

# Phyre2

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 Description RVBD2502c\_(accD1)\_2816895\_2818484  
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4q0gC_</a>	Alignment		100.0	100	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> probable acetyl-/propionyl-coa carboxylase (beta subunit) <b>PDBTitle:</b> crystal structure of beta subunit of acyl-coa carboxylase accd1 from2 mycobacterium tuberculosis
2	<a href="#">c3u9rB_</a>	Alignment		100.0	66	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> methylcrotonyl-coa carboxylase, beta-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
3	<a href="#">c5iklD_</a>	Alignment		100.0	47	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> geranyl-coa carboxylase, beta-subunit; <b>PDBTitle:</b> crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit
4	<a href="#">c1pixB_</a>	Alignment		100.0	25	<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
5	<a href="#">c3glmD_</a>	Alignment		100.0	25	<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 clostridium symbiosum co-2 crystallized with crotonyl-coa
6	<a href="#">c1on3E_</a>	Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> methylmalonyl-coa carboxyltransferase 12s <b>PDBTitle:</b> transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
7	<a href="#">c1vrgE_</a>	Alignment		100.0	34	<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
8	<a href="#">c1xnwD_</a>	Alignment		100.0	33	<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
9	<a href="#">c2a7sD_</a>	Alignment		100.0	33	<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
10	<a href="#">c1x0uB_</a>	Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical methylmalonyl-coa decarboxylase alpha subunit; <b>PDBTitle:</b> crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfobolus tokodaii
11	<a href="#">c5fifD_</a>	Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxylase; <b>PDBTitle:</b> carboxyltransferase domain of a single-chain bacterial carboxylase

12	<a href="#">c4rcnA_</a>	Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> long-chain acyl-coa carboxylase; <b>PDBTitle:</b> structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
13	<a href="#">c3n6rF_</a>	Alignment		100.0	35	<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)
14	<a href="#">c5ingC_</a>	Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> putative carboxyl transferase; <b>PDBTitle:</b> a crotonyl-coa reductase-carboxylase independent pathway for assembly2 of unusual alkylmalonyl-coa polyketide synthase extender unit
15	<a href="#">c4l6wA_</a>	Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> probable propionyl-coa carboxylase beta chain 6; <b>PDBTitle:</b> carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
16	<a href="#">c4l6wB_</a>	Alignment		100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> probable propionyl-coa carboxylase beta chain 6; <b>PDBTitle:</b> carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
17	<a href="#">c1uyvB_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain l1705j/2 v19671 mutant
18	<a href="#">c4wyoB_</a>	Alignment		100.0	23	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of human-yeast chimera acetyl coa carboxylase ct2 domain bound to compound 1
19	<a href="#">c3h0jA_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of2 acetyl-coenzyme a carboxylase in complex with compound 2
20	<a href="#">c2x24B_</a>	Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> bovine acc2 ct domain in complex with inhibitor
21	<a href="#">c3ff6D_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> human acc2 ct domain with cp-640186
22	<a href="#">c1od4C_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
23	<a href="#">c1uytC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> acetyl-coa carboxylase carboxyltransferase domain
24	<a href="#">c5i6fB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
25	<a href="#">c5i6fA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of c-terminal variant 1 of chaetomium thermophilum2 acetyl-coa carboxylase
26	<a href="#">c5i6hA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acetyl-coa carboxylase-like protein; <b>PDBTitle:</b> crystal structure of cd-ct domains of chaetomium thermophilum acetyl-2 coa carboxylase
27	<a href="#">c5cskB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of yeast acetyl-coa carboxylase, unbiotinylated
28	<a href="#">c6g2dC_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> acetyl-coa carboxylase 1; <b>PDBTitle:</b> citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
						<b>PDB header:</b> ligase

