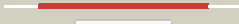



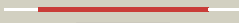














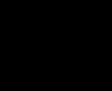



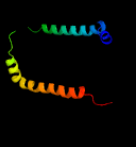
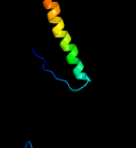





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2937_drrB_3273216_3274085
Date	Thu Aug 8 16:20:09 BST 2019
Unique Job ID	6ae7fd74135b9452

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6an7C_	 Alignment		100.0	10	PDB header: transport protein Chain: C: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
2	c6an7D_	 Alignment		100.0	10	PDB header: transport protein Chain: D: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
3	c5njgB_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: part of the structure that could be2 built de novo
4	c5nj3B_	 Alignment		100.0	11	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
5	c5do7B_	 Alignment		100.0	9	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
6	c5do7A_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
7	c5xjvA_	 Alignment		99.2	6	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
8	c5gasN_	 Alignment		45.1	10	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
9	c5ir6B_	 Alignment		12.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
10	c3cqyA_	 Alignment		11.4	38	PDB header: transferase Chain: A: PDB Molecule: anhidro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
11	c4yh5B_	 Alignment		10.2	43	PDB header: transferase Chain: B: PDB Molecule: levoglucosan kinase; PDBTitle: lipomyces starkeyi levoglucosan kinase bound to adp and manganese

12	c5n9yB_	Alignment		9.7	13	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
13	c3rkoF_	Alignment		8.4	11	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	c2k9yA_	Alignment		7.9	13	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
15	c2k9yB_	Alignment		7.9	13	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
16	c2x7lP_	Alignment		7.3	21	PDB header: immune system Chain: P: PDB Molecule: protein rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
17	c3lphD_	Alignment		6.1	21	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer

18

[c5ir6A_](#)

Alignment



5.1

16

PDB header: oxidoreductase

Chain: A: **PDB Molecule:** bd-type quinol oxidase subunit i;

PDB Title: the structure of bd oxidase from geobacillus
thermodenitrificans