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Comparative Analysis of Predictive 3D Atomic Modelling Programs with Mycobacteriophage Delylah Proteins

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Predictive 3D atomic models of proteins can be generated from amino acid sequences for unannotated Mycobacteriophage genes to assist in genome annotation by matching predictive 3D atomic models with 3D atomic models of similarly structured proteins with known functions. The structural comparison between unannotated Mycobacteriophage proteins and known function proteins can strengthen a function call if high-structural similarity is found. The goal of this analysis is to compare how different bioinformatic programs like Phyre, I-TASSER, and HHPRED Modeller generate predictive 3D atomic models for Mycobacteriophage Delylah proteins to elucidate which program may be a better predictor of 3D structure, and therefore, function. Currently, there are very few crystal structures of mycobacteriophage proteins in databases, which complicates the determination of which program is more accurate in 3D atomic model prediction. The structural output of genes with known functions from Mycobacteriophage Delylah will be analyzed in all three programs and compared based on program confidence levels. The structural outputs will also be super-imposed in PyMOL to visualize the differences and similarities between predicted structures for each protein analyzed. The findings of this analysis will demonstrate which protein structure modelling program is more comparable to known structures to improve protein analysis procedures.