29	<a href="#">c5cslA_</a>	Alignment	not modelled	100.0	23	<b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase; <b>PDBTitle:</b> crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
30	<a href="#">d1pixa3</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
31	<a href="#">d1on3a1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
32	<a href="#">d2a7sa1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
33	<a href="#">d1xnya1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
34	<a href="#">d1vrqa1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
35	<a href="#">d1on3a2</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
36	<a href="#">d1vrqa2</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
37	<a href="#">d2a7sa2</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
38	<a href="#">d1pixa2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
39	<a href="#">d1xnya2</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
40	<a href="#">d2f9yb1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
41	<a href="#">c2f9yB_</a>	Alignment	not modelled	100.0	22	<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
42	<a href="#">d1uyra1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
43	<a href="#">c5vipB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mdcd; <b>PDBTitle:</b> crystal structure of pseudomonas malonate decarboxylase mdcd-mdce2 hetero-dimer
44	<a href="#">d1uyra2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
45	<a href="#">c2f9iD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
46	<a href="#">d2f9ya1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
47	<a href="#">c2f9iC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acetyl-coenzyme a carboxylase carboxyl transferase subunit <b>PDBTitle:</b> crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
48	<a href="#">c5vj1M_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> mdce; <b>PDBTitle:</b> crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with coenzyme a
49	<a href="#">c4hnkl_</a>	Alignment	not modelled	98.9	12	<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
50	<a href="#">c3bezC_</a>	Alignment	not modelled	98.9	16	<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
51	<a href="#">c3r6hA_</a>	Alignment	not modelled	98.5	18	<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
52	<a href="#">d1q52a_</a>	Alignment	not modelled	98.3	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
53	<a href="#">c4iyjA_</a>	Alignment	not modelled	98.3	15	<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
54	<a href="#">c2f6qA_</a>	Alignment	not modelled	98.3	15	<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)

55	<a href="#">c4jccU_</a>	Alignment	not modelled	98.3	21	<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
56	<a href="#">c4fzwD_</a>	Alignment	not modelled	98.2	15	<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 from 2 e.coli
57	<a href="#">c3oc7A_</a>	Alignment	not modelled	98.2	18	<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
58	<a href="#">c4izbB_</a>	Alignment	not modelled	98.2	19	<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 that 2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa
59	<a href="#">d1yg6a1</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
60	<a href="#">d2f6ia1</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
61	<a href="#">c4kpkA_</a>	Alignment	not modelled	98.1	17	<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 pealeana 2 atcc 700345
62	<a href="#">c3moyA_</a>	Alignment	not modelled	98.1	19	<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 mycobacterium 2 smegmatis
63	<a href="#">c3i47A_</a>	Alignment	not modelled	98.1	11	<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/isomerase 2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
64	<a href="#">c4jcsA_</a>	Alignment	not modelled	98.1	16	<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 cupriavidus 2 metallidurans ch34
65	<a href="#">c3peaD_</a>	Alignment	not modelled	98.1	14	<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'
66	<a href="#">c3isaA_</a>	Alignment	not modelled	98.1	15	<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 from 2 bordetella parapertussis
67	<a href="#">c4jylE_</a>	Alignment	not modelled	98.1	16	<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 volcanium 2 gss1
68	<a href="#">d1xx4a_</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
69	<a href="#">c3njbA_</a>	Alignment	not modelled	98.1	16	<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
70	<a href="#">c3p2ID_</a>	Alignment	not modelled	98.1	17	<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 from 2 francisella tularensis
71	<a href="#">c5wybB_</a>	Alignment	not modelled	98.0	17	<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 dspl
72	<a href="#">c4b3hA_</a>	Alignment	not modelled	98.0	15	<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 acid 2 beta-oxidation complex
73	<a href="#">c3hrxD_</a>	Alignment	not modelled	98.0	16	<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
74	<a href="#">c4zu2A_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
75	<a href="#">c2qq3F_</a>	Alignment	not modelled	98.0	21	<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
76	<a href="#">c1y7oE_</a>	Alignment	not modelled	98.0	16	<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
77	<a href="#">c3i3sF_</a>	Alignment	not modelled	98.0	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 family 2 protein from silicibacter pomeroyi
78	<a href="#">c3gkbA_</a>	Alignment	not modelled	98.0	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 streptomyces 2 avermitilis

79	<a href="#">c5z7rA</a>	Alignment	not modelled	98.0	14	<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
80	<a href="#">c2vx2D</a>	Alignment	not modelled	98.0	12	<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)
81	<a href="#">c1rjnC</a>	Alignment	not modelled	98.0	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
82	<a href="#">d1rjma</a>	Alignment	not modelled	98.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
83	<a href="#">c5jxbB</a>	Alignment	not modelled	98.0	11	<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
84	<a href="#">d2fw2a1</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
85	<a href="#">c3h81A</a>	Alignment	not modelled	98.0	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
86	<a href="#">c5zaiB</a>	Alignment	not modelled	97.9	13	<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
87	<a href="#">d1nzya</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
88	<a href="#">c2fbmB</a>	Alignment	not modelled	97.9	13	<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
89	<a href="#">c3q7hM</a>	Alignment	not modelled	97.9	14	<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
90	<a href="#">c5xzdF</a>	Alignment	not modelled	97.9	16	<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 nubinhibens2 ism
91	<a href="#">c4olqD</a>	Alignment	not modelled	97.9	11	<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
92	<a href="#">c2ej5B</a>	Alignment	not modelled	97.9	14	<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
93	<a href="#">c3fduF</a>	Alignment	not modelled	97.9	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
94	<a href="#">c4kd6A</a>	Alignment	not modelled	97.9	13	<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
95	<a href="#">c2f6iG</a>	Alignment	not modelled	97.9	15	<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
96	<a href="#">c3lkeA</a>	Alignment	not modelled	97.9	12	<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
97	<a href="#">c3sllC</a>	Alignment	not modelled	97.9	13	<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
98	<a href="#">c4u0gG</a>	Alignment	not modelled	97.9	17	<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 adep and agonist
99	<a href="#">c3t88A</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> lyase/lyase inhibitor <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
100	<a href="#">d2f6qa1</a>	Alignment	not modelled	97.9	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
101	<a href="#">d1dcia</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
102	<a href="#">c3h0uB</a>	Alignment	not modelled	97.9	16	<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
103	<a href="#">c4di1A</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa17;

103	<a href="#">c4u1A_</a>	Alignment	not modelled	97.9	10	<b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum <b>PDB header:</b> lyase
104	<a href="#">c3omeE_</a>	Alignment	not modelled	97.9	20	<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
105	<a href="#">d1y7oa1</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
106	<a href="#">d1uiya_</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
107	<a href="#">c4lk5B_</a>	Alignment	not modelled	97.8	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
108	<a href="#">d1wz8a1</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
109	<a href="#">c3p5mB_</a>	Alignment	not modelled	97.8	14	<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
110	<a href="#">c4og1A_</a>	Alignment	not modelled	97.8	19	<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
111	<a href="#">c3kthD_</a>	Alignment	not modelled	97.8	16	<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 orthorombic crystal form
112	<a href="#">c3hp0B_</a>	Alignment	not modelled	97.8	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
113	<a href="#">c5o34C_</a>	Alignment	not modelled	97.8	14	<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
114	<a href="#">c2hw5F_</a>	Alignment	not modelled	97.8	17	<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
115	<a href="#">d1sg4a1</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
116	<a href="#">c4jfcA_</a>	Alignment	not modelled	97.8	10	<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
117	<a href="#">c3rsiA_</a>	Alignment	not modelled	97.8	21	<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
118	<a href="#">c4k3wA_</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 marinobacter aquaeolei
119	<a href="#">c3rrvC_</a>	Alignment	not modelled	97.8	16	<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
120	<a href="#">c2j5iF_</a>	Alignment	not modelled	97.8	15	<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