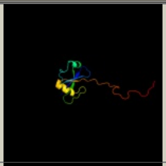
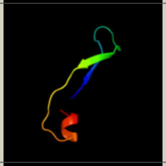
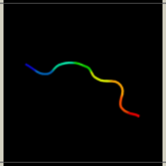
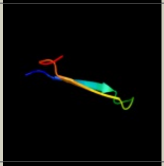
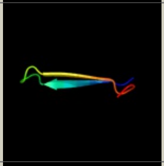
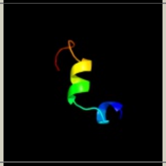
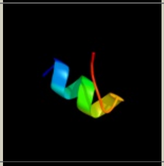
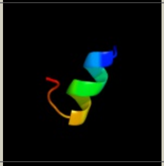
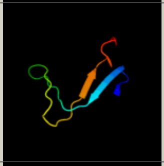
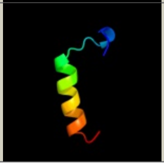
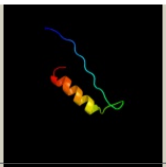
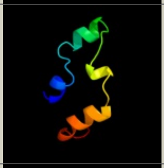
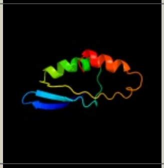
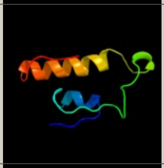
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AB43
Date	Thu Jan 5 11:14:35 GMT 2012
Unique Job ID	b4042a73e99574ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2h7aa1	Alignment		100.0	100	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
2	c2qz7B_	Alignment		22.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein sco6318; **PDBTitle:** the crystal structure of a homologue of telluride resistance protein2 (terd), sco6318 from streptomyces coelicolor a3(2)
3	c3ol0C_	Alignment		21.1	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
4	c2jn4A_	Alignment		20.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
5	d2jn4a1	Alignment		20.0	35	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
6	d1q8ka2	Alignment		17.8	16	**Fold:**Ferredoxin-like **Superfamily:**eIF-2-alpha, C-terminal domain **Family:**eIF-2-alpha, C-terminal domain
7	c1rrqA_	Alignment		17.0	38	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
8	c2hfqA_	Alignment		14.4	29	**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
9	d2hfqa1	Alignment		14.4	29	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
10	d1bb8a_	Alignment		13.5	30	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**DNA-binding domain from tn916 integrase
11	c2k4bA_	Alignment		12.6	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure

12	c2hzqA_	Alignment		11.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**apolipoprotein d; **PDBTitle:** crystal structure of human apolipoprotein d (apod) in2 complex with progesterone
13	d1ngna_	Alignment		11.5	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
14	d1lrza2	Alignment		9.8	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
15	d2g9wa1	Alignment		9.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
16	c3a52A_	Alignment		9.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
17	d1seda_	Alignment		9.2	39	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
18	d1sd4a_	Alignment		8.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
19	d1g8fa3	Alignment		8.4	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
20	d1orna_	Alignment		8.4	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
21	c3ogfA_	Alignment	not modelled	8.3	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
22	c1rrbA_	Alignment	not modelled	8.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**raf proto-oncogene serine/threonine-protein **PDBTitle:** the ras-binding domain of raf-1 from rat, nmr, 1 structure
23	d1y6va1	Alignment	not modelled	8.1	24	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
24	c3hi2D_	Alignment	not modelled	7.7	22	**PDB header:**dna binding protein/toxin **Chain:** D: **PDB Molecule:**motility quorum-sensing regulator mqsr; **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
25	d1pd0a4	Alignment	not modelled	7.3	20	**Fold:**Gelsolin-like **Superfamily:**C-terminal, gelsolin-like domain of Sec23/24 **Family:**C-terminal, gelsolin-like domain of Sec23/24
26	d1e7la1	Alignment	not modelled	7.2	15	**Fold:**LEM/SAP HeH motif **Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains **Family:**Recombination endonuclease VII, C-terminal and dimerization domains
27	d2abka_	Alignment	not modelled	6.9	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
						PDB header:hydrolase

28	c3n5nX_	Alignment	not modelled	6.9	38	**Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
29	d1fima_	Alignment	not modelled	6.8	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
30	d1jaea2	Alignment	not modelled	6.8	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	c2os5C_	Alignment	not modelled	6.7	10	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
32	c1nyqA_	Alignment	not modelled	6.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
33	d2bykb1	Alignment	not modelled	6.5	22	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
34	c2bykB_	Alignment	not modelled	6.5	22	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**chrac-14; **PDBTitle:** histone fold heterodimer of the chromatin accessibility2 complex
35	d1xova1	Alignment	not modelled	6.2	57	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Ply C-terminal domain-like
36	d1pu6a_	Alignment	not modelled	6.2	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
37	d2gdga1	Alignment	not modelled	6.0	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
38	d1kg2a_	Alignment	not modelled	6.0	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
39	d1lcda_	Alignment	not modelled	5.9	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
40	c2kxvA_	Alignment	not modelled	5.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein; **PDBTitle:** nmr structure and calcium-binding properties of the tellurite2 resistance protein terd from klebsiella pneumoniae
41	d1qupa2	Alignment	not modelled	5.8	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
42	c3m05A_	Alignment	not modelled	5.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
43	d1kyqa2	Alignment	not modelled	5.7	29	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
44	c3k0tA_	Alignment	not modelled	5.6	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**endoribonuclease l-psp, putative; **PDBTitle:** crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
45	c1pwaA_	Alignment	not modelled	5.5	11	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**fibroblast growth factor-19; **PDBTitle:** crystal structure of fibroblast growth factor 19
46	d1pwaa_	Alignment	not modelled	5.5	11	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
47	c2lcvA_	Alignment	not modelled	5.5	33	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
48	d1p6ra_	Alignment	not modelled	5.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
49	d2isba1	Alignment	not modelled	5.4	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
50	d1n1ja_	Alignment	not modelled	5.3	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs