

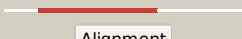

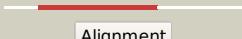



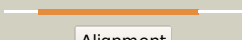

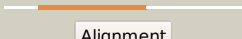

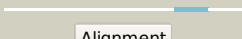
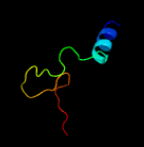
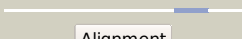


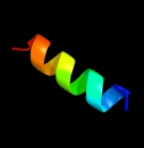

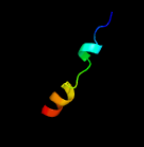

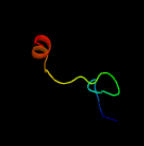
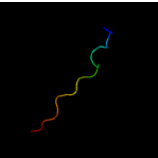

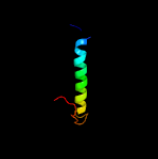
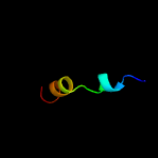

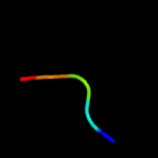
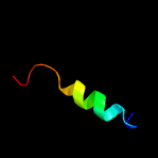
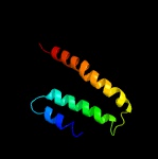



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2673 (-) _2989301_2990602
Date	Wed Aug 7 12:50:32 BST 2019
Unique Job ID	2083099fe5a590a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5f15A_	 Alignment		99.1	13	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to 2 undecaprenyl phosphate
2	c6p25A_	 Alignment		99.0	15	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
3	c6p2rB_	 Alignment		98.8	16	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
4	c3rceA_	 Alignment		94.9	15	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
5	c3wajA_	 Alignment		85.4	17	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
6	c6eznF_	 Alignment		84.9	15	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	c6nbxG_	 Alignment		35.8	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
8	c2lqtA_	 Alignment		22.0	17	PDB header: unknown function Chain: A: PDB Molecule: coiled-coil-helix-coiled-coil-helix domain-containing PDBTitle: solution structure of chcd7
9	c5z7lD_	 Alignment		14.0	47	PDB header: signaling protein Chain: D: PDB Molecule: 5-azacytidine-induced protein 2; PDBTitle: crystal structure of ndp52 skich region in complex with nap1
10	c1lrjA_	 Alignment		11.8	30	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
11	dlg12a_	 Alignment		10.5	25	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Fungal zinc peptidase

12	c5sxpG_	Alignment		10.5	24	PDB header: signaling protein/ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
13	c5sxpF_	Alignment		10.3	28	PDB header: signaling protein/ligase Chain: F: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
14	d2au5a1	Alignment		9.7	19	Fold: EF2947-like Superfamily: EF2947-like Family: EF2947-like
15	c2l64A_	Alignment		9.4	20	PDB header: hormone Chain: A: PDB Molecule: glucagon-like peptide 2; PDBTitle: nmr solution structure of glp-2 in dhpc micelles
16	c2mgyA_	Alignment		9.3	13	PDB header: membrane protein Chain: A: PDB Molecule: translocator protein; PDBTitle: solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
17	c2khsB_	Alignment		8.0	60	PDB header: hydrolase Chain: B: PDB Molecule: nuclease; PDBTitle: solution structure of snase121:snase(111-143) complex
18	c1d0rA_	Alignment		7.4	25	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
19	d2r6gf1	Alignment		7.3	17	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
20	c4mjkA_	Alignment		7.0	38	PDB header: protein binding Chain: A: PDB Molecule: crispr protein; PDBTitle: crystal structure of a crispr protein from archaeoglobus fulgidus
21	c2x3bB_	Alignment	not modelled	6.6	18	PDB header: hydrolase Chain: B: PDB Molecule: toxic extracellular endopeptidase; PDBTitle: asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
22	c1xb4C_	Alignment	not modelled	6.6	45	PDB header: unknown function Chain: C: PDB Molecule: hypothetical 23.6 kda protein in yuh1-ura8 intergenic PDBTitle: crystal structure of subunit vps25 of the endosomal trafficking2 complex escrt-ii
23	c3rq9B_	Alignment	not modelled	6.4	33	PDB header: tse2-binding protein Chain: B: PDB Molecule: type vi secretion immunity protein; PDBTitle: structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
24	c4auoH_	Alignment	not modelled	6.3	14	PDB header: hydrolase/peptide Chain: H: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
25	c4auoE_	Alignment	not modelled	6.3	14	PDB header: hydrolase/peptide Chain: E: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
26	c2na6B_	Alignment	not modelled	6.0	28	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
27	c2na6C_	Alignment	not modelled	6.0	28	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
						PDB header: apoptosis

28	c2na6A_	Alignment	not modelled	6.0	28	Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
29	d1xb4a1	Alignment	not modelled	5.9	45	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
30	c2zmeD_	Alignment	not modelled	5.9	45	PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
31	c4auoD_	Alignment	not modelled	5.9	14	PDB header: hydrolase/peptide Chain: D: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
32	c4auoG_	Alignment	not modelled	5.9	14	PDB header: hydrolase/peptide Chain: G: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
33	c4auoF_	Alignment	not modelled	5.9	14	PDB header: hydrolase/peptide Chain: F: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
34	d1e0na_	Alignment	not modelled	5.6	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
35	c4auoC_	Alignment	not modelled	5.4	14	PDB header: hydrolase/peptide Chain: C: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
36	c5a4hA_	Alignment	not modelled	5.3	41	PDB header: transferase Chain: A: PDB Molecule: 1-acylglycerol-3-phosphate o-acyltransferase abhd5; PDBTitle: solution structure of the lipid droplet anchoring peptide2 of cgi-58 bound to dpc micelles