**Targeting mechanisms of Pseudomonas aeruginosa pathogenesis**

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**KEYWORDS**

*Pseudomonas aeruginosa*, cystic fibrosis, carboxylesterase, a/b hydrolase

**COLLABORATIONS**

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**DESCRIPTION**

*Pseudomonas aeruginosa (PA)* is a ubiquitous gram-negative bacterium that is capable of surviving in a broad range of natural environments, contributing to a wide variety of clinical infections. As such, a better understanding of the mechanisms by which this bacterium causes disease is crucial for the development of novel therapeutic strategies.

We have purified an intracellular putative carboxylesterase encoded by the open reading frame PA3859 of PA and elucidated its 3D crystal structure. With the ultimate aim of gaining deeper insights into the PA3859 function, the binding properties of the enzyme active site are currently exploited by enzymatic assay and automated X-ray diffraction methods. In vitro binding studies have shown that PA3859 binds specifically to a range of carboxylic acids, suggesting a role in the degradation of extracellular substrates. These findings may provide new avenues for the treatment of infections caused by *Pseudomonas aeruginosa*.


Pesaresi A, Lamba D. Insights into the fatty acid chain length specificity of the carboxylesterase PA3859. *Biochemie* (2010) under revision
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