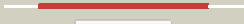



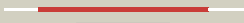




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2460c_clpP2_2762541_2763185
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	65452ce4640503ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4u0gG_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> G: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit 2; <b>PDBTitle:</b> crystal structure of m. tuberculosis clpp1p2 bound to adept and agonist
2	<a href="#">c3q7hM_</a>	 Alignment		100.0	49	<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
3	<a href="#">c1y7oE_</a>	 Alignment		100.0	37	<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
4	<a href="#">c3p2ID_</a>	 Alignment		100.0	49	<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
5	<a href="#">d1y7oa1</a>	 Alignment		100.0	38	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
6	<a href="#">d1yg6a1</a>	 Alignment		100.0	51	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
7	<a href="#">c1tg6G_</a>	 Alignment		100.0	44	<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
8	<a href="#">d1tg6a1</a>	 Alignment		100.0	46	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
9	<a href="#">c3kthD_</a>	 Alignment		100.0	50	<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		100.0	48	<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 protease proteolytic2 subunit 1 (clpp1) from mycobacterium tuberculosis
11	<a href="#">c2f6iG_</a>	 Alignment		100.0	44	<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

12	<a href="#">d2cbya1</a>	Alignment		100.0	48	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
13	<a href="#">d2f6ia1</a>	Alignment		100.0	43	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
14	<a href="#">c4hnl1</a>	Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> crystal structure of an enzyme
15	<a href="#">c4jqcU</a>	Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> U: <b>PDB Molecule:</b> atp-dependent clp protease proteolytic subunit; <b>PDBTitle:</b> clpp1 from listeria monocytogenes
16	<a href="#">c3bezC</a>	Alignment		100.0	21	<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
17	<a href="#">c2deoA</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 441aa long hypothetical nfd protein; <b>PDBTitle:</b> 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
18	<a href="#">c3rstH</a>	Alignment		99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> signal peptide peptidase sppa; <b>PDBTitle:</b> crystal structure of bacillus subtilis signal peptide peptidase a
19	<a href="#">c2ej5B</a>	Alignment		99.2	16	<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
20	<a href="#">c4jfcA</a>	Alignment		99.2	16	<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
21	<a href="#">c4fzwA</a>	Alignment	not modelled	99.2	16	<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
22	<a href="#">c3hrxD</a>	Alignment	not modelled	99.2	20	<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
23	<a href="#">c5o34C</a>	Alignment	not modelled	99.2	19	<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
24	<a href="#">c3i47A</a>	Alignment	not modelled	99.2	16	<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
25	<a href="#">c4zu2A</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
26	<a href="#">c3kqfC</a>	Alignment	not modelled	99.1	18	<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.
27	<a href="#">c2j5iF</a>	Alignment	not modelled	99.1	13	<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
						<b>PDB header:</b> isomerase

28	<a href="#">c4wczB_</a>	Alignment	not modelled	99.1	18	<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
29	<a href="#">c4fzWd_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> isomerase/lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,2-epoxyphenylacetyl-coa isomerase; <b>PDBTitle:</b> crystal structure of the paaf-paag hydratase isomerase complex from2 e.coli
30	<a href="#">c4f47A_</a>	Alignment	not modelled	99.1	14	<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
31	<a href="#">c5xzdF_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> structure of acryloyl-coa hydratase acuh from roseovarius nubinhbens2 ism
32	<a href="#">c3lkeA_</a>	Alignment	not modelled	99.1	18	<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
33	<a href="#">c2q35A_</a>	Alignment	not modelled	99.1	10	<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 lyngbya majuscula
34	<a href="#">c4nngB_</a>	Alignment	not modelled	99.1	15	<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
35	<a href="#">d1wdka4</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
36	<a href="#">c3peaD_</a>	Alignment	not modelled	99.1	12	<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'
37	<a href="#">d2fw2a1</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
38	<a href="#">c4lk5B_</a>	Alignment	not modelled	99.1	17	<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
39	<a href="#">c4q1jA_</a>	Alignment	not modelled	99.1	8	<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
40	<a href="#">d1dcia_</a>	Alignment	not modelled	99.1	12	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
41	<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
42	<a href="#">c2qq3F_</a>	Alignment	not modelled	99.1	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
43	<a href="#">c3moyA_</a>	Alignment	not modelled	99.1	18	<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="#">c3h81A_</a>	Alignment	not modelled	99.1	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
45	<a href="#">c3h02F_</a>	Alignment	not modelled	99.1	16	<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.
46	<a href="#">c3fduF_</a>	Alignment	not modelled	99.1	15	<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
47	<a href="#">d1xx4a_</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
48	<a href="#">c3rsia_</a>	Alignment	not modelled	99.1	14	<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
49	<a href="#">c3qreA_</a>	Alignment	not modelled	99.1	17	<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
50	<a href="#">c4nekD_</a>	Alignment	not modelled	99.1	12	<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
51	<a href="#">c3p85A_</a>	Alignment	not modelled	99.1	17	<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="#">c3omeE_</a>	Alignment	not modelled	99.1	17	<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
53	<a href="#">c3p5mB_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase;

53	<a href="#">c3p9mb_</a>	Alignment	not modelled	99.1	17	<b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium <b>PDB header:</b> hydrolase
54	<a href="#">c5zaiB_</a>	Alignment	not modelled	99.1	18	<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 <b>PDB header:</b> lyase
55	<a href="#">c3njbA_</a>	Alignment	not modelled	99.1	11	<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 <b>PDB header:</b> lyase
56	<a href="#">c5jbxB_</a>	Alignment	not modelled	99.1	19	<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 <b>PDB header:</b> lyase
57	<a href="#">d1q52a_</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like <b>PDB header:</b> lyase
58	<a href="#">c2hw5F_</a>	Alignment	not modelled	99.0	13	<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 <b>PDB header:</b> lyase/lyase inhibitor
59	<a href="#">c3t88A_</a>	Alignment	not modelled	99.0	17	<b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase; <b>PDBTitle:</b> crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa <b>PDB header:</b> isomerase
60	<a href="#">c4k2nA_</a>	Alignment	not modelled	99.0	10	<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 <b>PDB header:</b> hydrolase
61	<a href="#">c5yloA_</a>	Alignment	not modelled	99.0	19	<b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> structural of pseudomonas aeruginosa pa4980 <b>PDB header:</b> lyase
62	<a href="#">c2lexA_</a>	Alignment	not modelled	99.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynaphthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426 <b>PDB header:</b> isomerase,lyase
63	<a href="#">c5ve2j_</a>	Alignment	not modelled	99.0	18	<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. <b>PDB header:</b> isomerase,lyase
64	<a href="#">c2x58B_</a>	Alignment	not modelled	99.0	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 <b>PDB header:</b> isomerase
65	<a href="#">c4kpkA_</a>	Alignment	not modelled	99.0	15	<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 <b>PDB header:</b> lyase
66	<a href="#">c5z7rA_</a>	Alignment	not modelled	99.0	14	<b>Chain:</b> A: <b>PDB Molecule:</b> short-chain-enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of crotonase from clostridium acetobutylicum <b>PDB header:</b> structural genomics, unknown function
67	<a href="#">c2fbmB_</a>	Alignment	not modelled	99.0	17	<b>Chain:</b> B: <b>PDB Molecule:</b> y chromosome chromodomain protein 1, telomeric isoform b; <b>PDBTitle:</b> acetyltransferase domain of cdy1 <b>PDB header:</b> structural genomics, unknown function
68	<a href="#">d1nzya_</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like <b>PDB header:</b> isomerase
69	<a href="#">c4mi2C_</a>	Alignment	not modelled	99.0	14	<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 <b>PDB header:</b> isomerase
70	<a href="#">d1hzda_</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like <b>PDB header:</b> lyase
71	<a href="#">c3r6hA_</a>	Alignment	not modelled	99.0	16	<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 <b>PDB header:</b> lyase
72	<a href="#">c3qmjA_</a>	Alignment	not modelled	99.0	15	<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 <b>PDB header:</b> lyase
73	<a href="#">c4di1A_</a>	Alignment	not modelled	99.0	14	<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 <b>PDB header:</b> lyase
74	<a href="#">c3g64A_</a>	Alignment	not modelled	99.0	20	<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) <b>PDB header:</b> lyase
75	<a href="#">c4jcsA_</a>	Alignment	not modelled	99.0	20	<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 <b>PDB header:</b> isomerase
76	<a href="#">c4k3wA_</a>	Alignment	not modelled	99.0	14	<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 <b>PDB header:</b> hydrolase
77	<a href="#">c3isaA_</a>	Alignment	not modelled	99.0	14	<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 <b>PDB header:</b> lyase
78	<a href="#">c3qxiA_</a>	Alignment	not modelled	99.0	14	<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 <b>Fold:</b> ClpP/crotonase

79	<a href="#">d1uiya_</a>	Alignment	not modelled	99.0	19	<b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
80	<a href="#">c4o1qD_</a>	Alignment	not modelled	99.0	16	<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 hyphomona neptunium
81	<a href="#">c2d3tB_</a>	Alignment	not modelled	99.0	14	<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
82	<a href="#">c3l3sF_</a>	Alignment	not modelled	99.0	18	<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
83	<a href="#">c3sllC_</a>	Alignment	not modelled	99.0	14	<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
84	<a href="#">c3trrA_</a>	Alignment	not modelled	99.0	17	<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
85	<a href="#">c5wybB_</a>	Alignment	not modelled	99.0	14	<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
86	<a href="#">c3r0oA_</a>	Alignment	not modelled	99.0	13	<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
87	<a href="#">c3oc7A_</a>	Alignment	not modelled	99.0	13	<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
88	<a href="#">c4i4zE_</a>	Alignment	not modelled	99.0	17	<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
89	<a href="#">d2f6qa1</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
90	<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
91	<a href="#">c2vx2D_</a>	Alignment	not modelled	99.0	17	<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)
92	<a href="#">d1wz8a1</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
93	<a href="#">c3h0uB_</a>	Alignment	not modelled	99.0	18	<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
94	<a href="#">c4jotA_</a>	Alignment	not modelled	99.0	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
95	<a href="#">c2f6qa_</a>	Alignment	not modelled	98.9	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)
96	<a href="#">c2ppyE_</a>	Alignment	not modelled	98.9	13	<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
97	<a href="#">c4kd6A_</a>	Alignment	not modelled	98.9	18	<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
98	<a href="#">c4og1A_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
99	<a href="#">d1rjma_</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
100	<a href="#">d2a7ka1</a>	Alignment	not modelled	98.9	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
101	<a href="#">c4izbB_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa
102	<a href="#">d1mj3a_</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
103	<a href="#">c3ju1A_</a>	Alignment	not modelled	98.9	14	<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

104	<a href="#">c3mybA_</a>	Alignment	not modelled	98.9	17	<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
105	<a href="#">c3q1tB_</a>	Alignment	not modelled	98.9	16	<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
106	<a href="#">c4hdtA_</a>	Alignment	not modelled	98.9	14	<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
107	<a href="#">c3laoA_</a>	Alignment	not modelled	98.9	17	<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
108	<a href="#">c2wtbA_</a>	Alignment	not modelled	98.9	20	<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
109	<a href="#">c6iunB_</a>	Alignment	not modelled	98.9	11	<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
110	<a href="#">c4k29A_</a>	Alignment	not modelled	98.9	15	<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
111	<a href="#">c3swxB_</a>	Alignment	not modelled	98.9	17	<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
112	<a href="#">c4jylE_</a>	Alignment	not modelled	98.9	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 hydratase from thermoplasma volcanium2 gss1
113	<a href="#">c3hp0B_</a>	Alignment	not modelled	98.9	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
114	<a href="#">c5fusB_</a>	Alignment	not modelled	98.9	14	<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
115	<a href="#">c1rjnC_</a>	Alignment	not modelled	98.9	17	<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
116	<a href="#">c4b3hA_</a>	Alignment	not modelled	98.9	11	<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
117	<a href="#">c3m6nA_</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff
118	<a href="#">c4jvtA_</a>	Alignment	not modelled	98.8	17	<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
119	<a href="#">c4jyiA_</a>	Alignment	not modelled	98.8	11	<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
120	<a href="#">c4mouA_</a>	Alignment	not modelled	98.8	12	<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 member,2 nysgrc target 028282