAUGGAUCUAGCUCUGAG .........(((.....(((((((((..((((.........))))).....((.((((.........)))).)).)...((((((((..((((((.((((((.....(.(..(((....((..(.((((.((..(((((((...(((..((....))..)))

		))))......)))..)))))).)..)).)))..).)..((((....)))).)))))).))....(((..((...((((((((....)).))))))))..)))......))))..))))))).))))))))))).((((...((((.((((((.(((((. .((....)).))))))))))))....(((......)))))))...(((((.....))))).)))).))))..
74	395	AGUGGAGAAUGACAUCGCAUAAUUGCAUAGUAGUCCCCCGAACGGUUUGACAGCGACCGCACACUUGACAACAGUCCCUC UUUUAUUCUUGUGGGAACUAGUGGUAGCAAAGUACUCUACUGAAGUAAAGUACCGUCCGACCGCCAACAAGCCAAGAUUU CACUUCUUUGACCCAUAGGUUUCAGUUGCGUUGCGUCUUAGAAGUGUCGUACGAGAAAGUGGGUACCACCAAUUAGUAAC UGGCCUAUGGAGCAAGAGGUUGUCGUCCUUCUGUAGUGGGUCCAGAAAGUACUACAUAGGGUAAGCGAUAUCUAGUAAUU GAAUGCUCAGUUGUUGCGCCUCUUCGGACCGAAAGCCUUGGCUCCCGACACCCACCCAAACAAGUUGAGCGUCCC .((((...........(((....)))......(((.......(((((.(((.((.(((((.....((....)).((((.(..........).))))....))))).))...(((((.(((....))).))))).))).)))))......(((((((.((((.((((((.(..((((((((..(((((((..((((.(.........).))))......((((...))))......)))))))))))))))..)))))))....((((...(((((((..(.....)..)))))))..((((..((((((.((((((... ...)))).)).))))))))))....)))).)))))..)))))))...)))..)))))..................
75	400	UUUCUGUAUCCACUGUACUAAAUAGCAUGUGACUCGACGUCCUCGUUUACCUGGACACUUAGUUUGAAGGUUACGUUCAA GGGGUGUGAAAUGCGUUAUUAUUAGGUGCAACGAAUCGUUCCACUUGGACCAGCCCUCAUCCGCUCUUGCUUACAUAGGG GGCGCACUGCUCCGUGGGCGAAACGUAAUGACUAAUCGUUACCGAUAUAAUGUUUAGGGGCAGCUCUCGUUCGGUCUGAU CGCCGUAUUUUUCGAUAAACUUGUACAAUUUUAAGGCCGAUCAGGCUUAACUGGUGAACCUAUCACUGCGGCAAUCAAUA CCGGGAUUCCGGGCCCCUGUCUUGAAGCGGCGGUGCUGCCCUAACCGUAAGUCUACCCGGUUUACAUCCCCGAUCUCGAC ..........((((((........))).)))..((((.(((..(((..((((.(((.....)))...)))).)))..... (((((((((...........(((((((.((((...)))).)))))))............(((.....((((((....(((((((((((((.(..((((.....(((((((....)))))))............((((((.(((...(((.((((((((((((..........(((....)))..........)).))))))))))).))).(((((.....)))))..)))........ ((((....)))))))))))))))....).))))))))).)))))....))))))).....))))))))))))).))).))))).
76	405	CUUAAAUUUGUGACAGCAGCACUCACGUCUGUUCCGGUAGUGAAUGGAAUAGACACACCGAAGAAUACCAAUGCUUCGAG UCUACCUUCUUAAUGGUCUGCCAUCGGCAGGUUAGGAACCUAUAAUUAUACUAAAGUUUCUUCAGCCUAUUCCACCAUCC GGACUUUCAUCCAGGCCUGGGAGCGCCGCCGCGAUUUUGCCACAAGUCUAACCCGAAGUAACUGCCUUGGUAUAGGCUAC CUGCCUCUAGAGAGAGGGCCAUCGGACCUGAUAACGUCGGAACCGGCGAUGCUUUUAGACAAGUGACUUAUAGUGGCGAU CUACACAUUAGCAAAAACAUCUGUUACAUAUUUCUUUGGGACGUAGCAAGGCCCCAUCAGACCGGGUAGGCCCUCCGUUA CCCGC ...((((.((((((((..((.((((.(((((.(((((..(((..((((((((.(..(((((((.((....)).))))).)).....((((((((...(((((...)))))))))))))..........................).)))))))).))))))))........))))).)))).))..((((((......(.(((..((((((.((((.......((((......))))... ...(((((....)))))....))))........(((((....)))))......))))))..))).).....)))))).. ....))))))))).))))....((((((.((...((((..(((......))).)))))).)))..)))..
77	410	AUGUCGGGGCAGGCAUGACGCAAUAACAGACGAAUCGCCGAGCUUAGAGUAAGUGCCCUCGCUUGCCGCUGAGUGCGUUC GUGUACAACGUCCUCCGCUGUCAAUAUUUCGAAACUUGACUUAUAAUGUAUCAUAUGCGCCAGCCUUACGUAUGACCGAG AAUGUAAUUUUGAGUUAGCCUUCAUAUACAGGGGACACAUAGACGCGUUUUCUGUGAAGUGUGUUGCCCCCAAUCGCAAA UACCAGGGGGUACUGCUUACGGCGCCUCGAAUGGUUGCAACUUGCUGGCGACUAACAGACGGUGGAGUCAGCAAAGGACA ACUCAGCGAUCUAAAUCCAGAAAGGCACCUGUGGAUUACGAAGAGCUGUGCGGCGUUAGAACGUCAGUGUGGGUGGUUGA CCAAACUGAA ...(((((((((.(((..((((......((((...((((((((((...(((((((....)))))))((((((((..((((.(((........((((((((((.........((.((.............)).)).....(((((((....((.......)).. ..((((((((((((...(((......(((((..(((.(......).)))..)))))....((..(((((((.......... ......))))))))..))....)))..))))))..)))))))....))))))).......)))))))))))...))).))))).)))))))).....((((((...((....)).))))))).....))))))...))))))......)))))..))))).))).))))).))...))))).
78	415	CUUCCUGGCCGAGUUCCAGGAAGAGCGCAUUGGUCAACGCAGGAUCAUGCCAACUUAAGGAACGCAGUGAUAGCCAUGAG UCUAAUUGUGUAUUGAACGGAGUAUCGCUUUCGUAAGCCCGAUUACAGUCCACACUAGGCACUGUUUAAUGGAAAAUCGU CUCGCACAGCUGGCGCCCCUAGUCGCCGAAUGACCGGUUAGCGGUUGGCACCAUCGGGGGAUGUGAGUAGUCUGAUAGAC GUUAGGUGAGCCGCUUAGAUGGUCUCAAAGCGUACGCUCUGAUUGAUGGCCCAUCAGUGUGGUCCCCAGGCCACGCGGCG CCAUCCGGUAACUAUGUAUCAGGACAUGGGCUCGAAACCAUGCUGCUCGAAGCGAAGCGAGAUAGGGACAGCGGUUAUGC GGUAGACGGGAUGUU ..((((((.(((.(((((...(((...((((.((((.......))))))))...)))..))))).((((((...((.((... .....)).)).))))))..)))..((((((..((((...(((....(((((((......)).)))))).............(((((((...(((.(((((((..((.(((....(((((.....))))))))...))..)))).)))((((((.((((((.(. ((((...((((((((((.((.....)).))))))...))))).....((((((((....(((((((((....)))))))))).))))))...))))..).)))))))..(((((.........))))))))))))..)))...)))))))).)))...)))))....))))))..))))))....
79	420	AUUAACUUUCUUCGGUGGUGUCCGACUAUUUUCAGGUUCUCAAUAUGAUCAAUACUGCCCUGCGCCCGAAUGAUGAGCAU CAGGAGACGGUGGCCUUGCCCUUACCCCCAAUACCAAGCACUAAGAGUAGCCGCACCUAUACAGUGAAGGAGCAGAGUGG CUAGCACGAGUCCGCGUCGGCUUCACCAAGCGACUCUACGGGCGUAGCUAAGCGAGGCGAAUGAUUGUACAAGGAGAGAU AGCGGCGUAGGGAGACUUCCCUCAUCUGUCUUUUGAGUCAGACCCUUUUCAAGGGCAAGGACCCAGCUCUUAGCUAUAGC CGUCAGUGUGCAGCAUUCGAUCCAAGACCCAUACCAGCGGGCACGUCCACCGGCGCGGGGGAGUGGUAUGCAUACUCCCA GACCGAACUACUAAAAGAAG .....(((..((..(((((....((.......)).((((.....((((.....((((.(((((((((((((((((.((.((((.....((((((((((((((((((((.(((....((...((((..(.((((.......)))).)))))..))...(((((.((((((.((((....).))))))).......))).))))))..))).))).......((((.(..(((((.((.((((((.((((.(.((.(.((((....))))))).))))).))))))))))))..)))))....)))))))))).)).(((......)))...))))))).))))).)).)))))).......(.((((.........))))..........)))))))))).))))......))))......))))..))))))..))..)))
