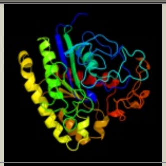
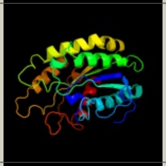
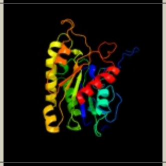
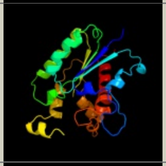
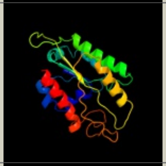
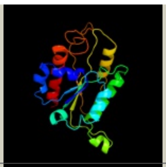
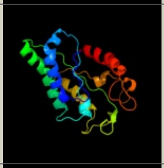
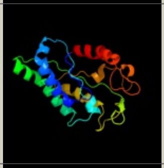
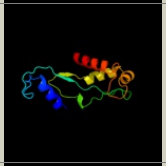
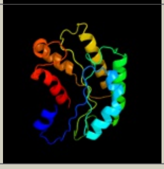
Email	l.a.kelley@imperial.ac.uk
Description	P39370
Date	Thu Jan 5 12:00:04 GMT 2012
Unique Job ID	5e84a698846cbfee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pt5A_	Alignment		100.0	97	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; **PDBTitle:** crystal structure of nans
2	d1zmba1	Alignment		100.0	22	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
3	d2apja1	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
4	d1jrla_	Alignment		97.4	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
5	c2o14A_	Alignment		97.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
6	c3hp4A_	Alignment		96.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-esterase; **PDBTitle:** crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
7	c3milA_	Alignment		95.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamyl acetate-hydrolyzing esterase; **PDBTitle:** crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae
8	d1yzfa1	Alignment		95.5	14	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
9	c3p94A_	Alignment		95.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-like lipase; **PDBTitle:** crystal structure of a gdsl-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
10	d1es9a_	Alignment		95.3	11	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
11	c2waaA_	Alignment		95.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylan esterase, putative, axe2c; **PDBTitle:** structure of a family two carbohydrate esterase from2 cellvibrio japonicus

12	d1fxwf_	Alignment		94.9	13	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
13	c3bzwA_	Alignment		94.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative lipase; **PDBTitle:** crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
14	d3bzwa1	Alignment		94.8	12	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**BT2961-like
15	c2vptA_	Alignment		94.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic enzyme; **PDBTitle:** clostridium thermocellum family 3 carbohydrate esterase
16	c2waoA_	Alignment		93.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase e; **PDBTitle:** structure of a family two carbohydrate esterase from2 clostridium thermocellum in complex with cellohexaose
17	c2q0qC_	Alignment		93.2	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aryl esterase; **PDBTitle:** structure of the native m. smegmatis aryl esterase
18	d2o14a2	Alignment		91.8	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**YxiM C-terminal domain-like
19	d1k7ca_	Alignment		86.2	12	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Rhamnogalacturonan acetylesterase
20	c3rjtA_	Alignment		82.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic protein g-d-s-l family; **PDBTitle:** crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
21	d3dc7a1	Alignment	not modelled	69.8	8	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**BT2961-like
22	c3dciB_	Alignment	not modelled	40.8	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**arylesterase; **PDBTitle:** the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58
23	d1vjga_	Alignment	not modelled	34.6	10	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Hypothetical protein alr1529
24	c3dc7B_	Alignment	not modelled	27.2	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein lp_3323; **PDBTitle:** crystal structure of the protein q88sr8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
25	c3d3qB_	Alignment	not modelled	26.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
26	d1a0da_	Alignment	not modelled	23.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
27	d1aq0a_	Alignment	not modelled	21.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
						Fold:TIM beta/alpha-barrel

28	d2cyga1	Alignment	not modelled	20.9	15	**Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
29	c2r2yA_	Alignment	not modelled	20.8	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** crystal structure of the proteasomal rpn13 pru-domain
30	c2z59A_	Alignment	not modelled	20.8	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** complex structures of mouse rpn13 (22-130aa) and ubiquitin
31	c3f55A_	Alignment	not modelled	20.2	12	**PDB header:**hydrolase, allergen **Chain:** A: **PDB Molecule:**beta-1,3-glucanase; **PDBTitle:** crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
32	d2hsja1	Alignment	not modelled	19.1	12	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
33	d1ghsa_	Alignment	not modelled	15.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
34	c3eplA_	Alignment	not modelled	15.0	18	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
35	c2y6eF_	Alignment	not modelled	13.3	6	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 4; **PDBTitle:** ubiquitin specific protease 4 is inhibited by its ubiquitin-2 like domain
36	d1a0ea_	Alignment	not modelled	12.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
37	c3exaD_	Alignment	not modelled	12.5	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
38	c3fozB_	Alignment	not modelled	11.6	18	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
39	d1bxda_	Alignment	not modelled	10.8	16	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Histidine kinase
40	d1a0ca_	Alignment	not modelled	10.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
41	c1y80A_	Alignment	not modelled	8.9	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
42	d1t1ra2	Alignment	not modelled	8.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	c2ibiA_	Alignment	not modelled	7.8	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 2; **PDBTitle:** covalent ubiquitin-usp2 complex
44	d1tdha3	Alignment	not modelled	7.2	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
45	c2yh6C_	Alignment	not modelled	6.5	6	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein 34; **PDBTitle:** structure of the n-terminal domain of bamc from e. coli
46	c3jsbA_	Alignment	not modelled	6.4	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** crystal structure of the n-terminal domain of the lymphocytic2 choriomeningitis virus l protein
47	d2jrxa1	Alignment	not modelled	6.1	27	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
48	d2oeba1	Alignment	not modelled	6.0	33	**Fold:**ATPD N-terminal domain-like **Superfamily:**AF1862-like **Family:**Cas Cmr5-like
49	d2jpqa1	Alignment	not modelled	6.0	23	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
50	c3aysA_	Alignment	not modelled	5.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
51	c3bjxB_	Alignment	not modelled	5.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
52	c3ieiD_	Alignment	not modelled	5.3	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine

53	d1wioa2	Alignment	not modelled	5.2	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
54	c2yihA_	Alignment	not modelled	5.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cel44c; **PDBTitle:** structure of a paenibacillus polymyxa xyloglucanase from gh2 family 44 with xyloglucan
55	d1onka_	Alignment	not modelled	5.1	15	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins