

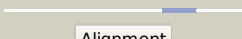
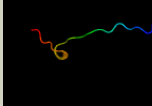
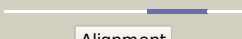
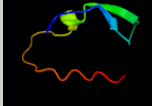

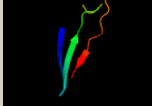





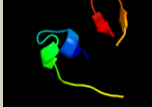


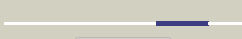
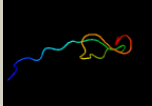

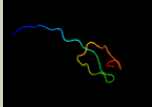


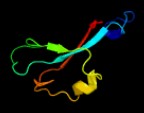


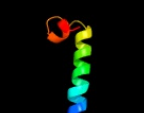



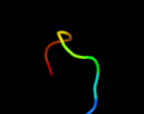


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3747_(-)_4196902_4197285
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	614f9702c783b084

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zjnA_	 Alignment		70.7	36	PDB header: transport protein Chain: A: PDB Molecule: portal protein; PDBTitle: crystal structure of the bacteriophage g20c portal protein
2	c3gasA_	 Alignment		21.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
3	d1pn0a2	 Alignment		16.8	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
4	c4knbE_	 Alignment		9.6	18	PDB header: transcription/replication Chain: E: PDB Molecule: uncharacterized protein spt16d; PDBTitle: structure of the spt16d pob3n heterodimer
5	c4b4rA_	 Alignment		9.1	62	PDB header: cell adhesion Chain: A: PDB Molecule: f18 fimbrial adhesin ac; PDBTitle: crystal structure of the lectin domain of f18 fimbrial2 adhesin fedf in complex with blood group b type 13 hexasaccharide
6	c3fkaD_	 Alignment		8.9	26	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized ntf-2 like protein; PDBTitle: crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
7	d1c4ka3	 Alignment		8.1	36	Fold: Ornithine decarboxylase C-terminal domain Superfamily: Ornithine decarboxylase C-terminal domain Family: Ornithine decarboxylase C-terminal domain
8	d2b1ya1	 Alignment		7.9	21	Fold: Atu1913-like Superfamily: Atu1913-like Family: Atu1913-like
9	d1zcca1	 Alignment		7.7	28	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
10	c5vugA_	 Alignment		7.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rv2277c; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 domain of uncharacterized protein rv2277c from mycobacterium3 tuberculosis
11	c5bjuA_	 Alignment		6.9	50	PDB header: membrane protein Chain: A: PDB Molecule: wlal protein; PDBTitle: x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)

12	d1wxaa1	Alignment		6.8	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
13	c2kxjA_	Alignment		6.2	50	PDB header: protein binding Chain: A: PDB Molecule: ubx domain-containing protein 4; PDBTitle: solution structure of ubx domain of human ubxd2 protein
14	c2ki8A_	Alignment		6.2	28	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
15	c5edlA_	Alignment		5.9	26	PDB header: transport protein Chain: A: PDB Molecule: putative hmp/thiamine permease protein ykoe; PDBTitle: crystal structure of an s-component of ecf transporter
16	c4d0uD_	Alignment		5.7	41	PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the atadenovirus snake2 adenovirus 1, selenomethionine-derivative
17	c6cj6B_	Alignment		5.6	22	PDB header: viral protein Chain: B: PDB Molecule: protein f9; PDBTitle: structure of the poxvirus protein f9
18	c6d10A_	Alignment		5.6	28	PDB header: cell adhesion Chain: A: PDB Molecule: alginate biosynthesis protein algf; PDBTitle: cs-rosetta determined structures of the c-terminal domain of algf from2 p. aeruginosa
19	d1aiwa_	Alignment		5.3	33	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain

20 [d1cb8a2](#)

Alignment



5.3

22

Fold: Hyaluronate lyase-like, C-terminal domain
Superfamily: Hyaluronate lyase-like, C-terminal domain
Family: Hyaluronate lyase-like, C-terminal domain