
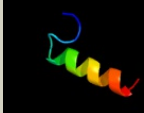





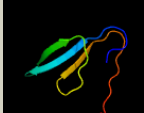
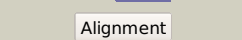



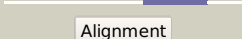

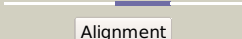
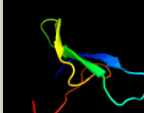
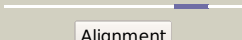

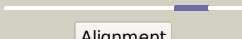
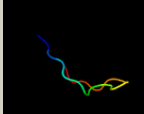
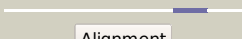
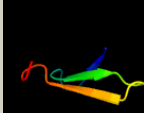


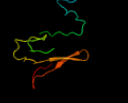
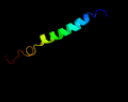
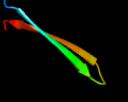






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0679c_(-) _779546_780043
Date	Fri Jul 26 01:50:24 BST 2019
Unique Job ID	03172b4b220a158a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ppiw_	 Alignment		33.5	35	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
2	c3sulA_	 Alignment		29.8	33	PDB header: unknown function Chain: A; PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 3 from m. perniciosa (mpcp3)
3	c5hceD_	 Alignment		24.5	24	PDB header: immune system Chain: D; PDB Molecule: rhhipcephalus appendiculatus rac1; PDBTitle: ternary complex of human complement c5 with ornithodoros moubata omc12 and rhhipcephalus appendiculatus rac1
4	c3d0jA_	 Alignment		24.1	15	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ca_c3497; PDBTitle: crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
5	d2pi2e1	 Alignment		16.6	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
6	d3cx5i1	 Alignment		16.2	25	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
7	d1vqoe1	 Alignment		16.1	15	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
8	c2pqaB_	 Alignment		15.1	18	PDB header: replication Chain: B; PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
9	c6az5A_	 Alignment		14.8	39	PDB header: sugar binding protein Chain: A; PDB Molecule: alpha-amylase; PDBTitle: crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k
10	c5muzA_	 Alignment		14.0	24	PDB header: viral protein Chain: A; PDB Molecule: l protein; PDBTitle: structure of a c-terminal domain of a reptarenavirus I protein
11	c3k8rA_	 Alignment		13.8	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution

12	c2fynO_	Alignment		13.3	29	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
13	c5e50A_	Alignment		13.0	16	PDB header: lyase Chain: A: PDB Molecule: aprataxin and pnk-like factor; PDBTitle: aplf/xrcc4 complex
14	c2kkIA_	Alignment		12.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mb1858; PDBTitle: solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
15	c6f0kA_	Alignment		12.4	14	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
16	c5avoA_	Alignment		12.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from2 sulfobolus tokodaii.
17	c3sukB_	Alignment		12.3	31	PDB header: unknown function Chain: B: PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 2 from m. perniciosa (mpcp2)
18	d1rl6a1	Alignment		11.6	18	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
19	c3sujA_	Alignment		10.2	27	PDB header: unknown function Chain: A: PDB Molecule: cerato-platanin 1; PDBTitle: crystal structure of cerato-platanin 1 from m. perniciosa (mpcp1)
20	c2n12A_	Alignment		10.1	38	PDB header: motor protein,protein transport Chain: A: PDB Molecule: unconventional myosin-vi; PDBTitle: solution structure of human myosin vi isoform3 (1050-1131)
21	c3sluB_	Alignment	not modelled	9.9	16	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
22	c3j21F_	Alignment	not modelled	9.4	13	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein l6p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
23	c3qr8A_	Alignment	not modelled	8.7	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
24	d1zata2	Alignment	not modelled	7.5	9	Fold: L,D-transpeptidase pre-catalytic domain-like Superfamily: L,D-transpeptidase pre-catalytic domain-like Family: L,D-transpeptidase pre-catalytic domain-like
25	c6hwhB_	Alignment	not modelled	7.0	12	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
26	c3llyA_	Alignment	not modelled	6.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: putative adhesin; PDBTitle: crystal structure of putative adhesin (yp_001304413.1) from2 parabacteroides distasonis atcc 8503 at 2.41 a resolution
27	c3ogga_	Alignment	not modelled	6.6	13	PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type d; PDBTitle: crystal structure of the receptor binding domain of botulinum2 neurotoxin d
28	c2lowA_	Alignment	not modelled	6.2	25	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip
						PDB header: transferase

29	c2kdcC_	Alignment	not modelled	6.1	17	Chain: C; PDB Molecule: diacylglycerol kinase; PDBTitle: nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
30	c4tmdA_	Alignment	not modelled	5.9	19	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: x-ray structure of putative uncharacterized protein (rv0999 ortholog)2 from mycobacterium smegmatis
31	c1vw4H_	Alignment	not modelled	5.9	14	PDB header: ribosome Chain: H; PDB Molecule: 54s ribosomal protein l23, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
32	c3j3wJ_	Alignment	not modelled	5.9	17	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l13; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
33	d1k4za_	Alignment	not modelled	5.8	18	Fold: Single-stranded right-handed beta-helix Superfamily: C-terminal domain of adenylcyclase associated protein Family: C-terminal domain of adenylcyclase associated protein
34	d1q8da_	Alignment	not modelled	5.7	38	Fold: GDNF receptor-like Superfamily: GDNF receptor-like Family: GDNF receptor-like
35	d1fcda3	Alignment	not modelled	5.7	17	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
36	c1yn3A_	Alignment	not modelled	5.6	41	PDB header: toxin, protein binding Chain: A; PDB Molecule: truncated cell surface protein map-w; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
37	d1l5pa_	Alignment	not modelled	5.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
38	c3petA_	Alignment	not modelled	5.5	15	PDB header: cell adhesion Chain: A; PDB Molecule: putative adhesin; PDBTitle: crystal structure of a putative adhesin (bf0245) from bacteroides2 fragilis nctc 9343 at 2.07 a resolution
39	c2m5sA_	Alignment	not modelled	5.4	22	PDB header: viral protein Chain: A; PDB Molecule: coat protein; PDBTitle: high-resolution nmr structure and cryo-em imaging support multiple2 functional roles for the accessory i-domain of phage p22 coat protein
40	c1yn4A_	Alignment	not modelled	5.3	29	PDB header: unknown function Chain: A; PDB Molecule: eaph1; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens
41	c1yn5B_	Alignment	not modelled	5.3	29	PDB header: unknown function Chain: B; PDB Molecule: eaph2; PDBTitle: crystal structures of eap domains from staphylococcus2 aureus reveal an unexpected homology to bacterial3 superantigens