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PROTEIN BINDING TO TETRACYCLINES: INHIBITOR, REGULATOR, SUBSTRATE

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This review will give a short overview on structural biology of tetracyclines. The group of tetracycline are one of the "big four" of antibiotic compounds. Tetracyclines block the bacterial protein synthesis by binding to the ribosomal 30S subunit. Crystal structure analyses of proteins that mediate resistance against the drug belong to a widespread efflux mechanism (Tet repressor controlled) and a chemical inactivation by a flavin monooxygenase (TetX). Non-antibiotic properties are also well known: tetracyclines interfere with inflammatory mechanisms by inhibiting Phospholipase A2. All these tetracycline binding proteins are characterized at atomic resolution. The tetracycline can act as a regulatory compound but is also a substrate or inhibitor for enzymatic mechanisms. The conclusion is that tetracyclines are an example for side effects of drugs that are more interesting than the obvious mode of action.

Biography

Winfried Hinrichs studied Chemistry and completed his PhD in 1983 at the University of Hamburg followed by Postdoctoral studies at the Rijksuniversiteit Leiden in 1984/5. He joined the group of Wolfram Saenger at the Free University of Berlin and expanded his crystallographic expertise to bio-crystallography (1986-1999). After a sabbatical in Strasbourg (IGBMC, Dino Moras) in 1998/99, he became a Full Professor in Biochemistry focused on Structural Biology at the University Of Greifswald, Germany. He was the Director of the Institute Of Biochemistry in 2008-2014 and retired in 2016. He has published about 120 papers in reputed journals and is serving as Topical Editor for *Biochemistry of Chemtexts*.

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