



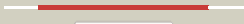




















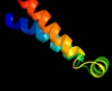




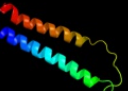


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P63235
Date	Thu Jan 5 12:08:01 GMT 2012
Unique Job ID	7ebb76997feab6cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c3lrcC_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
3	<a href="#">c2jlnA_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	<a href="#">c2xq2A_</a>	 Alignment		99.2	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsglT
5	<a href="#">c3dh4A_</a>	 Alignment		99.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	<a href="#">c2w8aC_</a>	 Alignment		97.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
7	<a href="#">d2a65a1</a>	 Alignment		97.1	11	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
8	<a href="#">c3hfxA_</a>	 Alignment		92.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
9	<a href="#">d1fftb2</a>	 Alignment		74.5	21	<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
10	<a href="#">c3qngD_</a>	 Alignment		61.3	19	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
11	<a href="#">c3rkoF_</a>	 Alignment		56.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution

12	<a href="#">c1fftG_</a>	Alignment		44.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> ubiquinol oxidase; <b>PDBTitle:</b> the structure of ubiquinol oxidase from escherichia coli
13	<a href="#">c2kncA_</a>	Alignment		21.3	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
14	<a href="#">d1iwga8</a>	Alignment		15.6	9	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
15	<a href="#">c2bbjB_</a>	Alignment		15.4	15	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
16	<a href="#">c2i5nH_</a>	Alignment		12.0	16	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodopseudomonas viridis:crystals grown by microfluidic technique
17	<a href="#">c1w8xP_</a>	Alignment		10.2	19	<b>PDB header:</b> virus <b>Chain:</b> P: <b>PDB Molecule:</b> protein p16; <b>PDBTitle:</b> structural analysis of prd1
18	<a href="#">c1qlcB_</a>	Alignment		9.9	16	<b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
19	<a href="#">c1ar1B_</a>	Alignment		9.9	16	<b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
20	<a href="#">c1m57H_</a>	Alignment		9.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
21	<a href="#">c2rddB_</a>	Alignment	not modelled	8.2	13	<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.
22	<a href="#">d3ehbb2</a>	Alignment	not modelled	7.7	16	<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
23	<a href="#">c1oy8A_</a>	Alignment	not modelled	7.6	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
24	<a href="#">d3dtub2</a>	Alignment	not modelled	7.3	13	<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
25	<a href="#">c2jp3A_</a>	Alignment	not modelled	5.8	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
26	<a href="#">c3mk7F_</a>	Alignment	not modelled	5.7	6	<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