80	425	UGAUCCGCACUUCGCUCUAGAUCACUUCUUAUGUAUAGCUCGUGUACACGUUUCAACCGCCCAUGGGACACCUUUAUAUA AAUAAGGUUGUUGGGAUAUAGAUCUUCACGUAGGGCUUAGAUACUUUCAUUCCGAAUGUUAACCCCCCUGGCAUGCAGGG GGUCGGUUGUACAAAUCAGCCGAAAAGCCAGGCCGUGUUUGCCCCGUCGAGGAUAAAUCCUGCAGCUGAUUCCGAAACAG UCGUCGUUAGAGGCUCGAAUGGCUCGUAUGAUUGACACGGGUCAUACUCCUAAUAGAACGUAUGUGGUGCAAUUCACCGC CCCUGUUCAUAAGGCCUACGUCAGGUAUACCUCAAAUAUAAGAACCAAGAAGUACAUCGAGACUCGGAUUCCCCCAUCUU

		UCUUCCAUGGGUCUUAACGCGCGGC ....((((..((((.(((.(((.(((((((..((((..(((((((....(((((....(((....)).)..... .....((((((.(((((....(((((((((..((((..((((((..((..............(((((((.....)))))))(((((((.......)))))))........))..))))))))))))).))))))..))))))))))).....))))).. ..(((((..(((.(......).)))..))))))..)))))))..))))........(((((...((((((.....)))))) ...)))))).....(((.....)))).....................)))))))..))).)))..))))....((((((... ......)))))).........)))).
81	430	GGACCGACGAACGGGAGUCGAACAGGGCGUAGACAGCAUCCACUAUCAUUAAUUACUCAGAUAGCCUCUUCUUACAGACA UCUAAGGAGACAACAACGACGGUACGGGCUUUGUUUGGAUCCUUGGCGAUAUUAUUAGGCCGGGUUAAGAAUUCCGUUAC AAGAGGGUGAUAUUUCCAAGCCCGUGCAUAUUUAAUAAAAUCGAUGCAACCACGCACUCAAAGGUGGCUGGACACAAUCG UUGUACUUCUUGUGGCGGCGGGUGUGUGCGUUAGUAGUACACGGGAUGAUCCUGUCCUUAUAUGCAUUCCAGCCAUGCUC UCUCAUGGAUGUCAACAUUGCCUUCAGCGGACCGAAGCGAUUUUAUGAAUUCGUCUACAUAUCACCUUUCUAAGGAACUU GGAGAUUCCAGCUACUGGGAGCCCAAAAAG .....((((((..(((((((....((.(((.((..(((....(((((.............)))))).....((((((((.(((((.....((((((((((.....((((..((((((..((....)).))))))..........(((((......)))))...)))))))))))))).....((((((.....))).))....((((((((((((..((((((((.....)).)))))).))))).((((....((...((((.....)))))).))...))))..)))))))))..)))))..)))))))).....)))..)).)))..))....)))))))).....))))))..........(((.....)))...((((.(.(((((((...))))))).))))))....
82	435	GUGGUGCGCGUAAAACGACAAUCACCAGGUAAUGACAAAACUAUAUACCUCAAUCUACGGUUGCAUCAGUGAUGUUUAGA ACGGGACGUUGAUAAAGUAACCGUUAUAAAGUGAACCGCCUCAUUCUUGAAUUGGGAUUUUCGGAUGCCGAAAGUUUACU GUAGUGCCCCCCCUUCGGUAUACCGUGGAUUGGUGGAUCGGCAAGAUAAGUAUAACAUGGUAUGGUCCUAGACGAGCCGC UUAUUCGCAUCCAAGAAUCGGUGAGUUGUGUUGCGGGUAAAGAAAUGAUACACAACAAUACACCACAAGAGGCGACCUAA UCUCCUAUGGCAUUGAGCUGCGUUCGGGGCCCGACUUUCGUGUACUCCUAAGUCAGCCGAUAAACCUCACCAGAAUGCGC GGACUGGAGCAUAGUCCGCCAGAUGCGAUAGGGUG (((((...((.....))...)))))).((((...................(((....(((((((((.....(((((((... ...)))))))).....))))))).......)))..((((((.............((((((.((((((.(((.(((((((((..((((((((((.(((....))).))...)).))...))))..)).)))).)))..(((.(.(((...))).)))).. ...)))))))))..))))))..(((.((.(((((((..((((.(....)..))))..)..)))))))))))..)))))))))).. ..((((((.(((((.....(((((((((((..(((((..(......)..)))))..))))..........)).)))))))(((((((.....))))))))..)))))..)))))).
83	440	CUUCGAGUGUAAGAUACUACUAAAUAUAUCCUUGAAUCGCCAUCGCUACACCUAGGGUCAGCUCAAGCCAUGCCGCCCGA ACGGGUUGUGUGUCCAGUAUCUAGGGUGAAAGUACCGAUGCUUGUUACCUAGGGAGUGUCUGUUCUGAAUGCAUGGUACA AAACCCAUCCUAACAUAGUCGGAGGCUUGUAGGUCUGGAAGGAAUGGUUGUUGAGUUCUUAGGGUUCGACAGUUUACCCC UUAUCGCUAAAUGUGAUAAGCCGAUACAUCCCUGCACUGGUUUAGCAUUAGUAAUUUUUAGUAAUAUCACACGGGCCUUG UUGUCUAAAGGCUCUUGUACCUCCCAAGUUUGGCACCCAUGCGAACCCCCGUAAGAUGUAAUGCCAUCACCGAGAAGGCU UUACCUCGUUGGGCAUACGACGCACACCGACGUGCGUCGG ....(((.(((.((((.(((((((...(((((.....((....)).....)))))..(((.((((((.(((..((((..(((((.((((.(((((((((((....((((((....)))))....)))))).(((.....))).)..)))).))))))) .)))))...(((...)))))))).))).((((((..((...((...((((((((((..(...)..)))))))....))).((((((((.....))))))))))....))..))))))..)))))))))..........)))))))..))))....(((((((. ....)))))))...))))))....(((((.((....)))))))..((((...((.((((.(((.((.....)).))).))))).))..))))....(((((((((.....)))))))).
84	445	AACCCUAGGGUACUCCACGCUAAAUAGAAGAUUCAGAAUAGCGAGAAGGUCUUAUUCUCAGAUACGACCCUGAUAGCUAC UCGCGUUUAGUUGGGGAAGUUUAUAUUGGUCAACCCGGCUGACUAAACAAGUCCUUUAGAUACAGAGCCAAAUGGCUGAA CAUUUUUAUUCUGAACUCGCUAAUUCCCCGUAAGGUAUUGUCCAAGUCCAGUAACAUGUUGGUAAUUGGCCCACCAACUG UGUUAAUUACUCUUUAUCACAAUGUACGAUAGUCCCGUAAUUUCAUAAAUCACUACGAACGGAAGGCCCCACGGUUUUAU CGUAAUCACUCGCGCACGAGGUAAAUCCCCGGCUUCACGCCGUGACCUCGACUUAUGGGGCCCGAUAAUACUUAGAGAAG ACUGCGGGGUCGAGAGGCUUCUCUCCAACGGAUUCAACCUCAGUC ....((..(((......((......(((((.(((........(((((.......))))).....(((((((.(((((.(((.........((((((.......(((((((.......)))))))...(((..((((((.....((((....)))))... ....))))))...)))..))))))...((((((((((....(((..((((((((((((.........))))))).))))))).((((...(((((.........)))))....)))).....................))).(((((((.((((.... ...)))).........(((((.......(((((.....)))))..)))))).....)))))))..)))))))))).))). .)))))))))).)))..)))))......))......)))..)).
85	450	GCGGGGGUAAUAUUGGUCCGGAGCUGAACAAGUGAGCAGGUGAGGUAUGGCCGUUCGCUUCCUGUCUCAGCGGGGGGAUG ACAUAUAAGUAGGUGCAAGUAGAAUAGCACCUGUCUUUAGUUUAGCUUAAGGAGAUCAGACCAAGUUUGUUGCGAUGAGG UCACUAAUUGUUCGCAACCAUUGGCACUCAUACUCGACAGUGUAGUAGGCCAUGAGACAGUGCACGUUUAAUGCCGAGGU ACGGGAGUAGGUAAACCGCGUAGGAUAGGGCUCGGGACUAGGCAUAACUUGGUUUCGAGUCAUAGAGCCUUUCAUAACUA UAUUAGCCAAUCACCUGAUUCCCUGUAUUUCCAUGCAACAAUGACACUUGUCAUUCCAACGCCACCAAUAGGGGAACUGA CAACGAAGGGGCCGAAAGACCUUAAGGACGCCAACCCACGUACUCGUCGU (((.((((..(((((((..((.((((((((((((((.(((.(....).)))))))))))..)))).)))))...(((((((((........((((((.........((((.((((((.......((((((.((........))....((((((.((((((((((....(((....)))....)))).)))))).).)))))).....))))))...)))))))))).........(((.(((((((((((((((((.....((..(((.((.(((((((..((((((.....))))))..))))))).))...)))......... .....)).....)))).)))))).)))))))...))).....)).)))))))))))....))))))))))((.(..((.. .....((((...(....).)))))).))..).)).)))).)))..........
86	455	AACUCAUUUAAGGUAACAACUGAUAGCCGGCCGAUUAAUGGUCUAAACUACGCCCUUAUGAUUUACAGUGCACCUGGGGA ACGGACAAUACUGUAUAAAACAGAUCAACGAUACAGUCCAAUGGGCAAGGCAGAAGUUGAGCGGAGACGGUGUAAGCGGU UUACGACCGGUAGUGGAAUUCGGUUGCUACGAUCCAACUUGACACUGGCGUCAAUGUAGAUGCAAACAACGCUUAUGAUU AAUAUGCCUAUACAAACUUUAAUGUAAGGCUCUUCCGCAAAUUUCGUUUCCGUGAAUUGACCCGGCGCUCGGGGGAACCU GGGUUGCAACAGUUCAACGCGUUUGGCUCAUUACUUGGUGGACUACUCUGAACAGAUCCCUCAUCUUGCGGUCCAUUCGG UGUGCAAGCGCUAAUUCCCUGCAGUCAACCGGAACGUCGCUCGGUUUAAUGUCAU .....((((((((.....)))))).....(((.....((..(((.....)))..)). ..(((....(((.....)))))((...)))...))))...)))).((.(((((((.(((.((..((...(((((...(((..((((.(((((((((.((((...((.(((...........(((((......)))))))....(((((.....

		.....((((.((((........))))))))....................(((((((.....(((((((((....)))))).)))..)))))))..))))))))).))..((((..((((((..(...((..((....))..))..)..))))))..)))).)))).))..))))))))))).))))))))..))..))))).)))))))).))..
87	460	AGGGCUCUGAAGACCACAGCGGCCUAGCAGGCAGGUAGAUAACAAGAGGUGAUUGUAUGCUUUAGAGAUAUGUAGUACCU UCUGAGAUAGACUGACUCCCAAAACUAAGUCAUCCCAUGGGAGCCCCUAGGGGGCAAUGGAGCAGGACUUUAGUAAUACA GUCCGUUAAAAGCUUGUCUUUGAUAUAGUCAAUGAUGUACCUGGAGUCAACCCAAUGUAAACGCCUCAUGUUUAGUUGAA GCCAGUUUGUGGUACAUUGCACGUUGACAUAACUAGGUUGCGGGAGACAGGCAAAUAGGCUACUCGUCCAAUUGAUUCCA AUACGAAUCGAAUACUGUCAAUCUGAUUGGACUCGUUUUUGACCCGGUGCUCCGGGAAAACUAAUACUUAUCUUAACGGA AGUUUAAGUGCAUUAACAAUUUUGGACUGAAGAUAGCAGGUAACCCCCGCCCCGCCGGU ..(((........((...(((((((((.((((((((.....((..(((((..(((((.((....)))))))...))))) ..))........(.((((.............(((....)))(((((...)))))...))))).(((((.((....)).)))))........))))))).........((((((((((((((((..(((((......((((((.....)))))))))))). .))).......))))))))....)))))))....))))))))).)).....(((......(((((((((((.(((((((.. ....)))))))..............(((((.....(((((...(((((....))))))))))...((((((.....(((... .))))))))).......))))).))))).).)).)))).((....))...)))..)))...
