DGK conference 2022



Contribution ID: 218 Type: Talk

The crystal structure of AMP deaminase as starting point for the design of new herbicides

Tuesday, 15 March 2022 15:00 (20 minutes)

The crystal structures of adenosine monophosphate deaminase (AMPD) from Arabidopsis thaliana were determined in an unligated form and in complex with the herbicidally active natural compound conformycin phosphate. Comparison of the structures revealed large conformational changes upon ligand binding and allowed a detailed view into the enzyme's mechanism. The results were used for the mechanism and structure based design of new AMPD inhibitors.

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Session Classification: Biocrystallography: Drug Design