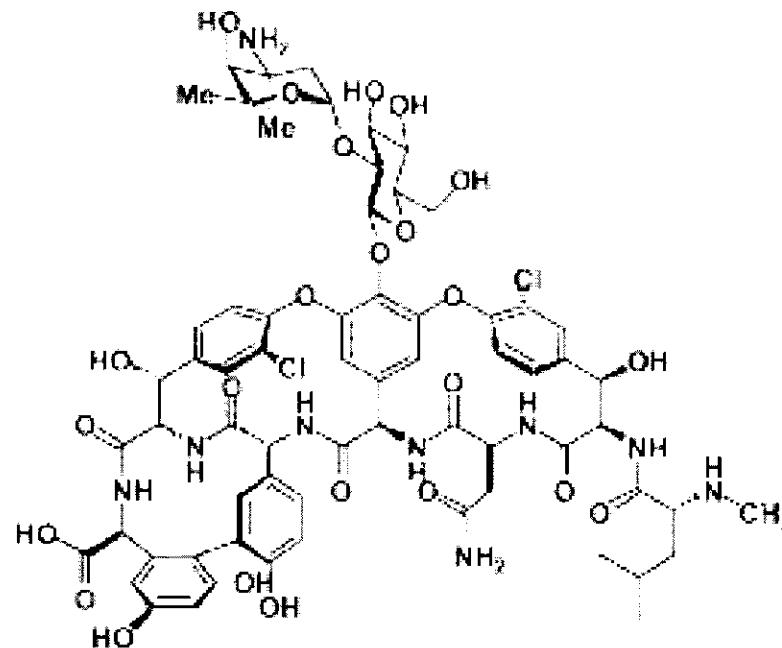
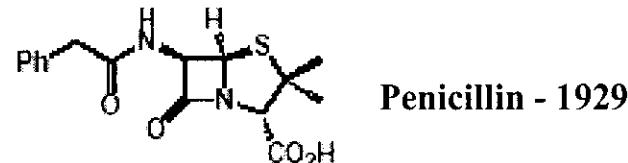


Partitioning the Loss in Vancomycin Binding Affinity for D-Ala-D-Lac into Lost H-Bond and Repulsive Lone Pair Contributions



Casey C. McComas, Brendan M. Crowley, and Dale L. Boger
J. Am. Chem. Soc. **2003**, 125, 9314

Antibiotics – Historical Perspective

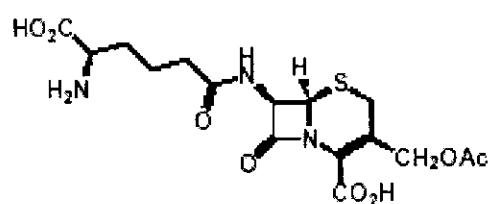


The Public Becomes Aware of Penicillin

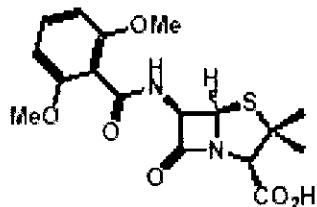
Given the political climate under which it was rediscovered and produced, it is not surprising that initially penicillin was used almost exclusively to treat soldiers injured during the war. That would change, though, with one fateful disaster.

Perhaps penicillin's most important clinical trial occurred after a fire at a Boston club, which resulted in numerous burn victims being sent to Boston-area hospitals. At that time, it was common for severe burn victims to die of bacterial infections, such as those from *Staphylococcus*. In response to this crisis, Merck rushed a large supply of a "priceless" drug (penicillin) to the Massachusetts General Hospital. The success that physicians had in treating severely burned victims that night was largely attributed to the effects of penicillin. The fire—and the success of penicillin—made national headlines, vaulting the drug into the public spotlight.

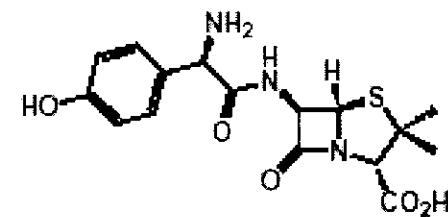
By 1946, the drug had become widespread for clinical use.



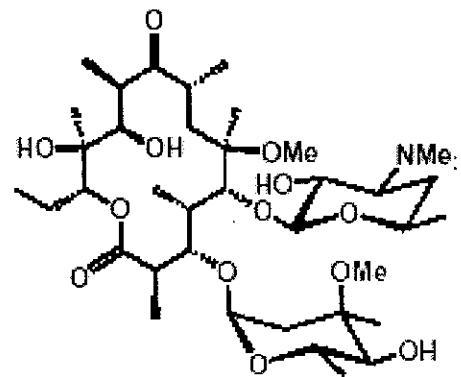
Cephalasporin - 1945



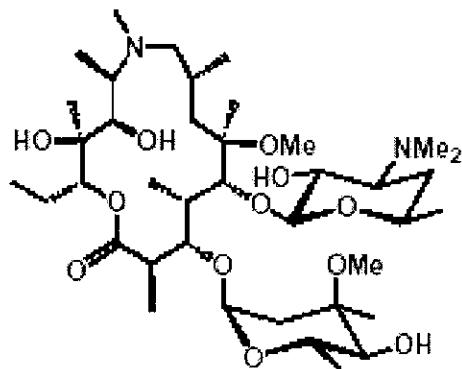
Methicillin - 1960



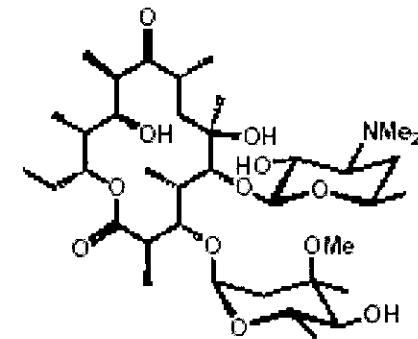
Amoxicillin - 1981



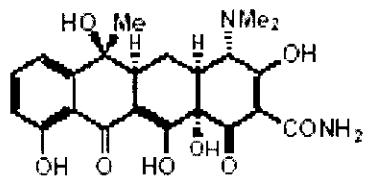
Erythromycin - 1952



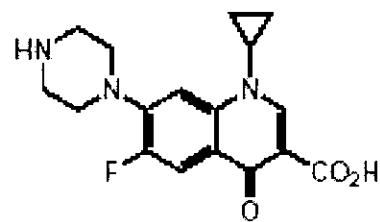
Azithromycin - 1988



Clarithromycin - 1990

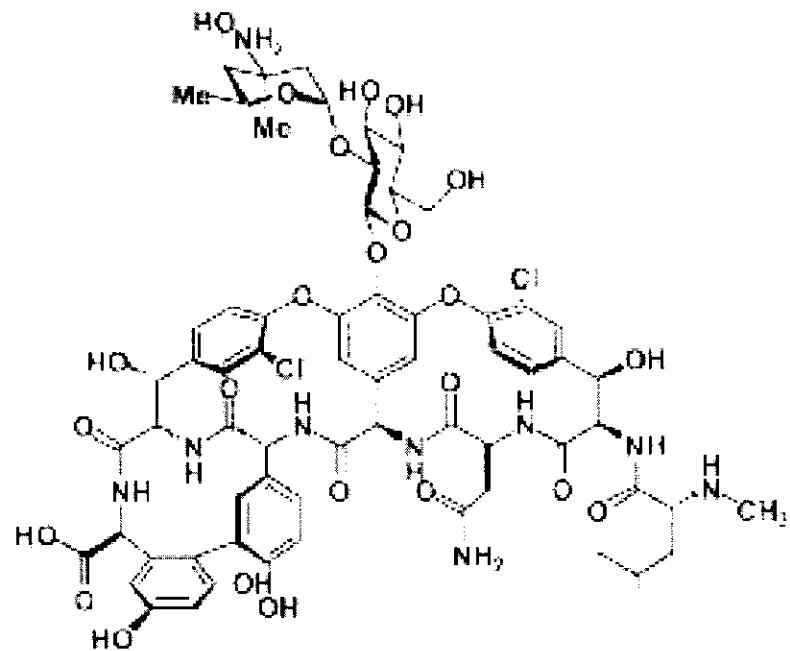


Tetracyclines - 1947

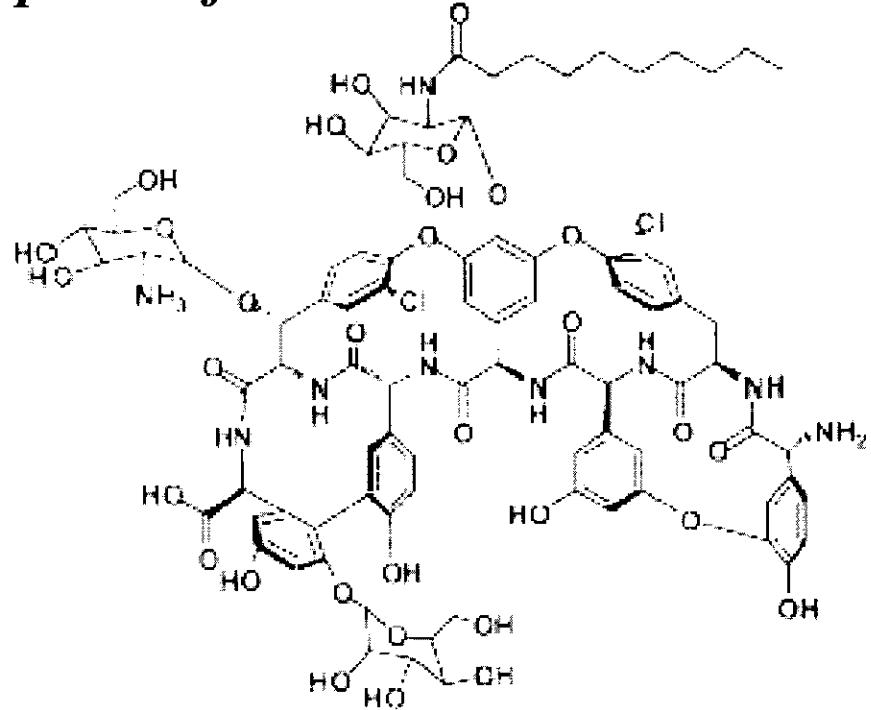


Ciprofloxacin

Glycopeptide Antibiotics Approved for Use in Humans

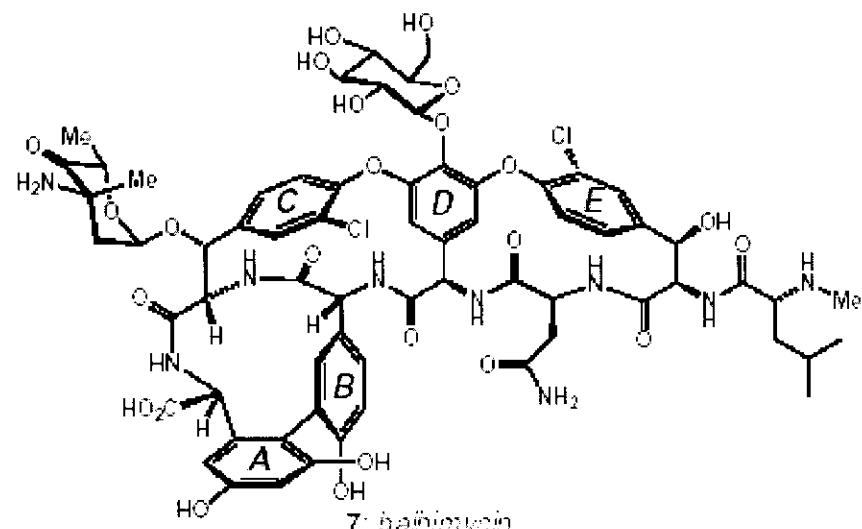


Vancomycin - 1956



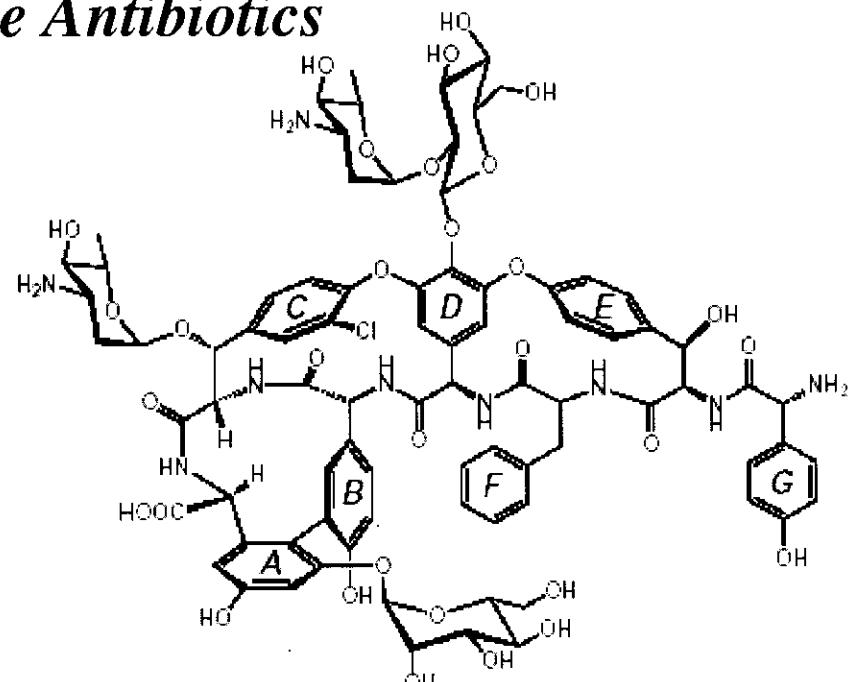
Teicoplanin - 1988

Other Glycopeptide Antibiotics



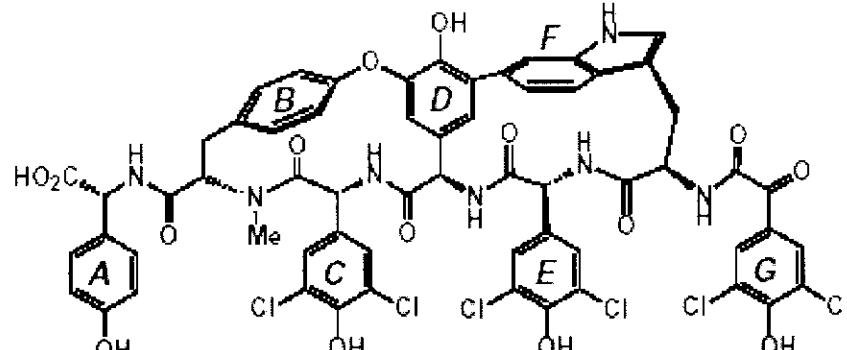
7: baflomycin

[type I: contain aliphatic chains in A4-1 and A4-3]

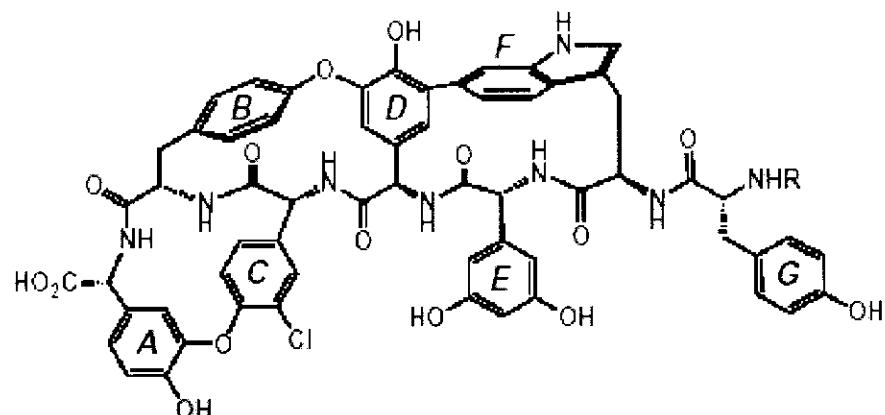


8: actinomycin A

[type II: contain aromatic chains in A4-1 and A4-3]



11: complestatin



13a: kistamicin A ($R = H$)

13b: kistamicin B ($R = CONHCH_2CH_2Ph$)

[type V: contain a tryptophan linked to central AA]

Sites of Action of Antimicrobial Agents

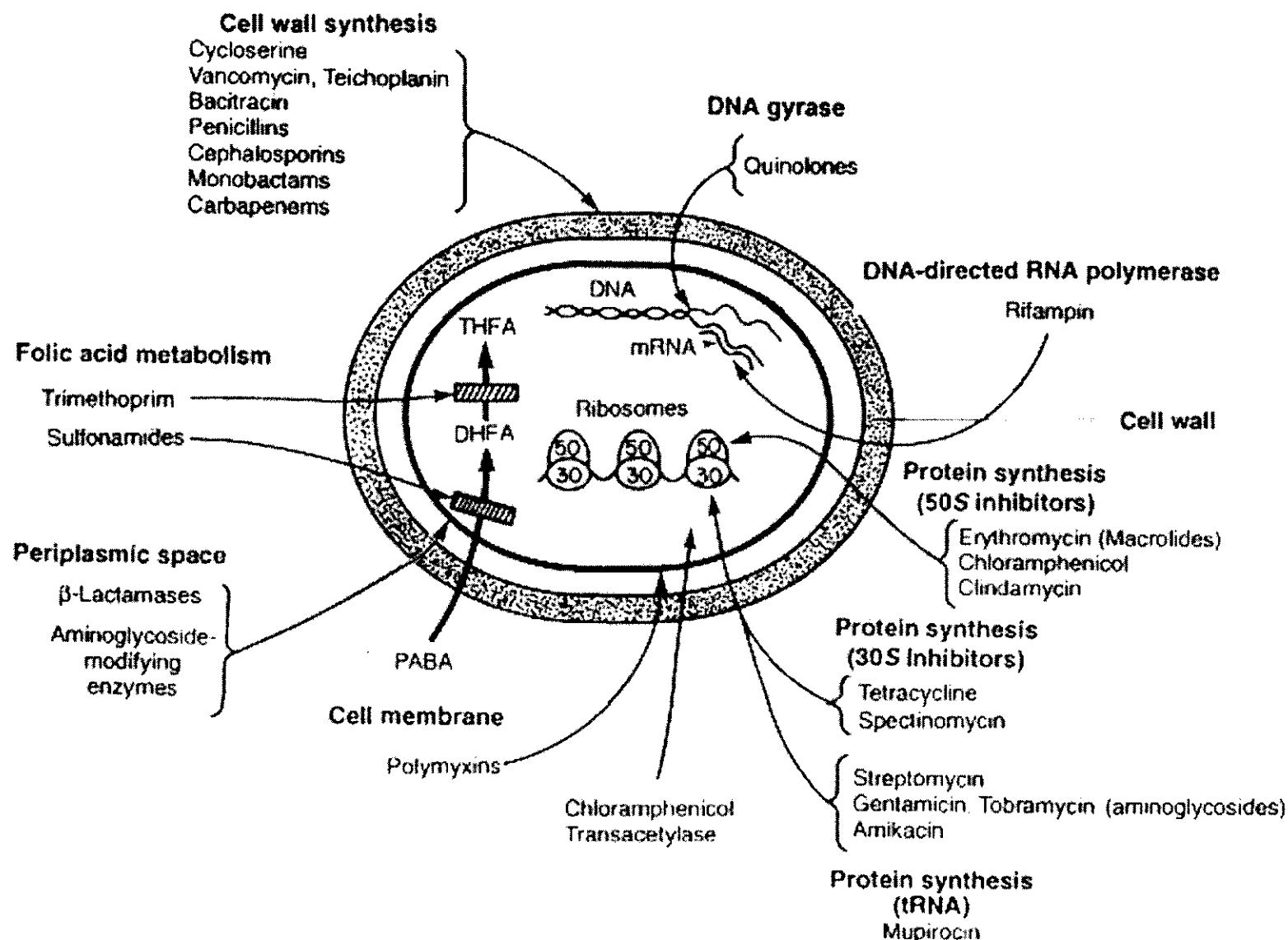


Fig. 1. Sites of action of various antimicrobial agents. mRNA, messenger RNA; tRNA, transfer RNA; PABA, p-aminobenzoic acid; DHFA, dihydrofolic acid; THFA, tetrahydrofolic acid.

Bacterial Targets and Resistance Mechanisms

Table 2: Antibiotic targets and resistance mechanisms.

Antibiotic	Target	Resistance mechanism
<i>cell wall</i>		
β -lactams	transpeptidase/transglycosylases (PBPs)	β -lactamases, PBP mutants
vancomycin	D-Ala-D-Ala termini of peptidoglycan and lipid II	reprogramming of D-Ala-D-Ala to D-Ala-D-Lac or D-Ala-D-Ser
teicoplanin	D-Ala-D-Ala termini of peptidoglycan and lipid II	reprogramming of D-Ala-D-Ala to D-Ala-D-Lac or D-Ala-D-Ser
<i>protein synthesis</i>		
erythromycins	peptidyl transferase/ribosome	rRNA methylation/efflux
tetracyclines	peptidyl transferase	drug efflux
aminoglycosides	peptidyl transferase	drug modification
oxazolidinones	peptidyl transferase	unknown
<i>DNA replication/ repair</i>		
fluoroquinolones	DNA gyrase	gyrase mutations

Modes of Transmission of Resistance

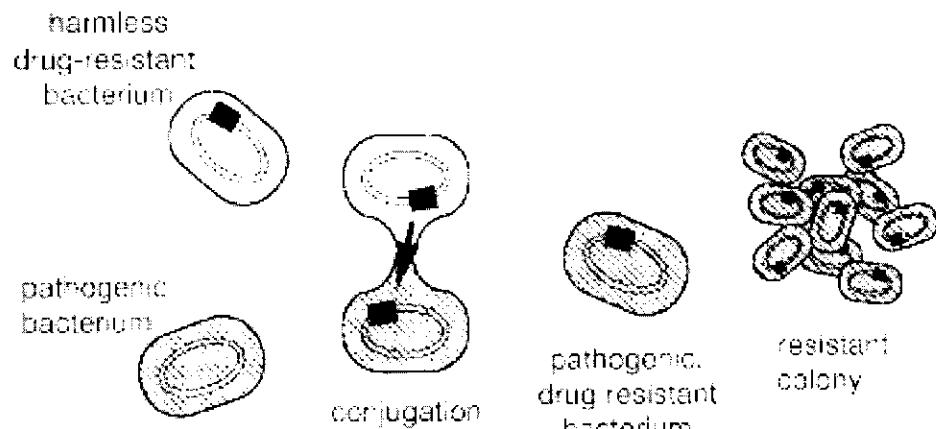


Figure 1. Drug resistance can be passed horizontally between species of bacteria. For example, a nonpathogenic, but antibiotic resistant bacterium can physically join with a disease-causing bacterium and pass on the genetic information required for antibiotic resistance through a process called conjugation. With the advantage of drug resistance, the pathogenic bacterium can then proliferate into an untreatable, disease-causing colony.

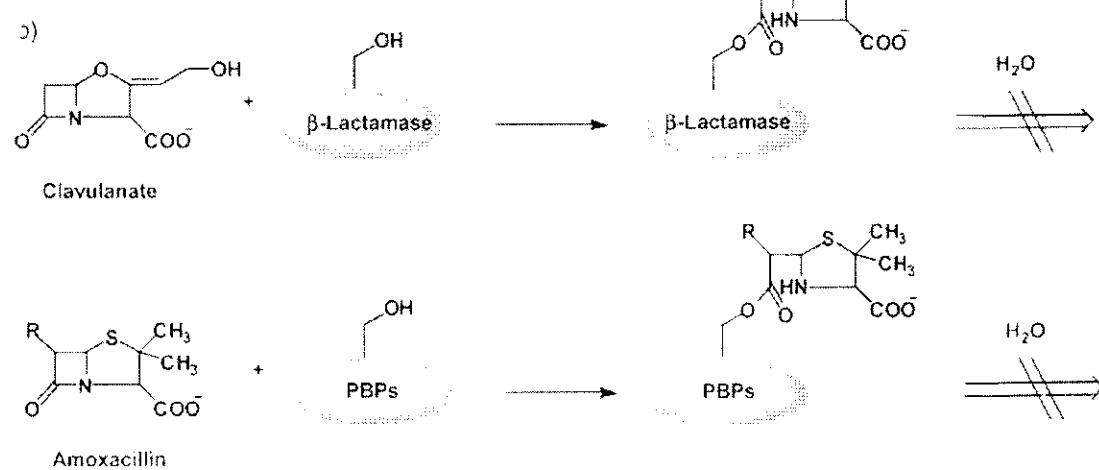
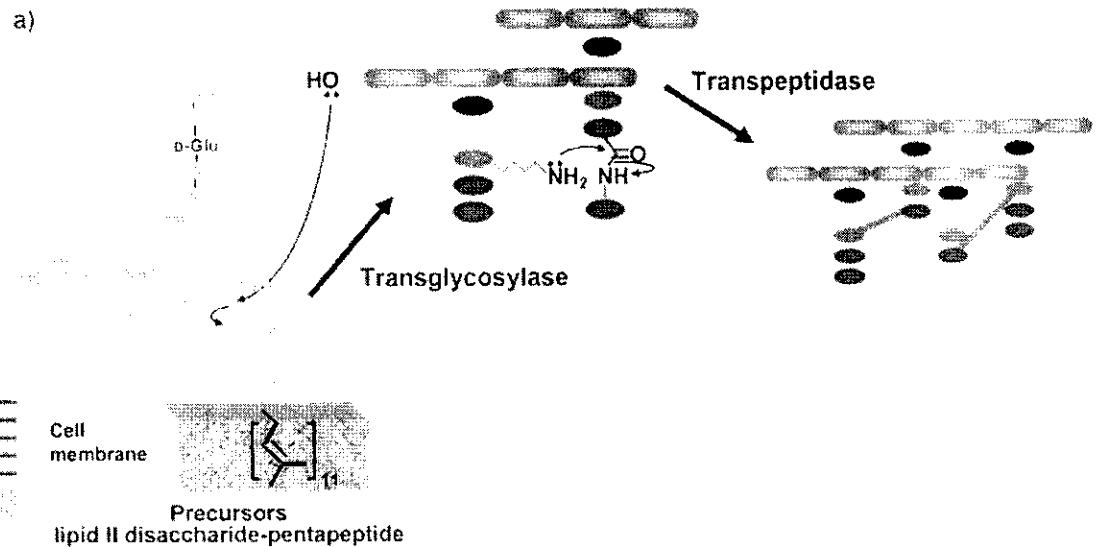
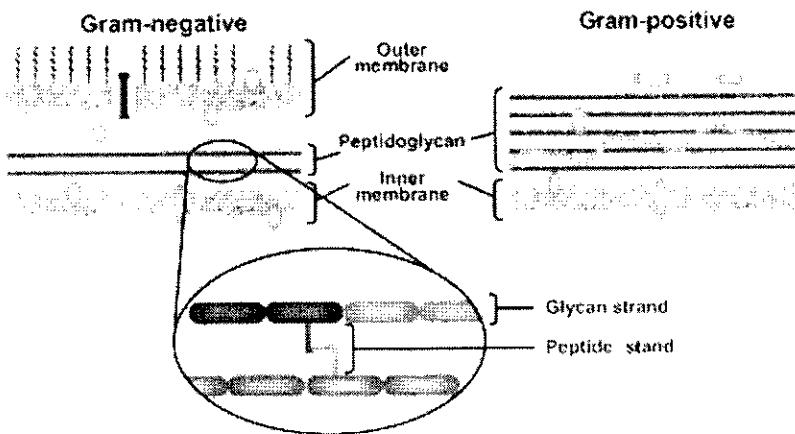
Williams, D. H.; Bardsley, B.
Angew. Chem. Int. Ed. Engl., 1999, 38, 1172



Figure 5. Three modes of resistance transfer between different bacteria: A) a plasmid containing the genes encoding for antibiotic resistance (yellow) is transferred from a donor bacterium to a new bacterium; B) bacterial DNA containing the genetic information for resistance is transferred through a virus to a new bacterium; C) incorporation of genes encoding for antibiotic resistance through DNA scavenged from dead cells.

Peptidoglycan Biosynthesis

Bacterial Cell Walls



How did Bacteria Become Vancomycin Resistant?

Vancomycin and other antimicrobial agents are themselves produced by bacteria. While evolving production of the anti-bacterials, these bacteria have also developed self-protection and immunity from these chemical weapons. The antibiotic production and antibiotic resistance genes are co-localized, enabling these genes to be turned on in concert. Often these genes code for transmembrane proteins that serve as efflux pumps keeping the intracellular concentration of the antibiotic below harmful levels. A more specialized resistance mechanism for two glycopeptide producing bacteria is shown below. This is believed to be the source of resistance for Vancomycin Resistant Enterococci (VRE).

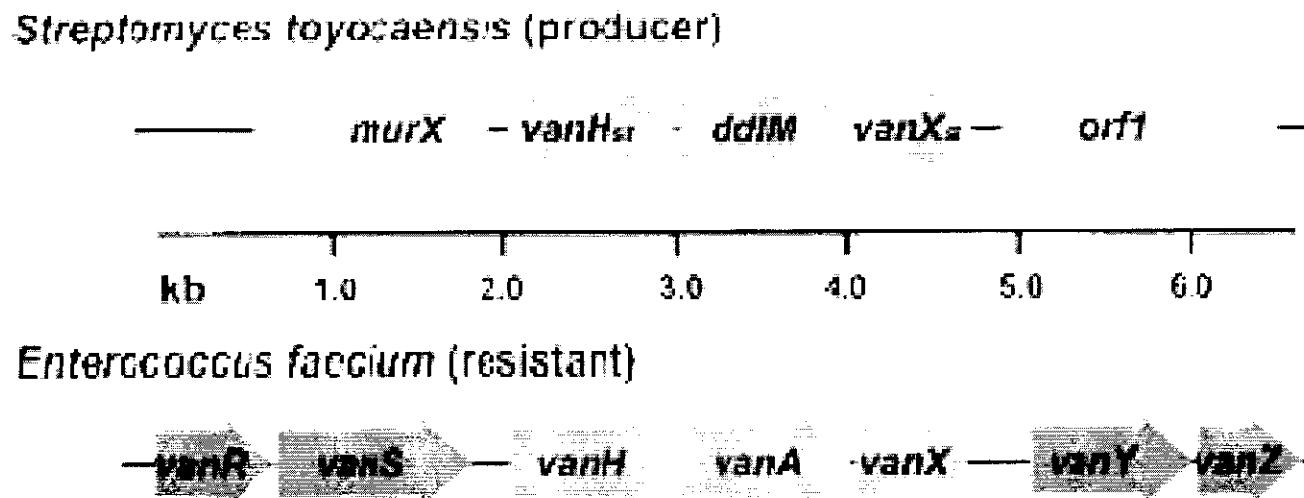
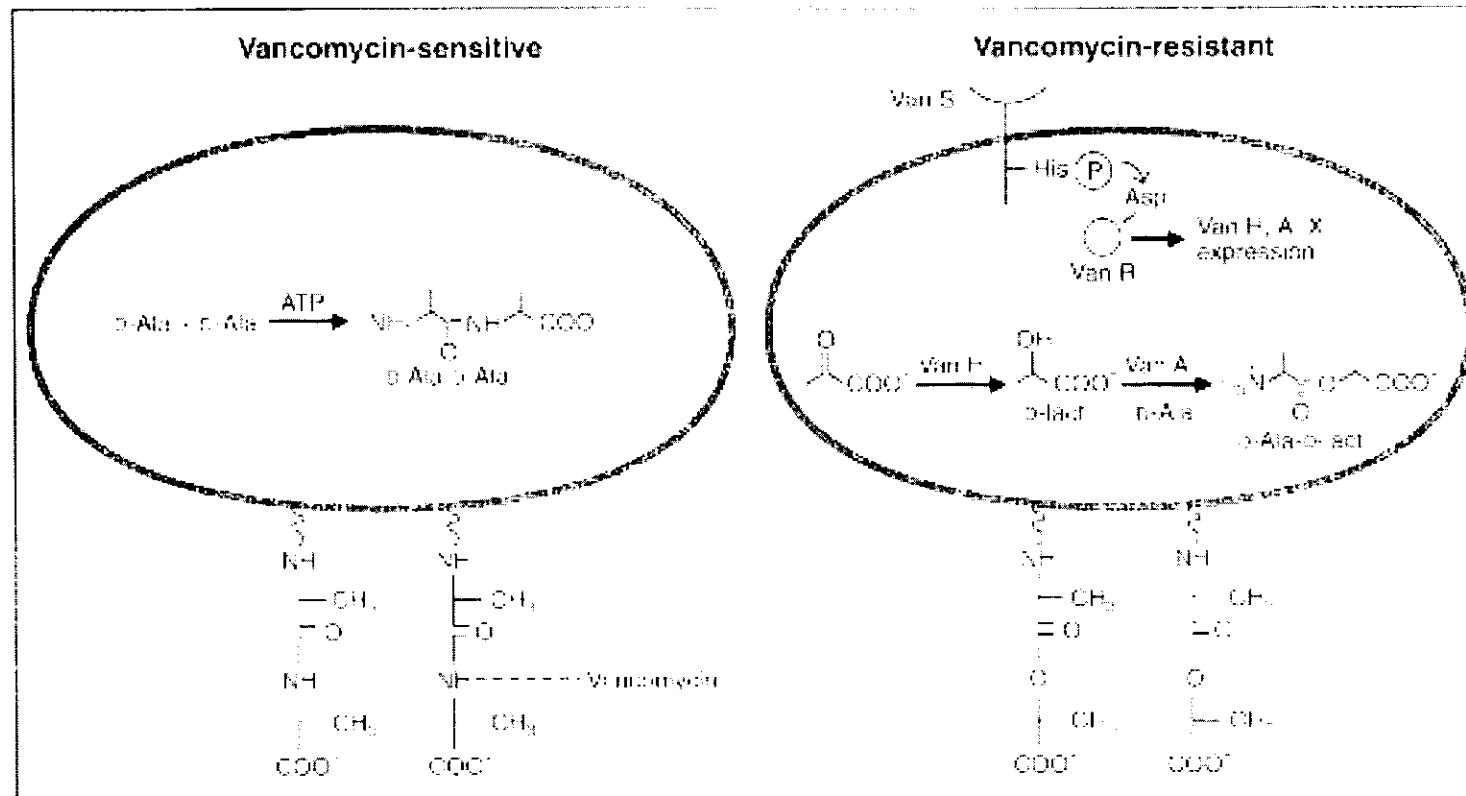


Figure 5. Gene cassettes for vancomycin resistance in the producing organism and resistant strains.



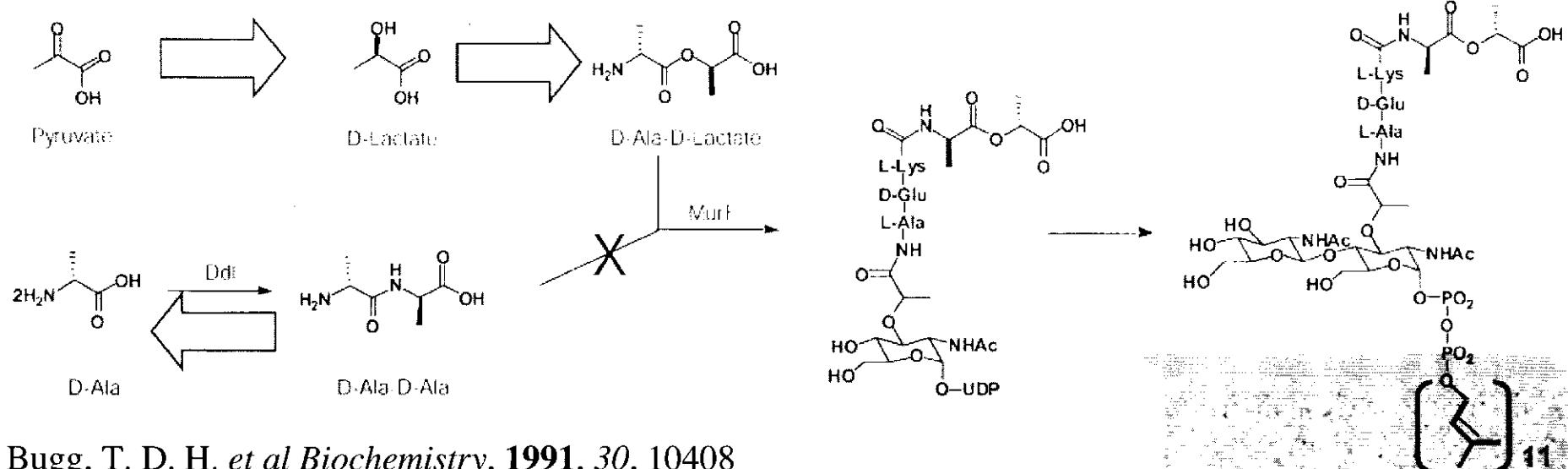
Molecular logic of vancomycin resistance. Vancomycin-sensitive and -resistant bacteria differ in a critical component of the cell wall. Sensitive bacteria (**left**) synthesize PG strands that terminate in D-Ala-D-Ala; vancomycin binds avidly to the α termini, thereby disrupting cell wall synthesis and leading to cell lysis. Resistant bacteria (**right**) harbor a transposable element encoding three proteins that contribute to the resistance phenotype. The gene products include a transcriptional regulator (Van S) that senses the presence of the drug and transmits a signal (by transfer of a phosphoryl group) to a response regulator protein (Van R) that activates transcription of the other resistance genes. The combined activities of Van H and Van A lead to synthesis of D-lactate, D-Ala-D-acetate, which can be incorporated into the PG strands of the cell wall. The altered PG termini do not affect the structural integrity of the cell wall, but substantially reduce its affinity for vancomycin, thereby rendering the bacteria resistant to the drug.

The Molecular Basis for Vancomycin Resistance

Table V: Vancomycin Binding Experiments^a

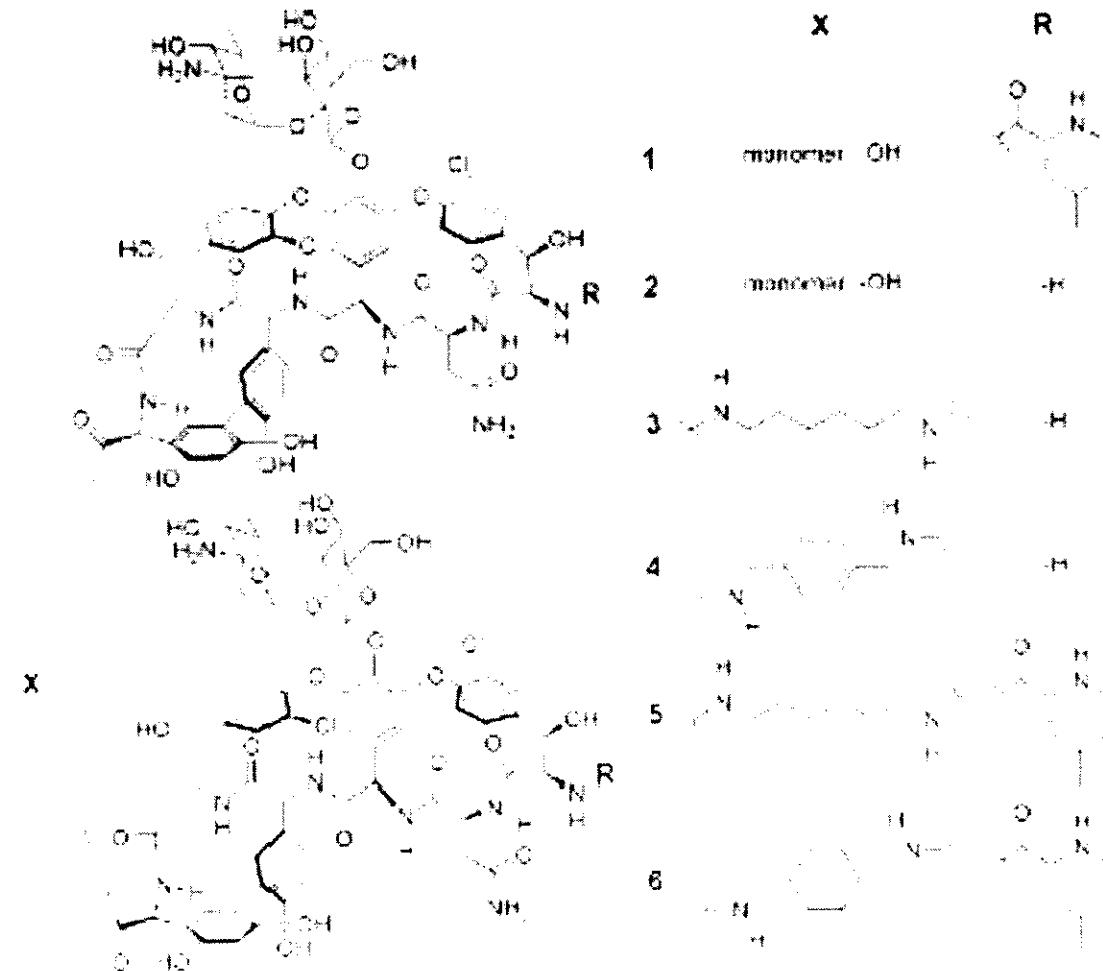
compound	K_d (mM)
NAc-D-Ala-D-Ala	0.054
NAc-D-Ala-D-Phe	>15 ^b
NAc-D-Ala-D-ABut	>18 ^b
NAc-D-Ala-D-Lac	>45 ^b
NAc-D-Ala-D-HBut	>73 ^b
N,N'-diacetyl-L-Lys-D-Ala-D-Ala	0.021
N,N'-diacetyl-L-Lys-D-Ala-D-Lac	>38 ^b

^a Binding assays were carried out using the UV binding assay of Nieto and Perkins (1971). ^b Little or no binding was observed at the highest ligand concentration (experimental error 10%). The lower limit quoted for K_d is five times the maximum concentration of ligand at which no binding is observed. Abbreviations: ABut, 2-amino-butyrate.



Synthesis and Activity of Vancomycin Dimers

Can pre-dimerization of Vancomycin lead to enhanced activity?



Glycopeptides Dimerize in the Presence of D-Ala-D-Ala

Table 1. Compound in Vitro Antibacterial Activity and Affinity for a Monomeric Model Peptide, dansyl-Lys(Ac)-D-Ala-D-Ala¹³

compound	MIC ($\mu\text{g/mL}$) ^a	K_d (μM) ^b
1	1200	1.3
2	> 1200	> 60
3	12	> 60
4	5.8	> 60
5	1.5	1.1
6	1.5	2.1

^a Measured against *E. faecium* (VanA phenotype).¹² ^b Determined at peptide = 1 μM , 25 °C, in 10 mM HEPES, 6 mM NaCl, pH = 7.0.

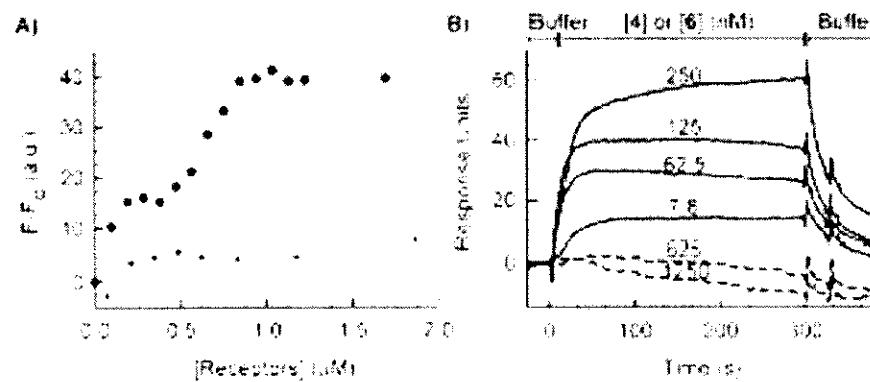
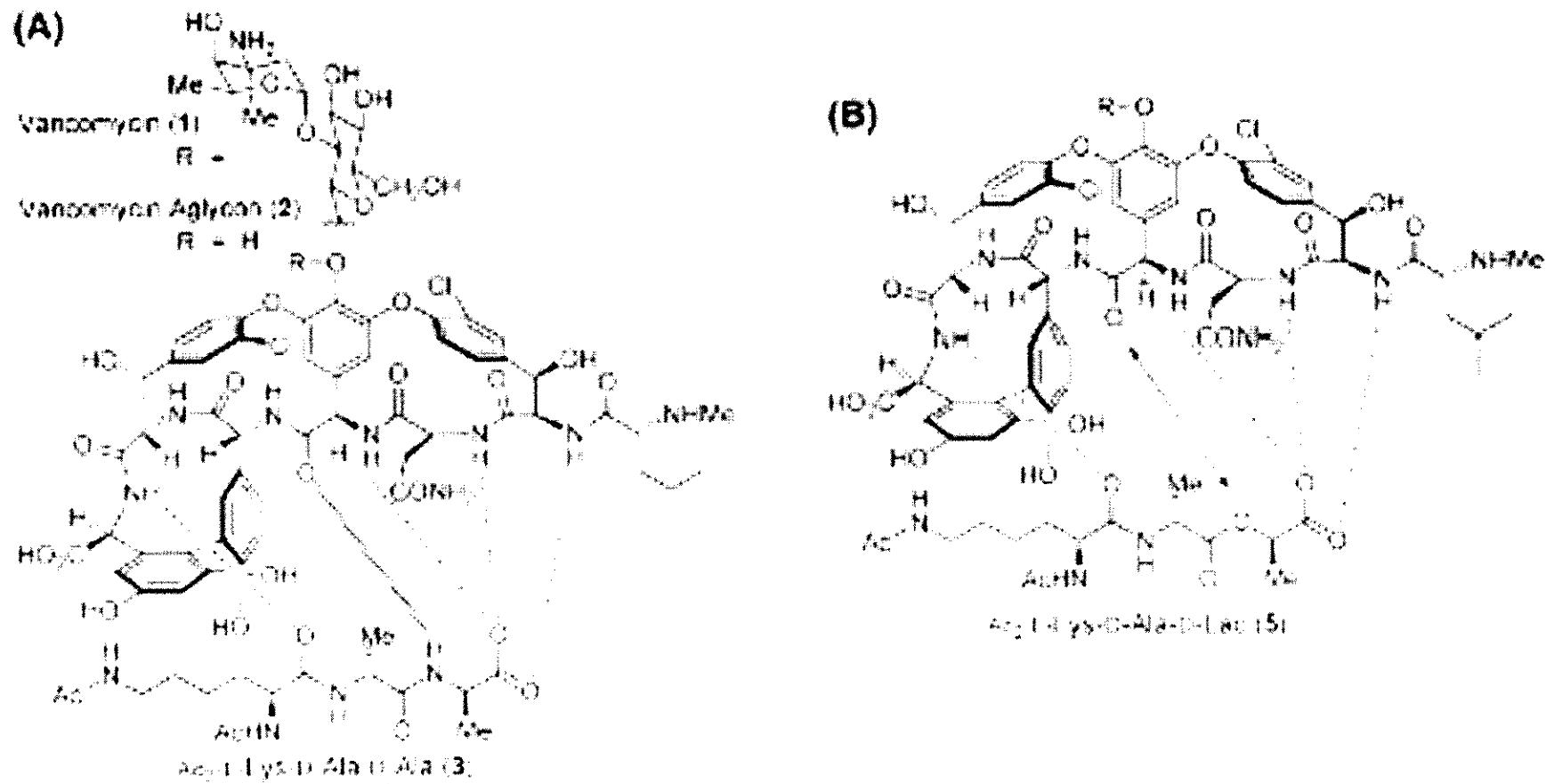


