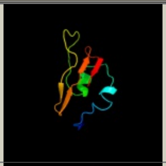
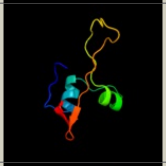
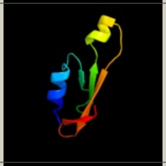
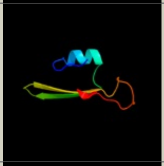
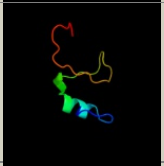
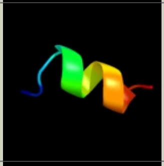
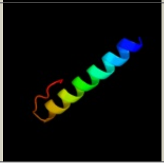
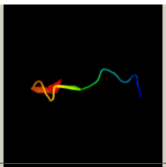
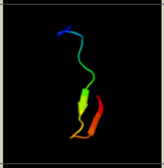
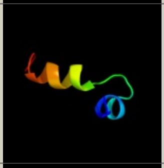
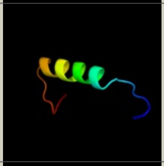
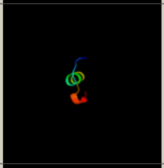
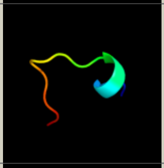
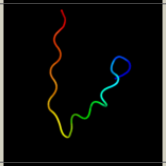
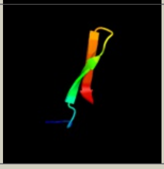
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADB1
Date	Thu Jan 5 11:20:30 GMT 2012
Unique Job ID	c08444166a67d157

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pxgA_	Alignment		96.9	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
2	c2kxxA_	Alignment		96.5	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
3	c3gmxB_	Alignment		79.0	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**blp; **PDBTitle:** crystal structure of beta-lactamse inhibitory protein-like2 protein (blp) at 1.05 angstrom resolution
4	c3d4eA_	Alignment		74.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-lactamase inhibitor protein; **PDBTitle:** crystal structure of putative beta-lactamase inhibitor protein2 (np_721579.1) from streptococcus mutans at 1.40 a resolution
5	d2g2ub1	Alignment		67.2	24	**Fold:**BLIP-like **Superfamily:**beta-lactamase-inhibitor protein, BLIP **Family:**beta-lactamase-inhibitor protein, BLIP
6	c3gmvX_	Alignment		64.4	42	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**beta-lactamase inhibitory protein blip-i; **PDBTitle:** crystal structure of beta-lactamse inhibitory protein-i2 (blip-i) in apo form
7	c2w7nA_	Alignment		19.8	25	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**trfb transcriptional repressor protein; **PDBTitle:** crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
8	d2ppxa1	Alignment		17.6	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
9	c2ppxA_	Alignment		17.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
10	c2fhdA_	Alignment		14.6	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
11	c3d0wD_	Alignment		11.9	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yflh protein; **PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326

12	c2a7yA_	Alignment		11.4	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
13	d2a7ya1	Alignment		11.4	35	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
14	d1bw6a_	Alignment		10.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
15	c2kq5A_	Alignment		9.7	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
16	c2xzmO_	Alignment		9.1	29	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
17	c3f6wE_	Alignment		8.7	30	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
18	d1tfra1	Alignment		8.7	7	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
19	d3eipa_	Alignment		8.4	40	**Fold:**FKBP-like **Superfamily:**Colicin E3 immunity protein **Family:**Colicin E3 immunity protein
20	c3o4aC_	Alignment		7.9	11	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed beta-trefoil architecture with symmetric **PDBTitle:** crystal structure of symfoil-2: de novo designed beta-trefoil2 architecture with symmetric primary structure
21	d1ihka_	Alignment	not modelled	7.7	31	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
22	c3mtjA_	Alignment	not modelled	7.2	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
23	d2oq1a2	Alignment	not modelled	7.2	18	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
24	d2a6ca1	Alignment	not modelled	7.0	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
25	c3f1rA_	Alignment	not modelled	7.0	38	**PDB header:**hormone **Chain:** A: **PDB Molecule:**fibroblast growth factor 20; **PDBTitle:** crystal structure of fgf20 dimer
26	d1ijwc_	Alignment	not modelled	7.0	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
27	d1f35a_	Alignment	not modelled	6.9	40	**Fold:**Olfactory marker protein **Superfamily:**Olfactory marker protein **Family:**Olfactory marker protein
28	c3bs3A_	Alignment	not modelled	6.4	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
29	d2hjqa1	Alignment	not modelled	6.3	38	**Fold:**LEM/SAP HeH motif **Superfamily:**Rho N-terminal domain-like

						Family: YqbF C-terminal domain-like
30	d2axwa1	Alignment	not modelled	6.0	9	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
31	d1pxza_	Alignment	not modelled	5.6	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
32	c2iurD_	Alignment	not modelled	5.6	41	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aromatic amine dehydrogenase beta subunit; **PDBTitle:** crystal structure of n-quinol form of aromatic amine2 dehydrogenase (aadh) from alcaligenes faecalis, form a3 cocrystal
33	c2p04B_	Alignment	not modelled	5.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
34	c1w78A_	Alignment	not modelled	5.2	15	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
35	c2o1uA_	Alignment	not modelled	5.2	44	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound