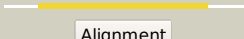

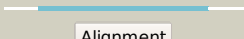

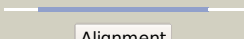
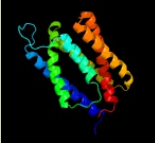

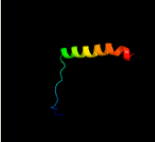
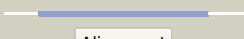






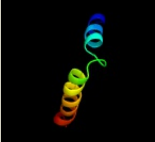



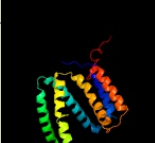



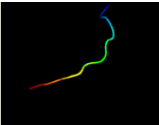

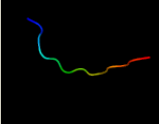

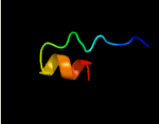
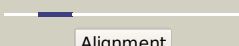
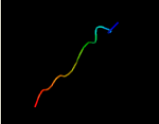
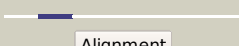

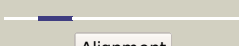




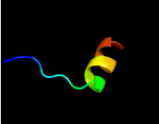


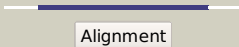


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1624c_(-)_1826005_1826592
Date	Fri Aug 2 13:30:21 BST 2019
Unique Job ID	919ebe74abbc4799

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		73.2	10	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	c6basA_	 Alignment		31.9	11	PDB header: transferase Chain: A: PDB Molecule: peptidoglycan glycosyltransferase roda; PDBTitle: crystal structure of thermus thermophilus rod shape determining2 protein roda d255a mutant (q5six3_thet8)
3	c4pquA_	 Alignment		25.7	12	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein yetj; PDBTitle: crystal structure of yetj from bacillus subtilis at ph 7 by soaking
4	c3arcL_	 Alignment		24.7	25	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
5	c3j1zP_	 Alignment		20.7	10	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
6	c5i20C_	 Alignment		15.4	11	PDB header: membrane protein Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
7	d1h59b_	 Alignment		14.9	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
8	c6bm8A_	 Alignment		14.7	23	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
9	c6btmC_	 Alignment		13.6	15	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
10	c5i20E_	 Alignment		13.4	14	PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein
11	c6g9xB_	 Alignment		11.9	14	PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution

12	c2ideE_	 Alignment		9.2	31	PDB header: biosynthetic protein Chain: E; PDB Molecule: molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8
13	d1ekra_	 Alignment		8.8	23	Fold: Ferredoxin-like Superfamily: Molybdenum cofactor biosynthesis protein C, MoaC Family: Molybdenum cofactor biosynthesis protein C, MoaC
14	c5wlbC_	 Alignment		8.2	26	PDB header: protein binding Chain: C; PDB Molecule: 225-15 b; PDBTitle: kras g12v, bound to gppnhp and miniprotein 225-15a/b
15	c2ohdB_	 Alignment		7.7	46	PDB header: biosynthetic protein Chain: B; PDB Molecule: probable molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of hypothetical molybdenum cofactor biosynthesis2 protein c from sulfolobus tokodaii
16	c2eeyA_	 Alignment		7.7	23	PDB header: biosynthetic protein Chain: A; PDB Molecule: molybdopterin biosynthesis; PDBTitle: structure of gk0241 protein from geobacillus kaustophilus
17	c3ue5B_	 Alignment		7.3	50	PDB header: contractile protein/transport protein Chain: B; PDB Molecule: protein spire; PDBTitle: ecp-cleaved actin in complex with spir domain d
18	c4fdFB_	 Alignment		6.2	23	PDB header: biosynthetic protein Chain: B; PDB Molecule: molybdenum cofactor biosynthesis protein c 2; PDBTitle: structural insights into putative molybdenum cofactor biosynthesis2 protein c (moac2) from mycobacterium tuberculosis h37rv
19	d1r89a3	 Alignment		5.9	19	Fold: Ferredoxin-like Superfamily: PAP/Archaeal CCA-adding enzyme, C-terminal domain Family: Archaeal tRNA CCA-adding enzyme
20	c5d92B_	 Alignment		5.4	14	PDB header: membrane protein Chain: B; PDB Molecule: af2299 protein, phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
21	c6f0kC_	 Alignment	not modelled	5.2	16	PDB header: membrane protein Chain: C; PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii