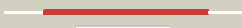



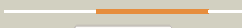
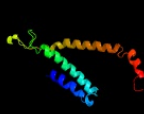

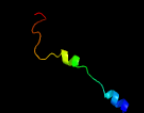

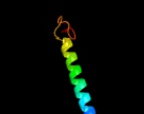



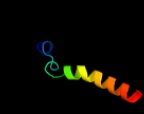





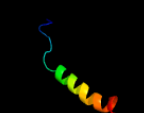






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1539_(lspA)_1742250_1742858
 Date Fri Aug 2 13:30:12 BST 2019
 Unique Job ID 57a923591a315621

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5dirD_	 Alignment		100.0	38	PDB header: hydrolase Chain: D: PDB Molecule: lipoprotein signal peptidase; PDBTitle: membrane protein at 2.8 angstroms
2	c5dirB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein signal peptidase; PDBTitle: membrane protein at 2.8 angstroms
3	c6btmC_	 Alignment		83.7	11	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
4	c2kncA_	 Alignment		43.1	25	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
5	d2oara1	 Alignment		36.5	23	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
6	c3qngD_	 Alignment		26.3	20	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
7	c2mfrA_	 Alignment		18.7	23	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
8	c6f0kC_	 Alignment		16.8	13	PDB header: membrane protein Chain: C: PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii
9	c5ireA_	 Alignment		16.7	24	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
10	c6fkip_	 Alignment		15.8	7	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
11	c5v8kB_	 Alignment		14.0	56	PDB header: photosynthesis Chain: B: PDB Molecule: proteinsubunit pshx; PDBTitle: homodimeric reaction center of h. modesticaldum

12	c6iuhC_	Alignment		12.0	33	PDB header: protein binding Chain: C: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of git1 pbd domain in complex with liprin-alpha2
13	c3rb8A_	Alignment		11.9	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of the phage tubulin phuz(semet)-gdp
14	c6btmF_	Alignment		10.6	9	PDB header: membrane protein Chain: F: PDB Molecule: alternative complex iii subunit f; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
15	d2d5ba1	Alignment		10.2	46	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
16	c2d46A_	Alignment		10.1	37	PDB header: metal transport Chain: A: PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
17	c2oarA_	Alignment		9.6	23	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
18	c6f0kF_	Alignment		9.1	16	PDB header: membrane protein Chain: F: PDB Molecule: actf; PDBTitle: alternative complex iii
19	c6oitG_	Alignment		8.4	26	PDB header: plant protein Chain: G: PDB Molecule: protein chromatin remodeling 35; PDBTitle: cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)
20	c3hzqA_	Alignment		7.8	15	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscl in an expanded intermediate state
21	c3uzeC_	Alignment	not modelled	7.4	21	PDB header: immune system Chain: C: PDB Molecule: envelope protein; PDBTitle: crystal structure of the dengue virus serotype 3 envelope protein2 domain iii in complex with the variable domains of mab 4e11
22	c4y7jE_	Alignment	not modelled	7.3	32	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
23	d1s7ba_	Alignment	not modelled	7.3	9	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
24	c3b9bA_	Alignment	not modelled	6.9	23	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
25	c1p58C_	Alignment	not modelled	6.7	16	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
26	c6iz4G_	Alignment	not modelled	6.3	20	PDB header: membrane protein Chain: G: PDB Molecule: trimeric intracellular cation channel type b-b; PDBTitle: crystal structure analysis of tric counter-ion channels in calcium2 release
27	c2voyC_	Alignment	not modelled	5.8	28	PDB header: hydrolase Chain: C: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus

28	d1ft8e_	 Alignment	not modelled	5.8	11	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Non-canonical RBD domain
29	c1x4pA_	 Alignment	not modelled	5.6	28	PDB header: rna binding protein Chain: A: PDB Molecule: putative splicing factor, arginine/serine-rich PDBTitle: solution structure of surp domain in sfrs14 protei