
































# Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3bezC_</a>	 Alignment		100.0	99	<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
2	<a href="#">c3p2lD_</a>	 Alignment		100.0	24	<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
3	<a href="#">c1tg6G_</a>	 Alignment		99.9	22	<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
4	<a href="#">c2deoA_</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 441aa long hypothetical nfed protein; <b>PDBTitle:</b> 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
5	<a href="#">c3q7hM_</a>	 Alignment		99.9	22	<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
6	<a href="#">d1tg6a1</a>	 Alignment		99.9	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
7	<a href="#">d1yg6a1</a>	 Alignment		99.9	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
8	<a href="#">d2cbya1</a>	 Alignment		99.9	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
9	<a href="#">c3kthD_</a>	 Alignment		99.9	21	<b>PDB header:</b> hydrolase <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
10	<a href="#">c2cbyG_</a>	 Alignment		99.9	27	<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
11	<a href="#">d1y7oa1</a>	 Alignment		99.9	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit

12	<a href="#">c2f6iG_</a>	Alignment		99.9	18	<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
13	<a href="#">d2f6ia1</a>	Alignment		99.9	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
14	<a href="#">c1y7oE_</a>	Alignment		99.9	24	<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
15	<a href="#">c2ej5B_</a>	Alignment		99.2	20	<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
16	<a href="#">c3he2C_</a>	Alignment		99.2	19	<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
17	<a href="#">c2q35A_</a>	Alignment		99.1	21	<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 lymgbya majuscula
18	<a href="#">c2x58B_</a>	Alignment		99.1	18	<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
19	<a href="#">c3peaD_</a>	Alignment		99.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'
20	<a href="#">c3kqfC_</a>	Alignment		99.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.
21	<a href="#">c3rrvC_</a>	Alignment	not modelled	99.1	18	<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
22	<a href="#">c3fduF_</a>	Alignment	not modelled	99.1	21	<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
23	<a href="#">d1q52a_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
24	<a href="#">c2iexA_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynapthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
25	<a href="#">c3p5mB_</a>	Alignment	not modelled	99.0	23	<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
26	<a href="#">d1rjma_</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
27	<a href="#">c3lkeA_</a>	Alignment	not modelled	99.0	19	<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
28	<a href="#">c2ppyE_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
						<b>PDB header:</b> isomerase

29	<a href="#">c3sII_C_</a>	Alignment	not modelled	99.0	21	<b>Chain:</b> C: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
30	<a href="#">c2j5iF_</a>	Alignment	not modelled	99.0	21	<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
31	<a href="#">c3r6hA_</a>	Alignment	not modelled	99.0	23	<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
32	<a href="#">c2hw5F_</a>	Alignment	not modelled	99.0	21	<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
33	<a href="#">d1xx4a_</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
34	<a href="#">d1sg4a1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
35	<a href="#">c2qq3F_</a>	Alignment	not modelled	99.0	20	<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
36	<a href="#">c2d3tB_</a>	Alignment	not modelled	99.0	25	<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
37	<a href="#">c2wtbA_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atnfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
38	<a href="#">d1wdka4</a>	Alignment	not modelled	98.9	27	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
39	<a href="#">c3moyA_</a>	Alignment	not modelled	98.9	23	<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
40	<a href="#">c3h81A_</a>	Alignment	not modelled	98.9	20	<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
41	<a href="#">d1nzva_</a>	Alignment	not modelled	98.9	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
42	<a href="#">c2w3pB_</a>	Alignment	not modelled	98.9	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa-dihydrodiol lyase; <b>PDBTitle:</b> boxc crystal structure
43	<a href="#">d1hzda_</a>	Alignment	not modelled	98.9	27	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
44	<a href="#">c3njbA_</a>	Alignment	not modelled	98.9	25	<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
45	<a href="#">c3l3sF_</a>	Alignment	not modelled	98.9	22	<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
46	<a href="#">c3i47A_</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl coa hydratase/isomerase (crotonase); <b>PDBTitle:</b> crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
47	<a href="#">c3rsiA_</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
48	<a href="#">c3oc7A_</a>	Alignment	not modelled	98.9	21	<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
49	<a href="#">c3hrxD_</a>	Alignment	not modelled	98.9	22	<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
50	<a href="#">d1wz8a1</a>	Alignment	not modelled	98.9	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
51	<a href="#">c3p85A_</a>	Alignment	not modelled	98.9	21	<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
52	<a href="#">c1rjnC_</a>	Alignment	not modelled	98.9	19	<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
53	<a href="#">c2vx2D_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase domain-containing protein 3; <b>PDBTitle:</b> crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)

54	<a href="#">d1uiya_</a>	Alignment	not modelled	98.9	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
55	<a href="#">c3qxiA_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa1; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
56	<a href="#">c2fbmB_</a>	Alignment	not modelled	98.9	22	<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
57	<a href="#">d2a7ka1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
58	<a href="#">c3h02F_</a>	Alignment	not modelled	98.8	20	<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.
59	<a href="#">c3mybA_</a>	Alignment	not modelled	98.8	21	<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 mycobacterium smegmatis
60	<a href="#">c3q1tB_</a>	Alignment	not modelled	98.8	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
61	<a href="#">c3g64A_</a>	Alignment	not modelled	98.8	27	<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)
62	<a href="#">c3omeE_</a>	Alignment	not modelled	98.8	24	<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
63	<a href="#">c3qreA_</a>	Alignment	not modelled	98.8	20	<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
64	<a href="#">d2fw2a1</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
65	<a href="#">c3h0uB_</a>	Alignment	not modelled	98.8	12	<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
66	<a href="#">c3trrA_</a>	Alignment	not modelled	98.8	23	<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
67	<a href="#">c3r0oA_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitinyl-coa dehydratase; <b>PDBTitle:</b> crystal structure of carnitinyl-coa hydratase from mycobacterium avium
68	<a href="#">c3ju1A_</a>	Alignment	not modelled	98.8	25	<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
69	<a href="#">c3qmiA_</a>	Alignment	not modelled	98.8	22	<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
70	<a href="#">d1dcia_</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
71	<a href="#">d2f6qa1</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
72	<a href="#">c3isaA_</a>	Alignment	not modelled	98.7	18	<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
73	<a href="#">c3hinA_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-hydroxybutyryl-coa dehydratase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
74	<a href="#">c3qxzA_</a>	Alignment	not modelled	98.7	19	<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
75	<a href="#">d1mj3a_</a>	Alignment	not modelled	98.7	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
76	<a href="#">c2j5gL_</a>	Alignment	not modelled	98.7	16	<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
77	<a href="#">c2f6qA_</a>	Alignment		98.7	17	<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)
78	<a href="#">c3gkbA_</a>	Alignment	not modelled	98.6	16	<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
79	<a href="#">d1szoa_</a>	Alignment	not modelled	98.6	22 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
80	<a href="#">c3swxB_</a>	Alignment	not modelled	98.6	20 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
81	<a href="#">d1pjha_</a>	Alignment	not modelled	98.6	16 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
82	<a href="#">c3ot6A_</a>	Alignment	not modelled	98.6	16 <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
83	<a href="#">c2pg8C_</a>	Alignment	not modelled	98.6	23 <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
84	<a href="#">d1ef8a_</a>	Alignment	not modelled	98.6	14 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
85	<a href="#">c1on3E_</a>	Alignment	not modelled	98.5	20 <b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> methyl malonyl-coa carboxyltransferase 12s <b>PDBTitle:</b> transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methyl malonyl-coenzyme a and methyl malonic acid bound)
86	<a href="#">c3bptA_</a>	Alignment	not modelled	98.5	19 <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
87	<a href="#">c3hp0B_</a>	Alignment	not modelled	98.5	14 <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
88	<a href="#">c3laoA_</a>	Alignment	not modelled	98.5	21 <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
89	<a href="#">c3u9rB_</a>	Alignment	not modelled	98.5	19 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl crotonyl-coa carboxylase, beta-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methyl crotonyl-coa carboxylase2 (mcc), beta subunit
90	<a href="#">c3m6nA_</a>	Alignment	not modelled	98.4	17 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff
91	<a href="#">c3qkaB_</a>	Alignment	not modelled	98.4	25 <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
92	<a href="#">c3n6rF_</a>	Alignment	not modelled	98.4	18 <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)
93	<a href="#">c1x0uB_</a>	Alignment	not modelled	98.3	19 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical methyl malonyl-coa decarboxylase alpha subunit; <b>PDBTitle:</b> crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfolobus tokodaii
94	<a href="#">c2f9iC_</a>	Alignment	not modelled	98.3	23 <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
95	<a href="#">c1vrgE_</a>	Alignment	not modelled	98.2	21 <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
96	<a href="#">c1xnwD_</a>	Alignment	not modelled	98.1	17 <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
97	<a href="#">c2a7sD_</a>	Alignment	not modelled	98.1	19 <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
98	<a href="#">d2f9ya1</a>	Alignment	not modelled	98.1	22 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
99	<a href="#">c3glmD_</a>	Alignment	not modelled	97.9	15 <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
100	<a href="#">d1pixa2</a>	Alignment	not modelled	97.9	19 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
101	<a href="#">c2f9iD_</a>	Alignment	not modelled	97.7	21 <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
102	<a href="#">d1on3a1</a>	Alignment	not modelled	97.6	14 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain



103	<a href="#">d1xnya2</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
104	<a href="#">d1vrqa2</a>	Alignment	not modelled	97.3	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
105	<a href="#">d2f9yb1</a>	Alignment	not modelled	97.2	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
106	<a href="#">c2f9yB_</a>	Alignment	not modelled	97.2	21	<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
107	<a href="#">d2a7sa2</a>	Alignment	not modelled	97.2	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
108	<a href="#">c2csuB_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
109	<a href="#">d1xnya1</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
110	<a href="#">d1on3a2</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
111	<a href="#">c1pixB_</a>	Alignment	not modelled	96.9	24	<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
112	<a href="#">d2a7sa1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
113	<a href="#">d1vrqa1</a>	Alignment	not modelled	96.8	12	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
114	<a href="#">d1euca2</a>	Alignment	not modelled	96.2	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
115	<a href="#">d1oi7a2</a>	Alignment	not modelled	96.1	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
116	<a href="#">c2nu9E_</a>	Alignment	not modelled	96.0	30	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> succinyl-coa synthetase beta chain; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
117	<a href="#">c3mwdB_</a>	Alignment	not modelled	95.6	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
118	<a href="#">d1pixa3</a>	Alignment	not modelled	95.6	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
119	<a href="#">c1oi7A_</a>	Alignment	not modelled	95.4	26	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
120	<a href="#">c2yv1A_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661