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Ansto



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The Structure of PaeDAH7PS: a Potentially Promiscuous Protein

Pseudomonas aeruginosa is an opportunistic human pathogen associated with the chronic infection of the lungs of Cystic Fibrosis patients –New Zealand's most common lethal genetic disease. *P. aeruginosa* has an innate resistance to antibiotics and concerns exist around the appearance of multi-drug resistant strains [1].

The shikimate pathway is responsible for the biosynthesis of key aromatic metabolites including the aromatic amino acids phenylalanine, tyrosine, and tryptophan; folic acid; and, in the case of *P. aeruginosa*, the toxic secondary metabolite pyocyanin [2].

The determination of the crystal structure of a key enzyme in the shikimate pathway from *P. aeruginosa* reveals a distinct regulatory mechanism and provides only the second example of a crystal structure of this type of enzyme.

References:

[1] Davies, J. (1994) Inactivation of antibiotics and the dissemination of resistance genes, *Science* 264, 375-382.

[2] Lau, G. W., Hassett, D. J., Ran, H. M., and Kong, F. S. (2004) The role of pyocyanin in *Pseudomonas aeruginosa* infection, *Trends in Molecular Medicine* 10, 599-606.

Are you a student?

Yes

Do you wish to take part in the Student Poster Slam?

Yes

Are you an ECR? (<5 yrs since PhD/Masters)

No

What is your gender?

Male

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Track Classification: Structural Biology