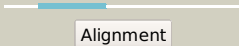





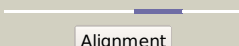

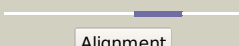
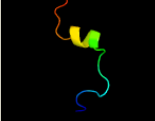
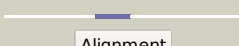

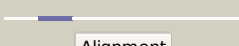




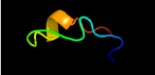

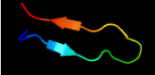

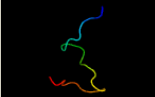

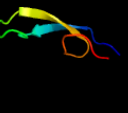
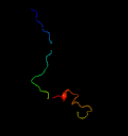

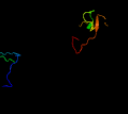
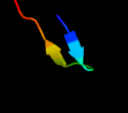





Phyre2





Email mdejesus@rockefeller.edu
 Description RVBD3136A_(RVBD3136A)_3502942_3503274
 Date Thu Aug 8 16:20:32 BST 2019
 Unique Job ID ccf17a9fb3c91aa8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h9iB_	 Alignment		39.5	26	PDB header: rna binding protein Chain: B; PDB Molecule: csf5; PDBTitle: csf5, crispr-cas type iv cas6 crrna endonuclease
2	d1okga3	 Alignment		33.6	34	Fold: FKBP-like Superfamily: FKBP-like Family: 3-mercaptopyruvate sulfurtransferase, C-terminal domain
3	c5v2sA_	 Alignment		16.6	17	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
4	c1nh1A_	 Alignment		15.1	26	PDB header: avirulence protein Chain: A; PDB Molecule: avirulence b protein; PDBTitle: crystal structure of the type iii effector avrb from2 pseudomonas syringae.
5	d1nh1a_	 Alignment		15.1	26	Fold: Antivirulence factor Superfamily: Antivirulence factor Family: Antivirulence factor
6	d1wvna1	 Alignment		14.9	22	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
7	c3sokB_	 Alignment		14.3	33	PDB header: cell adhesion Chain: B; PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
8	d1j4wa1	 Alignment		12.8	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
9	d1pama1	 Alignment		12.6	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
10	d2ctea1	 Alignment		11.9	37	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
11	c1okgA_	 Alignment		11.5	42	PDB header: transferase Chain: A; PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major

12	c4c47B_	Alignment		11.5	41	PDB header: cell adhesion Chain: B: PDB Molecule: inner membrane lipoprotein; PDBTitle: salmonella enterica trimeric lipoprotein sadb
13	c1gycA_	Alignment		11.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: laccase 2; PDBTitle: crystal structure determination at room temperature of a laccase from <i>Trametes versicolor</i> in its oxidised form containing a full complement of copper ions
14	d1el6a_	Alignment		11.1	26	Fold: Baseplate structural protein gp11 Superfamily: Baseplate structural protein gp11 Family: Baseplate structural protein gp11
15	c2x1kB_	Alignment		10.7	14	PDB header: hydrolase/rna Chain: B: PDB Molecule: csy4 endoribonuclease; PDBTitle: crystal structure of the csy4-crrna complex, orthorhombic form
16	c6j0mC_	Alignment		10.5	20	PDB header: protein transport Chain: C: PDB Molecule: pvc8; PDBTitle: cryo-em structure of an extracellular contractile injection system, 2 pvc baseplate in extended state (reconstructed with c3 symmetry)
17	c2wj7D_	Alignment		10.4	42	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alpha crystallin
18	d2ctda1	Alignment		9.1	31	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
19	d1tj1a1	Alignment		9.1	57	Fold: N-terminal domain of bifunctional PutA protein Superfamily: N-terminal domain of bifunctional PutA protein Family: N-terminal domain of bifunctional PutA protein
20	c6k4fU_	Alignment		8.9	38	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa
21	c5craB_	Alignment	not modelled	7.9	55	PDB header: hydrolase Chain: B: PDB Molecule: sdea; PDBTitle: structure of the sdea dub domain
22	d2pila_	Alignment	not modelled	7.9	22	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
23	c2hh3A_	Alignment	not modelled	7.8	17	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the third kh domain of ksrp
24	d3bmva1	Alignment	not modelled	7.7	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
25	c1v10A_	Alignment	not modelled	7.6	28	PDB header: oxidase Chain: A: PDB Molecule: laccase; PDBTitle: structure of rigidoporus lignosus laccase from hemihedrally 2 twinned crystals
26	d2ctma1	Alignment	not modelled	7.5	31	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
27	c5dgoA_	Alignment	not modelled	7.3	32	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 45 homolog; PDBTitle: crystal structure of cell division cycle protein 45 (cdc45)
28	c3kdpG_	Alignment	not modelled	7.0	18	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
29	c3kdpH_	Alignment	not modelled	7.0	18	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript

29	c3kupr1	Alignment	not modelled	7.0	10	variant a; PDB header: crystal structure of the sodium-potassium pump
30	c3lq9B	Alignment	not modelled	6.9	15	PDB header: signaling protein Chain: B; PDB Molecule: dna-damage-inducible transcript 4 protein; PDBTitle: crystal structure of human redd1, a hypoxia-induced regulator of mtor
31	d1x4na1	Alignment	not modelled	6.9	11	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
32	d2nsfa2	Alignment	not modelled	6.9	30	Fold: SCP-like Superfamily: SCP-like Family: Microthiol-dependent maleylpyruvate isomerase C-terminal domain-like
33	c3hj2B	Alignment	not modelled	6.8	27	PDB header: antimicrobial protein Chain: B; PDB Molecule: human neutrophil peptide 1; PDBTitle: crystal structure of covalent dimer of hnp1
34	c4hqjG	Alignment	not modelled	6.7	18	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
35	c2jp3A	Alignment	not modelled	6.6	29	PDB header: transcription Chain: A; PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
36	c3qphA	Alignment	not modelled	6.5	14	PDB header: transcription Chain: A; PDB Molecule: trmb, a global transcription regulator; PDBTitle: the three-dimensional structure of trmb, a global transcriptional2 regulator of the hyperthermophilic archaeon pyrococcus furiosus in3 complex with sucrose
37	c2m7gA	Alignment	not modelled	6.3	28	PDB header: cell adhesion, structural protein, elect Chain: A; PDB Molecule: geopilin domain 1 protein; PDBTitle: structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
38	c6nbxG	Alignment	not modelled	6.3	20	PDB header: oxidoreductase Chain: G; PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
39	c5m73H	Alignment	not modelled	6.3	46	PDB header: rna binding protein Chain: H; PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
40	d2axya1	Alignment	not modelled	6.2	21	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
41	c4hqjE	Alignment	not modelled	6.1	18	PDB header: hydrolase/transport protein Chain: E; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
42	c2qdjA	Alignment	not modelled	6.1	18	PDB header: antitumor protein Chain: A; PDB Molecule: retinoblastoma-associated protein; PDBTitle: crystal structure of the retinoblastoma protein n-domain2 provides insight into tumor suppression, ligand3 interaction and holoprotein architecture
43	c6rbkC	Alignment	not modelled	6.1	22	PDB header: virus like particle Chain: C; PDB Molecule: afp8; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate in2 extended state, 3-fold symmetrised
44	c2wmmA	Alignment	not modelled	6.0	11	PDB header: cell cycle Chain: A; PDB Molecule: chromosome partition protein mukb; PDBTitle: crystal structure of the hinge domain of mukb
45	c5b0uB	Alignment	not modelled	6.0	42	PDB header: luminescent protein Chain: B; PDB Molecule: oplophorus-luciferin 2-monoxygenase catalytic subunit; PDBTitle: crystal structure of the mutated 19 kda protein of oplophorus2 luciferase (nanokaz)
46	c2jo1A	Alignment	not modelled	5.8	24	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
47	c5wdaL	Alignment	not modelled	5.8	33	PDB header: protein transport Chain: L; PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
48	d1khma	Alignment	not modelled	5.7	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
49	d1oqwa	Alignment	not modelled	5.6	28	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
50	c5m8bB	Alignment	not modelled	5.6	27	PDB header: hydrolase Chain: B; PDB Molecule: alpha-l-arabinofuranosidase ii; PDBTitle: crystal structure of alpha-l-arabinofuranosidase from lactobacillus2 brevis
51	d1zka1	Alignment	not modelled	5.6	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
52	c5xf9E	Alignment	not modelled	5.6	24	PDB header: oxidoreductase Chain: E; PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
53	d1y7ba2	Alignment	not modelled	5.5	22	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
54	d1cgtal	Alignment	not modelled	5.4	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes

55	c2fugA_	 Alignment	not modelled	5.4	24	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
56	c3uv0B_	 Alignment	not modelled	5.1	28	PDB header: protein binding Chain: B; PDB Molecule: mutator 2, isoform b; PDBTitle: crystal structure of the drosophila mu2 fha domain
57	d1cyga1	 Alignment	not modelled	5.1	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
58	c5lc5F_	 Alignment	not modelled	5.1	24	PDB header: oxidoreductase Chain: F; PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2