



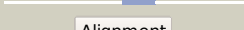

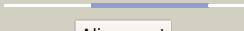




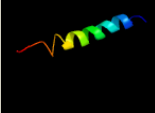




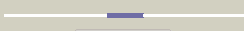
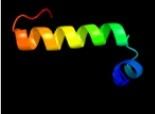

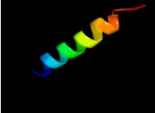




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2240c (-) _2511698_2512288
Date	Mon Aug 5 13:25:37 BST 2019
Unique Job ID	23d88115694f9935

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ke3A_	 Alignment		44.3	19	PDB header: hydrolase Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsq sorting domain in chaps
2	c2kdtA_	 Alignment		41.4	19	PDB header: protein transport Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsq sorting domain structure in dpc
3	c3k3wA_	 Alignment		25.3	29	PDB header: hydrolase Chain: A: PDB Molecule: penicillin g acylase; PDBTitle: thermostable penicillin g acylase from alcaligenes faecalis in2 orthorhombic form
4	c5h5mA_	 Alignment		25.0	10	PDB header: cell adhesion Chain: A: PDB Molecule: alpha-catenin-like protein hmp-1; PDBTitle: crystal structure of hmp-1 m domain
5	d1wiia_	 Alignment		21.1	19	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
6	c5fhya_	 Alignment		19.4	10	PDB header: structural protein Chain: A: PDB Molecule: b-type flagellar hook-associated protein 2; PDBTitle: crystal structure of flid (hap2) from pseudomonas aeruginosa pao1
7	c4c9yB_	 Alignment		17.7	10	PDB header: cell cycle Chain: B: PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex
8	c2lycA_	 Alignment		17.6	15	PDB header: protein binding Chain: A: PDB Molecule: spindle and kinetochore-associated protein 1 homolog; PDBTitle: structure of c-terminal domain of ska1
9	c2lfcA_	 Alignment		16.4	6	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit; PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
10	c2zxeG_	 Alignment		15.5	14	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+-pi2 state
11	c5xogM_	 Alignment		15.4	25	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor 1 homolog; PDBTitle: rna polymerase ii elongation complex bound with spt5 kow5 and elf1

12	c6d6rL_	Alignment		14.6	29	PDB header: hydrolase Chain: L: PDB Molecule: m-phase phosphoprotein 6; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
13	c6d6qL_	Alignment		14.6	29	PDB header: hydrolase Chain: L: PDB Molecule: m-phase phosphoprotein 6; PDBTitle: human nuclear exosome-mtr4 rna complex - overall reconstruction
14	c2mmpA_	Alignment		13.3	19	PDB header: ribosomal protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a ribosomal protein
15	d1st6a5	Alignment		13.0	26	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
16	c2kt5B_	Alignment		12.9	55	PDB header: rna binding protein / viral protein Chain: B: PDB Molecule: icp27; PDBTitle: rrm domain of mrna export adaptor ref2-i bound to hsv-1 icp27 peptide
17	d2asxa1	Alignment		10.4	9	Fold: HAMP domain-like Superfamily: HAMP domain-like Family: HAMP domain
18	d1d4ca3	Alignment		9.1	16	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
19	c5fimA_	Alignment		8.2	8	PDB header: unknown function Chain: A: PDB Molecule: ygau; PDBTitle: the structure of kbp.k from e. coli
20	d2ihoA2	Alignment		7.9	41	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: MOA C-terminal domain-like
21	c2jp3A_	Alignment	not modelled	7.8	17	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
22	c2k9yA_	Alignment	not modelled	7.4	35	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
23	c2k9yB_	Alignment	not modelled	7.4	35	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
24	c4odaC_	Alignment	not modelled	7.4	36	PDB header: hydrolase/replication Chain: C: PDB Molecule: dna polymerase processivity factor component a20; PDBTitle: crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
25	c4odaD_	Alignment	not modelled	7.4	36	PDB header: hydrolase/replication Chain: D: PDB Molecule: dna polymerase processivity factor component a20; PDBTitle: crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
26	c2ihoA_	Alignment	not modelled	7.2	41	PDB header: sugar binding protein Chain: A: PDB Molecule: lectin; PDBTitle: crystal structure of moa, a lectin from the mushroom marasmius oreades2 in complex with the trisaccharide gal(1,3)gal(1,4)glnac
27	c2m7xA_	Alignment	not modelled	6.8	50	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: structural and functional analysis of transmembrane segment iv of the2 salt tolerance protein sod2 PDB header: structural protein

28	c5h5vC_	Alignment	not modelled	6.7	10	Chain: C: PDB Molecule: flagellar hook-associated protein 2; PDBTitle: crystal structure of the flagellar cap protein flid d1-d2-d3 domains2 from escherichia coli
29	d1b3ta_	Alignment	not modelled	6.6	41	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
30	c5o1mA_	Alignment	not modelled	6.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: rubber oxygenase; PDBTitle: structure of latex clearing protein lcp in the closed state
31	c3phzA_	Alignment	not modelled	6.0	35	PDB header: sugar binding protein Chain: A: PDB Molecule: ricin b-related lectin; PDBTitle: crystal structure analysis of polyporus squamosus lectin bound to2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
32	d1sj7a1	Alignment	not modelled	5.9	14	Fold: A middle domain of Talin 1 Superfamily: A middle domain of Talin 1 Family: A middle domain of Talin 1
33	d1y0pa3	Alignment	not modelled	5.8	6	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
34	c5tw9D_	Alignment	not modelled	5.4	13	PDB header: lipid-binding protein Chain: D: PDB Molecule: iron uptake system component efeo; PDBTitle: 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
35	d1zeeA1	Alignment	not modelled	5.4	29	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
36	c2xrhA_	Alignment	not modelled	5.3	6	PDB header: unknown function Chain: A: PDB Molecule: protein hp0721; PDBTitle: crystal structure of the truncated form of hp0721
37	c2zqpE_	Alignment	not modelled	5.2	50	PDB header: protein transport Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of secey translocon from thermus2 thermophilus
38	c2zjsE_	Alignment	not modelled	5.2	50	PDB header: protein transport/immune system Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: crystal structure of secey translocon from thermus thermophilus with a2 fab fragment
39	c2yskA_	Alignment	not modelled	5.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha1432; PDBTitle: crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus