Utilizing Protein Crystallography and X-Ray Diffraction to Determine the Structure of TrmD (Crystallized with S-adenosylhomocysteine) from Mycobacterium abscessus

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Protein crystallography is a scientific process that typically involves solving the structure of the protein as a 3D model. The goal is to determine the structure of the tRNA (guanine-N(1)-)-methyltransferase (TrmD) protein from Mycobacterium abscessus bound with S-adenosylhomocysteine, a ligand required to execute the TrmD's process in bacteria. TrmD is a methyltransferase which uses S-Adenosylmethionine (SAM) to methylate the g37 nucleotide of a select group of tRNAs to reduce RNA wobble. Without methylation the ribosome is subject to frameshift errors that lead to nonfunctional proteins, and inhibition of bacterial growth and vitality1. This is exactly why we want to fully discover its structure, as it is a top ranking target for antibiotic inhibition since it's homolog in humans called Trm5 which does the same exact thing but with a different structure 1. Therefore, the goal is to understand the structure of the active site of TrmD by discovering and comparing models of the protein alone and bound to S-Adenosylhomocysteine (SAH) which is a product of the enzymatic reaction. This knowledge could help in finding inhibitors for TrmD. These potential inhibitors in the future could become new antibiotics to use against almost all bacteria (as TrmD is universal) and that may poses little risk of side effects in humans because of their enzyme's different structure.

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