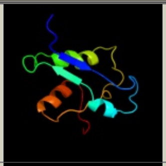
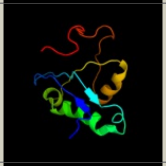
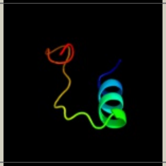
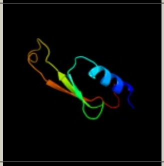
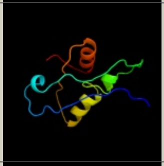
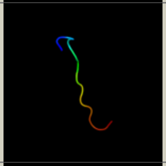
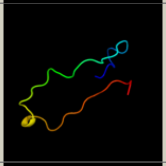
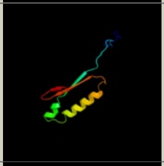
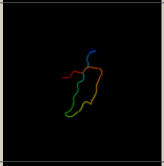
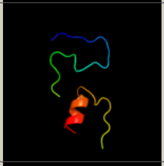
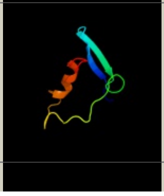
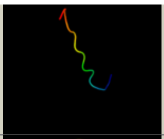
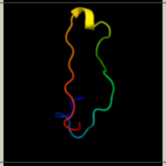
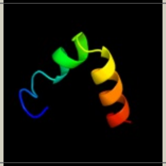
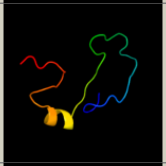
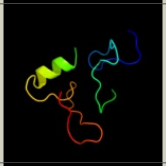
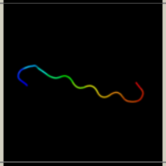
Email	l.a.kelley@imperial.ac.uk
Description	P39374
Date	Thu Jan 5 12:00:06 GMT 2012
Unique Job ID	7a9b0fecc10b9122

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2atra1	Alignment		38.9	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
2	c3s6fA_	Alignment		28.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical acetyltransferase; **PDBTitle:** crystal structure of a hypotetical acetyltransferase (dr_1678) from2 deinococcus radiodurans at 1.19 a resolution
3	d2odgc1	Alignment		24.2	33	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
4	d1yf9a1	Alignment		22.1	11	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
5	d1yx0a1	Alignment		19.5	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
6	c2xr4A_	Alignment		18.2	46	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** c-terminal domain of bc2l-c lectin from burkholderia cenocepacia
7	d2choa2	Alignment		17.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
8	c1m2oA_	Alignment		16.7	21	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
9	d1j58a_	Alignment		15.5	34	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
10	c3ijrF_	Alignment		14.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
11	d1fjra_	Alignment		14.6	19	**Fold:**Methuselah ectodomain **Superfamily:**Methuselah ectodomain **Family:**Methuselah ectodomain

12	c2vnvC_	Alignment		14.3	31	**PDB header:**sugar-binding protein **Chain:** C: **PDB Molecule:**bcla; **PDBTitle:** crystal structure of bcla lectin from burkholderia2 cenocepacia in complex with alpha-methyl-mannoside at 1.73 angstrom resolution
13	d2cbia2	Alignment		14.2	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
14	c2jvwA_	Alignment		13.6	52	**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
15	d1y9wa1	Alignment		13.1	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
16	d1x87a_	Alignment		13.0	29	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
17	d2cs3a1	Alignment		12.4	29	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
18	d1c4zd_	Alignment		11.5	15	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
19	c2boiA_	Alignment		11.3	15	**PDB header:**lectin **Chain:** A: **PDB Molecule:**cv-iil lectin; **PDBTitle:** 1.1a structure of chromobacterium violaceum lectin cv2l in2 complex with alpha-methyl-fucoside
20	d2chha1	Alignment		10.8	15	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
21	c3gemC_	Alignment	not modelled	10.6	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of short-chain dehydrogenase from pseudomonas2 syringae
22	d2nvuc1	Alignment	not modelled	10.4	11	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
23	d1uzva_	Alignment	not modelled	10.4	0	**Fold:**Calcium-mediated lectin **Superfamily:**Calcium-mediated lectin **Family:**Calcium-mediated lectin
24	c2xlfA_	Alignment	not modelled	10.2	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**sll1785 protein; **PDBTitle:** structure and metal-loading of a soluble periplasm cupro-protein:2 apo-cuca-closed (semet)
25	c3rl0j_	Alignment	not modelled	9.6	50	**PDB header:**membrane protein/exocytosis **Chain:** J: **PDB Molecule:**syntaxin-1a; **PDBTitle:** truncated snare complex with complexin (p1)
26	d1k2wa_	Alignment	not modelled	9.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
27	c2xsbA_	Alignment	not modelled	9.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** ogoga pugnac complex
28	c3gzaB_	Alignment	not modelled	9.0	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
29	d1xeba_	Alignment	not modelled	8.9	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat)

						Family:N-acetyl transferase, NAT
30	c2vxkA_	Alignment	not modelled	8.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate acetyltransferase; **PDBTitle:** structural comparison between aspergillus fumigatus and2 human gna1
31	d1hywa_	Alignment	not modelled	7.8	33	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
32	c2du7C_	Alignment	not modelled	7.6	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
33	d1su3a1	Alignment	not modelled	7.3	56	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
34	c2cbjA_	Alignment	not modelled	7.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase; **PDBTitle:** structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnacase in3 complex with pugnac
35	c3o2uB_	Alignment	not modelled	6.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nedd8-conjugating enzyme ubc12; **PDBTitle:** s. cerevisiae ubc12
36	c3topA_	Alignment	not modelled	6.6	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
37	c2qj8B_	Alignment	not modelled	6.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
38	d1ed7a_	Alignment	not modelled	6.5	42	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
39	c3pvlA_	Alignment	not modelled	6.4	28	**PDB header:**motor protein/protein transport **Chain:** A: **PDB Molecule:**myosin viia isoform 1; **PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
40	d2ae6a1	Alignment	not modelled	6.4	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
41	d1fasa_	Alignment	not modelled	6.4	50	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
42	d1o8ba1	Alignment	not modelled	6.2	45	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
43	c1kilE_	Alignment	not modelled	6.2	57	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**complexin i snare-complex binding region; **PDBTitle:** three-dimensional structure of the complexin/snare complex
44	d2jdca1	Alignment	not modelled	6.1	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	d2fiwa1	Alignment	not modelled	5.9	25	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
46	d1xs8a_	Alignment	not modelled	5.9	38	**Fold:**YggX-like **Superfamily:**YggX-like **Family:**YggX-like
47	d1d6za3	Alignment	not modelled	5.8	26	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
48	d2gx8a1	Alignment	not modelled	5.8	22	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
49	d1slma1	Alignment	not modelled	5.8	57	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
50	d1ejda_	Alignment	not modelled	5.7	16	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
51	d1yvoa1	Alignment	not modelled	5.6	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	c3nvaB_	Alignment	not modelled	5.5	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
53	d1wzva1	Alignment	not modelled	5.4	16	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
54	d2qtva3	Alignment	not modelled	5.2	17	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
55	c2pdoG_	Alignment	not modelled	5.1	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat


family2 from shigella flexneri