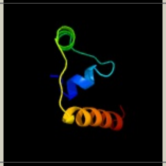
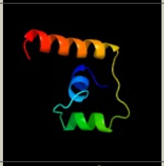
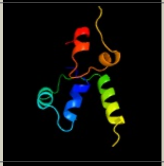
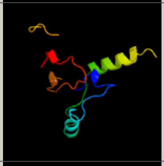
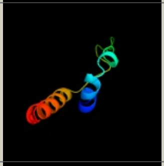
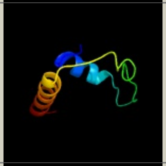
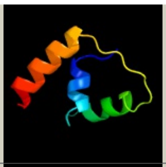
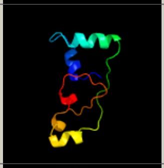
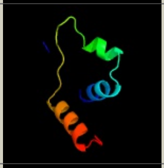
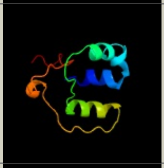
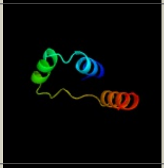
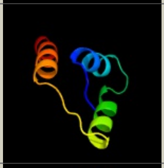
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1741_(-)_1967924_1968172
Date	Fri Aug 2 13:30:34 BST 2019
Unique Job ID	8bd1b648d5944159

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgrG_	Alignment		99.4	67	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc30; **PDBTitle:** crystal structure of addiction module from mycobacterial species
2	c5wzfB_	Alignment		97.4	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**23s rrna-specific endonuclease vapc20; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapc20 (rv2549c),2 sarcin-ricin loop cleaving toxin
3	c2fe1A_	Alignment		97.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein pae0151; **PDBTitle:** crystal structure of pae0151 from pyrobaculum aerophilum
4	d2fe1a1	Alignment		97.2	21	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
5	d2h1ca1	Alignment		97.0	14	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
6	c3dboB_	Alignment		96.8	23	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
7	c3zvkC_	Alignment		96.7	15	**PDB header:**antitoxin/toxin/dna **Chain:** C: **PDB Molecule:**toxin of toxin-antitoxin system; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
8	c3h87B_	Alignment		96.5	21	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
9	d1v8pa_	Alignment		95.9	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
10	c1v8pK_	Alignment		95.7	13	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**hypothetical protein pae2754; **PDBTitle:** crystal structure of pae2754 from pyrobaculum aerophilum
11	c6a7vG_	Alignment		95.7	19	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex

12	c5x3tD_	Alignment		95.2	29	**PDB header:**antitoxin/toxin **Chain:** D: **PDB Molecule:**ribonuclease vapc26; **PDBTitle:** vapbc from mycobacterium tuberculosis
13	c5sv2A_	Alignment		93.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease vapc21; **PDBTitle:** toxin vapc21 from mycobacterium tuberculosis
14	c3tndC_	Alignment		92.3	15	**PDB header:**translation, toxin **Chain:** C: **PDB Molecule:**trna(fmet)-specific endonuclease vapc; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
15	c5l6mC_	Alignment		91.9	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
16	c4chgC_	Alignment		91.8	23	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**probable ribonuclease vapc15; **PDBTitle:** crystal structure of vapbc15 complex from mycobacterium tuberculosis
17	c6nklA_	Alignment		90.6	14	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
18	d1y82a1	Alignment		65.8	15	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
19	d1v96a1	Alignment		50.6	18	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
20	d1w8ia_	Alignment		40.1	11	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
21	c3ix7A_	Alignment	not modelled	29.8	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ttha0540; **PDBTitle:** crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8
22	c2lcqA_	Alignment	not modelled	23.9	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
23	d1tqba_	Alignment	not modelled	18.8	38	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
24	d1b10a_	Alignment	not modelled	18.5	38	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
25	d1uw3a_	Alignment	not modelled	18.3	38	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
26	d1xyua_	Alignment	not modelled	17.9	38	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
27	c5ywwA_	Alignment	not modelled	14.3	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
28	c3i8oA_	Alignment	not modelled	13.7	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh domain-containing protein mj1533; **PDBTitle:** a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
						PDB header:hydrolase

29	c5f4hF_	Alignment	not modelled	13.7	44	**Chain:** F: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
30	d1xyqa_	Alignment	not modelled	12.4	36	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
31	d1xyxa_	Alignment	not modelled	11.8	36	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
32	c1dx0A_	Alignment	not modelled	11.6	45	**PDB header:**prion protein **Chain:** A: **PDB Molecule:**prion protein; **PDBTitle:** bovine prion protein residues 23-230
33	d1dwya_	Alignment	not modelled	11.6	45	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
34	d1xyka_	Alignment	not modelled	10.7	31	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
35	c3cinA_	Alignment	not modelled	9.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**myo-inositol-1-phosphate synthase-related protein; **PDBTitle:** crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
36	d1yj5a1	Alignment	not modelled	8.3	44	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
37	c1fo7A_	Alignment	not modelled	7.9	36	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**prion protein; **PDBTitle:** human prion protein mutant e200k fragment 90-231
38	d1fo7a_	Alignment	not modelled	7.9	36	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
39	d1fvpa_	Alignment	not modelled	7.7	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
40	c5jpqd_	Alignment	not modelled	7.3	12	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**wd40 domain proteins; **PDBTitle:** cryo-em structure of the 90s pre-ribosome
41	c6g5iy_	Alignment	not modelled	7.2	33	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** cryo-em structure of a late human pre-40s ribosomal subunit - state r
42	c1au7B_	Alignment	not modelled	6.9	33	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**protein pit-1; **PDBTitle:** pit-1 mutant/dna complex
43	d1jaea2	Alignment	not modelled	5.9	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
44	d1o4wa_	Alignment	not modelled	5.9	15	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
45	c5f4tA_	Alignment	not modelled	5.7	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**izumo sperm-egg fusion protein 1; **PDBTitle:** crystal structure of the human sperm izumo1 residues 22-254
46	c3c2qA_	Alignment	not modelled	5.4	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
47	c6em5r_	Alignment	not modelled	5.2	25	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**60s ribosomal protein l19-a; **PDBTitle:** state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes