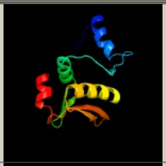
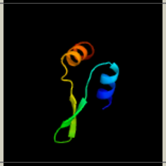
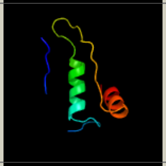
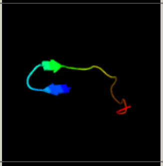
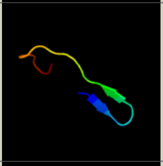
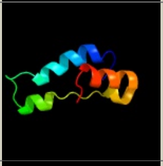
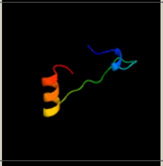
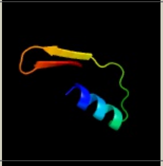
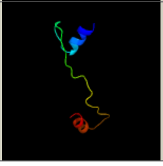
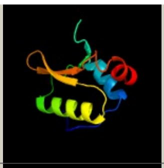
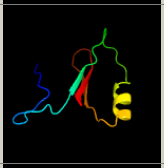
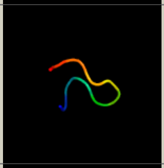
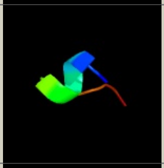
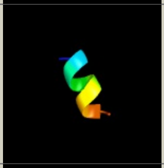
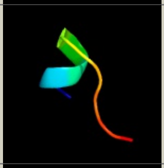
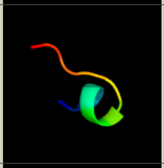
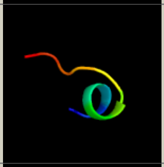
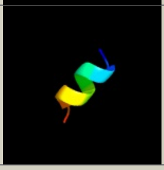
Email	mdejesus@rockefeller.edu
Description	RVBD3647c_(-)_4087789_4088367
Date	Fri Aug 9 18:20:33 BST 2019
Unique Job ID	309f901282018c07

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1r7mA_	Alignment		38.6	14	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**intron-encoded endonuclease i-scei; **PDBTitle:** the homing endonuclease i-scei bound to its dna recognition2 region
2	d1dq3a4	Alignment		19.6	18	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
3	d1em8a_	Alignment		16.7	20	**Fold:**DNA polymerase III chi subunit **Superfamily:**DNA polymerase III chi subunit **Family:**DNA polymerase III chi subunit
4	d1jala2	Alignment		13.9	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
5	c4za1A_	Alignment		13.4	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nosa; **PDBTitle:** crystal structure of nosa involved in nosiheptide biosynthesis
6	d1ni3a2	Alignment		11.8	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
7	d1jvaa3	Alignment		10.2	12	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
8	c2dzaA_	Alignment		8.8	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
9	d1k7ja_	Alignment		6.3	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
10	c3dluA_	Alignment		6.2	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
11	c2qsiB_	Alignment		5.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009

12	d1r7ma2	Alignment		5.5	15	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
13	c2faoB_	Alignment		5.5	25	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
14	c3ccmG_	Alignment		5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
15	c1vqkG_	Alignment		5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of ccda-phe-cap-bio bound to the a site of the ribosomal2 subunit of haloarcula marismortui
16	c1yitG_	Alignment		5.3	36	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of virginiamycin m and s bound to the 50s ribosomal2 subunit of haloarcula marismortui
17	c3i56G_	Alignment		5.3	36	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-crystal structure of triacetyloleandomcyin bound to the large2 ribosomal subunit
18	c1kc8I_	Alignment		5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of blasticidin s bound to the 50s2 ribosomal subunit
19	c1k73I_	Alignment		5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s2 ribosomal subunit
20	c1s72G_	Alignment		5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution
21	c1kqsG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
22	c1m90I_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of cca-phe-caproic acid-biotin and sparsomycin2 bound to the 50s ribosomal subunit
23	c1m1kI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of azithromycin bound to the 50s2 ribosomal subunit of haloarcula marismortui
24	c1yjwG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of quinupristin bound to the g2099a mutant 50s2 ribosomal subunit of haloarcula marismortui
25	c3cceG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535a
26	c1vq7G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "dca" bound to the2 large ribosomal subunit of haloarcula marismortui
27	c3ccuG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2482c
28	c1w2bG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** trigger factor ribosome binding domain in complex with 50s

29	c1kd1I_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of spiramycin bound to the 50s2 ribosomal subunit of haloarcula marismortui
30	c1qvgG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of cca oligonucleotide bound to the trna binding sites of2 the large ribosomal subunit of haloarcula marismortui
31	c1jj2G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** fully refined crystal structure of the haloarcula2 marismortui large ribosomal subunit at 2.4 angstrom3 resolution
32	c1k8aI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of carbomycin a bound to the 50s2 ribosomal subunit of haloarcula marismortui
33	c2otlG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** girodazole bound to the large subunit of haloarcula marismortui
34	c3cc2G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** the refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution with rrna sequence for3 the 23s rrna and genome-derived sequences for r-proteins
35	c1k9mI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l10; **PDBTitle:** co-crystal structure of tylosin bound to the 50s ribosomal2 subunit of haloarcula marismortui
36	c3cmaG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** the structure of cca and cca-phe-cap-bio bound to the large ribosomal2 subunit of haloarcula marismortui
37	c3i55G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-crystal structure of mycalamide a bound to the large ribosomal2 subunit
38	c1vqmG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "dan" bound to the2 large ribosomal subunit of haloarcula marismortui
39	c1q7yI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of ccdap-puromycin bound at the peptidyl transferase2 center of the 50s ribosomal subunit
40	c1vq5G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "raa" bound to the2 large ribosomal subunit of haloarcula marismortui
41	c2otjG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** 13-deoxytedanolide bound to the large subunit of haloarcula2 marismortui
42	c1qvfG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of a deacylated trna minihelix bound to the e site of the2 large ribosomal subunit of haloarcula marismortui
43	c1vq9G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of cca-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
44	c1yjnG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of clindamycin bound to the g2099a mutant 50s2 ribosomal subunit of haloarcula marismortui
45	c3ow2G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** crystal structure of enhanced macrolide bound to 50s ribosomal subunit
46	c1yi2G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of erythromycin bound to the g2099a mutant 50s2 ribosomal subunit of haloarcula marismortui
47	c1vq8G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
48	c1q86I_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of cca-phe-cap-biotin bound simultaneously at half2 occupancy to both the a-site and p-site of the the 50s ribosomal3 subunit.
49	c3g6eG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-crystal structure of homoharringtonine bound to the large ribosomal2 subunit
50	c1vqoG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of ccpmn bound to the large ribosomal subunit haloarcula2 marismortui
51	c1vq4G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "daa" bound to the2 large ribosomal subunit of haloarcula marismortui
52	c1yijG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of telithromycin bound to the g2099a mutant 50s2 ribosomal subunit of haloarcula marismortui
53	c3cxcG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**ribosomal protein l10;

		Alignment	not modelled			**PDBTitle:** the structure of an enhanced oxazolidinone inhibitor bound2 to the 50s ribosomal subunit of h. marismortui
54	c1q81I_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of minihelix with 3' puromycin bound to a-site of2 the 50s ribosomal subunit.
55	c1njiI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** structure of chloramphenicol bound to the 50s ribosomal2 subunit
56	c3ccvG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2616a
57	c3cd6G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-cystal of large ribosomal subunit mutant g2616a with cc-puromycin
58	c1yj9G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of the mutant 50s ribosomal subunit of haloarcula2 marismortui containing a three residue deletion in l22
59	c3cc4G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
60	c2qexG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** negamycin binds to the wall of the nascent chain exit tunnel of the2 50s ribosomal subunit
61	c3cclG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation u2535c. density for anisomycin is visible but not included3 in model.
62	c3cpwG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** the structure of the antibiotic linezolid bound to the large ribosomal2 subunit of haloarcula marismortui
63	c3cc7G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2487u
64	c1vq6G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of c-hpmn and cca-phe-cap-bio bound to the large2 ribosomal subunit of haloarcula marismortui
65	c1q82I_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of cc-puromycin bound to the a-site of the 50s2 ribosomal subunit
66	c1n8rI_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** structure of large ribosomal subunit in complex with2 virginiamycin m
67	c1vqpG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "rap" bound to the2 large ribosomal subunit of haloarcula marismortui
68	c1yhqG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** crystal structure of azithromycin bound to the g2099a mutant 50s2 ribosomal subunit of haloarcula marismortui
69	c3ccqG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation a2488u
70	c3ccjG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
71	c1vqlG_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0 homolog; **PDBTitle:** the structure of the transition state analogue "dcsn" bound to the2 large ribosomal subunit of haloarcula marismortui
72	c3g71G_	Alignment	not modelled	5.3	36	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** co-crystal structure of bruceantin bound to the large ribosomal2 subunit
73	c3ccsG_	Alignment	not modelled	5.1	33	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l10e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2482a