Phyre2

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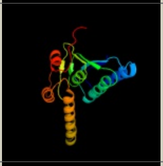
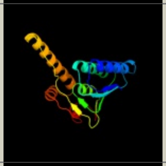
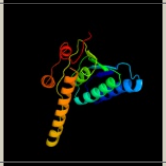
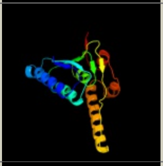
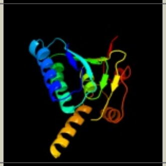
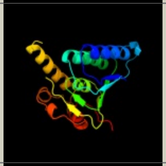
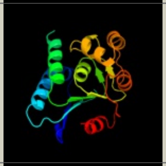
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bezC_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease 4; **PDBTitle:** crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
2	c3p2lD_	Alignment		100.0	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
3	c2deoA_	Alignment		99.9	16	**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
4	d1yg6a1	Alignment		99.9	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
5	c3kthD_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** structure of clpp from bacillus subtilis in orthorombic crystal form
6	c1tg6G_	Alignment		99.9	16	**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
7	c3q7hM_	Alignment		99.9	20	**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
8	d1tg6a1	Alignment		99.9	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
9	c2cbyG_	Alignment		99.9	22	**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
10	d2cbya1	Alignment		99.9	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
11	d1y7oa1	Alignment		99.9	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit

12	d2f6ia1	Alignment		99.9	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
13	c2f6iG_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp-dependent clp protease, putative; **PDBTitle:** crystal structure of the clpp protease catalytic domain from2 plasmodium falciparum
14	c1y7oE_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** the structure of streptococcus pneumoniae a153p clpp
15	c2ej5B_	Alignment		99.1	20	**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
16	c3peaD_	Alignment		99.1	16	**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	c2q35A_	Alignment		99.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curf; **PDBTitle:** crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
18	c3p5mB_	Alignment		99.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
19	c2iexA_	Alignment		99.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
20	c3fduF_	Alignment		98.9	20	**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
21	c2j5iF_	Alignment	not modelled	98.9	20	**PDB header:**lyase **Chain:** F: **PDB Molecule:**p-hydroxycinnamoyl coa hydratase/lyase; **PDBTitle:** crystal structure of hydroxycinnamoyl-coa hydratase-lyase
22	c2d3tB_	Alignment	not modelled	98.9	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
23	c3he2C_	Alignment	not modelled	98.9	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase echa6; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
24	d1rjma_	Alignment	not modelled	98.9	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
25	d1sg4a1	Alignment	not modelled	98.9	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
26	d1wz8a1	Alignment	not modelled	98.9	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
27	c3h81A_	Alignment	not modelled	98.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa8; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
28	c3r6hA_	Alignment	not modelled	98.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa3; **PDBTitle:** crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
						Fold: ClpP/crotonase

29	d1q52a_	Alignment	not modelled	98.9	18	**Superfamily:**ClpP/crotonase **Family:**Crotonase-like
30	c3lkeA_	Alignment	not modelled	98.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
31	c3hrxD_	Alignment	not modelled	98.8	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
32	d1xx4a_	Alignment	not modelled	98.8	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
33	c2x58B_	Alignment	not modelled	98.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
34	c3h0uB_	Alignment	not modelled	98.8	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
35	d2f6qa1	Alignment	not modelled	98.8	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
36	c2wtbA_	Alignment	not modelled	98.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2); **PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2
37	c3kqfC_	Alignment	not modelled	98.8	20	**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.
38	d1wdka4	Alignment	not modelled	98.8	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
39	c1rjnC_	Alignment	not modelled	98.8	19	**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
40	c3p85A_	Alignment	not modelled	98.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure enoyl-coa hydratase from mycobacterium avium
41	c3moyA_	Alignment	not modelled	98.8	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
42	d1nzya_	Alignment	not modelled	98.8	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
43	c3njbA_	Alignment	not modelled	98.8	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
44	c3h02F_	Alignment	not modelled	98.7	20	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
45	c3isaA_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
46	c3qreA_	Alignment	not modelled	98.7	16	**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
47	c3sllC_	Alignment	not modelled	98.7	20	**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
48	c3q1tB_	Alignment	not modelled	98.7	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium avium
49	c2qq3F_	Alignment	not modelled	98.7	21	**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
50	c3mybA_	Alignment	not modelled	98.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase mycobacterium smegmatis
51	c3rrvC_	Alignment	not modelled	98.7	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
52	c3rsiA_	Alignment	not modelled	98.7	20	**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
53	c3i47A_	Alignment	not modelled	98.7	21	**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
						PDB header:structural genomics, unknown function

54	c2fbmB_	Alignment	not modelled	98.7	16	**Chain:** B: **PDB Molecule:**y chromosome chromodomain protein 1, telomeric isoform b; **PDBTitle:** acetyltransferase domain of cdy1
55	c2f6qA_	Alignment	not modelled	98.7	19	**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)
56	d1hzda_	Alignment	not modelled	98.7	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
57	c2vx2D_	Alignment	not modelled	98.7	17	**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)
58	c2hw5F_	Alignment	not modelled	98.7	21	**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
59	c3l3sF_	Alignment	not modelled	98.7	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
60	c2ppyE_	Alignment	not modelled	98.6	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
61	d2a7ka1	Alignment	not modelled	98.6	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
62	c3omeE_	Alignment	not modelled	98.6	18	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
63	c3qxiA_	Alignment	not modelled	98.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa1; **PDBTitle:** crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
64	c3ju1A_	Alignment	not modelled	98.6	18	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase/isomerase family protein
65	d1szoa_	Alignment	not modelled	98.6	12	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
66	c3g64A_	Alignment	not modelled	98.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
67	d1mj3a_	Alignment	not modelled	98.6	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
68	d1dcia_	Alignment	not modelled	98.6	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
69	c3gkbA_	Alignment	not modelled	98.6	19	**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
70	d1ef8a_	Alignment	not modelled	98.6	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
71	c3oc7A_	Alignment	not modelled	98.5	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of an enoyl-coa hydratase from mycobacterium avium
72	c3hinA_	Alignment	not modelled	98.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 3-hydroxybutyryl-coa dehydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
73	d2fw2a1	Alignment	not modelled	98.5	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
74	d1uiya_	Alignment	not modelled	98.5	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
75	c3qmjA_	Alignment	not modelled	98.5	21	**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	98.5	17	**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	c3r0oA_	Alignment	not modelled	98.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carnitinyl-coa dehydratase; **PDBTitle:** crystal structure of carnitinyl-coa hydratase from mycobacterium avium
78	c3qxzA_	Alignment	not modelled	98.4	23	**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
						PDB header:lyase

79	c3hp0B_	Alignment	not modelled	98.4	18	**Chain:** B: **PDB Molecule:**putative polyketide biosynthesis enoyl-coa **PDBTitle:** crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
80	c2w3pB_	Alignment	not modelled	98.4	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
81	c3trrA_	Alignment	not modelled	98.4	17	**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
82	c3bptA_	Alignment	not modelled	98.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyryl-coa hydrolase; **PDBTitle:** crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
83	c3ot6A_	Alignment	not modelled	98.4	17	**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
84	c3swxB_	Alignment	not modelled	98.4	19	**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
85	c2j5gL_	Alignment	not modelled	98.3	19	**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
86	d1pjha_	Alignment	not modelled	98.3	12	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
87	c3laoA_	Alignment	not modelled	98.3	17	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
88	d2f9ya1	Alignment	not modelled	98.3	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
89	c3m6nA_	Alignment	not modelled	98.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rpff protein; **PDBTitle:** crystal structure of rpff
90	c2pg8C_	Alignment	not modelled	98.1	16	**PDB header:**ligand binding protein **Chain:** C: **PDB Molecule:**dpgc; **PDBTitle:** crystal structure of r254k mutanat of dpgc with bound substrate analog
91	c3qkaB_	Alignment	not modelled	98.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase, echa5; **PDBTitle:** crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
92	d1on3a2	Alignment	not modelled	97.8	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
93	d1vrga2	Alignment	not modelled	97.6	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
94	d1on3a1	Alignment	not modelled	97.5	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
95	d2a7sa2	Alignment	not modelled	97.5	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
96	c2f9iD_	Alignment	not modelled	97.5	19	**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	97.5	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
98	d2f9yb1	Alignment	not modelled	97.4	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
99	c2f9yB_	Alignment	not modelled	97.4	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
100	d1pixa2	Alignment	not modelled	97.4	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
101	c3glmD_	Alignment	not modelled	97.2	20	**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
102	c1on3E_	Alignment	not modelled	97.1	15	**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)
103	c3u9rB_	Alignment	not modelled	97.0	14	**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
						PDB header:ligase

104	c1vrgE_	Alignment	not modelled	96.9	17	**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
105	c1pixB_	Alignment	not modelled	96.8	17	**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
106	d2a7sa1	Alignment	not modelled	96.7	13	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
107	d1vrga1	Alignment	not modelled	96.7	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
108	c1xnwD_	Alignment	not modelled	96.7	18	**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	c3n6rF_	Alignment	not modelled	96.7	13	**PDB header:**ligase **Chain:** F: **PDB Molecule:**propionyl-coa carboxylase, beta subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
110	d1xnya1	Alignment	not modelled	96.7	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
111	c1x0uB_	Alignment	not modelled	96.5	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
112	c2a7sD_	Alignment	not modelled	96.5	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
113	d1pixa3	Alignment	not modelled	95.6	12	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
114	c1uytC_	Alignment	not modelled	90.5	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain
115	c1od4C_	Alignment	not modelled	89.7	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** acetyl-coa carboxylase carboxyltransferase domain
116	c2x24B_	Alignment	not modelled	88.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
117	c3h0jA_	Alignment	not modelled	86.8	19	**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
118	d1euca2	Alignment	not modelled	84.8	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
119	c3ff6D_	Alignment	not modelled	84.5	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
120	d1h4xa_	Alignment	not modelled	82.2	17	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa