


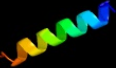

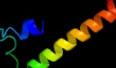

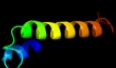







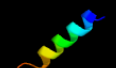

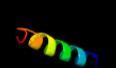




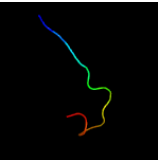
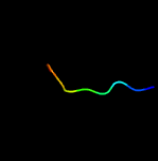
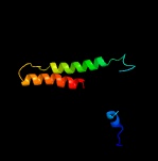
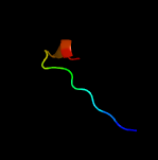
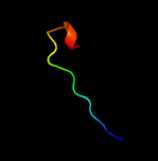
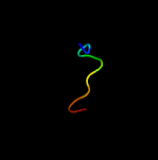
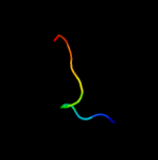

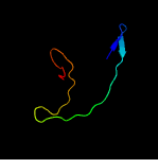


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2876 (-) _3187673_3187987
Date	Wed Aug 7 12:50:55 BST 2019
Unique Job ID	6c83819b6f60ec54

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6adqP_	 Alignment		100.0	61	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
2	c2rmzA_	 Alignment		59.7	26	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
3	c5n9yB_	 Alignment		59.1	22	PDB header: membrane protein Chain: B; PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
4	c4ev6E_	 Alignment		57.6	20	PDB header: metal transport Chain: E; PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
5	c5zazA_	 Alignment		37.0	22	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
6	c2ls2A_	 Alignment		35.4	40	PDB header: metal transport Chain: A; PDB Molecule: high affinity copper uptake protein 1; PDBTitle: 1h chemical shift assignments for the first transmembrane domain from2 human copper transport 1
7	c2kncB_	 Alignment		33.9	26	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
8	c2momB_	 Alignment		23.5	24	PDB header: membrane protein Chain: B; PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
9	c2momC_	 Alignment		23.4	24	PDB header: membrane protein Chain: C; PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
10	d1eu1a1	 Alignment		15.3	33	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
11	c5iqjB_	 Alignment		14.5	33	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: 1.9 angstrom crystal structure of protein with unknown function from2 vibrio cholerae.

12	c2d3aj_	Alignment		12.2	56	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
13	c4p5nB_	Alignment		11.5	50	PDB header: structural genomics Chain: B: PDB Molecule: hypothetical protein cnag_02591; PDBTitle: structure of cnag_02591 from cryptococcus neoformans
14	c2w2eA_	Alignment		10.6	21	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
15	c4baxH_	Alignment		9.4	50	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
16	c4is4G_	Alignment		9.2	56	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
17	c2xczA_	Alignment		8.6	45	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus
18	c3gacD_	Alignment		8.2	9	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
19	c6cuqB_	Alignment		8.2	27	PDB header: cytokine Chain: B: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica
20	c4c84B_	Alignment		7.8	27	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase znr3; PDBTitle: zebrafish znr3 ectodomain crystal form i
21	c3ug9A_	Alignment	not modelled	7.2	9	PDB header: membrane protein Chain: A: PDB Molecule: archaeal-type opsin 1, archaeal-type opsin 2; PDBTitle: crystal structure of the closed state of channelrhodopsin
22	d1uiza_	Alignment	not modelled	7.1	27	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
23	c3njaC_	Alignment	not modelled	6.5	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable ggdef family protein; PDBTitle: the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
24	c3icfB_	Alignment	not modelled	6.2	26	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase t; PDBTitle: structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
25	d1ppq1a_	Alignment	not modelled	6.1	19	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
26	c2mkvA_	Alignment	not modelled	5.9	21	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
27	c1hznA_	Alignment	not modelled	5.9	27	PDB header: hormone/growth factor Chain: A: PDB Molecule: cholecystokinin type a receptor; PDBTitle: nmr solution structure of the third extracellular loop of2 the cholecystokinin a receptor
28	c5unqF_	Alignment	not modelled	5.9	23	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of pt0534 inactivated by 2-oxo-3-

					pentynoate
29	c2mj2A_	Alignment	not modelled	5.8	25 PDB header: viral protein Chain: A: PDB Molecule: agnoprotein; PDBTitle: structure of the dimerization domain of the human polyoma, jc virus2 agnoprotein is an amphipathic alpha-helix.
30	c2os5C_	Alignment	not modelled	5.8	9 PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
31	c3rhtB_	Alignment	not modelled	5.7	22 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
32	d1dpta_	Alignment	not modelled	5.6	18 Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
33	c2jo1A_	Alignment	not modelled	5.5	38 PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
34	c2jp3A_	Alignment	not modelled	5.5	25 PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
35	c6cfwl_	Alignment	not modelled	5.4	25 PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
36	c2m59B_	Alignment	not modelled	5.3	13 PDB header: transferase Chain: B: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
37	c2m59A_	Alignment	not modelled	5.3	13 PDB header: transferase Chain: A: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
38	c2ks1A_	Alignment	not modelled	5.3	17 PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
39	c2jwaA_	Alignment	not modelled	5.3	17 PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
40	c4dh4A_	Alignment	not modelled	5.2	9 PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
41	c3mk7F_	Alignment	not modelled	5.2	16 PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
42	d1hfoa_	Alignment	not modelled	5.2	18 Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related