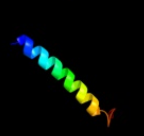
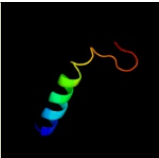
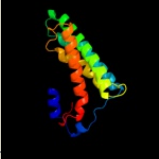
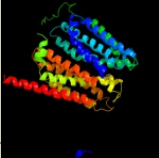
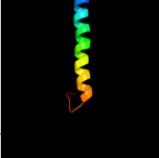
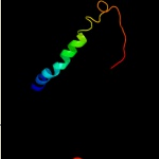
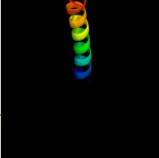
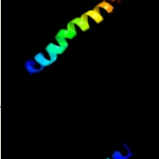
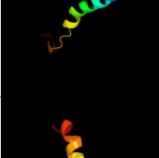
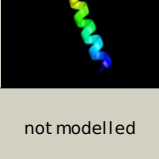


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AAE8
Date	Thu Jan 5 11:12:43 GMT 2012
Unique Job ID	265af434ac1e095b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
2	c3lrcC_	 Alignment		100.0	40	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
3	c2jlnA_	 Alignment		99.9	10	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c3dh4A_	 Alignment		99.2	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
5	c2xq2A_	 Alignment		99.1	11	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vs9lt
6	d2a65a1	 Alignment		95.8	19	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
7	c2w8aC_	 Alignment		91.4	13	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
8	c3rkoF_	 Alignment		60.5	11	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
9	c3hfxA_	 Alignment		50.9	10	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
10	d1eysh2	 Alignment		36.2	19	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
11	c2rddB_	 Alignment		22.4	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.

12	c2kluA_	Alignment		20.0	23	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
13	c3b9yA_	Alignment		17.6	4	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
14	d1pw4a_	Alignment		17.4	11	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
15	c2l2tA_	Alignment		17.4	11	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
16	d1fftb2	Alignment		14.9	9	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
17	c2yiuE_	Alignment		13.8	15	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
18	c2k21A_	Alignment		13.8	14	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
19	c2kncA_	Alignment		13.8	11	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
20	c1p84D_	Alignment		13.3	15	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
21	c2fynH_	Alignment	not modelled	13.2	19	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
22	c1zrtD_	Alignment	not modelled	12.4	11	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
23	d3ehbb2	Alignment	not modelled	12.0	11	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
24	c3cwbQ_	Alignment	not modelled	11.6	13	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
25	c2w2hD_	Alignment	not modelled	11.2	11	PDB header: rna-binding protein Chain: D: PDB Molecule: protein tat; PDBTitle: structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from e1av
26	d3dtub2	Alignment	not modelled	11.1	16	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
27	c2jo1A_	Alignment	not modelled	10.5	14	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
						PDB header: ribosomal protein/rna

28	c2zkry_	Alignment	not modelled	10.4	27	Chain: Y: PDB Molecule: 5s ribosomal rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
29	d2fq3a1	Alignment	not modelled	9.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: SWIRM domain
30	c3qngD_	Alignment	not modelled	9.7	11	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 the 2 n,n' -diacetylchitobiose-specific phosphotransferase system
31	c2jp3A_	Alignment	not modelled	9.7	14	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
32	d2auwa1	Alignment	not modelled	9.6	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
33	c1tz5A_	Alignment	not modelled	9.4	21	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
34	c2ks1B_	Alignment	not modelled	9.3	13	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
35	d1lmma_	Alignment	not modelled	9.2	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
36	c1ronA_	Alignment	not modelled	9.2	7	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
37	c2kncB_	Alignment	not modelled	9.1	26	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
38	c2dezA_	Alignment	not modelled	9.0	0	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy
39	c1d6uB_	Alignment	not modelled	9.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with 2 beta-phenylethylamine
40	c2bf9A_	Alignment	not modelled	8.9	7	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
41	c3njcA_	Alignment	not modelled	8.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yslb protein; PDBTitle: crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
42	c1uj1A_	Alignment	not modelled	8.7	24	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
43	d1qbic_	Alignment	not modelled	8.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
44	d1qgpa_	Alignment	not modelled	8.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
45	c2cpbA_	Alignment	not modelled	8.4	24	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of 2 filamentous bacteriophage m13 solubilized in 3 dodecylphosphocholine micelles, 25 lowest energy structures
46	d2e74g1	Alignment	not modelled	8.3	20	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
47	d2gxba1	Alignment	not modelled	8.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
48	c2b9sB_	Alignment	not modelled	8.0	15	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
49	d1ez3a_	Alignment	not modelled	7.8	15	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
50	c2auwB_	Alignment	not modelled	7.7	12	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from 2 nitrosomonas europaea atcc 19718
51	d1v54i_	Alignment	not modelled	7.4	28	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIc Family: Mitochondrial cytochrome c oxidase subunit VIc
52	d1zela1	Alignment	not modelled	7.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
						Fold: Transmembrane helix hairpin

