

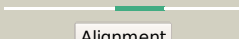

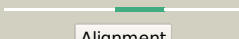
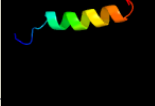



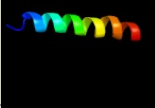

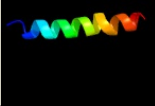
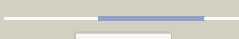
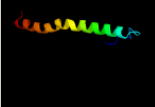
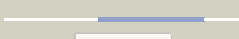
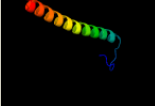
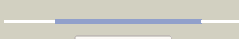





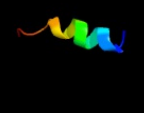

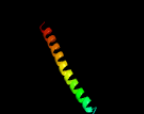




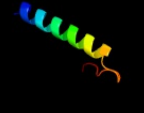



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0531 (-) _622332_622649
Date	Fri Jul 26 01:50:08 BST 2019
Unique Job ID	7e07750b7ed71fd3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k1kA_	 Alignment		44.8	52	PDB header: signaling protein Chain: A; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
2	c2k1kB_	 Alignment		44.8	52	PDB header: signaling protein Chain: B; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
3	c2k1lB_	 Alignment		44.8	52	PDB header: signaling protein Chain: B; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
4	c2k1lA_	 Alignment		44.8	52	PDB header: signaling protein Chain: A; PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
5	c2micA_	 Alignment		26.9	16	PDB header: membrane protein Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
6	c2micB_	 Alignment		26.9	16	PDB header: membrane protein Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
7	c2kb1A_	 Alignment		25.5	23	PDB header: membrane protein Chain: A; PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
8	d1r3jc_	 Alignment		23.0	19	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
9	c4wd7A_	 Alignment		20.5	34	PDB header: membrane protein Chain: A; PDB Molecule: bestrophin domain protein; PDBTitle: crystal structure of a bacterial bestrophin homolog from klebsiella2 pneumoniae by zn-sad phasing
10	c1ciiA_	 Alignment		18.4	32	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
11	c2lx0A_	 Alignment		15.7	36	PDB header: membrane protein Chain: A; PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles

12	c1pnbA	Alignment		13.3	33	PDB header: seed storage protein Chain: A: PDB Molecule: napin bnib; PDBTitle: structure of napin bnib, nmr, 10 structures
13	c2l1xA	Alignment		12.8	33	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone; PDBTitle: the solution structure of human parathyroid hormone-related protein
14	c5sv0C	Alignment		11.3	22	PDB header: transport protein Chain: C: PDB Molecule: biopolymer transport protein exbb; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 7.0
15	c2i88A	Alignment		9.0	53	PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin e1
16	c3lfmA	Alignment		8.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein fto; PDBTitle: crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
17	d2ib0a1	Alignment		8.0	16	Fold: Ferritin-like Superfamily: Ferritin-like Family: Rv2844-like
18	c2ib0A	Alignment		8.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical alanine rich protein; PDBTitle: crystal structure of a conserved hypothetical protein, rv2844, from2 mycobacterium tuberculosis
19	c2kktA	Alignment		7.8	36	PDB header: transcription Chain: A: PDB Molecule: ataxin-7-like protein 3; PDBTitle: solution structure of the sca7 domain of human ataxin-7-13 protein
20	c4g4gA	Alignment		7.7	17	PDB header: hydrolase Chain: A: PDB Molecule: 4-o-methyl-glucuronoyl methylesterase; PDBTitle: crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
21	c6gcsq	Alignment	not modelled	7.5	30	PDB header: oxidoreductase Chain: G: PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
22	d1cia1	Alignment	not modelled	7.4	32	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
23	c3m4wE	Alignment	not modelled	7.1	44	PDB header: signaling protein/signaling protein Chain: E: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: structural basis for the negative regulation of bacterial stress2 response by rseb
24	c6dftE	Alignment	not modelled	7.1	40	PDB header: transferase Chain: E: PDB Molecule: deoxyhypusine synthase; PDBTitle: trypanosoma brucei deoxyhypusine synthase
25	c5eofB	Alignment	not modelled	6.8	19	PDB header: protein binding/transferase Chain: B: PDB Molecule: optineurin; PDBTitle: crystal structure of optn ntd and tbk1 ctd complex
26	c5vkvA	Alignment	not modelled	6.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccda; PDBTitle: solution nmr structure of the membrane electron transporter ccda
27	c4ds7E	Alignment	not modelled	6.1	17	PDB header: protein binding Chain: E: PDB Molecule: spindle pole body component 110; PDBTitle: crystal structure of yeast calmodulin bound to the c-terminal fragment2 of spindle pole body protein spc110
28	d1p90a	Alignment	not modelled	5.4	23	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: Nitrogenase accessory factor

29

[c2hdiB_](#)

Alignment

not modelled

5.4

23

PDB header:protein transport,antimicrobial protein

Chain: B: **PDB Molecule:**colicin-ia;

PDBTitle: crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.