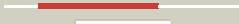
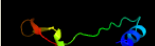
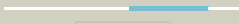




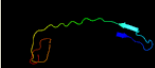

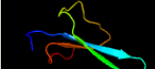

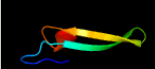



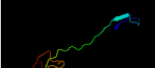

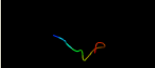




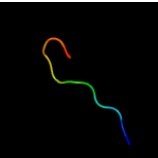
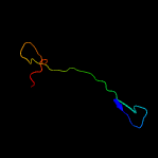

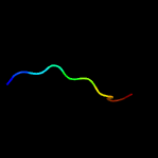
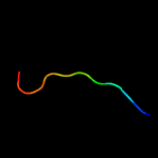
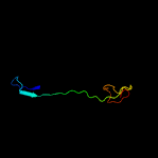

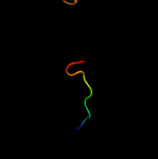
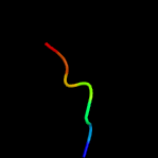


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1134 (-)_1261927_1262163
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	82f88a5c136add26

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s7ia_	 Alignment		98.5	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
2	c4pfeB_	 Alignment		31.1	33	PDB header: fluorescent protein Chain: B: PDB Molecule: green fluorescent protein; PDBTitle: crystal structure of vsfgfp-0
3	d1npha2	 Alignment		28.0	21	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Gelsolin-like
4	c6ce1A_	 Alignment		23.3	23	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-3; PDBTitle: crystal structure of peptidyl arginine deiminase type iii (padi3)
5	d1d0na5	 Alignment		20.5	23	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Gelsolin-like
6	c3f6hA_	 Alignment		16.9	28	PDB header: transferase Chain: A: PDB Molecule: alpha-isopropylmalate synthase; PDBTitle: crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
7	d1k28d1	 Alignment		16.5	43	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
8	c4n2gA_	 Alignment		16.2	25	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (d169a, 10 mm ca2+)
9	c2lcIA_	 Alignment		15.2	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator rfah; PDBTitle: solution structure of rfah carboxyterminal domain
10	d1nppa2	 Alignment		14.8	33	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
11	d2fh1a2	 Alignment		13.9	23	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Gelsolin-like

12	d1nz9a_	Alignment		12.9	33	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
13	c5hp5A_	Alignment		12.2	20	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-1; PDBTitle: srtucture of human peptidylarginine deiminase type i (pad1)
14	c1pdjF_	Alignment		11.5	43	PDB header: structural protein Chain: F: PDB Molecule: baseplate structural protein gp27; PDBTitle: fitting of gp27 into cryoem reconstruction of bacteriophage t42 baseplate
15	d1kr4a_	Alignment		11.3	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
16	d1vhfa_	Alignment		10.8	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
17	c4n2kA_	Alignment		10.5	25	PDB header: hydrolase Chain: A: PDB Molecule: protein-arginine deiminase type-2; PDBTitle: crystal structure of protein arginine deiminase 2 (q350a, 0 mm ca2+)
18	d1y60a_	Alignment		10.4	48	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Formaldehyde-activating enzyme, FAE
19	d1lukua_	Alignment		10.3	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
20	c6e2pC_	Alignment		9.7	71	PDB header: signaling protein Chain: C: PDB Molecule: leptin receptor; PDBTitle: structure of human jak2 ferm/sh2 in complex with leptin receptor
21	c2mi6A_	Alignment	not modelled	9.6	42	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
22	c6gdxA_	Alignment	not modelled	9.4	27	PDB header: metal binding protein Chain: A: PDB Molecule: periplasmic divalent cation tolerance protein; PDBTitle: structure of cuta from synechococcus elongatus pcc7942 complexed with2 3 molecules of bis-tris
23	c2jvvA_	Alignment	not modelled	9.3	42	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
24	c2kvqG_	Alignment	not modelled	9.3	42	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
25	d1p1la_	Alignment	not modelled	8.9	36	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
26	c5iiaH_	Alignment	not modelled	8.5	22	PDB header: cell adhesion Chain: H: PDB Molecule: vitelline envelope sperm lysin receptor; PDBTitle: crystal structure of red abalone egg ver1 repeat 3 in complex with2 sperm lysin at 1.7 a resolution (crystal form i)
27	c3n70F_	Alignment	not modelled	8.1	54	PDB header: transport protein Chain: F: PDB Molecule: transport activator; PDBTitle: the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
28	c1m1gB_	Alignment	not modelled	8.1	33	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2

					substance g (nusc), space group p2(1)
29	d1tg7a2	Alignment	not modelled	8.0	32 Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Beta-galactosidase LacA, domains 4 and 5
30	d2evra1	Alignment	not modelled	7.3	63 Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: Spr N-terminal domain-like
31	d1svya_	Alignment	not modelled	7.2	20 Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Gelsolin-like
32	c2xk0A_	Alignment	not modelled	6.9	31 PDB header: transcription Chain: A: PDB Molecule: polycomb protein pcl; PDBTitle: solution structure of the tudor domain from drosophila2 polycomblike (pcl)
33	d1sr9a3	Alignment	not modelled	6.8	32 Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
34	c5c2uA_	Alignment	not modelled	6.7	50 PDB header: transport protein Chain: A: PDB Molecule: nup54; PDBTitle: ferredoxin-like domain of nucleoporin nup54 bound to a nanobody
35	d1vtxa_	Alignment	not modelled	6.3	45 Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
36	c2zomC_	Alignment	not modelled	6.2	55 PDB header: unknown function Chain: C: PDB Molecule: protein cuta, chloroplast, putative, expressed; PDBTitle: crystal structure of cuta1 from oryza sativa
37	d1d1la_	Alignment	not modelled	6.1	32 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
38	c4e98C_	Alignment	not modelled	6.1	18 PDB header: signaling protein Chain: C: PDB Molecule: cuta1 divalent ion tolerance protein; PDBTitle: crystal structure of possible cuta1 divalent ion tolerance protein2 from cryptosporidium parvum iowa ii
39	c2ql8A_	Alignment	not modelled	6.0	21 PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
40	c1xk8A_	Alignment	not modelled	6.0	27 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: divalent cation tolerant protein cuta; PDBTitle: divalent cation tolerant protein cuta from homo sapiens o60888
41	d2zfha1	Alignment	not modelled	6.0	27 Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
42	c2zfha_	Alignment	not modelled	5.9	27 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cuta; PDBTitle: crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
43	c4za1A_	Alignment	not modelled	5.9	67 PDB header: transferase Chain: A: PDB Molecule: nosa; PDBTitle: crystal structure of nosa involved in nosiheptide biosynthesis
44	d1naqa_	Alignment	not modelled	5.2	36 Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
45	d4croa_	Alignment	not modelled	5.2	34 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors