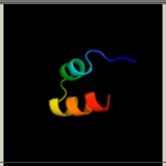
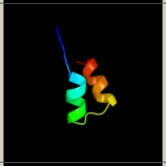
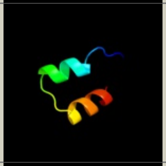
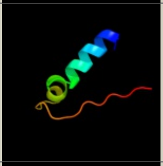
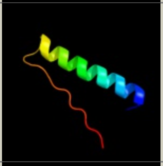
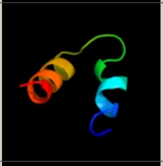
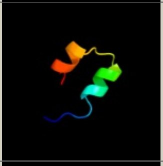
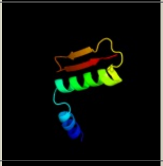
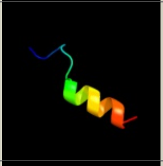
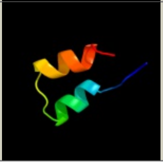
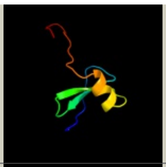
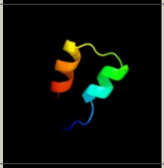
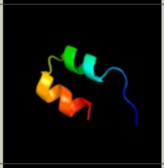
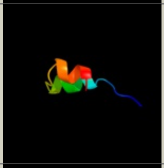
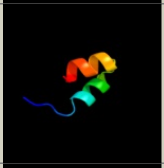
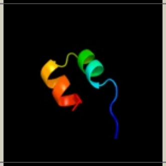
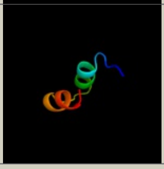
Email	l.a.kelley@imperial.ac.uk
Description	P76512
Date	Thu Jan 5 12:23:52 GMT 2012
Unique Job ID	798b780a78acf412

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cbra_	Alignment		27.6	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
2	d2fs6a1	Alignment		27.0	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
3	d1g7na_	Alignment		22.4	15	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
4	d1914a2	Alignment		21.2	21	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
5	d1e8ob_	Alignment		18.7	25	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
6	d1fx0a1	Alignment		18.4	21	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
7	d1pmpa_	Alignment		18.0	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
8	c3h4lB_	Alignment		17.8	6	**PDB header:**dna binding protein, protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
9	d2hnxa1	Alignment		17.6	16	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
10	c3si5X_	Alignment		16.7	37	**PDB header:**cell cycle **Chain:** X: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
11	d1fdqa_	Alignment		16.5	19	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like

12	c1t3bA_	Alignment		16.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
13	c3pptA_	Alignment		15.8	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**sodium-calcium exchanger; **PDBTitle:** rep1-nxsq fatty acid transporter
14	d1hmsa_	Alignment		15.1	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
15	d1ftpa_	Alignment		14.8	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
16	d1yiva1	Alignment		14.4	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
17	d1opaa_	Alignment		14.0	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
18	d1mdca_	Alignment		13.8	4	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
19	d1crba_	Alignment		13.5	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
20	c2q9sA_	Alignment		13.2	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fatty acid-binding protein; **PDBTitle:** linoleic acid bound to fatty acid binding protein 4
21	d1kqwa_	Alignment	not modelled	13.1	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
22	d1b56a_	Alignment	not modelled	12.8	28	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
23	c3na3A_	Alignment	not modelled	12.7	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
24	d1bwya_	Alignment	not modelled	12.3	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
25	d1lfoa_	Alignment	not modelled	12.2	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
26	d1o1va_	Alignment	not modelled	12.2	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
27	d1lpja_	Alignment	not modelled	12.0	17	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
28	d2a0aa1	Alignment	not modelled	11.8	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
29	d2ftba1	Alignment	not modelled	11.7	9	**Fold:**Lipocalins **Superfamily:**Lipocalins

						Family: Fatty acid binding protein-like
30	d1p6pa_	Alignment	not modelled	11.6	9	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
31	d1kzwa_	Alignment	not modelled	11.6	21	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
32	c1b9nA_	Alignment	not modelled	11.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein (mode); **PDBTitle:** regulator from escherichia coli
33	d1tw4a_	Alignment	not modelled	11.4	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
34	c1914A_	Alignment	not modelled	11.2	21	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
35	d1eala_	Alignment	not modelled	11.2	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
36	d1vyfa_	Alignment	not modelled	10.5	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
37	d1ifca_	Alignment	not modelled	9.8	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
38	d1h7sa2	Alignment	not modelled	9.7	13	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
39	c3gm8A_	Alignment	not modelled	9.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
40	c2lbaA_	Alignment	not modelled	8.7	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**babp protein; **PDBTitle:** solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
41	d1nuba2	Alignment	not modelled	8.1	53	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**Follistatin (FS) module N-terminal domain, FS-N
42	d2f73a1	Alignment	not modelled	7.9	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
43	c2hbpA_	Alignment	not modelled	7.9	14	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
44	c3em0A_	Alignment	not modelled	7.5	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ileal bile acid-binding protein; **PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
45	d1ggla_	Alignment	not modelled	7.3	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
46	d2j0na1	Alignment	not modelled	7.3	28	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
47	d2jdia1	Alignment	not modelled	7.0	21	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
48	d1o8va_	Alignment	not modelled	7.0	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
49	c3q0bX_	Alignment	not modelled	6.9	19	**PDB header:**transferase/dna **Chain:** X: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-9 specific **PDBTitle:** crystal structure of suvh5 sra- fully methylated cg dna complex in2 space group p42212
50	d1t3ba2	Alignment	not modelled	6.7	17	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
51	d1ukfa_	Alignment	not modelled	6.5	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3
52	c2kwaA_	Alignment	not modelled	6.2	20	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
53	d1xrsb2	Alignment	not modelled	5.9	33	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain