



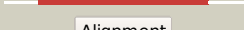

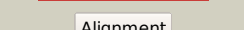

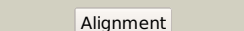





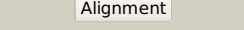

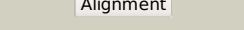

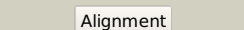




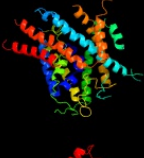

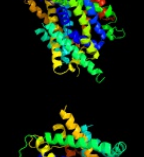

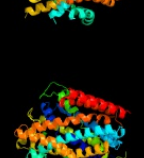


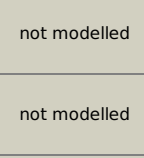


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1999c (-)_2243824_2245146
Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	1610a8c9da7e2b36

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oqtA_	 Alignment		100.0	25	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	c6f2wA_	 Alignment		100.0	22	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
3	c3giaA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
4	c6nplA_	 Alignment		100.0	19	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
5	c4djiA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
6	c6irtB_	 Alignment		100.0	22	PDB header: membrane protein Chain: B: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
7	c6jmqA_	 Alignment		100.0	22	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	c3lrcC_	 Alignment		100.0	21	PDB header: transport protein Chain: C: PDB Molecule: arginine/arginine antiporter; PDBTitle: structure of e. coli adic (p1)
9	c6csfC_	 Alignment		99.9	15	PDB header: membrane protein Chain: C: PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
10	c2jlnA_	 Alignment		99.9	11	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
11	c6c08F_	 Alignment		99.5	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

12	c5nvaA_	Alignment		99.4	12	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
13	c6c08C_	Alignment		99.3	13	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
14	c2xq2A_	Alignment		99.1	12	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsigl
15	c3dh4A_	Alignment		99.0	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
16	c4wqwa_	Alignment		98.5	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
17	c4wqvC_	Alignment		98.5	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
18	c5m87A_	Alignment		98.0	11	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
19	d2a65a1	Alignment		97.1	11	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
20	c4m48A_	Alignment		96.8	13	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
21	c5i6xA_	Alignment	not modelled	96.7	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
22	c4us3A_	Alignment	not modelled	96.1	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	c5kteA_	Alignment	not modelled	95.5	15	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
24	c2w8aC_	Alignment	not modelled	95.0	15	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
25	c4ainB_	Alignment	not modelled	92.2	12	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
26	c5t77A_	Alignment	not modelled	78.5	8	PDB header: transport protein Chain: A: PDB Molecule: putative lipid ii flippase murj; PDBTitle: crystal structure of the mop flippase murj
27	c3hfxA_	Alignment	not modelled	63.3	11	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
28	c5i20C_	Alignment	not modelled	62.4	16	PDB header: membrane protein Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein

29	c3qngD_	Alignment	not modelled	44.8	10	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
30	c4x5mB_	Alignment	not modelled	40.4	10	PDB header: transport protein Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of semisweet in the inward-open conformation
31	c2kncA_	Alignment	not modelled	39.2	7	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
32	c4kppA_	Alignment	not modelled	33.7	9	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
33	c5ldwL_	Alignment	not modelled	31.4	9	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1
34	c4heaT_	Alignment	not modelled	31.0	16	PDB header: oxidoreductase Chain: T; PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
35	c6gcs5_	Alignment	not modelled	30.9	8	PDB header: oxidoreductase Chain: 5; PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
36	d1ftfb2	Alignment	not modelled	29.5	10	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
37	c5i6cB_	Alignment	not modelled	28.6	15	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	c6humF_	Alignment	not modelled	26.5	13	PDB header: proton transport Chain: F; PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
39	c3rkoL_	Alignment	not modelled	24.2	13	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-quinone oxidoreductase subunit I; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
40	c2lonA_	Alignment	not modelled	23.3	22	PDB header: membrane protein Chain: A; PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
41	c5khnB_	Alignment	not modelled	21.2	11	PDB header: membrane protein Chain: B; PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
42	c2na6C_	Alignment	not modelled	19.9	12	PDB header: apoptosis Chain: C; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
43	c2na6A_	Alignment	not modelled	19.9	12	PDB header: apoptosis Chain: A; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
44	c2na6B_	Alignment	not modelled	19.9	12	PDB header: apoptosis Chain: B; PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
45	c4qtnB_	Alignment	not modelled	18.9	10	PDB header: transport protein Chain: B; PDB Molecule: nicotinamide riboside transporter pnuc; PDBTitle: crystal structure of the vitamin b3 transporter pnuc
46	c2mtpB_	Alignment	not modelled	18.8	31	PDB header: protein binding/cell adhesion Chain: B; PDB Molecule: integrin alpha-iib; PDBTitle: the structure of filamin repeat 21 bound to integrin
47	c1m8oA_	Alignment	not modelled	18.5	31	PDB header: membrane protein Chain: A; PDB Molecule: platelet integrin alfa-iib subunit: cytoplasmic PDBTitle: platelet integrin alfa-iib-beta3 cytoplasmic domain
48	c1s4wA_	Alignment	not modelled	18.5	31	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: nmr structure of the cytoplasmic domain of integrin aiib in2 dpc micelles
49	c1dpkA_	Alignment	not modelled	18.5	31	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib subunit; PDBTitle: solution structure of the cytoplasmic domain of the2 integrin alpha-iib subunit
50	c2rddB_	Alignment	not modelled	18.0	7	PDB header: membrane protein/transport protein Chain: B; PDB Molecule: supf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
51	c6agfB_	Alignment	not modelled	18.0	16	PDB header: membrane protein Chain: B; PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
52	c2m67A_	Alignment	not modelled	17.2	20	PDB header: transport protein Chain: A; PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
53	c5aexJ_	Alignment	not modelled	17.2	18	PDB header: membrane protein Chain: J; PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2

54	c1ujlA	Alignment	not modelled	17.0	18	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h PDBTitle: solution structure of the herg k+ channel s5-p2 extracellular linker
55	c5xpdA	Alignment	not modelled	17.0	14	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
56	c1oy8A	Alignment	not modelled	16.8	14	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
57	c6i1rA	Alignment	not modelled	16.8	9	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
58	c6g2jL	Alignment	not modelled	16.5	12	PDB header: oxidoreductase Chain: L: PDB Molecule: nahd-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
59	c5n9jC	Alignment	not modelled	16.4	21	PDB header: transcription Chain: C: PDB Molecule: mediator of rna polymerase ii transcription subunit 19; PDBTitle: core mediator of transcriptional regulation
60	c2gfpA	Alignment	not modelled	16.1	11	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
61	c5xsyB	Alignment	not modelled	16.0	3	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated sodium channel beta subunit 1; PDBTitle: structure of the nav1.4-beta1 complex from electric eel
62	c6csxA	Alignment	not modelled	15.7	14	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
63	d2oara1	Alignment	not modelled	15.5	10	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
64	d1nekd	Alignment	not modelled	15.1	14	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
65	c4mt1A	Alignment	not modelled	15.0	11	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
66	c5yd1B	Alignment	not modelled	14.8	12	PDB header: metal transport Chain: B: PDB Molecule: protein osca1; PDBTitle: structure of atosca1.1 channel
67	c2kluA	Alignment	not modelled	14.6	18	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
68	c6iu3A	Alignment	not modelled	14.6	7	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
69	c6buhH	Alignment	not modelled	14.4	12	PDB header: membrane protein Chain: H: PDB Molecule: d-alanyl transfer protein dlbt; PDBTitle: crystal structure of a membrane protein, crystal form ii
70	c4rfsS	Alignment	not modelled	14.4	20	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding prtein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
71	c6gcs4	Alignment	not modelled	14.1	14	PDB header: oxidoreductase Chain: 4: PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
72	c2l1nA	Alignment	not modelled	14.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
73	c5v2sA	Alignment	not modelled	14.1	23	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
74	c2lomA	Alignment	not modelled	13.8	17	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein higd1a
75	c5zazA	Alignment	not modelled	13.8	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
76	c2acmA	Alignment	not modelled	13.7	38	PDB header: structural protein Chain: A: PDB Molecule: mucin-1; PDBTitle: solution structure of the sea domain of human mucin 1 (muc1)
77	c4r4mB	Alignment	not modelled	13.6	32	PDB header: dna binding protein Chain: B: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of c42l cgmp dependent protein kinase i alpha (pkgi2 alpha) leucine zipper
78	c2micB	Alignment	not modelled	13.6	16	PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
						PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor

79	c2micA	Alignment	not modelled	13.6	16	superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
80	c2djrA	Alignment	not modelled	13.5	12	PDB header: metal binding protein Chain: A: PDB Molecule: zinc finger bed domain-containing protein 2; PDBTitle: solution structures of the c2h2 type zinc finger domain of2 human zinc finger bed domain containing protein 2
81	c4n7wA	Alignment	not modelled	13.4	14	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
82	c6hwhX	Alignment	not modelled	13.3	14	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
83	c1zxaB	Alignment	not modelled	13.3	31	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
84	c6c14A	Alignment	not modelled	13.2	7	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
85	c5wudA	Alignment	not modelled	12.9	18	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural basis for conductance through tric cation channels
86	c6b2zS	Alignment	not modelled	12.8	15	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
87	c6b2zi	Alignment	not modelled	12.8	15	PDB header: membrane protein Chain: I: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
88	c2hinA	Alignment	not modelled	12.7	35	PDB header: transcription Chain: A: PDB Molecule: repressor protein; PDBTitle: structure of n15 cro at 1.05 a: an ortholog of lambda cro2 with a completely different but equally effective3 dimerization mechanism
89	c5z62N	Alignment	not modelled	12.6	14	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
90	d2cupa3	Alignment	not modelled	12.5	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
91	c2n2aA	Alignment	not modelled	12.5	25	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
92	c5y79A	Alignment	not modelled	12.5	14	PDB header: transport protein Chain: A: PDB Molecule: putative hexose phosphate translocator; PDBTitle: crystal structure of the triose-phosphate/phosphate translocator in2 complex with 3-phosphoglycerate
93	c5oqmm	Alignment	not modelled	12.4	14	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
94	c6nbxG	Alignment	not modelled	12.3	11	PDB header: oxidoreductase Chain: G: PDB Molecule: ndh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
95	c2mkvA	Alignment	not modelled	12.2	11	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
96	c6m9tA	Alignment	not modelled	12.2	17	PDB header: membrane protein Chain: A: PDB Molecule: prostaglandin e2 receptor ep3 subtype, endolysin chimera; PDBTitle: crystal structure of ep3 receptor bound to misoprostol-fa
97	d1co4a	Alignment	not modelled	12.1	16	Fold: Zinc domain conserved in yeast copper-regulated transcription factors Superfamily: Zinc domain conserved in yeast copper-regulated transcription factors Family: Zinc domain conserved in yeast copper-regulated transcription factors
98	c2e76G	Alignment	not modelled	12.0	17	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
99	c2m20B	Alignment	not modelled	12.0	19	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.