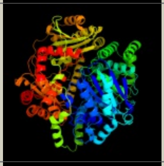
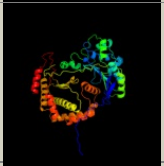
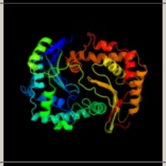
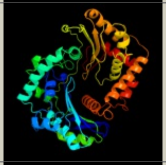
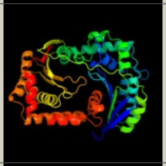
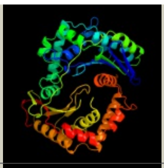
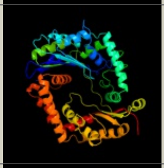
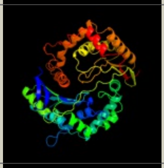
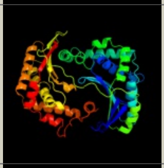
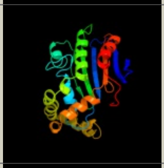
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P31828
Date	Thu Jan 5 11:48:53 GMT 2012
Unique Job ID	f5118e3e834c0a41

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jbuB_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**insulin-degrading enzyme; **PDBTitle:** crystal structure of human insulin degrading enzyme2 complexed with co-purified peptides.
2	c2wk3A_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulin degrading enzyme; **PDBTitle:** crystal structure of human insulin-degrading enzyme in2 complex with amyloid-beta (1-42)
3	c1q2lA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease iii; **PDBTitle:** crystal structure of pitrilysin
4	c2fgeA_	Alignment		100.0	10	**PDB header:**hydrolase, plant protein **Chain:** A: **PDB Molecule:**zinc metalloprotease (insulinase family); **PDBTitle:** crystal structure of presequence protease prep from2 arabidopsis thaliana
5	c3go9A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulinase family protease; **PDBTitle:** predicted insulinase family protease from yersinia pestis
6	c1sqpA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome-c reductase complex core protein i, **PDBTitle:** crystal structure analysis of bovine bc1 with myxothiazol
7	c1hr9D_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mitochondrial processing peptidase beta subunit; **PDBTitle:** yeast mitochondrial processing peptidase beta-e73q mutant2 complexed with malate dehydrogenase signal peptide
8	c1nu1A_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein i, **PDBTitle:** crystal structure of mitochondrial cytochrome bc1 complexed with 2-2 nonyl-4-hydroxyquinoline n-oxide (nqno)
9	c1hr6C_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mitochondrial processing peptidase alpha subunit; **PDBTitle:** yeast mitochondrial processing peptidase
10	c3amiB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase; **PDBTitle:** the crystal structure of the m16b metallopeptidase subunit from2 sphingomonas sp. a1
11	c3eoqB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of putative zinc protease beta-2 subunit from thermus thermophilus hb8

12	c3hdiA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**processing protease; **PDBTitle:** crystal structure of bacillus halodurans metallo peptidase
13	c1l0lB_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein 2; **PDBTitle:** structure of bovine mitochondrial cytochrome bc1 complex with a bound2 fungicide famoxadone
14	c3gwbA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m16 inactive domain family protein; **PDBTitle:** crystal structure of peptidase m16 inactive domain from pseudomonas2 fluorescens. northeast structural genomics target plr293l
15	c3amjB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase inactive subunit; **PDBTitle:** the crystal structure of the heterodimer of m16b peptidase from2 sphingomonas sp. a1
16	c3cx5L_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**cytochrome b-c1 complex subunit 1, mitochondrial; **PDBTitle:** structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
17	c3d3yA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein from enterococcus faecalis2 v583
18	d2fgea4	Alignment		100.0	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
19	d1ppja1	Alignment		100.0	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
20	c3cxhM_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**cytochrome b-c1 complex subunit 2, mitochondrial; **PDBTitle:** structure of yeast complex iii with isoform-2 cytochrome c2 bound and definition of a minimal core interface for3 electron transfer.
21	d1hr6b1	Alignment	not modelled	100.0	21	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
22	d1bcca1	Alignment	not modelled	100.0	22	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
23	d1hr6a1	Alignment	not modelled	100.0	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
24	d1q2la4	Alignment	not modelled	100.0	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
25	d1ppjb1	Alignment	not modelled	100.0	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
26	d1bccb1	Alignment	not modelled	100.0	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
27	d3cx5b1	Alignment	not modelled	100.0	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
28	d3cx5a1	Alignment	not modelled	100.0	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
29	d1q2la1	Alignment	not modelled	99.9	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase

						Family:MPP-like
30	d1hr6b2	Alignment	not modelled	99.9	10	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
31	d1ppjb2	Alignment	not modelled	99.9	7	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
32	d1q2la2	Alignment	not modelled	99.9	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
33	c3ivlA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of the inactive peptidase domain of a putative2 zinc protease from bordetella parapertussis to 2.2a
34	d1bcca2	Alignment	not modelled	99.9	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
35	d1hr6a2	Alignment	not modelled	99.9	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	d1ppja2	Alignment	not modelled	99.8	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
37	d2fgea2	Alignment	not modelled	99.8	6	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
38	d1bccb2	Alignment	not modelled	99.8	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
39	d3cx5a2	Alignment	not modelled	99.8	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
40	d2fgea1	Alignment	not modelled	99.5	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
41	d2fgea3	Alignment	not modelled	99.4	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
42	d1q2la3	Alignment	not modelled	99.2	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
43	d1nsha_	Alignment	not modelled	39.5	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
44	c2rgiA_	Alignment	not modelled	35.8	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein s100-a2; **PDBTitle:** crystal structure of ca2+-free s100a2 at 1.6 a resolution
45	d1a4pa_	Alignment	not modelled	35.2	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
46	d1qlsa_	Alignment	not modelled	33.8	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
47	d1g5ta_	Alignment	not modelled	23.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
48	c1ko7B_	Alignment	not modelled	22.8	15	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
49	c1g6uB_	Alignment	not modelled	22.2	37	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
50	d1ko7a1	Alignment	not modelled	20.8	15	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
51	c2kfvA_	Alignment	not modelled	20.5	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 3; **PDBTitle:** structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
52	d1e8aa_	Alignment	not modelled	20.3	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
53	d2rdea1	Alignment	not modelled	19.5	25	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
54	c2y5iF_	Alignment	not modelled	19.2	16	**PDB header:**metal-binding protein **Chain:** F: **PDB Molecule:**s100 calcium binding protein z; **PDBTitle:** s100z from zebrafish in complex with calcium
55	c1qpoA_	Alignment	not modelled	17.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
						PDB header:transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein

56	c3l7vA_	Alignment	not modelled	17.4	13	smu.1377c; **PDBTitle:** crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
57	d1ksoa_	Alignment	not modelled	15.7	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
58	c2uxsA_	Alignment	not modelled	15.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
59	d1knxa1	Alignment	not modelled	14.2	14	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
60	d1g64b_	Alignment	not modelled	13.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
61	c3llkA_	Alignment	not modelled	12.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
62	d3c1va1	Alignment	not modelled	12.3	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
63	d3cr5x1	Alignment	not modelled	11.8	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
64	d1zfsa1	Alignment	not modelled	11.3	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
65	c3fhkF_	Alignment	not modelled	11.2	17	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
66	d1qlka_	Alignment	not modelled	10.6	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
67	c2pbrB_	Alignment	not modelled	10.6	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
68	d2prda_	Alignment	not modelled	10.6	17	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
69	d3c7ba2	Alignment	not modelled	10.5	12	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
70	c3ostA_	Alignment	not modelled	10.1	8	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4; **PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p
71	c3lv8A_	Alignment	not modelled	9.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
72	d2ikba1	Alignment	not modelled	9.4	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
73	d1zavz1	Alignment	not modelled	9.2	21	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
74	c1zawZ_	Alignment	not modelled	9.2	21	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
75	c1zavZ_	Alignment	not modelled	9.2	21	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p21
76	d1l7ba_	Alignment	not modelled	9.0	22	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA ligase
77	c1zawY_	Alignment	not modelled	8.9	21	**PDB header:**structural protein **Chain:** Y: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
78	c1zawX_	Alignment	not modelled	8.9	21	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
79	d1pc2a_	Alignment	not modelled	8.9	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
80	c3pajA_	Alignment	not modelled	8.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
81	d1qpoa1	Alignment	not modelled	8.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like

						Family: NadC C-terminal domain-like
82	d1udea_	Alignment	not modelled	8.6	15	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
83	d1v33a_	Alignment	not modelled	8.6	17	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like
84	c1knxF_	Alignment	not modelled	8.6	12	**PDB header:**transferase/hydrolase **Chain:** F: **PDB Molecule:**probable hpr(ser) kinase/phosphatase; **PDBTitle:** hpr kinase/phosphatase from mycoplasma pneumoniae
85	d1tuza_	Alignment	not modelled	8.2	6	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
86	c2yw3E_	Alignment	not modelled	8.2	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
87	c3qf2B_	Alignment	not modelled	8.0	11	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**nacht, lrr and pyd domains-containing protein 3; **PDBTitle:** crystal structure of nalp3 pyd
88	d1u1qa_	Alignment	not modelled	8.0	7	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
89	c3dzzB_	Alignment	not modelled	8.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative pyridoxal 5'-phosphate-dependent c-s lyase; **PDBTitle:** crystal structure of a putative plp-dependent aminotransferase2 (lbul_1103) from lactobacillus delbrueckii subsp. at 1.61 a3 resolution
90	c3gnnA_	Alignment	not modelled	7.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
91	d1kyqa2	Alignment	not modelled	7.9	11	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
92	c2ebuA_	Alignment	not modelled	7.8	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor c subunit 1; **PDBTitle:** solution structure of the brct domain from human2 replication factor c large subunit 1
93	c1zawU_	Alignment	not modelled	7.7	21	**PDB header:**structural protein **Chain:** U: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
94	c1zawW_	Alignment	not modelled	7.7	21	**PDB header:**structural protein **Chain:** W: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
95	c1zawV_	Alignment	not modelled	7.7	21	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
96	c2b7pA_	Alignment	not modelled	7.7	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
97	c2ld7A_	Alignment	not modelled	7.6	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
98	c1zaxZ_	Alignment	not modelled	7.6	21	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
99	c1zaxV_	Alignment	not modelled	7.5	21	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b