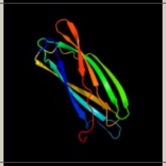
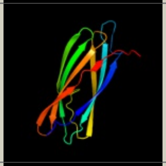
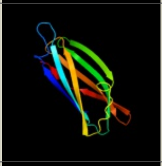
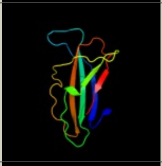
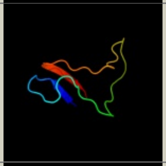
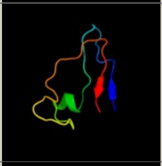
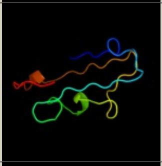
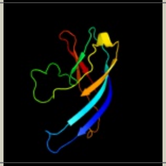
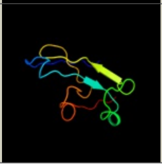
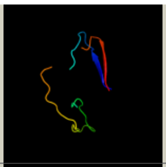
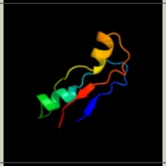
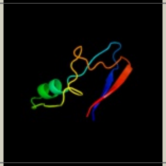
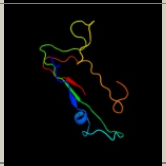
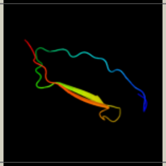
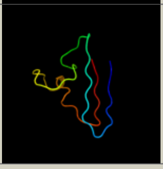
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P62672
Date	Thu Jan 5 12:07:46 GMT 2012
Unique Job ID	ee793427b130ce72

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tzaa_	Alignment		100.0	47	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
2	d1xq4a_	Alignment		100.0	47	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
3	d1xvsa_	Alignment		100.0	51	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ApaG-like **Family:**ApaG-like
4	c2f1eA_	Alignment		100.0	48	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
5	c3cfuA_	Alignment		81.2	13	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
6	c3cg8B_	Alignment		79.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**laccase; **PDBTitle:** laccase from streptomyces coelicolor
7	c3cdzB_	Alignment		70.2	23	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii light chain; **PDBTitle:** crystal structure of human factor viii
8	c2r7eB_	Alignment		67.6	23	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii; **PDBTitle:** crystal structure analysis of coagulation factor viii
9	c2uxtA_	Alignment		64.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein sufi; **PDBTitle:** sufi protein from escherichia coli
10	c3rfrI_	Alignment		64.3	19	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
11	d1cuoa_	Alignment		63.1	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like

12	c2x3bB_	Alignment		63.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
13	d1lm8v_	Alignment		60.0	25	**Fold:**Prealbumin-like **Superfamily:**VHL **Family:**VHL
14	c1sddA_	Alignment		59.9	17	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
15	d1hfua2	Alignment		59.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
16	c2fqeA_	Alignment		57.8	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**blue copper oxidase cueo; **PDBTitle:** crystal structures of e. coli laccase cueo under different2 copper binding situations
17	c1l9mB_	Alignment		56.2	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3; **PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
18	d1nepa_	Alignment		55.1	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**ML domain
19	c3zx1A_	Alignment		53.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** multicopper oxidase from campylobacter jejuni: a metallo-oxidase
20	c3cdzA_	Alignment		52.8	15	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
21	c2xu9A_	Alignment	not modelled	51.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of laccase from thermus thermophilus hb27
22	c3abgA_	Alignment	not modelled	50.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bilirubin oxidase; **PDBTitle:** x-ray crystal analysis of bilirubin oxidase from myrothecium2 verrucaria at 2.3 angstrom resolution using a twin crystal
23	c2zwnA_	Alignment	not modelled	50.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**two-domain type laccase; **PDBTitle:** crystal structure of the novel two-domain type laccase from a2 metagenome
24	c2k6zA_	Alignment	not modelled	50.0	37	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
25	c3m7oB_	Alignment	not modelled	48.7	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**lymphocyte antigen 86; **PDBTitle:** crystal structure of mouse md-1 in complex with phosphatidylcholine
26	c3isyA_	Alignment	not modelled	46.9	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
27	d1azca_	Alignment	not modelled	46.5	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
28	d2ccwa1	Alignment	not modelled	46.2	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins

						Family: Plastocyanin/azurin-like
29	d1v10a2	Alignment	not modelled	45.4	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
30	c1yewI_	Alignment	not modelled	45.2	24	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
31	c3kw8A_	Alignment	not modelled	42.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
32	d1ibya_	Alignment	not modelled	41.6	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
33	d1hc1a3	Alignment	not modelled	41.3	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arthropod hemocyanin, C-terminal domain
34	c3nrfA_	Alignment	not modelled	41.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**apag protein; **PDBTitle:** crystal structure of an apag protein (pa1934) from pseudomonas2 aeruginosa pao1 at 1.50 a resolution
35	c1sddB_	Alignment	not modelled	40.0	28	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
36	c3g5wC_	Alignment	not modelled	39.1	23	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**multicopper oxidase type 1; **PDBTitle:** crystal structure of blue copper oxidase from nitrosomonas europaea
37	d1ufga_	Alignment	not modelled	38.1	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
38	d2plta_	Alignment	not modelled	37.4	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
39	c3jt0B_	Alignment	not modelled	36.9	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
40	c1v10A_	Alignment	not modelled	35.1	17	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** structure of rigidoporus lignosus laccase from hemihedrally2 twinned crystals
41	d1cc3a_	Alignment	not modelled	34.8	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
42	c2bnoA_	Alignment	not modelled	34.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
43	d2j5wa3	Alignment	not modelled	34.0	32	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
44	c3rgbA_	Alignment	not modelled	33.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
45	c2zooA_	Alignment	not modelled	33.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
46	c1wa1X_	Alignment	not modelled	33.1	17	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
47	d1jzga_	Alignment	not modelled	31.6	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
48	c2h47C_	Alignment	not modelled	30.9	24	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**azurin; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
49	d1gyca2	Alignment	not modelled	30.7	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
50	d1ifra_	Alignment	not modelled	30.7	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
51	d1joia_	Alignment	not modelled	30.5	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
52	d1ejxb_	Alignment	not modelled	29.7	31	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
53	d4ubpb_	Alignment	not modelled	28.1	31	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
54	d1e9ya1	Alignment	not modelled	27.0	33	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit

55	d1sdda1	Alignment	not modelled	27.0	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	c3mu3A_	Alignment	not modelled	26.9	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein md-1; **PDBTitle:** crystal structure of chicken md-1 complexed with lipid iva
57	d2j5wa1	Alignment	not modelled	25.7	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
58	d1rkra_	Alignment	not modelled	24.9	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
59	d1nwpa_	Alignment	not modelled	24.8	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
60	d1kyaa2	Alignment	not modelled	23.9	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
61	d2q9oa1	Alignment	not modelled	23.2	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
62	d1hfua1	Alignment	not modelled	23.1	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
63	d1rutx4	Alignment	not modelled	21.9	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
64	c1mzzC_	Alignment	not modelled	21.6	37	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper-containing nitrite reductase; **PDBTitle:** crystal structure of mutant (m182t)of nitrite reductase
65	c3gdcC_	Alignment	not modelled	21.1	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**multicopper oxidase; **PDBTitle:** crystal structure of multicopper oxidase
66	d1qbaa2	Alignment	not modelled	21.0	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Bacterial chitobiase, n-terminal domain
67	d1kv7a2	Alignment	not modelled	20.7	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
68	c1kcwA_	Alignment	not modelled	20.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ceruloplasmin; **PDBTitle:** x-ray crystal structure of human ceruloplasmin at 3.0 angstroms
69	d1ndsa1	Alignment	not modelled	20.2	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
70	d1ivta_	Alignment	not modelled	20.1	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
71	c1e9zA_	Alignment	not modelled	19.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
72	d1hcza2	Alignment	not modelled	19.8	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
73	d1kv7a1	Alignment	not modelled	19.8	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
74	c3qgaD_	Alignment	not modelled	19.7	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
75	d1aoza2	Alignment	not modelled	18.8	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
76	d1sddb1	Alignment	not modelled	17.9	40	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
77	d1oe1a1	Alignment	not modelled	17.4	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
78	d1exha_	Alignment	not modelled	16.9	43	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
79	d1kbva2	Alignment	not modelled	16.8	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
80	c2yxwB_	Alignment	not modelled	16.6	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**blue copper oxidase cueo; **PDBTitle:** the deletion mutant of multicopper oxidase cueo
81	d2q9oa2	Alignment	not modelled	16.6	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
						PDB header:sugar binding protein

82	c3orjA_	Alignment	not modelled	16.3	20	**Chain:** A: **PDB Molecule:**sugar-binding protein; **PDBTitle:** crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
83	d1kyaa1	Alignment	not modelled	15.9	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
84	c3h8uA_	Alignment	not modelled	14.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
85	d1v97a4	Alignment	not modelled	13.4	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
86	c3hhsB_	Alignment	not modelled	13.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phenoloxidase subunit 1; **PDBTitle:** crystal structure of manduca sexta prophenoloxidase
87	d1gyca1	Alignment	not modelled	13.2	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
88	c1kbwA_	Alignment	not modelled	13.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**major outer membrane protein pan 1; **PDBTitle:** crystal structure of the soluble domain of ania from2 neisseria gonorrhoeae
89	d2ar1a1	Alignment	not modelled	13.0	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
90	d1m1ha1	Alignment	not modelled	12.9	33	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
91	d1aoza1	Alignment	not modelled	12.4	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
92	d2bnma2	Alignment	not modelled	12.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
93	c1asqB_	Alignment	not modelled	11.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ascorbate oxidase; **PDBTitle:** x-ray structures and mechanistic implications of three functional2 derivatives of ascorbate oxidase from zucchini: reduced-, peroxide-,3 and azide-forms
94	d2fdbm1	Alignment	not modelled	11.6	13	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
95	d1llaa3	Alignment	not modelled	11.5	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arthropod hemocyanin, C-terminal domain
96	c3ixvG_	Alignment	not modelled	10.6	25	**PDB header:**oxygen binding **Chain:** G: **PDB Molecule:**hemocyanin aa6 chain; **PDBTitle:** scorpion hemocyanin resting state pseudo atomic model built based on2 cryo-em density map
97	c3d5bN_	Alignment	not modelled	10.5	14	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
98	d2zjrg1	Alignment	not modelled	10.5	17	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
99	c3cf5G_	Alignment	not modelled	10.5	17	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans