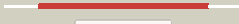



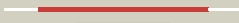



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0346c_(ansP2)_415502_416965
Date	Tue Jul 23 14:50:41 BST 2019
Unique Job ID	c2174d0ca2e96734

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4djiA_	 Alignment		100.0	15	PDB header: transport protein Chain: A; PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
2	c5oqtA_	 Alignment		100.0	20	PDB header: transport protein Chain: A; PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
3	c6f2wA_	 Alignment		100.0	18	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
4	c3giaA_	 Alignment		100.0	18	PDB header: transport protein Chain: A; PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
5	c6irtB_	 Alignment		100.0	16	PDB header: membrane protein Chain: B; PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
6	c3lrcC_	 Alignment		100.0	18	PDB header: transport protein Chain: C; PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
7	c6jmqA_	 Alignment		100.0	19	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
8	c6csfC_	 Alignment		100.0	11	PDB header: membrane protein Chain: C; PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
9	c2jlnA_	 Alignment		100.0	11	PDB header: membrane protein Chain: A; PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
10	c6c08F_	 Alignment		99.6	8	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
11	c5nvaA_	 Alignment		99.5	10	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

12	c2xq2A_	Alignment		99.3	9	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
13	c3dh4A_	Alignment		99.2	8	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
14	c6c08C_	Alignment		98.9	9	PDB header: membrane protein Chain: C: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
15	c5m87A_	Alignment		98.6	11	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
16	c4wqwA_	Alignment		98.6	15	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
17	c4wqvC_	Alignment		98.6	15	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
18	c4m48A_	Alignment		98.2	14	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
19	c5i6xA_	Alignment		98.2	10	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
20	d2a65a1	Alignment		98.0	10	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
21	c2w8aC_	Alignment	not modelled	97.5	11	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
22	c4us3A_	Alignment	not modelled	97.5	12	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
23	c4ainB_	Alignment	not modelled	97.4	12	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
24	c3hfxA_	Alignment	not modelled	94.4	11	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
25	c5kteA_	Alignment	not modelled	76.5	16	PDB header: transport protein/immune system Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
26	c6nbxG_	Alignment	not modelled	54.6	12	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
27	c4k1cB_	Alignment	not modelled	51.8	11	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
28	c5xpdA_	Alignment	not modelled	25.0	10	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog

29	c5sv0C_	Alignment	not modelled	22.7	9	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
30	c3ixzA_	Alignment	not modelled	21.4	8	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
31	c4x5mB_	Alignment	not modelled	18.1	9	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of semisweet in the inward-open conformation
32	c4px7A_	Alignment	not modelled	17.4	9	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggpb
33	c5ny0A_	Alignment	not modelled	17.1	21	PDB header: cell adhesion Chain: A: PDB Molecule: l. reuters srrp binding region; PDBTitle: l. reuters 100-23 srrp
34	c3qngD_	Alignment	not modelled	16.6	4	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
35	c2bbjB_	Alignment	not modelled	16.5	6	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
36	c5v2sA_	Alignment	not modelled	16.1	13	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
37	c5i6cB_	Alignment	not modelled	15.2	13	PDB header: transport protein Chain: B: PDB Molecule: uric acid-xanthine permease; PDBTitle: the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
38	c2momC_	Alignment	not modelled	15.2	19	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
39	d1fftb2	Alignment	not modelled	14.5	7	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
40	c3jlzP_	Alignment	not modelled	14.0	10	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yjip revealed by2 cryo-electron microscopy
41	d1pw4a_	Alignment	not modelled	13.9	7	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
42	d1j6ra_	Alignment	not modelled	13.3	22	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Hypothetical protein TM0269
43	c2momB_	Alignment	not modelled	13.0	17	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
44	c6hwhX_	Alignment	not modelled	12.8	10	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
45	c5cthB_	Alignment	not modelled	12.8	9	PDB header: transport protein Chain: B: PDB Molecule: bidirectional sugar transporter sweet2b; PDBTitle: the 3.7 a resolution structure of a eukaryotic sweet transporter
46	c4k1cA_	Alignment	not modelled	12.8	10	PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
47	c2m67A_	Alignment	not modelled	12.4	16	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
48	c3mkuA_	Alignment	not modelled	12.1	9	PDB header: transport protein Chain: A: PDB Molecule: multi antimicrobial extrusion protein (na(+))/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
49	c5xyiP_	Alignment	not modelled	11.6	13	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
50	c2lowA_	Alignment	not modelled	10.9	13	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp
51	c4o9tH_	Alignment	not modelled	10.8	12	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
52	c5oonA_	Alignment	not modelled	10.7	12	PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca
53	c3jcuS_	Alignment	not modelled	9.9	15	PDB header: membrane protein Chain: S: PDB Molecule: chlorophyll a-b binding protein 26 kd (cp26); PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution

54	c4o9uB	Alignment	not modelled	9.5	12	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
55	c5vkvA	Alignment	not modelled	9.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccda; PDBTitle: solution nmr structure of the membrane electron transporter ccda
56	c5ep6C	Alignment	not modelled	9.3	5	PDB header: protein binding/transferase Chain: C: PDB Molecule: 5-azacytidine-induced protein 2; PDBTitle: the crystal structure of nap1 in complex with tbk1
57	d3dhwa1	Alignment	not modelled	9.3	11	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
58	c6igz3	Alignment	not modelled	9.0	12	PDB header: plant protein Chain: 3: PDB Molecule: lhca-d; PDBTitle: structure of psi-lhci
59	c2ke4A	Alignment	not modelled	8.7	13	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
60	c5ep6A	Alignment	not modelled	8.6	5	PDB header: protein binding/transferase Chain: A: PDB Molecule: 5-azacytidine-induced protein 2; PDBTitle: the crystal structure of nap1 in complex with tbk1
61	c2l8sA	Alignment	not modelled	8.5	8	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
62	c6i1rA	Alignment	not modelled	8.5	7	PDB header: membrane protein Chain: A: PDB Molecule: cmp-sialic acid transporter 1; PDBTitle: crystal structure of cmp bound cst in an outward facing conformation
63	c4v1am	Alignment	not modelled	8.3	43	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
64	c2m7eA	Alignment	not modelled	8.2	18	PDB header: calmodulin-binding protein Chain: A: PDB Molecule: calcium-transporting atpase 2, plasma membrane-type; PDBTitle: solution structure of the calmodulin-binding domain of plant calcium-2 atpase aca2
65	c6c6lO	Alignment	not modelled	8.2	20	PDB header: membrane protein Chain: O: PDB Molecule: v-type proton atpase subunit f; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
66	d1rwta	Alignment	not modelled	8.1	21	Fold: Chlorophyll a-b binding protein Superfamily: Chlorophyll a-b binding protein Family: Chlorophyll a-b binding protein
67	c6bk5A	Alignment	not modelled	8.0	29	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin ligase cbl; PDBTitle: inactive choanoflagellate e3 ubiquitin ligase cbl tkb
68	c6fosK	Alignment	not modelled	8.0	23	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i
69	d2a90a1	Alignment	not modelled	8.0	6	Fold: WWE domain Superfamily: WWE domain Family: WWE domain
70	c2zxeA	Alignment	not modelled	7.7	10	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
71	c2kncA	Alignment	not modelled	7.6	7	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
72	c2na6A	Alignment	not modelled	7.6	4	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
73	c2na6C	Alignment	not modelled	7.6	4	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
74	c2na6B	Alignment	not modelled	7.6	4	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
75	d3buxb2	Alignment	not modelled	7.5	23	Fold: N-cbl like Superfamily: N-terminal domain of cbl (N-cbl) Family: N-terminal domain of cbl (N-cbl)
76	c2mkvA	Alignment	not modelled	7.5	16	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
77	c2lonA	Alignment	not modelled	7.4	13	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
78	d2yvxa3	Alignment	not modelled	7.4	19	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like

79	c6f0kF_	Alignment	not modelled	7.4	7	PDB header: membrane protein Chain: F; PDB Molecule: actf; PDBTitle: alternative complex iii
80	c5xxuP_	Alignment	not modelled	7.4	13	PDB header: ribosome Chain: P; PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
81	c6c6lN_	Alignment	not modelled	7.3	17	PDB header: membrane protein Chain: N; PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
82	c6b2zS_	Alignment	not modelled	7.3	6	PDB header: membrane protein Chain: S; PDB Molecule: atp synthase subunit j, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
83	c6b2zi_	Alignment	not modelled	7.3	6	PDB header: membrane protein Chain: l; PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
84	c5n9jF_	Alignment	not modelled	7.3	10	PDB header: transcription Chain: F; PDB Molecule: mediator complex subunit 9; PDBTitle: core mediator of transcriptional regulation
85	c6gcs3_	Alignment	not modelled	7.2	10	PDB header: oxidoreductase Chain: 3; PDB Molecule: nd3 subunit (nu3m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
86	c2w2eA_	Alignment	not modelled	7.2	12	PDB header: membrane protein Chain: A; PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
87	c2yevB_	Alignment	not modelled	7.1	7	PDB header: electron transport Chain: B; PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
88	c2kluA_	Alignment	not modelled	7.1	14	PDB header: immune system, membrane protein Chain: A; PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
89	c2m20B_	Alignment	not modelled	7.0	12	PDB header: signaling protein Chain: B; PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
90	c4r0cB_	Alignment	not modelled	7.0	9	PDB header: membrane protein Chain: B; PDB Molecule: abgt putative transporter family; PDBTitle: crystal structure of the alcanivorax borkumensis ydah transporter2 reveals an unusual topology
91	c2yadA_	Alignment	not modelled	7.0	25	PDB header: surfactant protein Chain: A; PDB Molecule: surfactant protein c brichos domain; PDBTitle: brichos domain of surfactant protein c precursor protein
92	c4xk88_	Alignment	not modelled	7.0	21	PDB header: photosynthesis Chain: 8; PDB Molecule: chlorophyll a-b binding protein 3, chloroplastic; PDB Fragment: unp residues 2-81; PDBTitle: crystal structure of plant photosystem i-lhci super-complex at 2.82 angstrom resolution
93	c4n7wA_	Alignment	not modelled	6.9	11	PDB header: transport protein Chain: A; PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
94	c3j20T_	Alignment	not modelled	6.9	17	PDB header: ribosome Chain: T; PDB Molecule: 30s ribosomal protein s19p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
95	c2rddB_	Alignment	not modelled	6.9	7	PDB header: membrane protein/transport protein Chain: B; PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
96	c2wsc1_	Alignment	not modelled	6.9	21	PDB header: photosynthesis Chain: 1; PDB Molecule: at3g54890; PDBTitle: improved model of plant photosystem i
97	c6igz7_	Alignment	not modelled	6.9	25	PDB header: plant protein Chain: 7; PDB Molecule: lhca-h; PDBTitle: structure of psi-lhci
98	c5zghK_	Alignment	not modelled	6.9	21	PDB header: photosynthesis Chain: K; PDB Molecule: psak; PDBTitle: cryo-em structure of the red algal psi-lhcr
99	d2otaa1	Alignment	not modelled	6.8	26	Fold: YejL-like Superfamily: YejL-like Family: YejL-like