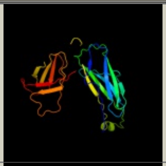
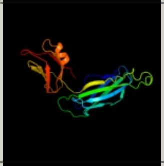
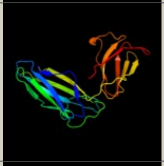
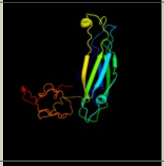
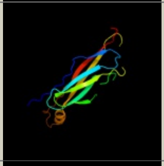
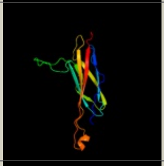
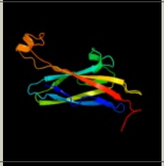
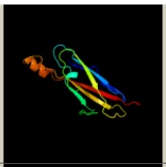
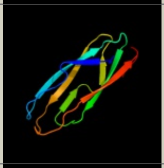
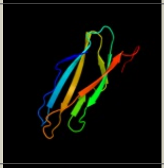
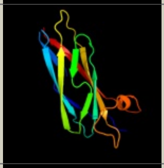
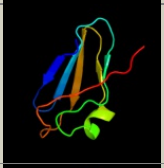
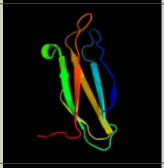
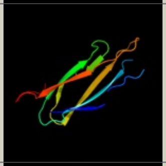
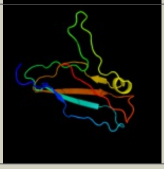
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77188
Date	Thu Jan 5 12:26:12 GMT 2012
Unique Job ID	92de6bd8a5aafb8a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z9sA_	Alignment		100.0	16	**PDB header:**chaperone/immune system **Chain:** A: **PDB Molecule:**chaperone protein caf1m; **PDBTitle:** crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
2	c2co7B_	Alignment		100.0	11	**PDB header:**fibril protein **Chain:** B: **PDB Molecule:**putative fimbriae assembly chaperone; **PDBTitle:** salmonella enterica safa pilin in complex with the safb2 chaperone (type ii)
3	c3q48B_	Alignment		100.0	13	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
4	c1qunA_	Alignment		100.0	14	**PDB header:**chaperone/structural protein **Chain:** A: **PDB Molecule:**papd-like chaperone fimc; **PDBTitle:** x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli
5	c1l4iA_	Alignment		100.0	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
6	c1qpxA_	Alignment		100.0	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
7	c3f6iB_	Alignment		99.9	14	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein faee; **PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee
8	d1p5va1	Alignment		99.9	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d2co7b1	Alignment		99.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d2j2za1	Alignment		99.9	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d3bwuc1	Alignment		99.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		99.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d1m1sa_	Alignment		97.9	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
14	d1rowa_	Alignment		97.7	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
15	c2qsvA_	Alignment		97.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
16	d1grwa_	Alignment		97.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
17	d3bwuc2	Alignment		96.7	14	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	c1z9oB_	Alignment		96.6	13	**PDB header:**protein binding/lipid binding protein **Chain:** B: **PDB Molecule:**vesicle-associated membrane protein-associated protein a; **PDBTitle:** 1.9 angstrom crystal structure of the rat vap-a msp homology domain in2 complex with the rat orp1 ffat motif
19	d1mspa_	Alignment		95.9	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	c2e6jA_	Alignment		95.5	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydin protein; **PDBTitle:** solution structure of the c-terminal papd-like domain from2 human hydin protein
21	c2ys4A_	Alignment	not modelled	95.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydrocephalus-inducing protein homolog; **PDBTitle:** solution structure of the n-terminal papd-like domain of2 hydin protein from human
22	d1wica_	Alignment	not modelled	94.3	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
23	d1w8oa1	Alignment	not modelled	94.2	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
24	d2j2za2	Alignment	not modelled	94.0	12	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
25	c3o0lB_	Alignment	not modelled	94.0	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
26	d1p5va2	Alignment	not modelled	94.0	10	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
27	d2co7b2	Alignment	not modelled	93.4	8	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
28	c3qbtH_	Alignment	not modelled	91.7	17	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp

29	d1l4ia2	Alignment	not modelled	88.4	14	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
30	c3qisA_	Alignment	not modelled	88.3	17	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** recognition of the f&h motif by the lowe syndrome protein ocrl
31	c2jwyA_	Alignment	not modelled	84.7	17	**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
32	c3ac0B_	Alignment	not modelled	80.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
33	d2vzsa2	Alignment	not modelled	75.7	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
34	c2x41A_	Alignment	not modelled	71.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
35	c1l9mB_	Alignment	not modelled	65.9	13	**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
36	c3isyA_	Alignment	not modelled	59.2	10	**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
37	c2r39A_	Alignment	not modelled	51.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
38	c3cfuA_	Alignment	not modelled	47.2	16	**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
39	d1exha_	Alignment	not modelled	47.1	14	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family II
40	d1yq2a1	Alignment	not modelled	45.7	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
41	d1ufga_	Alignment	not modelled	45.7	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
42	c2lllA_	Alignment	not modelled	44.8	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
43	d4ubpb_	Alignment	not modelled	44.1	11	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
44	d1e9ya1	Alignment	not modelled	43.6	15	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
45	c3qgaD_	Alignment	not modelled	38.0	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
46	c3jt0B_	Alignment	not modelled	37.8	13	**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
47	c2kl6A_	Alignment	not modelled	37.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
48	d1ejxb_	Alignment	not modelled	32.1	17	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
49	d1ifra_	Alignment	not modelled	31.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
50	c1yewI_	Alignment	not modelled	26.9	17	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
51	d1hmja_	Alignment	not modelled	26.7	26	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
52	c3rgbA_	Alignment	not modelled	26.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
						Fold: Ribosomal protein S19

53	d2uubs1	Alignment	not modelled	23.7	29	**Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
54	d2gy9s1	Alignment	not modelled	23.3	29	**Fold:**Ribosomal protein S19 **Superfamily:**Ribosomal protein S19 **Family:**Ribosomal protein S19
55	d1ivta_	Alignment	not modelled	20.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
56	d1vjja2	Alignment	not modelled	19.4	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
57	c3bbnS_	Alignment	not modelled	18.4	23	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**ribosomal protein s19; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
58	d1kyaa2	Alignment	not modelled	18.3	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
59	c1s1hS_	Alignment	not modelled	17.8	29	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**40s ribosomal protein s15; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
60	d2cj3a1	Alignment	not modelled	16.0	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
61	c3rfrI_	Alignment	not modelled	15.6	15	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
62	c2zkqs_	Alignment	not modelled	15.4	29	**PDB header:**ribosomal protein/rna **Chain:** S: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
63	c3ndyG_	Alignment	not modelled	15.4	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
64	c2xzmS_	Alignment	not modelled	14.5	29	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rps15e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
65	c1e9zA_	Alignment	not modelled	14.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
66	c2je8B_	Alignment	not modelled	12.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
67	d1plaa_	Alignment	not modelled	12.7	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
68	d1eika_	Alignment	not modelled	12.6	24	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
69	d1bxua_	Alignment	not modelled	12.1	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
70	d2q5ba1	Alignment	not modelled	12.0	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
71	d1pcsa_	Alignment	not modelled	11.4	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
72	c3mdjB_	Alignment	not modelled	11.3	10	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
73	d1gyca2	Alignment	not modelled	11.1	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
74	d1bqka_	Alignment	not modelled	10.9	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
75	d9pcya_	Alignment	not modelled	10.8	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
76	c2f1eA_	Alignment	not modelled	10.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein apag; **PDBTitle:** solution structure of apag protein
77	d1dzfa2	Alignment	not modelled	9.7	25	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
78	d1ag6a_	Alignment	not modelled	9.5	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like

79	d1g0da2	Alignment	not modelled	9.4	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
80	d1hfua2	Alignment	not modelled	9.3	5	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
81	d1plca_	Alignment	not modelled	9.1	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
82	c2kutA_	Alignment	not modelled	9.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
83	d1aoza2	Alignment	not modelled	8.8	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
84	d1hc1a3	Alignment	not modelled	8.7	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arthropod hemocyanin, C-terminal domain
85	d1v7wa2	Alignment	not modelled	8.6	16	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
86	d7pcya_	Alignment	not modelled	8.3	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
87	c2pmzV_	Alignment	not modelled	8.1	25	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
88	c1pzdA_	Alignment	not modelled	7.6	15	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**coatomer gamma subunit; **PDBTitle:** structural identification of a conserved appendage domain2 in the carboxyl-terminus of the copi gamma-subunit.
89	d3pmga4	Alignment	not modelled	7.6	11	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
90	d2jxma1	Alignment	not modelled	7.4	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
91	c3qnfA_	Alignment	not modelled	7.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
92	d1ex0a2	Alignment	not modelled	7.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
93	d1v10a2	Alignment	not modelled	6.9	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
94	d1pmya_	Alignment	not modelled	6.6	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
95	d1adwa_	Alignment	not modelled	6.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
96	d1bypa_	Alignment	not modelled	6.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
97	d2plta_	Alignment	not modelled	6.5	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
98	d1nc7a_	Alignment	not modelled	5.9	21	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
99	c3izbR_	Alignment	not modelled	5.6	31	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**40s ribosomal protein rps15 (s19p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome