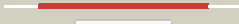




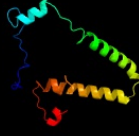



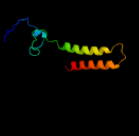
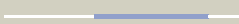











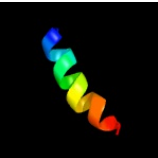
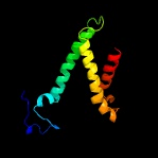

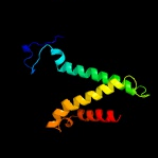




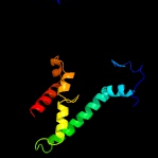


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1085c_(-)_1209761_1210489
Date	Wed Jul 31 22:05:16 BST 2019
Unique Job ID	50c4648a5c3e4e5c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3wxvA	 Alignment		100.0	20	PDB header: membrane protein/immune system Chain: A: PDB Molecule: adiponectin receptor protein 1; PDBTitle: crystal structure of the human adiponectin receptor 1
2	c6g7oA	 Alignment		98.0	15	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
3	c4ymkA	 Alignment		45.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
4	d1xl3c1	 Alignment		26.4	25	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: TyeA-like
5	c6adqP	 Alignment		25.5	10	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
6	c4pguA	 Alignment		20.3	7	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein yetj; PDBTitle: crystal structure of yetj from bacillus subtilis at ph 7 by soaking
7	c2khsB	 Alignment		17.8	15	PDB header: hydrolase Chain: B: PDB Molecule: nuclease; PDBTitle: solution structure of snase121:snase(111-143) complex
8	c5ajaC	 Alignment		17.3	25	PDB header: viral protein Chain: C: PDB Molecule: sam domain and hd domain-containing protein; PDBTitle: crystal structure of mandrill samhd1 (amino acid residues 1-114)2 bound to vpx isolated from mandrill and human dcaf1 (amino3 acid residues 1058-1396)
9	d1dxsa	 Alignment		17.2	15	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
10	d2e74g1	 Alignment		14.7	38	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
11	c1vf5G	 Alignment		14.5	38	PDB header: photosynthesis Chain: G: PDB Molecule: protein pet g; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus

12	d1vf5g_	Alignment		14.5	38	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
13	c6bwdC_	Alignment		12.3	12	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
14	c6bwdD_	Alignment		12.3	12	PDB header: membrane protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
15	c6bwdA_	Alignment		12.3	12	PDB header: membrane protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
16	c6bwdB_	Alignment		12.3	12	PDB header: membrane protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
17	c6bwfA_	Alignment		11.7	14	PDB header: membrane protein Chain: A: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
18	c6bwfD_	Alignment		11.7	14	PDB header: membrane protein Chain: D: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
19	c6bwfB_	Alignment		11.7	14	PDB header: membrane protein Chain: B: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
20	c6bwfC_	Alignment		11.7	14	PDB header: membrane protein Chain: C: PDB Molecule: trpm7; PDBTitle: 4.1 angstrom mg2+-unbound structure of mouse trpm7
21	c1yq3C_	Alignment	not modelled	10.9	9	PDB header: oxidoreductase Chain: C: PDB Molecule: succinate dehydrogenase cytochrome b, large subunit; PDBTitle: avian respiratory complex ii with oxaloacetate and ubiquinone
22	c5zx5D_	Alignment	not modelled	9.7	14	PDB header: transferase Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.3 angstrom structure of mouse trpm7 with edta
23	c2e76G_	Alignment	not modelled	9.7	35	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6-f complex subunit 5; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
24	c4lmoB_	Alignment	not modelled	9.5	19	PDB header: rna binding protein Chain: B: PDB Molecule: telomerase reverse transcriptase; PDBTitle: structure of a vertebrate rna binding domain of telomerase (trbd)
25	c4h9kA_	Alignment	not modelled	9.0	19	PDB header: hydrolase Chain: A: PDB Molecule: hog cholera virus; PDBTitle: crystal structure of cleavage site mutant of npro of classical swine2 fever virus.
26	c3ahrA_	Alignment	not modelled	8.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
27	c1rue4_	Alignment	not modelled	8.0	25	PDB header: virus Chain: 4: PDB Molecule: rhinovirus 14; PDBTitle: rhinovirus 14 site directed mutant n1219a complexed with2 antiviral compound win 52035
28	c3u5gh_	Alignment	not modelled	7.5	15	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s7-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome

					b
29	d1rp4a_	Alignment	not modelled	7.4	12 Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
30	c2koeA_	Alignment	not modelled	7.4	13 PDB header: membrane protein, signaling protein Chain: A: PDB Molecule: human cannabinoid receptor 1 - helix 7/8 peptide; PDBTitle: human cannabinoid receptor 1 - helix 7/8 peptide
31	c6p25A_	Alignment	not modelled	7.1	10 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
32	c5o6vE_	Alignment	not modelled	7.0	15 PDB header: virus Chain: E: PDB Molecule: small envelope protein m; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
33	d1jga_	Alignment	not modelled	6.5	6 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
34	c3t98A_	Alignment	not modelled	6.3	30 PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
35	d2v4ja2	Alignment	not modelled	6.3	19 Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
36	c6aksD_	Alignment	not modelled	6.1	11 PDB header: virus Chain: D: PDB Molecule: vp4; PDBTitle: cryo-em structure of cva10 mature virus
37	c1dgi4_	Alignment	not modelled	5.9	24 PDB header: virus/viral protein, receptor Chain: 4: PDB Molecule: vp4; PDB Fragment: poliovirus fragments vp1, vp2, vp3, vp4; PDBTitle:
38	c2r4gA_	Alignment	not modelled	5.8	4 PDB header: transferase Chain: A: PDB Molecule: telomerase reverse transcriptase; PDBTitle: the high resolution structure of the rna-binding domain of telomerase
39	c6iuaB_	Alignment	not modelled	5.7	29 PDB header: transport protein/protein binding Chain: B: PDB Molecule: peptide from tp53-binding protein 1; PDBTitle: crystal structure of importin-alpha1 bound to the 53bp1 nuclear2 localization signal (s1678d)
40	c4bz4D_	Alignment	not modelled	5.7	18 PDB header: copper-binding protein Chain: D: PDB Molecule: copper-repressible polypeptide; PDBTitle: cora is a surface-associated copper-binding protein2 important in methylomicrobium album bg8 copper acquisition
41	c5o6vF_	Alignment	not modelled	5.6	19 PDB header: virus Chain: F: PDB Molecule: small envelope protein m; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
42	c2k9pA_	Alignment	not modelled	5.4	12 PDB header: membrane protein Chain: A: PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles
43	c3vbhD_	Alignment	not modelled	5.3	11 PDB header: virus Chain: D: PDB Molecule: genome polyprotein, capsid protein vp4; PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group r32)