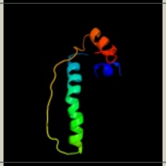
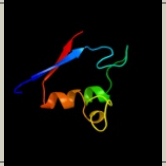
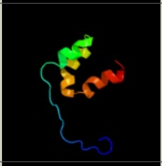
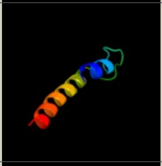
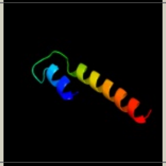
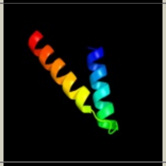
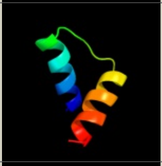
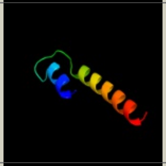
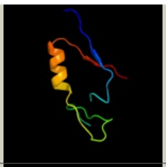
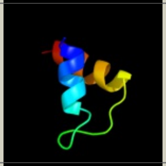
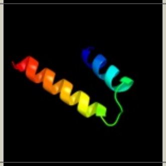
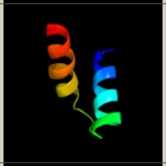
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P18006
Date	Thu Jan 5 11:36:33 GMT 2012
Unique Job ID	94ee705249be05e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u2ma_	Alignment		81.7	9	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
2	c2kkmA_	Alignment		75.1	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation machinery-associated protein 16; **PDBTitle:** solution nmr structure of yeast protein yor252w [residues2 38-178]: northeast structural genomics consortium target3 yt654
3	d2amya1	Alignment		40.1	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
4	c3nuqA_	Alignment		36.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nucleotide phosphatase; **PDBTitle:** structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
5	d1nh2d1	Alignment		31.1	11	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
6	d1nvpd1	Alignment		30.9	17	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
7	d2cbia1	Alignment		26.9	23	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
8	d1eb7a2	Alignment		26.7	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
9	c3o5cA_	Alignment		24.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
10	c1nvpD_	Alignment		24.1	17	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma chain; **PDBTitle:** human tfiia/tbp/dna complex
11	c1xviA_	Alignment		23.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12

12	d1xvia_	Alignment		23.5	25	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
13	c1zzhA_	Alignment		23.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c peroxidase; **PDBTitle:** structure of the fully oxidized di-heme cytochrome c2 peroxidase from r. capsulatus
14	c2fncA_	Alignment		20.9	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**maltose abc transporter, periplasmic maltose-binding **PDBTitle:** thermotoga maritima maltotriose binding protein bound with2 maltotriose.
15	d2qtia1	Alignment		20.0	14	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
16	d1v92a_	Alignment		20.0	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
17	c2vhdB_	Alignment		19.9	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
18	d1iqca2	Alignment		19.8	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
19	c2dalA_	Alignment		19.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein kiaa0794; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
20	d1b4ub_	Alignment		18.6	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
21	c3kfuJ_	Alignment	not modelled	18.5	14	**PDB header:**ligase/rna **Chain:** J: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** crystal structure of the transamidosome
22	d2jrxa1	Alignment	not modelled	18.1	21	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
23	d2f2ac1	Alignment	not modelled	17.9	11	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Glu-tRNAGln amidotransferase C subunit **Family:**Glu-tRNAGln amidotransferase C subunit
24	c1nh2D_	Alignment	not modelled	17.9	11	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia small chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
25	d2choa1	Alignment	not modelled	16.7	15	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
26	d1nmla2	Alignment	not modelled	16.2	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
27	c2q9rA_	Alignment	not modelled	15.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a duf416 family protein (sbal_3149) from2 shewanella baltica os155 at 1.91 a resolution
28	c3anoA_	Alignment	not modelled	15.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv

29	d2juwa1	Alignment	not modelled	15.5	15	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
30	d2juza1	Alignment	not modelled	15.4	14	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
31	c3h0mU_	Alignment	not modelled	15.3	11	**PDB header:**ligase **Chain: U: PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
32	d2jpqa1	Alignment	not modelled	14.7	21	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
33	c2kjwA_	Alignment	not modelled	14.1	22	**PDB header:**ribosomal protein **Chain: A: PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
34	d2c42a1	Alignment	not modelled	13.9	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR Pyr module
35	c3mpoD_	Alignment	not modelled	13.8	36	**PDB header:**hydrolase **Chain: D: PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
36	c2c1uB_	Alignment	not modelled	13.7	15	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
37	c1iqcB_	Alignment	not modelled	13.4	12	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**di-heme peroxidase; **PDBTitle:** crystal structure of di-heme peroxidase from nitrosomonas europaea
38	c3c8mA_	Alignment	not modelled	12.3	16	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
39	c3hq7A_	Alignment	not modelled	12.0	27	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
40	d1zyma1	Alignment	not modelled	11.9	17	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
41	d1u7pa_	Alignment	not modelled	11.7	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
42	c1odpA_	Alignment	not modelled	11.2	43	**PDB header:**lipid transport **Chain: A: PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
43	c1odrA_	Alignment	not modelled	11.2	43	**PDB header:**lipid transport **Chain: A: PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
44	c1odqA_	Alignment	not modelled	11.2	43	**PDB header:**lipid transport **Chain: A: PDB Molecule:**apoa-i peptide; **PDBTitle:** peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
45	c1lj2C_	Alignment	not modelled	10.8	60	**PDB header:**viral protein/ translation **Chain: C: PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
46	c3do5A_	Alignment	not modelled	10.7	11	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
47	d2fuea1	Alignment	not modelled	10.7	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
48	d1gefa_	Alignment	not modelled	10.4	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
49	d1xuba1	Alignment	not modelled	10.4	38	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
50	c3ingA_	Alignment	not modelled	10.1	16	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
51	c3mtjA_	Alignment	not modelled	10.1	24	**PDB header:**oxidoreductase **Chain: A: PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
52	d1x4pa1	Alignment	not modelled	9.7	20	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
53	d1ltqa1	Alignment	not modelled	9.5	27	**Fold:**HAD-like **Superfamily:**HAD-like

						Family:phosphatase domain of polynucleotide kinase
54	c2p11A_	Alignment	not modelled	9.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bxe_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
55	c1zzvA_	Alignment	not modelled	9.3	16	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter feca from3 escherichia coli.
56	c3rsiA_	Alignment	not modelled	9.2	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
57	c1lj2D_	Alignment	not modelled	8.9	60	**PDB header:**viral protein/ translation **Chain:** D: **PDB Molecule:**eukaryotic protein synthesis initiation factor; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
58	d2hcfa1	Alignment	not modelled	8.9	23	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
59	d1qy9a1	Alignment	not modelled	8.7	36	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
60	c2iexA_	Alignment	not modelled	8.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
61	c1nmlA_	Alignment	not modelled	8.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
62	c1or7C_	Alignment	not modelled	8.5	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
63	d1or7c_	Alignment	not modelled	8.5	14	**Fold:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Superfamily:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Family:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
64	d2otaa1	Alignment	not modelled	8.5	21	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
65	d1ng6a_	Alignment	not modelled	8.4	16	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/YqeY domain
66	d1mkza_	Alignment	not modelled	8.2	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
67	c3nzqB_	Alignment	not modelled	8.1	19	**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
68	d1w85b1	Alignment	not modelled	8.1	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
69	d2odfa1	Alignment	not modelled	8.1	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
70	c2d1uA_	Alignment	not modelled	7.8	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution strcuture of the periplasmic signaling domain of2 feca from escherichia coli
71	d1y5ea1	Alignment	not modelled	7.6	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
72	c3pgvB_	Alignment	not modelled	7.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
73	d1rkqa_	Alignment	not modelled	7.4	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
74	c3fduF_	Alignment	not modelled	7.3	10	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
75	d1mula_	Alignment	not modelled	7.3	25	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
76	d1nm8a1	Alignment	not modelled	7.1	30	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
77	d1t1ua1	Alignment	not modelled	7.1	30	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
78	d1ndba1	Alignment	not modelled	6.4	30	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases

						Family: Choline/Carnitine O-acyltransferase
79	d1s7za_	Alignment	not modelled	6.3	20	**Fold:**Another 3-helical bundle **Superfamily:**B-form DNA mimic Ocr **Family:**B-form DNA mimic Ocr
80	c2qniA_	Alignment	not modelled	6.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
81	d1nnla_	Alignment	not modelled	6.3	27	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
82	c1no1C_	Alignment	not modelled	6.1	30	**PDB header:**replication **Chain:** C: **PDB Molecule:**replisome organizer; **PDBTitle:** structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
83	d1no1a_	Alignment	not modelled	6.1	30	**Fold:**Replisome organizer (g39p helicase loader/inhibitor protein) **Superfamily:**Replisome organizer (g39p helicase loader/inhibitor protein) **Family:**Replisome organizer (g39p helicase loader/inhibitor protein)
84	c2l2dA_	Alignment	not modelled	6.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**otu domain-containing protein 7a; **PDBTitle:** solution nmr structure of human uba-like domain of otud7a_11_83, nesg2 target ht6304a/ocsp target otud7a_11_83/sgc-toronto
85	c3fxeA_	Alignment	not modelled	6.0	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein icmq; **PDBTitle:** crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
86	d1vcoa2	Alignment	not modelled	5.7	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
87	c1q6xA_	Alignment	not modelled	5.6	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline o-acetyltransferase; **PDBTitle:** crystal structure of rat choline acetyltransferase
88	d2vo1a1	Alignment	not modelled	5.5	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
89	d2q7sa1	Alignment	not modelled	5.4	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
90	d1wr8a_	Alignment	not modelled	5.4	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
91	c3fkeB_	Alignment	not modelled	5.2	12	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** structure of the ebola vp35 interferon inhibitory domain
92	d1rkua_	Alignment	not modelled	5.2	0	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
93	d1l6ra_	Alignment	not modelled	5.2	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
94	d1huua_	Alignment	not modelled	5.2	7	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
95	c3fvvA_	Alignment	not modelled	5.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
96	d1u02a_	Alignment	not modelled	5.1	6	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
97	c3l7yA_	Alignment	not modelled	5.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159