Restored Affinity

CHEMISTRY

Vancomycin is a powerful antibiotic, which functions by binding to a pair of alanine residues and thereby disrupting the formation of bacterial cell walls. However, several strains of bacteria can

evolve to resist vancomycin through replacement of the terminal alanine with lactate. This structural substitution of an O atom for an N-H group

reduces vancomycin binding affinity by a factor of 1000. In a preliminary effort to combat this resistance pathway, Crowley and Boger have modified the vancomycin structure. Their prior modeling studies attributed the reduced affinity to lone pair repulsion between the lactate oxygen and a carbonyl oxygen in the vancomycin framework. They therefore prepared a synthetic derivative with a

methylene group replacing the offending carbonyl. This backbone substitution was deemed too fundamental a change to attempt by modifying intact vancomycin. Instead, the authors were able to adapt their prior total

synthesis of the native compound by introducing Vancomycin structure and binding motif in nonresistant (X = NH) and resistant (X = 0) bacteria.

the methylene group at the outset and protectgen as a carbamate.

strains. - JSY

OH ing the adjacent nitro-The resulting compound NHAc showed a 40-fold improvement in activity against cultures of resistant bacteria, with only a 37-fold loss in affinity

toward the Ala-Ala motif present in nonresistant

J. Am. Chem. Soc. 10.1021/ja0572912 (2006).

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