

# Towards species-specific antibiotics that preserve the microbiome

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Many clinically useful antibiotics act by paralyzing ribosomes, the universal cellular machines that translate the genetic code into proteins. The so far available structures of ribosomes are from non-pathogenic bacteria that can be used as models for genuine pathogens, illuminated the antibiotics binding modes, inhibitory actions, synergism pathways, the differentiation between patients vs. pathogens and mechanisms leading to bacterial resistance. Nevertheless is Ribosomes, the universal cellular machines that translate the genetic code into proteins, are eless, species specific diversity was detected in susceptibility to infectious diseases. Consequently, our structural studies have been extended to ribosomes from genuine pathogens. The high resolution structures of the ribosomal particle from a genuine multi-resistant pathogen in complex with several antibiotics, highlighted subtle, albeit highly significant structural elements that can account partially or fully for species specificity and may lead to the design of species specific drug, while preserving the microbiome.