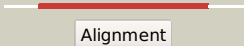

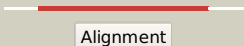

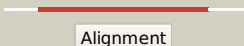


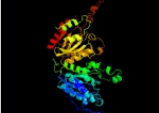



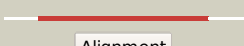









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0904c_(accD3)_1006696_1008183
Date	Fri Jul 26 01:50:49 BST 2019
Unique Job ID	77af5c407f0f84bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1on3E_</a>	 Alignment		100.0	23	<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)
2	<a href="#">c1x0uB_</a>	 Alignment		100.0	20	<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
3	<a href="#">c3n6rF_</a>	 Alignment		100.0	20	<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)
4	<a href="#">c1xnwD_</a>	 Alignment		100.0	21	<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
5	<a href="#">c1vrgE_</a>	 Alignment		100.0	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
6	<a href="#">c2a7sD_</a>	 Alignment		100.0	21	<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
7	<a href="#">c1pixB_</a>	 Alignment		100.0	17	<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
8	<a href="#">c5fifD_</a>	 Alignment		100.0	21	<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
9	<a href="#">c4rcnA_</a>	 Alignment		100.0	21	<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
10	<a href="#">c3glmD_</a>	 Alignment		100.0	16	<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
11	<a href="#">c5ingC_</a>	 Alignment		100.0	21	<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

12	<a href="#">c3u9rB_</a>	Alignment		100.0	18	<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
13	<a href="#">c5ikID_</a>	Alignment		100.0	17	<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
14	<a href="#">c4q0gC_</a>	Alignment		100.0	18	<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
15	<a href="#">c4l6wA_</a>	Alignment		100.0	21	<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	22	<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	16	<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 v1967i mutant
18	<a href="#">c2x24B_</a>	Alignment		100.0	19	<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
19	<a href="#">c1od4C_</a>	Alignment		100.0	18	<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
20	<a href="#">c4wyoB_</a>	Alignment		100.0	18	<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
21	<a href="#">c3h0jA_</a>	Alignment	not modelled	100.0	18	<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
22	<a href="#">c3ff6D_</a>	Alignment	not modelled	100.0	19	<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
23	<a href="#">c1uytC_</a>	Alignment	not modelled	100.0	19	<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	19	<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	19	<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	18	<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	18	<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="#">d2f9ya1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
29	<a href="#">c6g2dC_</a>	Alignment	not modelled	100.0	17	<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
30	<a href="#">c5cslA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> ligase <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
31	<a href="#">c2f9iC_</a>	Alignment	not modelled	100.0	27	<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
32	<a href="#">d2f9yb1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
33	<a href="#">c2f9yB_</a>	Alignment	not modelled	100.0	38	<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
34	<a href="#">c2f9iD_</a>	Alignment	not modelled	100.0	37	<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
35	<a href="#">d1on3a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
36	<a href="#">d2a7sa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
37	<a href="#">d1xnya1</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
38	<a href="#">d1vrga1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
39	<a href="#">d1pixa3</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
40	<a href="#">d1pixa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
41	<a href="#">d1on3a2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
42	<a href="#">d1vrga2</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
43	<a href="#">d2a7sa2</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
44	<a href="#">d1xnya2</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="#">c5vipB_</a>	Alignment	not modelled	100.0	28	<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
46	<a href="#">c5vj1M_</a>	Alignment	not modelled	100.0	19	<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
47	<a href="#">d1uyra1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
48	<a href="#">d1uyra2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
49	<a href="#">c3bezC_</a>	Alignment	not modelled	99.6	19	<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
50	<a href="#">c4hnl_</a>	Alignment	not modelled	99.4	9	<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
51	<a href="#">c3r6hA_</a>	Alignment	not modelled	99.0	13	<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="#">c2fbmB_</a>	Alignment	not modelled	99.0	18	<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
53	<a href="#">c4jcsA_</a>	Alignment	not modelled	98.9	13	<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
54	<a href="#">d2fw2a1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
55	<a href="#">c4fzwd_</a>	Alignment	not modelled	98.9	16	<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
56	<a href="#">c5zaiB_</a>	Alignment	not modelled	98.9	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
57	<a href="#">c3i47A_</a>	Alignment	not modelled	98.9	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
58	<a href="#">c3fduF_</a>	Alignment	not modelled	98.8	19	<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
59	<a href="#">c3rrvC_</a>	Alignment	not modelled	98.8	13	<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
60	<a href="#">d2a7ka1</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
61	<a href="#">c3peaD_</a>	Alignment	not modelled	98.8	16	<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'
62	<a href="#">c2f6qA_</a>	Alignment	not modelled	98.8	14	<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)
63	<a href="#">c2q35A_</a>	Alignment	not modelled	98.8	16	<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 lynngbya majuscula
64	<a href="#">c2vx2D_</a>	Alignment	not modelled	98.8	14	<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)
65	<a href="#">d1nzya_</a>	Alignment	not modelled	98.8	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
66	<a href="#">c4jfcA_</a>	Alignment	not modelled	98.8	15	<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
67	<a href="#">c5z7rA_</a>	Alignment	not modelled	98.8	17	<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
68	<a href="#">d1q52a_</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
69	<a href="#">d2f6ia1</a>	Alignment	not modelled	98.8	9	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
70	<a href="#">c3isaA_</a>	Alignment	not modelled	98.8	17	<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
71	<a href="#">d1xx4a_</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
72	<a href="#">d1uiya_</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
73	<a href="#">c4izbB_</a>	Alignment	not modelled	98.8	16	<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
74	<a href="#">c5jbxB_</a>	Alignment	not modelled	98.8	16	<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
75	<a href="#">c3oc7A_</a>	Alignment	not modelled	98.8	16	<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
76	<a href="#">c4zu2A_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
77	<a href="#">c4jvjA_</a>	Alignment	not modelled	98.8	16	<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
78	<a href="#">c5yloA_</a>	Alignment	not modelled	98.7	20	<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
79	<a href="#">d2f6qa1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like

80	<a href="#">d1hzda</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
81	<a href="#">c3njbA</a>	Alignment	not modelled	98.7	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 mycobacterium smegmatis,2 iodide soak
82	<a href="#">c3mybA</a>	Alignment	not modelled	98.7	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 mycobacterium smegmatis
83	<a href="#">c4kpkA</a>	Alignment	not modelled	98.7	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 pealeana2 atcc 700345
84	<a href="#">c4nekD</a>	Alignment	not modelled	98.7	15	<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
85	<a href="#">d1wz8a1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
86	<a href="#">c2ej5B</a>	Alignment	not modelled	98.7	17	<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
87	<a href="#">d1pjha</a>	Alignment	not modelled	98.7	10	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
88	<a href="#">c4kd6A</a>	Alignment	not modelled	98.7	20	<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
89	<a href="#">c2f6iG</a>	Alignment	not modelled	98.7	11	<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
90	<a href="#">c4jvtA</a>	Alignment	not modelled	98.7	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
91	<a href="#">c4di1A</a>	Alignment	not modelled	98.7	16	<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
92	<a href="#">c1y7oE</a>	Alignment	not modelled	98.7	10	<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
93	<a href="#">c4jylE</a>	Alignment	not modelled	98.7	14	<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
94	<a href="#">c4o1qD</a>	Alignment	not modelled	98.7	15	<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
95	<a href="#">c4lk5B</a>	Alignment	not modelled	98.7	18	<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
96	<a href="#">d1y7oa1</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
97	<a href="#">c5wybB</a>	Alignment	not modelled	98.7	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
98	<a href="#">d1szoa</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
99	<a href="#">c3hrxD</a>	Alignment	not modelled	98.7	18	<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
100	<a href="#">c3lkeA</a>	Alignment	not modelled	98.6	15	<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
101	<a href="#">c4jotA</a>	Alignment	not modelled	98.6	20	<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 hydrotase from deinococcus radiodurans2 r1
102	<a href="#">c3kqfC</a>	Alignment	not modelled	98.6	17	<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.
103	<a href="#">c3g64A</a>	Alignment	not modelled	98.6	18	<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)
104	<a href="#">c4jqcU</a>	Alignment	not modelled	98.6	11	<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
105	<a href="#">c2r9a</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase;

105	<a href="#">c3t68A_</a>	Alignment	not modelled	98.6	14	<b>PDBTitle:</b> crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa
106	<a href="#">d1rjma_</a>	Alignment	not modelled	98.6	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
107	<a href="#">c3q7hM_</a>	Alignment	not modelled	98.6	15	<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
108	<a href="#">c4wczB_</a>	Alignment	not modelled	98.6	17	<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
109	<a href="#">c2ppyE_</a>	Alignment	not modelled	98.6	12	<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
110	<a href="#">c3moyA_</a>	Alignment	not modelled	98.6	16	<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
111	<a href="#">c2deoA_</a>	Alignment	not modelled	98.6	11	<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
112	<a href="#">c1tg6G_</a>	Alignment	not modelled	98.6	10	<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
113	<a href="#">c4mi2C_</a>	Alignment	not modelled	98.6	15	<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
114	<a href="#">c2cbyG_</a>	Alignment	not modelled	98.6	16	<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
115	<a href="#">d1dcja_</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
116	<a href="#">c5xzdF_</a>	Alignment	not modelled	98.6	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
117	<a href="#">c2qq3F_</a>	Alignment	not modelled	98.6	11	<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
118	<a href="#">d2cbya1</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Clp protease, ClpP subunit
119	<a href="#">c2j5gL_</a>	Alignment	not modelled	98.6	14	<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
120	<a href="#">c4k2nA_</a>	Alignment	not modelled	98.6	12	<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