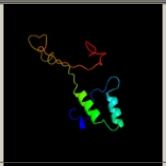
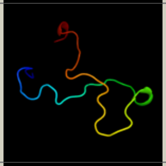
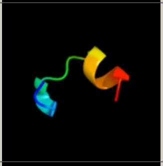
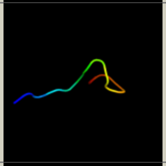
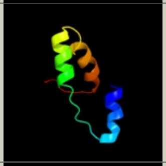
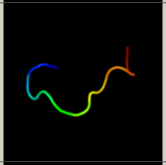
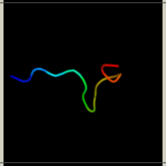
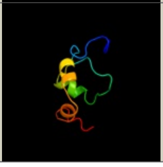
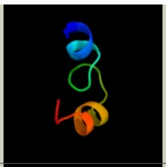
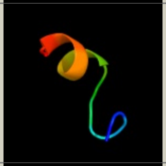
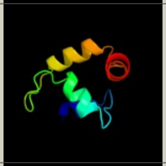
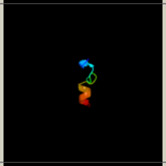
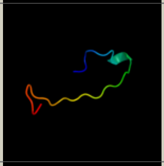
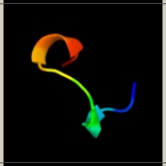
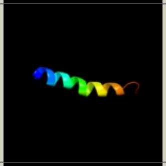
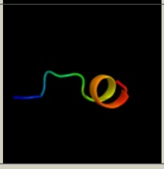
Email	l.a.kelley@imperial.ac.uk
Description	P76547
Date	Thu Jan 5 12:24:24 GMT 2012
Unique Job ID	579a475f46b22738

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a1oB_	Alignment		26.1	19	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
2	d2g39a1	Alignment		24.3	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
3	c2no8A_	Alignment		13.6	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**colicin-e2 immunity protein; **PDBTitle:** nmr structure analysis of the colicin immuntiy protein im2
4	c2l95A_	Alignment		13.5	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crammer; **PDBTitle:** solution structure of cytotoxic t-lymphocyte antigen-2(ctla protein),2 crammer at ph 6.0
5	c3bq7A_	Alignment		12.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
6	d1iv8a2	Alignment		12.3	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
7	d1zo0a1	Alignment		11.9	7	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Ornithine decarboxylase antizyme-like
8	d2csba4	Alignment		11.8	33	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
9	c2xqoA_	Alignment		11.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulosome enzyme, dockerin type i; **PDBTitle:** ctcel124: a cellulase from clostridium thermocellum
10	c3hjeA_	Alignment		11.1	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**704aa long hypothetical glycosyltransferase; **PDBTitle:** crystal structure of sulfolobus tokodaii hypothetical2 maltooligosyl trehalose synthase
11	c1v85A_	Alignment		10.3	11	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator

12	c3es5A_	Alignment		9.1	45	**PDB header:**virus **Chain:** A: **PDB Molecule:**putative capsid protein; **PDBTitle:** crystal structure of partitivirus (psv-f)
13	d1gxha_	Alignment		8.9	23	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
14	c3op0B_	Alignment		8.7	21	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
15	c2nogA_	Alignment		8.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**iswi protein; **PDBTitle:** sant domain structure of xenopus remodeling factor iswi
16	d2dlda2	Alignment		8.3	24	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
17	c3bs7A_	Alignment		8.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
18	c1l6lK_	Alignment		8.0	29	**PDB header:**lipid transport **Chain:** K: **PDB Molecule:**apolipoprotein a-ii; **PDBTitle:** structures of apolipoprotein a-ii and a lipid surrogate2 complex provide insights into apolipoprotein-lipid3 interactions
19	d2vlqa1	Alignment		7.4	23	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
20	d1j4aa2	Alignment		7.4	31	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
21	c1ofcX_	Alignment	not modelled	7.4	29	**PDB header:**nuclear protein **Chain:** X: **PDB Molecule:**iswi protein; **PDBTitle:** nucleosome recognition module of iswi atpase
22	d2cqqa1	Alignment	not modelled	7.3	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
23	d1f0la2	Alignment	not modelled	7.3	29	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
24	d2hqya2	Alignment	not modelled	6.9	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
25	c2wsfG_	Alignment	not modelled	6.7	47	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** improved model of plant photosystem i
26	c3f75P_	Alignment	not modelled	6.7	38	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**cathepsin l propeptide; **PDBTitle:** activated toxoplasma gondii cathepsin l (tgcpl) in complex with its2 propeptide
27	c2wscK_	Alignment	not modelled	6.5	26	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit psak, **PDBTitle:** improved model of plant photosystem i
28	d2fu5a1	Alignment	not modelled	6.5	25	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
29	d3buxb1	Alignment	not modelled	6.2	24	**Fold:**EF Hand-like **Superfamily:**EF-hand

		Alignment				**Family:**EF-hand modules in multidomain proteins
30	d1ayia_	Alignment	not modelled	6.2	23	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
31	d1wwva1	Alignment	not modelled	6.1	14	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
32	c3qodB_	Alignment	not modelled	6.1	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**heterocyst differentiation protein; **PDBTitle:** crystal structure of heterocyst differentiation protein, hetr from2 fischerella mv11
33	d1dpsa_	Alignment	not modelled	5.7	71	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
34	d1t92a_	Alignment	not modelled	5.7	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pseudopilin
35	c3cecA_	Alignment	not modelled	5.5	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
36	c2o01G_	Alignment	not modelled	5.3	47	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**photosystem i reaction center subunit v, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution