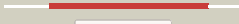
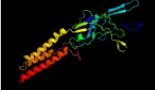


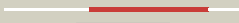


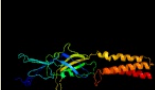







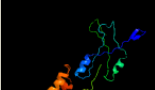





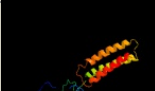

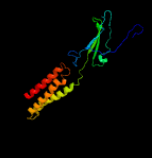

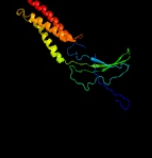



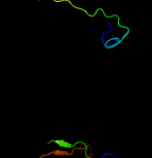



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0713 (-)_809949_810890
Date	Fri Jul 26 01:50:28 BST 2019
Unique Job ID	339702372ba40bcd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eamB_	 Alignment		96.8	18	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: glr4197 protein; PDBTitle: an open-pore structure of a bacterial pentameric ligand-2 gated ion channel
2	c4pirD_	 Alignment		96.5	10	PDB header: transport protein Chain: D: PDB Molecule: 5-hydroxytryptamine receptor 3a; PDBTitle: x-ray structure of the mouse serotonin 5-ht3 receptor
3	c3jadC_	 Alignment		96.2	15	PDB header: signaling protein/antagonist Chain: C: PDB Molecule: glycine receptor subunit alphaz1; PDBTitle: structure of alpha-1 glycine receptor by single particle electron2 cryo-microscopy, strychnine-bound state
4	c6d6uB_	 Alignment		96.0	16	PDB header: transport protein Chain: B: PDB Molecule: gamma-aminobutyric acid receptor subunit alpha-1,gamma- PDBTitle: human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation a
5	c4cofC_	 Alignment		95.8	15	PDB header: transport protein Chain: C: PDB Molecule: gamma-aminobutyric acid receptor subunit beta-3; PDBTitle: crystal structure of a human gamma-aminobutyric acid receptor, the2 gaba(a)r-beta3 homopentamer
6	c2vl0A_	 Alignment		95.7	20	PDB header: membrane protein Chain: A: PDB Molecule: elic pentameric ligand gated ion channel from PDBTitle: x-ray structure of a pentameric ligand gated ion channel2 from erwinia chrysanthemi (elic)
7	c3riaC_	 Alignment		95.0	14	PDB header: transport protein/immune system Chain: C: PDB Molecule: avermectin-sensitive glutamate-gated chloride channel glucl PDBTitle: c. elegans glutamate-gated chloride channel (glucl) in complex with2 fab, ivermectin and iodide.
8	c6hinA_	 Alignment		94.5	11	PDB header: membrane protein Chain: A: PDB Molecule: 5-hydroxytryptamine receptor 3a; PDBTitle: mouse serotonin 5-ht3 receptor, serotonin-bound, f conformation
9	c6fvqE_	 Alignment		91.6	16	PDB header: membrane protein Chain: E: PDB Molecule: cys-loop ligand-gated ion channel; PDBTitle: the active form of a pentameric ion channel (stelic) gated by alkaline2 ph - r86a
10	c5kxiA_	 Alignment		90.7	11	PDB header: transport protein Chain: A: PDB Molecule: neuronal acetylcholine receptor subunit alpha-4; PDBTitle: x-ray structure of the human alpha4beta2 nicotinic receptor
11	c4aq9E_	 Alignment		88.8	13	PDB header: membrane protein Chain: E: PDB Molecule: acetylcholine receptor gamma subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time- resolved2 electron cryo-microscopy (open class)

12	c4aq5B_	Alignment		86.5	13	PDB header: membrane protein Chain: B: PDB Molecule: acetylcholine receptor beta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
13	c2bg9E_	Alignment		85.2	13	PDB header: ion channel/receptor Chain: E: PDB Molecule: acetylcholine receptor protein, gamma chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
14	c4aq5C_	Alignment		84.2	16	PDB header: membrane protein Chain: C: PDB Molecule: acetylcholine receptor delta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
15	c5kxiC_	Alignment		82.9	15	PDB header: transport protein Chain: C: PDB Molecule: neuronal acetylcholine receptor subunit beta-2; PDBTitle: x-ray structure of the human alpha4beta2 nicotinic receptor
16	c4aq5A_	Alignment		79.1	13	PDB header: membrane protein Chain: A: PDB Molecule: acetylcholine receptor subunit alpha; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
17	c2bg9A_	Alignment		79.1	13	PDB header: ion channel/receptor Chain: A: PDB Molecule: acetylcholine receptor protein, alpha chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
18	c6d6uE_	Alignment		77.7	15	PDB header: transport protein Chain: E: PDB Molecule: gamma-aminobutyric acid receptor subunit gamma-2,gamma- PDBTitle: human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation a
19	c5jxfA_	Alignment		66.9	13	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
20	c5jxpA_	Alignment		63.9	11	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
21	c2bg9B_	Alignment	not modelled	59.4	14	PDB header: ion channel/receptor Chain: B: PDB Molecule: acetylcholine receptor protein, beta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
22	c4y01B_	Alignment	not modelled	57.5	12	PDB header: hydrolase Chain: B: PDB Molecule: peptidase s46; PDBTitle: crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
23	c3wolB_	Alignment	not modelled	54.9	24	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
24	c6iz4G_	Alignment	not modelled	44.9	30	PDB header: membrane protein Chain: G: PDB Molecule: trimeric intracellular cation channel type b-b; PDBTitle: crystal structure analysis of tric counter-ion channels in calcium2 release
25	c6d6tE_	Alignment	not modelled	44.8	15	PDB header: transport protein Chain: E: PDB Molecule: human gaba-a receptor subunit gamma-2; PDBTitle: human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation b
26	c2m59A_	Alignment	not modelled	44.3	20	PDB header: transferase Chain: A: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
27	c2m59B_	Alignment	not modelled	44.3	20	PDB header: transferase Chain: B: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
						PDB header: membrane protein

28	c5egiB_	Alignment	not modelled	40.4	25	Chain: B; PDB Molecule: uncharacterized protein y5/a10a.10; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
29	c6iz0A_	Alignment	not modelled	38.3	28	PDB header: membrane protein Chain: A; PDB Molecule: trimeric intracellular cation channel type a; PDBTitle: crystal structure analysis of a eukaryotic membrane protein
30	c5eikA_	Alignment	not modelled	38.1	28	PDB header: membrane protein Chain: A; PDB Molecule: uncharacterized protein y57a10a.28; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
31	c2bg9C_	Alignment	not modelled	36.6	14	PDB header: ion channel/receptor Chain: C; PDB Molecule: acetylcholine receptor protein, delta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
32	c5j09F_	Alignment	not modelled	28.7	16	PDB header: virus Chain: F; PDB Molecule: beak and feather disease virus capsid protein; PDBTitle: crystal structure of decameric bfdv capsid protein
33	c5jkkB_	Alignment	not modelled	26.0	50	PDB header: solute binding protein Chain: B; PDB Molecule: pfvft1; PDBTitle: crystal structure of plasmodium falciparum pf3d7_0606800 (pfvft1)
34	c2qc1B_	Alignment	not modelled	17.7	13	PDB header: protein binding Chain: B; PDB Molecule: acetylcholine receptor subunit alpha; PDBTitle: crystal structure of the extracellular domain of the nicotinic2 acetylcholine receptor 1 subunit bound to alpha-bungarotoxin at 1.9 a3 resolution
35	c2voyB_	Alignment	not modelled	12.0	30	PDB header: hydrolase Chain: B; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
36	c1zzaA_	Alignment	not modelled	11.5	38	PDB header: membrane protein Chain: A; PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
37	c4xbiA_	Alignment	not modelled	9.9	24	PDB header: chaperone Chain: A; PDB Molecule: clpb protein, putative,green fluorescent protein; PDBTitle: structure of a malarial protein involved in proteostasis
38	c3r0rA_	Alignment	not modelled	9.4	29	PDB header: virus Chain: A; PDB Molecule: porcine circovirus 2 (pcv2) capsid protein; PDBTitle: the 2.3 a structure of porcine circovirus 2
39	c1wcuA_	Alignment	not modelled	8.9	15	PDB header: carbohydrate binding Chain: A; PDB Molecule: non-catalytic protein 1; PDBTitle: cbm29_1, a family 29 carbohydrate binding module from2 piromyces equi
40	d1x4ka2	Alignment	not modelled	8.0	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
41	c4gx5D_	Alignment	not modelled	7.7	13	PDB header: transport protein Chain: D; PDB Molecule: trka domain protein; PDBTitle: gsuk channel
42	d1xmeb2	Alignment	not modelled	7.5	54	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
43	c6c14A_	Alignment	not modelled	7.5	14	PDB header: membrane protein, metal transport Chain: A; PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
44	c4d01A_	Alignment	not modelled	7.5	14	PDB header: signaling protein Chain: A; PDB Molecule: neuronal acetylcholine receptor subunit alpha-9; PDBTitle: crystal structure of the extracellular domain of the human2 alpha9 nicotinic acetylcholine receptor
45	c2na6B_	Alignment	not modelled	7.3	33	PDB header: apoptosis Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
46	c2na6A_	Alignment	not modelled	7.3	33	PDB header: apoptosis Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
47	c2na6C_	Alignment	not modelled	7.3	33	PDB header: apoptosis Chain: C; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
48	d1kp5a_	Alignment	not modelled	6.5	24	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
49	c4gucA_	Alignment	not modelled	6.4	20	PDB header: unknown function Chain: A; PDB Molecule: protein ba_2500; PDBTitle: 1.4 angstrom resolution crystal structure of uncharacterized protein2 ba_2500 from bacillus anthracis str. ames
50	d2a8ea1	Alignment	not modelled	6.3	40	Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: YktB-like
51	c3akoG_	Alignment	not modelled	6.3	27	PDB header: fluorescent protein Chain: G; PDB Molecule: venus; PDBTitle: crystal structure of the reassembled venus
52	c5xyhA_	Alignment	not modelled	6.2	50	PDB header: hydrolase Chain: A; PDB Molecule: cbbsa; PDBTitle: crystal structure of catalytic domain of 1,4-beta-

						cellobiosidase2 (cbsa) from xanthomonas oryzae pv. oryzae
53	c1vw4E_	Alignment	not modelled	6.0	14	PDB header: ribosome Chain: E: PDB Molecule: 54s ribosomal protein l7, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
54	c6n3qD_	Alignment	not modelled	5.9	12	PDB header: transport protein Chain: D: PDB Molecule: protein translocation protein sec63; PDBTitle: cryo-em structure of the yeast sec complex
55	d1ttza_	Alignment	not modelled	5.9	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
56	c3osrA_	Alignment	not modelled	5.8	24	PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
57	d1oxda_	Alignment	not modelled	5.5	24	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
58	c3mqzA_	Alignment	not modelled	5.4	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein duf1054; PDBTitle: crystal structure of conserved protein duf1054 from pink subaerial2 biofilm microbial leptospirillum sp. group ii uba.