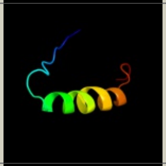
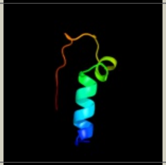
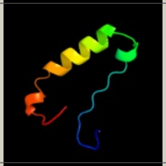
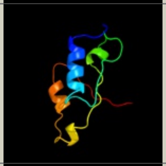
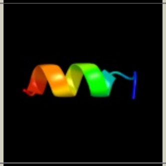
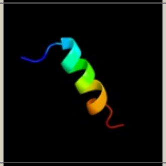
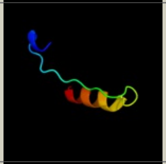
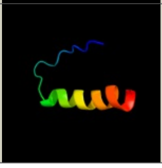
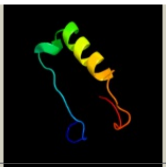
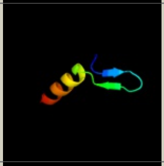
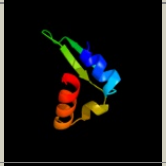
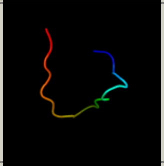
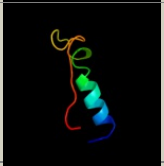
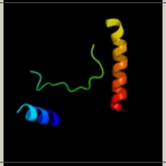
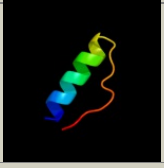
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P38521
Date	Thu Jan 5 11:58:12 GMT 2012
Unique Job ID	d66d09fb8c81485a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qd7X_	Alignment		51.9	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
2	c2kvoA_	Alignment		34.1	18	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
3	d1o0sa2	Alignment		24.6	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
4	c3h11A_	Alignment		22.8	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**casp8 and fadd-like apoptosis regulator; **PDBTitle:** zymogen caspase-8:c-flipl protease domain complex
5	d1nd9a_	Alignment		22.0	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**N-terminal subdomain of bacterial translation initiation factor IF2
6	d1kkha2	Alignment		21.7	22	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
7	d1pj3a2	Alignment		20.6	24	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
8	c3g6iA_	Alignment		18.1	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative outer membrane protein, part of carbohydrate **PDBTitle:** crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
9	d1gq2a2	Alignment		17.8	24	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
10	d1m72a_	Alignment		17.6	30	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
11	c2kjwA_	Alignment		17.5	10	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55

12	c2nn3D_	Alignment		17.5	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-1; **PDBTitle:** structure of pro-sf-caspase-1
13	d1yg2a_	Alignment		17.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
14	d1v33a_	Alignment		17.1	10	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like
15	c1kmcB_	Alignment		16.8	18	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of the caspase-7 / xiap-bir2 complex
16	c2wzpR_	Alignment		16.4	20	**PDB header:**viral protein **Chain:** R: **PDB Molecule:**lactococcal phage p2 orf16; **PDBTitle:** structures of lactococcal phage p2 baseplate shed light on2 a novel mechanism of host attachment and activation in3 siphoviridae
17	c1o0sB_	Alignment		16.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** crystal structure of ascaris suum malic enzyme complexed with nadh
18	d2fsqa1	Alignment		15.8	8	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
19	c2zqeA_	Alignment		15.3	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
20	d1t1ea2	Alignment		15.0	25	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
21	c2fp3A_	Alignment	not modelled	13.3	26	**PDB header:**hydrolysis/apoptosis **Chain:** A: **PDB Molecule:**caspase nc; **PDBTitle:** crystal structure of the drosophila initiator caspase dronc
22	d1e1oa2	Alignment	not modelled	13.0	10	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
23	d1k47a2	Alignment	not modelled	12.6	11	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
24	d1iyjb3	Alignment	not modelled	10.8	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
25	d1j9ia_	Alignment	not modelled	10.8	26	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
26	c2wdpA_	Alignment	not modelled	10.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of ligand free human caspase-6
27	d1g71a_	Alignment	not modelled	10.8	11	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like
28	d1miua3	Alignment	not modelled	10.6	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
29	c2aw5A_	Alignment	not modelled	10.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent malic enzyme;

						PDBTitle: crystal structure of a human malic enzyme
30	c1gz3B_	Alignment	not modelled	10.5	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
31	c1qr6A_	Alignment	not modelled	10.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
32	d2cxaa1	Alignment	not modelled	9.3	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
33	c2cxaA_	Alignment	not modelled	9.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
34	c2kl5A_	Alignment	not modelled	9.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yutd; **PDBTitle:** solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
35	c2hqrA_	Alignment	not modelled	9.2	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
36	c2ns6A_	Alignment	not modelled	9.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
37	d1jmxa1	Alignment	not modelled	9.0	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
38	c3e4cB_	Alignment	not modelled	9.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
39	c3f5bA_	Alignment	not modelled	8.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminoglycoside n(6')acetyltransferase; **PDBTitle:** the crystal structure of aminoglycoside n(6')acetyltransferase from2 legionella pneumophila subsp. pneumophila str. philadelphia 1.
40	c3ew8A_	Alignment	not modelled	8.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
41	c3mjhD_	Alignment	not modelled	8.4	50	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
42	d1pbya1	Alignment	not modelled	8.2	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
43	c3fo8D_	Alignment	not modelled	8.2	20	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**tail sheath protein gp18; **PDBTitle:** crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
44	c3k1tA_	Alignment	not modelled	8.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
45	c2hbzA_	Alignment	not modelled	7.9	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (arg286->ala, glu390->ala) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
46	c2p7vA_	Alignment	not modelled	7.7	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
47	d1zt2a1	Alignment	not modelled	7.6	14	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like
48	d2juza1	Alignment	not modelled	7.4	40	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
49	d1nw9b_	Alignment	not modelled	7.2	11	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
50	c3iukB_	Alignment	not modelled	7.1	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
51	d1c3pa_	Alignment	not modelled	6.8	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
52	c2zxyA_	Alignment	not modelled	6.7	0	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
53	c3kxeD_	Alignment	not modelled	6.6	20	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex

54	d1c75a_	Alignment	not modelled	6.6	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
55	d1dxxa2	Alignment	not modelled	6.5	22	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
56	d1t64a_	Alignment	not modelled	6.5	16	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
57	c1nmqB_	Alignment	not modelled	6.4	18	**PDB header:**apoptosis, hydrolase **Chain:** B: **PDB Molecule:**caspase-3; **PDBTitle:** extendend tethering: in situ assembly of inhibitors
58	c1cp3B_	Alignment	not modelled	6.4	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**apopain; **PDBTitle:** crystal structure of the complex of apopain with the tetrapeptide2 inhibitor ace-dvad-fmc
59	c2bpbB_	Alignment	not modelled	6.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
60	d2jrxa1	Alignment	not modelled	6.1	35	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
61	c1w2lA_	Alignment	not modelled	6.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
62	d2i7pa2	Alignment	not modelled	6.0	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
63	c2d89A_	Alignment	not modelled	5.8	15	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**ehbp1 protein; **PDBTitle:** solution structure of the ch domain from human eh domain2 binding protein 1
64	c3a9fA_	Alignment	not modelled	5.7	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the c-terminal domain of cytochrome cz2 from chlorobium tepidum
65	c3m3hA_	Alignment	not modelled	5.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
66	c1t1eA_	Alignment	not modelled	5.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kumamolisin; **PDBTitle:** high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
67	c1kjkA_	Alignment	not modelled	5.5	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** solution structure of the lambda integrase amino-terminal2 domain
68	d1z1ba1	Alignment	not modelled	5.5	43	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**lambda integrase N-terminal domain
69	d1cora_	Alignment	not modelled	5.5	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
70	d2qtia1	Alignment	not modelled	5.5	25	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
71	c3bboQ_	Alignment	not modelled	5.4	45	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein l18; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
72	d1a56a_	Alignment	not modelled	5.4	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
73	c3bqsB_	Alignment	not modelled	5.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
74	d1aoaa2	Alignment	not modelled	5.4	13	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
75	c2pebB_	Alignment	not modelled	5.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
76	d3c7bb2	Alignment	not modelled	5.2	36	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
77	d1otfa_	Alignment	not modelled	5.2	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
78	c1pyoA_	Alignment	not modelled	5.2	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
79	c1gd2G_	Alignment	not modelled	5.1	29	**PDB header:**transcription/dna **Chain:** G: **PDB Molecule:**transcription factor pap1; **PDBTitle:** crystal structure of bzip transcription factor pap1 bound2 to dna
						PDB header:transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr;

80	c2hwvA_	Alignment	not modelled	5.1	71	**PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.