

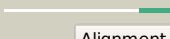
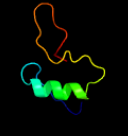













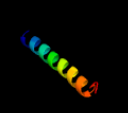

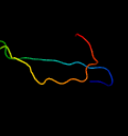



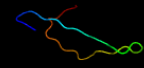
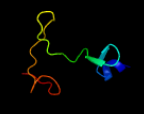

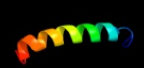
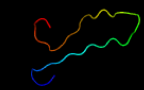





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2599_(-)_2927487_2927918
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	271adefbd37b61e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1veha_	 Alignment		45.8	20	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
2	c3fhkF_	 Alignment		43.8	31	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
3	d1th5a1	 Alignment		43.0	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
4	c2jnvA_	 Alignment		35.9	21	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
5	c6f0kA_	 Alignment		29.0	19	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
6	d3bmva3	 Alignment		27.4	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
7	d1pama3	 Alignment		27.0	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
8	d1cyga3	 Alignment		23.8	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
9	c5vhxE_	 Alignment		23.7	21	PDB header: transport protein Chain: E: PDB Molecule: glutamate receptor 2,germ cell-specific gene 1-like PDBTitle: glua2-1xgsg1I bound to zk
10	d1qhoa3	 Alignment		22.2	18	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
11	d1xhja_	 Alignment		18.7	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like

12	c6f46A_	Alignment		18.7	26	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs
13	d1cxa3	Alignment		18.5	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
14	c5mrwG_	Alignment		17.4	27	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpfabc complex
15	c2z51A_	Alignment		16.4	19	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 2, chloroplast; PDBTitle: crystal structure of arabidopsis cnfu involved in iron-sulfur cluster2 biosynthesis
16	c5ir6C_	Alignment		16.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
17	d1cgt3	Alignment		15.8	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
18	c4xydB_	Alignment		14.8	24	PDB header: oxidoreductase Chain: B: PDB Molecule: norc-like protein; PDBTitle: nitric oxide reductase from roseobacter denitrificans (rdnor)
19	c4akaA_	Alignment		14.2	34	PDB header: immune system Chain: A: PDB Molecule: il-4-inducing protein; PDBTitle: ipse alpha-1, an ige-binding crystallin
20	c1ifpA_	Alignment		14.0	46	PDB header: virus Chain: A: PDB Molecule: major coat protein assembly; PDBTitle: inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
21	c5doqC_	Alignment	not modelled	14.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
22	c2jp3A_	Alignment	not modelled	13.5	28	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
23	d1qm4a1	Alignment	not modelled	13.4	20	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
24	c5hhIA_	Alignment	not modelled	13.3	13	PDB header: rna binding protein Chain: A: PDB Molecule: retron-type reverse transcriptase; PDBTitle: reverse transcriptase domain of group ii intron maturase from2 eubacterium rectale in p21 space group
25	d1mxaa1	Alignment	not modelled	12.9	28	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
26	c2zzeG_	Alignment	not modelled	12.7	32	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
27	d2p02a1	Alignment	not modelled	12.3	20	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
28	c3o0rC_	Alignment	not modelled	12.1	14	PDB header: immune system/oxidoreductase Chain: C: PDB Molecule: nitric oxide reductase subunit c; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment

29	c2jo1A	Alignment	not modelled	11.9	22	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
30	d1qhxa	Alignment	not modelled	11.6	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Chloramphenicol phosphotransferase
31	d3pmga3	Alignment	not modelled	11.4	13	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
32	c6qt9Y	Alignment	not modelled	11.3	22	PDB header: virus Chain: Y: PDB Molecule: orf 31; PDBTitle: cryo-em structure of sh1 full particle.
33	c3pesA	Alignment	not modelled	11.2	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein gp49; PDBTitle: crystal structure of uncharacterized protein from pseudomonas phage2 yua
34	c2e76D	Alignment	not modelled	11.1	13	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
35	d2etna2	Alignment	not modelled	10.6	13	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
36	c2r9qD	Alignment	not modelled	9.9	16	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
37	c2eqjA	Alignment	not modelled	9.8	19	PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
38	c2mkvA	Alignment	not modelled	9.3	16	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
39	c2mc7A	Alignment	not modelled	8.9	17	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgrtr
40	c3fhoB	Alignment	not modelled	8.9	17	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase dbp5; PDBTitle: structure of s. pombe dbp5
41	d1jmx1	Alignment	not modelled	7.7	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
42	d1y4oa1	Alignment	not modelled	7.3	35	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
43	c2hxyC	Alignment	not modelled	6.3	17	PDB header: hydrolase Chain: C: PDB Molecule: probable atp-dependent rna helicase ddx48; PDBTitle: crystal structure of human apo-eif4aiii
44	c3iwdC	Alignment	not modelled	6.3	19	PDB header: lyase Chain: C: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with 5'-deoxy-5'-dimethyl thioadenosine
45	c5iv1A	Alignment	not modelled	6.1	17	PDB header: hydrolase Chain: A: PDB Molecule: dead-box atp-dependent rna helicase csha; PDBTitle: csha helicase
46	d1grja2	Alignment	not modelled	6.1	22	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
47	d1tqza1	Alignment	not modelled	5.8	41	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Necap1 N-terminal domain-like
48	d1pbya1	Alignment	not modelled	5.8	9	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
49	c2v9kA	Alignment	not modelled	5.7	27	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein flj32312; PDBTitle: crystal structure of human pus10, a novel pseudouridine2 synthase.
50	c4ct4B	Alignment	not modelled	5.6	19	PDB header: rna binding protein Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx6; PDBTitle: cnot1 mif4g domain - ddx6 complex
51	c6ohkA	Alignment	not modelled	5.5	11	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of fusobacterium nucleatum flavodoxin mutant k13g2 bound to flavin mononucleotide
52	c1s2mA	Alignment	not modelled	5.5	19	PDB header: rna binding protein Chain: A: PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p
53	c1xtkA	Alignment	not modelled	5.4	6	PDB header: gene regulation Chain: A: PDB Molecule: probable atp-dependent rna helicase p47; PDBTitle: structure of decd to dead mutation of human uap56
54	d2f23a2	Alignment	not modelled	5.2	14	Fold: FKBP-like Superfamily: FKBP-like

