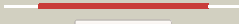

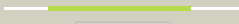


















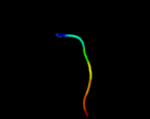






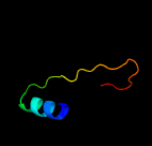
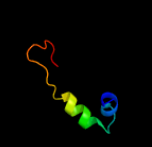
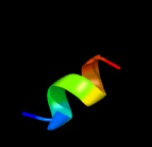


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3806c_(-)_4269103_4270011
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	42ec28e3ae5f8532

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4od5C_	 Alignment		100.0	15	PDB header: transferase Chain: C; PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
2	c3dh4A_	 Alignment		60.9	12	PDB header: transport protein Chain: A; PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
3	c2l4fA_	 Alignment		32.8	42	PDB header: protein binding Chain: A; PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: nmr structure of the uba domain of s. cerevisiae dcn1 bound to2 ubiquitin
4	c2xq2A_	 Alignment		28.1	12	PDB header: transport protein Chain: A; PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vs9t
5	d1dih2	 Alignment		23.9	28	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
6	c5us6L_	 Alignment		20.7	31	PDB header: oxidoreductase Chain: L; PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of dihydrodipicolinate reductase from vibrio vulnificus2 bound to nadh and 2,6 pyridine dicarboxylic acid with intact3 polyhistidine tag
7	c4o6mA_	 Alignment		16.9	13	PDB header: transferase Chain: A; PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
8	c3npgB_	 Alignment		16.4	18	PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: the crystal structure of geranyltranstransferase from campylobacter2 jejuni
9	c4ksnC_	 Alignment		14.3	33	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: sdbc; PDBTitle: c-terminal domain of sdbc protein from legionella pneumophila.
10	c5tenH_	 Alignment		13.2	31	PDB header: oxidoreductase Chain: H; PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
11	c2ww9O_	 Alignment		7.5	38	PDB header: ribosome Chain: O; PDB Molecule: 60s ribosomal protein l39; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome

12	c3m9uD_	Alignment		7.4	12	PDB header: transferase Chain: D: PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from <i>Lactobacillus brevis</i> atcc 367
13	c5wwoB_	Alignment		7.3	23	PDB header: rna binding protein Chain: B: PDB Molecule: essential nuclear protein 1; PDBTitle: crystal structure of enp1
14	c1drwA_	Alignment		7.2	28	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
15	c6g4ww_	Alignment		7.0	15	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
16	c4heoA_	Alignment		6.7	31	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
17	c2ogdB_	Alignment		6.6	14	PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527
18	c3iipA_	Alignment		6.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
19	d1vm6a2	Alignment		6.2	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
20	c2v6qB_	Alignment		6.2	33	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of a bhrf-1 : bim bh3 complex
21	c2wh6B_	Alignment	not modelled	6.1	33	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: crystal structure of anti-apoptotic bhrf1 in complex with the bim bh32 domain
22	c5vwzD_	Alignment	not modelled	6.0	33	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3pc
23	c5vwzB_	Alignment	not modelled	6.0	33	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3pc
24	c4nlbA_	Alignment	not modelled	5.9	32	PDB header: hydrolase Chain: A: PDB Molecule: ribosomal rna processing protein 6; PDBTitle: crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei
25	c3fdlB_	Alignment	not modelled	5.9	33	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bim bh3 peptide in complex with bcl-xl
26	c4ywjB_	Alignment	not modelled	5.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
27	c4a1bB_	Alignment	not modelled	5.6	38	PDB header: ribosome Chain: B: PDB Molecule: rp139; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
28	c2ndjA_	Alignment	not modelled	5.5	16	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3;

						PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
29	c5k4bA_	Alignment	not modelled	5.4	25	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit d; PDBTitle: structure of eukaryotic translation initiation factor 3 subunit d2 (eif3d) cap binding domain from nasonia vitripennis, crystal form 1
30	c2mpnB_	Alignment	not modelled	5.2	12	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
31	c2hbkA_	Alignment	not modelled	5.2	19	PDB header: hydrolase, gene regulation Chain: A: PDB Molecule: exosome complex exonuclease rrp6; PDBTitle: structure of the yeast nuclear exosome component, rrp6p, reveals an2 interplay between the active site and the hrdc domain; protein in3 complex with mn
32	c6nplA_	Alignment	not modelled	5.2	12	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride PDBTitle: cryo-em structure of nkcc1
33	c3izso_	Alignment	not modelled	5.2	38	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein rpl28 (l15p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
34	c6g2jY_	Alignment	not modelled	5.2	7	PDB header: oxidoreductase Chain: Y: PDB Molecule: mcg5603; PDBTitle: mouse mitochondrial complex i in the active state
35	c3ukwC_	Alignment	not modelled	5.2	40	PDB header: protein transport/inhibitor Chain: C: PDB Molecule: bimax1 peptide; PDBTitle: mouse importin alpha: bimax1 peptide complex
36	c2zkr3_	Alignment	not modelled	5.1	50	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
37	c3qy9C_	Alignment	not modelled	5.0	32	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: the crystal structure of dihydrodipicolinate reductase from2 staphylococcus aureus