

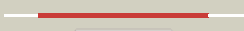

























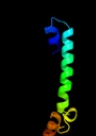
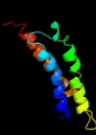
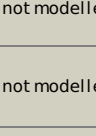


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P77610
Date	Thu Jan 5 12:31:02 GMT 2012
Unique Job ID	8e85d9766a526b93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		100.0	17	<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	17	<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	11	<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		99.4	11	<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 vsgl
5	<a href="#">c3dh4A_</a>	 Alignment		99.4	9	<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="#">d2a65a1</a>	 Alignment		98.3	9	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
7	<a href="#">c2w8aC_</a>	 Alignment		97.9	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
8	<a href="#">c3hfxA_</a>	 Alignment		96.2	8	<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="#">c2w2eA_</a>	 Alignment		49.6	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin; <b>PDBTitle:</b> 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
10	<a href="#">d1fftb2</a>	 Alignment		35.6	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
11	<a href="#">c2kncA_</a>	 Alignment		30.3	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex

12	<a href="#">d2fb5a1</a>	Alignment		15.0	11	<b>Fold:</b> Yojj-like <b>Superfamily:</b> Yojj-like <b>Family:</b> Yojj-like
13	<a href="#">c3m7bA</a>	Alignment		13.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog; <b>PDBTitle:</b> crystal structure of plant slac1 homolog teha
14	<a href="#">c2bbjB</a>	Alignment		12.3	12	<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
15	<a href="#">c3o7pA</a>	Alignment		9.7	5	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
16	<a href="#">c3entB</a>	Alignment		8.3	24	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of nitrollin, a betagamma-crystallin from2 nitrospira multiformis-in alternate space group (p65)
17	<a href="#">c3hd6A</a>	Alignment		8.2	12	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
18	<a href="#">c3p5tE</a>	Alignment		7.1	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor subunit 5; <b>PDBTitle:</b> cfim25-cfim68 complex
19	<a href="#">c3qngD</a>	Alignment		6.9	11	<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
20	<a href="#">c3ixzA</a>	Alignment		5.9	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> potassium-transporting atpase alpha; <b>PDBTitle:</b> pig gastric h+/k+-atpase complexed with aluminium fluoride
21	<a href="#">c2jwaA</a>	Alignment	not modelled	5.8	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
22	<a href="#">c2jo1A</a>	Alignment	not modelled	5.8	24	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
23	<a href="#">c2xutC</a>	Alignment	not modelled	5.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
24	<a href="#">d1iyjb2</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> BRCA2 tower domain <b>Superfamily:</b> BRCA2 tower domain <b>Family:</b> BRCA2 tower domain
25	<a href="#">d2oara1</a>	Alignment	not modelled	5.6	9	<b>Fold:</b> Gated mechanosensitive channel <b>Superfamily:</b> Gated mechanosensitive channel <b>Family:</b> Gated mechanosensitive channel
26	<a href="#">c2jp3A</a>	Alignment	not modelled	5.5	19	<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
27	<a href="#">c1m57H</a>	Alignment	not modelled	5.4	11	<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))
28	<a href="#">d1mjta</a>	Alignment	not modelled	5.3	11	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain

29	<a href="#">d2nr9a1</a>	Alignment	not modelled	5.2	16	<b>Fold:</b> Rhomboid-like <b>Superfamily:</b> Rhomboid-like <b>Family:</b> Rhomboid-like
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