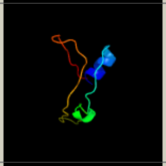
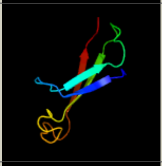
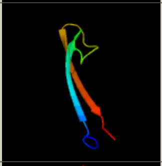
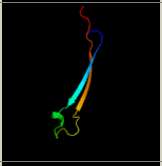
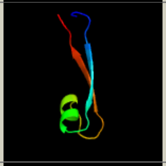
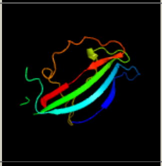
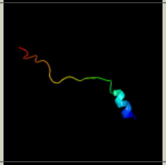
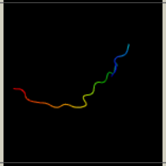
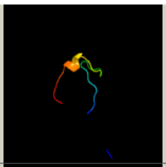
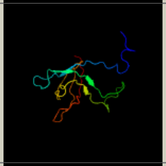
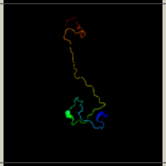
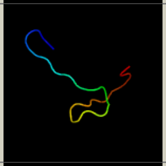
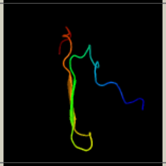
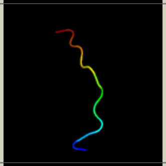
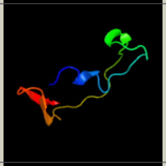
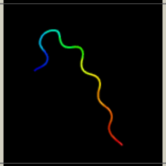
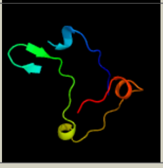
Phyre^{2}

Email	mdejesus@rockefeller.edu
Description	RVBD1926c_(mpt63)_2178964_2179443
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	ef52a856713e2637

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lmia_	Alignment		100.0	99	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Antigen MPT63/MPB63 (immunoprotective extracellular protein) **Family:**Antigen MPT63/MPB63 (immunoprotective extracellular protein)
2	c3cfuA_	Alignment		95.8	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus subtilis.2 northeast structural genomics consortium target sr562
3	c4r4gA_	Alignment		76.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative lipoprotein ycda; **PDBTitle:** crystal structure of a putative lipoprotein (ycda) from bacillus2 subtilis subsp. subtilis str. 168 at 2.62 a resolution
4	d1ix2a_	Alignment		74.6	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
5	c6nfqC_	Alignment		71.6	50	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**copc; **PDBTitle:** copc from pseudomonas fluorescens
6	c5icuA_	Alignment		69.2	35	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copc; **PDBTitle:** the crystal structure of copc from methylosinus trichosporium ob3b
7	d2c9qa1	Alignment		64.9	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
8	c4lesA_	Alignment		59.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein - conserved hypothetical; **PDBTitle:** 2.2 angstrom crystal structure of conserved hypothetical protein from2 bacillus anthracis.
9	c1avcA_	Alignment		35.7	41	**PDB header:**calcium/phospholipid-binding protein **Chain:** A: **PDB Molecule:**annexin vi; **PDBTitle:** bovine annexin vi (calcium-bound)
10	c4o3vA_	Alignment		35.2	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**virb8-like protein of type iv secretion system; **PDBTitle:** crystal structure of a virb8-like protein of type iv secretion system2 from rickettsia typhi
11	c5n1tM_	Alignment		26.5	35	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**copc; **PDBTitle:** crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus

12	d1wmxb_	Alignment		23.9	44	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
13	d1k0ha_	Alignment		23.6	17	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
14	c5az4A_	Alignment		18.9	15	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook subunit protein; **PDBTitle:** crystal structure of a 79kda fragment of flge, the hook protein from2 campylobacter jejuni
15	d1dmla2	Alignment		15.5	4	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
16	c6e8aA_	Alignment		15.0	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**duf1795 domain-containing protein; **PDBTitle:** crystal structure of dcrb from salmonella enterica at 1.92 angstroms2 resolution
17	c4r8aF_	Alignment		14.2	31	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of pafan1 - 5' flap dna complex
18	c2qp2A_	Alignment		13.1	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**unknown protein; **PDBTitle:** structure of a macpf/perforin-like protein
19	c2pr1B_	Alignment		12.9	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized n-acetyltransferase ylbp; **PDBTitle:** crystal structure of the bacillus subtilis n-acetyltransferase ylbp2 protein in complex with coenzyme-a
20	c5h9xA_	Alignment		12.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,3-glucanase; **PDBTitle:** crystal structure of gh family 64 laminaripentaose-producing beta-1,3-2 glucanase from paenibacillus barengoltzii
21	c3gqqD_	Alignment	not modelled	12.0	20	**PDB header:**splicing **Chain:** D: **PDB Molecule:**protein unc-119 homolog a; **PDBTitle:** crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
22	c2kykA_	Alignment	not modelled	10.7	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
23	c4m8aA_	Alignment	not modelled	10.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent zinc metalloprotease ftsh; **PDBTitle:** crystal structure of thermotoga maritima ftsh periplasmic domain
24	d1e88a3	Alignment	not modelled	9.7	27	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
25	d1dmla1	Alignment	not modelled	9.3	15	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
26	c6eorD_	Alignment	not modelled	8.4	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dipeptidyl peptidase 9; **PDBTitle:** dpp9 - 1g244
27	c1vw4V_	Alignment	not modelled	8.4	19	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**54s ribosomal protein l36, mitochondrial; **PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
28	d1ywka1	Alignment	not modelled	8.2	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like

29	d3dtub1	Alignment	not modelled	8.1	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
30	c4txvB_	Alignment	not modelled	7.7	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**cytochrome c oxidase subunit 2; **PDBTitle:** crystal structure of the mixed disulfide intermediate between2 thioredoxin-like tlpas(c110s) and subunit ii of cytochrome c oxidase3 coxbpd (c233s)
31	c5u6fA_	Alignment	not modelled	7.7	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**lpxtg-motif cell wall anchor domain protein; **PDBTitle:** bacterial adhesin from mobiluncus mulieris containing intramolecular2 disulfide, isopeptide, and ester bond cross-links (space group p21)
32	d1a6qa1	Alignment	not modelled	7.4	25	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
33	c4ribA_	Alignment	not modelled	7.3	31	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**fanconi-associated nuclease 1; **PDBTitle:** fan1 nuclease bound to 5' phosphorylated p(dt) single flap dna
34	c4g6vE_	Alignment	not modelled	7.2	19	**PDB header:**toxin **Chain:** E: **PDB Molecule:**adhesin/hemolysin; **PDBTitle:** cdia-ct/cdii toxin and immunity complex from burkholderia pseudomallei
35	d1iwla_	Alignment	not modelled	6.9	19	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**Outer-membrane lipoproteins carrier protein LolA
36	c2rttA_	Alignment	not modelled	6.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chic; **PDBTitle:** solution structure of the chitin-binding domain of chi18ac from2 streptomyces coelicolor
37	d3ehbb1	Alignment	not modelled	6.8	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
38	c1ymzA_	Alignment	not modelled	6.4	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
39	d1pf4a1	Alignment	not modelled	6.1	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
40	c2kt8A_	Alignment	not modelled	5.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable surface protein; **PDBTitle:** solution nmr structure of the cpe1231(468-535) protein from2 clostridium perfringens, northeast structural genomics3 consortium target cpr82b
41	d1w7ca3	Alignment	not modelled	5.8	35	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
42	d2ie7a1	Alignment	not modelled	5.8	53	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
43	d1nmva1	Alignment	not modelled	5.7	17	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
44	d1exha_	Alignment	not modelled	5.6	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
45	c6itcB_	Alignment	not modelled	5.6	42	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**translocating peptide; **PDBTitle:** structure of a substrate engaged seca-secy protein translocation2 machine
46	c4je3A_	Alignment	not modelled	5.5	43	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**central kinetochore subunit iml3; **PDBTitle:** an iml3-chl4 heterodimer links the core centromere to factors required2 for accurate chromosome segregation
47	c4lqzA_	Alignment	not modelled	5.4	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf4909 family protein (sav1798) from2 staphylococcus aureus subsp. aureus mu50 at 1.92 a resolution
48	d1v54b1	Alignment	not modelled	5.3	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
49	d1r2ja2	Alignment	not modelled	5.2	21	**Fold:**Acyl-CoA dehydrogenase NM domain-like **Superfamily:**Acyl-CoA dehydrogenase NM domain-like **Family:**Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains