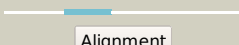
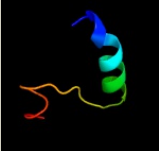
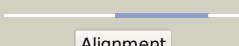

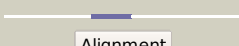
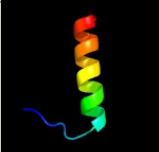
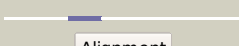
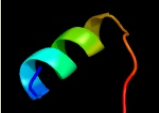







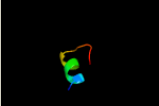

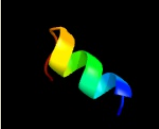

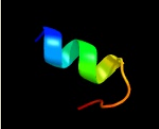






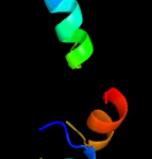
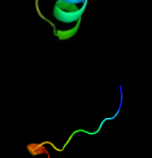

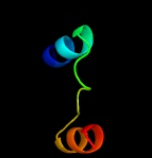
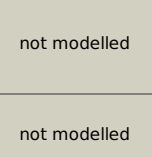


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3354 (-)_3769282_3769671
Date	Thu Aug 8 16:20:56 BST 2019
Unique Job ID	f1b1a1d65b06167c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2csua3	 Alignment		31.0	22	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
2	c6c3rB_	 Alignment		27.2	14	PDB header: viral protein Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
3	d1mkea1	 Alignment		19.5	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
4	c5uqda_	 Alignment		15.5	35	PDB header: oxidoreductase Chain: A: PDB Molecule: dummy; shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
5	c2ifsA_	 Alignment		11.6	22	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
6	c1vjqaB_	 Alignment		10.8	16	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
7	d1zara1	 Alignment		9.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rio2 serine protein kinase N-terminal domain
8	c2lweA_	 Alignment		9.2	13	PDB header: signaling protein Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: solution structure of mutant (t170e) second card of human rig-i
9	c4rl6A_	 Alignment		8.1	43	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04l03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
10	c4inaA_	 Alignment		7.9	36	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolfinella2 succinogenes. northeast structural genomics consortium target wsr35
11	d1xoda1	 Alignment		7.5	23	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)

12	c5tchG_	Alignment		7.5	36	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
13	c2hjmB_	Alignment		7.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein pf1176; PDBTitle: crystal structure of a singleton protein pf1176 from p. furiosus
14	c3ss4C_	Alignment		6.7	44	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
15	c5k9xA_	Alignment		6.6	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
16	d2j9ga2	Alignment		6.5	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
17	d1ulza2	Alignment		6.2	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
18	c4ph2A_	Alignment		6.0	46	PDB header: viral protein Chain: A: PDB Molecule: blv capsid - n-terminal domain; PDBTitle: mature n-terminal domain of capsid protein from bovine leukemia virus
19	c6a0aA_	Alignment		5.8	50	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
20	d1eucb1	Alignment		5.7	19	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
21	c1pemA_	Alignment	not modelled	5.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 2 alpha PDBTitle: ribonucleotide reductase protein r1e from salmonella2 typhimurium
22	c5dggB_	Alignment	not modelled	5.7	36	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
23	c2v75A_	Alignment	not modelled	5.6	13	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
24	c6a0aB_	Alignment	not modelled	5.4	50	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
25	c6a0aC_	Alignment	not modelled	5.4	50	PDB header: structural protein Chain: C: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
26	c6cgmA_	Alignment	not modelled	5.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: x-ray crystal structure of bacillus subtilis ribonucleotide reductase2 nrde alpha subunit (nucleotide free)
27	c5us3A_	Alignment	not modelled	5.3	75	PDB header: de novo protein Chain: A: PDB Molecule: heterogeneous-backbone variant of the sp1-3 zinc finger: n- PDBTitle: heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger
28	d1w2za3	Alignment	not modelled	5.1	22	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region

29	d1a6qa1	Alignment	not modelled	5.0	45	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
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