53	d2iuba2	Alignment	not modelled	7.3	5	Supertfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
54	c2k1aA	Alignment	not modelled	7.2	6	PDB header: signaling protein/transferase Chain: B: PDB Molecule: putative uncharacterized protein t20l15_90; PDBTitle: the crystal structure of plant specific calcium binding protein atcb122 in complex with the regulatory domain of atcpk14
55	c2zfdB	Alignment	not modelled	7.1	14	PDB header: ligase, cell cycle Chain: E: PDB Molecule: cell division control protein 53; PDBTitle: a dual e3 mechanism for rub1 ligation to cdc53: dcn1(p)-cdc53(whb)
56	c3o2pE	Alignment	not modelled	7.1	5	Fold: Preprotein translocase SecY subunit Superfamily: Preprotein translocase SecY subunit Family: Preprotein translocase SecY subunit
57	d1rh5a	Alignment	not modelled	7.0	11	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
58	c1fftG	Alignment	not modelled	7.0	11	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
59	d2r6gf1	Alignment	not modelled	6.9	15	PDB header: transcription regulation Chain: A: PDB Molecule: transactivator protein; PDBTitle: structure of the equine infectious anemia virus tat protein
60	c1vtA	Alignment	not modelled	6.9	11	PDB header: protein binding Chain: F: PDB Molecule: ring1 and yy1-binding protein; PDBTitle: ring1b c-terminal domain/rybp c-terminal domain complex
61	c3ixsF	Alignment	not modelled	6.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: bovine heart cytochrome c oxidase at the fully reduced state
62	c1v55B	Alignment	not modelled	6.8	5	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
63	c3rkoK	Alignment	not modelled	6.8	15	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
64	d1joya	Alignment	not modelled	6.8	15	Fold: Zinc domain conserved in yeast copper-regulated transcription factors Superfamily: Zinc domain conserved in yeast copper-regulated transcription factors Family: Zinc domain conserved in yeast copper-regulated transcription factors
65	d1co4a	Alignment	not modelled	6.8	18	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
66	d2h8pc1	Alignment	not modelled	6.7	17	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
67	d1iwga7	Alignment	not modelled	6.7	12	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
68	d1k18a	Alignment	not modelled	6.6	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
69	d1j75a	Alignment	not modelled	6.5	16	PDB header: de novo protein Chain: B: PDB Molecule: four-helix bundle model; PDBTitle: solution structure of a diiron protein model: due ferri(ii)2 turn mutant
70	c1u7mB	Alignment	not modelled	6.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: all0216 protein; PDBTitle: x-ray structure of all0216 protein from nostoc sp. pcc 7120 at the2 resolution 1.8a. northeast structural genomics consortium target3 nsr236
71	c3jsrA	Alignment	not modelled	6.5	15	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
72	c3iz5h	Alignment	not modelled	6.5	22	PDB header: photosynthesis Chain: G: PDB Molecule: protein pet g; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
73	c1vf5G	Alignment	not modelled	6.4	20	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
74	d1vf5g	Alignment	not modelled	6.4	20	PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein rps13 (s15p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
75	c3izbO	Alignment	not modelled	6.4	29	PDB header: rna binding protein/rna Chain: N: PDB Molecule: nucleoprotein; PDBTitle: respiratory syncytial virus ribonucleoprotein
76	c2wj8N	Alignment	not modelled	6.3	29	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
77	c3zquA	Alignment	not modelled	6.3	43	PDB header: antibiotic Chain: A: PDB Molecule: big defensin;
78	c3ra2A	Alignment	not modelled	6.2	24	

78	c2tq2A_	Alignment	not modelled	6.2	24	PDBTitle: the solution structure of the n-terminal fragment of big2 defensin
79	d2axti1	Alignment	not modelled	6.1	21	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, Psbl Family: Psbl-like
80	c2o5gB_	Alignment	not modelled	6.0	18	PDB header: metal binding protein Chain: B: PDB Molecule: smooth muscle myosin light chain kinase peptide; PDBTitle: calmodulin-smooth muscle light chain kinase peptide complex
81	d1ldja1	Alignment	not modelled	6.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
82	c4a1bB_	Alignment	not modelled	6.0	14	PDB header: ribosome Chain: B: PDB Molecule: rpl39; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 3.
83	d1iuya_	Alignment	not modelled	6.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
84	d2b8ta2	Alignment	not modelled	5.9	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
85	c2zkr3_	Alignment	not modelled	5.9	11	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
86	c2wwaA_	Alignment	not modelled	5.9	10	PDB header: ribosome Chain: A: PDB Molecule: sec sixty-one protein homolog; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
87	d1fcla_	Alignment	not modelled	5.9	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Immunoglobulin-binding domains Family: Immunoglobulin-binding domains
88	c3rj1P_	Alignment	not modelled	5.9	9	PDB header: transcription Chain: P: PDB Molecule: mediator of rna polymerase ii transcription subunit 17; PDBTitle: architecture of the mediator head module
89	d3cx5d2	Alignment	not modelled	5.9	12	Fold: Single transmembrane helix Superfamily: Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor Family: Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
90	c2egrA_	Alignment	not modelled	5.9	14	PDB header: transcription Chain: A: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
91	d1qzua_	Alignment	not modelled	5.8	14	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
92	c2xznZ_	Alignment	not modelled	5.8	15	PDB header: ribosome Chain: Z: PDB Molecule: rps21e; 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 2
93	d2bcgg3	Alignment	not modelled	5.7	15	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
94	d1mvka_	Alignment	not modelled	5.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Immunoglobulin-binding domains Family: Immunoglobulin-binding domains
95	c3p5nA_	Alignment	not modelled	5.7	15	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
96	c3ndhA_	Alignment	not modelled	5.7	8	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease thai; PDBTitle: restriction endonuclease in complex with substrate dna
97	c1m57H_	Alignment	not modelled	5.7	11	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
98	c2l9uA_	Alignment	not modelled	5.7	16	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
99	c1w8xP_	Alignment	not modelled	5.7	10	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1