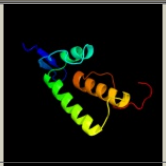
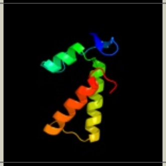
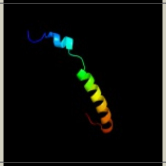
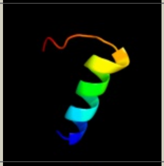
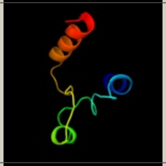
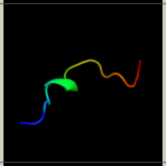
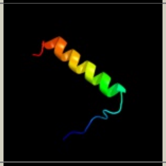
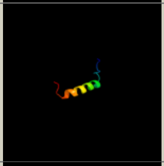
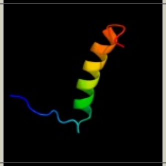
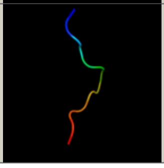
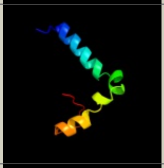
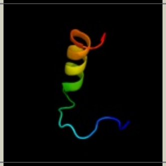
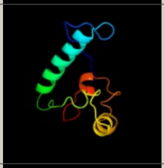
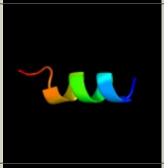
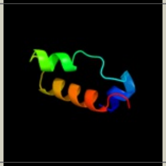
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8P3
Date	Thu Jan 5 11:08:25 GMT 2012
Unique Job ID	2667967ce8cfbae1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xs8a_	Alignment		100.0	95	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
2	d1t07a_	Alignment		100.0	47	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
3	d2fxaa1	Alignment		37.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
4	c2qm3A_	Alignment		32.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of a predicted methyltransferase from pyrococcus2 furiosus
5	d1fcdc2	Alignment		29.2	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
6	c2rfpA_	Alignment		29.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
7	c3mi6A_	Alignment		24.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
8	c2xn1B_	Alignment		24.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
9	c2voyK_	Alignment		23.4	40	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
10	c2yfnA_	Alignment		23.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
11	c2yf3F_	Alignment		21.0	46	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese

12	d1cyja_	Alignment		20.6	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
13	d1s29a_	Alignment		17.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
14	d2ijra1	Alignment		15.3	13	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
15	d1kb0a1	Alignment		14.8	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
16	d1u6ra2	Alignment		14.3	16	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
17	d1g0wa2	Alignment		13.4	16	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
18	d1ctja_	Alignment		13.4	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
19	d1hbka_	Alignment		13.1	11	**Fold:**Acyl-CoA binding protein-like **Superfamily:**Acyl-CoA binding protein **Family:**Acyl-CoA binding protein
20	d1vjga_	Alignment		12.8	30	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Hypothetical protein alr1529
21	d1xgsa1	Alignment	not modelled	12.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Methionine aminopeptidase, insert domain
22	d1c6ra_	Alignment	not modelled	11.5	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	c3fy6A_	Alignment	not modelled	11.1	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass3
24	c2kw3C_	Alignment	not modelled	10.8	24	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**regulatory factor x-associated protein; **PDBTitle:** heterotrimeric interaction between rfx5 and rfxap
25	c2kktA_	Alignment	not modelled	10.4	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ataxin-7-like protein 3; **PDBTitle:** solution structure of the sca7 domain of human ataxin-7-l3 protein
26	d1ngka_	Alignment	not modelled	9.9	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
27	d1gdva_	Alignment	not modelled	9.9	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
28	d1o22a_	Alignment	not modelled	9.8	31	**Fold:**Hypothetical protein TM0875 **Superfamily:**Hypothetical protein TM0875 **Family:**Hypothetical protein TM0875
29	d1zh5a1	Alignment	not modelled	9.6	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: La domain
30	d1qc7a_	Alignment	not modelled	9.4	18	**Fold:**alpha-alpha superhelix **Superfamily:**FliG **Family:**FliG
31	c2owlA_	Alignment	not modelled	9.1	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** crystal structure of e. coli rdgc
32	d1jmxa5	Alignment	not modelled	9.1	50	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
33	c3o2iB_	Alignment	not modelled	9.0	47	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
34	d1alca_	Alignment	not modelled	8.9	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
35	d1f6sa_	Alignment	not modelled	8.9	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
36	d1ykha1	Alignment	not modelled	8.8	25	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**MED7 hinge region
37	d1hb6a_	Alignment	not modelled	8.8	19	**Fold:**Acyl-CoA binding protein-like **Superfamily:**Acyl-CoA binding protein **Family:**Acyl-CoA binding protein
38	d1ls9a_	Alignment	not modelled	8.8	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
39	c2z2fA_	Alignment	not modelled	8.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
40	c3dr0B_	Alignment	not modelled	8.6	7	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
41	c3zs9C_	Alignment	not modelled	8.5	26	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 2; **PDBTitle:** s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
42	d1f08a_	Alignment	not modelled	8.3	44	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Replication initiation protein E1
43	d1co6a_	Alignment	not modelled	8.1	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
44	d1qc7b_	Alignment	not modelled	8.1	18	**Fold:**alpha-alpha superhelix **Superfamily:**FliG **Family:**FliG
45	d1r9wa_	Alignment	not modelled	8.0	22	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Replication initiation protein E1
46	d1nira1	Alignment	not modelled	7.8	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
47	c1x31D_	Alignment	not modelled	7.8	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
48	d1vrpa2	Alignment	not modelled	7.8	15	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
49	d1c52a_	Alignment	not modelled	7.7	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	d1cc5a_	Alignment	not modelled	7.7	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
51	d1gd6a_	Alignment	not modelled	7.7	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
52	c3flvA_	Alignment	not modelled	7.6	28	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa-binding domain-containing protein 5; **PDBTitle:** the crystal structure of human acyl-coenzymea binding domain2 containing 5
53	d1iiza_	Alignment	not modelled	7.5	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
54	d1x68a2	Alignment	not modelled	7.4	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
55	c3b08H_	Alignment	not modelled	7.3	15	**PDB header:**signaling protein/metal binding protein **Chain:** H: **PDB Molecule:**ranbp-type and c3hc4-type zinc finger-containing protein 1; **PDBTitle:** crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
						Fold: Lysozyme-like

