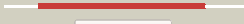

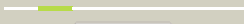








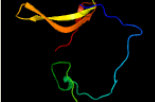







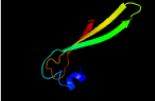

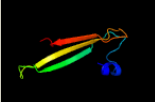



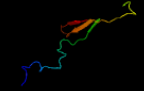
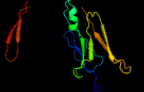
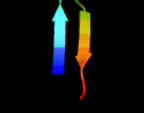
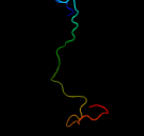








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3169_(-)_3537235_3538359
Date	Thu Aug 8 16:20:35 BST 2019
Unique Job ID	a57fda94982ed091

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2icha1	 Alignment		100.0	18	Fold: AttH-like Superfamily: AttH-like Family: AttH-like
2	c1cyjB_	 Alignment		62.3	16	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
3	c2v5iA_	 Alignment		45.0	62	PDB header: viral protein Chain: A: PDB Molecule: salmonella typhimurium db7155 bacteriophage det7 tailspike; PDBTitle: structure of the receptor-binding protein of bacteriophage det7: a2 podoviral tailspike in a myovirus
4	d1tywa_	 Alignment		38.4	62	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: P22 tailspike protein
5	c3riqA_	 Alignment		37.0	58	PDB header: viral protein Chain: A: PDB Molecule: tailspike protein; PDBTitle: siphovirus 9na tailspike receptor binding domain
6	c5lc0B_	 Alignment		34.9	22	PDB header: hydrolase Chain: B: PDB Molecule: ns2b-ns3 protease,ns2b-ns3 protease; PDBTitle: crystal structure of zika virus ns2b-ns3 protease in complex with a2 boronate inhibitor
7	c4qsgA_	 Alignment		34.4	18	PDB header: structural protein Chain: A: PDB Molecule: gas vesicle protein; PDBTitle: crystal structure of gas vesicle protein gvpf from microcystis2 aeruginosa
8	c2xc1A_	 Alignment		30.9	62	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional tail protein; PDBTitle: full-length tailspike protein mutant y108w of bacteriophage p22
9	c1h2iG_	 Alignment		21.3	23	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad52 homolog; PDBTitle: human rad52 protein, n-terminal domain
10	d2ea9a1	 Alignment		18.7	22	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
11	d2h28a1	 Alignment		17.5	18	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like

12	c5xf9F_	Alignment		16.2	29	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
13	d1kn0a_	Alignment		15.9	23	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: The homologous-pairing domain of Rad52 recombinase
14	d2inwa1	Alignment		14.7	18	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
15	c3j6vE_	Alignment		14.3	25	PDB header: ribosome Chain: E: PDB Molecule: 28s ribosomal protein s5, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
16	c5izrC_	Alignment		13.6	26	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: cytosolic phospholipase a2 delta; PDBTitle: human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride
17	c4g6tB_	Alignment		12.6	36	PDB header: chaperone Chain: B: PDB Molecule: type iii effector hopa1; PDBTitle: structure of the hopa1-scha chaperone-effector complex
18	c4k15A_	Alignment		8.3	20	PDB header: unknown function Chain: A: PDB Molecule: lmo2686 protein; PDBTitle: 2.75 angstrom crystal structure of hypothetical protein lmo2686 from2 listeria monocytogenes egd-e
19	c2z5dA_	Alignment		6.8	14	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 h; PDBTitle: human ubiquitin-conjugating enzyme e2 h
20	c6c23C_	Alignment		6.6	30	PDB header: gene regulation Chain: C: PDB Molecule: histone-lysine n-methyltransferase ezh2; PDBTitle: cryo-em structure of prc2 bound to cofactors aebp2 and jarid2 in the2 compact active state
21	c1ywke_	Alignment	not modelled	6.2	31	PDB header: isomerase Chain: E: PDB Molecule: 4-deoxy-l-threo-5-hexosulose-uronate ketol- PDBTitle: crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
22	d1xrua1	Alignment	not modelled	5.9	38	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Kdul-like
23	c2k7qA_	Alignment	not modelled	5.8	13	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: filamin a ig-like domains 18-19
24	d1ywka1	Alignment	not modelled	5.7	31	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Kdul-like
25	c5a52A_	Alignment	not modelled	5.7	14	PDB header: lipid binding protein Chain: A: PDB Molecule: calcium-dependent lipid-binding domain-containing protein; PDBTitle: the crystal structure of arabidopsis thaliana car1 in2 complex with one calcium ion
26	d1pkpa2	Alignment	not modelled	5.4	41	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
27	c1yx3A_	Alignment	not modelled	5.4	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrc; PDBTitle: nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
28	d2gria1	Alignment	not modelled	5.4	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: NSP3A-like Family: NSP3A-like

29	c2dylA	 Alignment	not modelled	5.3	21	PDB header: transferase Chain: A: PDB Molecule: dual specificity mitogen-activated protein kinase2 kinase 7 activated mutant (s287d, t291d)
30	d2cjsa1	 Alignment	not modelled	5.3	9	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
31	d2hjqa2	 Alignment	not modelled	5.2	27	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: YqbF N-terminal domain-like
32	d2cjta1	 Alignment	not modelled	5.0	9	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)