

SUPPLEMENTARY MATERIAL

Thermodynamic matchers for the construction of the cuckoo RNA family

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Methods

Deriving structure and sequence characteristics for TDM modeling

The design decisions of a TDM rest on observations of the extrema of the structural features and the deviation in sequence patterns. As a consequence, two sources of information based on the already known RNAs belonging to the family under consideration are needed to parameterize a TDM: (1) a multiple structure alignment for discovering conserved sequence motifs and to obtain the consensus secondary structure and (2) individual secondary structure folds to derive the range of structural variation. Implicitly, structural variation refers to the variation of RNAs folded into the family's overall structure, not to the variation of MFE structures. Thus, in order to guarantee that a cuckoo RNA folds into the characteristic shape of the family and yet in the energetically optimal way, three auxiliary TDMs, tdm_{AUX_HP2} , tdm_{AUX_HP3} , tdm_{AUX_HP4} , one for each structural variant, were designed (**Fig. S1**).

Like RNAfold, most software tools that implement constraint folding define structure constraints on the base or base-pair level. Such constraints can be easily derived for the cuckoo family from the existing structure alignments, but we have to bear in mind that there often is an underrepresentation of base-pairs and stacking in the consensus structure for some RNAs in the alignments, causing suboptimal energies if the RNAs are folded into the consensus. Therefore, the intention to use TDMs is to enable a cuckoo RNA to fold into the family's structure and only the family's structure, but with the highest degree of freedom (as few constraints as needed). For example, the grammar of tdm_{AUX_HP2} defines two hairpins with arbitrary lengths of stems and hairpin loops. The only restriction is that in every loop the cuckoo motif must be present. Except for the motif constraint this definition is equivalent to the RNASHAPES constraint folding using the most abstract level 5 (RNASHAPES -C '[][]'). The grammars of the other auxiliary TDMs, tdm_{AUX_HP3} and tdm_{AUX_HP4} , define three and four hairpins, respectively, and require the cuckoo motif in one of the motif variants observed with this number of hairpins.

The auxiliary TDMs described here were applied on the 145 previously known cuckoo RNAs (**Table S5**) and the feature information that was gathered from this analysis was used to build the initial skeleton and cuckoo TDMs.

Supplementary figures

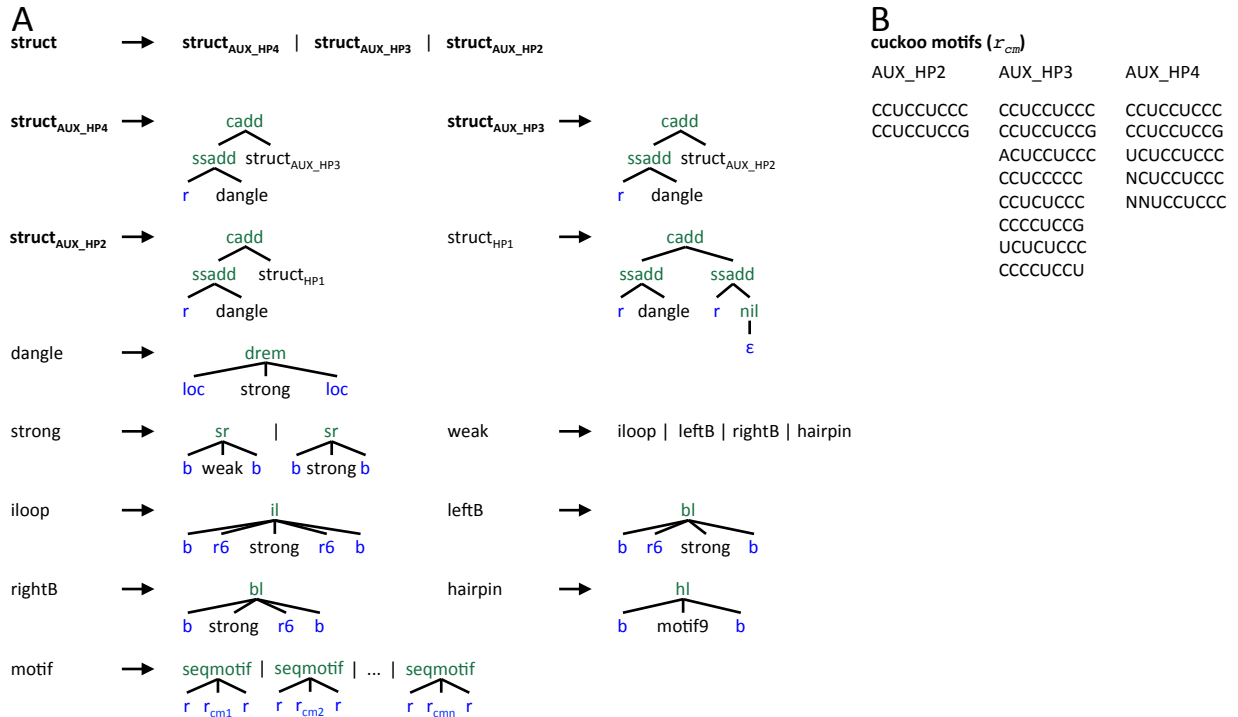


Figure S1. Unified grammar for auxiliary TDMs (A) and sequence constraints for cuckoo motifs (B). The auxiliary TDM grammars base on the same standard RNA folding grammar that is used by the cuckoo TDM grammar. $struct_{AUX_X}$ is the grammars axiom, where $X \in \{HP2, HP3, HP4\}$ denotes the structural variant of a cuckoo RNA that folds into two, three or four hairpins, respectively (A). Size thresholds are applied only for helix interruptions, which are restricted to a maximum of six bases ($r6$), and the length of hairpin loops, which must be at least nine bases long ($motif9$). For each cuckoo motif in (B) an alternative production of $seqmotif$ exists in the respective grammar, where r_{cm} corresponds to the cuckoo motif. The IUPAC convention is used to express cuckoo motifs.

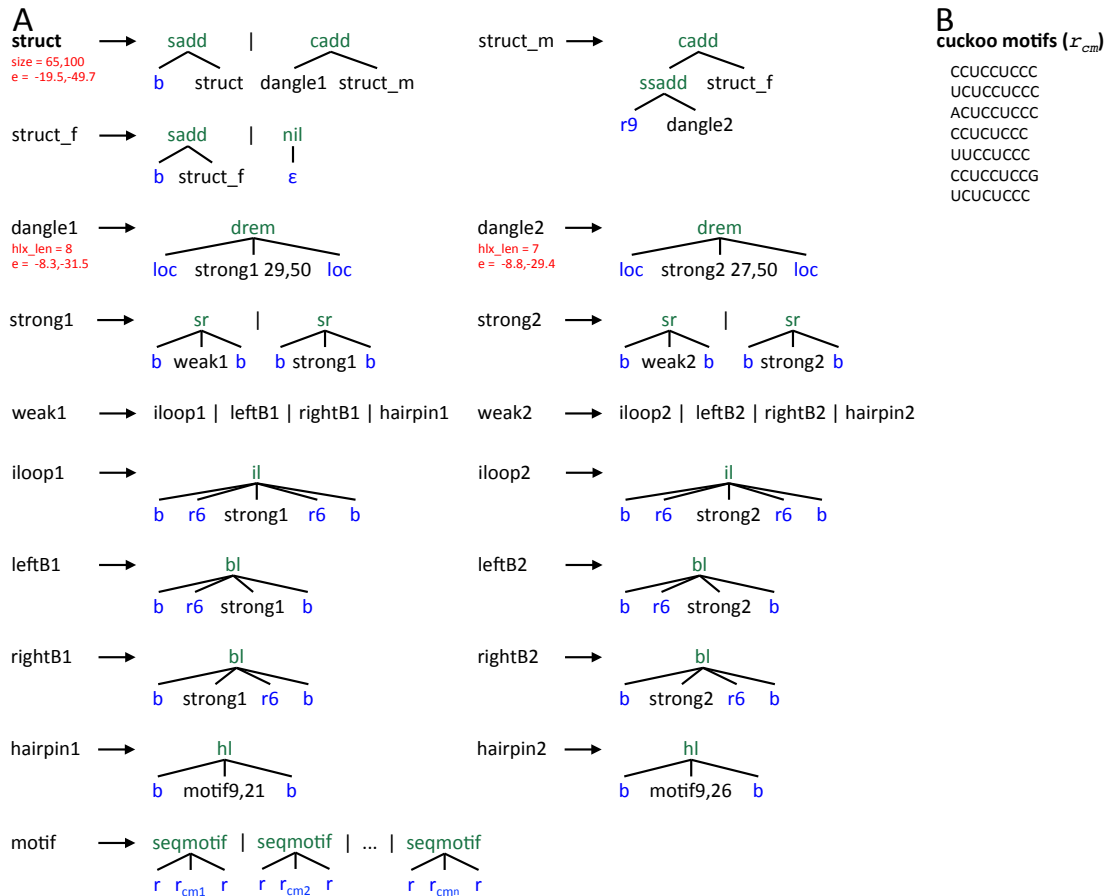


Figure S2. Grammar of HP2 cuckoo RNA specific TDM tdm_{HP2} (A) and sequence constraints for cuckoo motifs (B). Generally, the grammar of tdm_{HP2} is a less generic version of the cuckoo TDM grammar, and is tailored to cuckoo RNAs that consist of two hairpins (*struct*) (A). Both grammars apply the same algebra functions and production rules (see Methods for details). However, in order to apply specific constraints for the stem-loops separate nonterminals are defined, which are annotated at the end with a '1' for the first and a '2' for the second stem-loop. Vertical bars separate alternative productions that start at the same nonterminal. Algebra functions are colored in green and built the tree-like data structure from terminals and nonterminals. The functions call upon the energy functions of the thermodynamic model to compute free energies for the corresponding substructure. The following terminals (in blue) are used: ϵ denotes the empty word, b a single base from the RNA alphabet $\{A, C, G, U\}$, r a region of bases, and *loc* the end position of a neighbor subword. Numbers depict thresholds for size filters. A single number specifies the maximum size while two numbers determine a size range. Filter of nonterminals are colored red. Next to the helix length filter (*hlx_len*), an energy (*e*) and a global size filter (*size*) are introduced. These filter are applied either on the entire hairpin substructures (*dangle1*,

dangle2) or on the overall structure of the cuckoo RNA (*struct*). For each cuckoo motif in (B) an alternative production of *seqmotif* exists, where r_{cm} corresponds to the cuckoo motif. The IUPAC convention is used to express cuckoo motifs.

Table S1. Identified cuckoo RNAs.

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
1	<i>Brucella abortus</i> A13334	NC_016777	-	653262	653336	75	2
2	<i>Brucella abortus</i> S19	NC_010740	-	502220	502294	75	2
3	<i>Brucella abortus</i> bv. 1 str. 9-941	NC_006933	-	503016	503090	75	2
4	<i>Brucella canis</i> ATCC 23365	NC_010104	-	448045	448112	68	2
5	<i>Brucella canis</i> HSK A52141	NC_016796	+	347616	347683	68	2
6	<i>Brucella melitensis</i> ATCC 23457	NC_012442	+	693158	693235	78	2
7	<i>Brucella melitensis</i> M28	NC_017245	+	693239	693316	78	2
8	<i>Brucella melitensis</i> M5-90	NC_017247	+	693422	693500	79	2
9	<i>Brucella melitensis</i> NI	NC_017283	+	684915	684991	77	2
10	<i>Brucella melitensis</i> biovar Abortus 2308	NC_007624	-	503004	503078	75	2
11	<i>Brucella melitensis</i> biovar Abortus 2308	NC_007624	+	766870	766937	68	2
12	<i>Brucella melitensis</i> bv. 1 str. 16M	NC_003318	-	583662	583740	79	2
13	<i>Brucella melitensis</i> bv. 1 str. 16M	NC_003318	+	840862	840929	68	2
14	<i>Brucella microti</i> CCM 4915	NC_013118	-	449438	449505	68	2
15	<i>Brucella microti</i> CCM 4915	NC_013118	+	714994	715072	79	2
16	<i>Brucella ovis</i> ATCC 25840	NC_009504	+	715283	715365	83	2
17	<i>Brucella pinnipedialis</i> B2/94	NC_015858	+	769774	769858	85	2
18	<i>Brucella suis</i> 1330	NC_004311	+	714053	714140	88	2
19	<i>Brucella suis</i> ATCC 23445	NC_010167	+	701948	702026	79	2
20	<i>Brucella suis</i> VBI22	NC_016775	+	714103	714190	88	2
21	<i>Chelativorans</i> sp. BNC1	NC_008254	+	215078	215147	70	2
22	<i>Chelativorans</i> sp. BNC1	NC_008254	+	247442	247513	72	2
23	<i>Dinoroseobacter shibae</i> DFL 12	NC_009952	+	2630143	2630214	72	2
24	<i>Jannaschia</i> sp. CCS1	NC_007802	+	2789969	2790040	72	2
25	<i>Jannaschia</i> sp. CCS1	NC_007802	+	2790047	2790121	75	2
26	<i>Jannaschia</i> sp. CCS1	NC_007802	+	2790129	2790206	78	2
27	<i>Loktanella vestfoldensis</i> DSM 16212	ARNL01000047	+	167285	167363	79	2
28	<i>Loktanella vestfoldensis</i> DSM 16212	ARNL01000047	+	167366	167457	92	2
29	<i>Loktanella vestfoldensis</i> SKA53	AAMS01000006	+	20806	20885	80	2
30	<i>Loktanella vestfoldensis</i> SKA53	AAMS01000006	+	20888	20979	92	2
31	<i>Oceanicola batsensis</i> HTCC2597	AAMO01000006	-	253329	253403	75	2
32	<i>Oceanicola batsensis</i> HTCC2597	AAMO01000015	+	75594	75676	83	2
33	<i>Oceanicola granulosus</i> HTCC2516	AAOT01000003	+	159000	159071	72	2
34	<i>Oceanicola granulosus</i> HTCC2516	AAOT01000003	+	159079	159178	100	2
35	<i>Oceanicola granulosus</i> HTCC2516	AAOT01000003	+	159179	159271	93	2
36	<i>Oceanicola granulosus</i> HTCC2516	AAOT01000003	+	159276	159366	91	2
37	<i>Octadecabacter antarcticus</i> 307	NC_020911	-	1186564	1186643	80	2

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
38	Octadecabacter antarcticus 307	NC_020911	+	1586963	1587043	81	2
39	Octadecabacter arcticus 238	NC_020908	+	725520	725600	81	2
40	Octadecabacter arcticus 238	NC_020908	-	805823	805900	78	2
41	Octadecabacter arcticus 238	NC_020908	+	2229885	2229964	80	2
42	Paracoccus denitrificans PD1222	NC_008686	-	551382	551460	79	2
43	Paracoccus denitrificans PD1222	NC_008686	-	551461	551537	77	2
44	Paracoccus denitrificans PD1222	NC_008686	-	551548	551620	73	2
45	Paracoccus denitrificans PD1222	NC_008686	-	551632	551708	77	2
46	Parvibaculum lavamentivorans DS-1	NC_009719	-	2345729	2345812	84	2
47	Phaeobacter gallaeciensis 2.10	NC_018286	-	1028576	1028659	84	2
48	Phaeobacter gallaeciensis 2.10	NC_018286	-	1028692	1028768	77	2
49	Phaeobacter gallaeciensis DSM 17395 = CIP 105210	NC_018290	-	969366	969450	85	2
50	Phaeobacter gallaeciensis DSM 17395 = CIP 105210	NC_018290	-	969483	969559	77	2
51	Rhizobium etli CIAT 652	NC_010997	+	28126	28206	81	2
52	Rhizobium leguminosarum bv. trifolii WSM2304	NC_011369	+	2611417	2611512	96	2
53	Rhodobacter capsulatus SB 1003	NC_014034	+	2557456	2557534	79	2
54	Rhodobacter capsulatus SB 1003	NC_014034	+	2557567	2557644	78	2
55	Rhodobacter capsulatus SB 1003	NC_014034	+	2557654	2557718	65	2
56	Rhodobacter capsulatus SB 1003	NC_014034	+	2557722	2557797	76	2
57	Rhodobacter sphaeroides 2.4.1	NC_007493	-	691712	691787	76	2
58	Rhodobacter sphaeroides 2.4.1	NC_007493	-	691826	691901	76	2
59	Rhodobacter sphaeroides 2.4.1	NC_007493	-	691940	692015	76	2
60	Rhodobacter sphaeroides 2.4.1	NC_007493	-	692055	692130	76	2
61	Rhodobacter sphaeroides 2.4.1	NC_007493	-	692169	692245	77	2
62	Rhodobacter sphaeroides 2.4.1	NC_007493	-	692284	692355	72	2
63	Rhodobacter sphaeroides 2.4.1	NC_007493	-	692386	692458	73	2
64	Rhodobacter sphaeroides ATCC 17025	NC_009428	-	686801	686877	77	2
65	Rhodobacter sphaeroides ATCC 17025	NC_009428	-	686914	686990	77	2
66	Rhodobacter sphaeroides ATCC 17025	NC_009428	-	687030	687103	74	2
67	Rhodobacter sphaeroides ATCC 17025	NC_009428	-	687134	687206	73	2
68	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775209	775284	76	2
69	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775322	775397	76	2
70	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775436	775511	76	2
71	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775550	775625	76	2
72	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775664	775739	76	2
73	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775778	775853	76	2
74	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	775892	775968	77	2
75	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	776007	776078	72	2
76	Rhodobacter sphaeroides ATCC 17029	NC_009049	-	776109	776181	73	2

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
77	Rhodobacter sphaeroides KD131	NC_011963	-	388542	388617	76	2
78	Rhodobacter sphaeroides KD131	NC_011963	-	388655	388733	79	2
79	Rhodobacter sphaeroides KD131	NC_011963	-	388773	388848	76	2
80	Rhodobacter sphaeroides KD131	NC_011963	-	388886	388961	76	2
81	Rhodobacter sphaeroides KD131	NC_011963	-	389000	389076	77	2
82	Rhodobacter sphaeroides KD131	NC_011963	-	389115	389186	72	2
83	Rhodobacter sphaeroides KD131	NC_011963	-	389217	389289	73	2
84	Roseobacter denitrificans OCh 114	NC_008209	+	3236828	3236905	78	2
85	Roseobacter denitrificans OCh 114	NC_008209	+	3236958	3237038	81	2
86	Roseobacter litoralis OCh 149	NC_015730	+	2651702	2651779	78	2
87	Roseobacter litoralis OCh 149	NC_015730	+	2651849	2651925	77	2
88	Roseovarius nubinhibens ISM	AALY01000001	-	1448571	1448659	89	2
89	Roseovarius nubinhibens ISM	AALY01000001	-	1795550	1795645	96	2
90	Roseovarius sp. 217	AAMV01000014	-	60809	60892	84	2
91	Roseovarius sp. 217	AAMV01000014	-	60923	61000	78	2
92	Ruegeria pomeroyi DSS-3	NC_003911	-	1229325	1229402	78	2
93	Ruegeria pomeroyi DSS-3	NC_003911	-	1229435	1229515	81	2
94	Ruegeria pomeroyi DSS-3	NC_003911	-	1229541	1229615	75	2
95	Ruegeria sp. TM1040	NC_008044	+	2128236	2128310	75	2
96	Ruegeria sp. TM1040	NC_008044	+	2128342	2128421	80	2
97	Sagittula stellata E-37	AAYA01000003	-	288749	288824	76	2
98	Sagittula stellata E-37	AAYA01000003	-	288853	288928	76	2
99	Sagittula stellata E-37	AAYA01000003	-	288952	289032	81	2
100	Sinorhizobium medicae WSM419	NC_009636	-	1974715	1974785	71	2
101	Sulfitobacter sp. EE-36	AALV01000002	+	574043	574121	79	2
102	Sulfitobacter sp. NAS-14.1	AALZ01000003	+	477443	477521	79	2
103	Sulfitobacter sp. NAS-14.1	AALZ01000014	-	12834	12913	80	2
104	Phaeobacter gallaeciensis DSM 26640	NC_023137	+	2565404	2565480	77	2
105	Phaeobacter gallaeciensis DSM 26640	NC_023137	+	2565513	2565597	85	2
106	Agrobacterium fabrum str. C58	NC_003063	+	1230300	1230420	121	3
107	Agrobacterium radiobacter K84	NC_011985	+	597906	598019	114	3
108	Agrobacterium radiobacter K84	NC_011985	-	1693286	1693404	119	3
109	Agrobacterium radiobacter K84	NC_011985	-	3945513	3945635	123	3
110	Agrobacterium sp. H13-3	NC_015183	+	109376	109491	116	3
111	Agrobacterium sp. H13-3	NC_015508	+	1615158	1615278	121	3
112	Agrobacterium vitis S4	NC_011984	+	7323	7437	115	3
113	Agrobacterium vitis S4	NC_011989	+	115128	115250	123	3
114	Agrobacterium vitis S4	NC_011989	+	2043917	2044035	119	3
115	Brucella abortus A13334	NC_016777	+	917127	917244	118	3

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
116	<i>Brucella abortus</i> A13334	NC_016795	-	2057998	2058103	106	3
117	<i>Brucella abortus</i> S19	NC_010740	+	766085	766202	118	3
118	<i>Brucella abortus</i> S19	NC_010742	+	358314	358419	106	3
119	<i>Brucella abortus</i> bv. 1 str. 9-941	NC_006932	+	359929	360034	106	3
120	<i>Brucella canis</i> ATCC 23365	NC_010103	+	338025	338130	106	3
121	<i>Brucella canis</i> HSK A52141	NC_016778	-	716263	716368	106	3
122	<i>Brucella melitensis</i> ATCC 23457	NC_012441	+	358980	359085	106	3
123	<i>Brucella melitensis</i> M28	NC_017244	+	358975	359080	106	3
124	<i>Brucella melitensis</i> M5-90	NC_017246	+	359228	359333	106	3
125	<i>Brucella melitensis</i> NI	NC_017248	+	359170	359275	106	3
126	<i>Brucella melitensis</i> biovar Abortus 2308	NC_007618	+	356297	356402	106	3
127	<i>Brucella melitensis</i> bv. 1 str. 16M	NC_003317	-	1644164	1644269	106	3
128	<i>Brucella microti</i> CCM 4915	NC_013119	+	339703	339808	106	3
129	<i>Brucella ovis</i> ATCC 25840	NC_009505	+	359686	359791	106	3
130	<i>Brucella pinnipedialis</i> B2/94	NC_015857	+	359797	359902	106	3
131	<i>Brucella pinnipedialis</i> B2/94	NC_015858	-	432926	433043	118	3
132	<i>Brucella suis</i> 1330	NC_004311	-	448112	448229	118	3
133	<i>Brucella suis</i> 1330	NC_004310	+	338022	338127	106	3
134	<i>Brucella suis</i> ATCC 23445	NC_010167	-	449214	449331	118	3
135	<i>Brucella suis</i> ATCC 23445	NC_010169	+	355561	355666	106	3
136	<i>Brucella suis</i> VBI22	NC_016775	-	448084	448201	118	3
137	<i>Brucella suis</i> VBI22	NC_016797	+	337983	338088	106	3
138	<i>Chelativorans</i> sp. BNC1	NC_008242	-	32194	32312	119	3
139	<i>Chelativorans</i> sp. BNC1	NC_008242	-	135271	135381	111	3
140	<i>Chelativorans</i> sp. BNC1	NC_008254	+	1916700	1916818	119	3
141	<i>Chelativorans</i> sp. BNC1	NC_008254	-	3977087	3977203	117	3
142	<i>Ketogulonicigenium vulgare</i> WSH-001	NC_017384	+	1585028	1585148	121	3
143	<i>Ketogulonicigenium vulgare</i> Y25	NC_014625	-	363561	363681	121	3
144	<i>Loktanella vestfoldensis</i> DSM 16212	ARNL01000047	+	167460	167590	131	3
145	<i>Loktanella vestfoldensis</i> SKA53	AAMS01000006	+	20982	21115	134	3
146	<i>Mesorhizobium australicum</i> WSM2073	NC_019973	+	2514219	2514328	110	3
147	<i>Mesorhizobium australicum</i> WSM2073	NC_019973	-	3842524	3842639	116	3
148	<i>Mesorhizobium australicum</i> WSM2073	NC_019973	-	3842695	3842817	123	3
149	<i>Mesorhizobium australicum</i> WSM2073	NC_019973	-	3842878	3842995	118	3
150	<i>Mesorhizobium australicum</i> WSM2073	NC_019973	+	5250476	5250594	119	3
151	<i>Mesorhizobium ciceri</i> biovar biserrulae WSM1271	NC_014918	-	241411	241528	118	3
152	<i>Mesorhizobium ciceri</i> biovar biserrulae WSM1271	NC_014923	+	2545677	2545786	110	3
153	<i>Mesorhizobium ciceri</i> biovar biserrulae WSM1271	NC_014923	-	3674844	3674959	116	3
154	<i>Mesorhizobium ciceri</i> biovar biserrulae WSM1271	NC_014923	-	3675022	3675138	117	3

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
155	Mesorhizobium ciceri biovar biserrulae WSM1271	NC_014923	-	3675192	3675313	122	3
156	Mesorhizobium ciceri biovar biserrulae WSM1271	NC_014923	+	5265891	5266010	120	3
157	Mesorhizobium loti MAFF303099	NC_002678	+	890586	890708	123	3
158	Mesorhizobium loti MAFF303099	NC_002678	+	890764	890886	123	3
159	Mesorhizobium loti MAFF303099	NC_002678	+	890945	891060	116	3
160	Mesorhizobium loti MAFF303099	NC_002678	-	4952227	4952339	113	3
161	Mesorhizobium loti MAFF303099	NC_002678	+	5350765	5350884	120	3
162	Mesorhizobium loti MAFF303099	NC_002678	-	6092422	6092540	119	3
163	Mesorhizobium opportunistum WSM2075	NC_015675	+	2663741	2663850	110	3
164	Mesorhizobium opportunistum WSM2075	NC_015675	-	4112140	4112256	117	3
165	Mesorhizobium opportunistum WSM2075	NC_015675	-	4112319	4112435	117	3
166	Mesorhizobium opportunistum WSM2075	NC_015675	-	4112500	4112616	117	3
167	Mesorhizobium opportunistum WSM2075	NC_015675	+	5830416	5830540	125	3
168	Oceanicola granulosus HTCC2516	AAOT01000003	+	159369	159502	134	3
169	Ochrobactrum anthropi ATCC 49188	NC_009667	+	448505	448616	112	3
170	Ochrobactrum anthropi ATCC 49188	NC_009668	-	273977	274099	123	3
171	Ochrobactrum anthropi ATCC 49188	NC_009668	+	274692	274808	117	3
172	Ochrobactrum anthropi ATCC 49188	NC_009668	+	1275653	1275770	118	3
173	Octadecabacter arcticus 238	NC_020908	-	805678	805816	139	3
174	Pelagibacterium halotolerans B2	NC_016078	+	2112639	2112774	136	3
175	Pelagibacterium halotolerans B2	NC_016078	+	2112938	2113067	130	3
176	Polymorphum gilvum SL003B-26A1	NC_015259	-	2331457	2331575	119	3
177	Rhizobium etli CFN 42	NC_007761	+	462572	462689	118	3
178	Rhizobium etli CFN 42	NC_007761	-	1926237	1926353	117	3
179	Rhizobium etli CFN 42	NC_007761	-	4314389	4314500	112	3
180	Rhizobium etli CFN 42	NC_007766	+	22825	22932	108	3
181	Rhizobium etli CIAT 652	NC_010994	+	513999	514116	118	3
182	Rhizobium etli CIAT 652	NC_010994	-	1912478	1912592	115	3
183	Rhizobium etli CIAT 652	NC_010994	-	4444891	4445011	121	3
184	Rhizobium etli bv. mimosae str. Mim1	NC_021905	+	460364	460481	118	3
185	Rhizobium etli bv. mimosae str. Mim1	NC_021905	-	1884349	1884464	116	3
186	Rhizobium etli bv. mimosae str. Mim1	NC_021905	-	4217281	4217392	112	3
187	Rhizobium etli bv. mimosae str. Mim1	NC_021911	+	23172	23285	114	3
188	Rhizobium leguminosarum bv. trifolii WSM1325	NC_012848	+	112606	112722	117	3
189	Rhizobium leguminosarum bv. trifolii WSM1325	NC_012850	+	107069	107186	118	3
190	Rhizobium leguminosarum bv. trifolii WSM1325	NC_012850	-	1697043	1697151	109	3
191	Rhizobium leguminosarum bv. trifolii WSM1325	NC_012850	-	4296637	4296748	112	3
192	Rhizobium leguminosarum bv. trifolii WSM2304	NC_011368	-	306341	306452	112	3
193	Rhizobium leguminosarum bv. trifolii WSM2304	NC_011369	+	98056	98173	118	3

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
194	Rhizobium leguminosarum bv. trifolii WSM2304	NC_011369	-	1534501	1534616	116	3
195	Rhizobium leguminosarum bv. trifolii WSM2304	NC_011369	-	4019331	4019445	115	3
196	Rhizobium leguminosarum bv. viciae 3841	NC_008378	+	407204	407312	109	3
197	Rhizobium leguminosarum bv. viciae 3841	NC_008380	+	512664	512781	118	3
198	Rhizobium leguminosarum bv. viciae 3841	NC_008380	-	2174961	2175069	109	3
199	Rhizobium leguminosarum bv. viciae 3841	NC_008380	-	4988043	4988157	115	3
200	Rhizobium tropici CIAT 899	NC_020059	+	542312	542433	122	3
201	Rhizobium tropici CIAT 899	NC_020059	-	1631584	1631703	120	3
202	Rhizobium tropici CIAT 899	NC_020059	-	3775245	3775367	123	3
203	Sagittula stellata E-37	AAYA01000003	-	288595	288722	128	3
204	Sinorhizobium fredii HH103	NC_016812	-	1359348	1359467	120	3
205	Sinorhizobium fredii HH103	NC_016812	-	1359641	1359757	117	3
206	Sinorhizobium fredii HH103	NC_016812	+	4014538	4014654	117	3
207	Sinorhizobium fredii HH103	NC_016815	-	233468	233581	114	3
208	Sinorhizobium fredii HH103	NC_018299	+	158094	158203	110	3
209	Sinorhizobium fredii HH103	NT_187148	+	158094	158203	110	3
210	Sinorhizobium fredii NGR234	NC_012586	+	2205316	2205429	114	3
211	Sinorhizobium fredii NGR234	NC_012587	-	1434171	1434291	121	3
212	Sinorhizobium fredii NGR234	NC_012587	-	1434465	1434581	117	3
213	Sinorhizobium fredii NGR234	NC_012587	+	3720582	3720698	117	3
214	Sinorhizobium fredii USDA 257	NC_018000	+	1713249	1713362	114	3
215	Sinorhizobium fredii USDA 257	NC_018000	-	3752633	3752757	125	3
216	Sinorhizobium fredii USDA 257	NC_018000	-	3752930	3753043	114	3
217	Sinorhizobium fredii USDA 257	NC_018000	+	5733804	5733912	109	3
218	Sinorhizobium fredii USDA 257	NC_018000	+	6267166	6267283	118	3
219	Sinorhizobium fredii USDA 257	NC_018191	+	159232	159341	110	3
220	Sinorhizobium medicae WSM419	NC_009620	-	679042	679158	117	3
221	Sinorhizobium medicae WSM419	NC_009636	-	1258034	1258158	125	3
222	Sinorhizobium medicae WSM419	NC_009636	-	1258315	1258426	112	3
223	Sinorhizobium medicae WSM419	NC_009636	-	3590302	3590414	113	3
224	Sinorhizobium meliloti 1021	NC_003037	+	1220693	1220806	114	3
225	Sinorhizobium meliloti 1021	NC_003047	-	206865	206977	113	3
226	Sinorhizobium meliloti 1021	NC_003047	-	1667488	1667611	124	3
227	Sinorhizobium meliloti 1021	NC_003047	-	1667771	1667886	116	3
228	Sinorhizobium meliloti 1021	NC_003078	+	1605828	1605944	117	3
229	Sinorhizobium meliloti 2011	NC_020527	+	1219031	1219144	114	3
230	Sinorhizobium meliloti 2011	NC_020528	-	206866	206978	113	3
231	Sinorhizobium meliloti 2011	NC_020528	-	1667197	1667320	124	3
232	Sinorhizobium meliloti 2011	NC_020528	-	1667480	1667595	116	3

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
233	<i>Sinorhizobium meliloti</i> 2011	NC_020560	+	1605843	1605959	117	3
234	<i>Sinorhizobium meliloti</i> AK83	NC_015590	-	1369797	1369920	124	3
235	<i>Sinorhizobium meliloti</i> AK83	NC_015590	-	1370080	1370195	116	3
236	<i>Sinorhizobium meliloti</i> AK83	NC_015590	-	3626930	3627042	113	3
237	<i>Sinorhizobium meliloti</i> AK83	NC_015596	-	574044	574160	117	3
238	<i>Sinorhizobium meliloti</i> AK83	NC_015597	+	172172	172288	117	3
239	<i>Sinorhizobium meliloti</i> BL225C	NC_017322	-	1231897	1232020	124	3
240	<i>Sinorhizobium meliloti</i> BL225C	NC_017322	-	1232180	1232295	116	3
241	<i>Sinorhizobium meliloti</i> BL225C	NC_017322	-	3479601	3479713	113	3
242	<i>Sinorhizobium meliloti</i> BL225C	NC_017323	-	1376421	1376537	117	3
243	<i>Sinorhizobium meliloti</i> GR4	NC_019845	-	201602	201714	113	3
244	<i>Sinorhizobium meliloti</i> GR4	NC_019845	-	1637016	1637139	124	3
245	<i>Sinorhizobium meliloti</i> GR4	NC_019845	-	1637299	1637414	116	3
246	<i>Sinorhizobium meliloti</i> GR4	NC_019849	-	141338	141454	117	3
247	<i>Sinorhizobium meliloti</i> Rm41	NC_018683	-	532712	532828	117	3
248	<i>Sinorhizobium meliloti</i> Rm41	NC_018700	-	1308437	1308560	124	3
249	<i>Sinorhizobium meliloti</i> Rm41	NC_018700	-	1308720	1308835	116	3
250	<i>Sinorhizobium meliloti</i> Rm41	NC_018700	-	3485604	3485716	113	3
251	<i>Sinorhizobium meliloti</i> Rm41	NC_018701	-	135189	135305	117	3
252	<i>Sinorhizobium meliloti</i> SM11	NC_017325	+	2001062	2001177	116	3
253	<i>Sinorhizobium meliloti</i> SM11	NC_017325	+	2001337	2001460	124	3
254	<i>Sinorhizobium meliloti</i> SM11	NC_017325	-	3713437	3713549	113	3
255	<i>Sinorhizobium meliloti</i> SM11	NC_017326	-	141142	141258	117	3
256	<i>Agrobacterium fabrum</i> str. C58	NC_003062	+	109477	109645	169	4
257	<i>Agrobacterium fabrum</i> str. C58	NC_003063	+	1831446	1831604	159	4
258	<i>Agrobacterium radiobacter</i> K84	NC_011983	+	957654	957810	157	4
259	<i>Agrobacterium radiobacter</i> K84	NC_011983	-	1921118	1921278	161	4
260	<i>Agrobacterium radiobacter</i> K84	NC_011987	-	138502	138658	157	4
261	<i>Agrobacterium</i> sp. H13-3	NC_015508	-	164001	164157	157	4
262	<i>Agrobacterium</i> sp. H13-3	NC_015508	-	244664	244817	154	4
263	<i>Agrobacterium vitis</i> S4	NC_011988	-	598435	598589	155	4
264	<i>Agrobacterium vitis</i> S4	NC_011988	+	901000	901158	159	4
265	<i>Agrobacterium vitis</i> S4	NC_011989	-	2793811	2793967	157	4
266	<i>Brucella abortus</i> A13334	NC_016795	+	1527400	1527550	151	4
267	<i>Brucella abortus</i> S19	NC_010742	-	888878	889028	151	4
268	<i>Brucella abortus</i> bv. 1 str. 9-941	NC_006932	-	890577	890727	151	4
269	<i>Brucella canis</i> ATCC 23365	NC_010103	-	867218	867368	151	4
270	<i>Brucella canis</i> HSK A52141	NC_016778	+	185975	186125	151	4
271	<i>Brucella melitensis</i> ATCC 23457	NC_012441	-	890344	890494	151	4

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
272	<i>Brucella melitensis</i> M28	NC_017244	-	890289	890439	151	4
273	<i>Brucella melitensis</i> M5-90	NC_017246	-	890603	890753	151	4
274	<i>Brucella melitensis</i> NI	NC_017248	-	886872	887022	151	4
275	<i>Brucella melitensis</i> biovar Abortus 2308	NC_007618	-	886855	887005	151	4
276	<i>Brucella melitensis</i> bv. 1 str. 16M	NC_003317	+	1116628	1116778	151	4
277	<i>Brucella microti</i> CCM 4915	NC_013119	-	873050	873200	151	4
278	<i>Brucella ovis</i> ATCC 25840	NC_009505	-	895750	895898	149	4
279	<i>Brucella pinnipedialis</i> B2/94	NC_015857	-	897286	897436	151	4
280	<i>Brucella suis</i> 1330	NC_004310	-	868834	868984	151	4
281	<i>Brucella suis</i> ATCC 23445	NC_010169	-	888714	888864	151	4
282	<i>Brucella suis</i> VBI22	NC_016797	-	868801	868951	151	4
283	<i>Oceanicola batsensis</i> HTCC2597	AAMO01000006	-	253121	253287	167	4
284	<i>Ochrobactrum anthropi</i> ATCC 49188	NC_009667	+	2453942	2454091	150	4
285	<i>Octadecabacter antarcticus</i> 307	NC_020911	-	1086719	1086896	178	4
286	<i>Octadecabacter antarcticus</i> 307	NC_020911	-	1955581	1955758	178	4
287	<i>Octadecabacter antarcticus</i> 307	NC_020911	-	1992343	1992520	178	4
288	<i>Octadecabacter antarcticus</i> 307	NC_020911	+	3698830	3699006	177	4
289	<i>Octadecabacter arcticus</i> 238	NC_020908	-	670324	670504	181	4
290	<i>Octadecabacter arcticus</i> 238	NC_020908	+	2787008	2787181	174	4
291	<i>Octadecabacter arcticus</i> 238	NC_020908	+	3179240	3179417	178	4
292	<i>Paracoccus aminophilus</i> JCM 7686	NC_022041	+	2655475	2655630	156	4
293	<i>Paracoccus aminophilus</i> JCM 7686	NC_022041	+	2655655	2655805	151	4
294	<i>Paracoccus denitrificans</i> PD1222	NC_008686	-	551203	551352	150	4
295	<i>Polymorphum gilvum</i> SL003B-26A1	NC_015259	-	2332074	2332228	155	4
296	<i>Pseudovibrio</i> sp. FO-BEG1	NC_016642	+	3461369	3461532	164	4
297	<i>Rhizobium etli</i> CFN 42	NC_004041	+	77637	77794	158	4
298	<i>Rhizobium etli</i> CFN 42	NC_007765	-	443012	443161	150	4
299	<i>Rhizobium etli</i> CIAT 652	NC_010994	+	1173479	1173639	161	4
300	<i>Rhizobium etli</i> CIAT 652	NC_010996	+	112261	112418	158	4
301	<i>Rhizobium etli</i> CIAT 652	NC_010998	-	345903	346054	152	4
302	<i>Rhizobium etli</i> bv. mimosae str. Mim1	NC_021908	-	449725	449873	149	4
303	<i>Rhizobium leguminosarum</i> bv. trifolii WSM1325	NC_012848	+	265906	266069	164	4
304	<i>Rhizobium leguminosarum</i> bv. trifolii WSM1325	NC_012852	+	119283	119433	151	4
305	<i>Rhizobium leguminosarum</i> bv. trifolii WSM1325	NC_012854	-	2286	2441	156	4
306	<i>Rhizobium leguminosarum</i> bv. trifolii WSM1325	NC_012858	+	28612	28768	157	4
307	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304	NC_011366	+	50780	50933	154	4
308	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304	NC_011368	+	607606	607759	154	4
309	<i>Rhizobium leguminosarum</i> bv. viciae 3841	NC_008384	-	574470	574626	157	4
310	<i>Rhizobium tropici</i> CIAT 899	NC_020062	+	1038279	1038431	153	4

# Cuckoo RNA	Species	Replicon	Strand	Position	Length	# Cuckoo Modules	
311	<i>Sinorhizobium medicae</i> WSM419	NC_009621	+	316270	316428	159	4
312	<i>Sinorhizobium medicae</i> WSM419	NC_009621	+	338831	338988	158	4
313	<i>Sinorhizobium meliloti</i> 1021	NC_003037	-	1328176	1328333	158	4
314	<i>Sinorhizobium meliloti</i> 2011	NC_020527	-	1326513	1326670	158	4
315	<i>Sinorhizobium meliloti</i> AK83	NC_015591	+	252033	252190	158	4
316	<i>Sinorhizobium meliloti</i> BL225C	NC_017324	-	293093	293250	158	4
317	<i>Sinorhizobium meliloti</i> GR4	NC_019848	+	24154	24311	158	4
318	<i>Sinorhizobium meliloti</i> Rm41	NC_018683	+	26268	26425	158	4
319	<i>Sinorhizobium meliloti</i> SM11	NC_017327	+	29162	29319	158	4
320	<i>Sulfitobacter</i> sp. EE-36	AALV01000002	+	574555	574727	173	4
321	<i>Sulfitobacter</i> sp. NAS-14.1	AALZ01000003	+	477955	478127	173	4

Table S2. Synteny and genomic context of cuckoo RNAs.

# Cuckoo RNA	LEFT FLANKING FEATURE								OVERLAPPING FEATURE							RIGHT FLANKING FEATURE						
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product		
1	CIN1	Brucellaceae	OG1	653418	653564	-	CDS	BAA13334_I101032	hypothetical protein						OG15	652016	653245	+	CDS	BAA13334_I101030	flavorubredoxin reductase	
2	CIN1	Brucellaceae	OG1	502376	502534	-	CDS	BAb519_I104820	hypothetical protein						OG15	500974	502203	+	CDS	BAb519_I104810	pyridine nucleotide-disulfide oxidoreductase family protein	
3	CIN1	Brucellaceae	OG1	503172	503330	-	CDS	BruAb2_0503	hypothetical protein						OG15	501770	502999	+	CDS	BruAb2_0502	pyridine nucleotide-disulfide oxidoreductase	
4	CIN6	Brucellaceae	OG14	448555	449274	+	CDS	BCAN_B0464	TetR family transcriptional regulator	448064	448252	+	CDS	BCAN_B0463	hypothetical protein	OG13	446920	447978	+	CDS	BCAN_B0462	hypothetical protein
5	CIN6	Brucellaceae	OG14	346454	347173	-	CDS	BCA52141_I10534	regulatory protein LysR						OG13	347750	348814	-	CDS	BCA52141_I10535	hypothetical protein	
6	CIN1	Brucellaceae	OG1	692918	693076	+	CDS	BMEA_B0706	hypothetical protein							694594	695436	-	CDS	BMEA_B0708	RpiR family transcriptional regulator	
7	CIN1	Brucellaceae	OG1	693002	693157	+	CDS	BM28_B0696	hypothetical protein	OG15	693277	694563	-	CDS	BM28_B0697	pyridine nucleotide-disulfide oxidoreductase	694675	695517	-	CDS	BM28_B0698	transcriptional regulator
8	CIN1	Brucellaceae	OG1	693194	693340	+	CDS	BM590_B0694	hypothetical protein		693374	694747	-	CDS	BM590_B0695	rhodocoxin reductase	694859	695701	-	CDS	BM590_B0696	transcriptional regulator
9	CIN1	Brucellaceae	OG1	684687	684833	+	CDS	BMNI_I10677	hypothetical protein		684901	686238	-	CDS	BMNI_I10678	rhodocoxin reductase	686350	687192	-	CDS	BMNI_I10679	transcriptional regulator
10	CIN1	Brucellaceae	OG1	503160	503318	-	CDS	BAB2_0512	hypothetical protein						OG15	501758	502987	+	CDS	BAB2_0511	pyridine nucleotide-disulfide oxidoreductase class-II	
11	CIN6	Brucellaceae	OG14	765708	766427	-	CDS	BAB2_0774	transcriptional regulator TetR	766730	766918	-	CDS	BAB2_0775	hypothetical protein	OG13	767004	768062	-	CDS	BAB2_0776	hypothetical protein
12		Brucellaceae		584622	585725	+	CDS	BMEI10559	glycine cleavage system aminomethyltransferase T							583439	583645	+	CDS	BMEI10558	rhodocoxin reductase	
13	CIN6	Brucellaceae	OG14	839700	840419	-	CDS	BMEI10804	TETR family transcriptional regulator	840722	841036	-	CDS	BMEI10805	hypothetical protein	OG13	840996	842054	-	CDS	BMEI10806	transmembrane protein
14	CIN6	Brucellaceae	OG14	449948	450667	+	CDS	BMI_I1459	Tetr family transcriptional regulator	449457	449645	+	CDS	BMI_I1458	hypothetical protein	OG13	448313	449371	+	CDS	BMI_I1457	hypothetical protein
15	CIN1	Brucellaceae	OG1	714754	714912	+	CDS	BMI_I1721	hypothetical protein						OG15	715085	716314	-	CDS	BMI_I1722	pyridine nucleotide-disulfide oxidoreductase family protein	
16	CIN1	Brucellaceae	OG1	715043	715201	+	CDS	BOV_A0682	hypothetical protein						OG15	715378	716607	-	CDS	BOV_A0683	pyridine nucleotide-disulfide oxidoreductase family protein	
17	CIN1	Brucellaceae	OG1	769534	769692	+	CDS	BPI_I1781	hypothetical protein						OG15	769871	771100	-	CDS	BPI_I1782	pyridine nucleotide-disulfide oxidoreductase family protein	
18	CIN1	Brucellaceae	OG1	713813	713971	+	CDS	BS1330_I10721	hypothetical protein						OG15	714153	715382	-	CDS	BS1330_I10722	pyridine nucleotide-disulfide oxidoreductase family protein	
19	CIN1	Brucellaceae	OG1	701709	701867	+	CDS	BSUIS_B0720	hypothetical protein						OG15	702039	703268	-	CDS	BSUIS_B0721	hypothetical protein	
20	CIN1	Brucellaceae	OG1	713863	714021	+	CDS	BSVBI22_B0720	hypothetical protein						OG15	714203	715432	-	CDS	BSVBI22_B0721	pyridine nucleotide-disulfide oxidoreductase family protein	
21		Phyllobacteriaceae		214571	215014	+	CDS	Meso_0172	phasin							215234	215310	+	tRNA	Meso_R0004	tRNA-His	
22		Phyllobacteriaceae		247150	247416	+	CDS	Meso_0212	hypothetical protein							247697	247972	+	CDS	Meso_0213	hypothetical protein	
23	CIN1	Rhodobacteraceae		2628776	2629864	-	CDS	Dshi_2476	hypothetical protein						OG2	2630248	2630712	-	CDS	Dshi_2477	putative leucine-responsive regulatory protein	
24	CIN1	Rhodobacteraceae	OG1	2789478	2789852	+	CDS	Jann_2773	hypothetical protein						OG2	2790224	2790676	-	CDS	Jann_2774	AsnC family transcriptional regulator	
25	CIN1	Rhodobacteraceae	OG1	2789478	2789852	+	CDS	Jann_2773	hypothetical protein						OG2	2790224	2790676	-	CDS	Jann_2774	AsnC family transcriptional regulator	
26	CIN1	Rhodobacteraceae	OG1	2789478	2789852	+	CDS	Jann_2773	hypothetical protein						OG2	2790224	2790676	-	CDS	Jann_2774	AsnC family transcriptional regulator	
27		Rhodobacteraceae																				
28		Rhodobacteraceae																				
29	CIN1	Rhodobacteraceae	OG1	20582	20797	+	CDS	SKA53_07326	hypothetical protein						OG2	21202	21663	-	CDS	SKA53_07331	transcriptional regulator, AsnC family	
30	CIN1	Rhodobacteraceae	OG1	20582	20797	+	CDS	SKA53_07326	hypothetical protein						OG2	21202	21663	-	CDS	SKA53_07331	transcriptional regulator, AsnC family	

# Cuckoo RNA	LEFT FLANKING FEATURE									OVERLAPPING FEATURE						RIGHT FLANKING FEATURE					
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	
31	CIN1	Rhodobacteraceae	OG1	253412	253627	-	CDS	OB2597_16115	hypothetical protein	OG17	250382	252970	+	CDS	OB2597_16110	Putative uvrD/DNA Helicase II					
32		Rhodobacteraceae		74835	75470	+	CDS	OB2597_18721	hypothetical protein		76073	80383	+	CDS	OB2597_18726	putative methylase/helicase					
33	CIN1	Rhodobacteraceae	OG1	158763	158990	+	CDS	OG2516_05838	hypothetical protein		159616	160842	-	CDS	OG2516_05843	heat shock protein, Hsp70 family protein					
34	CIN1	Rhodobacteraceae	OG1	158763	158990	+	CDS	OG2516_05838	hypothetical protein		159616	160842	-	CDS	OG2516_05843	heat shock protein, Hsp70 family protein					
35	CIN1	Rhodobacteraceae	OG1	158763	158990	+	CDS	OG2516_05838	hypothetical protein		159616	160842	-	CDS	OG2516_05843	heat shock protein, Hsp70 family protein					
36	CIN1	Rhodobacteraceae	OG1	158763	158990	+	CDS	OG2516_05838	hypothetical protein		159616	160842	-	CDS	OG2516_05843	heat shock protein, Hsp70 family protein					
37	CIN1	Rhodobacteraceae		1186838	1187056	-	CDS	OAN307_c11810	hypothetical protein	OG2	1186093	1186545	+	CDS	OAN307_c11800	putative AsnC family transcriptional regulator					
38		Rhodobacteraceae		1586475	1586957	+	CDS	OAN307_c15980	hypothetical protein		1587107	1587649	+	CDS	OAN307_c15990	putative PHB synthesis repressor protein					
39		Rhodobacteraceae		725064	725513	+	CDS	OA238_c06950	hypothetical protein		725663	726205	+	CDS	OA238_c06960	putative PHB synthesis repressor protein					
40	CIN1	Rhodobacteraceae		805909	806127	-	CDS	OA238_c07730	hypothetical protein	OG2	805130	805633	+	CDS	OA238_c07720	putative AsnC family transcriptional regulator					
41		Rhodobacteraceae		2228456	2229466	-	CDS	OA238_c21140	putative IS481 family integrase		2230121	2230318	-	CDS	OA238_c21150	hypothetical protein					
42	CIN1	Rhodobacteraceae	OG1	551716	552015	-	CDS	Pden_0580	hypothetical protein		550394	551167	-	CDS	Pden_0579	hypothetical protein					
43	CIN1	Rhodobacteraceae	OG1	551716	552015	-	CDS	Pden_0580	hypothetical protein		550394	551167	-	CDS	Pden_0579	hypothetical protein					
44	CIN1	Rhodobacteraceae	OG1	551716	552015	-	CDS	Pden_0580	hypothetical protein		550394	551167	-	CDS	Pden_0579	hypothetical protein					
45	CIN1	Rhodobacteraceae	OG1	551716	552015	-	CDS	Pden_0580	hypothetical protein		550394	551167	-	CDS	Pden_0579	hypothetical protein					
46		Rhodobiaceae		2346100	2346174	+	tRNA	Plav_R0027	tRNA-Glu		2343868	2345316	-	CDS	Plav_2164	RluA family pseudouridine synthase					
47	CIN1	Rhodobacteraceae	OG1	1028770	1028988	-	CDS	PGA2_c09350	hypothetical protein	OG17	1026054	1028414	+	CDS	PGA2_c09340	DNA helicase II UvrD					
48	CIN1	Rhodobacteraceae	OG1	1028770	1028988	-	CDS	PGA2_c09350	hypothetical protein	OG17	1026054	1028414	+	CDS	PGA2_c09340	DNA helicase II UvrD					
49	CIN1	Rhodobacteraceae	OG1	969561	969779	-	CDS	PGA1_c09460	hypothetical protein	OG17	966842	969205	+	CDS	PGA1_c09450	DNA helicase II UvrD					
50	CIN1	Rhodobacteraceae	OG1	969561	969779	-	CDS	PGA1_c09460	hypothetical protein	OG17	966842	969205	+	CDS	PGA1_c09450	DNA helicase II UvrD					
51		Rhizobiaceae		27340	27705	-	CDS	RHECIAT_PC0000026	hypothetical protein		28423	28803	+	CDS	RHECIAT_PC0000027	dependent formaldehyde-activating protein					
52		Rhizobiaceae		2609131	2610966	-	CDS	Rleg2_2571	peptidase M24		2611835	2612713	-	CDS	Rleg2_2573	50S ribosomal protein L11 methyltransferase					
53	CIN1	Rhodobacteraceae	OG1	2557251	2557454	+	CDS	RCAP_rcc02385	hypothetical protein		2557937	2558734	+	CDS	RCAP_rcc02386	hypothetical protein					
54	CIN1	Rhodobacteraceae	OG1	2557251	2557454	+	CDS	RCAP_rcc02385	hypothetical protein		2557937	2558734	+	CDS	RCAP_rcc02386	hypothetical protein					
55	CIN1	Rhodobacteraceae	OG1	2557251	2557454	+	CDS	RCAP_rcc02385	hypothetical protein		2557937	2558734	+	CDS	RCAP_rcc02386	hypothetical protein					
56	CIN1	Rhodobacteraceae	OG1	2557251	2557454	+	CDS	RCAP_rcc02385	hypothetical protein		2557937	2558734	+	CDS	RCAP_rcc02386	hypothetical protein					
57	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
58	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
59	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
60	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
61	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
62	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
63	CIN1	Rhodobacteraceae	OG1	692464	692679	-	CDS	RSP_6037	hypothetical protein	OG18	690398	691543	-	CDS	RSP_2091	benzoate transporter, BenE					
64	CIN1	Rhodobacteraceae	OG1	687212	687427	-	CDS	Rsph17025_0680	hypothetical protein	OG18	685502	686647	-	CDS	Rsph17025_0679	benzoate transporter					
65	CIN1	Rhodobacteraceae	OG1	687212	687427	-	CDS	Rsph17025_0680	hypothetical protein	OG18	685502	686647	-	CDS	Rsph17025_0679	benzoate transporter					
66	CIN1	Rhodobacteraceae	OG1	687212	687427	-	CDS	Rsph17025_0680	hypothetical protein	OG18	685502	686647	-	CDS	Rsph17025_0679	benzoate transporter					
67	CIN1	Rhodobacteraceae	OG1	687212	687427	-	CDS	Rsph17025_0680	hypothetical protein	OG18	685502	686647	-	CDS	Rsph17025_0679	benzoate transporter					
68	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter					
69	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter					
70	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter					
71	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter					

# Cuckoo RNA	LEFT FLANKING FEATURE								OVERLAPPING FEATURE						RIGHT FLANKING FEATURE					
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product
72	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter				
73	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter				
74	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter				
75	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter				
76	CIN1	Rhodobacteraceae	OG1	776187	776402	-	CDS	Rsph17029_0768	hypothetical protein	OG18	773895	775040	-	CDS	Rsph17029_0767	benzoate transporter				
77	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
78	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
79	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
80	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
81	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
82	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
83	CIN1	Rhodobacteraceae	OG1	389295	389447	-	CDS	RSKD131_0402	hypothetical protein	OG18	387228	388373	-	CDS	RSKD131_0401	Benzoate transporter				
84	CIN1	Rhodobacteraceae	OG1	3236591	3236827	+	CDS	RD1_3372	hypothetical protein	OG18	3237115	3237792	-	CDS	RD1_3373	hypothetical protein				
85	CIN1	Rhodobacteraceae	OG1	3236591	3236827	+	CDS	RD1_3372	hypothetical protein	OG18	3237115	3237792	-	CDS	RD1_3373	hypothetical protein				
86	CIN1	Rhodobacteraceae	OG1	2650174	2651247	-	CDS	RLO149_c025820	hypothetical protein	OG1	2651466	2651705	+	CDS	RLO149_c025830	hypothetical protein				
87	CIN1	Rhodobacteraceae	OG1	2651466	2651705	+	CDS	RLO149_c025830	hypothetical protein	OG1	2651466	2651705	+	CDS	RLO149_c025830	hypothetical protein				
88	CIN1	Rhodobacteraceae	OG1	1448664	1448888	-	CDS	ISM_07085	hypothetical protein	OG18	1447445	1448407	+	CDS	ISM_07080	Sugar phosphate Isomerase				
89	CIN1	Rhodobacteraceae	OG1	1795806	1796783	-	CDS	ISM_08740	hypothetical protein	OG18	1794506	1795438	-	CDS	ISM_08735	Putative transporter, AEC family protein				
90	CIN1	Rhodobacteraceae	OG1	61009	61233	-	CDS	ROS217_16875	hypothetical protein	OG18	60216	60506	+	CDS	ROS217_16870	hypothetical protein				
91	CIN1	Rhodobacteraceae	OG1	61009	61233	-	CDS	ROS217_16875	hypothetical protein	OG18	60216	60506	+	CDS	ROS217_16870	hypothetical protein				
92	CIN1	Rhodobacteraceae	OG1	1229631	1229855	-	CDS	SPO1177	hypothetical protein	OG18	1228427	1229203	-	CDS	SPO1176	Ser/Thr protein phosphatase				
93	CIN1	Rhodobacteraceae	OG1	1229631	1229855	-	CDS	SPO1177	hypothetical protein	OG18	1228427	1229203	-	CDS	SPO1176	Ser/Thr protein phosphatase				
94	CIN1	Rhodobacteraceae	OG1	1229631	1229855	-	CDS	SPO1177	hypothetical protein	OG18	1228427	1229203	-	CDS	SPO1176	Ser/Thr protein phosphatase				
95	CIN1	Rhodobacteraceae	OG1	2128003	2128224	+	CDS	TM1040_2023	hypothetical protein	OG17	2128764	2131208	-	CDS	TM1040_2024	ATP-dependent DNA helicase Rep				
96	CIN1	Rhodobacteraceae	OG1	2128003	2128224	+	CDS	TM1040_2023	hypothetical protein	OG17	2128764	2131208	-	CDS	TM1040_2024	ATP-dependent DNA helicase Rep				
97	CIN1	Rhodobacteraceae	OG1	289036	289251	-	CDS	SSE37_24084	hypothetical protein	OG18	285278	288367	-	CDS	SSE37_24079	valyl-tRNA synthetase				
98	CIN1	Rhodobacteraceae	OG1	289036	289251	-	CDS	SSE37_24084	hypothetical protein	OG18	285278	288367	-	CDS	SSE37_24079	valyl-tRNA synthetase				
99	CIN1	Rhodobacteraceae	OG1	289036	289251	-	CDS	SSE37_24084	hypothetical protein	OG18	285278	288367	-	CDS	SSE37_24079	valyl-tRNA synthetase				
100	CIN1	Rhodobacteraceae	OG1	1975071	1975880	-	CDS	Smed_1916	hypothetical protein	OG18	1974057	1974461	-	CDS	Smed_1915	hypothetical protein				
101	CIN1	Rhodobacteraceae	OG1	572745	573815	-	CDS	EE36_17022	Putative Mrp (Multidrug resistance-associated proteins) family protein	OG1	574053	574133	-	CDS	EE36_17027	hypothetical protein				
102	CIN1	Rhodobacteraceae	OG1	476145	477215	-	CDS	NAS141_07243	Putative Mrp (Multidrug resistance-associated proteins) family protein	OG1	477730	477942	+	CDS	NAS141_07248	hypothetical protein				
103	CIN1	Rhodobacteraceae	OG1	13199	14455	+	CDS	NAS141_04568	putative sigma-54-dependent transcriptional regulator	OG18	10870	12810	+	CDS	NAS141_04563	type IV secretion system coupling protein				
104	CIN1	Rhodobacteraceae	OG1	2565184	2565402	+	CDS	Gal_02545	putative small protein	OG17	2565748	2568159	-	CDS	Gal_02546	Superfamily I DNA and RNA helicase				
105	CIN1	Rhodobacteraceae	OG1	2565184	2565402	+	CDS	Gal_02545	putative small protein	OG17	2565748	2568159	-	CDS	Gal_02546	Superfamily I DNA and RNA helicase				
106	CIN1	Rhodobacteraceae	OG1	1229247	1230176	+	CDS	Atu4110	serine dehydrogenase	OG18	1230719	1231906	+	CDS	Atu4112	proline dipeptidase				
107	CIN5	Rhizobiaceae	OG3	596785	597666	+	CDS	Arad_0725	oxidoreductase	OG4	598187	599503	+	CDS	Arad_0727	hypothetical protein				
108	CIN1	Rhizobiaceae	OG1	1693731	1694870	+	CDS	Arad_2145	hypothetical protein	OG1	1692677	1692823	-	CDS	Arad_2144	hypothetical protein				
109	CIN2	Rhizobiaceae	OG6	3946044	3946844	+	CDS	Arad_4883	molybdate ABC transporter substrate-binding protein	OG5	3944888	3945469	+	CDS	Arad_4880	nicotinic acid mononucleotide adenyltransferase				
110	CIN1	Rhizobiaceae	OG1	108794	109252	-	CDS	AGROH133_02958	hypothetical protein	OG18	109733	109942	+	CDS	AGROH133_02961	cold shock protein				
111	CIN1	Rhizobiaceae	OG1	1614286	1615035	+	CDS	AGROH133_12938	serine dehydrogenase	OG18	1615591	1616778	+	CDS	AGROH133_12940	proline dipeptidase				
112	CIN1	Rhizobiaceae	OG1	6113	7192	+	CDS	Avi_9007	two component sensor kinase	OG18	7500	8633	-	CDS	Avi_9008	phage integrase family protein				
113	CIN1	Rhizobiaceae	OG1	113190	114716	-	CDS	Avi_0122	sulfatase	OG18	115395	116840	+	CDS	Avi_0126	phosphomannomutase				
114	CIN1	Rhizobiaceae	OG1	2042548	2043660	-	CDS	Avi_2480	membrane protein	OG18	2044292	2044441	+	CDS	Avi_2481	hypothetical protein				
115	CIN6	Brucellaceae	OG14	915965	916684	-	CDS	BAA13334_0101436	regulatory protein LysR	OG13	917303	918367	-	CDS	BAA13334_0101437	permease				
116	CIN5	Brucellaceae	OG16	2058328	2059035	-	CDS	BAA13334_0103398	LrgB-like protein	OG4	2056541	2057788	-	CDS	BAA13334_0103396	hypothetical protein				

# Cuckoo RNA	LEFT FLANKING FEATURE								OVERLAPPING FEATURE							RIGHT FLANKING FEATURE							
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product			
117	CIN6	Brucellaceae	OG14	764923	765642	-	CDS	BAb519_I07190	regulatory protein TetR						OG13	766261	767346	-	CDS	BAb519_I07200	hypothetical protein		
118	CIN5	Brucellaceae	OG16	357382	358089	+	CDS	BAb519_I03260	LrgB-like protein						OG4	358635	359876	+	CDS	BAb519_I03270	esterase/lipase/thioesterase		
119	CIN5	Brucellaceae	OG16	358997	359704	+	CDS	BruAb1_0352	hypothetical protein						OG4	360250	361491	+	CDS	BruAb1_0354	lipoprotein		
120	CIN5	Brucellaceae	OG16	337093	337800	+	CDS	BCAN_A0335	LrgB family protein	337974	338309	+	CDS	BCAN_A0336	hypothetical protein	OG4	338347	339588	+	CDS	BCAN_A0337	hypothetical protein	
121	CIN5	Brucellaceae	OG16	716593	717300	-	CDS	BCA52141_I1159	LrgB family protein						OG4	714805	716052	-	CDS	BCA52141_I1158	hypothetical protein		
122	CIN5	Brucellaceae	OG16	358048	358755	+	CDS	BMEA_A0364	LrgB family protein	358929	359264	+	CDS	BMEA_A0365	hypothetical protein	OG4	359302	360543	+	CDS	BMEA_A0366	hypothetical protein	
123	CIN5	Brucellaceae	OG16	358043	358750	+	CDS	BM28_A0358	LrgB family protein						OG4	359291	360538	+	CDS	BM28_A0359	esterase/lipase/thioesterase		
124	CIN5	Brucellaceae	OG16	358296	359003	+	CDS	BM590_A0355	LrgB family protein						OG4	359550	360791	+	CDS	BM590_A0356	hypothetical protein		
125	CIN5	Brucellaceae	OG16	358238	358945	+	CDS	BMNI_I0353	hypothetical protein						OG4	359486	360733	+	CDS	BMNI_I0354	lipoprotein		
126	CIN5	Brucellaceae	OG16	355365	356072	+	CDS	BAB1_0356	LrgB-like protein						OG4	356618	357859	+	CDS	BAB1_0358	esterase/lipase/thioesterase		
127	CIN5	Brucellaceae	OG16	1644494	1645201	-	CDS	BMEI1596	LrgB protein	1643985	1644371	-	CDS	BMEI1595	hypothetical protein	OG4	1642706	1643914	-	CDS	BMEI1594	hypothetical protein	
128	CIN5	Brucellaceae	OG16	338771	339478	+	CDS	BMI_I332	LrgB family protein	339601	339987	+	CDS	BMI_I333	hypothetical protein	OG4	340025	341266	+	CDS	BMI_I334	lipoprotein, putative	
129	CIN5	Brucellaceae	OG16	358754	359461	+	CDS	BOV_0342	hypothetical protein							361342	361653	+	CDS	BOV_0344	transposase OrfA		
130	CIN5	Brucellaceae	OG16	358865	359572	+	CDS	BPI_I361	LrgB family protein	359695	360081	+	CDS	BPI_I362	hypothetical protein	OG4	360119	361360	+	CDS	BPI_I363	lipoprotein	
131	CIN6	Brucellaceae	OG14	433486	434205	+	CDS	BPI_I144	TetR family transcriptional regulator	432995	433183	+	CDS	BPI_I1443	hypothetical protein	OG13	431809	432867	+	CDS	BPI_I1442	hypothetical protein	
132	CIN6	Brucellaceae	OG14	448672	449391	+	CDS	BS1330_I10459	TetR family transcriptional regulator	448181	448369	+	CDS	BS1330_I10458	hypothetical protein	OG13	446995	448053	+	CDS	BS1330_I10457	hypothetical protein	
133	CIN5	Brucellaceae	OG16	337090	337797	+	CDS	BS1330_I0327	hypothetical protein	337920	338306	+	CDS	BS1330_I0328	hypothetical protein	OG4	338344	339585	+	CDS	BS1330_I0329	putative lipoprotein	
134	CIN6	Brucellaceae	OG14	449774	450493	+	CDS	BSUIS_B0463	hypothetical protein	449283	449471	+	CDS	BSUIS_B0462	hypothetical protein		447158	447865	-	CDS	BSUIS_B0460	hypothetical protein	
135	CIN5	Brucellaceae	OG16	354629	355336	+	CDS	BSUIS_A0355	LrgB family protein	355510	355845	+	CDS	BSUIS_A0356	hypothetical protein		357194	357562	+	CDS	BSUIS_A0358	transposase for insertion sequence element IS6501	
136	CIN6	Brucellaceae	OG14	448644	449363	+	CDS	BSVBI22_B0458	TetR family transcriptional regulator	448153	448341	+	CDS	BSVBI22_B0457	hypothetical protein	OG13	446967	448025	+	CDS	BSVBI22_B0456	hypothetical protein	
137	CIN5	Brucellaceae	OG16	337051	337758	+	CDS	BSVBI22_A0327	hypothetical protein	337881	338267	+	CDS	BSVBI22_A0328	hypothetical protein	OG4	338305	339546	+	CDS	BSVBI22_A0329	putative lipoprotein	
138		Phyllobacteriaceae		33959	34477	+	CDS	Meso_4137	hypothetical protein	32011	32697	+	CDS	Meso_4135	hypothetical protein		31210	31944	+	CDS	Meso_4134	hypothetical protein	
139		Phyllobacteriaceae		135539	136099	-	CDS	Meso_4236	hypothetical protein							134555	135097	-	CDS	Meso_4235	hypothetical protein		
140	CIN1	Phyllobacteriaceae	OG1	1916546	1916686	+	CDS	Meso_1791	hypothetical protein						OG7	1916819	1918300	+	CDS	Meso_1792	tRNA (uracil-5)-methyltransferase Gid		
141		Phyllobacteriaceae		3977363	3978682	+	CDS	Meso_3688	NAD-binding homoserine dehydrogenase							3975340	3976962	-	CDS	Meso_3687	alpha amylase		
142	CIN1	Rhodobacteraceae		1584816	1584983	+	CDS	KVU_1472	hypothetical protein						OG18	1585271	1586425	+	CDS	KVU_1473	benzoate transporter		
143	CIN1	Rhodobacteraceae		363726	363893	-	CDS	EIO_0391	hypothetical protein						OG18	362284	363438	-	CDS	EIO_0390	benzoate transporter		
144		Rhodobacteraceae																					
145	CIN1	Rhodobacteraceae	OG1	20582	20797	+	CDS	SKA53_07326	hypothetical protein						OG2	21202	21663	-	CDS	SKA53_07331	transcriptional regulator, AsnC family		
146		Phyllobacteriaceae		2513677	2514135	+	CDS	Mesau_02453	phasin							2514487	2514563	+	tRNA	Mesau_02454	tRNA-His		
147	CIN1	Phyllobacteriaceae	OG1	3843005	3843145	-	CDS	Mesau_03779	uncharacterized conserved small protein	OG7	3841019	3842611	-	CDS	Mesau_03778	tRNA:m(5)U-54 methyltransferase		3840645	3840947	-	CDS	Mesau_03777	putative addition module antidote protein, CC2985 family
148	CIN1	Phyllobacteriaceae	OG1	3843005	3843145	-	CDS	Mesau_03779	uncharacterized conserved small protein						OG7	3841019	3842611	-	CDS	Mesau_03778	tRNA:m(5)U-54 methyltransferase		
149	CIN1	Phyllobacteriaceae	OG1	3843005	3843145	-	CDS	Mesau_03779	uncharacterized conserved small protein						OG7	3841019	3842611	-	CDS	Mesau_03778	tRNA:m(5)U-54 methyltransferase		
150		Phyllobacteriaceae		5249354	5250376	+	CDS	Mesau_05196	ABC-type sugar transport system, periplasmic component							5250687	5251277	-	CDS	Mesau_05197	transcriptional regulator		
151		Phyllobacteriaceae		241784	242047	-	CDS	Mesci_6303	hypothetical protein							241107	241262	-	CDS	Mesci_6302	hypothetical protein		
152		Phyllobacteriaceae		2545134	2545592	+	CDS	Mesci_2426	phasin							2545962	2546038	+	tRNA	Mesci_R0032	tRNA-His		
153	CIN1	Phyllobacteriaceae	OG1	3675321	3675461	-	CDS	Mesci_3514	hypothetical protein						OG7	3673344	3674753	-	CDS	Mesci_3513	hypothetical protein		
154	CIN1	Phyllobacteriaceae	OG1	3675321	3675461	-	CDS	Mesci_3514	hypothetical protein						OG7	3673344	3674753	-	CDS	Mesci_3513	hypothetical protein		
155	CIN1	Phyllobacteriaceae	OG1	3675321	3675461	-	CDS	Mesci_3514	hypothetical protein						OG7	3673344	3674753	-	CDS	Mesci_3513	hypothetical protein		
156		Phyllobacteriaceae		5264750	5265772	+	CDS	Mesci_5119	LacI family transcriptional regulator	5265709	5265903	-	CDS	Mesci_5120	hypothetical protein		5266103	5266693	-	CDS	Mesci_5121	TetR family transcriptional regulator	
157	CIN1	Phyllobacteriaceae		890180	890389	+	CDS	msr1062	hypothetical protein						OG7	891150	892568	+	CDS	mlr1064	tRNA (uracil-5)-methyltransferase Gid		
158	CIN1	Phyllobacteriaceae		890180	890389	+	CDS	msr1062	hypothetical protein						OG7	891150	892568	+	CDS	mlr1064	tRNA (uracil-5)-methyltransferase Gid		
159	CIN1	Phyllobacteriaceae		890180	890389	+	CDS	msr1062	hypothetical protein						OG7	891150	892568	+	CDS	mlr1064	tRNA (uracil-5)-methyltransferase Gid		

# Cuckoo RNA	LEFT FLANKING FEATURE								OVERLAPPING FEATURE								RIGHT FLANKING FEATURE							
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product				
160		Phyllobacteriaceae		4952439	4952903	-	CDS	mll6119	transcriptional regulatory protein						4951975	4952181	+	CDS	mll6118	cold-shock protein				
161		Phyllobacteriaceae		5350228	5350686	+	CDS	mlr6541	hypothetical protein						5351042	5351115	+	tRNA	MAFF741	tRNA-His				
162		Phyllobacteriaceae		6092659	6093681	-	CDS	mll7360	hypothetical protein						6091731	6092324	+	CDS	mir7359	transcriptional regulator				
163		Phyllobacteriaceae		2663198	2663656	+	CDS	Mesop_2561	phasin						2664008	2664084	+	tRNA	Mesop_R0033	tRNA-His				
164	CIN1	Phyllobacteriaceae	OG1	4112624	4112764	-	CDS	Mesop_4003	hypothetical protein						OG7_4110639	4112048	-	CDS	Mesop_4002	gid protein				
165	CIN1	Phyllobacteriaceae	OG1	4112624	4112764	-	CDS	Mesop_4003	hypothetical protein						OG7_4110639	4112048	-	CDS	Mesop_4002	gid protein				
166	CIN1	Phyllobacteriaceae	OG1	4112624	4112764	-	CDS	Mesop_4003	hypothetical protein						OG7_4110639	4112048	-	CDS	Mesop_4002	gid protein				
167		Phyllobacteriaceae		5829273	5830295	+	CDS	Mesop_5703	LacI family transcriptional regulator						5830639	5831229	-	CDS	Mesop_5704	TetR family transcriptional regulator				
168	CIN1	Rhodobacteraceae	OG1	158763	158990	+	CDS	OG2516_05838	hypothetical protein						159616	160842	-	CDS	OG2516_05843	heat shock protein, Hsp70 family protein				
169	CIN5	Brucellaceae	OG16	447656	448351	+	CDS	Oant_0422	LrgB family protein						448748	450301	+	CDS	Oant_0423	glyoxalase/bleomycin resistance protein/dioxygenase				
170		Brucellaceae		275652	276380	+	CDS	Oant_2970	septum formation inhibitor						272174	273850	-	CDS	Oant_2969	hypothetical protein				
171		Brucellaceae		272174	273850	-	CDS	Oant_2969	hypothetical protein						275652	276380	+	CDS	Oant_2970	septum formation inhibitor				
172	CIN1	Brucellaceae	OG1	1275426	1275572	+	CDS	Oant_3865	hypothetical protein						1275787	1277010	-	CDS	Oant_3866	major facilitator superfamily transporter				
173	CIN1	Rhodobacteraceae		805909	806127	-	CDS	OA238_c07730	hypothetical protein						OG2_805130	805633	+	CDS	OA238_c07720	putative AsnC family transcriptional regulator				
174		Hyphomicrobiaceae		2111274	2112173	+	CDS	KKY_2127	LysR family transcriptional regulator						2113135	2114337	-	CDS	KKY_2128	aspartate aminotransferase				
175		Hyphomicrobiaceae		2111274	2112173	+	CDS	KKY_2127	LysR family transcriptional regulator						2113135	2114337	-	CDS	KKY_2128	aspartate aminotransferase				
176				2331701	2331850	-	CDS	SL003B_2210	hypothetical protein						2330776	2331393	+	CDS	SL003B_2209	hypothetical protein				
177	CIN5	Rhizobiaceae	OG3	461301	462182	+	CDS	RHE_CH00449	oxidoreductase						OG4_462794	464071	+	CDS	RHE_CH00450	hypothetical protein				
178		Rhizobiaceae		1926684	192778	+	CDS	RHE_CH01839	hypothetical protein						1925699	1926187	+	CDS	RHE_CH01838	hypothetical protein				
179	CIN2	Rhizobiaceae	OG6	4314798	4315589	+	CDS	RHE_CH04071	transporter, substrate-binding protein						OG5_4313781	4314359	+	CDS	RHE_CH04070	nicotinic acid mononucleotide adenyltransferase				
180		Rhizobiaceae		22159	22494	-	CDS	RHE_Pf00022	hypothetical protein						23286	23726	+	CDS	RHE_Pf00023	hypothetical protein				
181	CIN5	Rhizobiaceae	OG3	512732	513613	+	CDS	RHECIAT_CH0000515	oxidoreductase	513699	514148	+	CDS	RHECIAT_CH0000516	hypothetical protein	OG4_514221	515498	+	CDS	RHECIAT_CH0000517	hypothetical protein			
182		Rhizobiaceae		1912923	1914026	+	CDS	RHECIAT_CH0001926	hypothetical protein						1911937	1912446	+	CDS	RHECIAT_CH0001925	hypothetical protein				
183	CIN2	Rhizobiaceae		4445118	4445327	-	CDS	RHECIAT_CH0004360	hypothetical protein						OG5_4444289	4444867	+	CDS	RHECIAT_CH0004359	nicotinic acid mononucleotide adenyltransferase				
184	CIN5	Rhizobiaceae	OG3	459092	459973	+	CDS	REMIM1_CH00460	aldo/keto reductase protein						OG4_460586	461863	+	CDS	REMIM1_CH00462	alpha/beta hydrolase family protein				
185		Rhizobiaceae		1884795	1885889	+	CDS	REMIM1_CH01890	hypothetical protein						1883810	1884298	+	CDS	REMIM1_CH01888	hypothetical protein				
186	CIN2	Rhizobiaceae	OG6	4217687	4218478	+	CDS	REMIM1_CH04188	transporter substrate-binding protein ModA						OG5_4216673	4217251	+	CDS	REMIM1_CH04187	nicotinate-nucleotide adenyltransferase				
187		Rhizobiaceae		19546	20625	-	CDS	REMIM1_Pf00021	virulence factor BrkB family protein	23158	23391	-	CDS	REMIM1_Pf00023	hypothetical protein	23630	24070	+	CDS	REMIM1_Pf00024	GFA family glutathione-dependent formaldehyde-activating protein			
188		Rhizobiaceae		111695	112336	+	CDS	Rleg_4742	hypothetical protein	112352	112612	+	CDS	Rleg_4743	hypothetical protein	113441	114331	-	CDS	Rleg_4745	protein-L-isoaspartate(D-aspartate) O-methyltransferase			
189	CIN5	Rhizobiaceae	OG3	105825	106706	+	CDS	Rleg_0114	aldo/keto reductase						OG4_107377	108654	+	CDS	Rleg_0115	hypothetical protein				
190	CIN1	Rhizobiaceae		1697482	1698585	+	CDS	Rleg_1701	hypothetical protein						OG1_1696657	1696803	-	CDS	Rleg_1700	hypothetical protein				
191	CIN2	Rhizobiaceae	OG6	4297098	4297889	+	CDS	Rleg_4202	transporter periplasmic molybdenum ABC						OG5_4295976	4296575	+	CDS	Rleg_4201	nicotinic acid mononucleotide adenyltransferase				
192		Rhizobiaceae		306976	307923	-	CDS	Rleg2_4670	transposase IS110 family protein	306298	306825	+	CDS	Rleg2_4669	hypothetical protein	305380	306273	+	CDS	Rleg2_4668	protein-L-isoaspartate(D-aspartate) O-methyltransferase			
193	CIN5	Rhizobiaceae	OG3	96796	97677	+	CDS	Rleg2_0104	aldo/keto reductase						OG4_98282	99559	+	CDS	Rleg2_0105	hypothetical protein				
194	CIN1	Rhizobiaceae		1534947	1536050	+	CDS	Rleg2_1503	hypothetical protein						OG1_1533929	1534075	-	CDS	Rleg2_1502	hypothetical protein				

# Cuckoo RNA	LEFT FLANKING FEATURE									OVERLAPPING FEATURE						RIGHT FLANKING FEATURE				
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product
195	CIN2	Rhizobiaceae	OG6	4019781	4020572	+	CDS	Rleg2_3878	molybdenum ABC transporter periplasmic molybdate-binding protein	OG5	4018721	4019299	+	CDS	Rleg2_3877	nicotinic acid mononucleotide adenyltransferase				
196		Rhizobiaceae		407072	407087	-	repeat_region			405332	407214	+	repeat_region	405592	-					protein-L-isoaspartate O-methyltransferase
197	CIN5	Rhizobiaceae	OG3	511376	512272	+	CDS	RL0474	aldo-keto reductase		512816	513202	-	CDS	RL0475	hypothetical protein				
198	CIN1	Rhizobiaceae	OG7	2175400	2176503	+	CDS	RL2060	transmembrane protein	OG7	2172416	2173849	-	CDS	RL2059	tRNA (uracil-5-)-methyltransferase				Gid
199	CIN2	Rhizobiaceae	OG6	4988507	4989298	+	CDS	RL4685	solute-binding component of ABC transporter	OG5	4987413	4988012	+	CDS	RL4684	nicotinic acid mononucleotide adenyltransferase				
200	CIN5	Rhizobiaceae	OG3	541169	542050	+	CDS	RTCIA899_CH02665	putative oxidoreductase	OG4	542600	543904	+	CDS	RTCIA899_CH02670	putative esterase/lipase/thioesterase				
201		Rhizobiaceae		1632031	1633170	+	CDS	RTCIA899_CH08010	hypothetical protein		1631634	1631747	+	CDS	RTCIA899_CH08005	hypothetical protein				
202	CIN2	Rhizobiaceae	OG6	3775772	3776569	+	CDS	RTCIA899_CH18465	molybdate ABC transporter, substrate-binding protein	OG5	3774593	3775210	+	CDS	RTCIA899_CH18455	nicotinate nucleotide adenyltransferase				
203	CIN1	Rhodobacteraceae	OG1	289036	289251	-	CDS	SSE37_24084	hypothetical protein		285278	288367	-	CDS	SSE37_24079	valyl-tRNA synthetase				
204	CIN1	Rhizobiaceae		1359706	1359849	+	CDS	SFHH103_01270	hypothetical protein	OG1	1358962	1359105	-	CDS	SFHH103_01269	hypothetical protein				
205	CIN1	Rhizobiaceae		1360111	1361322	-	CDS	SFHH103_01271	hypothetical protein	OG1	1358962	1359105	-	CDS	SFHH103_01269	hypothetical protein				
206	CIN3	Rhizobiaceae		4014002	4014457	+	CDS	SFHH103_03688	putative endonuclease V	OG12	4014756	4015643	+	CDS	SFHH103_03689	hypothetical protein				
207	CIN4	Rhizobiaceae	OG10	233767	234051	+	CDS	SFHH103_05074	acylphosphatase	OG11	232648	233319	-	CDS	SFHH103_05073	RNA polymerase sigma factor sigW				Sigma-W factor
208		Rhizobiaceae		157772	157978	+	CDS	SFHH103_04704	hypothetical protein		158617	158883	-	CDS	SFHH103_04705	hypothetical protein				
209		Rhizobiaceae		157772	157978	+	CDS	SFHH103_04704	hypothetical protein		158617	158883	-	CDS	SFHH103_04705	hypothetical protein				
210	CIN4	Rhizobiaceae	OG10	2204845	2205168	-	CDS	NGR_b21490	acylphosphatase	OG11	2205588	2206316	+	CDS	NGR_b21500	RNA polymerase sigma factor				
211	CIN1	Rhizobiaceae	OG8	1434843	1434925	-	tRNA	NGR_c13910	tRNA-Leu	OG1	1433785	1433985	-	CDS	NGR_c13890	hypothetical protein				
212	CIN1	Rhizobiaceae	OG8	1434843	1434925	-	tRNA	NGR_c13910	tRNA-Leu	OG1	1433785	1433985	-	CDS	NGR_c13890	hypothetical protein				
213	CIN3	Rhizobiaceae	OG9	3718015	3720336	-	CDS	NGR_c35080	penicillin-binding protein		3720525	3721688	+	CDS	NGR_c35090	transmembrane protein				
214	CIN4	Rhizobiaceae	OG10	1712776	1713234	-	CDS	USDA257_c16100	acylphosphatase AcyP	OG11	1713523	1714206	+	CDS	USDA257_c16110	polymerase sigma-24 subunit				
215	CIN1	Rhizobiaceae	OG8	3753302	3753384	-	tRNA	USDA257_c35860	tRNA-Leu	OG1	3752255	3752398	-	CDS	USDA257_c35850	hypothetical protein				
216	CIN1	Rhizobiaceae	OG8	3753302	3753384	-	tRNA	USDA257_c35860	tRNA-Leu	OG1	3752255	3752398	-	CDS	USDA257_c35850	hypothetical protein				
217		Rhizobiaceae		5733195	5733668	+	CDS	USDA257_c55250	3-demethylubiquinone-9 3-methyltransferase		5733999	5734190	+	CDS	USDA257_c55260	hypothetical protein				
218	CIN3	Rhizobiaceae	OG9	6264591	6266813	-	CDS	USDA257_c60090	penicillin-binding protein 2D		6267110	6268270	+	CDS	USDA257_c60100	S-adenosylmethionine uptake transporter Sam				
219		Rhizobiaceae		158177	159061	+	CDS	USDA257_p01790	hypothetical protein		159299	159709	-	CDS	USDA257_p01800	hypothetical protein				
220	CIN4	Rhizobiaceae	OG10	679315	679599	+	CDS	Smed_4198	acylphosphatase	OG11	678214	678885	-	CDS	Smed_4197	RNA polymerase sigma factor				
221	CIN1	Rhizobiaceae	OG8	1258759	1258843	+	tRNA	Smed_R0020	tRNA-Leu	OG1	1257614	1257814	-	CDS	Smed_1180	hypothetical protein				
222	CIN1	Rhizobiaceae	OG8	1258759	1258843	+	tRNA	Smed_R0020	tRNA-Leu	OG1	1257614	1257814	-	CDS	Smed_1180	hypothetical protein				
223	CIN3	Rhizobiaceae		3590494	3590925	-	CDS	Smed_3387	pyrimidine dimer DNA glycosylase	OG12	3589318	3590205	-	CDS	Smed_3386	hypothetical protein				
224		Rhizobiaceae		1219615	1220355	+	CDS	SMa2165	short chain		1221480	1221947	+	CDS	SMa2167	Hypothetical/Global homology				
225	CIN3	Rhizobiaceae		207244	209547	+	CDS	SMc02856	cell envelope	OG12	205860	206783	-	CDS	SMc02855	hypothetical/global homology				
226	CIN1	Rhizobiaceae	OG8	1668357	1668441	+	tRNA	SMc02125	tRNA-Leu		1667262	1667434	-	repeat_region	REPEAT SM-4	Sm-4 OR SMc04537				
227	CIN1	Rhizobiaceae	OG8	1668357	1668441	+	tRNA	SMc02125	tRNA-Leu		1667262	1667434	-	repeat_region	REPEAT SM-4	Sm-4 OR SMc04537				
228	CIN4	Rhizobiaceae	OG10	1605382	1605705	-	CDS	SM_b20590	Hypothetical/Partial homology		1605767	1606063	-	CDS	SM_b20591	Unknown				
229		Rhizobiaceae		1217953	1218693	+	CDS	SM2011_a2165	short chain alcohol dehydrogenase-related dehydrogenase		1219818	1220285	+	CDS	SM2011_a2167	hypothetical protein				
230	CIN3	Rhizobiaceae	OG9	207245	209548	+	CDS	SM2011_c02856	Putative penicillin-binding protein	OG12	205861	206784	-	CDS	SM2011_c02855	putative transmembrane protein				
231	CIN1	Rhizobiaceae	OG8	1668066	1668150	+	tRNA	SM2011_c02125	tRNA-Leu		1666971	1667143	-	repeat_region	corresponds to SMc04537	Sm-4				

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	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product			
232	CIN1	Rhizobiaceae	OG8	1668066	1668150	+	tRNA	SM2011_c02125	tRNA-Leu						1666971	1667143	-	repeat_region	corresponds to SMc04537	Sm-4			
233	CIN4	Rhizobiaceae	OG10	1605397	1605720	-	CDS	SM2011_b20590	Putative acylphosphatase	1605782	1606105	-	CDS	SM2011_b20591	Hypothetical protein	OG11	1606104	1606787	+	CDS	SM2011_b20592	RNA polymerase sigma factor, ECF subfamily protein	
234	CIN1	Rhizobiaceae	OG8	1370668	1370752	+	tRNA	Sinme_R0020	tRNA-Leu	1369434	1369994	-	CDS	Sinme_1348	hypothetical protein	OG1	1369047	1369190	-	CDS	Sinme_1347	hypothetical protein	
235	CIN1	Rhizobiaceae	OG8	1370668	1370752	+	tRNA	Sinme_R0020	tRNA-Leu											CDS	Sinme_1348	hypothetical protein	
236	CIN3	Rhizobiaceae	OG9	3627309	3629612	+	CDS	Sinme_3508	penicillin-binding protein 1A family						OG12	3625925	3626848	-	CDS	Sinme_3507	hypothetical protein		
237	CIN4	Rhizobiaceae	OG10	574319	574603	+	CDS	Sinme_4239	acylphosphatase						OG11	573216	573899	-	CDS	Sinme_4238	ECF subfamily RNA polymerase sigma-24 subunit		
238		Rhizobiaceae		171097	171837	+	CDS	Sinme_6793	3-oxoacyl-(acyl-carrier-protein) reductase							172524	172853	-	CDS	Sinme_6794	hypothetical protein		
239	CIN1	Rhizobiaceae	OG8	1232766	1232850	+	tRNA	SinmeB_R0020	tRNA-Leu	OG1	1231144	1231287	-	CDS	SinmeB_1177	hypothetical protein	OG1	1231144	1231287	-	CDS	SinmeB_1177	hypothetical protein
240	CIN1	Rhizobiaceae	OG8	1232766	1232850	+	tRNA	SinmeB_R0020	tRNA-Leu						OG12	3478596	3479519	-	CDS	SinmeB_3284	hypothetical protein		
241	CIN3	Rhizobiaceae	OG9	3479980	3482283	+	CDS	SinmeB_3285	penicillin-binding protein						OG11	1375593	1376276	-	CDS	SinmeB_4732	ECF subfamily RNA polymerase sigma-24 subunit		
242	CIN4	Rhizobiaceae	OG10	1376696	1376980	+	CDS	SinmeB_4733	acylphosphatase						OG12	200597	201520	-	CDS	C770_GR4Chr0183	Permeases of the drug/metabolite transporter (DMT) superfamily		
243	CIN3	Rhizobiaceae	OG9	201981	204284	+	CDS	C770_GR4Chr0184	penicillin-binding protein, 1A family						OG1	1636263	1636406	-	CDS	C770_GR4Chr1564	putative conserved small protein		
244	CIN1	Rhizobiaceae	OG8	1637885	1637969	+	tRNA	C770_GR4Chr1565	tRNA-Leu						OG1	1636263	1636406	-	CDS	C770_GR4Chr1564	putative conserved small protein		
245	CIN1	Rhizobiaceae	OG8	1637885	1637969	+	tRNA	C770_GR4Chr1565	tRNA-Leu						OG11	140510	141193	-	CDS	C770_GR4pD0121	RNA polymerase sigma factor, sigma-70 family		
246	CIN4	Rhizobiaceae	OG10	141613	141897	+	CDS	C770_GR4pD0122	Acylphosphatase							532183	532512	+	CDS	BN406_04042	hypothetical protein		
247		Rhizobiaceae		533163	533903	-	CDS	BN406_04043	3-oxoacyl-(acyl-carrier-protein) reductase						OG1	1307688	1307831	-	CDS	BN406_01276	hypothetical protein		
248	CIN1	Rhizobiaceae	OG8	1309308	1309392	+	tRNA	BN406_RNA00021	tRNA-Leu	1308074	1308634	-	CDS	BN406_01277	hypothetical protein	OG1	1307688	1307831	-	CDS	BN406_01276	hypothetical protein	
249	CIN1	Rhizobiaceae	OG8	1309308	1309392	+	tRNA	BN406_RNA00021	tRNA-Leu						OG12	1308074	1308634	-	CDS	BN406_01277	hypothetical protein		
250	CIN3	Rhizobiaceae		3485983	3488286	+	CDS	BN406_03311	cell envelope						OG12	3484599	3485486	-	CDS	BN406_03310	hypothetical/global homology		
251	CIN4	Rhizobiaceae	OG10	135464	135748	+	CDS	BN406_05204	Hypothetical/Partial homology						OG11	134361	135044	-	CDS	BN406_05203	ECF subfamily RNA polymerase sigma-24 subunit		
252	CIN1	Rhizobiaceae	OG8	2000507	2000591	-	tRNA	SM11_chr2021	tRNA-Leu						OG1	2002070	2002213	+	CDS	SM11_chr2022	hypothetical protein		
253	CIN3	Rhizobiaceae	OG8	2000507	2000591	-	tRNA	SM11_chr2021	tRNA-Leu						OG1	2002070	2002213	+	CDS	SM11_chr2022	hypothetical protein		
254	CIN3	Rhizobiaceae	OG9	3713807	3716119	+	CDS	SM11_chr3653	penicillin-binding protein						OG12	3712432	3713355	-	CDS	SM11_chr3652	transmembrane protein		
255	CIN4	Rhizobiaceae	OG10	141417	141701	+	CDS	SM11_pD0122	putative acylphosphatase	141167	141319	+	CDS	SM11_pD0121	hypothetical protein	OG11	140314	140997	-	CDS	SM11_pD0120	RNA polymerase sigma factor, ECF subfamily protein	
256		Rhizobiaceae		108895	109353	-	CDS	Atu0104	hypothetical protein	109363	109557	-	CDS	Atu0105	hypothetical protein		109823	110032	+	CDS	Atu0106	cold shock protein	
257		Rhizobiaceae		1831052	1831294	-	CDS	Atu4670	hypothetical protein							1831642	1832085	-	CDS	Atu4671	response regulator		
258		Rhizobiaceae		957315	957461	+	CDS	Arad_8084	hypothetical protein							957909	958754	-	CDS	Arad_8086	hypothetical protein		
259		Rhizobiaceae		1921485	1921631	-	CDS	Arad_9217	hypothetical protein							1920052	1920927	-	CDS	Arad_9216	glutathione S-transferase YghU		
260		Rhizobiaceae		139226	140683	-	CDS	Arad_12193	Cytochrome c, mono- and diHEME variant							137950	138255	+	CDS	Arad_12190	FAD dependent oxidoreductase		
261	CIN1	Rhizobiaceae	OG1	164384	164530	-	CDS	AGROH133_09615	hypothetical protein							163498	163941	+	CDS	AGROH133_09614	response regulator		
262		Rhizobiaceae		244945	247116	-	CDS	AGROH133_09819	hydroxamate-type ferrisiderophore receptor							243567	244646	+	CDS	AGROH133_09818	DNA polymerase IV		
263	CIN1	Rhizobiaceae	OG1	598779	598925	-	CDS	Avi_5587	hypothetical protein							597555	598229	+	CDS	Avi_5586	hypothetical protein		
264		Rhizobiaceae		899428	900909	+	CDS	Avi_5890	sulfate permease							901178	902659	-	CDS	Avi_5891	siroheme synthase		
265		Rhizobiaceae		2794154	2794300	-	CDS	Avi_3375	hypothetical protein							2792636	2793793	+	CDS	Avi_3374	DNA polymerase IV		
266	CIN1	Bruceiaceae	OG1	1527241	1527387	+	CDS	BAA13334_I02542	hypothetical protein						OG7	1527593	1529029	+	CDS	BAA13334_I02543	tRNA:m(5)U-54 methyltransferase		
267	CIN1	Bruceiaceae	OG1	889041	889187	-	CDS	BAbS19_I08540	hypothetical protein						OG7	887399	888799	-	CDS	BAbS19_I08530	tRNA (uracil-5'-methyltransferase Gid		

#	LEFT FLANKING FEATURE								OVERLAPPING FEATURE								RIGHT FLANKING FEATURE						
	Cuckoo RNA	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product		
268	CIN1	Brucellaceae	OG1	890740	890886	-	CDS	BruAb1_0907	hypothetical protein	OG7	889098	890498	-	CDS	BruAb1_0906	OG7	889098	890498	-	CDS	BruAb1_0906	tRNA (uracil-5)-methyltransferase Gid	
269	CIN1	Brucellaceae	OG1	867399	867545	-	CDS	BCAN_A0909	hypothetical protein	OG7	865739	867139	-	CDS	BCAN_A0908	OG7	865739	867139	-	CDS	BCAN_A0908	tRNA (uracil-5)-methyltransferase Gid	
270	CIN1	Brucellaceae	OG1	185798	185944	+	CDS	BCA52141_I0298	hypothetical protein	OG7	186168	187604	+	CDS	BCA52141_I0299	OG7	186168	187604	+	CDS	BCA52141_I0299	tRNA (uracil-5)-methyltransferase Gid	
271	CIN1	Brucellaceae	OG1	890507	890653	-	CDS	BMEA_A0934	hypothetical protein	OG7	888865	890265	-	CDS	BMEA_A0933	OG7	888865	890265	-	CDS	BMEA_A0933	tRNA (uracil-5)-methyltransferase Gid	
272	CIN1	Brucellaceae	OG1	890452	890598	-	CDS	BM28_A0905	hypothetical protein	OG7	888810	890246	-	CDS	BM28_A0904	OG7	888810	890246	-	CDS	BM28_A0904	tRNA (uracil-5)-methyltransferase Gid	
273	CIN1	Brucellaceae	OG1	890766	890912	-	CDS	BM590_A0904	hypothetical protein	OG7	888971	890524	-	CDS	BM590_A0903	OG7	888971	890524	-	CDS	BM590_A0903	hypothetical protein	
274	CIN1	Brucellaceae	OG1	887035	887181	-	CDS	BMNI_I0882	hypothetical protein	OG7	885393	886829	-	CDS	BMNI_I0881	OG7	885393	886829	-	CDS	BMNI_I0881	hypothetical protein	
275	CIN1	Brucellaceae	OG1	887018	887164	-	CDS	BAB1_0914	hypothetical protein	OG7	885376	886776	-	CDS	BAB1_0913	OG7	885376	886776	-	CDS	BAB1_0913	tRNA (uracil-5)-methyltransferase Gid	
276	CIN1	Brucellaceae	OG1	1116469	1116615	+	CDS	BMEI1072	hypothetical protein	OG7	1116821	1118257	+	CDS	BMEI1073	OG7	1116821	1118257	+	CDS	BMEI1073	tRNA (uracil-5)-methyltransferase Gid	
277	CIN1	Brucellaceae	OG1	873231	873377	-	CDS	BMI_I893	hypothetical protein	OG7	871571	872971	-	CDS	BMI_I892	OG7	871571	872971	-	CDS	BMI_I892	tRNA (uracil-5)-methyltransferase Gid	
278	CIN1	Brucellaceae	OG1	895931	896077	-	CDS	BOV_0891	hypothetical protein	OG7	894271	895671	-	CDS	BOV_0890	OG7	894271	895671	-	CDS	BOV_0890	tRNA (uracil-5)-methyltransferase Gid	
279	CIN1	Brucellaceae	OG1	897467	897613	-	CDS	BPI_I934	hypothetical protein	OG7	895807	897207	-	CDS	BPI_I933	OG7	895807	897207	-	CDS	BPI_I933	tRNA (uracil-5)-methyltransferase Gid	
280	CIN1	Brucellaceae	OG1	869015	869161	-	CDS	BS1330_I0891	hypothetical protein	OG7	867355	868755	-	CDS	BS1330_I0890	OG7	867355	868755	-	CDS	BS1330_I0890	tRNA (uracil-5)-methyltransferase Gid	
281	CIN1	Brucellaceae	OG1	888895	889041	-	CDS	BSUIS_A0934	hypothetical protein	OG7	887235	888635	-	CDS	BSUIS_A0933	OG7	887235	888635	-	CDS	BSUIS_A0933	tRNA (uracil-5)-methyltransferase Gid	
282	CIN1	Brucellaceae	OG1	868982	869128	-	CDS	BSVB122_A0891	hypothetical protein	OG7	867322	868722	-	CDS	BSVB122_A0890	OG7	867322	868722	-	CDS	BSVB122_A0890	tRNA (uracil-5)-methyltransferase Gid	
283	CIN1	Rhodobacteraceae	OG1	253412	253627	-	CDS	OB2597_16115	hypothetical protein	OG17	250382	252970	+	CDS	OB2597_16110	OG17	250382	252970	+	CDS	OB2597_16110	Putative uvrD/DNA Helicase II	
284	CIN1	Brucellaceae	OG1	2453758	2453904	+	CDS	Oant_2332	hypothetical protein	OG7	2454171	2455601	+	CDS	Oant_2333	OG7	2454171	2455601	+	CDS	Oant_2333	tRNA (uracil-5)-methyltransferase Gid	
285		Rhodobacteraceae		1086993	1087208	-	CDS	OAN307_c10930	hypothetical protein		1085366	1086547	+	CDS	OAN307_c10920		1085366	1086547	+	CDS	OAN307_c10920	putative phytanoyl-CoA dioxygenase	
286		Rhodobacteraceae		1955857	1956072	-	CDS	OAN307_c19550	hypothetical protein		1953763	1955376	-	CDS	OAN307_c19540		1953763	1955376	-	CDS	OAN307_c19540	GMC oxidoreductase	
287		Rhodobacteraceae		1993118	1993552	+	CDS	OAN307_c19940	UV-repair and mutation protein Umud		1991682	1991852	+	CDS	OAN307_c19930		1991682	1991852	+	CDS	OAN307_c19930	hypothetical protein	
288		Rhodobacteraceae		3698516	3698731	+	CDS	OAN307_c37600	hypothetical protein		3700041	3700493	-	CDS	OAN307_c37610		3700041	3700493	-	CDS	OAN307_c37610	putative IS3-family mobile element-associated integrase	
289		Rhodobacteraceae		671570	672592	-	CDS	OA238_c06440	ketol-acid reductoisomerase IlvC		669138	670139	-	CDS	OA238_c06430		669138	670139	-	CDS	OA238_c06430	hypothetical protein	
290		Rhodobacteraceae		2783742	2784656	+	CDS	OA238_c26190	integrase/recombinase		2787435	2788697	+	CDS	OA238_c26210		2787435	2788697	+	CDS	OA238_c26210	MFS-type transporter protein	
291		Rhodobacteraceae		3178924	3179139	+	CDS	OA238_c29930	hypothetical protein		3179935	3180480	-	CDS	OA238_c29940		3179935	3180480	-	CDS	OA238_c29940	hypothetical protein	
292	CIN1	Rhodobacteraceae	OG1	2655172	2655465	+	CDS	JCM7686_2554	hypothetical protein		2655721	2656617	+	CDS	JCM7686_2555		2655721	2656617	+	CDS	JCM7686_2555	hypothetical protein	
293	CIN1	Rhodobacteraceae	OG1	2655172	2655465	+	CDS	JCM7686_2554	hypothetical protein	Cluster44	2655721	2656617	+	CDS	JCM7686_2555	hypothetical protein		2656642	2657070	-	CDS	JCM7686_2556	formaldehyde-activating GFA
294	CIN1	Rhodobacteraceae	OG1	551716	552015	-	CDS	Pden_0580	hypothetical protein		550394	551167	-	CDS	Pden_0579		550394	551167	-	CDS	Pden_0579	hypothetical protein	
295		Rhodobacteraceae		2332239	2332388	-	CDS	SLO038_2211	hypothetical protein		2331701	2331850	-	CDS	SLO038_2210		2331701	2331850	-	CDS	SLO038_2210	hypothetical protein	
296		Rhodobacteraceae		3461175	3461318	-	CDS	PSE_3225	hypothetical protein		3461660	3462184	-	CDS	PSE_3226		3461660	3462184	-	CDS	PSE_3226	hypothetical protein	
297		Rhizobiaceae		76971	77354	+	CDS	RHE_PD00068	hypothetical protein		77912	78484	+	CDS	RHE_PD00069		77912	78484	+	CDS	RHE_PD00069	hypothetical protein	
298	CIN1	Rhizobiaceae	OG1	443336	443482	-	CDS	RHE_PE00401	hypothetical protein	OG19	441962	442798	-	CDS	RHE_PE00400	OG19	441962	442798	-	CDS	RHE_PE00400	5-keto-4-deoxyuronate isomerase	
299		Rhizobiaceae		1172125	1173279	-	CDS	RHECIAT_CH0001166	polyhydroxybutyrate depolymerase		1173597	1173884	-	CDS	RHECIAT_CH0001167	hypothetical protein		1173948	1174214	+	CDS	RHECIAT_CH0001168	hypothetical protein
300		Rhizobiaceae		111975	112217	-	CDS	RHECIAT_PB0000101	hypothetical protein		112536	113108	+	CDS	RHECIAT_PB0000102		112536	113108	+	CDS	RHECIAT_PB0000102	hypothetical protein	
301	CIN1	Rhizobiaceae	OG1	346130	346366	-	CDS	RHECIAT_PA0000320	hypothetical protein	OG19	344808	345644	-	CDS	RHECIAT_PA0000319	OG19	344808	345644	-	CDS	RHECIAT_PA0000319	5-keto-4-deoxyuronate isomerase	

# Cuckoo RNA	LEFT FLANKING FEATURE								OVERLAPPING FEATURE							RIGHT FLANKING FEATURE						
	CIN	Family	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product	OG	Position	Strand	Region type	Locus tag	Product		
302	CIN1	Rhizobiaceae	OG1	450047	450193	-	CDS	REMIM1_PD00423	hypothetical protein						OG19	448675	449511	-	CDS	REMIM1_PD00421	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	
303		Rhizobiaceae		264545	265168	-	CDS	Rleg_4882	plasmid pRIA4b ORF-3 family protein							268316	268603	-	CDS	Rleg_4886	hypothetical protein	
304	CIN1	Rhizobiaceae	OG1	118943	119089	+	CDS	Rleg_6084	hypothetical protein							119664	120056	-	CDS	Rleg_6085	hypothetical protein	
305		Rhizobiaceae		2547	2873	-	CDS	Rleg_6289	hypothetical protein							122	1300	+	CDS	Rleg_6287	hypothetical protein	
306	CIN1	Rhizobiaceae	OG1	28280	28426	+	CDS	Rleg_6602	hypothetical protein						OG19	29055	29891	+	CDS	Rleg_6603	5-keto-4-deoxyuronate isomerase	
307	CIN1	Rhizobiaceae	OG1	50447	50593	+	CDS	Rleg2_5661	hypothetical protein						OG19	51199	52035	+	CDS	Rleg2_5662	5-keto-4-deoxyuronate isomerase	
308		Rhizobiaceae		607180	607512	+	CDS	Rleg2_4962	hypothetical protein							609168	609533	+	CDS	Rleg2_4966	hypothetical protein	
309	CIN1	Rhizobiaceae	OG1	574811	574957	-	CDS	pRL110532	hypothetical protein	574203	574637	-	CDS	pRL110531	hypothetical protein	OG19	573348	574184	-	CDS	pRL110530	5-keto-4-deoxyuronate isomerase
310	CIN1	Rhizobiaceae	OG1	1037924	1038070	+	CDS	RTC1AT899_PC04885	hypothetical protein							1038634	1039509	+	CDS	RTC1AT899_PC04890	glutathione S-transferase family protein	
311		Rhizobiaceae		313859	314596	-	CDS	Smed_5352	putative adenylate/guanylate cyclase							316485	317621	-	CDS	Smed_5353	DNA polymerase IV	
312	CIN1	Rhizobiaceae	OG1	338535	338681	+	CDS	Smed_5370	hypothetical protein							339017	339226	-	CDS	Smed_5371	hypothetical protein	
313		Rhizobiaceae		1329978	1330670	+	CDS	SMA2357	Global functions							1327042	1328151	+	CDS	SMA2355	Protection responses	
314		Rhizobiaceae		1328315	1329007	+	CDS	SM2011_a2357	adenylate/guanylate cyclase							1325379	1326488	+	CDS	SM2011_a2355	DNA polymerase IV	
315		Rhizobiaceae		251307	251429	-	CDS	Sinme_5530	hypothetical protein							252215	253351	-	CDS	Sinme_5531	DNA-directed DNA polymerase	
316		Rhizobiaceae		293847	293969	+	CDS	SinmeB_5363	hypothetical protein							291959	293068	+	CDS	SinmeB_5362	DNA-directed DNA polymerase	
317		Rhizobiaceae		23436	23558	-	CDS	C770_GR4pC0025	hypothetical protein							24336	25445	-	CDS	C770_GR4pC0026	Nucleotidyltransferase/DNA polymerase involved in DNA repair	
318		Rhizobiaceae		25550	25672	-	CDS	BN406_03525	hypothetical protein							26450	27586	-	CDS	BN406_03526	DNA polymerase IV 2	
319		Rhizobiaceae		27984	28274	-	CDS	SM11_pC0027	hypothetical protein							29344	30480	-	CDS	SM11_pC0028	Nucleotidyltransferase/DNA polymerase	
320	CIN1	Rhodobacteraceae	OG1	574330	574542	+	CDS	EE36_17032	hypothetical protein						OG17	574763	577183	-	CDS	EE36_17037	DNA helicase II, putative	
321	CIN1	Rhodobacteraceae	OG1	477730	477942	+	CDS	NAS141_07248	hypothetical protein						OG17	478163	480583	-	CDS	NAS141_07253	DNA helicase II, putative	

Table S3. Structure properties of cuckoo RNAs.

# Cuckoo RNA	Energy cuckoo TDM	MFE (RNAfold -d2)	Energy TDM / MFE	Abstract shape TDM structure	Abstract shape MFE structure	TDM hairpin centers	MFE hairpin centers	TDM structure and cuckoo motifs	MFE structure
1	-22.7	-21.7	1.05	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
2	-22.7	-21.7	1.05	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
3	-22.7	-21.7	1.05	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
4	-19.5	-17.9	1.09	□□	□□	19;54	19;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
5	-19.5	-17.9	1.09	□□	□□	19;54	19;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
6	-23.2	-22.2	1.05	□□	□□	19;60.5	19;60.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
7	-23.2	-22.2	1.05	□□	□□	19;60.5	19;60.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
8	-23.1	-22.1	1.05	□□	□□	19;61	19;61	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
9	-23.2	-22.2	1.05	□□	□□	19;60	19;60	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
10	-22.7	-21.7	1.05	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
11	-22.1	-20.5	1.08	□□	□□	19;54	19;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
12	-23.1	-22.1	1.05	□□	□□	19;61	19;61	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
13	-26.8	-25.2	1.06	□□	□□	19;54	19;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
14	-22.1	-20.5	1.08	□□	□□	19;54	19;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
15	-29.3	-28.4	1.03	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
16	-29.1	-28.2	1.03	□□	□□	19;61	19;61	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
17	-29.0	-28.1	1.03	□□	□□	19;62	19;62	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
18	-28.9	-28.0	1.03	□□	□□	19;63.5	19;63.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
19	-29.3	-28.4	1.03	□□	□□	19;59	19;59	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
20	-28.9	-28.0	1.03	□□	□□	19;63.5	19;63.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
21	-35.5	-38.0	0.93	□□	□□	15;51	15;51	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
22	-39.6	-40.2	0.99	□□	□□	14;52.5	14;52.5	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
23	-35.1	-34.5	1.02	□□	□□	15.5;54.5	15.5;54.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
24	-29.3	-28.2	1.04	□□	□□	15.5;54	15.5;54	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
25	-25.6	-25.1	1.02	□□	□□	16.5;58	16.5;58	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
26	-42.1	-43.2	0.97	□□	□□	15.5;57.5	15.5;57	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
27	-35.9	-35.2	1.02	□□	□□	18.5;57.5	18.5;57.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
28	-41.0	-41.3	0.99	□□	□□	20.5;69.5	20.5;69.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
29	-33.3	-33.3	1.00	□□	□□	18.5;58.5	18.5;58.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
30	-45.8	-47.1	0.97	□□	□□	20.5;69.5	20.5;69.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
31	-39.1	-38.0	1.03	□□	□□	17;57	17;57	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
32	-33.3	-32.7	1.02	□□	□□	18;58.5	18;58.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
33	-38.0	-36.7	1.04	□□	□□	17;54	17;54	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
34	-44.0	-42.2	1.04	□□	□□□	21;76	21;48;76	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
35	-36.7	-36.7	1.00	□□	□□	22;73.5	22;73.5	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
36	-38.2	-38.8	0.98	□□	□□	19;69	19;69	(((((.....cucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
37	-34.2	-38.9	0.88	□□	□□	14.5;58.5	16.5;58.5	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))
38	-34.1	-39.5	0.86	□□	□□	23.5;63.5	23.5;63.5	(((((.....ucucucc.....)))))).....(((.....ucucucc.....))))))	(((((.....)))))).....(((.....))))))

# Cuckoo RNA	Energy cuckoo TDM	MFE (RNAfold -d2)	Energy TDM / MFE	Abstract shape TDM structure	Abstract shape MFE structure	TDM hairpin centers	MFE hairpin centers	TDM structure and cuckoo motifs	MFE structure
39	-35.7	-40.9	0.87	□□	□□	22.5;62.5	22.5;62.5	(((((.....(((ucucucc))))))))).....(((.....(((ucucucc)))))).....	((.....(((.....)))).....(((.....)))).....
40	-23.1	-23.3	0.99	□□	□□	19;58.5	21.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
41	-32.3	-31.2	1.04	□□	□□	18.5;60.5	18.5;60.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
42	-45.5	-44.9	1.01	□□	□□	20.5;60	20.5;60	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
43	-41.9	-41.8	1.00	□□	□□	14.5;54	14.5;54	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
44	-37.7	-37.0	1.02	□□	□□	15.5;55	15.5;55	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
45	-40.2	-39.4	1.02	□□	□□	19.5;58	19.5;58	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
46	-40.9	-40.4	1.01	□□	□□	18;62	18;62	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
47	-40.6	-40.0	1.02	□□	□□	16;57.5	16;57.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
48	-35.6	-34.8	1.02	□□	□□	21;59.5	21;59.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
49	-42.2	-41.1	1.03	□□	□□	16.5;58.5	16.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
50	-35.6	-34.8	1.02	□□	□□	21;59.5	21;59.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
51	-39.2	-39.0	1.01	□□	□□	17;60	17;60	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
52	-31.1	-33.9	0.92	□□	□□□	21.5;74	21.5;45;74	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
53	-43.1	-42.5	1.01	□□	□□	21;60	21;60	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
54	-42.8	-42.0	1.02	□□	□□	16;55.5	16;55.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
55	-39.9	-39.9	1.00	□□	□□	15;48.5	15;48.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
56	-41.5	-41.3	1.00	□□	□□	18;57	18;57	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
57	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
58	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
59	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
60	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
61	-43.5	-42.5	1.02	□□	□□	20.5;59.5	20.5;59.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
62	-36.8	-36.0	1.02	□□	□□	17;54.5	17;54.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
63	-38.9	-37.9	1.03	□□	□□	16.5;55	16.5;55	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
64	-47.5	-46.1	1.03	□□	□□	19.5;59	19.5;59	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
65	-45.5	-44.9	1.01	□□	□□	19.5;59	19.5;59	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
66	-36.7	-35.6	1.03	□□	□□	18.5;56.5	18.5;56.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
67	-38.2	-37.9	1.01	□□	□□	16.5;55	16.5;55	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
68	-41.1	-40.1	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
69	-42.3	-41.3	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
70	-42.3	-41.3	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
71	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
72	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
73	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
74	-46.2	-45.2	1.02	□□	□□	20.5;59.5	20.5;59.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
75	-36.8	-36.0	1.02	□□	□□	17;54.5	17;54.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
76	-38.3	-37.3	1.03	□□	□□	16.5;55	16.5;55	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
77	-45.0	-44.0	1.02	□□	□□	19.5;58.5	19.5;58.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....
78	-43.0	-42.0	1.02	□□	□□	19.5;60.5	19.5;60.5	((.....(((ucucucc)))).....(((.....(((ucucucc)))).....	((.....(((.....)))).....(((.....)))).....

# Cuckoo RNA	Energy cuckoo TDM	MFE (RNAfold -d2)	Energy TDM / MFE	Abstract shape TDM structure	Abstract shape MFE structure	TDM hairpin centers	MFE hairpin centers	TDM structure and cuckoo motifs	MFE structure
79	-43.0	-42.0	1.02	00	00	19.5;58.5	19.5;58.5	((...(((((((.cucucucc)))))))))-.(((((((.cucucucc)))))))))	((-((((((.....)))))))))-.((((((.....)))))))))
80	-42.3	-41.3	1.02	00	00	19.5;58.5	19.5;58.5	((...(((((((.cucucucc)))))))))-.(((((((.cucucucc)))))))))	((-((((((.....)))))))))-.((((((.....)))))))))
81	-46.2	-45.2	1.02	00	00	20.5;59.5	20.5;59.5	((...(((((((.cucucucc)))))))))-.(((((((.cucucucc)))))))))	((-((((((.....)))))))))-.((((((.....)))))))))
82	-36.8	-36.0	1.02	00	00	17;54.5	17;54.5	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))
83	-38.9	-37.9	1.03	00	00	16.5;55	16.5;55	((((((.cucucucc))))))-.(((((((.cucucucc)))))))))	((((((.cucucucc))))))-.(((((((.cucucucc)))))))))
84	-37.3	-38.2	0.98	00	00	22;61	22.5;61	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))
85	-45.8	-44.8	1.02	00	00	20.5;62	20.5;62	((-(((((((.cucucucc)))))))))-.(((((((.cucucucc)))))))))	((-((((((.....)))))))))-.((((((.....)))))))))
86	-33.4	-34.8	0.96	00	00	22;61	23.5;61	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))	((((((.cucucucc...))))))-.(((((((.cucucucc...)))))))))
87	-42.5	-41.5	1.02	00	00	16.5;58	16.5;58	((((((.cucucucc))))))-.(((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
88	-37.1	-35.5	1.05	00	00	20.5;64.5	20.5;64.5	((-(((((((.cucucucc...)))))))))-.(((((((.cucucucc...)))))))))	((-(((.....))))-.((((((.....)))))))))
89	-38.6	-37.5	1.03	00	00	22.5;70.5	22.5;70.5	((((((((((((.cucucucc...)))))))))-.((((((((((.cucucucc...)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
90	-43.6	-43.2	1.01	00	00	17;59	17;59	((-(((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
91	-39.1	-38.5	1.02	00	00	16;56	16;56	(((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
92	-41.1	-40.5	1.01	00	00	15;57	15;57	(((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
93	-49.7	-47.6	1.04	00	00	22;63	22;63	((-(((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
94	-39.8	-39.2	1.02	00	00	19;57.5	19;57.5	((-(((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
95	-37.7	-36.0	1.05	00	00	18.5;57.5	18.5;57.5	((-(((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
96	-40.5	-40.0	1.01	00	00	16;59	16;59	(((((((((.cucucucc...)))))))))-.((((((((((.cucucucc...)))))))))	(((((.....))))-.((((((.....)))))))))
97	-37.2	-36.6	1.02	00	00	19;58	19;58	(((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
98	-43.4	-42.6	1.02	00	00	19;58	19;58	(((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
99	-42.2	-41.5	1.02	00	00	16.5;56	16.5;56	((-(((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
100	-39.3	-37.8	1.04	00	00	16;52	16;52	(((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
101	-32.5	-31.4	1.04	00	00	21;60.5	21;60.5	((((((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
102	-32.5	-31.4	1.04	00	00	21;60.5	21;60.5	((((((((((((.cucucucc)))))))))-.((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
103	-40.4	-40.3	1.00	00	00	14.5;54.5	14.5;54.5	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
104	-35.6	-34.8	1.02	00	00	21;59.5	21;59.5	((-(((((((.cucucucc...)))))))))-.((((((((((.cucucucc...)))))))))	((-(((.....))))-.((((((.....)))))))))
105	-46.6	-45.5	1.02	00	00	16.5;58.5	16.5;58.5	((((((((((((.cucucucc...)))))))))-.(((((((((((((.cucucucc...)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
106	-56.4	-55.8	1.01	000	000	20;58;97.5	20;58;97.5	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
107	-52.9	-52.3	1.01	000	000	17.5;54;95	17.5;54;95	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
108	-54.2	-53.2	1.02	000	000	18;54;97	18;54;97	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
109	-49.8	-49.5	1.01	000	000	19;57;97.5	19;57;97.5	((((((((((((.cucucucc...)))))))))-.(((((((((((((.cucucucc...)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
110	-53.4	-51.9	1.03	000	000	19;56;96.5	19;56;96.5	((-(((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
111	-57.0	-55.8	1.02	000	000	20;58;97.5	20;58;97.5	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
112	-51.3	-50.9	1.01	000	000	16.5;52.5;93.5	16.5;52.5;93.5	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
113	-58.3	-57.1	1.02	000	000	21;59;100	21;59;100	((-((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
114	-58.0	-57.0	1.02	000	000	19;56;98.5	19;56;98.5	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
115	-50.7	-50.1	1.01	000	000	19;53;95	19;53;95	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((((((((.....)))))))))-.(((((((((.....)))))))))
116	-43.5	-43.1	1.01	000	000	14;47.5;84	14;47.5;84	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))
117	-50.7	-50.1	1.01	000	000	19;53;95	19;53;95	((-((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	((-(((.....))))-.((((((.....)))))))))
118	-43.5	-43.1	1.01	000	000	14;47.5;84	14;47.5;84	((((((((((((.cucucucc)))))))))-.(((((((((((((.cucucucc)))))))))	(((((.....))))-.((((((.....)))))))))

# Cuckoo RNA	Energy cuckoo TDM	MFE (RNAfold -d2)	Energy TDM / MFE	Abstract shape TDM structure	Abstract shape MFE structure	TDM hairpin centers	MFE hairpin centers	TDM structure and cuckoo motifs	MFE structure
159	-61.5	-60.6	1.01	□□□	□□□	17.5;54.5;95.5	17.5;54.5;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
160	-56.7	-57.6	0.98	□□□	□□□	18;56.5;95.5	20.5;56.5;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
161	-57.6	-57.2	1.01	□□□	□□□	23.5;59.5;96.5	23.5;59.5;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
162	-54.1	-53.5	1.01	□□□	□□□	19;57.5;96.5	19;57.5;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
163	-54.4	-54.1	1.01	□□□	□□□	17.5;53.5;90.5	17.5;53.5;90.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
164	-57.8	-56.9	1.02	□□□	□□□	17.5;54.5;96.5	17.5;54.5;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
165	-61.0	-60.0	1.02	□□□	□□□	17.5;54.5;95.5	17.5;54.5;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
166	-70.6	-69.4	1.02	□□□	□□□	17.5;54;95.5	17.5;54;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
167	-54.4	-53.6	1.01	□□□	□□□	25;63.5;102.5	25;63.5;102.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
168	-64.5	-72.3	0.89	□□□	□□□	22;72.5;113	22;72.5;113	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
169	-45.8	-45.9	1.00	□□□	□□□	19;53.5;90	19;53.5;90	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
170	-49.8	-49.2	1.01	□□□	□□□	23;58;100	23;58;100	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
171	-53.4	-52.6	1.02	□□□	□□□	15.5;50;92.5	15.5;50;92.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
172	-49.8	-53.4	0.93	□□□	□□□	20;59;99.5	20;59;99.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
173	-55.4	-62.1	0.89	□□□	□□□	23;76.5;119.5	23;76.5;119.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
174	-43.4	-45.2	0.96	□□□	□□□	25;76;118	25;74;118	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
175	-47.0	-46.5	1.01	□□□	□□□	25;72;112	25;72;112	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
176	-63.7	-63.8	1.00	□□□	□□□	17.5;54.5;96.5	17.5;54.5;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
177	-53.0	-52.7	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
178	-58.3	-64.0	0.91	□□□	□□□	18.5;55;94.5	18.5;55;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
179	-46.0	-45.3	1.02	□□□	□□□	18;55;95.5	18;55;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
180	-48.1	-53.5	0.90	□□□	□□□	16;52.5;91.5	16;52.5;91.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
181	-55.3	-55.0	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
182	-56.0	-61.9	0.90	□□□	□□□	18.5;55;94.5	18.5;55;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
183	-48.2	-48.0	1.00	□□□	□□□	18.5;56;96.5	18.5;56;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
184	-53.0	-52.7	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
185	-56.5	-62.8	0.90	□□□	□□□	18.5;55;94.5	18.5;55;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
186	-46.0	-45.3	1.02	□□□	□□□	18;55;95.5	18;55;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
187	-48.9	-53.7	0.91	□□□	□□□	16;52.5;91.5	16;52.5;91.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
188	-58.6	-59.9	0.98	□□□	□□□	18;55;94	18;55;94	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
189	-49.6	-49.3	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
190	-51.4	-57.3	0.90	□□□	□□□	18;54;93.5	18;54;93.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
191	-46.3	-52.9	0.88	□□□	□□□	20.5;57;96.5	20.5;57;96.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
192	-49.2	-57.0	0.86	□□□	□□□	18;54.5;93.5	18;54.5;93.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
193	-55.3	-55.0	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
194	-55.4	-61.3	0.90	□□□	□□□	18.5;56;95.5	18.5;56;95.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
195	-43.8	-50.4	0.87	□□□	□□□	22.5;60;99.5	22.5;60;99.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
196	-60.5	-60.1	1.01	□□□	□□□	17.5;53;92	17.5;53;92	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
197	-51.5	-51.2	1.01	□□□	□□□	17;54;94.5	17;54;94.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))
198	-49.1	-55.0	0.89	□□□	□□□	18;54;93.5	18;54;93.5	(((((...(((...(((...)))...)))))))	(((((...(((...(((...)))...)))))))

# Cuckoo RNA	Energy cuckoo TDM	MFE (RNAfold -d2)	Energy TDM / MFE	Abstract shape TDM structure	Abstract shape MFE structure	TDM hairpin centers	MFE hairpin centers	TDM structure and cuckoo motifs	MFE structure
319	-64.4	-67.2	0.96	□□□□	□□□□	17.5;54.5;90.5;136.5	17.5;54.5;92;136.5	((((((((cuccuccc)))))...))))	((((((((cuccuccc)))))...))))
320	-74.8	-79.2	0.94	□□□□	□□□□	15;55.5;101.5;146.5	15;55.5;103;146.5	((((((((accucccu)))))...))))	((((((((accucccu)))))...))))
321	-74.3	-78.7	0.94	□□□□	□□□□	15;55.5;101.5;146.5	15;55.5;103;146.5	((((((((accucccu)))))...))))	((((((((accucccu)))))...))))

Table S4. Sequences of cuckoo RNAs.

# Cuckoo RNA	Cuckoo RNA sequence
1	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
2	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
3	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
4	GGUGUUCGGUUUACUCCUCCCAAAAAUCGAAACUGAGCGCGGCACUCCUCCCAAGUGCAGCG
5	GGUGUUCGGUUUACUCCUCCCAAAAAUCGAAACUGAGCGCGGCACUCCUCCCAAGUGCAGCG
6	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
7	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
8	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
9	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
10	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
11	GGUGUUCGGUUUACUCCUCCCAAAAAACCGAAACUGAGCGCGGCACUCCUCCCAAGUGCAGCG
12	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGU
13	GGUGUUCGGUUUACUCCUCCCAAAAAACCGAAACUGAGCGCGGCACUCCUCCCAAGUGCAGCG
14	GGUGUUCGGUUUACUCCUCCCAAAAAACCGAAACUGAGCGCGGCACUCCUCCCAAGUGCAGCG
15	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
16	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
17	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
18	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
19	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
20	AUCGCCGGUGUUUCUCCUCCCAUUCUCCGCGCAUAAAAACCGGGACUCUCCUCCCCCAAGUCCGGUCUUU
21	GGGUGCGGUAUCUCCUCCCGAUCUCCUAAGAAAAGACCGGGUUCUCCUCCGGUCUUUUUU
22	UCACCGUCCUUCUCCUCCGCGGUGACUCCAGCCAGCAGGGGUGUUUCUCCUCCGCCUUCGUCGGC
23	CAGAAAGCCUUCUCCUCCGUGUUUCUUGUAUAUAGCGGCGGCUUUCUCCUCCUAGCGUCGCGC
24	AUCGGGCCUUCUCCUCCAUUAGGCCGUGAUCAGCGAACCUCUCCUCCUUCGAGCGGUC
25	CAGACCGCCUUCUCCUCCAUUCGGAUCGGAUCAACGGCAAGCUUCUCCUCCUUGGACGUGCGCC
26	GGCCUUGCCUUCUCCUCCAUUGGGCGGGCAGAUUUCGGCGGUGAUGUUCUCCUCCAGAACUUGCACCGCC
27	UCGGAUCUCCGCGCUUCCUCCGAAAAGGACAGUUCGAGACCCACCGCUUACUCCUCCAGGGACGGGUCAU
28	UAAAGCGGCGCAUCACCUCCUCCGCGGUGCCCGCUUUAUGAAACAAGUUCGGAACCGCCACUCCUCCGCGGUGGAACCGAUGAU
29	UCGGAUCUCCGCGCUUCCUCCGAAAAGGACAGUUCGAGACCCCGCGCUUACUCCUCCGAGCCAGGGUCAUG
30	UAAGGCGGCGGCCACCUCCUCCGCGGUGCCCGCUUUAUGACACAGGUUUCGGAACCGCCACUCCUCCGCGGUGGACCGAUUUU
31	UCAGGCGGUCUCCUCCUCCUCCGAGCGAUAACUCCGCGGCGAUCUCCUCCUCCUUGAUGCCCGCC
32	UGUGAUCGGUUCUCCUCCUCCGAGCGGAUCCGGAUUAAGCGGCGAUCUCCUCCUCCUCCUUGGAGCGGUC
33	UCGGAGCCUUCUCCUCCUCCGAAAGGCUUGACCGCGGUCGCUUCUCCUCCUCCUAGCGGUGCG
34	AGAAGCGGCGGCUUCCUCCUCCGCGGUGGUCGCUUCCUCCGAAACAGAAUUCGAGGUGUUCUCCUCCUCCUUGAAGCGGCGAUGAGC
35	AAGACGCGGCGGCGCUUCCUCCUCCGCGGUGGCAUCGUCGCGGCUUCGACCAUCAUGCAGGCGGCGUCCUCCUCCUUGGACCGGCGA
36	AGACGCGCGGCGCUUCCUCCUCCUCCGCGGUGGCAUCAUGGAAAGUUCGCGGCGGUCUCCUCCUCCUUGAAGCGGUCUCCGAG
37	GGCCUUCUCCUCCUCCAGAGGUGGCGCACAUUAGAAAGUACGAGACCUUCCUCCGCGGUCGUCGCUUUU
38	AGAAAUAAGUAACGCGCUUUCUCCUCCGAAAGGCUUUCUUAAGGGGUGGUGUUCUCCGACAGCAGCCCUU
39	GAAAAUAGUAACGCGCUUUCUCCUCCGAAAGCGCGAGUCUUUCAAAGGGGUGGUGUUCUCCGACAGCAGCCCUU
40	GAAACGGGCUUUCUCCUCCGAAAGGUGUUCGGAUCGUGCCACCCUCCUCCUCCUUGGGUUCGAGCAC
41	UUUCGAAACCGCCACCUCUCCCGGUGGAAACGAAAUAACCGCUGACGGCGCUUCCUCCCGGACAAUGUUGGCG
42	GAUACGGUAGAGCCUCCUCCUCCGCGGUCUCCCGUUCAGCGCGCACCUCCUCCUCCUUGAGGGUGCGCC
43	GCGAGACCCUCCUCCUCCGUGGUCUGCGGUUCGCGGCGGCGGCUUCCUCCUCCUCCGAGGCGGCGCCAAACC
44	GCGAAGUCUGUUCUCCUCCUCCAGGCUUCGCGUUCGAGCGGCUUCCUCCUCCUCCUUGGGUGUUGCGCC
45	GAAACCCGACCCUCCUCCUCCUUGGUGCAGGGUGUUCAGCGGCAUCUCCUCCUCCUCCUUGAGGUGCGCC
46	GAAACGUCGUGCAUCCUCCCGACCUCAUUCAGAAUGCCGCGGUGCAUCCUCCUCCUCCCGGCGGCGGCA

Cuckoo
RNA

Cuckoo RNA sequence

47 ACACCCUGCCUUCUCCUCCUUCUGGCCGGUGUUGUACAGAACGGCGGUGCCUCCUCCUCCUGGCACCGCCGUUUUUUGUG
48 GAGUUCAGGCUCUCUUCUCCUCCUUCAGGGCCUGUAAUCGCGGUGACAUCCUCCUCCUCCUGAUGUACCCGC
49 ACACCUUGCCUUCUCCUCCUUCUGGCCGGUGUUGUACAGAACGGCGGUGCCUCCUCCUCCUGGCACCGCCGUUUUUUGUGC
50 GAGUUCAGGCUCUCUUCUCCUCCUUCAGGGCCUGUAAUCGCGGUGACAUCCUCCUCCUCCUGAUGUACCCGC
51 GACGGGCGACUCUCUCCUCCUAGGCUUCGUGUACAUAGCCGGCGCAUCUCCUCCUCCUCCCGGCGGCUUC
52 UCUGAAAGCCCGUCCUCCUCCUCCCGGACCGGCCUUAUGGAAUGCAGUAGAGCCCGCUCCAGCAGCUCUCCUCCUCCUGAGCUCGCGGGCAUUG
53 GACUUCGAGACCCUCCUCCUCCUCCUGGGUUCGGAUUCGGCGCAUCCUCCUCCUCCUCCUGAGGAUGCCGCC
54 AUAAGCCCUCCUCCUCCUCCUGGGGUUCGUAAGAAGACGGCGGCUCCUCCUCCUCCAGAGCCGCCGCUUC
55 CUGCCGCCUCCUCCUCCUGGGGGGUGUGGUGUCCACCUCCUCCCGGGCGGACCG
56 AACCCGAGGCCUCCUCCUCCUCCUGGGCGGAGGUUAUCGCGGGGCGUCUCCUCCUCCUCCUGAGCGCCGCCG
57 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGAGCCGCCGC
58 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
59 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
60 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
61 UGGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGUCG
62 UUCGAAAGCCGUCUCCUCCUCCUGGCAGUCCGAAACCGCAGCGGCCUCCUCCUCCUGGGGUGCGUUC
63 CUGCGAGGUCCACCUCCUCCCGGGACCUUAAGCAGCAGCGGCGACGCCUCCUCCUCCUCCUGGUGUCGCGU
64 GGGCUCGCGCUGCACCUCCUCCCGGGCGGCAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
65 GGGCUCGCGCUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
66 GUUCGAAAGCCCUCCUCCUCCUGGGCGGACUCCGCAACCGCAGCGGCCUCCUCCUCCUGGGGUGCGUUC
67 CUGCGAGGUCCACCUCCUCCCGGGACCUUAAGCAGCAGCGGCGACGCCUCCUCCUCCUCCUGGUGUCGCGU
68 GGACUUCGGCACUGCACCUCCUCCCGGGCGGCAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
69 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGUCG
70 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGUCG
71 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
72 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
73 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
74 UGGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
75 UUCGAAAGCCGUCUCCUCCUCCUGGCAGUCCGAAACCGCAGCGGCCUCCUCCUCCUGGGGUGCGUUC
76 CUGCGAGGUCCACCUCCUCCCGGGGCUUAAGCAGCAGCGGCGACGCCUCCUCCUCCUCCUGGUGUCGCGU
77 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUCCUGGAGCCGCCGC
78 GGACUUCGGCACUGCACCUCCUCCCGGAGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
79 GGACUUCGGUACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
80 GGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUCCUGGAGCCGUCG
81 UGGACUUCGGCACUGCACCUCCUCCCGGGUGCCGAUGACCAAGCGGGCGUCUCCUCCUCCUGGAGCCGCCGC
82 UUCGAAAGCCGUCUCCUCCUCCUGGCAGUCCGAAACCGCAGCGGCCUCCUCCUCCUGGGGUGCGUUC
83 CUGCGAGGUCCACCUCCUCCCGGGACCUUAAGCAGCAGCGGCGACGCCUCCUCCUCCUCCUGGUGUCGCGU
84 CUGAGGUUCGGGCAUCCUCCUCCUCCUGGAGAGAGCGCCGCAUGUUGGGGGGCAUUAUCCUCCUCCAGAUUCGCGC
85 GGAUCAGGUCAACCCUCCUCCUCCUGGUGAUCUUAUACCAAGGGGUGGGCGCUAUCUCCUCCAGGCGCAACCGUC
86 CUGAGGUUCGGGCUUAUUCUCCUCCUGAGAGCGCCGCAUGUUGGGGGGCAUUAUCCUCCUCCAGAUUCGCGC
87 CAGAUCAUCCUCCUCCUCCUGGGUUGUUAACAAAGGCGGUGGCGCUAUCUCCUCCCGGGGCGCACCGUC
88 GUUUAGAUGCCTGUUUCUCCUCCUUAAGGGGCAUACAUACCAGGAGCUCAGUGGUUUCUCCUCCUUAAGCCACUUGCCACUCCGG
89 CCGGACGGUCUCUCCUCCUCCUCCUUAUAGCAGGGGUCGCGGAAACGGUUCGUAUGGCGUGCAUCCUCCUCCUGCCCGCAUAAAGGACCG
90 GCGAAUGCCUCCUCCUCCUCCUGGGGACGUAUAGGAAACGGCGGACCUCCUCCUCCUCCUGGUGCGCGGCUUUUUUAU
91 CAGAUACCCCUCCUCCUCCUCCUGGGUUAUCUUAACGGUACAGGGCAUUCUCCUCCUCCUGAUGCCUGGGGCCGU
92 ACUUCGGGCGUCUCCUCCUCCUGGAGUUGCAUAGAACGGCGGUGCCUCCUCCUCCUGGGCGCGCGUUC
93 CGCGGAUACACCGGUCUCUCCUCCUCCUGCCGGUGUAGAAGCGCGCGGGUGUCUCUCCUCCUCCUGCACCGCCCGC
94 GGAAUCAGGCCUUCUCCUCCUCCUGGGGCUUAGACUACGCGGCGCAUCCUCCUCCUCCUGAUGCCGCCGC
95 GAUCAGGCCUUCUCCUCCUCCUUAAGGGGUCUCCUUAAGGGGUGCAUCCUCCUCCUCCUGAUGCCACCGC

Cuckoo
RNA

Cuckoo RNA sequence

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194 UCGCAGCCGCGCACUCCUCCUCCCAAGCGCGUCGCAUAAGACUGGCAACACUCCUCCUCCAGUUGCCAGUCAUAUAGCGCCGCCGGAUCCUCCCCGCGGGCGUUUUUAU
195 CCUAUCGAAACGGCUUUCUCCUCCUCCAUAGCGGUUCGACAGGGUGGCAACACUCCUCCUCCAGUUGUCGAGUCAGUUUAUAGCCCGACGGAUCCUCCCCGUCGGGCUU
196 GGACCGAAGCGCUUCCCCUCCUAGCCGCUUCGUGCCGACGACAGCACUUCUCCUCCAGCUGUCGGUCACUUCGAAAGCCCGCGCAUUCUCCCGCGCCGGGCUU
197 GUAAAGCAGCGCACUCCUCCUCCAGCGCUUACAUUCGACUGACAACACUCCUCCUCCAGUUGUCAGUCAGGAUCAAGAGCCCGCGCACCUCCUCCCGGUCGGGCUUUUUUUUU
198 UCGUAGCCGCGCACUCCUCCUCCAGCGGCUUCGCAUAGACUGGCAACACUCCUCCUCCAGUUGUCAGUCACCAUAAACGCGCCCGCGGAUCCUCCCCGCGGGGCGU
199 CUCAUCGACACGGCUUCUCCUCCUCCUAGCCGCUUCGUAAGGGUCGACAACACUCCUCCUCCAGUUGUCGAGUCAGUUUAUAGCCCGACGGAUUCUCCUCCCCGUCGGGCUU
200 GAAGGUAGCGCACUCCUCCUCCUCCUCCGCGCUUCAUAGAUUGGCAACACUCCUCCUCCUCCAGUUGCCAAUCCGGAUCAAGAGCCCGAUGCAUCCUCCUCCCGGUCGGGCUU
201 UCGGAGCGCAUACUCCUCCUCCAAUUGCGUCGGAUCGUAUGGCGAGCUCUCCUCCUCCAGUUGCAUACACCAAUAGCGCCACCGCAUCCUCCUCCCGGUGGGGCUUUUU
202 CAUAAUACUCGAGAGCGGCUUCCUCCUCCAAUUGCCGUCGGAUUGGAUCAGCAACUCCUCCUCCAGUUGUCGAGUCAGGUCAAAGCCCGACGCAUCCUCCCGGUCGGGCUUU
203 UAUGCCUGACCCUUCUCCUCCUCCUCCGCGGCUUCGAGCAUAGCGGCGGCAACUCCUCCUCCUCCUUGGUCGCGCGCACUCCAUUUCGGAUCGAGGCCCCUCCUCCUCCUGGGGCGUCUAUAC
204 CGGUCGCGAGCGCACUCCUCCUCCAGCGUCUCCGUAUCGGAUUGGCAACACUCCUCCUCCAGUUGCCAAUAGAGAACGGCAACGCCCGCGGGAUCCUCCCCAGCGGGCGUUUU
205 UCGAAACAGCGUACUCCUCCUCCAGCGCUGUUCGUAAGGUUGGCAACACUCCUCCUCCGCUUGCCAAUUCUAUUCAGACGCCCGCGGAUCCUCCCCAGCGGGCGUCGU
206 CAUCGAAGCGCUGCACCUCCUCCCGCGGCGCCGUAUGCGGGUCGGUUCACUCCUCCUCCAGGAACCGGCCGAGUUUAAGAGCCCGACGCCACCUCCUCCCGGUCGGGCUUU
207 UCGAUGGAGCACUCCGCGUCCAGCUCUGUCGAGGGGAUCGGCAACCCUCCUCCUCCAGUUGCCGUAUCAGGAUCAGGAUCGAAAGCCCGCGCACCUCCUCCCGCGCGGGCUU
208 ACCGAGGCGAUUUACCUCCUCCCGAGUCGUAUGCGGUCGACGGACAGCACUCCUCCUCCAGCUGUCAGUCACUUUUAAGAGCCCGCGCACCUCCUCCCGCGCGGGC
209 ACCGAGGCGAUUUACCUCCUCCCGAGUCGUAUGCGGUCGACGGACAGCACUCCUCCUCCAAAGCUGUCAGUCACUUUUAAGAGCCCGCGCACCUCCUCCCGCGCGGGC
210 UCGAGGAAGCACUCCUCCUCCAGCUUCAUCGAGGGGAUCGGCGACCCUCCUCCUCCAGUUGCCGUAUCAGGAUCGAAAGCCCGCGCACUCCUCCCGCGCGGGCUU
211 CGGUCGCGAGCGCACUCCUCCUCCAGCGUCUCCGUAUCGGAUUGGCGACAACUCCUCCUCCGCUUGCCAAUCAGAACAGGCAACGCCCGCGGACCUCCUCCCCAGUGGGGCUUUUU
212 UCGAAACAGCGCACUCCUCCUCCAGCGCUGUUCGUAAGGUUGGCAACACUCCUCCUCCGCUUGCCAAUUCUAUUCAGACGCCCGCGGAUCCUCCUCCGCGGGCGUCGU
213 CAUCGAAGCGCUGCACCUCCUCCCGCGGCGCCGUAUGCGGGUCGGUUCACUCCUCCUCCAGGAACCGGCCAAGUUUAAGAGCCCGACGCCACCUCCUCCCGGUCGGGCUUU
214 UCGGUAAGAGCACUCCUCCUCCGGGCUUCAUCGAGGGGAUCGGCAACCCUCCUCCUCCAGUUGCCGUAUCAGGAUCGAAAGCCCGCGCACCUCCUCCCGCGCGGGCUU
215 CGGUCGCGAGCGCACUCCUCCUCCCGCGCUCUCCGUAUCGGAUUGGCGACACUCCUCCUCCAGUUGCCAAUCAGAACAGGCAACGCCCGCGGGAUCCUCCCCAGCGGGCGU
216 UCGAAACAGCACAUUCCUCCUCCUCCAGCUGUUCGUAAGCAUUGGCAACACUCCUCCUCCGCUUGCCAAUCACCUUAUAGAGCGCCCGCGGACCUCCUCCCCGCGGGGCUU
217 UCGAAGUCAGCACUCCUCCUCCCGUCGCGACGACUCGUAUCGCUUCACUCCUCCUCCAGCUCUCCUCCUCCAGGACCGGAUUGGUUUUAAGAGCCCGCGCACCUCCUCCCGGUCGGGCUU
218 CAUCGAAGCGCUGCACCUCCUCCCGCGGCGCCGUAUCGGGAUCGGUUCACUCCUCCUCCAGGAACCGGCCGAGUUUAAGAGCCCGACGCCACCUCCUCCCGGUCGGGCUUU
219 ACCGAGGCGAUUUACCUCCUCCCGAGUCGUAUGCGGUCGACGGACAGCACUCCUCCUCCAAAGCUGUCAGUCACUUUUAAGAGCCCGCGCACCUCCUCCCGCGCGGGC
220 UUGUCGAUGGAACACUCCUCCUCCAGUUCGCGGGAUCGGCAACCCUCCUCCUCCGCUUGCCGUAUCAGGAUCGGAAGCCCGCGCACCUCCUCCCGCGCGGGCUU
221 CGAUCGGGAGCGCACUCCUCCUCCAGCGCACCGGUAUCGGAUUGGCAACACUCCUCCUCCAGUUGCCAAUCAGAACAGCGACGCCUCGUGGACCUCCUCCCCAGCGGGGCUUUUU
222 UCGAAGCAGCGCACUCCUCCUCCAGCGCGCUUUGUAAGGAUUGGCAACACUCCUCCUCCGCUUGCCAAUCGCCUUAUUGAGCGCCCGCGGUCUCCUCCCGCGGGGCUU
223 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCCCGGAUUCGUAUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
224 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCAAGAGCGCGGAUCGGUUCACUCCUCCUCCAGGACCGAUCAAGUUCAGAGACCCCGAUGCAUCCUCCCGCAUCGGGCUUU
225 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCCCGGAUUCGGUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
226 CGAUCGGGAGCGCACUCCUCCUCCAGCGCGCCCGAUACGGAUUGGCGACACUCCUCCUCCGCUUGCCAAUCAGAUCAAGCAACGCCCGCGGACCUCCUCCCCAGCGGGGCUUUUU
227 UCGAAGCAGCGCACUCCUCCUCCUCCAGCGCUGUUCGUAUGGAUUGGCAACACUCCUCCUCCGCUUGCCAAUCGCUUUAUAGAGCGCCCGCGGUCUCCUCCCGAGCGGGGCUU
228 CUGUCGAUGGAACACUCCUCCUCCAGUUCUCCUCCGCGGAUCGGCAACCCUCCUCCUCCAGUUGCCGCUUCAGGAUCGAAAGCCCGCGCACCUCCUCCCGCGCGGGUUUUCU
229 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCAAGAGCGCGGAUCGGUUCACUCCUCCUCCAGGACCGAUCAAGUUCAGAGACCCCGAUGCAUCCUCCCGCAUCGGGCUUU
230 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCCCGGAUUCGGUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
231 CGAUCGGGAGCGCACUCCUCCUCCAGCGCGCCCGAUUCGGAUUGGCGACACUCCUCCUCCGCUUGCCAAUCAGAUCAAGCAACGCCCGCGGACCUCCUCCCCAGCGGGGCUUUUU
232 UCGAAGCAGCGCACUCCUCCUCCUCCAGCGCUGUUCGUAUGGAUUGGCAACACUCCUCCUCCGCUUGCCAAUCGCUUUAUAGAGCGCCCGCGGUCUCCUCCCCAGCGGGGCUU
233 CUGUCGAUGGAACACUCCUCCUCCAGUUCUCCUCCGCGGAUCGGCAACCCUCCUCCUCCAGUUGCCGCUUCAGGAUCGAAAGCCCGCGCACCUCCUCCCGCGCGGGUUUUCU
234 CGAUCGGGAGCGCACUCCUCCUCCAGCGCGCCGUAUCGGAUUGGCGACACUCCUCCUCCGCUUGCCAAUCAGAUCAAAACAGCCCGCGGACCUCCUCCCCAGCGGGGCUUUUU
235 UCGAAGCAGCGCACUCCUCCUCCUCCAGCGCUCGUAUGGAUUGGCAACACUCCUCCUCCGCUUGCCAAUCGCCUUAUAGAGCGCCCGCGGUCUCCUCCCCAGCGGGGCUU
236 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCCCGGAUUCGGUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
237 CUGUCGAUGGAACACUCCUCCUCCAGUUCUCCUCCGCGGAUCGGCAACCCUCCUCCUCCAGGACCGAUCAAGUUCAGAGACCCCGAUGCAUCCUCCCGCAUCGGGCUUUUCG
238 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCAAGAGCGCGGAUCGGUUCACUCCUCCUCCAGGACCGAUCAAGUUCAGAGACCCCGAUGCAUCCUCCCGCAUCGGGCUUUUCG
239 CGAUCGGGAGCGCACUCCUCCUCCAGCGCGCCGUAUCGGAUUGGCGACACUCCUCCUCCGCUUGCCAAUCAGAUCAAGCAACGCCCGCGGACCUCCUCCCCAGCGGGGCUUU
240 UCGAAGCAGCGCACUCCUCCUCCUCCAGCGCGCCGGAUUCGGUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
241 UGUCGAAGCGCUGUACCUCCUCCAGCGCGCCCGGAUUCGGUCGGUUCACUCCUCCUCCAGAACCGAUCAAGUUUAAGAGCCCGAGCCACCUCCUCCCGGUCGGGCUUU
242 CUGUCGAUGGAACACUCCUCCUCCAGUUCUCCUCCGCGGAUCGGCAACCCUCCUCCUCCAGUUGCCGCUUCAGGAUCGAAAGCCCGCGCACCUCCUCCCGCGCGGGUUUUCU
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Cuckoo
RNA

Cuckoo RNA sequence

292 ACCCGCCCGCUCUCCUCCUUGGGGCGGGUUCAGGCGACAUCCUCCUCCUCCUAGGAGUUCGCGCCACCAACACGGAAGCCUCCUCCUCCUUGGGUUCUGUUAAGGCGGCGACCCUCCUCCUCCUUGGGUUCGCCGACU
293 UACGAUGGCCUCCUCCUCCUUGGGGUCGUCUGAGCGGUAUUGGCACUCCUCCUCCAGCAUUGCGCACCUUUAACGCGGCCUCCUCCUCCUUGGGCCAGCGUUGCGGGCGGUGCCUCCUCCUCCUUGGGACCGCCGC
294 UGCGACGGUCCUCCUCCUCCUUGGGUUCGUCAGCACGGGUAUUGGCGUCCUCCUCCUCCUCCUUGCCGACCCCAUACGCGGCCUCCUCCUCCUUGGGCCAGCGUUGCGGGCGGUGCCUCCUCCUCCUUGGGACCGCCGC
295 CGCGUUCACGGGGCUCUCCUCCUCCAAAGCCUUGAGCGUGCAACGCCGGGACCUCCUCCUCCAAUCCCGCAGUCUCCAACGACGCCAGUACCAACGCGGCCUCCUCCUCCUUGGGCGGGGCGCCCG
296 AGGCGCGUAGGAAUCUCCCAAUCAAACUCGCGAGCCUAAAUCAAAUCCUCAAAGUGGCACUCCUCCCAAGCGCUGUAGUUGUUUCAAACAGAGAUUUCUCCCAAGUUCUGUUAUACUAGCUUCCGCGUCUCCUCCAUAGCGGGCGUUAAGCUG
297 UCGAAGCGAUGCUUCCUCCCGCAACGCUUCGAAGUUUAGACGGCCACUCCUCCUCCAAAGGGACGUCUGUGGGAACAGCGGCACUCCUCCAGGUCGCGGUUCGUGUUUAGGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
298 AUCGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUGCAGGCGCUCAUCCUCCUCCAGGGACGUCUGCGGGAACAGCCGACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCGCACUCCUCCCGGGCAGGCUUUU
299 CUCGAAGCGAUGCUUCCUCCCGCACCGCUUCGAGUUAAGAUUGGCCCACUCCUCCUCCGAAAGGACGUCUGUUGGAAACAGCGGCACUCCUCCUCCAAAGUCGUGUUCGGUUCUUUAGGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
300 UCGAAGCGAUGCUUCCUCCCGCAACGCUUCGAAGUUUAGACGGCCACUCCUCCUCCAAAGGGACGUCUGUGGGAACAGCGGCACUCCUCCAGGUCGCGGUUCGUGUUUAGGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
301 AUCGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUGCAGGCGCCUCCUCCUCCAGGGUCGCUUGCGGGAACAACAGCACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCGCACUCCUCCCGGGCAGGCUUUU
302 AUCGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUGCAGGCGCUCAUCCUCCUCCAGGGACGUCUGCGGGAACAGCGGCACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCGCACUCCUCCCGGGCAGGCUUUU
303 GGCUCAACGAAGCAAUGCACCUCUCCCGCAGAGCUUCGUGGUUUCAGGCGACCCACUCCUCCUCCAAAGGGGAGCUCGACGGAACAGCGGCACUCCUCCUCCAGCGUUGUCAAUUUUAGGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
304 CGAAGCAAUGCACCUCUCCCGCAAGCUUCGCUUUCAGCCGACCCUCCUCCUCCAAAGGGGAGCUCGUAUAAACAGCGGCACUCCUCCUCCAGCUGCGUUCGUAUUCAGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
305 ACGAAGCAAUGCACCUCUCCCGCAGAGCUUCGUGUCACAGGCGACCAUCCUCCUCCCGGGGGCGCCUGACGGAACAGCGGCGCUCCUCCUCCAGCGGUUGUUAUUAUUGGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
306 UACGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUCAGGCGCCCAUCCUCCUCCAGGGUCGUCUGUGGAUUCAGCACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
307 UACGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUCAGGCGCCCAUCCUCCUCCAGGGUCGUCUGUGGAUUCAGCACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
308 CGAAGUAGUAGCACCUCUCCCGCAAGCUUCGUGUUUAGGCGACCCGCUCCUCCUCCAAAGGGCGCCUUCAGGAACAGCGGCACUCCUCCUCCAGCGGUUGUUAUUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
309 UACGAAGCGAUGCACCUCUCCCGCAUCCUUGAUUUCAGGCGCCCAUCCUCCUCCAGGGUCGUCUGUGGAUUCAGCACUCCUCCUCCAGCUGUUGUUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
310 CGAAGCGAUGAUCUCCUCCCGCAUCCUUCGCUUGGCGAGAGCUCUUAUCCUCCUCCAGGGGACGUCGAGGAUAGCGGAACUCCUCCUCCUCCAGCUGUUGGUAUUAUUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
311 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGUGGGGACCUUCCUCCUCCCGGGUUCUUCGCUACAGAGAUUCAGCGCCACUCCUCCUCCCGGGGUCGUAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
312 UCAACGAAGCGAUGCACCUCUCCCGCAGAGCUUCGUGAUUCAGGCGGCCACUCCUCCUCCAGGGACGUCUGAAGGACAGCGGCACUCCUCCUCCUUGCGUAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
313 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
314 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
315 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
316 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
317 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGCAGGCUUUUUA
318 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGGAGGCUUUUUA
319 AUCGAAGCGAUGCACCUCUCCCGCAGAGCUUCGAUUGCGAGCGACCUUCCUCCUCCGAGUUCGCUUGCGGGAUACAGCGCUACUCCUCCUCCGAAUGCUGAUCGUAUUCGAAAGCCUGCCGACCCUCCUCCCGGGUAGGCUUUUUA
320 CGGGCACACGACCCUCCUGUUGUGGCUUGAAGAAAGCUUCGGGUCUCCUCCUCCUCCGAGACCGCGGCUUUAUAAACGUCCUCCUCCUCCUCCGAAUGGUAUGGGGACGUAAGAAAGACGGCGGUGCUUCCUCCAAAGCACCGCCGUUCUGCAUCU
321 CGGGCACACGACCCUCCUGUUGUGGCUUGAAGAAAGCUUCGGGUCUCCUCCUCCUCCGAGACCGCGGCUUUAUAAACGUCCUCCUCCUCCUCCGAAUGGUAUGGGGACGUAAGAAAGACGGCGGUGCUUCCUCCAAAGCACCGCCGUUCUGCAUCU

Cuckoo
RNA del Val et al. 2007 Valverde et al. 2008 Livny et al. 2008 Berghoff et al. 2009 Vercruyse et al. 2010 Schlüter et al. 2010 Reinkensmeier et al. 2011 del Val et al. 2012 Wilms et al. 2012

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RSs0680d
RSs0680c repeat3
RSs0680c repeat2
RSs0680c repeat1
RSs0680c
RSs0680b
RSs0680a

RSs0680a homolog

RSs0680a homolog

RSs0680a homolog
RSs0680a homolog

# Cuckoo RNA	del Val et al. 2007	Valverde et al. 2008	Livny et al. 2008	Berghoff et al. 2009	Vercruyse et al. 2010	Schlüter et al. 2010	Reinkensmeier et al. 2011	del Val et al. 2012	Wilms et al. 2012
94				RSs0680a homolog					
95				RSs0680a homolog					
96									
97									
98									
99				RSs0680a homolog					
100									
101									
102									
103									
104				RSs0680a homolog					
105									
106							RNA10	Atr14C2	
107							RNA15	Arr14Cl1	
108							RNA37	Arr14Cl2	
109							RNA20	Arr14Cl3	
110							RNA7	AH13r14C1	
111							RNA9		
112							RNA23	Avr14Atc	
113							RNA38	Avr14Cl1	
114							RNA48	Avr14Cl2	
115									
116									
117							RNA78		
118							RNA63	BaS19r14Cl1	
119							RNA62	Ba19941r14Cl1	
120							RNA59	Bcr14Cl1	
121									
122							RNA66	Bm23457r14Cl1	
123							RNA65		
124									
125									
126							RNA64	Bmar14Cl1	
127							RNA67	Bm16Mr14Cl2	
128							RNA57	Bmir14Cl1	
129							RNA61	Bor14Cl1	
130									
131									
132							RNA77		
133							RNA70	Bs1330r14Cl1	
134							RNA79		
135							RNA58	Bs23445r14Cl1	
136									
137									
138							RNA82		
139								MsBCNr14p1	
140							RNA28	MsBCNr14Cl1	
141							RNA32	MsBCNr14C2	

# Cuckoo RNA	del Val et al. 2007	Valverde et al. 2008	Livny et al. 2008	Berghoff et al. 2009	Vercruyse et al. 2010	Schlüter et al. 2010	Reinkensmeier et al. 2011	del Val et al. 2012	Wilms et al. 2012
142									
143									
144									
145				RSs0680a homolog					
146									
147									
148									
149									
150									
151							RNA69	Mcr14p01	
152							RNA80	Mcr14C4	
153							RNA50	Mcr14C1	
154							RNA53	Mcr14C2	
155							RNA36	Mcr14C3	
156							RNA71	Mcr14C5	
157							RNA52	Mlr14C1	
158							RNA51	Mlr14C2	
159							RNA49	Mlr14C3	
160							RNA68		
161							RNA81	Mlr14C4	
162							RNA72	Mlr14C5	
163									
164									
165									
166									
167									
168									
169							RNA75	Oar14CI1	
170							RNA76		
171							RNA60	Oar14CI1	
172			Candidate_13_NC_009668				RNA56	Oar14CI2	
173									
174									
175									
176									
177			Candidate_154_NC_007761		ReC11		RNA13	ReCFNr14C1	
178			Candidate_69_NC_007761				RNA34	ReCFNr14C2	
179			Candidate_150_NC_007761				RNA24	ReCFNr14C3	
180								ReCFNr14f	
181							RNA11	ReCIATr14C1	
182							RNA29	ReCIATr14C3	
183							RNA14	ReCIATr14C4	
184									
185									
186									
187									
188							RNA55	Rlt1325r14p011	
189							RNA16	Rlt1325r14C1	

# Cuckoo RNA	del Val et al. 2007	Valverde et al. 2008	Livny et al. 2008	Berghoff et al. 2009	Vercruyse et al. 2010	Schlüter et al. 2010	Reinkensmeier et al. 2011	del Val et al. 2012	Wilms et al. 2012
190							RNA31	Rlt1325r14C2	
191							RNA25	Rlt1325r14C3	
192							RNA73	Rlt2304r14p011	
193							RNA12	Rlt2304r14C1	
194							RNA35	Rlt2304r14C2	
195							RNA26	Rlt2304r14C3	
196							RNA54	Rlvr14p12	
197			Candidate_152_NC_008380				RNA17	Rlvr14C1	
198							RNA42	Rlvr14C2	
199							RNA19	Rlvr14C3	
200									
201									
202									
203									
204									
205									
206									
207									
208									
209									
210							RNA74	Sfr14b	
211							RNA33	Sfr14C1	
212							RNA39	Sfr14C2	
213							RNA6	Sfr14C3	
214									
215									
216									
217									
218									
219									
220							RNA43	Smedr14p01	
221							RNA27	Smedr14C1	
222							RNA47	Smedr14C2	
223			Candidate_35_NC_009636				RNA5	Smedr14C3	
224						SmelA075	SmelA075	Smr14A1	
225						SmelC025	RNA4	Smr14C1	
226	C14	smrC14				SmelC397	RNA22	Smr14C2	
227		sm7				SmelC398	RNA45	Smr14C3	
228						SmelB161	RNA30	Smr14B	
229									
230									
231									
232									
233									
234							RNA18		
235							RNA44		
236							RNA3		
237							RNA40		

# Cuckoo RNA	del Val et al. 2007	Valverde et al. 2008	Livny et al. 2008	Berghoff et al. 2009	Vercruyse et al. 2010	Schlüter et al. 2010	Reinkensmeier et al. 2011	del Val et al. 2012	Wilms et al. 2012
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Candidate_7_NC_004041
Candidate_5_NC_007765

RNA22 ReCFNr14d
RNA15 ReCFNr14e
RNA13 ReCIATr14C2
RNA23 ReCIATr14B
RNA7 ReCIATr14A

RNA21 Rlt1325r14p012
RNA24 Rlt1325r14p04
RNA18 Rlt1325r14p05
RNA14 Rlt1325r14p02
RNA9 Rlt2304r14p02
RNA17 Rlt2304r14p012
RNA16 Rlvr14p11

Candidate_14_NC_009621

A6

SmelA099

RNA3 Smedr14p021
RNA4 Smedr14p022
SmelA099 Smr14A2

RNA1
RNA2