88	465	GACCAUGCGUCAGACAACCUUAAAUUCAAGGACGACACACGAUUUUCGUCGUGUCGAGUCUCCUACUUUCUGCUAUACGU AGCCCCCCCGUUGACUCCGUCCUCGCAUUCUUAGGAACAAGGUUCGGGAUUGAAGAAAUUAUGGCUAGACUAUGGCCUGU CAUCGGAGUAAACCACAGUUCCGCAAUAUGAAAUCGGACCCAACAGCUGGCCUGUGCACUGCAGGGUGAAUGUAACGUAA UGGUCACGGCGGACCGCUCACGACGUAAUCAGCGAUCAUCCGGAGGAUCCUAAUGGGUCUUAAAUCCUUCAGAUCGUCUC CUUAUUCAUACAGUGUGGCUAACUGACUGGGUAAACCAGCACCCCGGCUCCCGGCCAGAUAACGCCCCAGGGGUAGGAAU GAUAAGGACGGAUCCGGGACGAGUAGUAGCUGACGCACUUGGCGGUGACUACUCUGCGAUUAUCC .....((((((((...............(((((((((((((.....))).))))))).....)))).....((((((((.(((......((((..((.((((((((..(((((((........((((((((((((..........(((((.....)))))... ....((.......)).))))))))...............(((((.(((.(((((...((((((....(((((((..((((.. (((((......)))))......)))).....((((((....((((((((((....)))))))....))).....)))))))... ..))))))).))))))))))).)))..))))).))))...(((((((.....(((.........))))).))))))))))))...))))))))))))))))))).))))))))))))))))....((((.........))))........
89	470	CCGCUACAGGCGAGAUACAAUGUCCCACAUUCUCCUGGAGAGCCUACCCGCUUCUCGCCCAGUCUCUGGAAGAGCCUAUU CCGGAAGUCCUAAACCGAUCUUGGCGUUUCUAUCCAGCUCUACGAACAGCAUUAGUGUCACAAGAUGUUCCGAAAAAGUG GCUGGAUCUUUUCACAGUAGAAGCGAGUAGUCUUGGGCCAUCCUAAUAAGCCGUGGGUUAGGAGAUCACACCCCACGUAG CGACCUCUUGCGAUAAUGCAGUAUCUGGUUUAGACAUCAUGGGCUUGGCUUACUCGAAGCAAUCUACUUAAUCUGGCGGC ACGAAAACAGAUGGGCGUUUCCAUCAGCCUCGCCGUUAUUAUACCACCCUGGGUGAAGAGAUCCUCCCGGUAGUUGCUCU GGGUCGCUAGUCACAGUGCACAACACGAAGUCAUCAUGGUGGCGCGUUAGAGAAAUGGACCGGCUCCGAG ......((((.((......(((.....))))).))))..(((((...(((.(((((....((...(((((((((((.... .(((...........)))......)))...))).))))))..))..............(((((((..((((..........(((((((((((((((((.(((((..((((((((((..((.((((.....(((((((((((....(.....)....)))))))...(((((....))))...................))))))).......)))).)).))).)))))).......)))))).......((((((..(.....).((((((.....))))))......)))))))......................)))))))))))).(((((.........)))))......))))))).(((......))).....)))).....)))))))....))))).)))...))))))....
90	475	CCUUACGUCCUCGUACGUCUUAUUACACGCUGCUGAGUCCCCAAUUAAUGAAGUGAGCUAUUCUAAACGCAGAUCUUAGC AGCCGCCCUUCUAAGAAUUCCUCGACCAAACAUUAGGCGAGGGGCUUAACGACGAAAGGCGACGAGUGACUGCGCGGACC AAGUUAUACGUAACGCCCAUAUUCUGCUGGGUAUUCAACGAGAGUAGUCCUUAUGUGAGACGAAAGGCGCGUCCCGAGAC UAUAUGAAUAUGAGGGCCUUAGACAAUGGCACGGCCCUUCGACUCCGUGAGAGAUCUCUUGGAUUUUGCGUGUUCGCUGA GCCCAAGGGCUGUACAUAGAUUCUUCAGAGCUAGUGUUCAGCCUGUUUGGAGCAUGCUGUUCCACUCCGAGCGGAAAGUG GCCCAGCCGUCCAGGGCCUUGACUCGGCAUUCUAUAAUGUUCCACUUCACUCCUCUGGUUCAGCGACGACUGCUC ......((((((((.((((((.......(((((((((............(((.........)))...........)))))))))........((((...((((((.((.........))))))).)))).......)))))))))))).)))...((((... .....((((((((.(((((.........)))))......((((((..((((((((((.(((.((((.(((..(((....))) ................(((..........)))...))).)))).)))))))))).)))))))))....))))))))(((((((((...((((((.((((((.(((....)))))).)))).)))))))...(((((((((((((..(((((((....)))..))))..)))).........(((........)))........))))))))...........)))))))))))...))))..
91	480	CUCACGGGCCGGUGACGGCGGUGUAUGGCUAAGGGAAGCGAACCUGCAGGCGCCUCGAUGUUAGCUUCAGCGUGCAUUCA GUGCAUUUUCUAAACAGCCGAGCGGACCUCCUGUGAGCUCCCUUGUCUGGUUGUCCACGCCGUCAUACCAUGAUAAAGGA GUCGCGCUUCGCUAAUUCGCUGAGUUUGCUGCUGGAACUUAGUAUUACACGUAAUUGGUUCUAGGUGUGUUUAUCAACAU CACAUUCCCAGUUCGGCUAAGCACUUAAUUCGUCCGGCAUGCAGGGCAAGGAAAUAUACCUAUCCUUGGAGUUGGCUGAC CGUCUACAUAAUUCUGAGAGUAUCGUCAUCCCUGUAAAAACGAAAACUGGAUUCCCUCUGACGAGCUGGUAAACCCGCAA GUCCCCUCCUUGUCGGAUUAACGUGUUUCAUCGCCUAGCUGCCGCCAGCAUUAACGACUCCGAACGACCGAUGCCGCUA ......(((((((...((((((((..(((..(((((.((((((((.((((......((((((((((((((((.((((...))))...........(((.((((((((.((((((((..(..((.......))..)..)))...(((((...)))))..))))))).))))).)))....)))))).((((((((((((....(((.(((..((.((((((......((((((....)))).)))....))))))))..)))..)))........))))))).))))).((((((..........)))))).....)))))).))))........)))))).)).)))..))))).........((((((((........(((((((((..((.......(....)...))..)))))))))....)).))))))...)))..)).)))))).........((....))....))))..)))....
92	485	AUAAGAAUGCCACGCUCUAUAGAUGUCUCUUGACAAACGCCUUACUAAGCGACUUUGACACCCCCCGACCAGACGAGAUA UAAAUAAGGUUAUUCCUUUACAGAUGUCCGUCGAAGCCCUUCCUCUAGAGGACGCCUCCAAUAAAACACCUGGCGCCUCA UUAGGCCCAUACUGAUACUCUAUUAGGUGUCCUGUAGACCGUAAAAACCUACGGAGAGACAGGGCGAUAGUAAAGGCGCG UUAUUUGGCUGAACUUCCCAAGUGGGGGUUCGCGUCUAGGACGUCUCUGGCGAAACGAUCACAUGUGGCUGUUCGGAUGA CUUAUGAUCUGCCGCUCAGCCAUACAUCCUUCUCUAACUCGCUUCCCAUGCGGCCAGAUAUCGUGGUGCGCGGAGUGAUC GAGAAUACCAGUGCUUAACGAUAGAUUAGUUUGUCACGUCGGGCUGCAUGCGCGCUAGGCCCUCCAACCCGUAUGCGGCC GUCCA .((((..((...((((....(((((((.((.(((....(((.......(((.((((.((............((((.(((((....((((.....))))......))))))))))...(((((((.((((.((((((((((..........((..(((.((((.. ..))))))))...))..........)))))))))).))))(((((.......)))))...)).)))))....)).)))))))). ....))).((((((((......))))))))..))).))))))))))..))))...(((((((.((((((((..(((..(((.....).))..)))..))))))))......................((.((((.((((.....).)))))))).)).)))))))).......))...))))..((((((.....))))))......((((((((((((.(...((.....))...))))))))))))

		.....
93	490	CUUGGGAAUUCACGUGGUGAUCAUACCACACAGGGCACUCACUAAGUAUUAUCGCUAGAAGACGCAUGACCCACCUGCAG GCGCGUGUCGGAAGUCUGUAGCGUCAACUUUUGGCGCUGUCGUCGUCUAAGGACGUAGGAGUGACUCUUCACAGGUGCUU CCCUCAUACGUUGGCUGUGAUCCUCCGAACAACUCCUGCGCUAUGACUUAUUACUUGCCUAUGACUUACCCUCCAUCGGA UGGCUAUCGCGGACGUGAGCUCUAACAUACAUUUGUAAUGACACCAAGGCGACUGACGCGCUUUCAGCGGAUAUGUAUGC CUCCGGGUCGCCGUGGGAAAAAUUACUAACAGAUACAUUCUCUAAUUCCAGAUUUAUGCGGAGUUCGAUCCGCGAUGCUG GGUAAUUUCAACUUGUUUCGCCGGUUAAAUAGGACCCAAAGAUCGCAACACAGUGAGUGCGGAUGGGUUGGUAAGGGCAA ACUCGCAUUU ...((((((..((((((((((....))))))..((((((((((.(((........(((((((((..(((.(......)))).(((((..(.(....).)....))))))..)))))))))).......((((....))))))))))))).))))......)))).)))))(((((((((.((...((.((....)).))...)).))).)))))........((((((...(((.(((((((..... .(((.(((((((((..(((((((((..((((.(((((.(((....(((.(((((((..(((.......))).....(....) .....)))))))..)))..............(((.....))).))).)))))).))))).)))))))).)))))))))))((((.((((.((((.(.....).)))))))).))))).....((((......))))....))).))))..))))) ....
94	495	UAUUGACUACCGGCGGUGUACUUCCUUGGCAUAUGUUCUGCAGAAACUGACGGGAUAUACCAAAAUUCGUGUACUGUCAU GGGAUUACCCAGAAAAAGCAGGACGACCGUUCCUCAGUGUGUACGGGGCCGCCAUUCCUUCCCAGCCCAAGUCCUAACCC ACGAUUCUAGAGGCUCAGGAAGGAAAGAGAUCGCUACAAGUUGAGUUGACUUAGGUCACGUAGGAGUGGUUUGGAGAACG AGUUCAACCAAUAUCAGCGUUAGCCAAGGGAAGGGGCAACGUCACAGUCCAGGCCUCGCGGUCCAUGAACGAACACAGGA GAUUAGACGUGAUUAUGAGAAAGAUCCUUGCUACUCUAAAGAGAGCUCCCUACGCCGAAGGCUAGUUGUCGUGCUUGGUUC CAACGACAGAUUCGGUAACCGGACUUCUUCUAAACACUGGUCACCCAAUGCUCCUAUUGCCAGACGUGGACUUUGUGAUA ACUCUACCAGGCGCG ....((((...((((.(((.((((((((((....(((((((.......(((((..(((((........)))))))))).((((....))))......)))))))((((.(..(((((..((((.(.(..(..(.(((((((((.(((((.((......... ......)).).))))..)))))))).).).)..).)))))..)))))..).....)))).(((..((.(((((.(((..... ..))))))))...)).)))...)))))).)))))..))).)))))..))))...(((((((((((((((.........(((((.......(((((((((((((..((((..(((.(((...)))))).......((((((......(((((((...((....)))))))))).))))))....))).)..))))...)).)))))))......)))))........))))))))..)))).. ....))).
95	500	GUACUGAGCGGACUAAUCUGUAUAAUGUCGACGAAGCCGGCCUUCGCCGUUAACUACUCUCUCAUACAUAUAUGUAAACA GGAAAAAAAGGUCGUCCCACUGAGUGCUCUCUUGGUAUUCAGCUUCCAAGUGGCGGCACCGUAUCGGUUUAAGCAGAUAG ACGGAAGGAGCGCGGCUGCGCCGUCUGCGUACUGAUAUCUUCUCCGGAGCAUUUUGUAGGGUCGUGACGCUUCUCUGAGC ACACUCAGCUCAAACCUAUAUCCCGCUCUCCACCCAAAGGGAGAUCAUGUAUAUUAAGCACUCCUUCAGUCGGAACCUAA AUAAGUAUAACAGUUCUACCGAGACUAAGGGCACAAUGUAGUACCGUUGUAGCGCAACGAAACCCCGAAAAACGGCAAGC GUCUAUUAACGAUGUACGGGCCCUUUCGCCAUUUGUGAAAGAACGUAGAGUUAACGAUACGCGAAGCGCCGGAGUUGCGU CAUACGCCCGCUACAUUCAU ....(((((((.......(((((.(((.((((....(((((((((((((((((((..(((.(((((............. ((((.....((....))..(((((((((.....)))))))))..))))).(((((((((.((((((((((....)).(((((((((((((((.((...(((((.....)))))...((((..((((((((((....((((((....((((.((((.....(((. ...)))))))))..))))))....)))))..........)))))..))))).......)).)))))))..(((((..... ....((((.(((.......((........)).....))).))))(((((.....)))))).....)))).........))))))))..)))..)))))))).....))))))))))).)))......)))))))....))))))).)))))).))))))) .)))))..)))))..))....