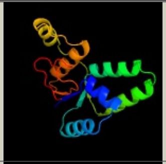
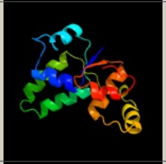
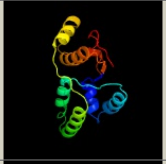
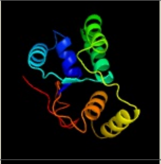
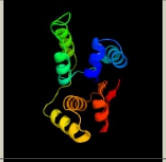
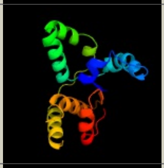
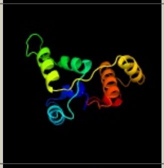
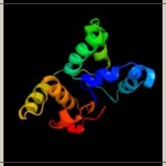
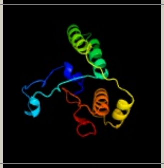
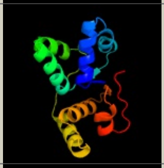
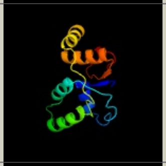
Email	mdejesus@rockefeller.edu
Description	RVBD0617_(-)_711009_711410
Date	Fri Jul 26 01:50:18 BST 2019
Unique Job ID	bfbd01529d9a995e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zvkC_	Alignment		99.9	10	**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
2	c5x3tD_	Alignment		99.8	17	**PDB header:**antitoxin/toxin **Chain:** D: **PDB Molecule:**ribonuclease vapc26; **PDBTitle:** vapbc from mycobacterium tuberculosis
3	c3tndC_	Alignment		99.8	14	**PDB header:**translation, toxin **Chain:** C: **PDB Molecule:**trna(fmet)-specific endonuclease vapc; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
4	c6nklA_	Alignment		99.8	13	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
5	d2fe1a1	Alignment		99.8	18	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
6	c2fe1A_	Alignment		99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein pae0151; **PDBTitle:** crystal structure of pae0151 from pyrobaculum aerophilum
7	c5l6mC_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease vapc; **PDBTitle:** structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
8	c5wzfB_	Alignment		99.8	17	**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
9	c4xgrG_	Alignment		99.8	10	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc30; **PDBTitle:** crystal structure of addiction module from mycobacterial species
10	c6a7vG_	Alignment		99.8	13	**PDB header:**toxin/antitoxin **Chain:** G: **PDB Molecule:**ribonuclease vapc11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
11	c4chgC_	Alignment		99.8	12	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**probable ribonuclease vapc15; **PDBTitle:** crystal structure of vapbc15 complex from mycobacterium tuberculosis

12	d2h1ca1	Alignment		99.7	20	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
13	c3h87B_	Alignment		99.7	14	**PDB header:**toxin/antitoxin **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
14	c5sv2A_	Alignment		99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease vapc21; **PDBTitle:** toxin vapc21 from mycobacterium tuberculosis
15	d1v96a1	Alignment		99.6	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
16	c3dboB_	Alignment		99.6	21	**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
17	d1y82a1	Alignment		99.5	13	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
18	d1v8pa_	Alignment		99.4	22	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
19	c1v8pK_	Alignment		99.4	22	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**hypothetical protein pae2754; **PDBTitle:** crystal structure of pae2754 from pyrobaculum aerophilum
20	d1w8ia_	Alignment		99.3	14	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
21	c3i8oA_	Alignment	not modelled	98.7	11	**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.
22	c3ix7A_	Alignment	not modelled	98.5	21	**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
23	d1o4wa_	Alignment	not modelled	98.2	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
24	c5ywwA_	Alignment	not modelled	97.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
25	c5f4hF_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nucleotide binding protein pinc; **PDBTitle:** archael ruvb-like holiday junction helicase
26	c2lcqA_	Alignment	not modelled	97.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
27	c2hwwC_	Alignment	not modelled	97.3	16	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**telomerase-binding protein est1a; **PDBTitle:** structure of pin domain of human smg6
28	c5yz4A_	Alignment	not modelled	96.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rrna-processing protein fcf1; **PDBTitle:** structure of the pin domain endonuclease utp24
						PDB header:ribosome

29	c5jpqd_	Alignment	not modelled	95.7	22	**Chain:** D: **PDB Molecule:**wd40 domain proteins; **PDBTitle:** cryo-em structure of the 90s pre-ribosome
30	c4mj7B_	Alignment	not modelled	91.1	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**rrna-processing protein utp23; **PDBTitle:** crystal structure of the pin domain of saccharomyces cerevisiae utp23
31	c2hwyB_	Alignment	not modelled	82.3	10	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
32	c6g5iy_	Alignment	not modelled	78.3	25	**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
33	c3v33A_	Alignment	not modelled	74.7	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 conserved domain with zinc-finger motif
34	c3v32B_	Alignment	not modelled	73.7	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease zc3h12a; **PDBTitle:** crystal structure of mcpip1 n-terminal conserved domain
35	c2mdtA_	Alignment	not modelled	18.9	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** a pilt n-terminus domain protein sso1118 from hyperthemophilic2 archaeon sulfolobus solfataricus p2
36	c3al0B_	Alignment	not modelled	8.5	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
37	c2g5iB_	Alignment	not modelled	6.5	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
38	c3h0mE_	Alignment	not modelled	6.4	19	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
39	c3kfuF_	Alignment	not modelled	6.3	11	**PDB header:**ligase/rna **Chain:** F: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the transamidosome
40	c4wj3K_	Alignment	not modelled	6.1	19	**PDB header:**ligase/rna **Chain:** K: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
41	c4wj3H_	Alignment	not modelled	6.0	19	**PDB header:**ligase/rna **Chain:** H: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
42	c4wj3E_	Alignment	not modelled	6.0	19	**PDB header:**ligase/rna **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
43	c4wj3B_	Alignment	not modelled	6.0	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the asparagine transamidosome from pseudomonas2 aeruginosa
44	c3zddA_	Alignment	not modelled	5.7	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein xni; **PDBTitle:** structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium