

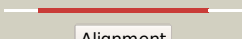













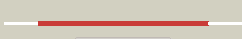
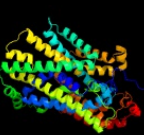






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1704c_cycA_1929793_1931463
 Date Fri Aug 2 13:30:30 BST 2019
 Unique Job ID 09f5ba1cc43102b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oqtA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
2	c4djiA_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
3	c6f2wA_	 Alignment		100.0	19	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	c6irtB_	 Alignment		100.0	21	PDB header: membrane protein Chain: B: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
5	c3giaA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
6	c3lrcC_	 Alignment		100.0	19	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
7	c6jmqA_	 Alignment		100.0	21	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	14	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	8	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
10	c5nvaA_	 Alignment		99.7	9	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
11	c6c08F_	 Alignment		99.7	9	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

12	c2xq2A_	Alignment		99.6	9	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsgl
13	c3dh4A_	Alignment		99.4	12	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		99.3	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		99.2	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		99.0	10	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		99.0	10	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		97.7	15	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
19	c5i6xA_	Alignment		97.7	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
20	c4us3A_	Alignment		97.2	13	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
21	d2a65a1	Alignment	not modelled	97.2	15	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
22	c2w8aC_	Alignment	not modelled	97.1	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
23	c4ainB_	Alignment	not modelled	95.4	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	93.9	9	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
25	c5kteA_	Alignment	not modelled	85.3	14	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	c3g40A_	Alignment	not modelled	60.3	8	PDB header: transport protein Chain: A: PDB Molecule: na-k-cl cotransporter; PDBTitle: crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
27	c6nbxG_	Alignment	not modelled	44.9	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
28	d1fftb2	Alignment	not modelled	33.2	6	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region

29	c3j1zP_	Alignment	not modelled	23.2	12	PDB header: metal transport Chain: P: PDB Molecule: scation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
30	c5xpdA_	Alignment	not modelled	20.4	10	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
31	c5mg3D_	Alignment	not modelled	19.7	12	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
32	c2kluA_	Alignment	not modelled	19.4	11	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
33	c6hwhL_	Alignment	not modelled	16.7	10	PDB header: electron transport Chain: L: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
34	d1g2913	Alignment	not modelled	16.5	30	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
35	c2m67A_	Alignment	not modelled	14.9	22	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
36	c2m20B_	Alignment	not modelled	13.6	18	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.
37	c3rkoF_	Alignment	not modelled	12.7	17	PDB header: oxidoreductase Chain: F: PDB Molecule: nahd-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
38	c1k6nH_	Alignment	not modelled	12.4	16	PDB header: photosynthesis Chain: H: PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
39	c2yevB_	Alignment	not modelled	11.6	15	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
40	c2wj8N_	Alignment	not modelled	8.4	55	PDB header: rna binding protein/rna Chain: N: PDB Molecule: nucleoprotein; PDBTitle: respiratory syncytial virus ribonucleoprotein
41	c2auhB_	Alignment	not modelled	6.9	24	PDB header: transferase/signaling protein Chain: B: PDB Molecule: growth factor receptor-bound protein 14; PDBTitle: crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
42	c5gapG_	Alignment	not modelled	6.9	11	PDB header: transcription Chain: G: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: body region of the u4/u6.u5 tri-snrnp
43	c6adqP_	Alignment	not modelled	6.6	15	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
44	c5h93C_	Alignment	not modelled	6.6	43	PDB header: hydrolase Chain: C: PDB Molecule: geobacter metallireducens smug1; PDBTitle: crystal structure of geobacter metallireducens smug1
45	d1qnta2	Alignment	not modelled	6.5	21	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
46	c2l9uB_	Alignment	not modelled	6.5	13	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
47	c2l9uA_	Alignment	not modelled	6.5	13	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb3-3; PDBTitle: spatial structure of dimeric erb3 transmembrane domain
48	c4o9uB_	Alignment	not modelled	6.3	12	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
49	c2w2eA_	Alignment	not modelled	6.1	18	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
50	c1m57H_	Alignment	not modelled	5.9	8	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
51	c6eznH_	Alignment	not modelled	5.8	9	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
52	c3ixzA_	Alignment	not modelled	5.8	13	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
53	d2qw7a1	Alignment	not modelled	5.8	13	Fold: OB-fold Superfamily: EutN/CcmL-like Family: EutN/CcmL-like
54	c1fftG_	Alignment	not modelled	5.6	6	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli

55	c5xamA_	Alignment	not modelled	5.6	10	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution
56	c5ofxF_	Alignment	not modelled	5.5	11	PDB header: sugar binding protein Chain: F: PDB Molecule: plla; PDBTitle: plla lectin, trisaccharide complex
57	d1xcra1	Alignment	not modelled	5.3	10	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: PTD012-like