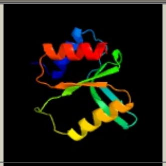
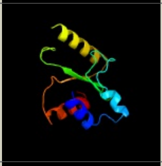
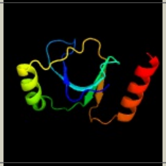
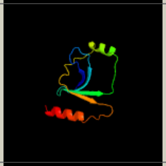
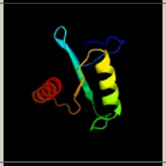
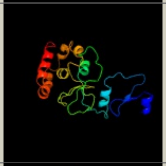
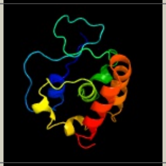
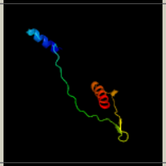
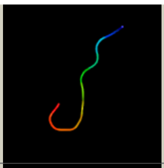
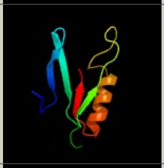
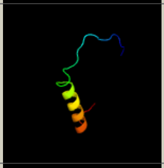
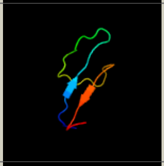
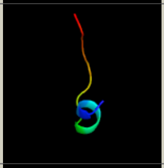
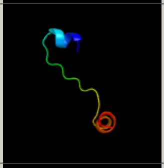
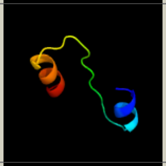
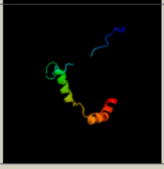
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3517_(-)_3953610_3954449
Date	Fri Aug 9 18:20:19 BST 2019
Unique Job ID	45b0a52329944cce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	Alignment		99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobile intron protein; **PDBTitle:** homing endonuclease i-bth0305i catalytic domain
2	c3hrlA_	Alignment		99.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
3	d1cw0a_	Alignment		99.3	18	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
4	d1vsra_	Alignment		98.1	18	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
5	c4oq2A_	Alignment		96.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease pvurts1 i; **PDBTitle:** 5hmc specific restriction endonuclease pvurts1i
6	c4parC_	Alignment		96.1	22	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**uncharacterized protein abasi; **PDBTitle:** the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a2 complex with product-like dna
7	c6rdu2_	Alignment		95.7	12	**PDB header:**proton transport **Chain:** 2: **PDB Molecule:**asa-2: polytomella f-atp synthase associated subunit 2; **PDBTitle:** cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
8	c1zelA_	Alignment		81.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2827c; **PDBTitle:** crystal structure of rv2827c protein from mycobacterium tuberculosis
9	d1zela2	Alignment		74.9	19	**Fold:**Rv2827c C-terminal domain-like **Superfamily:**Rv2827c C-terminal domain-like **Family:**Rv2827c C-terminal domain-like
10	d1m0da_	Alignment		59.9	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
11	d2fcla1	Alignment		25.0	15	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like

12	c4ytkA_	Alignment		11.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** structure of the kow1-linker1 domain of transcription elongation2 factor spt5
13	d2fuka1	Alignment		11.2	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
14	d1tfea_	Alignment		10.7	10	**Fold:**EF-Ts domain-like **Superfamily:**Elongation factor Ts (EF-Ts), dimerisation domain **Family:**Elongation factor Ts (EF-Ts), dimerisation domain
15	c2hw2A_	Alignment		10.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
16	c4gqzB_	Alignment		9.5	22	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**putative periplasmic or exported protein; **PDBTitle:** crystal structure of s.cuep
17	d1jg5a_	Alignment		9.0	21	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
18	d2ieaa2	Alignment		7.0	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like PP module
19	d1ccwa_	Alignment		6.9	21	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
20	c5vrvA_	Alignment		6.4	13	**PDB header:**hydrolase,oxidoreductase **Chain:** A: **PDB Molecule:**protein regulated by acid ph; **PDBTitle:** 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
21	d7reqa2	Alignment	not modelled	5.7	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
22	c2qqdG_	Alignment	not modelled	5.5	14	**PDB header:**lyase **Chain:** G: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase (ec **PDBTitle:** n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
23	c3n53B_	Alignment	not modelled	5.5	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
24	c5xoxD_	Alignment	not modelled	5.3	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of trna(his) guanylyltranserase from saccharomyces2 cerevisiae