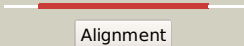

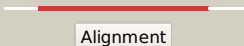

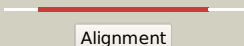
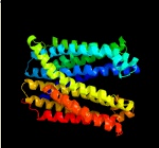






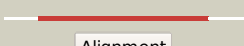















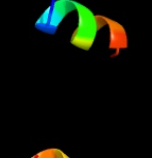

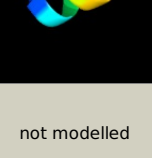


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2836c_(dinF)_3142319_3143638
 Date Wed Aug 7 12:50:50 BST 2019
 Unique Job ID 75a292a9171c2a93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5y50A_	 Alignment		100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
2	c6idrA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: mate family efflux transporter; PDBTitle: crystal structure of vibrio cholerae mate transporter vcmn in the bent2 form
3	c5xjxA_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
4	c3mkuA_	 Alignment		100.0	21	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
5	c3mkuB_	 Alignment		100.0	21	PDB header: transport protein Chain: B: PDB Molecule: multi antimicrobial extrusion protein (na(+))/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
6	c4z3pA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
7	c4lz9A_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: bh2163 protein; PDBTitle: structure of mate multidrug transporter dinf-bh in complex with r6g
8	c3vvpA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
9	c6fv6A_	 Alignment		100.0	17	PDB header: membrane protein Chain: A: PDB Molecule: aq128; PDBTitle: monomer structure of the mate family multidrug resistance transporter2 aq_128 from aquifex aeolicus in the outward-facing state
10	c6cc4A_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
11	c5t77A_	 Alignment		100.0	9	PDB header: transport protein Chain: A: PDB Molecule: putative lipid ii flippase murj; PDBTitle: crystal structure of the mop flippase murj

12	c4hunA_	Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux protein; PDBTitle: mate transporter norm-ng in complex with r6g and monobody
13	c5aymA_	Alignment		76.0	9	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
14	c5aynA_	Alignment		47.1	9	PDB header: transport protein Chain: A: PDB Molecule: solute carrier family 39 (iron-regulated transporter); PDBTitle: crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
15	c4iu8A_	Alignment		44.2	10	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
16	c3wdoA_	Alignment		41.6	11	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
17	c5jthB_	Alignment		28.6	40	PDB header: transferase Chain: B: PDB Molecule: myosin light chain kinase, smooth muscle; PDBTitle: crystal structure of e67a calmodulin - cam:rm20 complex
18	c5jqdB_	Alignment		28.6	40	PDB header: calcium binding protein/protein binding Chain: B: PDB Molecule: myosin light chain kinase, smooth muscle; PDBTitle: cam:rm20 complex
19	c1qtxB_	Alignment		26.3	40	PDB header: signaling protein Chain: B: PDB Molecule: protein (rs20); PDBTitle: the 1.65 angstrom structure of calmodulin rs20 peptide2 complex
20	c1cdIF_	Alignment		26.1	40	PDB header: calcium-binding protein Chain: F: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
21	c1cdIE_	Alignment	not modelled	26.1	40	PDB header: calcium-binding protein Chain: E: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
22	c2o5gB_	Alignment	not modelled	25.8	40	PDB header: metal binding protein Chain: B: PDB Molecule: smooth muscle myosin light chain kinase peptide; PDBTitle: calmodulin-smooth muscle light chain kinase peptide complex
23	c1cdIG_	Alignment	not modelled	25.0	40	PDB header: calcium-binding protein Chain: G: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
24	c6adqP_	Alignment	not modelled	16.2	11	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
25	d1pw4a_	Alignment	not modelled	14.6	10	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
26	c1cdIH_	Alignment	not modelled	14.4	44	PDB header: calcium-binding protein Chain: H: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
27	c5njgB_	Alignment	not modelled	13.8	10	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: part of the structure that

						could be2 built de novo
28	c6e9oA_	Alignment	not modelled	12.5	8	PDB header: membrane protein Chain: A: PDB Molecule: d-galactonate transport; PDBTitle: e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
29	c5n9yB_	Alignment	not modelled	11.7	19	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
30	c2nzza_	Alignment	not modelled	10.2	13	PDB header: membrane protein Chain: A: PDB Molecule: penetratin conjugated gas (374-394) peptide; PDBTitle: nmr structure analysis of the penetratin conjugated gas2 (374-394) peptide
31	c6j5if_	Alignment	not modelled	9.1	16	PDB header: membrane protein Chain: F: PDB Molecule: atp synthase subunit beta; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
32	c2k5kA_	Alignment	not modelled	8.9	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein rhr2; PDBTitle: solution structure of rhr2 from rhodobacter sphaeroides.2 northeast structural genomics consortium
33	c4u1eG_	Alignment	not modelled	8.8	25	PDB header: translation Chain: G: PDB Molecule: eukaryotic translation initiation factor 3 subunit g; PDBTitle: crystal structure of the eif3b-ctd/eif3i/eif3g-ntd translation2 initiation complex
34	c6hu9o_	Alignment	not modelled	8.7	17	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: cytochrome c1, heme protein, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
35	c3wmmP_	Alignment	not modelled	8.4	11	PDB header: photosynthesis Chain: P: PDB Molecule: lh1 beta polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
36	c2m7tA_	Alignment	not modelled	8.0	57	PDB header: protein binding Chain: A: PDB Molecule: cystine knot protein 2.5d; PDBTitle: solution nmr structure of engineered cystine knot protein 2.5d
37	c6agfB_	Alignment	not modelled	7.8	6	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
38	c4ev6E_	Alignment	not modelled	7.6	11	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
39	c1wrgA_	Alignment	not modelled	7.4	11	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
40	c6iz4G_	Alignment	not modelled	7.4	16	PDB header: membrane protein Chain: G: PDB Molecule: trimeric intracellular cation channel type b-b; PDBTitle: crystal structure analysis of tric counter-ion channels in calcium2 release
41	c6et5u_	Alignment	not modelled	7.3	16	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
42	d2d5ba1	Alignment	not modelled	7.1	8	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
43	c2x9aA_	Alignment	not modelled	6.8	44	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
44	d1lghb_	Alignment	not modelled	6.7	13	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
45	c2l0gA_	Alignment	not modelled	6.4	60	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
46	c2khuA_	Alignment	not modelled	6.3	60	PDB header: transferase/protein binding Chain: A: PDB Molecule: immunoglobulin g-binding protein g, dna PDBTitle: solution structure of the ubiquitin-binding motif of human2 polymerase iota
47	c3ipdB_	Alignment	not modelled	6.1	6	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
48	c2bbmB_	Alignment	not modelled	5.8	33	PDB header: calcium-binding protein Chain: B: PDB Molecule: myosin light chain kinase; PDBTitle: solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
49	c2lv6B_	Alignment	not modelled	5.8	33	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: myosin light chain kinase 2, skeletal/cardiac muscle; PDBTitle: the complex between ca-calmodulin and skeletal muscle myosin light2 chain kinase from combination of nmr and aqueous and contrast-matched3 saxs data
50	c2bbnB_	Alignment	not modelled	5.8	33	PDB header: calcium-binding protein Chain: B: PDB Molecule: myosin light chain kinase; PDBTitle: solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
51	c1b9uA_	Alignment	not modelled	5.7	5	PDB header: hydrolase Chain: A: PDB Molecule: protein (atp synthase); PDBTitle: membrane domain of the subunit b of the e.coli atp

						synthase
52	c4yczC_	Alignment	not modelled	5.6	21	PDB header: structural protein Chain: C; PDB Molecule: nup120; PDBTitle: y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)
53	d1g3pa1	Alignment	not modelled	5.5	44	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
54	c2kwuA_	Alignment	not modelled	5.4	50	PDB header: protein binding/signaling protein Chain: A; PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
55	c2kogA_	Alignment	not modelled	5.3	7	PDB header: membrane protein Chain: A; PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
56	d1htaa_	Alignment	not modelled	5.3	7	Fold: Histone-fold Superfamily: Histone-fold Family: Archaeal histone
57	c6iz0A_	Alignment	not modelled	5.2	13	PDB header: membrane protein Chain: A; PDB Molecule: trimeric intracellular cation channel type a; PDBTitle: crystal structure analysis of a eukaryotic membrane protein
58	d1v54c_	Alignment	not modelled	5.1	12	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
59	c2jvwA_	Alignment	not modelled	5.0	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117