

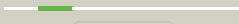


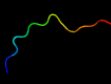

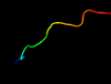












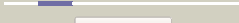



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0040c_(mtc28)_42433_43365
 Date Tue Jul 23 14:50:07 BST 2019
 Unique Job ID 2265ad596623c6fe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ibwC_	 Alignment		57.7	25	PDB header: motor protein Chain: C: PDB Molecule: myosin ic heavy chain; PDBTitle: complex of mlcc bound to the tandem iq motif of myoc
2	c6g2dC_	 Alignment		54.2	43	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
3	c5cskB_	 Alignment		48.3	43	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
4	c5cslA_	 Alignment		46.3	43	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
5	d1uyra2	 Alignment		20.3	38	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
6	c5i6fB_	 Alignment		14.9	43	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
7	c4umoB_	 Alignment		14.1	40	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt member 1; PDBTitle: crystal structure of the kv7.1 proximal c-terminal domain in complex2 with calmodulin
8	c6butB_	 Alignment		14.1	40	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel protein type 2 subunit alpha; PDBTitle: solution structure of full-length apo mammalian calmodulin bound to2 the iq motif of the human voltage-gated sodium channel nav1.2
9	c5i6fA_	 Alignment		13.8	43	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
10	c2m5eB_	 Alignment		13.6	40	PDB header: calcium-binding protein/metal transport Chain: B: PDB Molecule: sodium channel protein type 2 subunit alpha; PDBTitle: structure of the c-domain of calcium-saturated calmodulin bound to the2 iq motif of nav1.2
11	c2kxwB_	 Alignment		13.6	40	PDB header: calcium-binding protein/metal transport Chain: B: PDB Molecule: sodium channel protein type 2 subunit alpha; PDBTitle: structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2

12	c5i6hA_	Alignment		12.0	43	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase
13	c1od4C_	Alignment		10.7	43	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
14	c5j03A_	Alignment		9.6	40	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 3, PDBTitle: crystal structure of a chimeric kv7.2 - kv7.3 proximal c-terminal2 domain in complex with calmodulin
15	c6fegA_	Alignment		9.4	24	PDB header: metal transport Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 2, PDBTitle: solution structure of cam/kv7.2-hab complex
16	c6b8qG_	Alignment		9.3	40	PDB header: metal transport Chain: G: PDB Molecule: potassium voltage-gated channel subfamily kqt member 5; PDBTitle: crystal structure of the mg2+/cam:kv7.5 (kcnq5) ab domain complex
17	c4r8gE_	Alignment		9.3	40	PDB header: protein binding/calcium-binding protein Chain: E: PDB Molecule: unconventional myosin-ic; PDBTitle: crystal structure of myosin-1c tail in complex with calmodulin
18	c6b8pG_	Alignment		8.8	30	PDB header: metal transport Chain: G: PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of the mg2+/cam:kv7.4 (kcnq4) ab domain complex
19	c3ff6D_	Alignment		8.6	50	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
20	c3h0jA_	Alignment		8.5	43	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
21	c3ostA_	Alignment	not modelled	8.1	13	PDB header: lipid binding protein Chain: A: PDB Molecule: serine/threonine-protein kinase kcc4; PDBTitle: structure of the kinase associated-1 (ka1) from kcc4p
22	c1uytC_	Alignment	not modelled	7.7	43	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
23	c2ix7C_	Alignment	not modelled	7.3	40	PDB header: contractile protein/metal binding Chain: C: PDB Molecule: myosin-5a; PDBTitle: structure of apo-calmodulin bound to unconventional myosin v
24	c2m76A_	Alignment	not modelled	6.7	22	PDB header: signaling protein Chain: A: PDB Molecule: carnitine o-palmitoyltransferase 1, brain isoform; PDBTitle: structure of the regulatory domain of human brain carnitine2 palmitoyltransferase 1
25	c4wyoB_	Alignment	not modelled	5.7	43	PDB header: ligase/ligase inhibitor Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1
26	c2mlgA_	Alignment	not modelled	5.5	60	PDB header: dna binding protein Chain: A: PDB Molecule: sulfolobus transcription factor 76 aminoacid protein, PDBTitle: stf76 from the sulfolobus islandicus plasmid-virus pssvx
27	c4bbkA_	Alignment	not modelled	5.5	9	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 1; PDBTitle: structural and functional characterisation of the kindlin-12 pleckstrin homology domain
28	c5fu7H_	Alignment	not modelled	5.1	58	PDB header: gene regulation Chain: H: PDB Molecule: nanos, isoform b; PDBTitle: drosophila nanos nbr peptide bound to the not module2 of the human ccr4-not complex