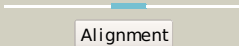



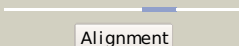

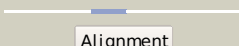

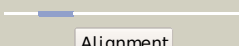

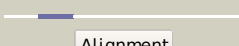



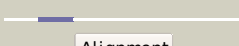




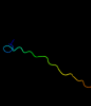



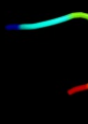
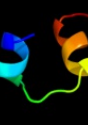
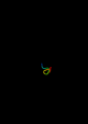

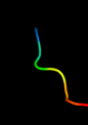
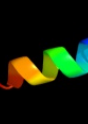
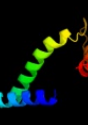



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PJX8
Date	Thu Apr 26 09:45:40 BST 2012
Unique Job ID	b4ebfd22d6e3dfe0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gb5B_	 Alignment		33.7	36	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
2	c2jp3A_	 Alignment		30.1	27	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
3	d1q7ha2	 Alignment		22.8	29	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Hypothetical protein Ta1423, N-terminal domain
4	c2jt1A_	 Alignment		21.9	40	PDB header: transcription Chain: A: PDB Molecule: pefi protein; PDBTitle: solution nmr structure of pefi (plasmid-encoded fimbriae regulatory)2 protein from salmonella typhimurium. northeast structural genomics3 target str82
5	d1bsma1	 Alignment		21.4	50	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
6	d1ma1a1	 Alignment		14.4	50	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
7	c2wff4_	 Alignment		12.7	44	PDB header: virus Chain: 4: PDB Molecule: p1; PDB Fragment: capsid protein vp4, residues 1-80 PDBTitle: equine rhinitis a virus
8	d1mnga1	 Alignment		12.1	50	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
9	d1nlna_	 Alignment		12.0	33	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
10	d1uffa_	 Alignment		12.0	16	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
11	c3htuE_	 Alignment		11.7	56	PDB header: protein transport Chain: E: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: crystal structure of the human vps25-vps20 subcomplex

12	c2q2fA_	Alignment		11.5	38	PDB header: membrane protein Chain: A: PDB Molecule: selenoprotein s; PDBTitle: structure of the human selenoprotein s (vcp-interacting membrane2 protein)
13	d1x6aa2	Alignment		11.4	80	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
14	c3eyiB_	Alignment		11.4	32	PDB header: dna binding protein/dna Chain: B: PDB Molecule: z-dna-binding protein 1; PDBTitle: the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
15	c3ks7D_	Alignment		11.3	53	PDB header: hydrolase Chain: D: PDB Molecule: putative putative pngase f; PDBTitle: crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
16	c1junB_	Alignment		11.3	29	PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
17	c3js4C_	Alignment		11.2	63	PDB header: oxidoreductase Chain: C: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of iron superoxide dismutase from anaplasma2 phagocytophilum
18	d2axtm1	Alignment		11.1	42	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein M, PsbM Family: PsbM-like
19	d1wc9a_	Alignment		10.9	16	Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: TRAPP components
20	c1qqp4_	Alignment		10.6	44	PDB header: virus Chain: 4: PDB Molecule: protein (genome polyprotein); PDBTitle: foot-and-mouth disease virus/ oligosaccharide receptor complex.
21	c1bdeA_	Alignment	not modelled	10.3	27	PDB header: aids Chain: A: PDB Molecule: vpr protein; PDBTitle: helical structure of polypeptides from the c-terminal half2 of hiv-1 vpr, nmr, 20 structures
22	c2e62A_	Alignment	not modelled	9.9	86	PDB header: rna binding protein Chain: A: PDB Molecule: protein at5g25060; PDBTitle: solution structure of the cwf21 domain in protein aak25922
23	d1vava_	Alignment	not modelled	9.6	38	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Alginate lyase
24	c3ceiA_	Alignment	not modelled	9.6	63	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase; PDBTitle: crystal structure of superoxide dismutase from helicobacter2 pylori
25	c1avmA_	Alignment	not modelled	9.5	50	PDB header: oxidoreductase Chain: A: PDB Molecule: superoxide dismutase; PDBTitle: the cambialistic superoxide dismutase (fe-sod) of p. shermanii2 coordinated by azide
26	c1byvA_	Alignment	not modelled	9.5	63	PDB header: membrane protein Chain: A: PDB Molecule: protein (sodium channel alpha-subunit); PDBTitle: sodium channel iia inactivation gate
27	c2zrrA_	Alignment	not modelled	9.4	28	PDB header: antimicrobial protein Chain: A: PDB Molecule: mundticin ks immunity protein; PDBTitle: crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
28	c3bj4B_	Alignment	not modelled	9.4	50	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt PDBTitle: the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2

						subunit assembly and protein interaction
29	c1ciiA	Alignment	not modelled	9.3	22	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
30	d1x68a2	Alignment	not modelled	9.2	60	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
31	d1nkza	Alignment	not modelled	9.2	50	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
32	c3zquA	Alignment	not modelled	9.1	60	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
33	c2gpcB	Alignment	not modelled	9.1	75	PDB header: oxidoreductase Chain: B: PDB Molecule: iron superoxide dismutase; PDBTitle: the crystal structure of the enzyme fe-superoxide dismutase2 from trypanosoma cruzi
34	d1jgka	Alignment	not modelled	9.0	36	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
35	d2pw4a1	Alignment	not modelled	8.9	50	Fold: Jann2411-like Superfamily: Jann2411-like Family: Jann2411-like
36	d1tg7a1	Alignment	not modelled	8.9	33	Fold: Beta-galactosidase LacA, domain 3 Superfamily: Beta-galactosidase LacA, domain 3 Family: Beta-galactosidase LacA, domain 3
37	c1mngA	Alignment	not modelled	8.6	50	PDB header: oxidoreductase(superoxide acceptor) Chain: A: PDB Molecule: manganese superoxide dismutase; PDBTitle: structure-function in e. coli iron superoxide dismutase: comparisons2 with the manganese enzyme from t. thermophilus
38	d1j7na3	Alignment	not modelled	8.5	44	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
39	c1x9vA	Alignment	not modelled	8.3	27	PDB header: viral protein Chain: A: PDB Molecule: vpr protein; PDBTitle: dimeric structure of the c-terminal domain of vpr
40	d1duga1	Alignment	not modelled	8.3	30	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
41	c1bl1A	Alignment	not modelled	8.3	63	PDB header: hormone receptor Chain: A: PDB Molecule: parathyroid hormone receptor; PDBTitle: pth receptor n-terminus fragment, nmr, 1 structure
42	d2k4xa1	Alignment	not modelled	8.2	40	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
43	c2kn0A	Alignment	not modelled	8.0	18	PDB header: apoptosis Chain: A: PDB Molecule: fn14; PDBTitle: solution nmr structure of xenopus fn14
44	d1iida	Alignment	not modelled	7.8	44	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
45	c2kwzA	Alignment	not modelled	7.8	38	PDB header: viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution structure of ns2 [60-99]
46	c2jo1A	Alignment	not modelled	7.8	41	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-ATPase regulatory protein fxyd1 in 2 micelles
47	c1ma1E	Alignment	not modelled	7.7	50	PDB header: oxidoreductase Chain: E: PDB Molecule: superoxide dismutase; PDBTitle: structure and properties of the atypical iron superoxide2 dismutase from methanobacterium thermoautotrophicum
48	c2ejbA	Alignment	not modelled	7.6	60	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
49	d2es9a1	Alignment	not modelled	7.6	60	Fold: YoaC-like Superfamily: YoaC-like Family: YoaC-like
50	d1m72a	Alignment	not modelled	7.5	11	Fold: Caspase-like Superfamily: Caspase-like Family: Caspase catalytic domain
51	d1w6ka2	Alignment	not modelled	7.4	50	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
52	c1y32A	Alignment	not modelled	7.4	50	PDB header: unknown function Chain: A: PDB Molecule: humanin; PDBTitle: nmr structure of humanin in 30% tfe solution
53	d2j3wb1	Alignment	not modelled	7.4	21	Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: TRAPP components
54	d2phcb1	Alignment	not modelled	7.2	25	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
55	c2zp2B	Alignment	not modelled	7.2	17	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis

56	c3no7A_	Alignment	not modelled	7.2	47	PDB header: dna binding protein Chain: A: PDB Molecule: putative plasmid related protein; PDBTitle: crystal structure of the centromere-binding protein parb from plasmid2 pxc100
57	d1u2ca1	Alignment	not modelled	7.2	55	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Dystroglycan, N-terminal domain
58	c2bn3A_	Alignment	not modelled	7.1	63	PDB header: radiation damage Chain: A: PDB Molecule: insulin; PDBTitle: insulin before a high dose x-ray burn
59	c3prrl_	Alignment	not modelled	7.1	53	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
60	d2axtl1	Alignment	not modelled	7.1	53	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein L, PsbL Family: PsbL-like
61	c1s5L_	Alignment	not modelled	7.1	53	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
62	c3prql_	Alignment	not modelled	7.1	53	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
63	c2axtl_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
64	c1s5I_	Alignment	not modelled	7.1	53	PDB header: photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
65	c3arcL_	Alignment	not modelled	7.1	53	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
66	c2axtl_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center I protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
67	c3bz2L_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
68	c3kziL_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
69	c3a0bL_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
70	c3bz1L_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
71	c3a0hl_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
72	c3a0hL_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
73	c3a0bl_	Alignment	not modelled	7.1	53	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
74	d1whqa_	Alignment	not modelled	7.1	19	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
75	d1lc0a2	Alignment	not modelled	7.1	73	Fold: FwdE/GAPDH domain-like Superfamily: Glycerol dehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Biliverdin reductase
76	d1xb4a2	Alignment	not modelled	7.0	71	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
77	d2v4jb1	Alignment	not modelled	7.0	50	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
78	d2axtl1	Alignment	not modelled	7.0	24	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, PsbI Family: PsbI-like
79	c1skhA_	Alignment	not modelled	7.0	40	PDB header: unknown function Chain: A: PDB Molecule: major prion protein 2; PDBTitle: n-terminal (1-30) of bovine prion protein
80	c1mk2B_	Alignment	not modelled	7.0	27	PDB header: transcription Chain: B: PDB Molecule: madh-interacting protein; PDBTitle: smad3 sbd complex
81	c2cfhA_	Alignment	not modelled	6.9	13	PDB header: transport Chain: A: PDB Molecule: trafficking protein particle complex subunit 3; PDBTitle: structure of the bet3-tpc6b core of trapp PDB header: rna binding protein

82	c3kwrA_	Alignment	not modelled	6.9	56	Chain: A: PDB Molecule: putative rna-binding protein; PDBTitle: crystal structure of putative rna-binding protein (np_785364.1) from2 lactobacillus plantarum at 1.45 a resolution
83	c2qqpD_	Alignment	not modelled	6.8	50	PDB header: virus Chain: D: PDB Molecule: small capsid protein; PDBTitle: crystal structure of authentic providence virus
84	c2phcB_	Alignment	not modelled	6.6	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
85	c3hieA_	Alignment	not modelled	6.6	14	PDB header: exocytosis Chain: A: PDB Molecule: exocyst complex component sec3; PDBTitle: structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex
86	d1nuba3	Alignment	not modelled	6.6	23	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
87	c2xb0X_	Alignment	not modelled	6.5	13	PDB header: hydrolase Chain: X: PDB Molecule: chromo domain-containing protein 1; PDBTitle: dna-binding domain from saccharomyces cerevisiae chromatin-2 remodelling protein chd1
88	c3e5yB_	Alignment	not modelled	6.5	29	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
89	d1j5wa_	Alignment	not modelled	6.5	28	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
90	d2d4pa1	Alignment	not modelled	6.5	35	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
91	d1xmka1	Alignment	not modelled	6.5	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
92	c2becB_	Alignment	not modelled	6.4	33	PDB header: metal binding protein/transport protein Chain: B: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: crystal structure of chp2 in complex with its binding2 region in nhe1 and insights into the mechanism of ph3 regulation
93	c1znmA_	Alignment	not modelled	6.4	36	PDB header: zinc finger Chain: A: PDB Molecule: yy1; PDBTitle: a zinc finger with an artificial beta-turn, original2 sequence taken from the third zinc finger domain of the3 human transcriptional repressor protein yy1 (ying and yang4 1, a delta transcription factor), nmr, 34 structures
94	c2k1vA_	Alignment	not modelled	6.4	60	PDB header: hormone Chain: A: PDB Molecule: insulin-like peptide insl5; PDBTitle: r3/i5 relaxin chimera
95	c2kbcA_	Alignment	not modelled	6.4	60	PDB header: hormone Chain: A: PDB Molecule: insl5_a-chain; PDBTitle: solution structure of human insulin-like peptide 5 (insl5)
96	d1w2ya_	Alignment	not modelled	6.3	25	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: Type II deoxyuridine triphosphatase
97	c1facA_	Alignment	not modelled	6.3	45	PDB header: coagulation factor Chain: A: PDB Molecule: coagulation factor viii; PDBTitle: coagulation factor viii, nmr, 1 structure
98	c2lgbA_	Alignment	not modelled	6.3	57	PDB header: hormone Chain: A: PDB Molecule: insulin a chain; PDBTitle: human insulin mutant a22gly-b31arg
99	d1ecib_	Alignment	not modelled	6.3	86	Fold: Ectatomin subunits Superfamily: Ectatomin subunits Family: Ectatomin subunits