

Cologne Evolution Colloquium

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A journey from an ancient finger print of Rossmann fold enzymes to cofactor engineering

Nucleoside-based cofactors are presumed to have preceded proteins. The Rossmann fold is one of the most ancient and functionally diverse protein folds. We analyzed an omnipresent Rossmann ribose binding interaction and identified a canonical motif, defined by unique geometry. This motif is uniquely found in Rossmann enzymes that use different cofactors. Overall, these data indicate the divergence of several major Rossmann-fold enzyme classes from a common pre-Last Universal Common Ancestor (LUCA).

While we were studying how Rossmann fold enzyme binding ribose based cofactor evolves, the adenosine mode of binding attracted our attention. Based on this observation we started our cofactor engineering studies to remodel the catalytic site for a new cofactor. Our approach may provide a powerful tool to study the cellular roles of cofactor binding enzymes in cell.

Wednesday, December 5, 2018, 16:00

University of Cologne

Institute for Biological Physics, Zùlpicher Str. 77a

Seminar Room 0.03, Ground Floor

Hosted by Michael Lässig