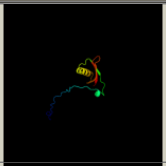
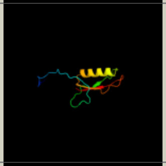
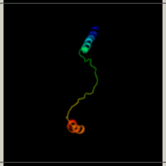
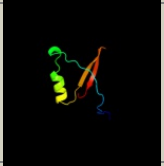
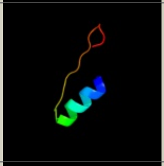
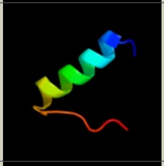
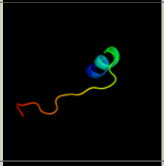
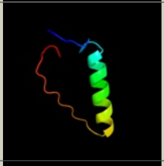
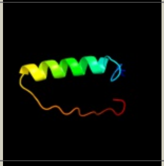
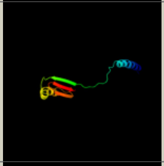
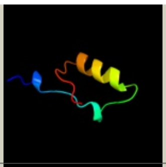
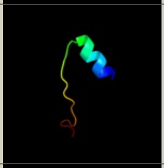
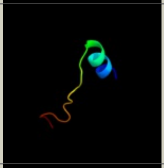
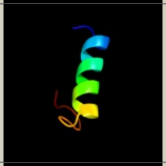
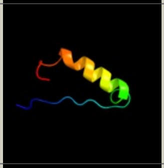
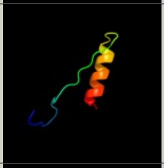
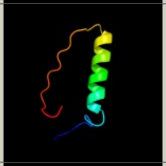
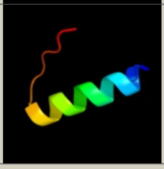
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P64614
Date	Wed Jan 25 15:21:00 GMT 2012
Unique Job ID	4fb8efb9b8bf9656

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jnaa1	Alignment		100.0	41	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
2	d2noca1	Alignment		100.0	36	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
3	c1oy8A_	Alignment		48.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
4	c2k4qA_	Alignment		39.9	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major tail protein v; **PDBTitle:** the solution structure of gpv, the major tail protein from2 bacteriophage lambda
5	c3dfeA_	Alignment		36.2	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative pii-like signaling protein; **PDBTitle:** crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
6	c3b9nB_	Alignment		31.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
7	c1hl8B_	Alignment		25.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
8	c3no4A_	Alignment		22.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
9	c3lubE_	Alignment		21.4	11	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
10	c3k07A_	Alignment		19.6	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
11	c3dnfB_	Alignment		18.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway

12	d1tqxa_	Alignment		18.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
13	c3eypB_	Alignment		18.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
14	c3mo4B_	Alignment		17.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
15	c3sdoB_	Alignment		16.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
16	c3ke8A_	Alignment		16.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
17	d3etja1	Alignment		15.9	10	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
18	d1kjqa1	Alignment		14.8	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
19	d1v7za_	Alignment		14.2	13	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
20	d1luca_	Alignment		13.9	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
21	d1f07a_	Alignment	not modelled	13.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
22	d1hl9a2	Alignment	not modelled	13.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
23	c3qkbB_	Alignment	not modelled	12.9	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
24	c2wvsD_	Alignment	not modelled	12.5	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
25	c3rofA_	Alignment	not modelled	11.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
26	d1lucb_	Alignment	not modelled	11.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
27	d1txka2	Alignment	not modelled	10.7	21	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
28	c1txkA_	Alignment	not modelled	10.3	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g;

						PDBTitle: crystal structure of escherichia coli opgg
29	c1f02T_	Alignment	not modelled	9.9	33	**PDB header:**cell adhesion **Chain:** T: **PDB Molecule:**translocated intimin receptor; **PDBTitle:** crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
30	d1nfpa_	Alignment	not modelled	9.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
31	c2y1bA_	Alignment	not modelled	9.8	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
32	c2jz7A_	Alignment	not modelled	8.5	25	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
33	d1rpxa_	Alignment	not modelled	8.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
34	c2w1sB_	Alignment	not modelled	7.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** unique ligand binding specificity of a family 322 carbohydrate-binding module from the mu toxin produced by3 clostridium perfringens
35	c3gzaB_	Alignment	not modelled	7.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
36	d1h1ya_	Alignment	not modelled	7.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
37	c1z69D_	Alignment	not modelled	7.2	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)- **PDBTitle:** crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
38	c2i7gA_	Alignment	not modelled	7.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
39	c2k38A_	Alignment	not modelled	7.0	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cupiennin-1a; **PDBTitle:** cupiennin 1a, nmr, minimized average structure
40	c3ir9A_	Alignment	not modelled	6.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
41	d1r3sa_	Alignment	not modelled	6.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
42	c3qc3B_	Alignment	not modelled	6.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
43	d2flia1	Alignment	not modelled	6.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
44	d1l7ba_	Alignment	not modelled	6.2	31	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA ligase
45	d1nqka_	Alignment	not modelled	6.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
46	c2gi4A_	Alignment	not modelled	6.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
47	d1p5vb_	Alignment	not modelled	6.1	13	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
48	c2cokA_	Alignment	not modelled	6.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1
49	c2zfdB_	Alignment	not modelled	5.5	15	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
50	d1tvla_	Alignment	not modelled	5.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
51	c1tvlA_	Alignment	not modelled	5.5	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein ytnj; **PDBTitle:** structure of ytnj from bacillus subtilis
52	d2g39a1	Alignment	not modelled	5.4	31	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
53	d1mnta_	Alignment	not modelled	5.3	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors

54	d1cdwa2	Alignment	not modelled	5.1	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain