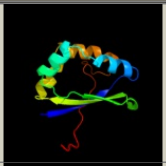
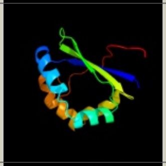
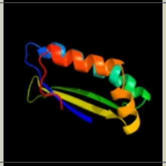
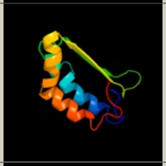
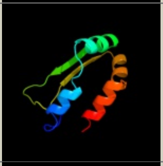
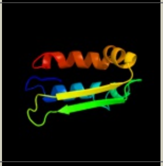
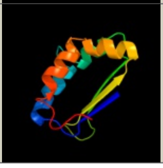
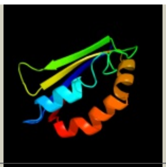
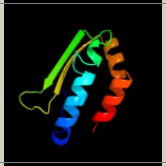
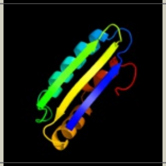
Email	l.a.kelley@imperial.ac.uk
Description	P32156
Date	Thu Jan 5 11:49:38 GMT 2012
Unique Job ID	62b68b5c4698fcf8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1x8da1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
2	c2qlwA_	Alignment		100.0	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
3	c2qlxA_	Alignment		100.0	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
4	c3bm7A_	Alignment		97.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein of unknown function with ferredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
5	c2fb0A_	Alignment		97.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
6	c3e8oB_	Alignment		96.9	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein with erredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
7	d2omoa1	Alignment		96.8	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
8	c3f44A_	Alignment		96.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative monooxygenase; **PDBTitle:** crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
9	c2omoC_	Alignment		96.6	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**duf176; **PDBTitle:** putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
10	d1y0ha_	Alignment		96.6	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
11	c2gffB_	Alignment		96.5	10	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**lsrg protein; **PDBTitle:** crystal structure of yersinia pestis lsrg

12	c2bbeA_	Alignment		96.5	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein so0527; **PDBTitle:** crystal structure of protein so0527 from shewanella oneidensis
13	d2pd1a1	Alignment		96.3	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
14	d1x7va_	Alignment		96.2	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
15	c3gz7B_	Alignment		96.0	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_888398.1) from bordetella bronchiseptica3 at 2.15 a resolution
16	c3mcsB_	Alignment		96.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative monooxygenase; **PDBTitle:** crystal structure of putative monooxygenase (fn1347) from2 fusobacterium nucleatum subsp. nucleatum atcc 25586 at 2.55 a3 resolution
17	c3fgvB_	Alignment		95.5	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein with ferredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution
18	c3kkfA_	Alignment		95.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_810307.1) from bacteriodes3 thetaiotaomicron vpi-5482 at 1.30 a resolution
19	d1tuva_	Alignment		93.8	20	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
20	d1iuja_	Alignment		90.0	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
21	d1vqsa_	Alignment	not modelled	89.1	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**NIPSNAP
22	d1vqya1	Alignment	not modelled	87.3	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**NIPSNAP
23	c3kngA_	Alignment	not modelled	84.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**snoab; **PDBTitle:** crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
24	d1q8ba_	Alignment	not modelled	70.9	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
25	c3hx9B_	Alignment	not modelled	64.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein rv3592; **PDBTitle:** structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
26	d2atza1	Alignment	not modelled	55.8	19	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**HP0184-like
27	d1tuwa_	Alignment	not modelled	29.0	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Polyketide synthesis cyclase
28	c3louB_	Alignment	not modelled	21.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a

						resolution
29	c3fj2A_	Alignment	not modelled	21.5	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**monooxygenase-like protein; **PDBTitle:** crystal structure of a monooxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution
30	d2cz4a1	Alignment	not modelled	20.5	33	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
31	d2zdpa1	Alignment	not modelled	18.9	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
32	c2x7vA_	Alignment	not modelled	18.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
33	c3thdD_	Alignment	not modelled	18.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
34	d2ns1b1	Alignment	not modelled	16.1	17	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
35	c2jdjB_	Alignment	not modelled	12.2	5	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**redy-like protein; **PDBTitle:** crystal structure of hapk from hahella chejuensis
36	c2rodB_	Alignment	not modelled	11.7	33	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**noxa; **PDBTitle:** solution structure of mcl-1 complexed with noxaa
37	c3obiC_	Alignment	not modelled	10.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
38	c2qqdG_	Alignment	not modelled	10.8	31	**PDB header:**lyase **Chain:** G: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase (ec **PDBTitle:** n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
39	d1vfja_	Alignment	not modelled	10.3	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
40	c3mhyC_	Alignment	not modelled	10.2	22	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
41	c3o8wA_	Alignment	not modelled	10.1	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-1); **PDBTitle:** archaeoglobus fulgidus glnk1
42	d2hh8a1	Alignment	not modelled	10.1	21	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
43	c3hfkB_	Alignment	not modelled	9.8	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-methylmuconolactone methylisomerase; **PDBTitle:** crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone
44	c3d3aA_	Alignment	not modelled	9.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
45	c2hfqA_	Alignment	not modelled	9.4	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
46	d2hfqa1	Alignment	not modelled	9.4	33	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
47	c2rd5D_	Alignment	not modelled	9.2	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
48	c2pfuA_	Alignment	not modelled	9.1	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
49	d1tafa_	Alignment	not modelled	9.0	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
50	c3bzqA_	Alignment	not modelled	8.9	11	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
51	c3ncpD_	Alignment	not modelled	8.4	26	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
52	d1qy7a_	Alignment	not modelled	8.1	17	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
53	c2lf3A_	Alignment	not modelled	7.6	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab3; **PDBTitle:** solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
						PDB header:hydrolase

54	c3ogrA_	Alignment	not modelled	7.5	15	**Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
55	c1xc6A_	Alignment	not modelled	7.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
56	c2k42A_	Alignment	not modelled	7.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
57	d2piia_	Alignment	not modelled	7.0	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
58	c1ceeB_	Alignment	not modelled	7.0	18	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
59	c2dclB_	Alignment	not modelled	6.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
60	c3s8sA_	Alignment	not modelled	6.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd1a; **PDBTitle:** crystal structure of the rrm domain of human setd1a
61	c2j9dG_	Alignment	not modelled	6.0	11	**PDB header:**membrane transport **Chain:** G: **PDB Molecule:**hypothetical nitrogen regulatory pii-like **PDBTitle:** structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
62	d1gx5a_	Alignment	not modelled	5.7	11	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
63	c3n0vD_	Alignment	not modelled	5.7	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
64	d1hwua_	Alignment	not modelled	5.5	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
65	c3mjkE_	Alignment	not modelled	5.2	20	**PDB header:**hormone **Chain:** E: **PDB Molecule:**platelet-derived growth factor subunit a; **PDBTitle:** structure of a growth factor precursor
66	c3nrbD_	Alignment	not modelled	5.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
67	d1p42a1	Alignment	not modelled	5.1	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
68	d1qw1a1	Alignment	not modelled	5.1	8	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like