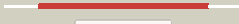



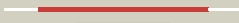



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0632c_(echA3)_728586_729281
Date	Fri Jul 26 01:50:19 BST 2019
Unique Job ID	c7b08c32d6bc01fb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3r6hA_</a>	 Alignment		100.0	84	<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
2	<a href="#">c4di1A_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase echa17; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum
3	<a href="#">c4jcsA_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34
4	<a href="#">d1nzya_</a>	 Alignment		100.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
5	<a href="#">c5zaiB_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-hydroxypropionyl-coenzyme a dehydratase; <b>PDBTitle:</b> crystal structure of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula
6	<a href="#">c5jbxB_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydratase; <b>PDBTitle:</b> crystal structure of liuc in complex with coenzyme a and malonic acid
7	<a href="#">c5z7rA_</a>	 Alignment		100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> short-chain-enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of crotonase from clostridium acetobutylicum
8	<a href="#">c3hinA_</a>	 Alignment		100.0	18	<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 rhodospseudomonas palustris cga009
9	<a href="#">d2f6qa1</a>	 Alignment		100.0	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
10	<a href="#">c2f6qA_</a>	 Alignment		100.0	21	<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)
11	<a href="#">c3rrvC_</a>	 Alignment		100.0	21	<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

12	<a href="#">c3g64A_</a>	Alignment		100.0	24	<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)
13	<a href="#">c3ot6A_</a>	Alignment		100.0	39	<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
14	<a href="#">c2qq3F_</a>	Alignment		100.0	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
15	<a href="#">c4jfcA_</a>	Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from polaromonas sp. js666
16	<a href="#">c3lkeA_</a>	Alignment		100.0	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 from bacillus halodurans
17	<a href="#">c5wybB_</a>	Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa dspi
18	<a href="#">c2ej5B_</a>	Alignment		100.0	22	<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
19	<a href="#">c3peaD_</a>	Alignment		100.0	22	<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="#">c3p5mB_</a>	Alignment		100.0	26	<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
21	<a href="#">d1xx4a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
22	<a href="#">d2fw2a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
23	<a href="#">c2fbmB_</a>	Alignment	not modelled	100.0	16	<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
24	<a href="#">c3hrxD_</a>	Alignment	not modelled	100.0	27	<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
25	<a href="#">c3h81A_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c4jylE_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1
27	<a href="#">c4zu2A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
28	<a href="#">c2vx2D_</a>	Alignment	not modelled	100.0	20	<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)

29	<a href="#">c3njbA</a>	Alignment	not modelled	100.0	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 from mycobacterium smegmatis,2 iodide soak
30	<a href="#">c4fzwA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase/lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-dehydroadipyl-coa hydratase; <b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli
31	<a href="#">c3q1tB</a>	Alignment	not modelled	100.0	22	<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
32	<a href="#">c3trrA</a>	Alignment	not modelled	100.0	27	<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
33	<a href="#">c2ppyE</a>	Alignment	not modelled	100.0	19	<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
34	<a href="#">d2a7ka1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
35	<a href="#">c4jvtA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of tfu_1878, a putative enoyl-coa hydratase2 fromthermobifida fusca yx in complex with coa
36	<a href="#">c4mi2C</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
37	<a href="#">c3i47A</a>	Alignment	not modelled	100.0	19	<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
38	<a href="#">c4q1iA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis enoyl-coa isomerase pksi; <b>PDBTitle:</b> structure and mechanism of a dehydratase/decarboxylase enzyme couple2 involved in polyketide beta-branching
39	<a href="#">c4k2nA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/ carnithine racemase from2 magnetospirillum magneticum
40	<a href="#">c3isaA</a>	Alignment	not modelled	100.0	22	<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
41	<a href="#">c5ve2J</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase,lyase <b>Chain:</b> J: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution.
42	<a href="#">c2j5iF</a>	Alignment	not modelled	100.0	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
43	<a href="#">c3moyA</a>	Alignment	not modelled	100.0	20	<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
44	<a href="#">c5yloA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> structural of pseudomonas aeruginosa pa4980
45	<a href="#">c4lk5B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10
46	<a href="#">c3kqfC</a>	Alignment	not modelled	100.0	16	<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.
47	<a href="#">c4olqD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
48	<a href="#">c3h0uB</a>	Alignment	not modelled	100.0	17	<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 from streptomyces2 avermitilis
49	<a href="#">c3r0oA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitiny-coa dehydratase; <b>PDBTitle:</b> crystal structure of carnitiny-coa hydratase from mycobacterium avium
50	<a href="#">c4hdtA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase; <b>PDBTitle:</b> crystal structure of a carnitiny-coa dehydratase from mycobacterium2 thermoresistibile
51	<a href="#">d1sg4a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
52	<a href="#">c4nekD</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase; <b>PDBTitle:</b> putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1
53	<a href="#">c3nkaB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase, echa5;

53	<a href="#">c3qkaB</a>	Alignment	not modelled	100.0	23	<b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;
54	<a href="#">c4izbB</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;
55	<a href="#">c3mybA</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of enoyl-coa hydratase mycobacterium smegmatis <b>PDB header:</b> isomerase/lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,2-epoxyphenylacetyl-coa isomerase;
56	<a href="#">c4fzwD</a>	Alignment	not modelled	100.0	21	<b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli
57	<a href="#">d1wz8a1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
58	<a href="#">c2d3tB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit;
59	<a href="#">c3bptA</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase;
60	<a href="#">c4mouA</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein;
61	<a href="#">d1wdka4</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family member,2 nysgrc target 028282 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
62	<a href="#">c2hw5F</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase;
63	<a href="#">c4j2uA</a>	Alignment	not modelled	100.0	26	<b>PDBTitle:</b> the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase;
64	<a href="#">c3t88A</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from rhodobacter2 sphaeroides 2.4.1 <b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase;
65	<a href="#">d1dcia</a>	Alignment	not modelled	100.0	22	<b>PDBTitle:</b> crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
66	<a href="#">c2iexA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynapthoic acid synthetase;
67	<a href="#">d1pjha</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
68	<a href="#">d1szoa</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
69	<a href="#">c3gkBA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase;
70	<a href="#">c3rsiA</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase;
71	<a href="#">c5xzdF</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196 <b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase;
72	<a href="#">d1uiya</a>	Alignment	not modelled	100.0	27	<b>PDBTitle:</b> structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
73	<a href="#">c3swxB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase;
74	<a href="#">d1mj3a</a>	Alignment	not modelled	100.0	22	<b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
75	<a href="#">c3qxzA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;
76	<a href="#">c2q35A</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> curf;
77	<a href="#">c4og1A</a>	Alignment	not modelled	100.0	25	<b>PDBTitle:</b> crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;
78	<a href="#">d1hzda</a>	Alignment	not modelled	100.0	20	<b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444 <b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like

79	<a href="#">c4jotA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, putative; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from deinococcus radiodurans2 r1
80	<a href="#">c3omeE</a>	Alignment	not modelled	100.0	21	<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
81	<a href="#">c2x58B</a>	Alignment	not modelled	100.0	22	<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
82	<a href="#">c4i4zE</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa
83	<a href="#">c3l3sF</a>	Alignment	not modelled	100.0	23	<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 hydratase/isomerase family2 protein from silicibacter pomeroyi
84	<a href="#">c4kd6A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m
85	<a href="#">c3laoA</a>	Alignment	not modelled	100.0	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
86	<a href="#">c3qxiA</a>	Alignment	not modelled	100.0	24	<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
87	<a href="#">c4b3hA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid beta-oxidation complex alpha-chain fadb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
88	<a href="#">c3ju1A</a>	Alignment	not modelled	100.0	18	<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
89	<a href="#">c4f47A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa19; <b>PDBTitle:</b> the structure of enoyl-coa hydratase echa19 from mycobacterium marinum
90	<a href="#">d1ef8a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
91	<a href="#">c3p85A</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure enoyl-coa hydratase from mycobacterium avium
92	<a href="#">c6ojmB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase; <b>PDBTitle:</b> crystal structure of 1,4-dihydroxy-2-naphthoyl-coa synthase2 elizabethkingia anophelis nuhp1
93	<a href="#">c4kpkA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from shewanella pealeana2 atcc 700345
94	<a href="#">c3fduF</a>	Alignment	not modelled	100.0	26	<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
95	<a href="#">c4k3wA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 marinobacter aquaeolei
96	<a href="#">d1q52a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
97	<a href="#">c3tiff</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
98	<a href="#">c3h02F</a>	Alignment	not modelled	100.0	22	<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.
99	<a href="#">c4jvwA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of putative short chain enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
100	<a href="#">c2j5gL</a>	Alignment	not modelled	100.0	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
101	<a href="#">c4iyjA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans dsm 12444
102	<a href="#">c2wtbA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
103	<a href="#">c3sllC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <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

104	<a href="#">c3oc7A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from mycobacterium avium
105	<a href="#">c4k29A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 xanthobacter autotrophicus py2
106	<a href="#">c6iunB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
107	<a href="#">c2w3pB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa-dihydrodiol lyase; <b>PDBTitle:</b> boxc crystal structure
108	<a href="#">c3hp0B_</a>	Alignment	not modelled	100.0	16	<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
109	<a href="#">c1rjnC_</a>	Alignment	not modelled	100.0	18	<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
110	<a href="#">c4nnqB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of lnmf protein from streptomyces amphibiosporus
111	<a href="#">c2pg8C_</a>	Alignment	not modelled	100.0	24	<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
112	<a href="#">d1rjma_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
113	<a href="#">c5fusB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl coa hydratase; <b>PDBTitle:</b> crystal structure of b. cenocepacia dfsa
114	<a href="#">c5zqzC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase,hydrolase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trifunctional enzyme subunit alpha, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, tetramer
115	<a href="#">c3he2C_</a>	Alignment	not modelled	100.0	26	<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
116	<a href="#">c4wczB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans
117	<a href="#">c3qmjA_</a>	Alignment	not modelled	100.0	21	<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
118	<a href="#">c3m6nA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff
119	<a href="#">c3qreA_</a>	Alignment	not modelled	100.0	28	<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
120	<a href="#">c5o34C_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase carb homologue; <b>PDBTitle:</b> thne from s.clavuligerus