























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qq3F_</a>	 Alignment		100.0	41	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase subunit i; <b>PDBTitle:</b> crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
2	<a href="#">c3h81A_</a>	 Alignment		100.0	44	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa8; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
3	<a href="#">c3moyA_</a>	 Alignment		100.0	45	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
4	<a href="#">c3g64A_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
5	<a href="#">c3trrA_</a>	 Alignment		100.0	37	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
6	<a href="#">c3hrxD_</a>	 Alignment		100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> probable enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of phenylacetic acid degradation protein paag
7	<a href="#">c2hw5F_</a>	 Alignment		100.0	44	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
8	<a href="#">c3p5mB_</a>	 Alignment		100.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
9	<a href="#">c2ej5B_</a>	 Alignment		100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase subunit ii; <b>PDBTitle:</b> crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
10	<a href="#">c3qxzA_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
11	<a href="#">c3r0oA_</a>	 Alignment		100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitiny-coa dehydratase; <b>PDBTitle:</b> crystal structure of carnitiny-coa hydratase from mycobacterium avium



29	<a href="#">c3hinA_</a>	Alignment	not modelled	100.0	32	<b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-hydroxybutyryl-coa dehydratase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from2 rhodospseudomonas palustris cga009
30	<a href="#">c3bptA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase; <b>PDBTitle:</b> crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
31	<a href="#">d1ef8a_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
32	<a href="#">d1wz8a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
33	<a href="#">d1q52a_</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
34	<a href="#">c3ju1A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase family protein
35	<a href="#">c3he2C_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase echa6; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
36	<a href="#">c3oc7A_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from mycobacterium avium
37	<a href="#">d1xx4a_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
38	<a href="#">d1wdka4</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
39	<a href="#">c3lkeA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus2 halodurans
40	<a href="#">c3gkbA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
41	<a href="#">c3njba_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
42	<a href="#">c3rrvC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
43	<a href="#">c2d3tB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
44	<a href="#">c2x58B_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa
45	<a href="#">c3h0uB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
46	<a href="#">c2fbmB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> y chromosome chromodomain protein 1, telomeric isoform b; <b>PDBTitle:</b> acetyltransferase domain of cdy1
47	<a href="#">d2f6qa1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
48	<a href="#">c2q35A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> curf; <b>PDBTitle:</b> crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from l yngbya majuscula
49	<a href="#">c3q1tB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium avium
50	<a href="#">c2f6qA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal 3,2-trans-enoyl-coa isomerase; <b>PDBTitle:</b> the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
51	<a href="#">c2wtbA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
52	<a href="#">c3qkaB_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase, echa5; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
53	<a href="#">c3hp0B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide biosynthesis enoyl-coa <b>PDBTitle:</b> crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
54	<a href="#">d1sg4a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase

						<b>Family:</b> Crotonase-like
55	<a href="#">c3isaA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
56	<a href="#">c3l3sF_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi
57	<a href="#">c3r6hA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa3; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
58	<a href="#">c3omeE_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
59	<a href="#">d1pjha_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
60	<a href="#">c3p85A_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure enoyl-coa hydratase from mycobacterium avium
61	<a href="#">c2j5iF_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> p-hydroxycinnamoyl coa hydratase/lyase; <b>PDBTitle:</b> crystal structure of hydroxycinnamoyl-coa hydratase-lyase
62	<a href="#">d2a7ka1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
63	<a href="#">c3laoA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
64	<a href="#">c3fduF_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
65	<a href="#">c3ot6A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae
66	<a href="#">c2pg8C_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ligand binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dpgc; <b>PDBTitle:</b> crystal structure of r254k mutanat of dpgc with bound substrate analog
67	<a href="#">c3h02F_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
68	<a href="#">d1szoa_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
69	<a href="#">c2w3pB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa-dihydrodiol lyase; <b>PDBTitle:</b> boxc crystal structure
70	<a href="#">c1rjnC_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> menb; <b>PDBTitle:</b> the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
71	<a href="#">d1rjma_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
72	<a href="#">c3m6nA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff
73	<a href="#">c3qmjA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa8_6; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
74	<a href="#">c2j5gL_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> alr4455 protein; <b>PDBTitle:</b> the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
75	<a href="#">c3greA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa12_1; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum
76	<a href="#">c3bezC_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease 4; <b>PDBTitle:</b> crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
77	<a href="#">c2f9iC_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
78	<a href="#">d2cbya1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
79	<a href="#">d2f9ya1</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
						<b>PDB header:</b> hydrolase

80	<a href="#">c3kthD_</a>	Alignment	not modelled	99.3	16	<b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> structure of clpp from bacillus subtilis in orthorhombic crystal form
81	<a href="#">c2deoA_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 441aa long hypothetical nfd protein; <b>PDBTitle:</b> 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
82	<a href="#">c1tg6G_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> putative atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> crystallography and mutagenesis point to an essential role for the n-2 terminus of human mitochondrial clpp
83	<a href="#">c2cbyG_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit 1; <b>PDBTitle:</b> crystal structure of the atp-dependent clp protease2 proteolytic subunit 1 (clpp1) from mycobacterium3 tuberculosis
84	<a href="#">d1yg6a1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
85	<a href="#">c3p21D_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis
86	<a href="#">d1tg6a1</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
87	<a href="#">c3q7hM_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> structure of the clpp subunit of the atp-dependent clp protease from2 coxiella burnetii
88	<a href="#">d2f6ia1</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
89	<a href="#">c2f6iG_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp-dependent clp protease, putative; <b>PDBTitle:</b> crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
90	<a href="#">d1y7oa1</a>	Alignment	not modelled	99.0	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
91	<a href="#">c1y7oE_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> the structure of streptococcus pneumoniae a153p clpp
92	<a href="#">d1on3a1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
93	<a href="#">d2f9yb1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
94	<a href="#">c2f9yB_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
95	<a href="#">d1pixa2</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
96	<a href="#">d2a7sa1</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
97	<a href="#">c2f9iD_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
98	<a href="#">d1vrga2</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
99	<a href="#">d1xnya2</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
100	<a href="#">c3glmD_</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> glutaconyl-coa decarboxylase subunit a; <b>PDBTitle:</b> glutaconyl-coa decarboxylase a subunit from clostridium2 symbiosum co-crystallized with crotonyl-coa
101	<a href="#">c1x0uB_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical methylmalonyl-coa decarboxylase alpha subunit; <b>PDBTitle:</b> crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
102	<a href="#">d2a7sa2</a>	Alignment	not modelled	98.4	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
103	<a href="#">c1on3E_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> methylmalonyl-coa carboxyltransferase 12s <b>PDBTitle:</b> transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
						<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, beta-



104	<a href="#">c3u9rB_</a>	Alignment	not modelled	98.4	18	subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
105	<a href="#">d1on3a2</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
106	<a href="#">d1xnya1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
107	<a href="#">c2a7sD_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> probable propionyl-coa carboxylase beta chain 5; <b>PDBTitle:</b> crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
108	<a href="#">d1vrqa1</a>	Alignment	not modelled	98.3	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
109	<a href="#">c1pixB_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaconyl-coa decarboxylase a subunit; <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
110	<a href="#">c1vrgE_</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> propionyl-coa carboxylase, beta subunit; <b>PDBTitle:</b> crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
111	<a href="#">c3n6rF_</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> propionyl-coa carboxylase, beta subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
112	<a href="#">c1xnwD_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> propionyl-coa carboxylase complex b subunit; <b>PDBTitle:</b> acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
113	<a href="#">c1od4C_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
114	<a href="#">d1pixa3</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
115	<a href="#">c3ff6D_</a>	Alignment	not modelled	97.2	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> human acc2 ct domain with cp-640186
116	<a href="#">c1uytC_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
117	<a href="#">d1uyra1</a>	Alignment	not modelled	97.1	12	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
118	<a href="#">c2x24B_</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> bovine acc2 ct domain in complex with inhibitor
119	<a href="#">c3h0jA_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
120	<a href="#">d1zq1a2</a>	Alignment	not modelled	74.5	21	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase