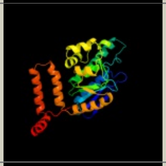
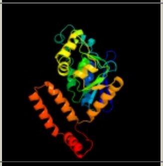
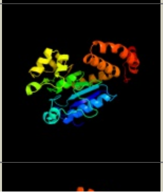
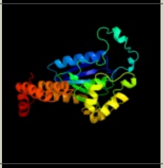
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77467
Date	Thu Jan 5 12:29:31 GMT 2012
Unique Job ID	725b3cc6406f82c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g64A_	Alignment		100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
2	c2qq3F_	Alignment		100.0	35	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase subunit i; **PDBTitle:** crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
3	c2ej5B_	Alignment		100.0	44	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase subunit ii; **PDBTitle:** crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
4	c3trrA_	Alignment		100.0	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
5	c3h81A_	Alignment		100.0	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa8; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
6	c3hrxD_	Alignment		100.0	45	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
7	d1nzya_	Alignment		100.0	27	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
8	c3moyA_	Alignment		100.0	34	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
9	c2hw5F_	Alignment		100.0	31	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
10	c3p5mB_	Alignment		100.0	37	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
11	c3swxB_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
						

12	c3kqfC_	Alignment		100.0	33	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.
13	c2vx2D_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase domain-containing protein 3; **PDBTitle:** crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
14	c3rsiA_	Alignment		100.0	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
15	c3r0oA_	Alignment		100.0	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carnitinyl-coa dehydratase; **PDBTitle:** crystal structure of carnitinyl-coa hydratase from mycobacterium avium
16	c3peaD_	Alignment		100.0	30	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'
17	c3qxzA_	Alignment		100.0	30	**PDB header:**lyase,isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
18	c3i47A_	Alignment		100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl coa hydratase/isomerase (crotonase); **PDBTitle:** crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
19	d2fw2a1	Alignment		100.0	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
20	c2ppyE_	Alignment		100.0	27	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
21	d1mj3a_	Alignment	not modelled	100.0	32	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
22	d1hzda_	Alignment	not modelled	100.0	30	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
23	c3mybA_	Alignment	not modelled	100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase mycobacterium smegmatis
24	c3qxiA_	Alignment	not modelled	100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa1; **PDBTitle:** crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
25	d1uiya_	Alignment	not modelled	100.0	28	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
26	c3hinA_	Alignment	not modelled	100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 3-hydroxybutyryl-coa dehydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
27	d1dcia_	Alignment	not modelled	100.0	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
28	c2iexA_	Alignment	not modelled	100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
29	c3bptA_	Alignment	not modelled	100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyryl-coa hydrolase;

29	c3bptA_	Alignment	not modelled	100.0	29	**PDBTitle:** crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
30	c3sllC_	Alignment	not modelled	100.0	29	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
31	d1wz8a1	Alignment	not modelled	100.0	28	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
32	d1ef8a_	Alignment	not modelled	100.0	25	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
33	d1q52a_	Alignment	not modelled	100.0	28	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
34	c3oc7A_	Alignment	not modelled	100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of an enoyl-coa hydratase from mycobacterium avium
35	c3ju1A_	Alignment	not modelled	100.0	23	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase/isomerase family protein
36	c3lkeA_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
37	d1wdka4	Alignment	not modelled	100.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
38	c3he2C_	Alignment	not modelled	100.0	31	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase echa6; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
39	d1xx4a_	Alignment	not modelled	100.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
40	c3njbA_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
41	c3rrvC_	Alignment	not modelled	100.0	29	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
42	c3gkbA_	Alignment	not modelled	100.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
43	c2d3tB_	Alignment	not modelled	100.0	22	**PDB header:**lyase, oxidoreductase/transferase **Chain:** B: **PDB Molecule:**fatty oxidation complex alpha subunit; **PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
44	c2fbmB_	Alignment	not modelled	100.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**y chromosome chromodomain protein 1, telomeric isoform b; **PDBTitle:** acetyltransferase domain of cdy1
45	c2x58B_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
46	c3h0uB_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
47	c2q35A_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curf; **PDBTitle:** crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
48	d2f6qa1	Alignment	not modelled	100.0	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
49	c3q1tB_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium avium
50	c2f6qA_	Alignment	not modelled	100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peroxisomal 3,2-trans-enoyl-coa isomerase; **PDBTitle:** the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
51	c2wtbA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2); **PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2
52	c3hp0B_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide biosynthesis enoyl-coa **PDBTitle:** crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
53	d1pjha_	Alignment	not modelled	100.0	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
54	d1sg4a1	Alignment	not modelled	100.0	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
						PDB header:hydrolase

55	c3isaA_	Alignment	not modelled	100.0	20	**Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
56	c3qkaB_	Alignment	not modelled	100.0	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase, echa5; **PDBTitle:** crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
57	c2j5iF_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** F: **PDB Molecule:**p-hydroxycinnamoyl coa hydratase/lyase; **PDBTitle:** crystal structure of hydroxycinnamoyl-coa hydratase-lyase
58	c3l3sF_	Alignment	not modelled	100.0	27	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi
59	c3r6hA_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa3; **PDBTitle:** crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
60	c3p85A_	Alignment	not modelled	100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure enoyl-coa hydratase from mycobacterium avium
61	c3omeE_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
62	c3ot6A_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae
63	d2a7ka1	Alignment	not modelled	100.0	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
64	c3fduF_	Alignment	not modelled	100.0	34	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
65	c3laoA_	Alignment	not modelled	100.0	24	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
66	c2pg8C_	Alignment	not modelled	100.0	25	**PDB header:**ligand binding protein **Chain:** C: **PDB Molecule:**dpgc; **PDBTitle:** crystal structure of r254k mutanat of dpgc with bound substrate analog
67	c2w3pB_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
68	c3h02F_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
69	d1szoa_	Alignment	not modelled	100.0	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
70	c3m6nA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rpff protein; **PDBTitle:** crystal structure of rpff
71	c1rjnC_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** C: **PDB Molecule:**menb; **PDBTitle:** the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
72	d1rjma_	Alignment	not modelled	100.0	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
73	c2j5gL_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**alr4455 protein; **PDBTitle:** the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
74	c3qreA_	Alignment	not modelled	100.0	37	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa12_1; **PDBTitle:** crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum
75	c3qmjA_	Alignment	not modelled	100.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa8_6; **PDBTitle:** crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
76	c2f9iC_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
77	c3bezC_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease 4; **PDBTitle:** crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
78	d2cbya1	Alignment	not modelled	99.3	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
79	d2f9ya1	Alignment	not modelled	99.2	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
80	c2deoA_	Alignment	not modelled	99.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**441aa long hypothetical nfed protein; **PDBTitle:** 1510-n membrane protease specific for a stomatin

						homolog from2 pyrococcus horikoshii
81	c3kthD_	Alignment	not modelled	99.2	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of clpp from bacillus subtilis in orthorombic crystal form
82	c1tg6G_	Alignment	not modelled	99.1	12	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**putative atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
83	c2cbyG_	Alignment	not modelled	99.1	20	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease proteolytic subunit 1; **PDBTitle:** crystal structure of the atp-dependent clp protease2 proteolytic subunit 1 (clpp1) from mycobacterium3 tuberculosis
84	c3p2lD_	Alignment	not modelled	99.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis
85	d1yg6a1	Alignment	not modelled	99.0	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
86	d1tg6a1	Alignment	not modelled	99.0	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
87	d2f6ia1	Alignment	not modelled	99.0	12	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
88	c3q7hM_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii
89	c2f6iG_	Alignment	not modelled	98.8	12	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease, putative; **PDBTitle:** crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
90	d1y7oa1	Alignment	not modelled	98.8	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
91	c1y7oE_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** the structure of streptococcus pneumoniae a153p clpp
92	d1on3a1	Alignment	not modelled	98.7	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
93	c2f9yB_	Alignment	not modelled	98.5	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
94	d2f9yb1	Alignment	not modelled	98.5	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
95	d1xnya2	Alignment	not modelled	98.4	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
96	c2f9iD_	Alignment	not modelled	98.4	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
97	d2a7sa2	Alignment	not modelled	98.4	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
98	c2a7sD_	Alignment	not modelled	98.3	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**probable propionyl-coa carboxylase beta chain 5; **PDBTitle:** crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
99	d1vrga2	Alignment	not modelled	98.3	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
100	c1x0uB_	Alignment	not modelled	98.3	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical methylmalonyl-coa decarboxylase alpha subunit; **PDBTitle:** crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
101	d1on3a2	Alignment	not modelled	98.2	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
102	d2a7sa1	Alignment	not modelled	98.2	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
103	c1vrgE_	Alignment	not modelled	98.2	16	**PDB header:**ligase **Chain:** E: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
104	d1pixa2	Alignment	not modelled	98.2	14	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
						PDB header:transferase **Chain:** E: **PDB Molecule:**methylmalonyl-coa carboxyltransferase

105	c1on3E_	Alignment	not modelled	98.2	20	12s **PDBTitle:** transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
106	c1xnwD_	Alignment	not modelled	98.2	17	**PDB header:**ligase **Chain:** D: **PDB Molecule:**propionyl-coa carboxylase complex b subunit; **PDBTitle:** acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
107	c3n6rF_	Alignment	not modelled	98.1	14	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
108	d1vrga1	Alignment	not modelled	97.9	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
109	d1xnya1	Alignment	not modelled	97.8	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
110	c3u9rB_	Alignment	not modelled	97.7	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**methylcrotonyl-coa carboxylase, beta-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
111	c1pixB_	Alignment	not modelled	97.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutaconyl-coa decarboxylase a subunit; **PDBTitle:** crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
112	c3glmD_	Alignment	not modelled	97.4	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**glutaconyl-coa decarboxylase subunit a; **PDBTitle:** glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
113	d1pixa3	Alignment	not modelled	97.4	12	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
114	c1od4C_	Alignment	not modelled	96.3	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain
115	c3ff6D_	Alignment	not modelled	96.0	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
116	c3h0jA_	Alignment	not modelled	95.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
117	d1uyra1	Alignment	not modelled	95.8	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
118	c1uytC_	Alignment	not modelled	93.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain
119	c2x24B_	Alignment	not modelled	83.7	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
120	d1uyra2	Alignment	not modelled	78.9	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain