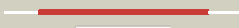



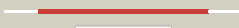
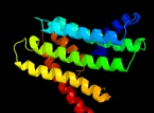

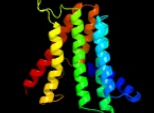









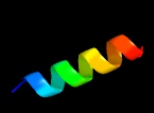



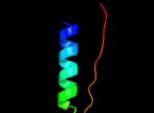
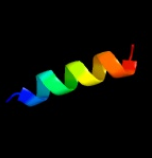
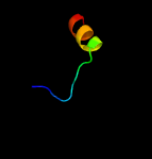

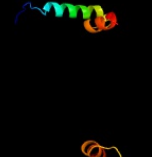
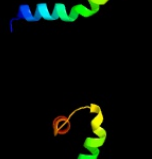
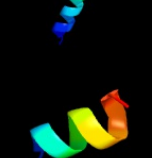
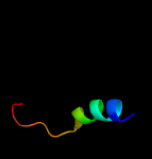
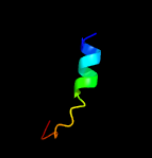
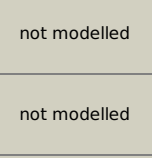


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2612c_(pgsA1)_2939969_2940622
Date	Wed Aug 7 12:50:25 BST 2019
Unique Job ID	88acd89247079527

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6h59B_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: cdp-diacylglycerol--inositol 3-phosphatidyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis phosphatidylinositol2 phosphate synthase (pgsa1) with cdp-dag bound
2	c5d92B_	 Alignment		100.0	43	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
3	c4o6mA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
4	c4mndA_	 Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: ctp l-myo-inositol-1-phosphate cytidyltransferase/cdp-l- PDBTitle: crystal structure of archaeoglobus fulgidus ipct-dipps bifunctional2 membrane protein
5	c2voyG_	 Alignment		52.3	17	PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
6	c5gufA_	 Alignment		26.3	14	PDB header: transferase Chain: A: PDB Molecule: cdp-archaeol synthase; PDBTitle: structural insight into an intramembrane enzyme for archaeal membrane2 lipids biosynthesis
7	c5zc2B_	 Alignment		25.4	13	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
8	d1ou8a_	 Alignment		22.6	31	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
9	d1zszc1	 Alignment		22.2	19	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
10	d1ou9a_	 Alignment		20.1	31	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
11	c2rkhA_	 Alignment		19.1	29	PDB header: transcription Chain: A: PDB Molecule: putative apha-like transcription factor; PDBTitle: crystal structure of a putative apha-like transcription factor2 (zp_00208345.1) from magnetospirillum magnetotacticum ms-1 at 2.00 a3 resolution

12	d1yfa1	Alignment		18.2	25	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
13	c6mjbC	Alignment		16.0	28	PDB header: cell cycle Chain: C: PDB Molecule: kinetochore-associated protein dsn1; PDBTitle: structure of candida glabrata csm1:dsn1(14-72) complex
14	c3cjnA	Alignment		13.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
15	c6c28C	Alignment		12.0	21	PDB header: dna binding protein Chain: C: PDB Molecule: transcriptional regulator, marr family; PDBTitle: transcriptional repressor, cour, bound to p-coumaroyl-coa
16	c3cdhB	Alignment		11.5	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
17	d2fbha1	Alignment		10.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
18	c4n3xD	Alignment		9.8	64	PDB header: endocytosis Chain: D: PDB Molecule: rab5 gdp/gtp exchange factor; PDBTitle: crystal structure of rabex-5 cc domain
19	c2zxqA	Alignment		9.6	21	PDB header: hydrolase Chain: A: PDB Molecule: endo-alpha-n-acetylgalactosaminidase; PDBTitle: crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
20	c3ecqA	Alignment		9.2	32	PDB header: hydrolase Chain: A: PDB Molecule: endo-alpha-n-acetylgalactosaminidase; PDBTitle: endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
21	c4i0xJ	Alignment	not modelled	8.5	22	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
22	c3bj6B	Alignment	not modelled	6.8	29	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
23	d1bvp11	Alignment	not modelled	6.7	29	Fold: A virus capsid protein alpha-helical domain Superfamily: A virus capsid protein alpha-helical domain Family: Orbivirus capsid
24	c3hrmA	Alignment	not modelled	5.9	22	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarz; PDBTitle: crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
25	c2le7A	Alignment	not modelled	5.6	29	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: solution nmr structure of the s4s5 linker of herg potassium channel
26	c3ecoB	Alignment	not modelled	5.4	16	PDB header: transcription Chain: B: PDB Molecule: mepR; PDBTitle: crystal structure of mepR, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepA
27	c3oopA	Alignment	not modelled	5.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2960 protein; PDBTitle: the structure of a protein with unknown function from listeria innocua2 clip11262