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

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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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