

preQ1 riboswitch

Number	PDB code	Identity (%)		Similar region in the riboswitch (local alignment)	Length (bp)	Local alignment
		local	global			
1	1rngA	66.7	20.6	4-12	12	GGUUCUAGC GGCCUUTUC
2	1afxA	100.0	26.5	14-18	12	ACACC ACACC
3	1g1xI	85.7	13.1	1-7	41	AGAGGSU .. AGAGGSU
4	361dB	70.0	27.0	11-20	20	GCUACACCCU GGACCCGCCU
5	1uuuA	68.8	24.4	3-18	19	AGGUUCAGCUACACC ACGUU-UCG-UCAGCC
6	1wtsA	83.3	14.6	3-8	14	AGGUUC .. AGGUCC
7	1fhkA	80.0	23.5	2-6	14	GAGGU .. GCGGU
8	1hs8A	71.4	15.8	18-24	13	CCUCUAD CCUCUAA
9	1vopA	80.0	10.0	2-6	13	GAGGU .. G
10	1zihA	66.7	23.5	4-12	12	GGUUCUAGC GCAAGC
11	1i3yA	66.7	28.2	5-19	19	GGUUCUAGCUACACC GUUC--GC--CAGC
12	1k5iA	80.0	31.0	11-20	23	GCUACACCCU .. GCU-CAACCU
13	1mt4A	66.7	19.6	1-12	24	GGUUCUAGC GGUUCUAGC
14	1jurA	55.0	12.2	1-17	22	GGUUCUAGC GGUUCUAGC
15	1qwaA	70.0	27.5	5-14	21	GGUUCUAGC GGUUCUAGC
16	483dA	62.5	11.1	1-16	27	GGUUCUAGC GGA----CCGAGUG
17	1mjiC	63.2	32.6	3-17	34	AUGC----CUCCGAGUGC AUGCAGACUCAGAGUGC
18	1q93C	41.9	27.7	2-20	27	GAGUCCUCCGAGU-----GCAUC GGU-CTC--AGAGGAGACGAAACCCGACC
19	1pbrA	69.2	31.8	6-18	27	CCUCCGAGUGCA CCU-UCGGUGAA
20	1fyoA	69.2	13.7	6-18	27	CCUCCGAGUGCA CCU-UCGGUGAA
21	1bgzA	50.0	30.0	1-20	23	GGUUCUAGC GGAU-----ACUGCUC
22	1i6uD	56.5	23.2	1-17	37	GGUUCUAGC GUAAGUCUCUUGGAGUAUCUGC
23	1d6kB	61.1	11.1	1-18	37	GGUUCUAGC GGAU-----CGAGAGUA
24	1mzpB	43.9	25.0	1-21	55	GGUUCUAGC GGUUCUAGC
25	1fypA	69.2	13.7	6-18	27	CCUCCGAGUGCA CCU-UCGGUGAA
26	1qa6D	100.0	33.3	1-5	58	GGUUCUAGC GGUUCUAGC
27	1un6F	54.2	28.4	1-17	61	GGUUCUAGC GGAAACCGGAAUACAG-GUGC
28	1f7yB	68.8	23.9	1-14	57	GGUUCUAGC GGUUCUAGC
29	1g1xJ	66.7	27.5	1-21	44	GGUUCUAGC GGUUCUAGC