BIOMOLECULAR CONCEPTS

DE GRUYTER

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COVER ILLUSTRATION

The cover illustration represents MurD enzyme from *Escherichia coli* showing superposition of its closed conformation (green, PDB entry: 2UAG) with two open conformations (blue, PDB entry: 1E0D; red, PDB entry: 1EEH). MurD belongs to the Mur ligase family. It participates in the biosynthesis of bacterial peptidoglycan, and as such it constitutes an attractive target for new antibacterial compounds. Recent research efforts have led to the deciphering of its reaction mechanism, the characterization of several orthologs from pathogenic bacteria, the availability of several co-crystal structures, and the discovery of different classes of inhibitors. With the great amount of data accumulated, efforts can now be devoted to the design and synthesis of panactive MurD inhibitors that could be developed into broad-spectrum antibacterial agents. For further information about recent developments in MurD enzyme research including suggestions for the improvement of the enzyme's inhibitors, see the review article by Šink et al. on pp. 539–556 in this issue.

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Short Conceptual Overviews