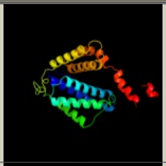
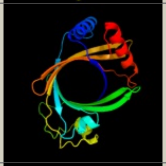
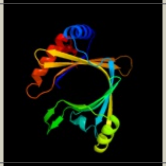
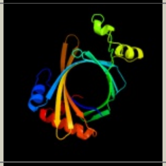
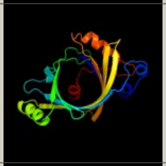
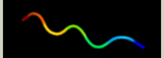
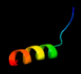
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P30871
Date	Thu Jan 5 11:46:46 GMT 2012
Unique Job ID	a12f3ea2bcde6bab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e0sA_	Alignment		100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 chlorobium tepidum
2	c2gfgB_	Alignment		100.0	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**bh2851; **PDBTitle:** crystal structure of a putative adenylate cyclase (bh2851) from2 bacillus halodurans at 2.12 a resolution
3	d2jmua1	Alignment		100.0	19	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
4	c3sy3D_	Alignment		100.0	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**gbaa_1210 protein; **PDBTitle:** gbaa_1210 protein, a putative adenylate cyclase, from bacillus2 anthracis
5	c2fjtA_	Alignment		99.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylyl cyclase class iv; **PDBTitle:** adenylyl cyclase class iv from yersinia pestis
6	d2acaa1	Alignment		99.8	16	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
7	c2dc4A_	Alignment		99.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**165aa long hypothetical protein; **PDBTitle:** structure of ph1012 protein from pyrococcus horikoshii ot3
8	d1yema_	Alignment		99.7	17	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
9	c2eenA_	Alignment		99.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1819; **PDBTitle:** structure of ph1819 protein from pyrococcus horikoshii ot3
10	c3g3rA_	Alignment		98.5	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 4; **PDBTitle:** crystal structure of a eukaryotic polyphosphate polymerase2 in complex with appnhp-mn2+
11	c3g3oA_	Alignment		98.3	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 2; **PDBTitle:** crystal structure of the cytoplasmic tunnel domain in yeast2 vtc2p

12	d2fbla1	Alignment		97.2	28	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
13	c3oq0D_	Alignment		21.0	43	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**dbf4; **PDBTitle:** crystal structure of motif n of saccharomyces cerevisiae dbf4
14	d1b77a2	Alignment		9.5	20	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
15	c2y3yC_	Alignment		9.4	26	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** holo-ni(ii) hpnikr is a symmetric tetramer containing four2 canonic square-planar ni(ii) ions at physiological ph
16	c2aghA_	Alignment		8.9	63	**PDB header:**transcription **Chain:** A: **PDB Molecule:**myb proto-oncogene protein; **PDBTitle:** structural basis for cooperative transcription factor2 binding to the cbp coactivator
17	d1czda2	Alignment		8.8	20	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
18	d1nh1a_	Alignment		8.4	15	**Fold:**Antivirulence factor **Superfamily:**Antivirulence factor **Family:**Antivirulence factor
19	c1nh1A_	Alignment		8.4	15	**PDB header:**avirulence protein **Chain:** A: **PDB Molecule:**avirulence b protein; **PDBTitle:** crystal structure of the type iii effector avrb from2 pseudomonas syringae.
20	c2y9xG_	Alignment		7.8	28	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**lectin-like fold protein; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
21	c1sb0B_	Alignment	not modelled	7.6	63	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein c-myb; **PDBTitle:** solution structure of the kix domain of cbp bound to the2 transactivation domain of c-myb
22	d1n8ia_	Alignment	not modelled	7.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
23	c3ectA_	Alignment	not modelled	7.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase; **PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
24	c2imuA_	Alignment	not modelled	7.2	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**structural polyprotein (pp) p1; **PDBTitle:** nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc).
25	d2oyza1	Alignment	not modelled	7.1	33	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
26	d1qr5a_	Alignment	not modelled	6.8	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
27	d1ka5a_	Alignment	not modelled	6.8	25	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
28	c2eqeA_	Alignment	not modelled	6.6	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** solution structure of the fourth a20-type zinc finger2 domain from human tumor necrosis factor, alpha-induced3 protein3

29	d2ae8a2	Alignment	not modelled	6.6	16	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
30	c2bnoA_	Alignment	not modelled	6.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
31	d2ofya1	Alignment	not modelled	6.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
32	d1ok7a2	Alignment	not modelled	6.2	15	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
33	d2nzul1	Alignment	not modelled	6.1	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
34	c3eo6B_	Alignment	not modelled	6.1	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of unknown function (duf1255); **PDBTitle:** crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
35	c3pxpA_	Alignment	not modelled	6.0	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
36	c3hqxA_	Alignment	not modelled	5.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0345 protein aciad0356; **PDBTitle:** crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
37	c3fbnC_	Alignment	not modelled	5.8	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 7; **PDBTitle:** structure of the mediator submodule med7n/31
38	c1y9qA_	Alignment	not modelled	5.8	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
39	c3eusB_	Alignment	not modelled	5.8	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
40	d1w0ba_	Alignment	not modelled	5.8	20	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
41	c3f3bA_	Alignment	not modelled	5.7	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdh; **PDBTitle:** structure of the phage-like element pbsx protein xkdh from2 bacillus subtilus. northeast structural genomics3 consortium target sr352.
42	d2j0oa1	Alignment	not modelled	5.6	9	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
43	c2j0oA_	Alignment	not modelled	5.6	9	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**invasin ipad; **PDBTitle:** shigella flexneri ipad
44	d1d8ca_	Alignment	not modelled	5.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
45	c2hw2A_	Alignment	not modelled	5.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
46	d1xu2r_	Alignment	not modelled	5.3	25	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
47	c1xu2R_	Alignment	not modelled	5.3	25	**PDB header:**cytokine, hormone/growth factor receptor **Chain:** R: **PDB Molecule:**tumor necrosis factor receptor superfamily member 17; **PDBTitle:** the crystal structure of april bound to bcma
48	d1d8ia_	Alignment	not modelled	5.3	23	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**mRNA triphosphatase CET1
49	c1b8hA_	Alignment	not modelled	5.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase processivity component; **PDBTitle:** sliding clamp, dna polymerase
50	d1z8ua1	Alignment	not modelled	5.1	20	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
51	c3sr2A_	Alignment	not modelled	5.1	3	**PDB header:**dna binding protein/protein binding **Chain:** A: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of human xlf-xrcc4 complex
52	d1v7wa2	Alignment	not modelled	5.1	5	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain