Mycobacterium abscessus is a Gram - positive multidrug-resistant bacteria that is structurally related to M.tuberculosis and is a persistent problem in healthcare, especially for cystic fibrosis and immunocompromised patients. *M.abscesses* contains a bacterial protein called TrmD, which allows the bacteria to function by preventing frameshift errors at m'G37-tRNA during protein synthesis. This occurs through the transfer of a methyl group from a donor molecule, Adomet to the G37 codon. Inhibition of the TrmD enzymatic cycle will cause frameshift errors to occur, preventing the synthesis of membrane proteins resulting in cell growth inhibition. This gives TrmD the potential to be a key resource in the development of new antibiotics. Specific ligands, when bound to the TrmD active site, have the potential to inhibit methyltransferase reaction responsible for preventing +1 frameshift errors. Two possible inhibitors, 5'-Deoxy-5'-Methylthioadenosine (MTA) and Sinefungin, were used in co-crystallization experiments in our school lab. Trays with candidate crystals were delivered to BNL. Crystals that formed were harvested and stored in unipucks by Brookhaven National Laboratory scientists. X-ray diffraction data was collected remotely at FMX and AMX beamlines at the NSLS-II Synchrotron by SPARK teachers and students. Protein crystallization and computational methods were used to observe ligand interactions and conformational changes at the binding site to assess the potential for TrmD-specific antibiotic drugs.