







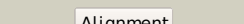

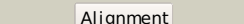

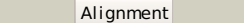

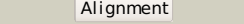

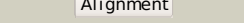

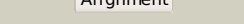

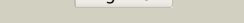



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r0oA_	 Alignment		100.0	40	PDB header: lyase Chain: A: PDB Molecule: carnitiny-coa dehydratase; PDBTitle: crystal structure of carnitiny-coa hydratase from mycobacterium avium
2	c3g64A_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
3	c3trrA_	 Alignment		100.0	39	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
4	c3hrxD_	 Alignment		100.0	33	PDB header: lyase Chain: D: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of phenylacetic acid degradation protein paag
5	c2qq3F_	 Alignment		100.0	38	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
6	c2ppyE_	 Alignment		100.0	35	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
7	c3h81A_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa8; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
8	c2ej5B_	 Alignment		100.0	32	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
9	c3moyA_	 Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
10	c3qxzA_	 Alignment		100.0	31	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
11	c3kqfC_	 Alignment		100.0	34	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.

12	dlhzda_	Alignment		100.0	31	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
13	c3p5mB_	Alignment		100.0	30	PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
14	dlnzya_	Alignment		100.0	26	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
15	c3peaD_	Alignment		100.0	31	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'
16	c2vx2D_	Alignment		100.0	30	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)
17	c3rsiA_	Alignment		100.0	35	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
18	c2hw5F_	Alignment		100.0	32	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
19	c3bptA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: 3-hydroxyisobutyryl-coa hydrolase; PDBTitle: crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
20	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
21	c3i47A_	Alignment	not modelled	100.0	27	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
22	c2iexA_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: A: PDB Molecule: dihydroxynapthoic acid synthetase; PDBTitle: crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
23	dl1ef8a_	Alignment	not modelled	100.0	29	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
24	c3hinA_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: A: PDB Molecule: putative 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from2 rhodospseudomonas palustris cga009
25	c3qxiA_	Alignment	not modelled	100.0	40	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa1; PDBTitle: crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
26	dlmj3a_	Alignment	not modelled	100.0	34	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
27	c3mybA_	Alignment	not modelled	100.0	29	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase mycobacterium smegmatis
						Fold: ClpP/crotonase

28	dlwz8a1	Alignment	not modelled	100.0	24	Superfamily: ClpP/crotonase Family: Crotonase-like
29	c3sllC_	Alignment	not modelled	100.0	25	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
30	d2fw2a1	Alignment	not modelled	100.0	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
31	d1uiya_	Alignment	not modelled	100.0	28	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
32	c3ju1A_	Alignment	not modelled	100.0	22	PDB header: lyase, isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase family protein
33	d1dcia_	Alignment	not modelled	100.0	33	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
34	d1xx4a_	Alignment	not modelled	100.0	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
35	d1q52a_	Alignment	not modelled	100.0	25	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
36	c3gkbA_	Alignment	not modelled	100.0	24	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
37	d1wdka4	Alignment	not modelled	100.0	26	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
38	c3njbA_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium smegmatis, 2 iodide soak
39	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
40	c3oc7A_	Alignment	not modelled	100.0	27	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of an enoyl-coa hydratase from mycobacterium avium
41	c2d3tB_	Alignment	not modelled	100.0	25	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
42	c3lkeA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus2 halodurans
43	c3h0uB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
44	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
45	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
46	c3q1tB_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium avium
47	d1sg4a1	Alignment	not modelled	100.0	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
48	c2wtbA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atnfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
49	c2fbmB_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: y chromosome chromodomain protein 1, telomeric isoform b; PDBTitle: acetyltransferase domain of cdy1
50	d2f6qa1	Alignment	not modelled	100.0	25	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
51	c2f6qA_	Alignment	not modelled	100.0	25	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)
52	c2q35A_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: curf; PDBTitle: crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
53	c3hp0B_	Alignment	not modelled	100.0	18	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

54	c3isaA	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
55	d1pjha	Alignment	not modelled	100.0	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
56	c3r6hA	Alignment	not modelled	100.0	22	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase, echa3; PDBTitle: crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
57	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
58	d2a7ka1	Alignment	not modelled	100.0	25	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
59	c3qkaB	Alignment	not modelled	100.0	31	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase, echa5; PDBTitle: crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
60	c2j5iF	Alignment	not modelled	100.0	30	PDB header: lyase Chain: F: PDB Molecule: p-hydroxycinnamoyl coa hydratase/lyase; PDBTitle: crystal structure of hydroxycinnamoyl-coa hydratase-lyase
61	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
62	c2w3pB	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: benzoyl-coa-dihydrodiol lyase; PDBTitle: boxc crystal structure
63	c3laaA	Alignment	not modelled	100.0	28	PDB header: lyase, isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
64	c3omeE	Alignment	not modelled	100.0	31	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
65	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.
66	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
67	c2pg8C	Alignment	not modelled	100.0	30	PDB header: ligand binding protein Chain: C: PDB Molecule: dpgc; PDBTitle: crystal structure of r254k mutanat of dpgc with bound substrate analog
68	c3m6nA	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: rpff protein; PDBTitle: crystal structure of rpff
69	d1szoa	Alignment	not modelled	100.0	24	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
70	c3fduF	Alignment	not modelled	100.0	27	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
71	c1rjnC	Alignment	not modelled	100.0	24	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	24	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
73	c2j5gL	Alignment	not modelled	100.0	23	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	31	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	c3qmiA	Alignment	not modelled	100.0	29	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	99.5	18	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	99.5	21	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
78	d2f9ya1	Alignment	not modelled	99.2	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
79	d2cbya1	Alignment	not modelled	99.2	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase

					Family: Clp protease, ClpP subunit
80	c2deoA	Alignment	not modelled	99.2	18 PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfd protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
81	c3kthD	Alignment	not modelled	99.2	19 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	15 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	17 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	d2f6ia1	Alignment	not modelled	99.1	15 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
85	c3p2ID	Alignment	not modelled	99.1	17 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
86	d1tg6a1	Alignment	not modelled	99.0	15 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
87	d1yg6a1	Alignment	not modelled	99.0	19 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
88	c2f6iG	Alignment	not modelled	98.9	15 PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease, putative; PDBTitle: crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
89	c3q7hM	Alignment	not modelled	98.9	14 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
90	d1y7oa1	Alignment	not modelled	98.9	16 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
91	d1on3a1	Alignment	not modelled	98.8	21 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
92	d1pixa2	Alignment	not modelled	98.7	17 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
93	c2f9yB	Alignment	not modelled	98.7	13 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	98.7	13 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
95	c1y7oE	Alignment	not modelled	98.7	19 PDB header: hydrolase Chain: E: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: the structure of streptococcus pneumoniae a153p clpp
96	c2f9iD	Alignment	not modelled	98.6	11 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	d1xnya2	Alignment	not modelled	98.6	18 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
98	c1on3E	Alignment	not modelled	98.6	21 PDB header: transferase Chain: E: PDB Molecule: methylmalonyl-coa carboxyltransferase 12s PDBTitle: transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
99	d2a7sa1	Alignment	not modelled	98.5	18 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
100	d2a7sa2	Alignment	not modelled	98.5	13 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
101	d1on3a2	Alignment	not modelled	98.5	15 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
102	c2a7sD	Alignment	not modelled	98.5	13 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
103	d1vrga2	Alignment	not modelled	98.5	13 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain

104	c3n6rF_	Alignment	not modelled	98.5	18	PDB header: ligase Chain: F: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
105	c1x0uB_	Alignment	not modelled	98.5	18	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
106	c1vrgE_	Alignment	not modelled	98.4	13	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
107	c3u9rB_	Alignment	not modelled	98.4	21	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
108	c1xnwD_	Alignment	not modelled	98.3	15	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
109	d1vrga1	Alignment	not modelled	98.3	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
110	d1xnya1	Alignment	not modelled	98.2	21	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
111	c3glmD_	Alignment	not modelled	98.2	14	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
112	c1pixB_	Alignment	not modelled	98.0	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
113	d1pixa3	Alignment	not modelled	98.0	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
114	c1od4C_	Alignment	not modelled	97.8	22	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
115	c1uytC_	Alignment	not modelled	97.7	22	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
116	c3h0jA_	Alignment	not modelled	97.6	22	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	c3ff6D_	Alignment	not modelled	97.4	17	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
118	c2x24B_	Alignment	not modelled	97.4	21	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
119	d1uyra1	Alignment	not modelled	96.8	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
120	d1auza_	Alignment	not modelled	74.3	14	Fold: SpolIaa-like Superfamily: SpolIaa-like Family: Anti-sigma factor antagonist SpolIaa