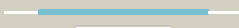

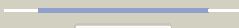


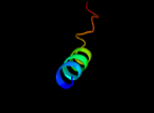
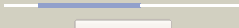
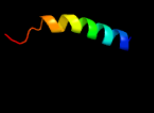


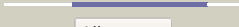
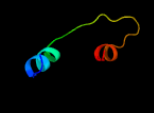
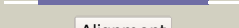

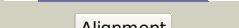
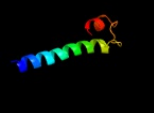
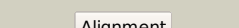

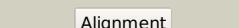

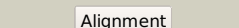
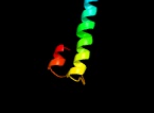
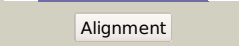


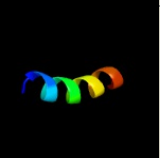
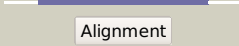
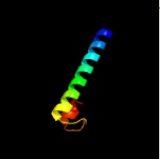


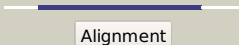
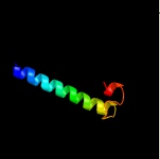
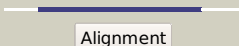
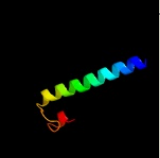
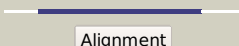
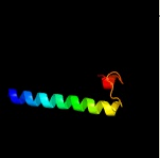
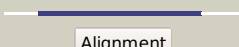
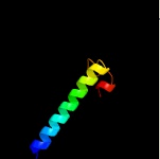
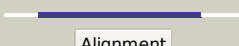
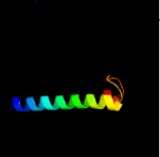
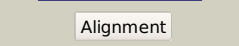
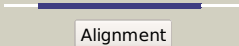
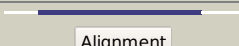
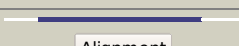

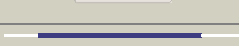
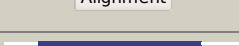
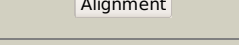
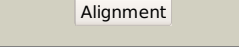


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0530Ac_(RVBD0530Ac)_622124_622285
 Date Fri Jul 26 01:50:08 BST 2019
 Unique Job ID 0145789096882a76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2mi2A_	 Alignment		39.7	36	PDB header: transport protein Chain: A: PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
2	c4ntfA_	 Alignment		23.4	24	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: mus musculus ltc4 synthase in s-hexyl-gsh complex form
3	c2k1aA_	 Alignment		23.0	32	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
4	c2kncA_	 Alignment		22.5	29	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
5	c3ktbD_	 Alignment		19.4	36	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
6	c3tj0B_	 Alignment		16.9	16	PDB header: rna binding protein Chain: B: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of influenza b virus nucleoprotein
7	c2i16A_	 Alignment		16.2	40	PDB header: protein transport Chain: A: PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
8	d2q7ra1	 Alignment		14.9	17	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
9	c3hkkA_	 Alignment		13.2	26	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: structure of human leukotriene c4 synthase in complex with glutathione2 sulfonate
10	c2lzsE_	 Alignment		12.8	24	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
11	c2uuiA_	 Alignment		11.4	30	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase

12	c2uuhA	 Alignment		11.1	26	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase in2 complex with substrate glutathione
13	c3j00Z	 Alignment		11.0	35	PDB header: ribosome/ribosomal protein Chain: Z: PDB Molecule: cell division protein ftsq; PDBTitle: structure of the ribosome-secye complex in the membrane environment
14	c3leoA	 Alignment		10.3	26	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: structure of human leukotriene c4 synthase mutant r31q in complex with2 glutathione
15	c3arcL	 Alignment		8.8	70	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
16	c2pnoK	 Alignment		8.4	28	PDB header: lyase Chain: K: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
17	c2pnoF	 Alignment		8.4	28	PDB header: lyase Chain: F: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
18	c2pnoB	 Alignment		8.4	28	PDB header: lyase Chain: B: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
19	c2pnoA	 Alignment		8.4	28	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
20	c2pnoJ	 Alignment		8.4	28	PDB header: lyase Chain: J: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
21	c2pnoG	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: G: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
22	c2pnoI	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: I: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
23	c2pnoC	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: C: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
24	c2pnoD	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: D: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
25	c2pnoE	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: E: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
26	c2pnoL	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: L: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
27	d2uuia1	 Alignment	not modelled	8.4	28	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
28	c2pnoH	 Alignment	not modelled	8.4	28	PDB header: lyase Chain: H: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
29	c5nhuL	 Alignment	not modelled	8.0	67	PDB header: hydrolase Chain: I: PDB Molecule: agap008004-pa; PDBTitle: human alpha thrombin complexed with anopheles

56	c4tnkL	Alignment	not modelled	6.3	64	PDB header: electron transport,photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third illumination at 5.2 a resolution
57	c4rvyl	Alignment	not modelled	6.3	64	PDB header: oxidoreductase Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: serial time resolved crystallography of photosystem ii using a 2 femtosecond x-ray laser. the s state after two flashes (s3)
58	c5e7cL	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
59	c4rvyl	Alignment	not modelled	6.3	64	PDB header: oxidoreductase Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: serial time resolved crystallography of photosystem ii using a 2 femtosecond x-ray laser. the s state after two flashes (s3)
60	c4ub6L	Alignment	not modelled	6.3	64	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray laser
61	c5e7cL	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
62	c4ub6L	Alignment	not modelled	6.3	64	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray laser
63	c1s5L	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
64	c3a0bL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
65	c3a0hL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
66	c3bz1L	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
67	c4ixqL	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
68	c3a0hL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
69	c2axtL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
70	c4ixrL	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
71	c3kziL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
72	c3arcL	Alignment	not modelled	6.3	64	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
73	c2axtL	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
74	c3prqL	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with 2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
75	c1s5L	Alignment	not modelled	6.3	64	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
76	c3bz2L	Alignment	not modelled	6.3	64	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
77	c4ogqF	Alignment	not modelled	5.9	67	PDB header: electron transport Chain: F: PDB Molecule: cytochrome b6-f complex subunit 7; PDBTitle: internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
78	c2zt9F	Alignment	not modelled	5.9	67	PDB header: photosynthesis Chain: F: PDB Molecule: cytochrome b6-f complex subunit 7; PDBTitle: crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
79	c4h44F	Alignment	not modelled	5.9	67	PDB header: photosynthesis Chain: F: PDB Molecule: cytochrome b6-f complex subunit 7; PDBTitle: 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
80	c3pcvA	Alignment	not modelled	5.7	28	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure analysis of human leukotriene c4 synthase at 1.92 angstrom resolution
81	c3idwA	Alignment	not modelled	5.5	50	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2

82	c3b29A_	Alignment	not modelled	5.5	28	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: human leukotriene c4 synthase in complex with dodecyl-beta-d-2 selenomaltoside
83	c3fxeA_	Alignment	not modelled	5.2	54	PDB header: unknown function Chain: A: PDB Molecule: protein icmq; PDBTitle: crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
84	c5nhuj_	Alignment	not modelled	5.2	67	PDB header: hydrolase Chain: J: PDB Molecule: agap008004-pa; PDBTitle: human alpha thrombin complexed with anopheles gambiae ce52 anticoagulant