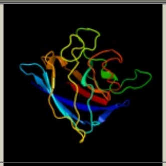
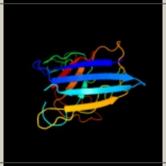
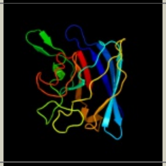
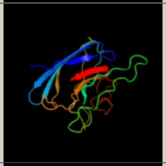
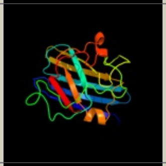
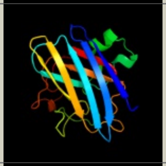
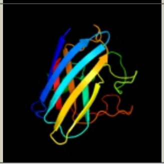
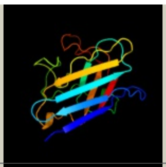
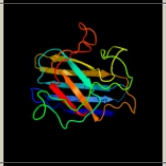
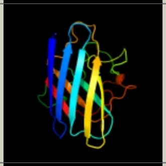
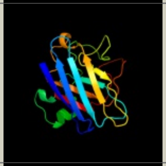
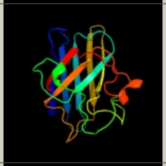
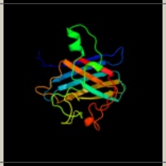
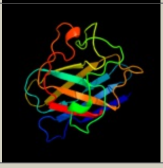
Email	l.a.kelley@imperial.ac.uk
Description	P0AGD1
Date	Thu Jan 5 11:28:47 GMT 2012
Unique Job ID	6a99b1bd4c3487c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1esoa_	Alignment		100.0	100	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
2	c2aqmA_	Alignment		100.0	55	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** cu/zn superoxide dismutase from brucella abortus
3	d1eqwa_	Alignment		100.0	57	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
4	c1pzsA_	Alignment		100.0	29	**PDB header:**oxidoreductase, metal binding protein **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** crystal structure of a cu-zn superoxide dismutase from mycobacterium2 tuberculosis at 1.63 resolution
5	d1pzsa_	Alignment		100.0	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
6	d1oala_	Alignment		100.0	47	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
7	d2apsa_	Alignment		100.0	51	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
8	c1s4iC_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**superoxide dismutase-like protein yojm; **PDBTitle:** crystal structure of a sod-like protein from bacillus subtilis
9	d1do5a_	Alignment		100.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
10	d1q0ea_	Alignment		100.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
11	c3f7lA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper,zinc superoxide dismutase; **PDBTitle:** x-ray crystal structure of alvinella pompejana cu,zn2 superoxide dismutase

12	d1srda_	Alignment		100.0	30	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
13	c2q2lB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from p.2 atrosanguina
14	d2c9va1	Alignment		100.0	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
15	d1to4a_	Alignment		100.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
16	c3ce1A_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** crystal structure of the cu/zn superoxide dismutase from2 cryptococcus liquefaciens strain n6
17	d1xsoa_	Alignment		100.0	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
18	c2e47A_	Alignment		100.0	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**time interval measuring enzyme time; **PDBTitle:** crystal structure analysis of the clock protein ea4 (glycosylation2 form)
19	d1f1ga_	Alignment		100.0	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
20	c3l9eC_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** crystal structures of holo and cu-deficient cu/znsod from the silkworm2 bombyx mori and the implications in amyotrophic lateral sclerosis
21	c2jlpA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**extracellular superoxide dismutase (cu-zn); **PDBTitle:** crystal structure of human extracellular copper-zinc2 superoxide dismutase.
22	d1ej8a_	Alignment	not modelled	100.0	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
23	c3kbeA_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn]; **PDBTitle:** metal-free c. elegans cu,zn superoxide dismutase
24	c1jk9D_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
25	c1qupA_	Alignment	not modelled	100.0	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
26	c3hogA_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn], chloroplastic; **PDBTitle:** metal-free tomato chloroplast superoxide dismutase
27	d1jk9b1	Alignment	not modelled	100.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
28	c1zpuE_	Alignment	not modelled	48.1	30	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3; **PDBTitle:** crystal structure of fet3p, a multicopper oxidase that

						functions in2 iron import
29	d1gska3	Alignment	not modelled	31.0	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
30	c1of0A_	Alignment	not modelled	25.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**spore coat protein a; **PDBTitle:** crystal structure of bacillus subtilis cota after 1h2 soaking with ebs
31	c3zx1A_	Alignment	not modelled	23.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** multicopper oxidase from campylobacter jejuni: a metallo-oxidase
32	d1e30a_	Alignment	not modelled	21.5	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
33	c2g23G_	Alignment	not modelled	20.5	33	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**phenoxazinone synthase; **PDBTitle:** the crystal structure of hexameric phenoxazinone synthase
34	d1kyaa3	Alignment	not modelled	13.7	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
35	d1ibya_	Alignment	not modelled	13.1	29	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
36	d1bf2a1	Alignment	not modelled	11.7	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
37	c2fqeA_	Alignment	not modelled	11.2	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**blue copper oxidase cueo; **PDBTitle:** crystal structures of e. coli laccase cueo under different2 copper binding situations
38	d1kv7a3	Alignment	not modelled	10.7	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
39	d1x53a1	Alignment	not modelled	10.1	14	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
40	c2yxwB_	Alignment	not modelled	10.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**blue copper oxidase cueo; **PDBTitle:** the deletion mutant of multicopper oxidase cueo
41	c2jwyA_	Alignment	not modelled	9.2	24	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yaji; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540
42	c2f2bA_	Alignment	not modelled	8.6	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin aqpm; **PDBTitle:** crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
43	c3ottB_	Alignment	not modelled	8.5	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two-component system sensor histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
44	d1y02a2	Alignment	not modelled	8.3	18	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
45	c2q9oA_	Alignment	not modelled	7.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase-1; **PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase
46	c2kpsA_	Alignment	not modelled	7.5	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafniense
47	d1aoza3	Alignment	not modelled	7.5	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
48	d1od3a_	Alignment	not modelled	7.4	13	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
49	d1gyca3	Alignment	not modelled	7.2	30	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
50	d2q9oa3	Alignment	not modelled	7.1	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
51	d1h6ia_	Alignment	not modelled	7.1	67	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
52	c2w2eA_	Alignment	not modelled	7.0	67	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
53	c2kq1A_	Alignment	not modelled	6.7	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh0266 protein; **PDBTitle:** solution structure of protein bh0266 from bacillus2 halodurans. northeast structural genomics consortium target3 bhr97a
54	c3iyzA_	Alignment	not modelled	6.7	67	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** structure of aquaporin-4 s180d mutant at 10.0 a

						resolution from2 electron micrograph
55	c3c02A_	Alignment	not modelled	6.7	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaglyceroporin; **PDBTitle:** x-ray structure of the aquaglyceroporin from plasmodium falciparum
56	c3llqB_	Alignment	not modelled	6.6	67	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
57	c2wnyB_	Alignment	not modelled	6.6	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved protein mth689; **PDBTitle:** structure of mth689, a duf54 protein from methanothermobacter2 thermautotrophicus
58	c2d57A_	Alignment	not modelled	6.5	67	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
59	d1hfua3	Alignment	not modelled	6.5	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
60	c2xu9A_	Alignment	not modelled	6.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of laccase from thermus thermophilus hb27
61	c3gd8A_	Alignment	not modelled	6.2	67	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin-4; **PDBTitle:** crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
62	d1fx8a_	Alignment	not modelled	6.1	67	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
63	c1ldaA_	Alignment	not modelled	6.0	67	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycerol uptake facilitator protein; **PDBTitle:** crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
64	d1ymga1	Alignment	not modelled	6.0	50	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
65	c1ymgA_	Alignment	not modelled	6.0	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
66	c3d9sB_	Alignment	not modelled	6.0	67	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
67	d1j4na_	Alignment	not modelled	5.9	67	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
68	c2b5fD_	Alignment	not modelled	5.8	67	**PDB header:**transport protein,membrane protein **Chain:** D: **PDB Molecule:**aquaporin; **PDBTitle:** crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
69	d2ysca1	Alignment	not modelled	5.6	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
70	c2zshB_	Alignment	not modelled	5.6	33	**PDB header:**hormone receptor **Chain:** B: **PDB Molecule:**della protein gai; **PDBTitle:** structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
71	d2qfra1	Alignment	not modelled	5.5	6	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Purple acid phosphatase, N-terminal domain **Family:**Purple acid phosphatase, N-terminal domain
72	d2pa7a1	Alignment	not modelled	5.5	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
73	c3l1eA_	Alignment	not modelled	5.5	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin a chain; **PDBTitle:** bovine alphaa crystallin zinc bound
74	c3htrB_	Alignment	not modelled	5.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized prc-barrel domain protein; **PDBTitle:** crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
75	c1gycA_	Alignment	not modelled	5.3	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase 2; **PDBTitle:** crystal structure determination at room temperature of a2 laccase from trametes versicolor in its oxidised form3 containing a full complement of copper ions
76	d1rc2a_	Alignment	not modelled	5.3	67	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
77	d2ozka1	Alignment	not modelled	5.2	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Nsp15 N-terminal domain-like
78	c2r1fB_	Alignment	not modelled	5.2	57	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**predicted aminodeoxychorismate lyase; **PDBTitle:** crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli
79	d1akpa_	Alignment	not modelled	5.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Actinoxanthin-like **Family:**Actinoxanthin-like