

***Arabidopsis thaliana* Acyl-CoA Oxidase 1 in Complex with Acetoacetyl-CoA**

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Fatty acid breakdown is an essential process in all organisms, and the complex pathway require several sets of enzymes working in different cellular compartments. β -oxidation cycles are the center of the fatty acid breakdown, in each round the lipid chain shortening by a C_2 unit. The acyl-CoA oxidase family catalyzes the first and rate limiting step in the peroxosomal β -oxidation cycle, where acyl-CoA is converted to *trans*-2-enoyl-CoA. *Arabidopsis thaliana* have 4 different acyl-CoA oxidases, each with different chain length specificities. The structure of acyl-CoA oxidase 1 (ACX1), specific for long chain lipids, has previously been determined in our group.

We here present ACX1 in complex with acetoacetyl-CoA; the first structure of an acyl-CoA oxidase in complex with a substrate analogue. The fatty acyl moiety could be modeled between the isoalloxazine ring of FAD and the putative catalytic residue Glu424, forming hydrogen bonds to the backbone nitrogen of Glu424 and to N5 of FAD. Glu424 has moved to better accomodate the inhibitor, and is also more ordered in the complex structure. This confirms Glu424 to be the catalytic residue. The beginning of helix G and the end of helix H has moved slightly, and an interesting rotamer change of His374 and Tyr278 can be observed, bringing both residues closer to the CoA tail of the modeled ligand.

Keywords: acylCoA oxidase, beta oxidation, peroxisome