Structure-Guided Antibiotic Discovery Platform for MRSA

(No. T4-1760)

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Overview

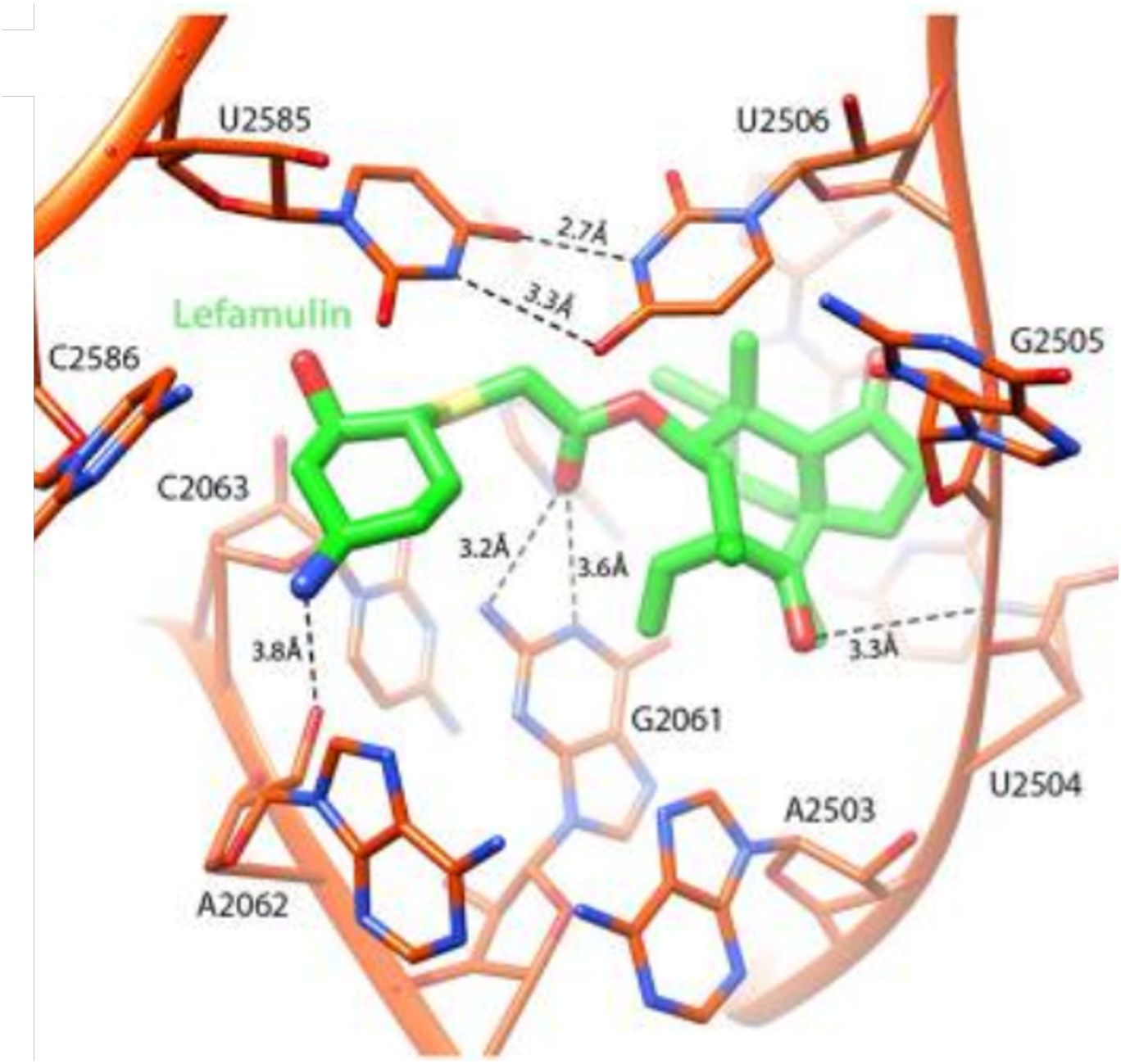
Antibiotic-resistant bacteria such as Staphylococcus aureus (MRSA) are a growing threat, causing severe infections that are increasingly untreatable by existing drugs. This technology provides a high-resolution crystal structure of the large ribosomal subunit (50S) from pathogenic S. aureus, enabling structure-based discovery of new antibiotic classes. Derived from a clinically relevant strain, the structure reveals novel, species-specific binding sites that can be exploited for precision antibiotic development.

Applications

- Structure-guided design of novel antibiotics targeting S. aureus and MRSA
- Computational screening and virtual docking of compound libraries
- Rational optimization of existing antibiotic scaffolds
- Structural biology resource for elucidating bacterial ribosomal mechanisms

Differentiation

- First high-resolution ribosome structure from a pathogenic S. aureus strain
- Antibiotic-soaked crystal structures reveal drugâ€“ribosome interaction sites
- Species-specific ribosomal differences provide unique antibacterial target



Zoom into the lefamulin (green) pocket in 23S rRNA (orange), showing U2585â€“U2506 interactions that stabilize binding and elucidate the antibioticâ€™s mechanism of action.

Development Stage

The 50S ribosomal subunit was crystallized from a pathogenic S. aureus strain, and several antibiotic-complex structures were resolved at high resolution, defining new binding pockets for rational drug design. The platform supports computational and experimental screening of next-generation antibiotic candidates.