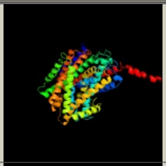
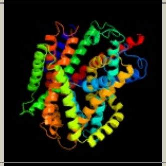
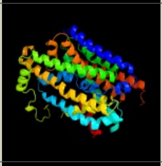
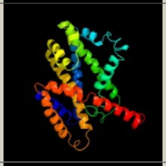
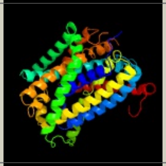
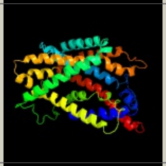
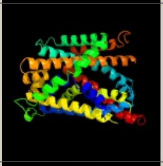
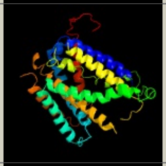
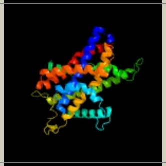
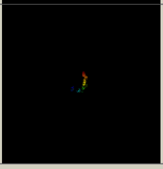
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD0917_(betP)_1022091_1023872
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	239d7fb2851e7bcb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8aC_	Alignment		100.0	41	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
2	c3hfxA_	Alignment		100.0	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
3	c4ainB_	Alignment		100.0	41	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of betp with asymmetric protomers.
4	c5nvaA_	Alignment		99.3	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative sodium:solute symporter; **PDBTitle:** substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
5	c2xq2A_	Alignment		97.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
6	c5i6xA_	Alignment		97.6	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium-dependent serotonin transporter; **PDBTitle:** x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
7	c4m48A_	Alignment		97.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter; **PDBTitle:** x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
8	d2a65a1	Alignment		97.4	13	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
9	c4us3A_	Alignment		97.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter; **PDBTitle:** crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
10	c5oqtA_	Alignment		97.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid transporter; **PDBTitle:** crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
11	c3dh4A_	Alignment		97.1	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus

12	c2jlnA_	Alignment		96.9	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
13	c3giaA_	Alignment		96.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
14	c4djiA_	Alignment		95.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable glutamate/gamma-aminobutyrate antiporter; **PDBTitle:** structure of glutamate-gaba antiporter gadc
15	c6irtB_	Alignment		95.5	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**large neutral amino acids transporter small subunit 1; **PDBTitle:** human lat1-4f2hc complex bound with bch
16	c6f2wA_	Alignment		92.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative amino acid/polyamine transport protein; **PDBTitle:** bacterial asc transporter crystal structure in open to in conformation
17	c3lrcC_	Alignment		91.9	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
18	c4wgvC_	Alignment		68.2	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
19	c4wgwA_	Alignment		68.2	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
20	c6bm8A_	Alignment		40.7	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** crystal structure of glycoprotein b from herpes simplex virus type i
21	c5xmjG_	Alignment	not modelled	33.6	13	**PDB header:**electron transport **Chain:** G: **PDB Molecule:**fumarate reductase respiratory complex; **PDBTitle:** crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
22	c5m87A_	Alignment	not modelled	26.8	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** crystal structure of eremococcus coleocola manganese transporter
23	c3gztF_	Alignment	not modelled	24.1	40	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
24	c2kvlA_	Alignment	not modelled	22.8	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
25	c1f59C_	Alignment	not modelled	18.7	67	**PDB header:**transport protein receptor **Chain:** C: **PDB Molecule:**fxfg nucleoporin repeats; **PDBTitle:** importin-beta-fxfg nucleoporin complex
26	c3s2xB_	Alignment	not modelled	17.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
27	c6jmqA_	Alignment	not modelled	16.1	13	**PDB header:**membrane protein/immune system **Chain:** A: **PDB Molecule:**large neutral amino acids transporter small subunit 1; **PDBTitle:** lat1-cd98hc complex bound to mem-108 fab
28	c4p6vB_	Alignment	not modelled	16.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**na(+)-translocating nadh-quinone reductase subunit b; **PDBTitle:** crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae

29	c4iu9A_	Alignment	not modelled	15.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter
30	c1x59A_	Alignment	not modelled	14.4	40	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** solution structures of the whep-trs domain of human2 histidyl-trna synthetase
31	c3jcuM_	Alignment	not modelled	14.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
32	c3jcum_	Alignment	not modelled	14.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
33	c1xb4C_	Alignment	not modelled	13.9	14	**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
34	c2qksA_	Alignment	not modelled	12.8	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
35	d2f2ha1	Alignment	not modelled	12.3	33	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
36	c1zzaA_	Alignment	not modelled	12.3	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
37	c6c08F_	Alignment	not modelled	11.5	13	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**sodium-coupled neutral amino acid transporter 9; **PDBTitle:** zebrafish slc38a9 with arginine bound in the cytosol open state
38	c5azcA_	Alignment	not modelled	10.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**prolipoprotein diacylglyceryl transferase; **PDBTitle:** crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
39	c6hwhB_	Alignment	not modelled	10.0	15	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
40	c5xnlM_	Alignment	not modelled	9.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** structure of stacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
41	c5xnmM_	Alignment	not modelled	9.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
42	c5xnlm_	Alignment	not modelled	9.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** structure of stacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
43	c5xnmm_	Alignment	not modelled	9.2	41	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
44	c3syaA_	Alignment	not modelled	8.3	30	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**g protein-activated inward rectifier potassium channel 2; **PDBTitle:** crystal structure of the g protein-gated inward rectifier k+ channel2 girk2 (kir3.2) in complex with sodium and pip2
45	c3s0xB_	Alignment	not modelled	8.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
46	c2lcoA_	Alignment	not modelled	8.0	40	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**walp19-p8 peptide; **PDBTitle:** 1h and 15n assignments of walp19-p8 peptide in sds micelles
47	c3j2wH_	Alignment	not modelled	7.3	24	**PDB header:**virus **Chain:** H: **PDB Molecule:**glycoprotein e1; **PDBTitle:** electron cryo-microscopy of chikungunya virus
48	c3j2wE_	Alignment	not modelled	7.3	24	**PDB header:**virus **Chain:** E: **PDB Molecule:**glycoprotein e1; **PDBTitle:** electron cryo-microscopy of chikungunya virus
49	c5mdxm_	Alignment	not modelled	7.3	44	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** cryo-em structure of the psii supercomplex from arabidopsis thaliana
50	c5mdxM_	Alignment	not modelled	7.3	44	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**photosystem ii reaction center protein m; **PDBTitle:** cryo-em structure of the psii supercomplex from arabidopsis thaliana
51	c2qwuB_	Alignment	not modelled	6.9	25	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**intracellular growth locus, subunit c; **PDBTitle:** crystal structure of f. tularensis pathogenicity island protein c
52	d1m56d_	Alignment	not modelled	6.8	17	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
53	c3qf4B_	Alignment	not modelled	6.8	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized abc transporter atp-binding protein **PDBTitle:** crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation

54	d2nwwa1	Alignment	not modelled	6.6	12	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
55	c5gasN_	Alignment	not modelled	6.5	11	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**archaeal/vacuolar-type h+-atpase subunit i; **PDBTitle:** thermus thermophilus v/a-atpase, conformation 2
56	c3f1iH_	Alignment	not modelled	6.5	50	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
57	c5hdjA_	Alignment	not modelled	6.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nfra1; **PDBTitle:** structure of b. megaterium nfra1
58	c3l09B_	Alignment	not modelled	6.1	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
59	c6djyC_	Alignment	not modelled	5.9	13	**PDB header:**virus **Chain:** C: **PDB Molecule:**major capsid protein; **PDBTitle:** fako virus
60	c3pcqX_	Alignment	not modelled	5.9	38	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
61	c4iu8A_	Alignment	not modelled	5.9	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter (selenomethionine2 derivative)
62	d2axtm1	Alignment	not modelled	5.8	46	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein M, PsbM **Family:**PsbM-like
63	c5kpeA_	Alignment	not modelled	5.8	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo beta sheet design protein or664; **PDBTitle:** solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664
64	c6csfC_	Alignment	not modelled	5.7	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**sodium/alanine symporter agcs; **PDBTitle:** crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
65	c1jb0X_	Alignment	not modelled	5.6	38	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
66	d1jb0x_	Alignment	not modelled	5.6	38	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
67	c4fe1X_	Alignment	not modelled	5.6	38	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** improving the accuracy of macromolecular structure refinement at 7 a2 resolution
68	c4j29A_	Alignment	not modelled	5.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**engineered protein or258; **PDBTitle:** crystal structure of engineered protein. northeast structural genomics2 consortium target or258.
69	c5o9zP_	Alignment	not modelled	5.5	32	**PDB header:**splicing **Chain:** P: **PDB Molecule:**u4/u6.u5 tri-snrnp-associated protein 1; **PDBTitle:** cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
70	c3kv1A_	Alignment	not modelled	5.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
71	c2n28A_	Alignment	not modelled	5.2	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein vpu; **PDBTitle:** solid-state nmr structure of vpu
72	c5o31Z_	Alignment	not modelled	5.2	14	**PDB header:**oxidoreductase **Chain:** Z: **PDB Molecule:**nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit **PDBTitle:** mitochondrial complex i in the deactive state
73	c4k1cB_	Alignment	not modelled	5.1	15	**PDB header:**membrane protein/metal transport **Chain:** B: **PDB Molecule:**vacuolar calcium ion transporter; **PDBTitle:** vcx1 calcium/proton exchanger