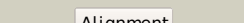
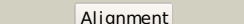
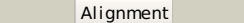
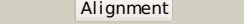
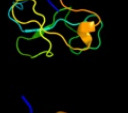
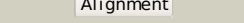
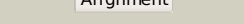
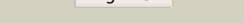
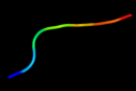
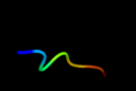
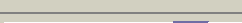
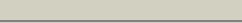


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ACC3
Date	Thu Jan 5 11:17:53 GMT 2012
Unique Job ID	68a48847d847e235

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2apnA_	 Alignment		100.0	82	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
2	c2d2aA_	 Alignment		100.0	29	PDB header: metal transport Chain: A: PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
3	c1x0gA_	 Alignment		100.0	32	PDB header: metal binding protein Chain: A: PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
4	d1s98a_	 Alignment		100.0	33	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
5	c2k4zA_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
6	d1nwba_	 Alignment		100.0	38	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
7	d2p2ea1	 Alignment		98.7	20	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
8	c2qgoA_	 Alignment		98.6	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative fe-s biosynthesis protein; PDBTitle: crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
9	d1vsra_	 Alignment		23.3	7	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
10	d1sp2a_	 Alignment		19.1	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
11	c2kvfA_	 Alignment		17.5	45	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein

12	dlzfda_	Alignment			16.9	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	dlalial	Alignment			15.4	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
14	dlaaya1	Alignment			14.9	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
15	dlubdc3	Alignment			14.5	71	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
16	dla1ha1	Alignment			13.9	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
17	c2nq2C_	Alignment			13.1	20	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
18	dla1ga1	Alignment			13.1	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
19	d1tf3a2	Alignment			13.1	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
20	d1f2ig1	Alignment			12.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
21	d1u86a1	Alignment		not modelled	12.6	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
22	d2a6sa1	Alignment		not modelled	12.6	5	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
23	clbcrA_	Alignment		not modelled	12.3	28	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
24	d2ns1b1	Alignment		not modelled	12.1	10	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
25	d1wmia1	Alignment		not modelled	12.0	11	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
26	c3kxeD_	Alignment		not modelled	11.9	20	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
27	d2yt9a1	Alignment		not modelled	11.2	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	d1x6ea2	Alignment		not modelled	10.1	67	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
							Fold: beta-beta-alpha zinc fingers

29	d2glia3	Alignment	not modelled	10.1	36	Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
30	c3g5oC	Alignment	not modelled	10.0	24	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
31	c1znmA	Alignment	not modelled	9.6	50	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
32	d2dlka2	Alignment	not modelled	9.3	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
33	d1ncsa	Alignment	not modelled	9.3	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
34	c2ab3A	Alignment	not modelled	9.1	67	PDB header: rna binding protein Chain: A: PDB Molecule: znf29; PDBTitle: solution structures and characterization of hiv rre iib rna2 targeting zinc finger proteins
35	c2kdxA	Alignment	not modelled	8.7	13	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
36	d1jj7a	Alignment	not modelled	8.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
37	d1wgea1	Alignment	not modelled	8.3	50	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
38	c2kdnA	Alignment	not modelled	8.2	60	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein pfe0790c; PDBTitle: solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
39	d1m0sa2	Alignment	not modelled	8.1	23	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
40	d1v9ja	Alignment	not modelled	7.7	20	Fold: Alpha-lytic protease prodomain-like Superfamily: BolA-like Family: BolA-like
41	d1lk5a2	Alignment	not modelled	7.6	16	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
42	c1va1A	Alignment	not modelled	7.6	43	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
43	c1zc1A	Alignment	not modelled	7.4	21	PDB header: protein turnover Chain: A: PDB Molecule: ubiquitin fusion degradation protein 1; PDBTitle: ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
44	d2cota1	Alignment	not modelled	7.3	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	d1ji0a	Alignment	not modelled	7.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
46	c2kheA	Alignment	not modelled	7.2	22	PDB header: hydrolase Chain: A: PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
47	c2jn4A	Alignment	not modelled	7.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein fixu, nift; PDBTitle: solution nmr structure of protein rp4601 from2 rhodospseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
48	d2jn4a1	Alignment	not modelled	7.1	22	Fold: NifT/FixU barrel-like Superfamily: NifT/FixU-like Family: NifT/FixU
49	d2hq2a1	Alignment	not modelled	7.1	20	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
50	c3a44D	Alignment	not modelled	7.1	20	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
51	c2wh44	Alignment	not modelled	6.9	67	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome
52	c2yujA	Alignment	not modelled	6.5	28	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
53	d1ywsa1	Alignment	not modelled	6.4	56	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
						PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: solution structure of protein l31 from thermophilus

54	c3f1f4_	Alignment	not modelled	6.2	67	PDB title: crystal structure of a translation termination complex2 formed with release factor rf2. this file contains the 50s3 subunit of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.
55	d2j0pa1	Alignment	not modelled	6.2	17	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
56	d2j7ja1	Alignment	not modelled	6.2	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
57	c1gxsC_	Alignment	not modelled	6.2	23	PDB header: lyase Chain: C: PDB Molecule: p-(s)-hydroxymandelonitrile lyase chain a; PDBTitle: crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
58	d2a2ua_	Alignment	not modelled	6.2	9	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
59	c3hlzA_	Alignment	not modelled	6.2	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bt_1490; PDBTitle: crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
60	c2jr7A_	Alignment	not modelled	6.1	67	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
61	c3kxeB_	Alignment	not modelled	6.1	12	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
62	c2cbzA_	Alignment	not modelled	5.9	26	PDB header: transport Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: structure of the human multidrug resistance protein 12 nucleotide binding domain 1
63	d1a1ia3	Alignment	not modelled	5.9	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
64	d2cota2	Alignment	not modelled	5.9	83	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
65	d3b60a1	Alignment	not modelled	5.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
66	d1adta2	Alignment	not modelled	5.7	40	Fold: Zn-binding domains of ADDBP Superfamily: Zn-binding domains of ADDBP Family: Zn-binding domains of ADDBP
67	d1ubdc2	Alignment	not modelled	5.7	60	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
68	d2j0141	Alignment	not modelled	5.6	40	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
69	c2j034_	Alignment	not modelled	5.6	40	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
70	d1ewfa1	Alignment	not modelled	5.6	0	Fold: Aha1/BPI domain-like Superfamily: Bactericidal permeability-increasing protein, BPI Family: Bactericidal permeability-increasing protein, BPI
71	c3gfoA_	Alignment	not modelled	5.6	18	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
72	d1u85a1	Alignment	not modelled	5.6	67	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
73	c3a0rA_	Alignment	not modelled	5.5	19	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
74	c3c3ja_	Alignment	not modelled	5.5	38	PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
75	d1llmc2	Alignment	not modelled	5.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
76	c2entA_	Alignment	not modelled	5.4	63	PDB header: transcription Chain: A: PDB Molecule: krueppel-like factor 15; PDBTitle: solution structure of the second c2h2-type zinc finger2 domain from human krueppel-like factor 15
77	c2k6la_	Alignment	not modelled	5.2	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
78	c3t7la_	Alignment	not modelled	5.2	21	PDB header: transport protein Chain: A: PDB Molecule: zinc finger fyve domain-containing protein 16; PDBTitle: crystal structure of the fyve domain of endofin (zfvyve16) at 1.1a2 resolution

79	d2h85a2	Alignment	not modelled	5.2	43	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
80	c2l72A_	Alignment	not modelled	5.0	6	PDB header: protein binding Chain: A: PDB Molecule: actin depolymerizing factor, putative; PDBTitle: solution structure and dynamics of adf from toxoplasma gondii (tgadf)
81	clareA_	Alignment	not modelled	5.0	33	PDB header: transcription regulation Chain: A: PDB Molecule: yeast transcription factor adr1; PDBTitle: structures of dna-binding mutant zinc finger domains:2 implications for dna binding