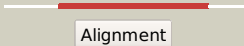
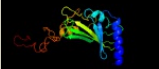
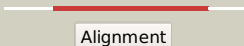

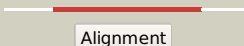
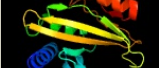



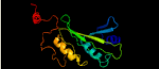


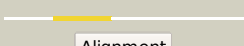










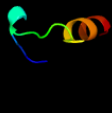

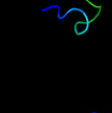

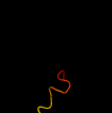


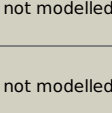


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3147_(nuoC)_3512625_3513335
 Date Thu Aug 8 16:20:33 BST 2019
 Unique Job ID ea2b5581ea2db6f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gcsG_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: G: PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
2	c5ldwC_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class1
3	c3mcrA_	 Alignment		100.0	63	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
4	d2fug51	 Alignment		100.0	32	Fold: Nqo5-like Superfamily: Nqo5-like Family: Nqo5-like
5	c6cfwK_	 Alignment		100.0	24	PDB header: membrane protein Chain: K: PDB Molecule: membrane-bound hydrogenase subunit beta; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
6	c6humJ_	 Alignment		100.0	33	PDB header: proton transport Chain: J: PDB Molecule: nad(p)h-quinone oxidoreductase subunit j; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
7	d2p06a1	 Alignment		70.4	45	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: AF0060-like
8	c2p06A_	 Alignment		70.4	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af_0060; PDBTitle: crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
9	c3s2xB_	 Alignment		59.1	25	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
10	d1ru3a_	 Alignment		49.8	25	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
11	c3gitA_	 Alignment		35.4	28	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase/acetyl-coa synthase subunit PDBTitle: crystal structure of a truncated acetyl-coa synthase

12	d1oaoc_	Alignment		34.9	28	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Acetyl-CoA synthase
13	c3kfwX_	Alignment		21.7	36	PDB header: structural genomics, unknown function Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein rv0674 from mycobacterium tuberculosis
14	c1bl1A_	Alignment		14.1	46	PDB header: hormone receptor Chain: A: PDB Molecule: parathyroid hormone receptor; PDBTitle: pth receptor n-terminus fragment, nmr, 1 structure
15	c3kw1A_	Alignment		13.8	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
16	c2fq8A_	Alignment		12.1	29	PDB header: unknown function Chain: A: PDB Molecule: 2f; PDBTitle: nmr structure of 2f associated with lipid disc
17	c2fq5A_	Alignment		12.1	29	PDB header: unknown function Chain: A: PDB Molecule: peptide 2f; PDBTitle: nmr structure of 2f associated with lipid disc
18	d2f05a1	Alignment		11.5	22	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
19	c3v8vB_	Alignment		9.7	16	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase I; PDBTitle: crystal structure of bifunctional methyltransferase ycby (rlmk) from2 escherichia coli, sam binding
20	c5a96A_	Alignment		9.1	44	PDB header: viral protein Chain: A: PDB Molecule: polyhedrin; PDBTitle: crystal structure of lymantria dispar cpv14 polyhedra
21	d1es6a2	Alignment	not modelled	8.6	50	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
22	c5o60D_	Alignment	not modelled	8.1	25	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l3; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
23	c4wfbB_	Alignment	not modelled	8.0	19	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l3; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
24	c2mcdA_	Alignment	not modelled	7.9	47	PDB header: hydrolase Chain: A: PDB Molecule: murine norovirus 1; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for murine2 norovirus ns1/2 d94e mutant
25	c3tcqA_	Alignment	not modelled	7.8	40	PDB header: viral protein Chain: A: PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of matrix protein vp40 from ebola virus sudan
26	c3hq2A_	Alignment	not modelled	7.6	16	PDB header: hydrolase Chain: A: PDB Molecule: bacillus subtilis m32 carboxypeptidase; PDBTitle: bsucp crystal structure
27	c1es6A_	Alignment	not modelled	7.5	50	PDB header: viral protein Chain: A: PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of the matrix protein of ebola virus
28	c5b0vA_	Alignment	not modelled	7.0	50	PDB header: viral protein Chain: A: PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of marburg virus vp40 dimer
						PDB header: ribosome

29	c1vw3C	Alignment	not modelled	6.7	21	Chain: C: PDB Molecule: 54s ribosomal protein I9, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
30	c6ogdB	Alignment	not modelled	6.7	23	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
31	d2gycb1	Alignment	not modelled	6.7	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3
32	c3oe3B	Alignment	not modelled	6.3	16	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of plic-st, periplasmic lysozyme inhibitor of c-type2 lysozyme from salmonella typhimurium
33	c3echC	Alignment	not modelled	6.3	36	PDB header: transcription, transcription regulation Chain: C: PDB Molecule: 25-mer fragment of protein armr; PDBTitle: the marr-family repressor mexr in complex with its antirepressor armr
34	c5mlcE	Alignment	not modelled	6.3	19	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein I3, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
35	c5nz8A	Alignment	not modelled	6.1	12	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
36	d1s5qb	Alignment	not modelled	5.9	25	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
37	c1odpA	Alignment	not modelled	5.9	33	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
38	c1odrA	Alignment	not modelled	5.9	33	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
39	c1odqA	Alignment	not modelled	5.9	33	PDB header: lipid transport Chain: A: PDB Molecule: apoa-i peptide; PDBTitle: peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
40	c5uz9B	Alignment	not modelled	5.7	25	PDB header: immune system/rna Chain: B: PDB Molecule: crispr-associated protein csy2; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
41	c2ks1B	Alignment	not modelled	5.6	42	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
42	c5nz7A	Alignment	not modelled	5.3	12	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
43	d2j01e1	Alignment	not modelled	5.2	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3
44	c6e1cB	Alignment	not modelled	5.1	19	PDB header: metal binding protein Chain: B: PDB Molecule: di-heme enzyme; PDBTitle: crystal structure of a maug-like protein associated with microbial2 copper homeostasis
45	d2ga5a1	Alignment	not modelled	5.1	24	Fold: N domain of copper amine oxidase-like Superfamily: Fratxin/Nqo15-like Family: Fratxin-like
46	c4dz4D	Alignment	not modelled	5.1	24	PDB header: hydrolase Chain: D: PDB Molecule: agmatinase; PDBTitle: x-ray crystal structure of a hypothetical agmatinase from burkholderia2 thailandensis