

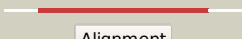




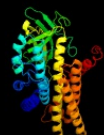








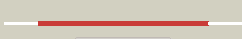
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3560c_(fadE30)_4000611_4001768
Date	Fri Aug 9 18:20:24 BST 2019
Unique Job ID	1f1704ad714c9f7a

Detailed template information



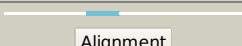
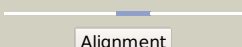
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6es9A_</a>	 Alignment		100.0	26	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> methylsuccinyl-coa dehydrogenase of paracoccus denitrificans with2 bound flavin adenine dinucleotide
2	<a href="#">c2z1qA_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of acyl coa dehydrogenase
3	<a href="#">c3owaC_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of acyl-coa dehydrogenase complexed with fad from2 bacillus anthracis
4	<a href="#">c2ix5A_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase 4, peroxisomal; <b>PDBTitle:</b> short chain specific acyl-coa oxidase from arabidopsis thaliana, acx42 in complex with acetoacetyl-coa
5	<a href="#">c2a1tC_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-coa dehydrogenase, medium-chain specific, <b>PDBTitle:</b> structure of the human mcad:etf e165betaa complex
6	<a href="#">c2pg0B_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of acyl-coa dehydrogenase from geobacillus2 kaustophilus
7	<a href="#">c6ijcA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase family protein; <b>PDBTitle:</b> structure of mmpa-coa dehydrogenase from roseovarius nubinhibens ism
8	<a href="#">c1rx0B_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase family member 8, mitochondrial; <b>PDBTitle:</b> crystal structure of isobutyryl-coa dehydrogenase complexed with2 substrate/ligand.
9	<a href="#">c2uxwA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> very-long-chain specific acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of human very long chain acyl-coa dehydrogenase2 (acadvl)
10	<a href="#">c1ivhD_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> isovaleryl-coa dehydrogenase; <b>PDBTitle:</b> structure of human isovaleryl-coa dehydrogenase at 2.62 angstroms resolution: structural basis for substrate3 specificity
11	<a href="#">c5zw2A_</a>	 Alignment		100.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-prolyl-[peptidyl-carrier protein] dehydrogenase; <b>PDBTitle:</b> fad complex of piga

12	<a href="#">c1egcB_</a>	Alignment		100.0	26	<b>PDB header:</b> electron transfer <b>Chain:</b> B: <b>PDB Molecule:</b> medium chain acyl-coa dehydrogenase; <b>PDBTitle:</b> structure of t255e, e376g mutant of human medium chain acyl-2 coa dehydrogenase complexed with octanoyl-coa
13	<a href="#">c3oibB_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak
14	<a href="#">c4hr3A_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-coa dehydrogenase; <b>PDBTitle:</b> structure of a putative acyl-coa dehydrogenase from mycobacterium2 abscessus
15	<a href="#">c4x28B_</a>	Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the chse4-chse5 complex from mycobacterium2 tuberculosis
16	<a href="#">c4irnF_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> prolyl-accp dehydrogenase; <b>PDBTitle:</b> crystal structure of the prolyl acyl carrier protein oxidase anab
17	<a href="#">c5ol2F_</a>	Alignment		100.0	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> F: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
18	<a href="#">c5ahsB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> 3-sulfinopropionyl-coenzyme a (3sp-coa) desulfinate from advenella2 mimgardefordensis dpn7t: holo crystal structure with the substrate3 analog succinyl-coa
19	<a href="#">c1ukwA_</a>	Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of medium-chain acyl-coa dehydrogenase2 from thermus thermophilus hb8
20	<a href="#">c4n5fA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative acyl-coa dehydrogenase with bound2 fadh2 from burkholderia cenocepacia j2315
21	<a href="#">c5iduB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase domain protein; <b>PDBTitle:</b> crystal structure of an acyl-coa dehydrogenase domain protein from2 burkholderia phymatum bound to fad
22	<a href="#">c2jifA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short/branched chain specific acyl-coa dehydrogenase; <b>PDBTitle:</b> structure of human short-branched chain acyl-coa dehydrogenase2 (acadsb)
23	<a href="#">c2cx9C_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of acyl-coa dehydrogenase
24	<a href="#">c3sf6A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of glutaryl-coa dehydrogenase from mycobacterium2 smegmatis
25	<a href="#">c4ktoB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> isovaleryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative isovaleryl-coa dehydrogenase (psi-2 nysgrc-012251) from sinorhizobium meliloti 1021
26	<a href="#">c4iv6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase fade3; <b>PDBTitle:</b> x-ray crystal structure of an isovaleryl-coa dehydrogenase from2 mycobacterium smegmatis
27	<a href="#">c3swoA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a glutaryl-coa dehydrogenase from mycobacterium2 smegmatis in complex with fadh2
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain specific acyl-coa

28	<a href="#">c2vigC_</a>	Alignment	not modelled	100.0	26	dehydrogenase.; <b>PDBTitle:</b> crystal structure of human short-chain acyl coa dehydrogenase
29	<a href="#">c1siqA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaryl-coa dehydrogenase; <b>PDBTitle:</b> the crystal structure and mechanism of human glutaryl-coa2 dehydrogenase
30	<a href="#">c3mpjG_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> glutaryl-coa dehydrogenase; <b>PDBTitle:</b> structure of the glutaryl-coenzyme a dehydrogenase
31	<a href="#">c6fahD_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit carc; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
32	<a href="#">c3pfdB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of an acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to reduced flavin adenine dinucleotide solved3 by combined iodide ion sad mr
33	<a href="#">c3r7kB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable acyl coa dehydrogenase; <b>PDBTitle:</b> crystal structure of a probable acyl coa dehydrogenase from2 mycobacterium abscessus atcc 19977 / dsm 44196
34	<a href="#">c4l1fB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase domain protein; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
35	<a href="#">c3eomD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glutaryl-coa dehydrogenase; <b>PDBTitle:</b> 2.4 a crystal structure of native glutaryl-coa dehydrogenase from2 burkholderia pseudomallei
36	<a href="#">c1r2jA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein fkbj; <b>PDBTitle:</b> fkbj for biosynthesis of methoxymalonyl extender unit of fk5202 polyketide immunosuppresant
37	<a href="#">c3nf4B_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of acyl-coa dehydrogenase from mycobacterium2 thermoresistibile bound to flavin adenine dinucleotide
38	<a href="#">c6cy8B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> butyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of fad-dependent dehydrogenase
39	<a href="#">c2dvlB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of project tt0160 from thermus thermophilus hb8
40	<a href="#">c4u83A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> structure of brucella abortus butyryl-coa dehydrogenase
41	<a href="#">c3mkhC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitroalkane oxidase; <b>PDBTitle:</b> podospora anserina nitroalkane oxidase
42	<a href="#">c5lnxC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of mmgc, an acyl-coa dehydrogenase from bacillus2 subtilis.
43	<a href="#">c2ebaI_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> putative glutaryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the putative glutaryl-coa dehydrogenase from2 thermus thermophilus
44	<a href="#">c4w9uD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of an acyl-coa dehydrogenase from brucella2 melitensis
45	<a href="#">c4doyE_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme c; <b>PDBTitle:</b> crystal structure of dibenzothiophene desulfurization enzyme c
46	<a href="#">c2rehD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitroalkane oxidase; <b>PDBTitle:</b> mechanistic and structural analyses of the roles of arg4092 and asp402 in the reaction of the flavoprotein nitroalkane3 oxidase
47	<a href="#">c1bucB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> butyryl-coa dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of butyryl-coa dehydrogenase from2 megasphaera elsdenii
48	<a href="#">c2wbiB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase family member 11; <b>PDBTitle:</b> crystal structure of human acyl-coa dehydrogenase 11
49	<a href="#">c4rm7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> the crystal structure of acyl-coa dehydrogenase from slackia2 heliotrinireducens dsm 20476
50	<a href="#">c4m6zB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein] dehydrogenase mbtn; <b>PDBTitle:</b> crystal structure of an acyl-acp dehydrogenase
51	<a href="#">c3m9vA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent oxidoreductase; <b>PDBTitle:</b> x-ray structure of a kjid3 in complex with dtdp
52	<a href="#">c5xdcB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thermophilic dibenzothiophene desulfurization enzyme c;

						<b>PDBTitle:</b> crystal structure of indole-bound tdsc from paenibacillus sp. a11-2
53	<a href="#">c5ez3B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure acyl-coa dehydrogenase from brucella melitensis in2 complex with fad
54	<a href="#">c4x28D_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> acyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the chse4-chse5 complex from mycobacterium2 tuberculosis
55	<a href="#">c2jbtA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p-hydroxyphenylacetate hydroxylase c2\oxygenase <b>PDBTitle:</b> structure of the monooxygenase component of p-2 hydroxyphenylacetate hydroxylase from acinetobacter3 baumannii
56	<a href="#">c5mr6R_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> xiaf protein; <b>PDBTitle:</b> xiaf from streptomyces sp. in complex with fadh2 and glycerol
57	<a href="#">c5gj7A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa dehydrogenase type 2 domain protein; <b>PDBTitle:</b> putative acyl-coa dehydrogenase
58	<a href="#">c3djlA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein aidb; <b>PDBTitle:</b> crystal structure of alkylation response protein e. coli aidb
59	<a href="#">c4y9lB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein acdh-11, isoform b; <b>PDBTitle:</b> crystal structure of caenorhabditis elegans acdh-11
60	<a href="#">c2rfqA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hsa hydroxylase, oxygenase; <b>PDBTitle:</b> crystal structure of 3-hsa hydroxylase from rhodococcus sp. rha1
61	<a href="#">c2or0B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxylase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative hydroxylase2 from rhodococcus sp. rha1
62	<a href="#">c4zxvB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dnmz; <b>PDBTitle:</b> streptomyces peucetius nitrososynthase dnmz in ligand-free state
63	<a href="#">c1w07A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa oxidase; <b>PDBTitle:</b> arabidopsis thaliana acyl-coa oxidase 1
64	<a href="#">c2ddhA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa oxidase; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
65	<a href="#">c2fonA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal acyl-coa oxidase 1a; <b>PDBTitle:</b> x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
66	<a href="#">c5k3jA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase; <b>PDBTitle:</b> crystals structure of acyl-coa oxidase-2 in caenorhabditis elegans2 bound with fad, ascaroside-coa, and atp
67	<a href="#">c3mxiB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrososynthase; <b>PDBTitle:</b> crystal structure of nitrososynthase from micromonospora carbonacea2 var. africana
68	<a href="#">c5y9dA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase 1; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase1 from yarrowia lipolytica
69	<a href="#">c5k3iH_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> acyl-coenzyme a oxidase; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase-1 in caenorhabditis elegans2 complexed with fad and atp
70	<a href="#">c5ys9A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase 3; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase3 from yarrowia lipolytica
71	<a href="#">d2c12a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
72	<a href="#">d1rx0a2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
73	<a href="#">d3mdea2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
74	<a href="#">d1jqia2</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
75	<a href="#">d2d29a2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
76	<a href="#">d1ukwa2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
77	<a href="#">d1egda2</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
						<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like

78	<a href="#">d1ivha2</a>	Alignment	not modelled	100.0	23	<b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
79	<a href="#">d1r2ja2</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
80	<a href="#">c3hwcD</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> chlorophenol-4-monoxygenase component 2; <b>PDBTitle:</b> crystal structure of chlorophenol 4-monoxygenase (tftd) of2 burkholderia cepacia ac1100
81	<a href="#">d1buca2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
82	<a href="#">d2ddha3</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> acyl-CoA oxidase N-terminal domains
83	<a href="#">d1sqa2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
84	<a href="#">d1w07a3</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> acyl-CoA oxidase N-terminal domains
85	<a href="#">c4g5eD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,4,6-trichlorophenol 4-monoxygenase; <b>PDBTitle:</b> 2,4,6-trichlorophenol 4-monoxygenase
86	<a href="#">c1u8vA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-aminobutyrate metabolism dehydratase/isomerase; <b>PDBTitle:</b> crystal structure of 4-hydroxybutyryl-coa dehydratase from clostridium2 aminobutyricum: radical catalysis involving a [4fe-4s] cluster and3 flavin
87	<a href="#">c2yyjA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylacetate-3-hydroxylase; <b>PDBTitle:</b> crystal structure of the oxygenase component (hpab) of 4-2 hydroxyphenylacetate 3-monoxygenase complexed with fad and 4-3 hydroxyphenylacetate
88	<a href="#">d1sqa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
89	<a href="#">d3mdea1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
90	<a href="#">d1egda1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
91	<a href="#">d1r2ja1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
92	<a href="#">d1ivha1</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
93	<a href="#">d1rx0a1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
94	<a href="#">d2d29a1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
95	<a href="#">d1jqia1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
96	<a href="#">d1lukwa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
97	<a href="#">d2c12a1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
98	<a href="#">d1buca1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
99	<a href="#">c6eb0A</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monoxygenase, oxygenase subunit; <b>PDBTitle:</b> structure of 4-hydroxyphenylacetate 3-monoxygenase (hpab), oxygenase2 compnon from escherichia coli
100	<a href="#">d2ddha1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> acyl-CoA oxidase C-terminal domains
101	<a href="#">d1w07a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> acyl-CoA oxidase C-terminal domains
102	<a href="#">d1u8va2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Acyl-CoA dehydrogenase NM domain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase NM domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains

103	<a href="#">c4oo2D_</a>	 Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase; <b>PDBTitle:</b> streptomyces globisporus c-1027 fad dependent (s)-3-chloro-β-2 tyrosine-s-sgcc2 c-5 hydroxylase sgcc apo form
104	<a href="#">d1u8va1</a>	 Alignment	not modelled	94.4	15	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Acyl-CoA dehydrogenase C-terminal domain-like <b>Family:</b> Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
105	<a href="#">c5okzj_</a>	 Alignment	not modelled	31.1	40	<b>PDB header:</b> rna binding protein <b>Chain:</b> J: <b>PDB Molecule:</b> m-phase phosphoprotein 6 homolog; <b>PDBTitle:</b> crystal structure of the mpp6 exosome complex
106	<a href="#">c2i9zB_</a>	 Alignment	not modelled	20.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative septation protein spovg; <b>PDBTitle:</b> structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228