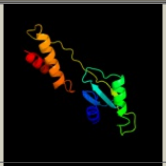
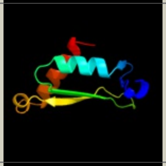
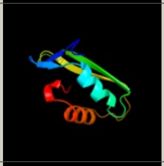
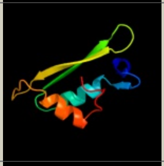
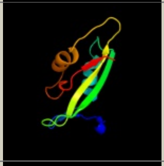
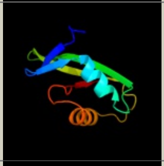
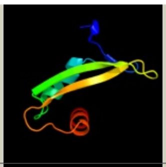
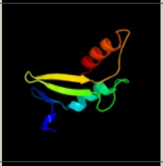
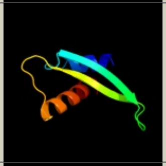
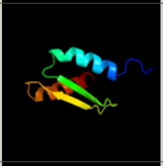
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75981
Date	Thu Jan 5 12:16:54 GMT 2012
Unique Job ID	4959ab4a0e631b96

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h3yF_	Alignment		98.1	13	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp6; **PDBTitle:** fitting of the gp6 crystal structure into 3d cryo-em2 reconstruction of bacteriophage t4 star-shaped baseplate
2	c3etcB_	Alignment		71.0	7	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
3	c3eynB_	Alignment		45.1	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acyl-coenzyme a synthetase acsm2a; **PDBTitle:** crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
4	c3iplB_	Alignment		44.2	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**2-succinylbenzoate--coa ligase; **PDBTitle:** crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
5	c3nyrA_	Alignment		39.7	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
6	c3dhvA_	Alignment		33.7	5	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
7	c2d1tA_	Alignment		32.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**luciferin 4-monooxygenase; **PDBTitle:** crystal structure of the thermostable japanese firefly2 luciferase red-color emission s286n mutant complexed with3 high-energy intermediate analogue
8	d1amua_	Alignment		32.0	8	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
9	d1lcia_	Alignment		25.8	9	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
10	c1amuB_	Alignment		25.6	8	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
11	c3e7wA_	Alignment		23.2	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains

12	d1mdba_	Alignment		23.2	7	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
13	c3gqwB_	Alignment		21.4	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fatty acid amp ligase; **PDBTitle:** crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
14	d1u9la_	Alignment		20.9	23	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**NusA extra C-terminal domains
15	d1pg4a_	Alignment		18.8	8	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
16	d1xhja_	Alignment		17.6	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
17	c3l8cA_	Alignment		12.5	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** structure of probable d-alanine--poly(phosphoribitol) ligase2 subunit-1 from streptococcus pyogenes
18	c2aj1A_	Alignment		10.0	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
19	d2qifa1	Alignment		9.8	3	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	c2l3mA_	Alignment		8.9	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
21	c3ni2A_	Alignment	not modelled	8.8	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**4-coumarate:coa ligase; **PDBTitle:** crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
22	d1veha_	Alignment	not modelled	8.6	12	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
23	d1p6ta2	Alignment	not modelled	7.3	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	c3qovD_	Alignment	not modelled	7.2	9	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
25	d1osda_	Alignment	not modelled	7.0	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c2y27B_	Alignment	not modelled	7.0	6	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
27	d1sb6a_	Alignment	not modelled	7.0	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
28	c1y96D_	Alignment	not modelled	6.8	9	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**gem-associated protein 7; **PDBTitle:** crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex

29	d1ry2a_	Alignment	not modelled	6.7	14	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
30	c3l48B_	Alignment	not modelled	6.6	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** crystal structure of the c-terminal domain of the papc usher
31	c2k2pA_	Alignment	not modelled	6.5	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
32	c2kt2A_	Alignment	not modelled	6.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
33	c2ofhX_	Alignment	not modelled	6.1	6	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
34	c2v7bB_	Alignment	not modelled	6.1	7	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
35	d1mnta_	Alignment	not modelled	6.1	6	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
36	c1yjrA_	Alignment	not modelled	5.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
37	c3dxsX_	Alignment	not modelled	5.6	10	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
38	d1cpza_	Alignment	not modelled	5.3	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c2kkhA_	Alignment	not modelled	5.2	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
40	c2ga7A_	Alignment	not modelled	5.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
41	c3laxA_	Alignment	not modelled	5.2	3	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
42	c3qu3A_	Alignment	not modelled	5.1	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**interferon regulatory factor 7; **PDBTitle:** crystal structure of irf-7 dbd apo form
43	c2uwjE_	Alignment	not modelled	5.0	12	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**type iii export protein psce; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
44	d1q8la_	Alignment	not modelled	5.0	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain