

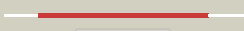





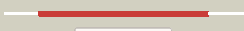















Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1on3E_	 Alignment		100.0	39	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)
2	c1xnwD_	 Alignment		100.0	43	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
3	c2a7sD_	 Alignment		100.0	43	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
4	c1x0uB_	 Alignment		100.0	40	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 sulfobolus tokodaii
5	c1vrgE_	 Alignment		100.0	40	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
6	c3n6rF_	 Alignment		100.0	42	PDB header: ligase Chain: F; PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
7	c5ingC_	 Alignment		100.0	40	PDB header: transferase Chain: C; PDB Molecule: putative carboxyl transferase; PDBTitle: a crotonyl-coa reductase-carboxylase independent pathway for assembly2 of unusual alkylmalonyl-coa polyketide synthase extender unit
8	c3u9rB_	 Alignment		100.0	32	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
9	c4q0gC_	 Alignment		100.0	31	PDB header: ligase Chain: C; PDB Molecule: probable acetyl-/propionyl-coa carboxylase (beta subunit) PDBTitle: crystal structure of beta subunit of acyl-coa carboxylase accd1 from2 mycobacterium tuberculosis
10	c5fifD_	 Alignment		100.0	28	PDB header: ligase Chain: D; PDB Molecule: carboxylase; PDBTitle: carboxyltransferase domain of a single-chain bacterial carboxylase
11	c5ikID_	 Alignment		100.0	28	PDB header: ligase Chain: D; PDB Molecule: geranyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit

12	c1pixB_	Alignment		100.0	21	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
13	c3glmD_	Alignment		100.0	20	PDB header: lyase Chain: D: PDB Molecule: glutaconyl-coa decarboxylase subunit a; PDBTitle: glutaconyl-coa decarboxylase a subunit from clostridium symbiosum co-2 crystallized with crotonyl-coa
14	c4rcnA_	Alignment		100.0	26	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
15	c4l6wB_	Alignment		100.0	100	PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
16	c4l6wA_	Alignment		100.0	100	PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
17	c2x24B_	Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
18	c4wyoB_	Alignment		100.0	23	PDB header: ligase/ligase inhibitor Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1
19	c3h0jA_	Alignment		100.0	23	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
20	c3ff6D_	Alignment		100.0	25	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
21	c1od4C_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
22	c1uyvB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain l1705i/2 v1967i mutant
23	c1uytC_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
24	c5i6fA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
25	c5i6fB_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
26	c5i6hA_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase-like protein; PDBTitle: crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase
27	c5cskB_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
28	c6g2dC_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution PDB header: ligase

29	c5cslA_	Alignment	not modelled	100.0	24	Chain: A; PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
30	d1pixa3	Alignment	not modelled	100.0	23	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
31	d1on3a2	Alignment	not modelled	100.0	41	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
32	d2a7sa2	Alignment	not modelled	100.0	45	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
33	d1vrqa2	Alignment	not modelled	100.0	42	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
34	d1xnaya2	Alignment	not modelled	100.0	43	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
35	d1on3a1	Alignment	not modelled	100.0	36	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
36	d2a7sa1	Alignment	not modelled	100.0	40	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
37	d1xnaya1	Alignment	not modelled	100.0	42	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
38	d1vrqa1	Alignment	not modelled	100.0	37	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
39	d1pixa2	Alignment	not modelled	100.0	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
40	d2f9yb1	Alignment	not modelled	100.0	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
41	c2f9yB_	Alignment	not modelled	100.0	22	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
42	c5vipB_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: B; PDB Molecule: mdcd; PDBTitle: crystal structure of pseudomonas malonate decarboxylase mdcd-mdce2 hetero-dimer
43	d1uyra2	Alignment	not modelled	100.0	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
44	d1uyra1	Alignment	not modelled	100.0	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
45	c2f9iD_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: D; PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
46	d2f9ya1	Alignment	not modelled	100.0	26	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
47	c2f9iC_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: C; PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
48	c5vj1M_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: M; PDB Molecule: mdce; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with coenzyme a
49	c3bezC_	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: C; PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
50	c4hnkl_	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: I; PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: crystal structure of an enzyme
51	c3r6hA_	Alignment	not modelled	98.7	18	PDB header: lyase Chain: A; PDB Molecule: enoyl-coa hydratase, echa3; PDBTitle: crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
52	c4iyjA_	Alignment	not modelled	98.7	15	PDB header: isomerase Chain: A; PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans dsm 12444
53	d2a7ka1	Alignment	not modelled	98.6	14	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
54	d2f6ia1	Alignment	not modelled	98.6	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
						PDB header: lyase

55	c3oc7A	Alignment	not modelled	98.5	20	Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of an enoyl-coa hydratase from mycobacterium avium
56	c4fzwD	Alignment	not modelled	98.5	15	PDB header: isomerase/lyase Chain: D: PDB Molecule: 1,2-epoxyphenylacetyl-coa isomerase; PDBTitle: crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli
57	c4lk5B	Alignment	not modelled	98.5	18	PDB header: lyase Chain: B: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10
58	c4kpkA	Alignment	not modelled	98.5	15	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a enoyl-coa hydratase from shewanella pealeana2 atcc 700345
59	c4jylE	Alignment	not modelled	98.5	16	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1
60	c3fduF	Alignment	not modelled	98.5	15	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
61	c4izbB	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa
62	c4kd6A	Alignment	not modelled	98.5	20	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m
63	c3isaA	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
64	c3rrvC	Alignment	not modelled	98.5	16	PDB header: isomerase Chain: C: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
65	c2iexA	Alignment	not modelled	98.5	15	PDB header: lyase Chain: A: PDB Molecule: dihydroxynaphthoic acid synthetase; PDBTitle: crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
66	c3njbA	Alignment	not modelled	98.5	17	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
67	c3hrxD	Alignment	not modelled	98.5	18	PDB header: lyase Chain: D: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of phenylacetic acid degradation protein paag
68	c4jqcU	Alignment	not modelled	98.5	19	PDB header: hydrolase Chain: U: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: clpp1 from listeria monocytogenes
69	d1dcia	Alignment	not modelled	98.5	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
70	c4jcsA	Alignment	not modelled	98.5	17	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34
71	c4zu2A	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: A: PDB Molecule: putative isohexenylglutaconyl-coa hydratase; PDBTitle: pseudomonas aeruginosa atue
72	c2vx2D	Alignment	not modelled	98.4	14	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)
73	c3peaD	Alignment	not modelled	98.4	13	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'
74	c3i47A	Alignment	not modelled	98.4	11	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
75	c2q35A	Alignment	not modelled	98.4	19	PDB header: lyase Chain: A: PDB Molecule: curf; PDBTitle: crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
76	d2fw2a1	Alignment	not modelled	98.4	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
77	c3l3sF	Alignment	not modelled	98.4	18	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
78	c2f6qA	Alignment	not modelled	98.4	14	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)
						PDB header: structural genomics, unknown function

79	c2fbmB_	Alignment	not modelled	98.4	12	Chain: B: PDB Molecule: y chromosome chromodomain protein 1, telomeric isoform b; PDBTitle: acetyltransferase domain of cdy1
80	c5jbxB_	Alignment	not modelled	98.4	12	PDB header: lyase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of liuc in complex with coenzyme a and malonic acid
81	d1yg6a1	Alignment	not modelled	98.4	17	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
82	c2j5iF_	Alignment	not modelled	98.4	16	PDB header: lyase Chain: F: PDB Molecule: p-hydroxycinnamoyl coa hydratase/lyase; PDBTitle: crystal structure of hydroxycinnamoyl-coa hydratase-lyase
83	c3lkeA_	Alignment	not modelled	98.4	13	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from bacillus halodurans
84	d1xx4a_	Alignment	not modelled	98.4	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
85	c2f6iG_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: G: PDB Molecule: atp-dependent clp protease, putative; PDBTitle: crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
86	c3hp0B_	Alignment	not modelled	98.4	8	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
87	c4og1A_	Alignment	not modelled	98.4	20	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
88	c3omeE_	Alignment	not modelled	98.4	18	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
89	c5xzdF_	Alignment	not modelled	98.4	18	PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase; PDBTitle: structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism
90	c3p5mB_	Alignment	not modelled	98.4	19	PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
91	c4nekD_	Alignment	not modelled	98.4	20	PDB header: isomerase Chain: D: PDB Molecule: enoyl-coa hydratase/carnithine racemase; PDBTitle: putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1
92	c2deoA_	Alignment	not modelled	98.4	15	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
93	c4jfcA_	Alignment	not modelled	98.4	15	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from polaromonas sp. js666
94	c5zaiB_	Alignment	not modelled	98.3	12	PDB header: hydrolase Chain: B: PDB Molecule: 3-hydroxypropionyl-coenzyme a dehydratase; PDBTitle: crystal structure of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula
95	c3mybA_	Alignment	not modelled	98.3	20	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase mycobacterium smegmatis
96	c5z7rA_	Alignment	not modelled	98.3	16	PDB header: lyase Chain: A: PDB Molecule: short-chain-enoyl-coa hydratase; PDBTitle: crystal structure of crotonase from clostridium acetobutylicum
97	d1uiya_	Alignment	not modelled	98.3	18	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
98	c3q7hM_	Alignment	not modelled	98.3	15	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
99	c1y7oE_	Alignment	not modelled	98.3	20	PDB header: hydrolase Chain: E: PDB Molecule: atp-dependent clp protease proteolytic subunit; PDBTitle: the structure of streptococcus pneumoniae a153p clpp
100	c4nnqB_	Alignment	not modelled	98.3	18	PDB header: lyase Chain: B: PDB Molecule: putative enoyl-coa hydratase; PDBTitle: crystal structure of lnmf protein from streptomyces amphibiosporus
101	d2f6qa1	Alignment	not modelled	98.3	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
102	c5yloA_	Alignment	not modelled	98.3	13	PDB header: hydrolase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structural of pseudomonas aeruginosa pa4980
103	c4di1A_	Alignment	not modelled	98.3	13	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa17; PDBTitle: crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum
104	c2qq3F_	Alignment	not modelled	98.3	19	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
105	c3moyA_	Alignment	not modelled	98.3	15 PDB header: lyase Chain: A: PDB Molecule: probable enoyl-coa hydratase; PDBTitle: crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
106	c4olqD_	Alignment	not modelled	98.3	15 PDB header: lyase Chain: D: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
107	c4i4zE_	Alignment	not modelled	98.3	17 PDB header: lyase Chain: E: PDB Molecule: naphthoate synthase; PDBTitle: synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa
108	c2ej5B_	Alignment	not modelled	98.3	15 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
109	c3rsiA_	Alignment	not modelled	98.3	19 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
110	d1hzda_	Alignment	not modelled	98.3	19 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
111	c3t88A_	Alignment	not modelled	98.3	17 PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa synthase; PDBTitle: crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa
112	d1y7oa1	Alignment	not modelled	98.3	22 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
113	c4k3wA_	Alignment	not modelled	98.3	18 PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 marinobacter aquaeolei
114	d1wz8a1	Alignment	not modelled	98.3	14 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
115	d1nzya_	Alignment	not modelled	98.3	14 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
116	c4k2nA_	Alignment	not modelled	98.3	15 PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/carnithine racemase; PDBTitle: crystal structure of an enoyl-coa hydratase/ carnithine racemase from2 magnetospirillum magneticum
117	c3kqfC_	Alignment	not modelled	98.3	17 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.
118	c3ju1A_	Alignment	not modelled	98.2	13 PDB header: lyase, isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase family protein
119	d2cbya1	Alignment	not modelled	98.2	18 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
120	c4u0gG_	Alignment	not modelled	98.2	18 PDB header: hydrolase/antibiotic Chain: G: PDB Molecule: atp-dependent clp protease proteolytic subunit 2; PDBTitle: crystal structure of m. tuberculosis clpp1p2 bound to adep and agonist