

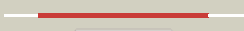














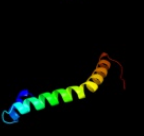

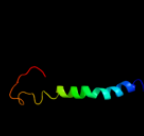


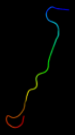



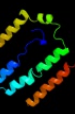
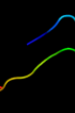





Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q5H778
Date	Thu Jan 5 12:37:23 GMT 2012
Unique Job ID	64d1a13b67ca8869

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
2	c3lrcC_	 Alignment		100.0	17	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
3	c2jlnA_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c2xq2A_	 Alignment		99.1	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vs9lt
5	c3dh4A_	 Alignment		99.1	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	c2w8aC_	 Alignment		94.6	11	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
7	d2a65a1	 Alignment		91.6	11	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
8	c3hfxA_	 Alignment		78.7	11	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
9	c3qngD_	 Alignment		51.3	17	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
10	d1fftb2	 Alignment		46.2	15	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
11	c2kluA_	 Alignment		37.6	12	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4

12	c2kvtA_	Alignment		11.0	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yaia; PDBTitle: solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244
13	c3le4A_	Alignment		10.9	27	PDB header: nuclear protein Chain: A: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: crystal structure of the dgcr8 dimerization domain
14	d1qhda2	Alignment		10.7	32	Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein
15	c1ujlA_	Alignment		10.3	0	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h PDBTitle: solution structure of the herg k+ channel s5-p2 extracellular linker
16	c3rkoF_	Alignment		9.6	12	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
17	c1zgxB_	Alignment		9.2	28	PDB header: hydrolase Chain: B: PDB Molecule: guanyl-specific ribonuclease sa; PDBTitle: crystal structure of ribonuclease mutant
18	c3bcyA_	Alignment		8.8	17	PDB header: unknown function Chain: A: PDB Molecule: protein yer067w; PDBTitle: crystal structure of yer067w
19	c2l1nA_	Alignment		8.5	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
20	c2elmA_	Alignment		8.4	21	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 10th c2h2 zinc finger of human2 zinc finger protein 406
21	c2rddB_	Alignment	not modelled	8.0	22	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.
22	c2v6xB_	Alignment	not modelled	7.8	25	PDB header: protein transport Chain: B: PDB Molecule: doa4-independent degradation protein 4; PDBTitle: structural insight into the interaction between escrt-iii2 and vps4
23	d1eg3a3	Alignment	not modelled	7.6	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
24	c3m7bA_	Alignment	not modelled	7.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
25	c2owrD_	Alignment	not modelled	7.4	17	PDB header: hydrolase Chain: D: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of vaccinia virus uracil-dna glycosylase
26	c2wmpB_	Alignment	not modelled	7.3	29	PDB header: chaperone Chain: B: PDB Molecule: papg protein; PDBTitle: structure of the e. coli chaperone papd in complex with the pilin2 domain of the papgii adhesin
27	d1p35a_	Alignment	not modelled	7.3	23	Fold: Baculovirus p35 protein Superfamily: Baculovirus p35 protein Family: Baculovirus p35 protein
28	c2i6kA_	Alignment	not modelled	7.2	29	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 1; PDBTitle: crystal structure of human type i ipp isomerase complexed2 with a substrate analog

29	d2r6gf1	Alignment	not modelled	7.2	14	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
30	d2oara1	Alignment	not modelled	6.8	10	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
31	c2gfpA	Alignment	not modelled	6.8	6	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
32	d2iuba2	Alignment	not modelled	6.7	5	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
33	c2y69Z	Alignment	not modelled	6.7	24	PDB header: electron transport Chain: Z: PDB Molecule: cytochrome c oxidase polypeptide 8h; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
34	c1qo8A	Alignment	not modelled	6.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
35	d1qmha2	Alignment	not modelled	6.5	23	Fold: IF3-like Superfamily: EPT/RTPC-like Family: RNA 3'-terminal phosphate cyclase, RTPC
36	c2kncA	Alignment	not modelled	6.5	8	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
37	c1qhdA	Alignment	not modelled	6.5	32	PDB header: viral protein Chain: A: PDB Molecule: viral capsid vp6; PDBTitle: crystal structure of vp6, the major capsid protein of group a2 rotavirus
38	c3kz5E	Alignment	not modelled	6.5	44	PDB header: dna binding protein Chain: E: PDB Molecule: protein sobp; PDBTitle: structure of cdomain
39	d1roca	Alignment	not modelled	6.4	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
40	d1kp6a	Alignment	not modelled	6.4	21	Fold: Ferredoxin-like Superfamily: Killer toxin KP6 alpha-subunit Family: Killer toxin KP6 alpha-subunit
41	d2joza1	Alignment	not modelled	6.4	15	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
42	c3c0fB	Alignment	not modelled	6.4	36	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein af_1514; PDBTitle: crystal structure of a novel non-pfam protein af1514 from archeoglobus2 fulgidus dsm 4304 solved by s-sad using a cr x-ray source
43	c2l9uA	Alignment	not modelled	6.3	32	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
44	c1bzka	Alignment	not modelled	6.2	50	PDB header: transport protein Chain: A: PDB Molecule: protein (band 3 anion transport protein); PDBTitle: structural studies on the effects of the deletion in the2 red cell anion exchanger (band3, ae1) associated with3 south east asian ovalocytosis.
45	c1iijA	Alignment	not modelled	6.2	21	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
46	c2embA	Alignment	not modelled	6.1	36	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region 342-2 372) of human zinc finger protein 473
47	d1f6ga	Alignment	not modelled	6.1	14	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
48	d2h8pc1	Alignment	not modelled	6.0	13	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
49	c3pqvD	Alignment	not modelled	5.9	9	PDB header: unknown function Chain: D: PDB Molecule: rcl1 protein; PDBTitle: cyclase homolog
50	c2k9yB	Alignment	not modelled	5.9	17	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
51	c2k9yA	Alignment	not modelled	5.9	17	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
52	c3nzqB	Alignment	not modelled	5.9	11	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
53	d2cu9a1	Alignment	not modelled	5.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: ASF1-like Family: ASF1-like
54	c2xzmO	Alignment	not modelled	5.8	12	PDB header: ribosome Chain: O: PDB Molecule: rps13e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the

						40s subunit and initiation factor for4 molecule 1
55	c2zx6A_	Alignment	not modelled	5.8	9	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
56	d1t98a2	Alignment	not modelled	5.7	14	Fold: STAT-like Superfamily: MukF C-terminal domain-like Family: MukF C-terminal domain-like
57	d1f8ea_	Alignment	not modelled	5.5	12	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
58	c3n2oA_	Alignment	not modelled	5.4	11	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
59	c1qmiC_	Alignment	not modelled	5.4	23	PDB header: rna 3'-terminal phosphate cyclase Chain: C: PDB Molecule: rna 3'-terminal phosphate cyclase; PDBTitle: crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
60	c3imkA_	Alignment	not modelled	5.4	13	PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
61	c1nmbN_	Alignment	not modelled	5.4	12	PDB header: complex (hydrolase/immunoglobulin) Chain: N: PDB Molecule: n9 neuraminidase; PDBTitle: the structure of a complex between the nc10 antibody and influenza2 virus neuraminidase and comparison with the overlapping binding site3 of the nc41 antibody
62	c2rmhA_	Alignment	not modelled	5.4	30	PDB header: hormone Chain: A: PDB Molecule: urocortin-3; PDBTitle: human urocortin 3
63	d1v54m_	Alignment	not modelled	5.3	24	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) Family: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
64	c2d46A_	Alignment	not modelled	5.3	5	PDB header: metal transport Chain: A: PDB Molecule: calcium channel, voltage-dependent, beta 4 PDBTitle: solution structure of the human beta4a-a domain
65	c1w21D_	Alignment	not modelled	5.2	3	PDB header: hydrolase Chain: D: PDB Molecule: neuraminidase; PDBTitle: structure of neuraminidase from english duck subtype n62 complexed with 30 mm sialic acid (nana, neu5ac), crystal3 soaked for 43 hours at 291 k.
66	c2cpbA_	Alignment	not modelled	5.2	18	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
67	c2vdaB_	Alignment	not modelled	5.2	63	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex