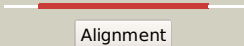

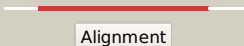

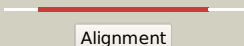







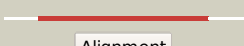










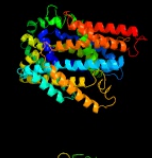
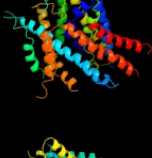
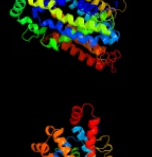
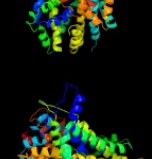
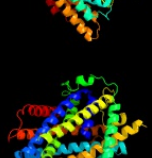
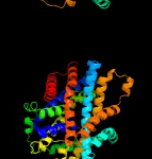

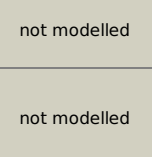


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2127_(ansP1)_2388624_2390093
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	61eacad64defc057

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4djiA_	 Alignment		100.0	14	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	19	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	17	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	18	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	c6nplA_	 Alignment		100.0	14	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
7	c3lrcC_	 Alignment		100.0	18	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
8	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
9	c6csfC_	 Alignment		100.0	13	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		100.0	11	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
11	c6c08F_	 Alignment		99.7	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	c5nvaA	Alignment		99.6	11	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	c2xq2A	Alignment		99.5	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
14	c6c08C	Alignment		99.3	10	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	c3dh4A	Alignment		99.3	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
16	c5i6xA	Alignment		99.0	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
17	c5m87A	Alignment		98.8	11	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
18	c4wqwA	Alignment		98.8	11	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
19	c4wgvC	Alignment		98.8	11	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
20	c4m48A	Alignment		98.6	12	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
21	d2a65a1	Alignment	not modelled	98.2	13	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
22	c2w8aC	Alignment	not modelled	97.9	12	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	c4us3A	Alignment	not modelled	97.8	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
24	c4ainB	Alignment	not modelled	97.2	10	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
25	c3hfxA	Alignment	not modelled	91.5	9	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
26	c5xpdA	Alignment	not modelled	83.6	11	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
27	c6nbxG	Alignment	not modelled	79.0	10	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
28	c4n7wA	Alignment	not modelled	66.2	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
29	c5kteA	Alignment	not modelled	65.9	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
30	c6hwhX	Alignment	not modelled	18.4	15	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
31	c2dhzA	Alignment	not modelled	17.6	14	PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor (gef)- PDBTitle: solution structure of the ra domain in the human link2 guanine nucleotide exchange factor ii (link-gefi)
32	c5b52B	Alignment	not modelled	16.1	19	PDB header: transcription Chain: B: PDB Molecule: h-ns family protein mvat; PDBTitle: crystal structure of the n-terminal domain of h-ns family protein turb
33	c3aygA	Alignment	not modelled	14.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
34	c2l1nA	Alignment	not modelled	14.1	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
35	c4x5mB	Alignment	not modelled	10.4	8	PDB header: transport protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of semisweet in the inward-open conformation
36	c6eznH	Alignment	not modelled	9.3	12	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
37	c3jlzP	Alignment	not modelled	8.1	8	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
38	c2bbjB	Alignment	not modelled	7.8	8	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
39	d1fftb2	Alignment	not modelled	7.5	6	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
40	c2m67A	Alignment	not modelled	7.4	11	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
41	c2kncB	Alignment	not modelled	7.2	9	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
42	c5i6cB	Alignment	not modelled	7.0	14	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
43	c3h5fB	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: B: PDB Molecule: coil ser I16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
44	c3h5gA	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: A: PDB Molecule: coil ser I16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
45	c5u9tA	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: A: PDB Molecule: zn(ii)cl(coilser I16(dcy))3 2-; PDBTitle: the tris-thiolate zn(ii)s3cl binding site engineered by d-cysteine2 ligands in de novo three-stranded coiled coil environment
46	c5u9uB	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: B: PDB Molecule: apo-(coilser I16(dcy))3; PDBTitle: de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
47	c3h5gB	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: B: PDB Molecule: coil ser I16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
48	c5u9uA	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: A: PDB Molecule: apo-(coilser I16(dcy))3; PDBTitle: de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
49	c3h5gC	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: C: PDB Molecule: coil ser I16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
50	c5u9uC	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: C: PDB Molecule: apo-(coilser I16(dcy))3; PDBTitle: de novo three-stranded coiled coil peptide containing a tris-thiolate2 site engineered by d-cysteine ligands
51	c3h5fA	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: A: PDB Molecule: coil ser I16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
52	c3h5fC	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: C: PDB Molecule: coil ser I16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
53	c5u9tC	Alignment	not modelled	6.8	21	PDB header: de novo protein Chain: C: PDB Molecule: zn(ii)cl(coilser I16(dcy))3 2-; PDBTitle: the tris-thiolate zn(ii)s3cl binding site engineered by d-cysteine2 ligands in de novo three-stranded coiled coil environment
						PDB header: de novo protein

54	c5u9tB_	Alignment	not modelled	6.8	21	Chain: B; PDB Molecule: zn(ii)cl(coilser l16(dcy))3 2-; PDBTitle: the tris-thiolate zn(ii)s3cl binding site engineered by d-cysteine2 ligands in de novo three-stranded coiled coil environment
55	c6nd1E_	Alignment	not modelled	6.6	15	PDB header: protein transport Chain: E; PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast
56	c5oonA_	Alignment	not modelled	6.5	12	PDB header: membrane protein Chain: A; PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca
57	c4kppA_	Alignment	not modelled	6.4	10	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
58	c3bd1B_	Alignment	not modelled	6.4	14	PDB header: transcription Chain: B; PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
59	c3ixzA_	Alignment	not modelled	6.2	7	PDB header: hydrolase Chain: A; PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
60	c2m7eA_	Alignment	not modelled	6.0	15	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
61	c6f0kF_	Alignment	not modelled	6.0	8	PDB header: membrane protein Chain: F; PDB Molecule: actf; PDBTitle: alternative complex iii
62	d3buxb2	Alignment	not modelled	5.9	17	Fold: N-cbl like Superfamily: N-terminal domain of cbl (N-cbl) Family: N-terminal domain of cbl (N-cbl)
63	c6cghA_	Alignment	not modelled	5.8	21	PDB header: chaperone Chain: A; PDB Molecule: dnaj homolog subfamily c member 2; PDBTitle: solution structure of the four-helix bundle region of human j-protein2 zootin, a component of ribosome-associated complex (rac)
64	c4px7A_	Alignment	not modelled	5.8	7	PDB header: hydrolase Chain: A; PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb
65	c6gcs3_	Alignment	not modelled	5.6	12	PDB header: oxidoreductase Chain: 3; PDB Molecule: nd3 subunit (nu3m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
66	c4k1cB_	Alignment	not modelled	5.5	10	PDB header: membrane protein/metal transport Chain: B; PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
67	c2m20B_	Alignment	not modelled	5.5	15	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.
68	c2luvA_	Alignment	not modelled	5.4	16	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-x; PDBTitle: structure and binding interface of the cytosolic tails of axb22 integrin
69	c1w8xP_	Alignment	not modelled	5.1	11	PDB header: virus Chain: P; PDB Molecule: protein p16; PDBTitle: structural analysis of prd1