56	d1juga_	Alignment	not modelled	7.3	33	**Superfamily:**Lysozyme-like **Family:**C-type lysozyme
57	c3cu4A_	Alignment	not modelled	7.3	8	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
58	d1jmxa1	Alignment	not modelled	7.3	10	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
59	d1h4ra3	Alignment	not modelled	7.2	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
60	c2wh5A_	Alignment	not modelled	7.1	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa-binding domain-containing protein 4; **PDBTitle:** crystal structure of human acyl-coa binding domain 42 complexed with stearoyl-coa
61	d2dloa2	Alignment	not modelled	7.0	31	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
62	d1f1fa_	Alignment	not modelled	7.0	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
63	d1f1ca_	Alignment	not modelled	6.9	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
64	d1kv9a1	Alignment	not modelled	6.8	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
65	c2cfhA_	Alignment	not modelled	6.7	16	**PDB header:**transport **Chain:** A: **PDB Molecule:**trafficking protein particle complex subunit 3; **PDBTitle:** structure of the bet3-tpc6b core of trapp
66	c2zonG_	Alignment	not modelled	6.6	17	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
67	d1b9oa_	Alignment	not modelled	6.6	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
68	c3fo8D_	Alignment	not modelled	6.5	37	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**tail sheath protein gp18; **PDBTitle:** crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
69	c2v07A_	Alignment	not modelled	6.5	14	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
70	d1ef1a3	Alignment	not modelled	6.4	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
71	c2crcA_	Alignment	not modelled	6.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin conjugating enzyme 7 interacting **PDBTitle:** solution structure of the zf-ranbp domain of the protein2 hbv associated factor
72	c3epyA_	Alignment	not modelled	6.3	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa-binding domain-containing protein 7; **PDBTitle:** crystal structure of human acyl-coa binding domain 72 complexed with palmitoyl-coa
73	d2nwdx1	Alignment	not modelled	6.2	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
74	d1gg3a3	Alignment	not modelled	6.1	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
75	d2q9oa3	Alignment	not modelled	5.9	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
76	c2wweA_	Alignment	not modelled	5.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoinositide-3-kinase, class 2, gamma **PDBTitle:** crystal structure of the phox homology domain of human2 phosphoinositide-3-kinase-c2-gamma
77	d1e29a_	Alignment	not modelled	5.9	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
78	d1wvec1	Alignment	not modelled	5.8	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
79	d2c8sa1	Alignment	not modelled	5.6	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
80	d1hfxa_	Alignment	not modelled	5.6	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
81	c2goiC_	Alignment	not modelled	5.5	28	**PDB header:**cell adhesion, sugar binding protein **Chain:** C: **PDB Molecule:**sperm lysozyme-like protein 1; **PDBTitle:** crystal structure of mouse sperm c-type lysozyme-like2 protein 1
						PDB header:transcription

82	c2kjeB_	Alignment	not modelled	5.5	38	**Chain:** B: **PDB Molecule:**early e1a 32 kda protein; **PDBTitle:** nmr structure of cbp taz2 and adenoviral e1a complex
83	d1yroa1	Alignment	not modelled	5.5	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
84	d2zpya3	Alignment	not modelled	5.4	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
85	d1ghla_	Alignment	not modelled	5.2	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
86	c3cp5A_	Alignment	not modelled	5.2	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** cytochrome c from rhodothermus marinus