
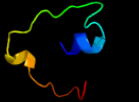
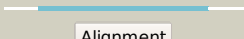

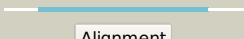
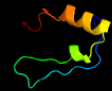

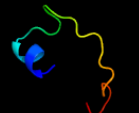
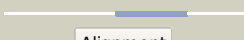


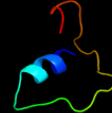
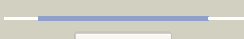


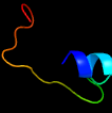


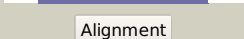
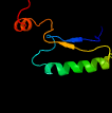
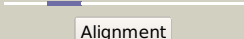
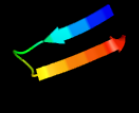
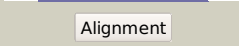


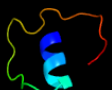
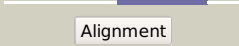
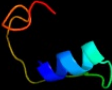








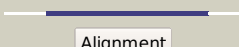
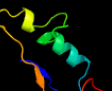
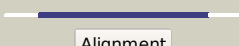

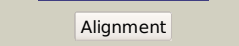
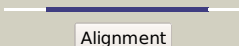

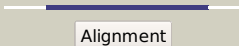
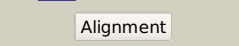

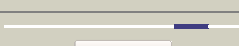
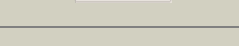


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1366A_(RVBD1366A)_1539186_1539446
 Date Wed Jul 31 22:05:47 BST 2019
 Unique Job ID 013e540ca768ed05

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1i32D_	 Alignment		53.9	24	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
2	c5zojE_	 Alignment		37.5	27	PDB header: dna binding protein Chain: E: PDB Molecule: inner nuclear membrane protein man1; PDBTitle: crystal structure of human smad2-man1 complex
3	c3s6eB_	 Alignment		37.1	27	PDB header: rna binding protein Chain: B: PDB Molecule: rna-binding protein 39; PDBTitle: crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
4	d1k3ta1	 Alignment		30.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
5	d1i32a1	 Alignment		29.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
6	d2b4ro1	 Alignment		23.4	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
7	c3dlbA_	 Alignment		22.3	25	PDB header: nucleic acid binding protein/dna Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of the guide-strand-containing argonaute2 protein silencing complex
8	d1ggaa1	 Alignment		19.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	d1azpa_	 Alignment		17.2	22	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: "Histone-like" proteins from archaea
10	c3ho1A_	 Alignment		17.0	27	PDB header: nucleic acid binding protein/dna/rna Chain: A: PDB Molecule: argonaute; PDBTitle: crystal structure of t. thermophilus argonaute n546 mutant protein2 complexed with dna guide strand and 12-nt rna target strand
11	c3aqjQ_	 Alignment		14.6	29	PDB header: metal binding protein Chain: Q: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of a c-terminal domain of the bacteriophage p2 tail2 spike protein, gpv

12	c4yh8A_	 Alignment		13.7	30	PDB header: splicing Chain: A: PDB Molecule: splicing factor u2af 23 kda subunit; PDBTitle: structure of yeast u2af complex
13	d1u8fo1	 Alignment		12.9	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	d1j0xo1	 Alignment		12.6	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
15	c3cieC_	 Alignment		12.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
16	d1od6a_	 Alignment		9.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Adenylyltransferase
17	d3gpdg1	 Alignment		9.8	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	d1o0pa_	 Alignment		9.0	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
19	c4k29A_	 Alignment		8.8	18	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 xanthobacter autotrophicus py2
20	d1yvua2	 Alignment		8.7	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain
21	d1w9ha1	 Alignment	not modelled	8.7	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: PIWI domain
22	c3sllC_	 Alignment	not modelled	7.9	16	PDB header: isomerase Chain: C: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
23	d1fjca_	 Alignment	not modelled	7.0	22	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
24	c4nekD_	 Alignment	not modelled	6.9	13	PDB header: isomerase Chain: D: PDB Molecule: enoyl-coa hydratase/carnithine racemase; PDBTitle: putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1
25	c3j60I_	 Alignment	not modelled	6.7	47	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8e; PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
26	c2q3vB_	 Alignment	not modelled	6.5	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein at2g34160; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160
27	c4quvB_	 Alignment	not modelled	6.3	63	PDB header: oxidoreductase, membrane protein Chain: B: PDB Molecule: delta(14)-sterol reductase; PDBTitle: structure of an integral membrane delta(14)-sterol reductase
28	c1yz7A_	 Alignment	not modelled	6.2	15	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of a c-terminal segment of the alpha2 subunit of aif2 from pyrococcus abyssi

29	c4mouA_	Alignment	not modelled	6.1	17	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase family member,2 nysgrc target 028282
30	c2vkzH_	Alignment	not modelled	6.0	13	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
31	d1vm0a_	Alignment	not modelled	5.9	26	Fold: IF3-like Superfamily: AlbA-like Family: Hypothetical protein At2g34160
32	d1h6da1	Alignment	not modelled	5.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	d2pkqo1	Alignment	not modelled	5.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	c3rrvC_	Alignment	not modelled	5.7	12	PDB header: isomerase Chain: C: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
35	c3h02F_	Alignment	not modelled	5.7	21	PDB header: lyase Chain: F: PDB Molecule: naphthoate synthase; PDBTitle: 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
36	c2uval_	Alignment	not modelled	5.6	20	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
37	d1jmta_	Alignment	not modelled	5.5	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Splicing factor U2AF subunits
38	c4i4zE_	Alignment	not modelled	5.2	23	PDB header: lyase Chain: E: PDB Molecule: naphthoate synthase; PDBTitle: synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa