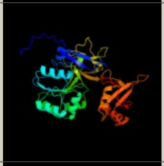
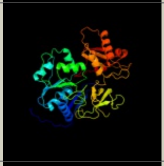
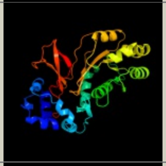
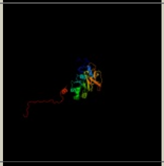
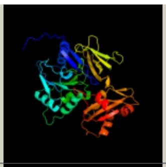
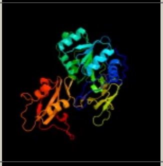
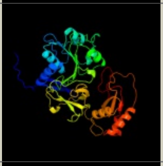
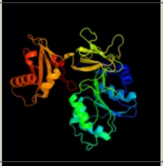
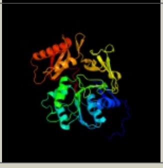
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76085
Date	Thu Jan 5 12:18:37 GMT 2012
Unique Job ID	73b621d8230540d1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y4oA_	Alignment		100.0	67	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak2 in complex with phenylacetyl adenylate
2	c2y27B_	Alignment		100.0	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylacetate-coenzyme a ligase; **PDBTitle:** crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
3	c3qovD_	Alignment		100.0	41	**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
4	d1pg4a_	Alignment		100.0	20	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
5	c2vsqA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**surfactin synthetase subunit 3; **PDBTitle:** structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
6	d1ry2a_	Alignment		100.0	19	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
7	c3hguB_	Alignment		100.0	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ehpf; **PDBTitle:** structure of phenazine antibiotic biosynthesis protein
8	c3tsyA_	Alignment		100.0	17	**PDB header:**ligase, transferase **Chain:** A: **PDB Molecule:**fusion protein 4-coumarate--coa ligase 1, resveratrol **PDBTitle:** 4-coumaroyl-coa ligase::stilbene synthase fusion protein
9	d3cw9a1	Alignment		100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
10	c3e7wA_	Alignment		100.0	12	**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
11	c3gqwB_	Alignment		100.0	18	**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

12	d1mdba_	Alignment		100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
13	c3etcB_	Alignment		100.0	16	**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
14	c3ni2A_	Alignment		100.0	17	**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
15	c3kxwA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**saframycin mx1 synthetase b; **PDBTitle:** the crystal structure of fatty acid amp ligase from legionella2 pneumophila
16	c3iteB_	Alignment		100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
17	c3eynB_	Alignment		100.0	15	**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
18	c3nyrA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**malonyl-coa ligase; **PDBTitle:** malonyl-coa ligase ternary product complex with malonyl-coa and amp2 bound
19	c2d1tA_	Alignment		100.0	17	**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
20	c2v7bB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**benzoate-coenzyme a ligase; **PDBTitle:** crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
21	c3iplB_	Alignment	not modelled	100.0	19	**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
22	d1v25a_	Alignment	not modelled	100.0	18	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
23	c3g7sA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
24	c3dhvA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-poly(phosphoribitol) ligase; **PDBTitle:** crystal structure of dlta protein in complex with d-alanine2 adenylate
25	d1lcia_	Alignment	not modelled	100.0	13	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
26	c1amuB_	Alignment	not modelled	100.0	15	**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
27	d1amua_	Alignment	not modelled	100.0	16	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
28	c3l8cA_	Alignment	not modelled	100.0	17	**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
29	c3o82B_	Alignment	not modelled	99.9	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
30	c3ivrA_	Alignment	not modelled	99.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
31	c3e53A_	Alignment	not modelled	99.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
32	c3o82A_	Alignment	not modelled	99.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
33	c3laxA_	Alignment	not modelled	99.6	28	**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
34	c2wh7A_	Alignment	not modelled	34.7	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-phage associated; **PDBTitle:** the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
35	d1whua_	Alignment	not modelled	34.0	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 **Family:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
36	c2i2xD_	Alignment	not modelled	29.9	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
37	d3bula2	Alignment	not modelled	29.2	11	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
38	d1hska2	Alignment	not modelled	29.1	18	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
39	d1pk1c1	Alignment	not modelled	27.0	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
40	d1wwva1	Alignment	not modelled	23.6	15	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
41	c2c3fA_	Alignment	not modelled	19.1	44	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hyaluronidase, phage associated; **PDBTitle:** the structure of a group a streptococcal phage-encoded2 tail-fibre showing hyaluronan lyase activity.
42	d2c3fa1	Alignment	not modelled	19.1	44	**Fold:**Triple-stranded beta-helix **Superfamily:**Phage fibre proteins **Family:**HylP-like
43	c1bmtB_	Alignment	not modelled	16.1	13	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
44	d1dpta_	Alignment	not modelled	15.1	6	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
45	c1pk1A_	Alignment	not modelled	14.5	28	**PDB header:**transcription repression **Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein; **PDBTitle:** hetero sam domain structure of ph and scm.
46	c2ormA_	Alignment	not modelled	14.4	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase hp0924; **PDBTitle:** crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
47	d2o70a1	Alignment	not modelled	13.8	13	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
48	c3ry0A_	Alignment	not modelled	13.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
49	d1bjpa_	Alignment	not modelled	13.3	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
50	c3ezxA_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
51	d1otfa_	Alignment	not modelled	12.5	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
52	c3kk1B_	Alignment	not modelled	11.6	12	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**reverse transcriptase p51 subunit; **PDBTitle:** hiv-1 reverse transcriptase-dna complex with nuceotide inhibitor gs-2 9148-diphosphate bound in nucleotide site
53	c3ebrA_	Alignment	not modelled	11.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein

						(reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
54	c1hskA_	Alignment	not modelled	11.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
55	c3abfB_	Alignment	not modelled	11.1	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
56	c2op8A_	Alignment	not modelled	11.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
57	c2x4kB_	Alignment	not modelled	10.5	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
58	d1kw4a_	Alignment	not modelled	10.2	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
59	d1iwga3	Alignment	not modelled	10.0	8	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
60	d1h80a_	Alignment	not modelled	10.0	31	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**iota-carrageenase
61	d2zd1b1	Alignment	not modelled	9.3	12	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
62	c1rthA_	Alignment	not modelled	8.6	12	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**hiv-1 reverse transcriptase; **PDBTitle:** high resolution structures of hiv-1 rt from four rt-2 inhibitor complexes
63	d1ucra_	Alignment	not modelled	8.3	57	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Dissimilatory sulfite reductase DsvD
64	d2qfia1	Alignment	not modelled	8.3	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
65	c1y80A_	Alignment	not modelled	8.1	17	**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
66	c1x4rA_	Alignment	not modelled	7.9	71	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**parp14 protein; **PDBTitle:** solution structure of wwe domain in parp14 protein
67	c3mb2G_	Alignment	not modelled	7.7	12	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
68	c2pmzV_	Alignment	not modelled	7.6	22	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
69	d2icwg1	Alignment	not modelled	7.5	31	**Fold:**Superantigen MAM **Superfamily:**Superantigen MAM **Family:**Superantigen MAM
70	c2do9A_	Alignment	not modelled	6.6	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nacht-, lrr- and pyd-containing protein 10; **PDBTitle:** solution structure of the pyrin/paad-dapin domain in mouse2 nalp10 (nacht, leucine rich repeat and pyd containing 10)
71	c2pjkA_	Alignment	not modelled	6.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
72	c2bcmB_	Alignment	not modelled	6.2	43	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**f1845 fimbrial protein; **PDBTitle:** daae adhesin
73	c2epbA_	Alignment	not modelled	6.2	63	**PDB header:**transcription **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 6; **PDBTitle:** solution structure of chromo domain 2 in chromodomain-2 helicase-dna-binding protein 6
74	d1uhra_	Alignment	not modelled	6.2	36	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
75	c2qfiB_	Alignment	not modelled	6.2	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ferrous-iron efflux pump fief; **PDBTitle:** structure of the zinc transporter yiip
76	c3idwA_	Alignment	not modelled	6.1	18	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
77	d2edua1	Alignment	not modelled	6.1	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
						Fold: Tautomerase/MIF

78	d1mwwa_	Alignment	not modelled	6.0	11	**Superfamily:**Tautomerase/MIF **Family:**Hypothetical protein HI1388.1
79	c2zztA_	Alignment	not modelled	6.0	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
80	c1pk1B_	Alignment	not modelled	6.0	15	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
81	d2f3na1	Alignment	not modelled	6.0	12	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
82	c1k98A_	Alignment	not modelled	5.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
83	d1gyxa_	Alignment	not modelled	5.9	6	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
84	c2fvnA_	Alignment	not modelled	5.8	36	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**protein afad; **PDBTitle:** the fibrillar tip complex of the afa/dr adhesins from2 pathogen e. coli displays synergistic binding to 5 1 and v3 3 integrins
85	c3bs7A_	Alignment	not modelled	5.6	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
86	d2aala1	Alignment	not modelled	5.6	26	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
87	c3bs5A_	Alignment	not modelled	5.6	15	**PDB header:**signaling protein/membrane protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex
88	c2dn5A_	Alignment	not modelled	5.4	45	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
89	c3cmqA_	Alignment	not modelled	5.1	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine trna2 synthetase
90	d1f06a2	Alignment	not modelled	5.1	9	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
91	d7reqa2	Alignment	not modelled	5.0	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain