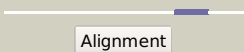

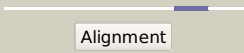

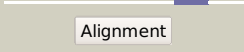





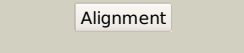

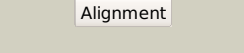



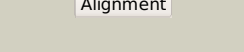

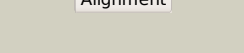

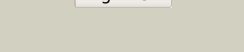
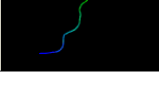


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0076c_(-)_85180_85569
Date	Tue Jul 23 14:50:11 BST 2019
Unique Job ID	7b3c7a2ac713d0ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pcqX_	 Alignment		19.6	33	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i 4.8k protein; PDBTitle: femtosecond x-ray protein nanocrystallography
2	c4fe1X_	 Alignment		19.4	35	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i 4.8k protein; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution
3	d1jb0X_	 Alignment		19.2	33	Fold: Single transmembrane helix Superfamily: Subunit PsaX of photosystem I reaction centre Family: Subunit PsaX of photosystem I reaction centre
4	c1jb0X_	 Alignment		19.2	33	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i subunit psax; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
5	c2n4nA_	 Alignment		13.7	54	PDB header: de novo protein Chain: A: PDB Molecule: designed beta sheet; PDBTitle: nmr structure for a 3-stranded parallel beta-sheet
6	c4hbzA_	 Alignment		12.5	20	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartita.
7	c2yn0A_	 Alignment		11.7	20	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
8	c3eozB_	 Alignment		11.3	14	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
9	c1vryA_	 Alignment		11.3	29	PDB header: membrane protein Chain: A: PDB Molecule: glycine receptor alpha-1 chain; PDBTitle: second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
10	c2zqtB_	 Alignment		11.1	15	PDB header: hydrolase Chain: B: PDB Molecule: anti-tumor lectin; PDBTitle: crystal structure of agrocybe aegerita lectin aal mutant2 f93g
11	c2r0fA_	 Alignment		11.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: cgl3 lectin; PDBTitle: ligand free structure of fungal lectin cgl3

12	c5wylB_	Alignment		11.0	44	PDB header: ribosomal protein/nuclear protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
13	c4f77t_	Alignment		10.8	17	PDB header: splicing Chain: T: PDB Molecule: small nuclear ribonucleoprotein f; PDBTitle: the 8s snrnp assembly intermediate
14	c2rf1B_	Alignment		10.7	14	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
15	d1xq9a_	Alignment		10.4	10	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
16	c5wylD_	Alignment		10.3	44	PDB header: ribosomal protein/nuclear protein Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
17	c2k42B_	Alignment		10.2	38	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehc effector
18	c2kv5A_	Alignment		10.1	50	PDB header: toxin Chain: A: PDB Molecule: putative uncharacterized protein rnai; PDBTitle: solution structure of the par toxin fst in dpc micelles
19	c3mxoB_	Alignment		10.0	30	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
20	c1q68A_	Alignment		9.5	89	PDB header: membrane protein/transferase Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
21	c1ujcA_	Alignment	not modelled	9.4	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
22	d1ofcx2	Alignment	not modelled	8.6	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: SLIDE domain
23	d1ppjf_	Alignment	not modelled	8.5	18	Fold: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
24	d2hhja1	Alignment	not modelled	8.5	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
25	d1ulea_	Alignment	not modelled	8.3	26	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
26	d3cx5g1	Alignment	not modelled	8.3	23	Fold: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
27	d1riia_	Alignment	not modelled	8.2	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
						Fold: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)

28	d1bccf_	Alignment	not modelled	8.0	14	Superfamily: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: 14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
29	c6mqu_	Alignment	not modelled	7.9	63	PDB header: de novo protein Chain: J: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
30	c6mquE_	Alignment	not modelled	7.9	63	PDB header: de novo protein Chain: E: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
31	c2lnhC_	Alignment	not modelled	7.8	38	PDB header: signaling protein/protein binding Chain: C: PDB Molecule: secreted effector protein espf(u); PDBTitle: enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
32	c6mquG_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: G: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
33	c6mquI_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: I: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
34	c6mquD_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: D: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
35	c6mquH_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: H: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
36	c6mquF_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: F: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
37	c6mquA_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: A: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
38	c6mquB_	Alignment	not modelled	7.8	63	PDB header: de novo protein Chain: B: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
39	c6mquC_	Alignment	not modelled	7.7	63	PDB header: de novo protein Chain: C: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
40	d1c0pa2	Alignment	not modelled	7.4	57	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
41	c6qtrD_	Alignment	not modelled	7.3	63	PDB header: transcription Chain: D: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat y144f mutant toxin bound to the c-terminus of2 the antitoxin atar and acetyl-coa
42	c4nutB_	Alignment	not modelled	6.7	50	PDB header: rna binding protein Chain: B: PDB Molecule: ribosome assembly 1 protein; PDBTitle: crystal structure of the complex between snu13p and the pep domain of2 rsa1
43	c3ra3D_	Alignment	not modelled	6.5	44	PDB header: de novo protein Chain: D: PDB Molecule: p2f; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
44	c6c62D_	Alignment	not modelled	6.5	38	PDB header: hydrolase Chain: D: PDB Molecule: atzg; PDBTitle: an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme.
45	c3bbnM_	Alignment	not modelled	6.3	100	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein s13; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
46	d1edqa1	Alignment	not modelled	6.3	35	Fold: immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
47	c2yn2A_	Alignment	not modelled	6.3	25	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
48	c3h87D_	Alignment	not modelled	6.2	27	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
49	c3f2iD_	Alignment	not modelled	6.2	10	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr0221 protein; PDBTitle: crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
50	c2ee7A_	Alignment	not modelled	6.2	20	PDB header: structural protein Chain: A: PDB Molecule: sperm flagellar protein 1; PDBTitle: solution structure of the ch domain from human sperm2 flagellar protein 1
51	c4g5oG_	Alignment	not modelled	6.1	50	PDB header: cell cycle/signaling protein Chain: G: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of lgn gl4/galphai3(q147l) complex
52	c4embD_	Alignment	not modelled	6.1	15	PDB header: isomerase Chain: D: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpma from borrelia2 burgdorferi b31
53	c5mmjm_	Alianment	not modelled	6.1	80	PDB header: ribosome Chain: M: PDB Molecule:

						PDBTitle: structure of the small subunit of the chloroplast ribosome
54	c4g5rG_	Alignment	not modelled	6.1	50	PDB header: cell cycle/signaling protein Chain: G; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3 complex
55	c4g5rZ_	Alignment	not modelled	6.0	50	PDB header: cell cycle/signaling protein Chain: Z; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3 complex
56	c4g5rE_	Alignment	not modelled	6.0	50	PDB header: cell cycle/signaling protein Chain: E; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3 complex
57	c5o5jM_	Alignment	not modelled	6.0	100	PDB header: ribosome Chain: M; PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
58	c2m6iC_	Alignment	not modelled	5.9	31	PDB header: membrane protein Chain: C; PDB Molecule: full-length transmembrane domains of human glycine receptor PDBTitle: putative pentameric open-channel structure of full-length2 transmembrane domains of human glycine receptor alpha1 subunit
59	d1ryia2	Alignment	not modelled	5.9	57	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
60	d3b2ua2	Alignment	not modelled	5.9	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
61	d1pyya3	Alignment	not modelled	5.8	50	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
62	d1e58a_	Alignment	not modelled	5.7	15	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
63	c3ra3B_	Alignment	not modelled	5.7	44	PDB header: de novo protein Chain: B; PDB Molecule: p2f; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
64	d1kifa2	Alignment	not modelled	5.6	71	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
65	c4ui9E_	Alignment	not modelled	5.6	36	PDB header: cell cycle Chain: E; PDB Molecule: anaphase-promoting complex subunit 16; PDBTitle: atomic structure of the human anaphase-promoting complex
66	c5gg7A_	Alignment	not modelled	5.5	33	PDB header: hydrolase Chain: A; PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
67	d2gy9m1	Alignment	not modelled	5.4	100	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
68	c2y69Z_	Alignment	not modelled	5.4	26	PDB header: electron transport Chain: Z; PDB Molecule: cytochrome c oxidase polypeptide 8h; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
69	d2uubm1	Alignment	not modelled	5.3	100	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
70	c4g5qG_	Alignment	not modelled	5.3	50	PDB header: cell cycle/signaling protein Chain: G; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai1 complex
71	c4g5oE_	Alignment	not modelled	5.2	50	PDB header: cell cycle/signaling protein Chain: E; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3(q147l) complex
72	c4g5qF_	Alignment	not modelled	5.2	50	PDB header: cell cycle/signaling protein Chain: F; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai1 complex
73	c4g5oF_	Alignment	not modelled	5.2	50	PDB header: cell cycle/signaling protein Chain: F; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3(q147l) complex
74	c4g5rF_	Alignment	not modelled	5.2	50	PDB header: cell cycle/signaling protein Chain: F; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai3 complex
75	d1kxpd3	Alignment	not modelled	5.2	21	Fold: Serum albumin-like Superfamily: Serum albumin-like Family: Serum albumin-like
76	c4g5qE_	Alignment	not modelled	5.2	50	PDB header: cell cycle/signaling protein Chain: E; PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structure of Ign gl4/galpai1 complex