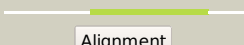

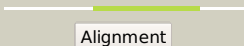


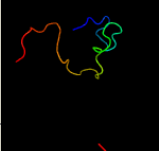
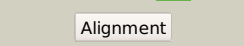


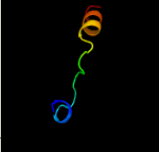

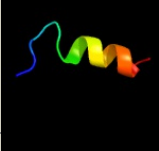
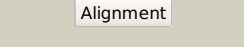
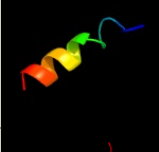











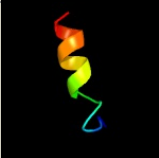

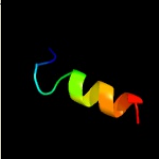
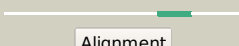

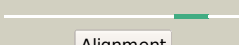
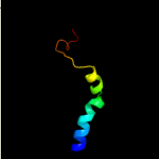
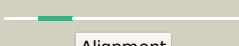
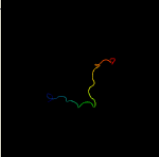
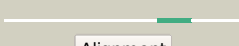


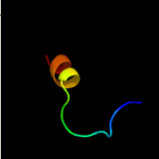

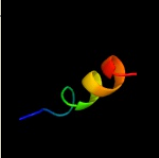




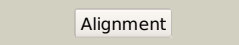


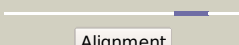


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0204c_(-)_241976_243214
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	cdb52a5bd69b9f74

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ky0B_	 Alignment		69.2	19	PDB header: transport protein, membrane protein Chain: B; PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
2	c6gctA_	 Alignment		63.4	13	PDB header: membrane protein Chain: A; PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2
3	c5nf2A_	 Alignment		51.9	16	PDB header: cell adhesion Chain: A; PDB Molecule: minor fimbrium subunit mfa1; PDBTitle: the fimbrial shaft protein mfa1 from porphyromonas gingivalis
4	c2c2xB_	 Alignment		51.1	17	PDB header: oxidoreductase Chain: B; PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
5	c4a5oB_	 Alignment		49.6	24	PDB header: oxidoreductase Chain: B; PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
6	c5zf1A_	 Alignment		49.3	24	PDB header: oxidoreductase Chain: A; PDB Molecule: 5,10-methylenetetrahydrofolate dehydrogenase; PDBTitle: molecular structure of a novel 5,10-methylenetetrahydrofolate2 dehydrogenase from the silkworm, bombyx mori
7	c4cxA_	 Alignment		48.4	29	PDB header: oxidoreductase Chain: A; PDB Molecule: c-1-tetrahydrofolate synthase, cytoplasmic, putative; PDBTitle: the crystal structure of trypanosoma brucei n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor and inhibitor
8	c3p2oA_	 Alignment		48.0	24	PDB header: oxidoreductase, hydrolase Chain: A; PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
9	c3p2oB_	 Alignment		47.6	24	PDB header: oxidoreductase, hydrolase Chain: B; PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
10	c3l07B_	 Alignment		47.6	24	PDB header: oxidoreductase,hydrolase Chain: B; PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
11	c1b0aA_	 Alignment		47.2	24	PDB header: oxidoreductase,hydrolase Chain: A; PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.

12	c6apeA	 Alignment		47.0	24	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
13	c4b4uB	 Alignment		46.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of acinetobacter baumannii n5,2 n10-methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor
14	c4a26B	 Alignment		46.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
15	c5tc4A	 Alignment		46.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional methylenetetrahydrofolate PDBTitle: crystal structure of human mitochondrial methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase (mthfd2) in complex with ly345899 and3 cofactors
16	d1l3ac	 Alignment		45.1	16	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Plant transcriptional regulator PBF-2
17	c2lnhC	 Alignment		41.5	28	PDB header: signaling protein/protein binding Chain: C: PDB Molecule: secreted effector protein espf(u); PDBTitle: enterohaemorrhagic e. coli (ehc) exploits a tryptophan switch to2 hijack host f-actin assembly
18	d1b0aa1	 Alignment		41.2	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
19	c5nhsB	 Alignment		40.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
20	d1a4ia1	 Alignment		38.5	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
21	c1a4iB	 Alignment	not modelled	38.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
22	c3nglA	 Alignment	not modelled	34.5	29	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
23	c4djiA	 Alignment	not modelled	29.9	4	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
24	c5mdxt	 Alignment	not modelled	24.2	24	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
25	c5mdxT	 Alignment	not modelled	24.2	24	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
26	c3jcut	 Alignment	not modelled	24.0	24	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein tc; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
27	c3jcuT	 Alignment	not modelled	24.0	24	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein tc; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
28	c5xnmT	 Alignment	not modelled	16.0	30	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii

						supercomplex from pisum2 sativum
29	c2rddb_	Alignment	not modelled	13.8	14	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
30	c5lc5d_	Alignment	not modelled	13.3	17	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class2
31	c5ldwd_	Alignment	not modelled	13.3	17	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class1
32	c5ldxd_	Alignment	not modelled	13.3	17	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class3.
33	c6hwhb_	Alignment	not modelled	11.2	19	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
34	c4a54B_	Alignment	not modelled	11.0	31	PDB header: rna binding protein/hydrolase Chain: B: PDB Molecule: mrna decapping complex subunit 2; PDBTitle: structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
35	c6hwhX_	Alignment	not modelled	11.0	8	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
36	c3u02C_	Alignment	not modelled	10.1	16	PDB header: transcription Chain: C: PDB Molecule: putative transcription-associated protein tfiis; PDBTitle: crystal structure of the trna modifier tias from pyrococcus furiosus,2 northeast structural genomics consortium target pfr225
37	d1ydha_	Alignment	not modelled	9.3	44	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
38	c2q4dB_	Alignment	not modelled	9.2	44	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
39	c5zba_	Alignment	not modelled	9.0	56	PDB header: hydrolase Chain: A: PDB Molecule: putative cytokinin riboside 5'-monophosphate PDBTitle: crystal structure of type-i log from pseudomonas aeruginosa pa01
40	d1t35a_	Alignment	not modelled	8.7	44	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
41	c2l2iB_	Alignment	not modelled	8.6	45	PDB header: transcription Chain: B: PDB Molecule: krueppel-like factor 1; PDBTitle: nmr structure of the complex between the tfb1 subunit of tfiih and the2 activation domain of ekf
42	c5itsD_	Alignment	not modelled	8.5	56	PDB header: hydrolase Chain: D: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of log from corynebacterium glutamicum
43	c2q4oA_	Alignment	not modelled	8.4	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
44	d2q4oa1	Alignment	not modelled	8.4	44	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
45	c5aezA_	Alignment	not modelled	8.4	15	PDB header: membrane protein Chain: A: PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2
46	c6cfwl_	Alignment	not modelled	7.5	9	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
47	c3aygA_	Alignment	not modelled	7.5	7	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
48	d2r6gf1	Alignment	not modelled	7.4	23	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
49	d2nwwa1	Alignment	not modelled	7.4	18	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
50	d1m6ya1	Alignment	not modelled	7.4	14	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
51	c6gwsD_	Alignment	not modelled	7.4	35	PDB header: replication Chain: D: PDB Molecule: pcna-associated factor; PDBTitle: crystal structure of human pcna in complex with three p15 peptides
52	c6gwsE_	Alignment	not modelled	7.4	35	PDB header: replication Chain: E: PDB Molecule: pcna-associated factor; PDBTitle: crystal structure of human pcna in complex with three p15 peptides

53	c5xpdA	Alignment	not modelled	7.3	13	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
54	c4mt1A	Alignment	not modelled	7.2	9	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
55	c5twvG	Alignment	not modelled	7.2	21	PDB header: transport protein Chain: G: PDB Molecule: atp-sensitive inward rectifier potassium channel 11; PDBTitle: cryo-em structure of the pancreatic atp-sensitive k+ channel2 sur1/kir6.2 in the presence of atp and glibenclamide
56	c5ajtA	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: A: PDB Molecule: phosphoribohydrolase lonely guy; PDBTitle: crystal structure of ligand-free phosphoribohydrolase lonely guy from2 claviceps purpurea
57	d2g7la2	Alignment	not modelled	7.0	28	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
58	d1wg8a1	Alignment	not modelled	7.0	6	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
59	c6nbxG	Alignment	not modelled	6.4	14	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
60	c5a63D	Alignment	not modelled	6.3	22	PDB header: hydrolase Chain: D: PDB Molecule: gamma-secretase subunit pen-2; PDBTitle: cryo-em structure of the human gamma-secretase complex at 3.4 angstrom2 resolution.
61	d1ikpa2	Alignment	not modelled	6.3	29	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
62	c4d2gD	Alignment	not modelled	6.1	35	PDB header: transcription Chain: D: PDB Molecule: p15; PDBTitle: crystal structure of human pcna in complex with p15 peptide
63	c4d2gE	Alignment	not modelled	6.1	35	PDB header: transcription Chain: E: PDB Molecule: p15; PDBTitle: crystal structure of human pcna in complex with p15 peptide
64	c1vjqB	Alignment	not modelled	6.1	26	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.
65	d1h6pa	Alignment	not modelled	6.1	21	Fold: Telomeric repeat binding factor (TRF) dimerisation domain Superfamily: Telomeric repeat binding factor (TRF) dimerisation domain Family: Telomeric repeat binding factor (TRF) dimerisation domain
66	c5l6nI	Alignment	not modelled	5.9	42	PDB header: hydrolase Chain: I: PDB Molecule: thrombin inhibitor madanin 1; PDBTitle: disulfated madanin-thrombin complex
67	c2rfIB	Alignment	not modelled	5.9	18	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
68	c2mfrA	Alignment	not modelled	5.7	21	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
69	d1nmla1	Alignment	not modelled	5.7	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
70	c6c6lO	Alignment	not modelled	5.6	24	PDB header: membrane protein Chain: O: PDB Molecule: v-type proton atpase subunit f; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
71	c5wq3A	Alignment	not modelled	5.6	33	PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from corynebacterium glutamicum
72	d1x7da	Alignment	not modelled	5.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
73	c3syaA	Alignment	not modelled	5.5	19	PDB header: metal transport Chain: A: PDB Molecule: g protein-activated inward rectifier potassium channel 2; PDBTitle: crystal structure of the g protein-gated inward rectifier k+ channel2 girk2 (kir3.2) in complex with sodium and pip2
74	c5lnko	Alignment	not modelled	5.5	13	PDB header: oxidoreductase Chain: O: PDB Molecule: PDBTitle: entire ovine respiratory complex i
75	c2c9kA	Alignment	not modelled	5.5	19	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry4aa; PDBTitle: structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
76	c2i5nH	Alignment	not modelled	5.5	24	PDB header: photosynthesis Chain: H: PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
77	d2vkva2	Alignment	not modelled	5.3	19	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain

					Family: Tetracyclin repressor-like, C-terminal domain	
78	d1pw4a_	Alignment	not modelled	5.2	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
79	d1o5ha_	Alignment	not modelled	5.2	44	Fold: Methenyltetrahydrofolate cyclohydrolase-like Superfamily: Methenyltetrahydrofolate cyclohydrolase-like Family: Methenyltetrahydrofolate cyclohydrolase-like