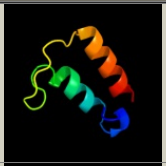
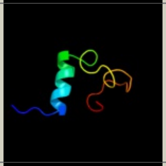
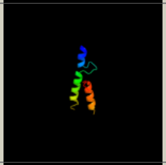
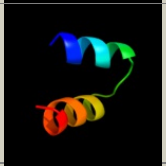
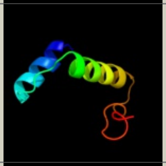
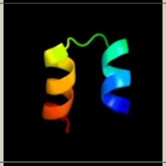
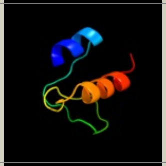
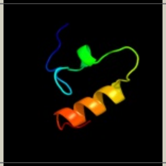
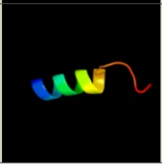
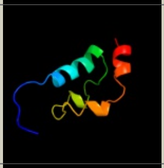
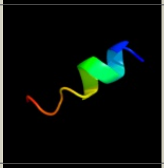
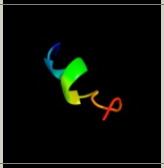
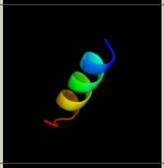
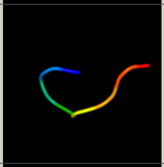
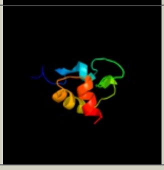
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77692
Date	Thu Jan 5 12:31:42 GMT 2012
Unique Job ID	587bb26ed7f880e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fwtA_	Alignment		71.5	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
2	c2jvwA_	Alignment		67.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
3	d1zeea1	Alignment		30.6	33	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
4	c2bh7A_	Alignment		27.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
5	c2hl7A_	Alignment		21.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
6	c1yx3A_	Alignment		19.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
7	c2kw0A_	Alignment		18.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
8	c2dnwA_	Alignment		17.9	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
9	c3g2bA_	Alignment		17.6	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
10	d1wj7a1	Alignment		16.9	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
11	c3hieA_	Alignment		15.8	56	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex

12	c1ziiA_	Alignment		11.7	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
13	c1ziiB_	Alignment		11.7	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
14	c2d86A_	Alignment		11.6	21	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**vav-3 protein; **PDBTitle:** solution structure of the ch domain from human vav-3 protein
15	c1zijA_	Alignment		11.1	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
16	c1zijC_	Alignment		11.1	46	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
17	c1zijB_	Alignment		11.1	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
18	d1whra_	Alignment		10.9	13	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
19	d1sr9a1	Alignment		10.6	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
20	c1wr1B_	Alignment		10.4	23	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
21	c2pjwH_	Alignment	not modelled	10.4	18	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
22	d1nq4a_	Alignment	not modelled	9.8	17	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
23	d1veja1	Alignment	not modelled	9.5	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
24	d1gjja2	Alignment	not modelled	9.3	20	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
25	d1t8ka_	Alignment	not modelled	9.1	23	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
26	c2cnrA_	Alignment	not modelled	9.0	13	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
27	c2fq2A_	Alignment	not modelled	8.4	25	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
28	d1q9ja1	Alignment	not modelled	8.3	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
						Fold: Transducin (alpha subunit), insertion domain

29	d1zcba1	Alignment	not modelled	8.0	32	**Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
30	c2yfvC_	Alignment	not modelled	7.9	24	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
31	d1tada1	Alignment	not modelled	7.6	38	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
32	c2kwlA_	Alignment	not modelled	7.5	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
33	c3ce7A_	Alignment	not modelled	7.3	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochondrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochondrial acyl2 carrier protein, 59.m03510
34	c2ae8C_	Alignment	not modelled	7.3	25	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
35	c2g2qB_	Alignment	not modelled	7.3	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the crystal structure of g4, the poxviral disulfide oxidoreductase2 essential for cytoplasmic disulfide bond formation
36	d1cipa1	Alignment	not modelled	7.3	38	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
37	c1vngA_	Alignment	not modelled	7.0	14	**PDB header:**haloperoxidase **Chain:** A: **PDB Molecule:**vanadium chloroperoxidase; **PDBTitle:** chloroperoxidase from the fungus curvularia inaequalis:2 mutant h404a
38	c3pcqX_	Alignment	not modelled	7.0	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
39	d1whca_	Alignment	not modelled	6.9	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
40	d1jb0x_	Alignment	not modelled	6.9	58	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
41	c1jb0X_	Alignment	not modelled	6.9	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
42	c2kebA_	Alignment	not modelled	6.8	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
43	d1zcaa1	Alignment	not modelled	6.8	41	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
44	d2hlya1	Alignment	not modelled	6.7	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
45	c2fvfA_	Alignment	not modelled	6.3	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
46	c2pbyB_	Alignment	not modelled	6.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
47	d1n7va_	Alignment	not modelled	6.2	50	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
48	c2dakA_	Alignment	not modelled	6.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
49	d1yo5c1	Alignment	not modelled	6.1	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ets domain
50	c2nnyA_	Alignment	not modelled	6.1	29	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**c-ets-1 protein; **PDBTitle:** crystal structure of the ets1 dimer dna complex.
51	d2af8a_	Alignment	not modelled	6.1	27	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
52	d1vkua_	Alignment	not modelled	5.9	28	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
53	c3ejbC_	Alignment	not modelled	5.7	23	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
54	d2bcjq1	Alignment	not modelled	5.6	29	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
55	d1d0qa_	Alignment	not modelled	5.4	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger

56	d1oqya2	Alignment	not modelled	5.3	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
57	d1hfes_	Alignment	not modelled	5.2	30	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Fe-only hydrogenase smaller subunit **Family:**Fe-only hydrogenase smaller subunit
58	c1hfeT_	Alignment	not modelled	5.2	30	**PDB header:**hydrogenase **Chain:** T: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans