










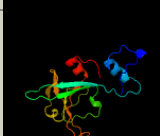












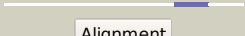
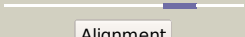

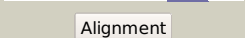
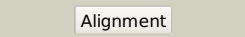
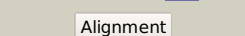
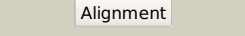
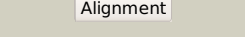
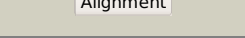
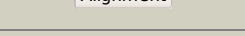
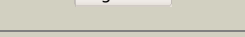
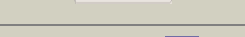

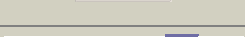






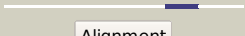
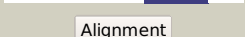
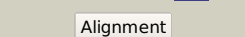
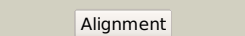


Phyre2



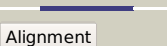
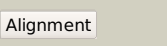
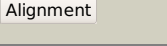
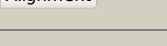
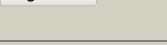
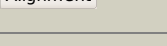
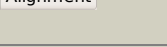
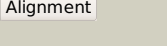
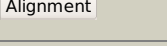
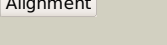
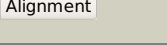
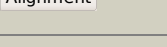


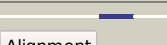
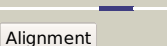



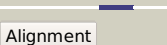
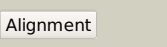


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Date	Tue Jul 23 14:50:10 BST 2019
Unique Job ID	268cb09d808ebe73

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ws4A_	 Alignment		100.0	20	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
2	c5nikK_	 Alignment		100.0	18	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
3	c5xu1M_	 Alignment		100.0	18	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
4	c5lj7B_	 Alignment		100.0	18	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
5	c5naaB_	 Alignment		98.0	16	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: lipoprotein-releasing system transmembrane protein lolc
6	c5f9qA_	 Alignment		97.6	14	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein yknz; PDBTitle: crystal structure of the extracellular domain of noncanonic abc-type2 transporter yknz from gram-positive bacteria
7	c5udfB_	 Alignment		97.5	18	PDB header: protein transport Chain: B: PDB Molecule: lipoprotein-releasing system transmembrane protein lolc; PDBTitle: structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lolc from acinetobacter baumannii
8	c3ftjA_	 Alignment		97.0	17	PDB header: hydrolase Chain: A: PDB Molecule: macrolide export atp-binding/permease protein PDBTitle: crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
9	c5c59F_	 Alignment		96.6	23	PDB header: hydrolase Chain: F: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of the periplasmic region of macb from e. coli
10	c5c59G_	 Alignment		94.2	19	PDB header: hydrolase Chain: G: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of the periplasmic region of macb from e. coli
11	c5x5yF_	 Alignment		90.1	20	PDB header: membrane protein Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex

12	c5I75F_	Alignment		88.3	19	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
13	c5I75G_	Alignment		85.6	20	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
14	c5x5yG_	Alignment		85.6	18	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
15	c6mjpG_	Alignment		85.3	19	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
16	c6mjpF_	Alignment		80.8	19	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
17	d1cola_	Alignment		71.1	13	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
18	c1ciiA_	Alignment		68.5	14	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
19	c3fewX_	Alignment		53.7	11	PDB header: immune system Chain: X; PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
20	c6btmD_	Alignment		53.6	9	PDB header: membrane protein Chain: D; PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
21	d2yvxa3	Alignment	not modelled	50.8	18	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
22	c2yvxD_	Alignment	not modelled	45.7	13	PDB header: transport protein Chain: D; PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
23	c3ltiA_	Alignment	not modelled	33.3	19	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta14 domains
24	c4ymuC_	Alignment	not modelled	32.1	11	PDB header: protein binding/transport protein Chain: C; PDB Molecule: abc-type amino acid transport system, permease component; PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
25	c3is6A_	Alignment	not modelled	26.9	17	PDB header: transport protein Chain: A; PDB Molecule: putative permease protein, abc transporter; PDBTitle: the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a
26	c5v2sA_	Alignment	not modelled	26.0	15	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
27	c5xjyA_	Alignment	not modelled	20.0	17	PDB header: transport protein Chain: A; PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
28	c5a43B_	Alignment	not modelled	18.6	21	PDB header: transport protein Chain: B; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.

29	c2i88A	 Alignment	not modelled	17.1	18	PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin e1
30	c4kbmA	 Alignment	not modelled	15.5	25	PDB header: transferase/transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
31	c4av3A	 Alignment	not modelled	13.3	18	PDB header: hydrolase Chain: A: PDB Molecule: k(+)-stimulated pyrophosphate-energized sodium pump; PDBTitle: crystal structure of thermotoga maritima sodium pumping membrane2 integral pyrophosphatase with metal ions in active site
32	d1a87a	 Alignment	not modelled	13.2	14	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
33	c1a87A	 Alignment	not modelled	13.2	14	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
34	c2cwbA	 Alignment	not modelled	12.9	4	PDB header: protein binding Chain: A: PDB Molecule: chimera of immunoglobulin g binding protein g PDBTitle: solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
35	c5a40C	 Alignment	not modelled	12.0	22	PDB header: transport protein Chain: C: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
36	c1wr1B	 Alignment	not modelled	12.0	4	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like protein dsk2; PDBTitle: the complex sturcture of dsk2p uba with ubiquitin
37	d2bwba1	 Alignment	not modelled	11.7	4	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
38	d2dnaa1	 Alignment	not modelled	11.6	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
39	c2dahA	 Alignment	not modelled	11.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-3; PDBTitle: solution structure of the c-terminal uba domain in the2 human ubiquilin 3
40	d1ciia1	 Alignment	not modelled	11.5	14	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
41	c2dnaA	 Alignment	not modelled	10.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
42	c2v50A	 Alignment	not modelled	10.9	16	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
43	d1veja1	 Alignment	not modelled	10.9	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
44	d1rh1a2	 Alignment	not modelled	10.7	14	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
45	d2daha1	 Alignment	not modelled	10.5	8	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
46	c6f0kD	 Alignment	not modelled	10.3	13	PDB header: membrane protein Chain: D: PDB Molecule: actd; PDBTitle: alternative complex iii
47	c4r4eA	 Alignment	not modelled	10.0	17	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
48	c5jefA	 Alignment	not modelled	9.6	21	PDB header: transferase Chain: A: PDB Molecule: nitrate/nitrite sensor protein narq; PDBTitle: fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
49	c3hd7A	 Alignment	not modelled	9.6	9	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
50	c2jy5A	 Alignment	not modelled	9.4	12	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
51	d2r6gg1	 Alignment	not modelled	9.3	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
52	d2i76a1	 Alignment	not modelled	9.2	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
53	d1q08a	 Alignment	not modelled	8.8	29	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
54	d2hyda2	 Alignment	not modelled	8.8	23	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region

55	c2ndjA_		Alignment	not modelled	8.7	17	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
56	d1dv0a_		Alignment	not modelled	8.6	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
57	c6owsB_		Alignment	not modelled	8.3	16	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
58	c2hydB_		Alignment	not modelled	7.9	23	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
59	c2k29A_		Alignment	not modelled	7.8	11	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
60	c4yn3B_		Alignment	not modelled	7.7	11	PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin complex with pro-peptide
61	c5mpyB_		Alignment	not modelled	7.5	11	PDB header: plant protein Chain: B: PDB Molecule: multiple organellar rna editing factor 9, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana rna editing factor morf9
62	c4fxeB_		Alignment	not modelled	7.5	11	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
63	c5mpwA_		Alignment	not modelled	7.4	11	PDB header: plant protein Chain: A: PDB Molecule: multiple organellar rna editing factor 1, mitochondrial; PDBTitle: crystal structure of arabidopsis thaliana rna editing factor morf1
64	c2k21A_		Alignment	not modelled	7.2	0	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and 2 40 degree c
65	c2jpcA_		Alignment	not modelled	7.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
66	c5ydgB_		Alignment	not modelled	7.1	11	PDB header: rna binding protein Chain: B: PDB Molecule: multiple organellar rna editing factor 2, chloroplastic; PDBTitle: crystal structure of the arabidopsis thaliana chloroplast rna editing2 factors 2(morf2)
67	c4r24B_		Alignment	not modelled	7.0	37	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
68	c5oy0m_		Alignment	not modelled	6.7	11	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
69	c5oy0M_		Alignment	not modelled	6.7	11	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
70	c6hqbM_		Alignment	not modelled	6.7	11	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: monomeric cyanobacterial photosystem i
71	c5oy09_		Alignment	not modelled	6.7	11	PDB header: photosynthesis Chain: 9: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
72	c4l6v7_		Alignment	not modelled	6.7	11	PDB header: electron transport Chain: 7: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
73	c4l6vM_		Alignment	not modelled	6.7	11	PDB header: electron transport Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
74	c5fgnA_		Alignment	not modelled	6.7	13	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
75	c3idwA_		Alignment	not modelled	6.6	13	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
76	d1scjb_		Alignment	not modelled	6.5	10	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
77	c2kncA_		Alignment	not modelled	6.5	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
78	d1oqya2		Alignment	not modelled	6.5	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
79	c5gacN		Alignment	not modelled	6.4	10	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit

79	c2gasi_	Alignment	not modelled	6.4	10	PDBTitle: thermus thermophilus v/a-atpase, conformation 2 PDB header: membrane protein
80	c2lorA_	Alignment	not modelled	6.4	17	Chain: A: PDB Molecule: transmembrane protein 141; PDBTitle: backbone structure of human membrane protein tmem141
81	c3vw4B_	Alignment	not modelled	6.4	17	PDB header: dna binding protein/dna Chain: B: PDB Molecule: rep; PDBTitle: crystal structure of the dna-binding domain of cole2-p9 rep in complex2 with the replication origin
82	c6csxA_	Alignment	not modelled	6.3	15	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
83	c2kr6A_	Alignment	not modelled	6.2	14	PDB header: hydrolase Chain: A: PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit
84	c4ev6E_	Alignment	not modelled	6.2	9	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
85	c3sztB_	Alignment	not modelled	6.2	22	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
86	c2kncB_	Alignment	not modelled	6.1	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
87	d1nosa_	Alignment	not modelled	6.1	23	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
88	c4q2uM_	Alignment	not modelled	6.1	7	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
89	c1y698_	Alignment	not modelled	6.1	20	PDB header: ribosome Chain: 8: PDB Molecule: ribosome-recycling factor; PDB Fragment: unp residues 1-30 and 106-185; PDBTitle: rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
90	c2jnhA_	Alignment	not modelled	6.0	14	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b
91	c5mg3D_	Alignment	not modelled	6.0	12	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secD; PDBTitle: em fitted model of bacterial holo-translocon
92	c3gp4B_	Alignment	not modelled	6.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
93	c2m0qA_	Alignment	not modelled	5.9	6	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
94	d2e1za2	Alignment	not modelled	5.8	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetkinase-like
95	c5zazA_	Alignment	not modelled	5.8	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
96	c5mkkB_	Alignment	not modelled	5.7	4	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
97	c4z3pA_	Alignment	not modelled	5.7	20	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
98	d1wpga4	Alignment	not modelled	5.7	8	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
99	c2krfB_	Alignment	not modelled	5.7	17	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a