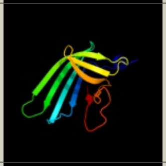
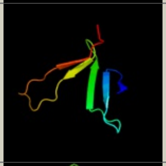
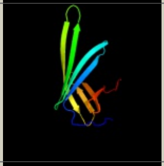
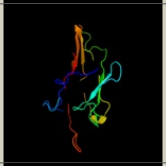
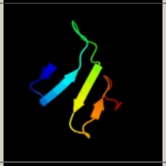
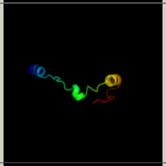
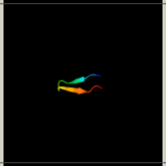
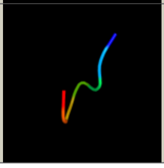
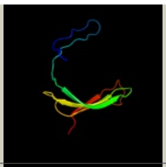
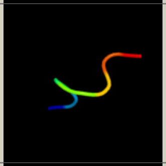
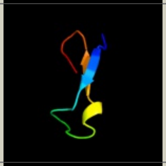
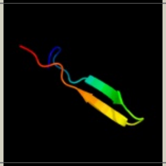
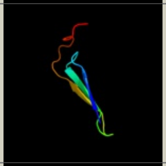
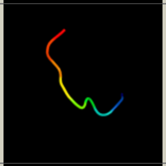
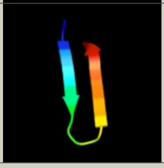
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P40710
Date	Thu Jan 5 12:01:13 GMT 2012
Unique Job ID	e36d1a927fa628c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z4hB_	Alignment		100.0	100	**PDB header:**signaling protein activator **Chain:** B: **PDB Molecule:**copper homeostasis protein cutf; **PDBTitle:** crystal structure of the cpx pathway activator nlpe from2 escherichia coli
2	c3lhnB_	Alignment		100.0	36	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution
3	d1jiwi_	Alignment		74.1	16	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
4	c3ge2A_	Alignment		65.8	16	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein, putative; **PDBTitle:** crystal structure of putative lipoprotein sp_0198 from streptococcus2 pneumoniae
5	c3p02A_	Alignment		34.4	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein of unknown function (bacova_00267) from2 bacteroides ovatus at 1.55 a resolution
6	d2q4ma1	Alignment		27.2	29	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
7	c1zxuA_	Alignment		27.2	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750
8	c3o0rC_	Alignment		22.9	11	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
9	c1brvA_	Alignment		18.2	47	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**protein g; **PDBTitle:** solution nmr structure of the immunodominant region of2 protein g of bovine respiratory syncytial virus, 483 structures
10	d1jhna4	Alignment		18.0	21	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Calnexin/calreticulin
11	d1hxra_	Alignment		17.6	86	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4

12	c3p43A_	Alignment		17.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
13	d2fu5a1	Alignment		17.4	86	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
14	d1rc9a2	Alignment		15.3	57	**Fold:**Crisp domain-like **Superfamily:**Crisp domain-like **Family:**Crisp domain
15	c1nuiA_	Alignment		15.3	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
16	d2fm8a1	Alignment		15.2	17	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
17	d2hh8a1	Alignment		15.1	6	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
18	c2l6nA_	Alignment		14.1	43	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_001092504.1; **PDBTitle:** nmr solution structure of the protein yp_001092504.1
19	c3hyxC_	Alignment		13.9	56	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfide-quinone reductase; **PDBTitle:** 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
20	c3rg0A_	Alignment		13.8	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**calreticulin; **PDBTitle:** structural and functional relationships between the lectin and arm2 domains of calreticulin
21	c2bx9J_	Alignment	not modelled	12.9	38	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
22	d1j8ra_	Alignment	not modelled	12.6	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**PapG adhesin receptor-binding domain
23	c2l6pA_	Alignment	not modelled	11.5	43	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
24	c2ktsA_	Alignment	not modelled	10.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hslj; **PDBTitle:** nmr structure of the protein np_415897.1
25	c1jhnA_	Alignment	not modelled	10.4	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**calnexin; **PDBTitle:** crystal structure of the lumenal domain of calnexin
26	d1oyvi_	Alignment	not modelled	10.0	29	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
27	d1r7aa1	Alignment	not modelled	9.9	30	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
28	c2ovsB_	Alignment	not modelled	9.8	8	**PDB header:**gene regulation, ligand binding protein **Chain:** B: **PDB Molecule:**I0044; **PDBTitle:** crystal strcuture of a type three secretion system protein
						Fold:beta-beta-alpha zinc fingers

29	d2eppa1	Alignment	not modelled	9.2	45	**Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
30	d2dsya1	Alignment	not modelled	8.8	24	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA0281-like
31	c2dcrA_	Alignment	not modelled	8.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fes/fps; **PDBTitle:** fully automated solution structure determination of the fes2 sh2 domain
32	c3kg9A_	Alignment	not modelled	8.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curk; **PDBTitle:** dehydratase domain from curk module of curacin polyketide synthase
33	d1vlya1	Alignment	not modelled	8.1	16	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
34	d2aqaa1	Alignment	not modelled	8.1	40	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
35	d2bpa2_	Alignment	not modelled	8.0	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
36	c3luuA_	Alignment	not modelled	7.9	60	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
37	d1w0na_	Alignment	not modelled	7.9	25	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 36 carbohydrate binding module, CBM36
38	d1o6da_	Alignment	not modelled	7.9	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
39	d1wgea1	Alignment	not modelled	7.9	38	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
40	d1gff2_	Alignment	not modelled	7.8	36	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
41	c1n1uA_	Alignment	not modelled	7.6	25	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** nmr structure of [ala1,15]kalata b1
42	d1n1ua_	Alignment	not modelled	7.6	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
43	c1r8oA_	Alignment	not modelled	7.6	38	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kunitz trypsin inhibitor; **PDBTitle:** crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
44	c3cjtP_	Alignment	not modelled	7.5	6	**PDB header:**transferase/ribosomal protein **Chain:** P: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
45	c3ld0Q_	Alignment	not modelled	7.4	38	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
46	d2gvia2	Alignment	not modelled	7.4	67	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**FwdE C-terminal domain-like
47	c3n9dA_	Alignment	not modelled	7.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** monoclinic structure of p. aeruginosa ligd phosphoesterase domain
48	d1mila_	Alignment	not modelled	7.2	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
49	d1ns5a_	Alignment	not modelled	7.2	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
50	c2knnA_	Alignment	not modelled	7.2	50	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin-o2; **PDBTitle:** solution structure of the cyclotide cycloviolacin o2 with2 glu6 methylated (cyo2me)
51	c2qn4B_	Alignment	not modelled	7.2	29	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**alpha-amylase/subtilisin inhibitor; **PDBTitle:** structure and function study of rice bifunctional alpha-2 amylase/subtilisin inhibitor from oryza sativa
52	d1to0a_	Alignment	not modelled	7.1	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
53	d1vh0a_	Alignment	not modelled	7.1	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
54	c2f2iA_	Alignment	not modelled	6.8	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [p20d,v21k]-kalata b1
55	d1avwb_	Alignment	not modelled	6.7	57	**Fold:**beta-Trefoil **Superfamily:**STI-like

						Family: Kunitz (STI) inhibitors
56	d1nb1a_	Alignment	not modelled	6.6	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
57	d1ha8a_	Alignment	not modelled	6.6	63	**Fold:**Pheromone ER-23 **Superfamily:**Pheromone ER-23 **Family:**Pheromone ER-23
58	d1lrva_	Alignment	not modelled	6.6	38	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Leucine-rich repeat variant
59	c3o6uB_	Alignment	not modelled	6.6	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cpe2226; **PDBTitle:** crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
60	d1fnoa3	Alignment	not modelled	6.5	9	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
61	d1pt4a_	Alignment	not modelled	6.5	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
62	c2l6lA_	Alignment	not modelled	6.5	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
63	c2kzxA_	Alignment	not modelled	6.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
64	d1cf1a1	Alignment	not modelled	6.4	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
65	c2f2jA_	Alignment	not modelled	6.4	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [w19k, p20n, v21k]-kalata b1
66	c2zkrk_	Alignment	not modelled	6.3	9	**PDB header:**ribosomal protein/rna **Chain:** K: **PDB Molecule:**rna expansion segment es19; **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
67	c2khbA_	Alignment	not modelled	6.3	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of linear kalata b1 (loop 6)
68	c1iebD_	Alignment	not modelled	6.0	20	**PDB header:**histocompatibility antigen **Chain:** D: **PDB Molecule:**mhc class ii i-ek; **PDBTitle:** histocompatibility antigen
69	d1m3va1	Alignment	not modelled	6.0	57	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
70	d1r8na_	Alignment	not modelled	5.8	36	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
71	d1mmsa2	Alignment	not modelled	5.7	6	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
72	c2xvoB_	Alignment	not modelled	5.7	32	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**sso1725; **PDBTitle:** sso1725, a protein involved in the crispr/cas pathway
73	d1vqok1	Alignment	not modelled	5.7	14	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
74	c3swrA_	Alignment	not modelled	5.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** structure of human dnmt1 (601-1600) in complex with sinefungin
75	d3cjsb1	Alignment	not modelled	5.6	6	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
76	d1v1qa_	Alignment	not modelled	5.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
77	d2hz5a1	Alignment	not modelled	5.4	26	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
78	c2jmbA_	Alignment	not modelled	5.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens
79	d1whia_	Alignment	not modelled	5.4	23	**Fold:**Ribosomal protein L14 **Superfamily:**Ribosomal protein L14 **Family:**Ribosomal protein L14
80	d1sg1x2	Alignment	not modelled	5.3	31	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
81	c2p57A_	Alignment	not modelled	5.3	55	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
						PDB header:structural genomics, unknown function

82	c2p3yA_	Alignment	not modelled	5.3	25	**Chain:** A: **PDB Molecule:**hypothetical protein vpa0735; **PDBTitle:** crystal structure of vpa0735 from vibrio parahaemolyticus. northeast2 structural genomics target vpr109
83	d2p3ya1	Alignment	not modelled	5.3	25	**Fold:**VPA0735-like **Superfamily:**VPA0735-like **Family:**VPA0735-like
84	d2f2ha1	Alignment	not modelled	5.3	27	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
85	d1tiea_	Alignment	not modelled	5.3	29	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
86	d1eyla_	Alignment	not modelled	5.3	43	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
87	c3g12A_	Alignment	not modelled	5.2	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
88	d3bx1c1	Alignment	not modelled	5.1	29	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
89	c1y7jA_	Alignment	not modelled	5.1	80	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**agouti signaling protein; **PDBTitle:** nmr structure family of human agouti signalling protein (80-2 132: q115y, s124y)
90	c2owaB_	Alignment	not modelled	5.1	27	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**arfgap-like finger domain containing protein; **PDBTitle:** crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
91	c2dreA_	Alignment	not modelled	5.1	36	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**water-soluble chlorophyll protein; **PDBTitle:** crystal structure of water-soluble chlorophyll protein from2 lepidium virginicum at 2.00 angstrom resolution