Figure 1. (a) Fluorescence titration of dimeric model peptide ϵ -N-succinyl-(dansyl-Lys-D-Ala-D-Ala)₂ with compounds 4 (+) and 6 (●). Determined at 25 °C, peptide = 1 μM , in 10 mM HEPES, 6 mM NaCl, pH = 7.0. (b) SPR sensorgrams of Ac-Lys-D-Ala-D-Ala immobilized surfaces eluted by indicated concentrations of 4 (dashed lines) or 6 (solid lines). Determined at 25 °C, in 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, 0.005% surfactant P-20.

The dimers prepared in this study show no binding to D-Ala-D-Lac, yet regain the activity of Vancomycin.

Partitioning the Loss in Vancomycin Binding Affinity for D-Ala-D-Lac into Lost H-Bond and Repulsive Lone Pair Contributions



Partitioning the Loss in Vancomycin Binding Affinity for D-Ala-D-Lac into Lost H-Bond and Repulsive Lone Pair Contributions

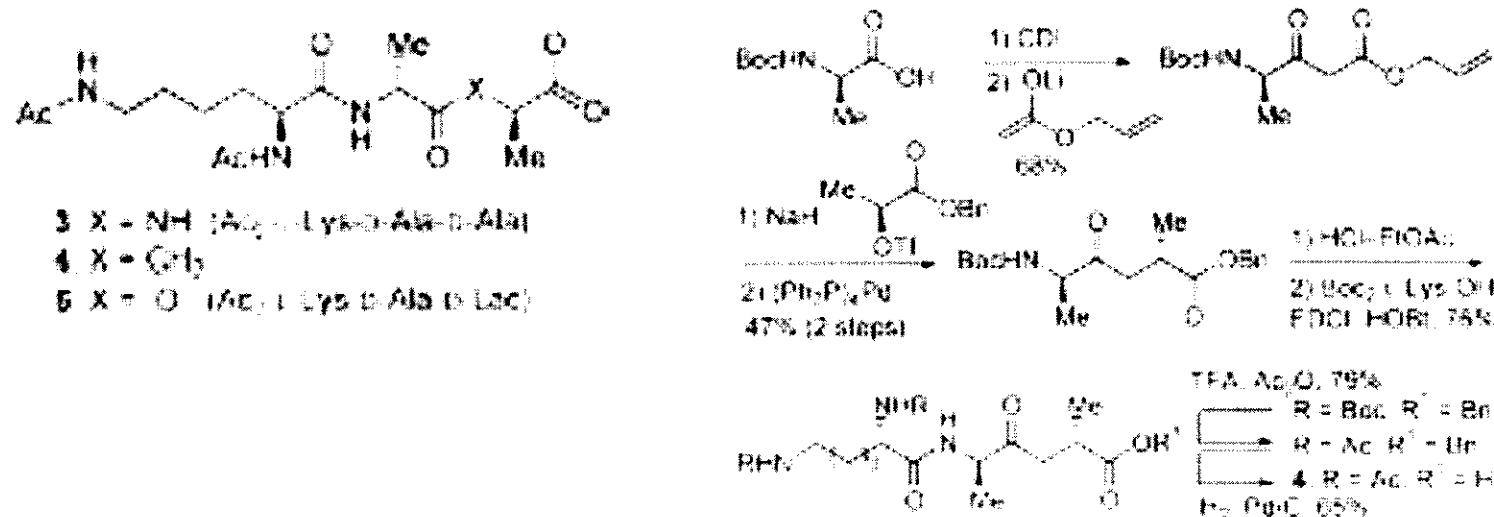


Table 1. Association Constants (K) and Binding Free Energy ($-ΔG'$, 25 °C)^a

Ligand	Vancomycin (1) K (M ⁻¹)	Vancomycin (2) K (M ⁻¹)	$-ΔG'$ (kcal/mol)
	(ΔΔE, kcal/mol)	(ΔΔE, kcal/mol)	
3 (X = NH)	4.4 × 10 ³ (7.7)	5.8 × 10 ³ (7.8)	1.5-1.8 kcal/mol
4 (X = CH ₂)	3.3 × 10 ³ (6.2)	2.5 × 10 ³ (6.0)	
5 (X = O)	4.3 × 10 ² (3.6)	3.1 × 10 ² (3.4)	2.6 kcal/mol

^a 25 °C, 0.0001 M vancomycin in 0.02 M sodium citrate, pH 5.1, observed at 270 nm. (cf 12)

Summary

- A number of model peptides or depsipeptides were prepared and their binding constants to Vancomycin and its aglycon were measured.
- The free energies of binding of the model compounds delineated the effect of H-Bond loss and repulsive lone-pair interactions.
- The loss in H-Bonding capability from D-Ala-D-Ala to D-Ala-D-Lac was determined to account for ~1.5 kcal/mol of the 4.1 kcal/mol (~1000 fold decrease in binding) that is lost. The lone-pair repulsion was found to account for the majority of the loss in binding affinity at 2.6 kcal/mol.