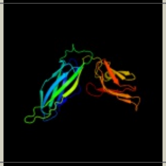
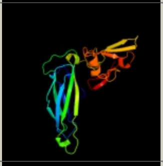
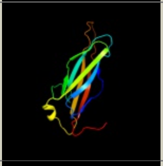
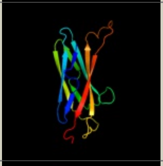
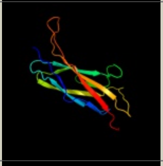
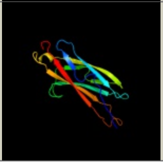
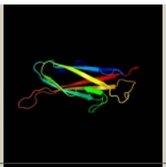
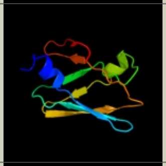
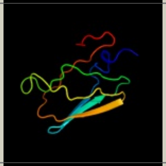
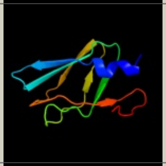
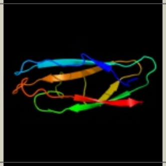
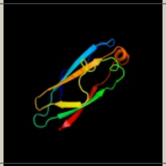
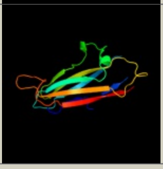
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77599
Date	Thu Jan 5 12:30:55 GMT 2012
Unique Job ID	6ad886b7c1716f56

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qpxA_	Alignment		100.0	42	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
2	c1qunA_	Alignment		100.0	32	**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
3	c2co7B_	Alignment		100.0	22	**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)
4	c1z9sA_	Alignment		100.0	26	**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
5	c1l4iA_	Alignment		100.0	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
6	c3f6iB_	Alignment		100.0	26	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein faee; **PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee
7	c3q48B_	Alignment		100.0	29	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone
8	d2j2za1	Alignment		100.0	54	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
9	d3bwuc1	Alignment		100.0	37	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
10	d1p5va1	Alignment		100.0	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	d2co7b1	Alignment		100.0	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone

12	d1l4ia1	Alignment		100.0	37	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
13	d2j2za2	Alignment		99.9	28	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
14	d1p5va2	Alignment		99.7	17	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	d3bwuc2	Alignment		99.7	24	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
16	d2co7b2	Alignment		99.7	18	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
17	d1l4ia2	Alignment		99.6	26	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
18	d1m1sa_	Alignment		96.0	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
19	d1rowa_	Alignment		95.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
20	d1grwa_	Alignment		94.8	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
21	c2qsvA_	Alignment	not modelled	94.2	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
22	c1z9oB_	Alignment	not modelled	94.1	17	**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
23	d1mspa_	Alignment	not modelled	93.9	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
24	c3qisA_	Alignment	not modelled	92.8	15	**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
25	c2e6jA_	Alignment	not modelled	91.9	14	**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
26	d1e42a1	Alignment	not modelled	83.3	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
27	c2ys4A_	Alignment	not modelled	80.5	15	**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
						PDB header:protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase

28	c3qbtH_	Alignment	not modelled	80.5	12	ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp
29	c3ac0B_	Alignment	not modelled	74.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
30	d2vzsa2	Alignment	not modelled	69.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
31	d1hfua2	Alignment	not modelled	67.7	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
32	d1wica_	Alignment	not modelled	67.1	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
33	c1e42A_	Alignment	not modelled	65.2	15	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**ap-2 complex subunit beta; **PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2
34	c2qvkA_	Alignment	not modelled	62.4	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** the second ca2+-binding domain of the na+-ca2+ exchanger is2 essential for regulation: crystal structures and3 mutational analysis
35	c1yycA_	Alignment	not modelled	54.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
36	c3eujB_	Alignment	not modelled	51.8	25	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer
37	d2fwua1	Alignment	not modelled	48.4	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
38	d1w8oa1	Alignment	not modelled	42.8	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
39	d1aoza2	Alignment	not modelled	42.4	3	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
40	c3h6aB_	Alignment	not modelled	42.3	6	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-4; **PDBTitle:** structure of the calx-beta domain of integrin beta42 crystallized in the presence of calcium
41	c2x41A_	Alignment	not modelled	41.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
42	d1k3ra1	Alignment	not modelled	40.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
43	d1v10a2	Alignment	not modelled	40.6	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
44	c2oxgE_	Alignment	not modelled	39.3	11	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**soxz protein; **PDBTitle:** the soxyz complex of paracoccus pantotrophus
45	c3ts3D_	Alignment	not modelled	32.4	27	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
46	c3ginB_	Alignment	not modelled	31.2	6	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1; **PDBTitle:** crystal structure of e454k-cbd1
47	d1gyca2	Alignment	not modelled	29.5	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
48	d4ubpb_	Alignment	not modelled	28.2	13	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
49	c3rb7E_	Alignment	not modelled	27.0	6	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of cbd12 from calx1.2
50	d1kyaa2	Alignment	not modelled	26.9	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
51	d2dpka1	Alignment	not modelled	26.6	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CalX-like **Family:**CalX-beta domain
52	c3o0lB_	Alignment	not modelled	25.0	15	**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
53	c1wkwB_	Alignment	not modelled	24.0	44	**PDB header:**translation/protein binding **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 4e **PDBTitle:** crystal structure of the ternary complex of eif4e-m7gpppa-2 4ebp1 peptide
54	d1e9ya1	Alignment	not modelled	22.1	17	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit

						Family: Urease, beta-subunit
55	d1v8ha1	Alignment	not modelled	21.0	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SoxZ-like
56	c2qziA_	Alignment	not modelled	19.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311.
57	c3butA_	Alignment	not modelled	18.8	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
58	d2q9oa2	Alignment	not modelled	17.2	10	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
59	c1e9zA_	Alignment	not modelled	16.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
60	d1ejxb_	Alignment	not modelled	16.6	12	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
61	d1ufga_	Alignment	not modelled	16.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
62	c3jt0B_	Alignment	not modelled	16.0	12	**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
63	c2lllA_	Alignment	not modelled	13.6	15	**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
64	d1ifra_	Alignment	not modelled	12.3	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
65	c3qgaD_	Alignment	not modelled	12.3	18	**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
66	c3e9uA_	Alignment	not modelled	11.9	4	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
67	c3rfrI_	Alignment	not modelled	11.5	15	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
68	c3e9tD_	Alignment	not modelled	10.8	8	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of apo-form calx cbd1 domain
69	d1r7aa1	Alignment	not modelled	10.8	27	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
70	c2z4dA_	Alignment	not modelled	10.7	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn13; **PDBTitle:** nmr structures of yeast proteasome component rpn13
71	c2frgP_	Alignment	not modelled	10.6	14	**PDB header:**immune system **Chain:** P: **PDB Molecule:**trem-like transcript-1; **PDBTitle:** structure of the immunoglobulin-like domain of human tlt-1
72	d2huha1	Alignment	not modelled	9.4	27	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
73	d1xo8a_	Alignment	not modelled	9.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
74	c2phgB_	Alignment	not modelled	8.9	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to tfiib
75	d1u00a2	Alignment	not modelled	8.9	17	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
76	c2pheC_	Alignment	not modelled	8.5	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**alpha trans-inducing protein; **PDBTitle:** model for vp16 binding to pc4
77	d1eg3a3	Alignment	not modelled	7.6	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
78	d2f7fa1	Alignment	not modelled	7.5	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
79	c3k6sB_	Alignment	not modelled	7.4	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
80	c3hzpA_	Alignment	not modelled	7.2	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of ntf2-like protein of unknown function

						mn2a_05052 from prochlorococcus marinus (yp_291699.1) from prochlorococcus sp.3 natl2a at 1.40 a resolution
81	d2o2aa1	Alignment	not modelled	7.1	12	**Fold:**SecB-like **Superfamily:**SecB-like **Family:**SP1558-like
82	d1ivta_	Alignment	not modelled	6.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
83	c3dqgC_	Alignment	not modelled	6.4	13	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70 kda protein f; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
84	d1nyna_	Alignment	not modelled	6.1	23	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein Yhr087W
85	c3fyfA_	Alignment	not modelled	6.1	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein bvu-3222; **PDBTitle:** crystal structure of uncharacterized protein bvu_3222 from2 bacteroides vulgatus
86	c3of6D_	Alignment	not modelled	5.8	24	**PDB header:**immune system **Chain:** D: **PDB Molecule:**pre t-cell antigen receptor alpha; **PDBTitle:** human pre-t cell receptor crystal structure
87	c2l3bA_	Alignment	not modelled	5.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
88	c3smuD_	Alignment	not modelled	5.5	50	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
89	c3u7xC_	Alignment	not modelled	5.5	50	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
90	c3smuC_	Alignment	not modelled	5.5	50	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
91	c3u7xD_	Alignment	not modelled	5.5	50	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
92	c2vzvB_	Alignment	not modelled	5.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
93	d1dkza2	Alignment	not modelled	5.4	19	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
94	d1x9la_	Alignment	not modelled	5.4	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
95	c1u00A_	Alignment	not modelled	5.3	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
96	c3czuB_	Alignment	not modelled	5.3	50	**PDB header:**transferase/signaling protein **Chain:** B: **PDB Molecule:**ephrin-a1; **PDBTitle:** crystal structure of the human ephrin a2- ephrin a1 complex
97	d1pkoa_	Alignment	not modelled	5.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
98	d2olra1	Alignment	not modelled	5.2	35	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
99	d2vj0a1	Alignment	not modelled	5.1	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like