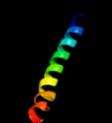
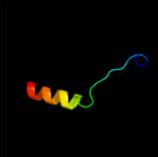
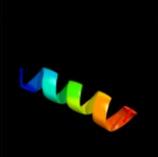


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P69789
Date	Thu Jan 5 12:11:55 GMT 2012
Unique Job ID	5e3c372065dbe99f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ibaA_</a>	 Alignment		99.9	33	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose permease; <b>PDBTitle:</b> glucose permease (domain iib), nmr, 11 structures
2	<a href="#">d3bp8c1</a>	 Alignment		99.9	35	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Glucose permease domain IIB <b>Family:</b> Glucose permease domain IIB
3	<a href="#">c3ipjB_</a>	 Alignment		99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts system, iiabc component; <b>PDBTitle:</b> the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
4	<a href="#">c2rddB_</a>	 Alignment		72.7	17	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> upf0092 membrane protein yajc; <b>PDBTitle:</b> x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
5	<a href="#">c3arct_</a>	 Alignment		33.9	25	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
6	<a href="#">c3hd7A_</a>	 Alignment		32.8	8	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
7	<a href="#">d3dtub2</a>	 Alignment		26.2	12	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
8	<a href="#">c3mk7F_</a>	 Alignment		19.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
9	<a href="#">c2dlaB_</a>	 Alignment		18.0	17	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> 397aa long hypothetical protein; <b>PDBTitle:</b> primase large subunit amino terminal domain from pyrococcus horikoshii
10	<a href="#">c3a0bT_</a>	 Alignment		16.4	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
11	<a href="#">c1iijA_</a>	 Alignment		12.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> erbB-2 receptor protein-tyrosine kinase; <b>PDBTitle:</b> solution structure of the neu/erbB-2 membrane spanning2 segment

12	<a href="#">d2cfua2</a>	Alignment		12.8	19	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Alkylsulfatase-like
13	<a href="#">c2zjsE_</a>	Alignment		12.5	50	<b>PDB header:</b> protein transport/immune system <b>Chain:</b> E: <b>PDB Molecule:</b> preprotein translocase sece subunit; <b>PDBTitle:</b> crystal structure of sece translocon from thermus thermophilus with a2 fab fragment
14	<a href="#">c3tixB_</a>	Alignment		11.3	8	<b>PDB header:</b> gene regulation/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> chromo domain-containing protein 1; <b>PDBTitle:</b> crystal structure of the chp1-tas3 complex core
15	<a href="#">d1fftb2</a>	Alignment		10.8	8	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
16	<a href="#">c3bz1T_</a>	Alignment		10.4	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
17	<a href="#">c3prqT_</a>	Alignment		10.4	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
18	<a href="#">c3bz2T_</a>	Alignment		10.4	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
19	<a href="#">c3prrT_</a>	Alignment		10.4	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
20	<a href="#">c1s5tT_</a>	Alignment		10.3	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii psbt protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
21	<a href="#">c1s5t_</a>	Alignment	not modelled	10.3	25	<b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii psbt protein; <b>PDBTitle:</b> architecture of the photosynthetic oxygen evolving center
22	<a href="#">c3kziT_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of monomeric form of cyanobacterial photosystem ii
23	<a href="#">c3arcT_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
24	<a href="#">d2axtt1</a>	Alignment	not modelled	10.2	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein T, PsbT <b>Family:</b> PsbT-like
25	<a href="#">c3a0bt_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
26	<a href="#">c3a0ht_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
27	<a href="#">c2axtT_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center t protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
28	<a href="#">c2axtt_</a>	Alignment	not modelled	10.2	25	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center t protein; <b>PDBTitle:</b> crystal structure of photosystem ii from thermosynechococcus elongatus
						<b>PDB header:</b> electron transport

29	<a href="#">c3a0hT_</a>	Alignment	not modelled	10.2	25	<b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
30	<a href="#">c2cfuA_</a>	Alignment	not modelled	10.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sdsa1; <b>PDBTitle:</b> crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
31	<a href="#">c3zqsB_</a>	Alignment	not modelled	8.0	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase fanc1; <b>PDBTitle:</b> human fanc1 central domain
32	<a href="#">c3d22A_</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin h-type; <b>PDBTitle:</b> crystal structure of a poplar thioredoxin h mutant,2 pptrxh4c61s
33	<a href="#">d1fzda_</a>	Alignment	not modelled	6.7	22	<b>Fold:</b> Fibrinogen C-terminal domain-like <b>Superfamily:</b> Fibrinogen C-terminal domain-like <b>Family:</b> Fibrinogen C-terminal domain-like
34	<a href="#">d1t57a_</a>	Alignment	not modelled	5.9	24	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
35	<a href="#">c3qd1X_</a>	Alignment	not modelled	5.8	45	<b>PDB header:</b> sugar binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> platelet binding protein gspb; <b>PDBTitle:</b> gspb plus alpha-2,3-sialyl (1-thioethyl)galactose
36	<a href="#">d3pvia_</a>	Alignment	not modelled	5.5	30	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease Pvull