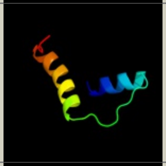
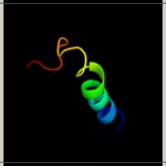
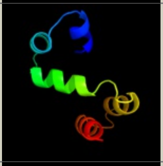
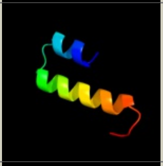
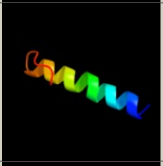
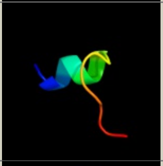
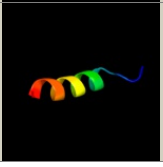
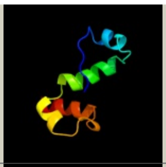
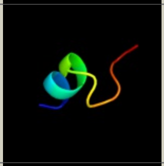
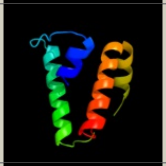
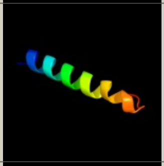
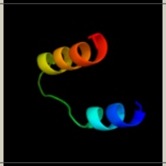
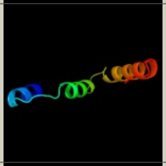
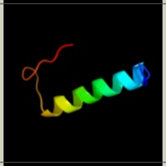
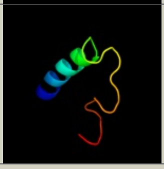
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77528
Date	Thu Jan 5 12:30:18 GMT 2012
Unique Job ID	0050b119bee98158

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1c52a_	Alignment		69.9	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
2	c3nufB_	Alignment		58.9	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**prd-containing transcription regulator; **PDBTitle:** crystal structure of a prd-containing transcription regulator2 (lsei_2718) from lactobacillus casei atcc 334 at 1.38 a resolution
3	c2yumA_	Alignment		35.1	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger zz-type-containing protein 3; **PDBTitle:** solution structure of the myb-like dna-binding domain of2 human zzz3 protein
4	d1vz0a1	Alignment		30.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
5	d2es9a1	Alignment		25.3	9	**Fold:**YoaC-like **Superfamily:**YoaC-like **Family:**YoaC-like
6	c2cjjA_	Alignment		25.3	20	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**radialis; **PDBTitle:** crystal structure of the myb domain of the rad2 transcription factor from antirrhinum majus
7	d2cjja1	Alignment		25.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
8	d1m98a1	Alignment		18.6	20	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
9	d1h99a1	Alignment		17.2	14	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
10	c2l66B_	Alignment		15.5	40	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
11	c3nzlA_	Alignment		14.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b

12	c1zx4B_	Alignment		13.8	13	**PDB header:**translation **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
13	c1m98A_	Alignment		12.9	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
14	d1h99a2	Alignment		11.4	8	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
15	d1up8a_	Alignment		11.0	23	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
16	d2dsya1	Alignment		10.7	26	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA0281-like
17	d2b7ma1	Alignment		10.2	17	**Fold:**alpha-alpha superhelix **Superfamily:**Cullin repeat-like **Family:**Exocyst complex component
18	c3gwhB_	Alignment		9.5	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional antiterminator (bglg family); **PDBTitle:** crystallographic ab initio protein solution far below atomic2 resolution
19	d1hwxa2	Alignment		9.2	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
20	c2wj8N_	Alignment		8.8	19	**PDB header:**rna binding protein/rna **Chain:** N: **PDB Molecule:**nucleoprotein; **PDBTitle:** respiratory syncitial virus ribonucleoprotein
21	d1ufza_	Alignment	not modelled	8.8	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
22	d1ddba_	Alignment	not modelled	8.7	19	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
23	d2gmya1	Alignment	not modelled	8.7	23	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
24	d1b5qa2	Alignment	not modelled	8.0	18	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
25	c2wvmA_	Alignment	not modelled	7.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
26	d1toha_	Alignment	not modelled	7.6	21	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
27	c3gocB_	Alignment	not modelled	7.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
						PDB header:transferase

28	c2zu8A_	Alignment	not modelled	7.2	23	**Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
29	d2v5za2	Alignment	not modelled	7.2	18	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
30	d1j8ua_	Alignment	not modelled	7.1	18	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
31	d1phza2	Alignment	not modelled	6.9	18	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
32	d1l1fa2	Alignment	not modelled	6.8	22	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
33	d2fhzb1	Alignment	not modelled	6.7	5	**Fold:**Colicin D/E5 nuclease domain **Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin E5 nuclease domain
34	d1mlwa_	Alignment	not modelled	6.6	18	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
35	d1ppjb2	Alignment	not modelled	6.6	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	d1dgsa2	Alignment	not modelled	6.4	50	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
37	c1uixA_	Alignment	not modelled	6.4	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rho-associated kinase; **PDBTitle:** coiled-coil structure of the rhoa-binding domain in rho-2 kinase
38	c3bboW_	Alignment	not modelled	6.4	33	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosomal protein l24; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
39	d1szaa_	Alignment	not modelled	6.3	13	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**RPR domain (SMART 00582)
40	d1tjla2	Alignment	not modelled	6.2	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Prokaryotic DksA/TraR C4-type zinc finger
41	c3jroA_	Alignment	not modelled	6.1	20	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
42	c1s1cY_	Alignment	not modelled	6.1	67	**PDB header:**signaling protein **Chain:** Y: **PDB Molecule:**rho-associated, coiled-coil containing protein **PDBTitle:** crystal structure of the complex between the human rhoa and2 rho-binding domain of human rocki
43	c2d3jA_	Alignment	not modelled	6.0	19	**PDB header:**signaling protein inhibitor **Chain:** A: **PDB Molecule:**wnt inhibitory factor-1; **PDBTitle:** nmr structure of the wif domain from human wif-1
44	c2vo4A_	Alignment	not modelled	5.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
45	c2phmA_	Alignment	not modelled	5.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
46	d2fzva1	Alignment	not modelled	5.7	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
47	d1b8za_	Alignment	not modelled	5.6	13	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
48	c3hahA_	Alignment	not modelled	5.5	18	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**human pacsin1 f-bar; **PDBTitle:** crystal structure of human pacsin1 f-bar domain (c2 lattice)
49	c3bg1F_	Alignment	not modelled	5.4	20	**PDB header:**protein transport, hydrolase **Chain:** F: **PDB Molecule:**nucleoporin nup145; **PDBTitle:** architecture of a coat for the nuclear pore membrane
50	c2p1iA_	Alignment	not modelled	5.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, small chain; **PDBTitle:** plasmodium yoelii ribonucleotide reductase subunit r2 (py03671)
51	d1bgva2	Alignment	not modelled	5.3	22	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
52	d1oyja1	Alignment	not modelled	5.3	15	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain