

Cover Picture

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The cover picture shows two representations of two potent competitive inhibitors of *Mycobacterium tuberculosis* and *Streptomyces coelicolor* dehydroquinase with a bacterial culture in the background. These enzymes operate in the shikimic acid pathway, which is an important target for the development of new antibiotics. On the right, the bioactive conformation of the 3-nitrophenyl derivative as bound to the *Mycobacterium tuberculosis* active site, obtained from NMR spectroscopy, is highlighted. On the left, the picture depicts the proposed binding mode for the most potent inhibitor reported to date against any dehydroquinase, a 6-benzothiophenyl derivative (4 nM). For more details, see the Full Paper by C. González-Bello et al. on p. 194 ff.

