

# The Structure of The Translating Bacterial Ribosome At 1.55 Å Resolution

Dr Simon Fromm<sup>1</sup>, Kate Marie O'Connor<sup>2</sup>, Dr Michael Purdy<sup>3</sup>, Dr Pramod R. Bhatt<sup>2</sup>, Dr Gary Longharn<sup>2</sup>, Dr John F Atkins<sup>2</sup>, Dr Ahmad Jomaa<sup>2</sup>, Dr Simone Mattei<sup>4</sup>

<sup>1</sup>*EMBL Heidelberg*, <sup>2</sup>*University College Cork*, <sup>3</sup>*University of Virginia*, <sup>4</sup>*EMBL Heidelberg*

[simon.fromm@embl.de](mailto:simon.fromm@embl.de)

Our understanding of protein synthesis has been conceptualised around the structure and function of the bacterial ribosome. This complex macromolecular machine is the target of important antimicrobial drugs, an integral line of defence against infectious diseases. Here, we present the structure of the translating ribosome from *Escherichia coli* at 1.55 Å resolution. A combination of improvements in sample preparation, microscopy hardware, data collection, and processing schemes with respect to previous studies allowed for this substantial advancement of the achievable resolution for an asymmetric and compositionally heterogeneous complex like the ribosome. The obtained structures allow for direct determination of the rRNA sequence to identify ribosome polymorphism sites in the *E. coli* strain used in this study and enable interpretation of the ribosomal active and peripheral sites at unprecedented resolution. This includes scarcely populated chimeric hybrid states of the ribosome engaged in several tRNA translocation steps resolved at ~2 Å resolution. The current map not only improves our understanding of protein synthesis but also allows for more precise structure-based drug design of antibiotics to tackle rising bacterial resistance.