



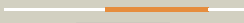


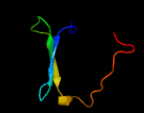









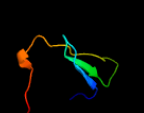
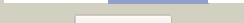

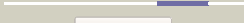
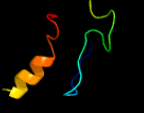











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3278c_(-)_3660648_3661166
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	9454938b178c2e19

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dcxa1	 Alignment		95.2	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: BPHL domain
2	c4tyzB_	 Alignment		92.8	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal domain of an unknown protein from2 leishmania infantum
3	d2hthb1	 Alignment		83.8	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: VPS36 N-terminal domain-like
4	d2caya1	 Alignment		83.7	13	Fold: PH domain-like barrel Superfamily: PH domain-like Family: VPS36 N-terminal domain-like
5	c3fssA_	 Alignment		56.3	15	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: structure of the tandem ph domains of rtt106
6	c3gypA_	 Alignment		48.6	12	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: rtt106p
7	d2gcla1	 Alignment		46.6	31	Fold: PH domain-like barrel Superfamily: PH domain-like Family: SSRP1-like
8	c5yqrA_	 Alignment		32.8	19	PDB header: transport protein Chain: A: PDB Molecule: endolysin/membrane-anchored lipid-binding protein lam6 PDBTitle: crystal structure of the ph-like domain of lam6
9	d2dx5a1	 Alignment		22.0	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: VPS36 N-terminal domain-like
10	d3b77a1	 Alignment		20.2	14	Fold: PH domain-like barrel Superfamily: PH domain-like Family: BPHL domain
11	c4uaqA_	 Alignment		14.6	19	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca 2; PDBTitle: crystal structure of the accessory translocation atpase, seca2, from2 mycobacterium tuberculosis

12	d1omwa2	Alignment		14.1	16	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
13	c6irtA	Alignment		13.8	26	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
14	c4r8gE	Alignment		12.8	8	PDB header: protein binding/calcium-binding protein Chain: E: PDB Molecule: unconventional myosin-ic; PDBTitle: crystal structure of myosin-1c tail in complex with calmodulin
15	c4ifsA	Alignment		10.6	20	PDB header: transcription, replication Chain: A: PDB Molecule: fact complex subunit sssr1; PDBTitle: crystal structure of the hssr1 middle domain
16	d1zj8a1	Alignment		9.6	19	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
17	c3aqoD	Alignment		8.9	13	PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
18	d1hyua3	Alignment		7.7	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
19	c4chjA	Alignment		7.2	19	PDB header: cell cycle Chain: A: PDB Molecule: imc sub-compartment protein isp3; PDBTitle: structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
20	c3g9wA	Alignment		6.4	14	PDB header: cell adhesion Chain: A: PDB Molecule: tal1n-2; PDBTitle: crystal structure of talin2 f2-f3 in complex with the integrin beta1d2 cytoplasmic tail
21	d1zj8a2	Alignment	not modelled	5.7	18	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
22	d3c7bb2	Alignment	not modelled	5.5	15	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
23	d1w1ha	Alignment	not modelled	5.4	9	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)