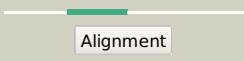
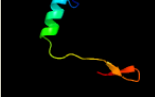
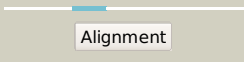
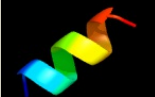
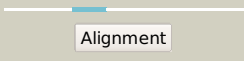

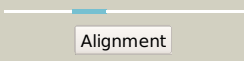

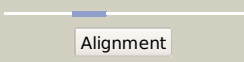

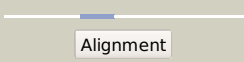

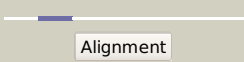

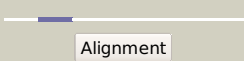

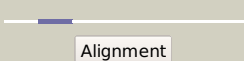
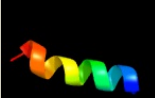
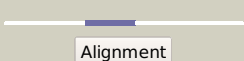

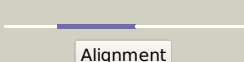

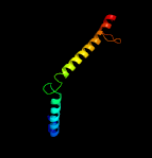



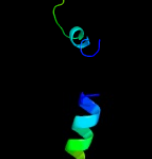

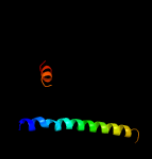
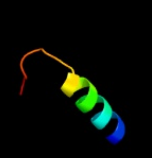
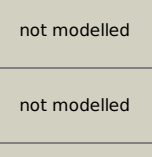


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3675 (-)_4116180_4116557
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	6fdf82facc7329bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rfea_	 Alignment		40.5	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
2	c6gqaD_	 Alignment		39.8	36	PDB header: cell cycle Chain: D: PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb
3	c2wukD_	 Alignment		35.3	45	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
4	c4ug3C_	 Alignment		32.9	36	PDB header: cell cycle Chain: C: PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb n-terminal domain
5	c4ug1A_	 Alignment		29.9	45	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
6	c3h36A_	 Alignment		29.6	53	PDB header: transferase Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of an uncharacterized domain in polyribonucleotide2 nucleotidyltransferase from streptococcus mutans ua159
7	c4fe1M_	 Alignment		15.5	31	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution
8	d1jb0m_	 Alignment		15.5	31	Fold: Single transmembrane helix Superfamily: Subunit XII of photosystem I reaction centre, PsaM Family: Subunit XII of photosystem I reaction centre, PsaM
9	c1jb0M_	 Alignment		15.5	31	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem 1 reaction centre subunit xii; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
10	c5da9D_	 Alignment		15.3	24	PDB header: hydrolase Chain: D: PDB Molecule: putative double-strand break protein; PDBTitle: atp-gamma-s bound rad50 from chaetomium thermophilum in complex with2 the rad50-binding domain of mre11
11	c6g04A_	 Alignment		13.5	17	PDB header: transport protein Chain: A: PDB Molecule: pre-rrna-processing protein tsr2; PDBTitle: nmr solution structure of yeast tsr2(1-152) in complex with s26a(100-2 119)

12	d2py8a1	Alignment		12.4	20	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
13	c5xj0Y_	Alignment		12.2	24	PDB header: transferase/transcription Chain: Y: PDB Molecule: gp76; PDBTitle: t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
14	d1w4ha1	Alignment		12.1	38	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
15	c3tgvD_	Alignment		11.4	19	PDB header: heme binding protein Chain: D: PDB Molecule: heme-binding protein hutz; PDBTitle: crystal structure of hutz,the heme storage protein from vibrio2 cholerae
16	c3f7eB_	Alignment		11.1	19	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeq_3380 f420 reductase
17	d1k4ta1	Alignment		10.3	43	Fold: Long alpha-hairpin Superfamily: Eukaryotic DNA topoisomerase I, dispensable insert domain Family: Eukaryotic DNA topoisomerase I, dispensable insert domain
18	c2ksdA_	Alignment		10.3	24	PDB header: transferase Chain: A: PDB Molecule: aerobic respiration control sensor protein arcb; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor arcb, center for structures of membrane proteins (csm)3 target 4310c
19	c1kmiZ_	Alignment		9.9	10	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
20	d1j5ya2	Alignment		9.6	19	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
21	c1pk1A_	Alignment	not modelled	8.9	14	PDB header: transcription repression Chain: A: PDB Molecule: polyhomeotic-proximal chromatin protein; PDBTitle: hetero sam domain structure of ph and scm.
22	d2f66c1	Alignment	not modelled	8.5	27	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like
23	c2hhzA_	Alignment	not modelled	8.4	31	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
24	d1w9aa_	Alignment	not modelled	8.0	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	c5j8yC_	Alignment	not modelled	8.0	25	PDB header: nuclear protein Chain: C: PDB Molecule: polycomb protein sfmbt; PDBTitle: crystal structure of the scm-sam and sfmbt-sam heterodimer
26	c1pk1B_	Alignment	not modelled	7.7	18	PDB header: transcription repression Chain: B: PDB Molecule: sex comb on midleg cg9495-pa; PDBTitle: hetero sam domain structure of ph and scm.
27	d1dda_	Alignment	not modelled	7.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
28	c4pzoE_	Alignment	not modelled	7.5	14	PDB header: dna binding protein Chain: E: PDB Molecule: polyhomeotic-like protein 3; PDBTitle: crystal structure of phc3 sam l967r

29	c3bq7A_	Alignment	not modelled	7.1	18	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
30	d1pk1c1	Alignment	not modelled	7.1	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
31	d1pk3a1	Alignment	not modelled	7.1	18	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
32	d1z0jb1	Alignment	not modelled	7.0	21	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like Family: Rabenosyn-5 Rab-binding domain-like
33	c2dkzA_	Alignment	not modelled	6.9	14	PDB header: signaling protein Chain: A: PDB Molecule: hypothetical protein loc64762; PDBTitle: solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762
34	d1kw4a_	Alignment	not modelled	6.9	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
35	c3kfuj_	Alignment	not modelled	6.6	21	PDB header: ligase/rna Chain: J: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c; PDBTitle: crystal structure of the transamidosome
36	c5lkdB_	Alignment	not modelled	6.6	32	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase omega-like 2; PDBTitle: crystal structure of the xi glutathione transferase ecm4 from2 saccharomyces cerevisiae in complex with glutathione
37	c4qoyE_	Alignment	not modelled	6.4	23	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
38	d2af7a1	Alignment	not modelled	6.3	21	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
39	c3iz5n_	Alignment	not modelled	5.9	25	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l14 (l14e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
40	d2hq9a1	Alignment	not modelled	5.6	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
41	d2fgca1	Alignment	not modelled	5.6	27	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
42	c3fhkF_	Alignment	not modelled	5.5	54	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
43	d1rp1a2	Alignment	not modelled	5.5	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
44	c1zwwA_	Alignment	not modelled	5.4	19	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
45	c3u0iA_	Alignment	not modelled	5.3	12	PDB header: unknown function Chain: A: PDB Molecule: probable fad-binding, putative uncharacterized protein; PDBTitle: crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
46	c1v06A_	Alignment	not modelled	5.3	22	PDB header: dna-binding protein Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: axh domain of the transcription factor hbp1 from m.musculus
47	c3j39k_	Alignment	not modelled	5.2	33	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l12; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
48	c2penE_	Alignment	not modelled	5.2	20	PDB header: chaperone Chain: E: PDB Molecule: orf134; PDBTitle: crystal structure of rbxc, crystal form i
49	d1bala_	Alignment	not modelled	5.1	38	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
50	c1w4kA_	Alignment	not modelled	5.1	22	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
51	c3izcn_	Alignment	not modelled	5.0	47	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein rpl14 (l14e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome