***Pseudomonas Aeruginosa* PA3859: from Structure to Function**

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We have recently purified a carboxylesterase from *Pseudomonas aeruginosa* that corresponds to the open reading frame PA3859 [1]. The biochemical characterization of this enzyme showed that it hydrolyzes short chain fatty acid esters with a broad substrate specificity. However, its biochemical characterization did not provide insights into a clearly defined *in vivo* function.

Neither bioinformatics tools did provide hints on its physiological function: useful information could not be gained by data mining for homologs or orthologs.

The successful crystallization and 3D structure determination of PA3859 at 2.1Å resolution provided new insights into the structural basis for its *in vivo* substrate(s) specificity. The presence on the protein surface, next to the active site, of an hydrophobic cleft exposed to the solvent has been hypothesized as the possible protein *hot spot* binding site that may accommodate an alkylic chain. This hypothesis was also supported by the localization of genes involved in lipid metabolism in the vicinity of the PA3859 locus. Docking of a variety of phospholipids suggested lysophopsphatidylcholine as potential substrate. We have established, by an enzymatic bioassay, that PA3859 is indeed able to release free fatty acid from lysophosphatidylcholine.

[1] Pesaresi A., Devescovi G., Lamba D., Venturi V., Degrassi G., *Curr. Microbiol.,* 2005, **50**, 102.

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