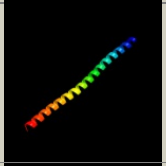
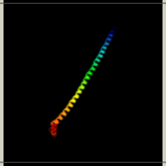
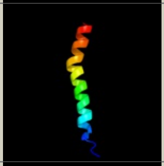
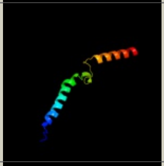
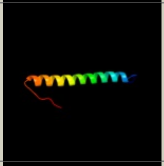
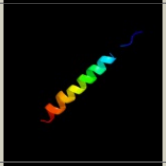
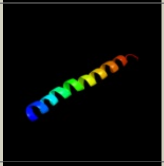
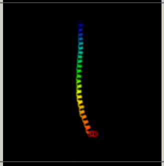
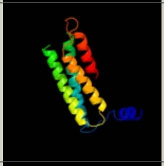
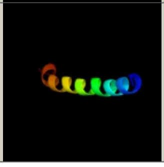
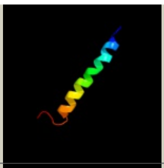
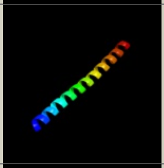
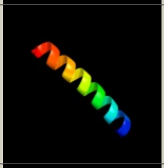
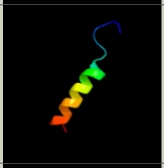
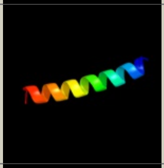
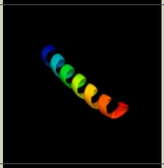
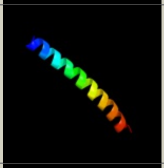
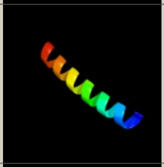
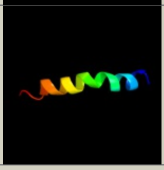
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ABA0
Date	Thu Jan 5 11:15:01 GMT 2012
Unique Job ID	844336a0421fe333

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1b9uA_	Alignment		98.3	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
2	d1l2pa_	Alignment		97.6	100	**Fold:**Single transmembrane helix **Superfamily:**F1F0 ATP synthase subunit B, membrane domain **Family:**F1F0 ATP synthase subunit B, membrane domain
3	c3k5bE_	Alignment		96.3	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
4	d2oara1	Alignment		90.9	24	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
5	c2oarA_	Alignment		90.1	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
6	c2khkA_	Alignment		87.9	100	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp synthase subunit b; **PDBTitle:** nmr solution structure of the b30-82 domain of subunit b of2 escherichia coli f1fo atp synthase
7	c3hzqA_	Alignment		81.0	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
8	c2rddB_	Alignment		77.0	15	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
9	c3k5bB_	Alignment		76.3	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase, subunit (vapc-therm); **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
10	c1y4cA_	Alignment		70.0	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
11	c1qcrD_	Alignment		43.6	6	**PDB header:** **PDB COMPND:**

12	c3rfrI_	Alignment		37.3	3	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
13	c2k88A_	Alignment		33.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vacuolar proton pump subunit g; **PDBTitle:** association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase
14	d3dtub2	Alignment		24.9	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
15	c1jdmA_	Alignment		20.4	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sarcolipin; **PDBTitle:** nmr structure of sarcolipin
16	c1ar1B_	Alignment		17.0	4	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
17	c1qleB_	Alignment		17.0	4	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
18	c2kk7A_	Alignment		16.5	46	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
19	d3ehbb2	Alignment		14.6	4	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
20	d1fftb2	Alignment		12.7	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
21	c1bctA_	Alignment	not modelled	11.5	15	**PDB header:**photoreceptor **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
22	c3mk7F_	Alignment	not modelled	10.2	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
23	d1v54d_	Alignment	not modelled	9.5	17	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
24	c2y69Q_	Alignment	not modelled	9.3	17	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
25	c1ei3E_	Alignment	not modelled	8.9	9	**PDB header:** **PDB COMPND:**
26	c3ghgK_	Alignment	not modelled	8.9	15	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
27	c1dxzA_	Alignment	not modelled	8.5	28	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**acetylcholine receptor protein, alpha chain; **PDBTitle:** m2 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 203 structures
						PDB header:transport protein

28	c2k59B_	Alignment	not modelled	8.3	30	**Chain:** B: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2; **PDBTitle:** nmr structures of the second transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
29	c1m57H_	Alignment	not modelled	7.9	16	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
30	c1fftG_	Alignment	not modelled	7.5	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
31	c2ww9B_	Alignment	not modelled	7.4	16	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
32	c1kilE_	Alignment	not modelled	6.2	28	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**complexin i snare-complex binding region; **PDBTitle:** three-dimensional structure of the complexin/snare complex
33	c3bz1T_	Alignment	not modelled	5.4	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
34	c3prrT_	Alignment	not modelled	5.4	17	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
35	c3prqT_	Alignment	not modelled	5.4	17	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
36	c3bz2T_	Alignment	not modelled	5.4	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
37	c1s5lT_	Alignment	not modelled	5.2	16	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii psbt protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
38	c1s5lt_	Alignment	not modelled	5.2	16	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii psbt protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
39	c2axtt_	Alignment	not modelled	5.2	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center t protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
40	c2axtT_	Alignment	not modelled	5.2	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center t protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
41	c3a0ht_	Alignment	not modelled	5.2	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
42	c3kziT_	Alignment	not modelled	5.2	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
43	d2axtt1	Alignment	not modelled	5.2	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein T, PsbT **Family:**PsbT-like
44	c3a0hT_	Alignment	not modelled	5.2	17	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
45	c3arcT_	Alignment	not modelled	5.2	17	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution