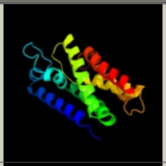
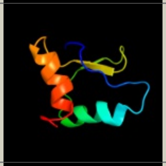
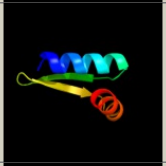
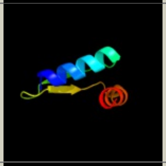
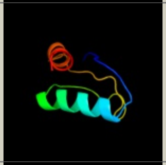
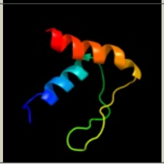
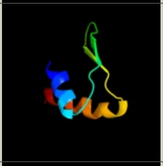
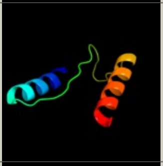
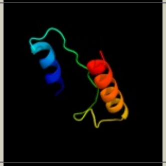
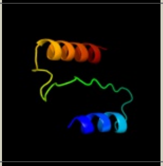
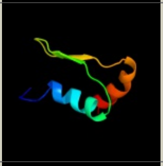
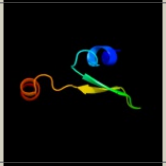
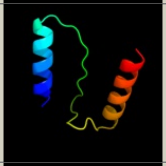
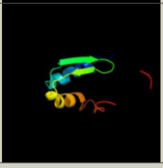
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P09391
Date	Thu Jan 5 11:02:20 GMT 2012
Unique Job ID	4edf742f2c378ddc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3b45a1	Alignment		100.0	100	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
2	d2nr9a1	Alignment		100.0	36	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like **Family:**Rhomboid-like
3	c2gqcA_	Alignment		98.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rhomboid intramembrane protease; **PDBTitle:** solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
4	d1utaa_	Alignment		93.9	19	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
5	c1x60A_	Alignment		93.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
6	c2y9jt_	Alignment		93.5	4	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
7	c1yj7A_	Alignment		92.7	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
8	d1zhva2	Alignment		60.8	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
9	c2hfvA_	Alignment		53.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
10	d1zvpa2	Alignment		51.5	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
11	d2hmfa2	Alignment		44.3	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like

12	d2hfva1	Alignment		37.7	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
13	c1zvpB_	Alignment		30.6	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein vc0802; **PDBTitle:** crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
14	d2bgra2	Alignment		29.2	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
15	c3jw8A_	Alignment		28.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
16	c3hjuB_	Alignment		27.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
17	c1zhvA_	Alignment		23.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
18	c2v1nA_	Alignment		22.7	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein kin homolog; **PDBTitle:** solution structure of the region 51-160 of human kin172 reveals a winged helix fold
19	d1orva2	Alignment		22.4	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
20	c3l76B_	Alignment		19.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
21	c2wirB_	Alignment	not modelled	19.2	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein; **PDBTitle:** hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
22	d1u4na_	Alignment	not modelled	19.2	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
23	c2dtjA_	Alignment	not modelled	18.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
24	c3qwuA_	Alignment	not modelled	17.6	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
25	d2cdqa3	Alignment	not modelled	15.8	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
26	d1sbpa_	Alignment	not modelled	15.1	27	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
27	c3d7rB_	Alignment	not modelled	14.9	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a putative esterase from staphylococcus aureus
28	d1xfda2	Alignment	not modelled	14.2	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
						PDB header:oxidoreductase

29	c1yq3C_	Alignment	not modelled	12.8	10	**Chain:** C: **PDB Molecule:**succinate dehydrogenase cytochrome b, large subunit; **PDBTitle:** avian respiratory complex ii with oxaloacetate and ubiquinone
30	c2voyG_	Alignment	not modelled	12.4	23	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
31	d2hu7a2	Alignment	not modelled	12.0	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
32	c3aikB_	Alignment	not modelled	11.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**303aa long hypothetical esterase; **PDBTitle:** crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
33	d2boaa2	Alignment	not modelled	11.1	22	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
34	c3gr0D_	Alignment	not modelled	10.7	11	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
35	d1jqga2	Alignment	not modelled	10.6	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
36	c2re1A_	Alignment	not modelled	10.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
37	c1nauA_	Alignment	not modelled	8.8	36	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
38	d1tc3c_	Alignment	not modelled	8.5	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
39	c3fakA_	Alignment	not modelled	8.2	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase/lipase; **PDBTitle:** structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
40	c2ecfA_	Alignment	not modelled	8.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
41	c3ga7A_	Alignment	not modelled	7.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
42	d1udxa3	Alignment	not modelled	7.6	20	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
43	d1o6xa_	Alignment	not modelled	7.5	21	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
44	c2k9yB_	Alignment	not modelled	7.2	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
45	c2k9yA_	Alignment	not modelled	7.2	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
46	c1bh0A_	Alignment	not modelled	6.4	33	**PDB header:**synthetic hormone **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** structure of a glucagon analog
47	c1jrjA_	Alignment	not modelled	6.2	7	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
48	d1h97a_	Alignment	not modelled	6.2	5	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
49	d2hmfa3	Alignment	not modelled	5.8	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
50	d2c0ra1	Alignment	not modelled	5.6	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
51	d1lzla_	Alignment	not modelled	5.6	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
52	c1d0rA_	Alignment	not modelled	5.4	17	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
53	c2zhoB_	Alignment	not modelled	5.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
54	c3ofeB_	Alignment	not modelled	5.3	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**ldlr chaperone boca; **PDBTitle:** structured domain of drosophila melanogaster boca p41 2 2 crystal form