
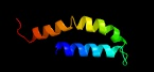

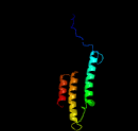



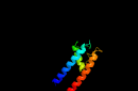

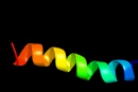



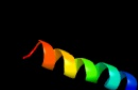

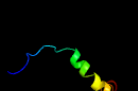



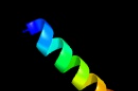

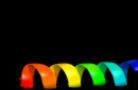



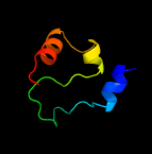


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2707 (-) _3020583_3021557
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	28f818df056636be

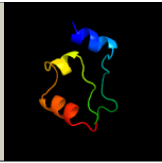
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gf1	 Alignment		94.1	20	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
2	c6eznH	 Alignment		29.7	7	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
3	c2yn9B	 Alignment		10.9	10	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: cryo-em structure of gastric h+,k+-atpase with bound rubidium
4	c2qksA	 Alignment		10.1	17	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
5	c5lnkW	 Alignment		9.5	17	PDB header: oxidoreductase Chain: W: PDB Molecule: mitochondrial complex i, sgdh subunit; PDBTitle: entire ovine respiratory complex i
6	c3echC	 Alignment		9.1	21	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
7	c3b8eB	 Alignment		8.8	20	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
8	c2voyB	 Alignment		8.2	14	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
9	c3ixzB	 Alignment		7.9	10	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
10	c2zxeB	 Alignment		7.5	19	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: :na+,k+-atpase beta subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
11	c3kdpD	 Alignment		7.1	20	PDB header: hydrolase Chain: D: PDB Molecule: sodium/potassium-transporting atpase subunit beta-1; PDBTitle: crystal structure of the sodium-potassium pump

12	c2xzbB_	 Alignment		6.6	10 PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h,k-atpase with bound bef and sch28080
13	d1m9dc_	 Alignment		5.9	17 Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain

14 [d2pxrc1](#)

Alignment



5.5

19

Fold:Retrovirus capsid protein, N-terminal core domain
Superfamily:Retrovirus capsid protein, N-terminal core domain
Family:Retrovirus capsid protein, N-terminal core domain