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Determining the Function of the Hypothetical Protein Encoded By Gene Twenty-Two of the Makai Bacteriophage Genome

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Of the eighty-nine genes in the sequenced Makai bacteriophage genome, we used BLAST and HHpred to define sixty-four genes as coding for the function of “hypothetical proteins”. Due to the abundance of these proteins with unknown functions, we decided to investigate the function of one of these hypothetical proteins. After running the amino acid sequences of identified “hypothetical proteins” through SWISS-MODEL, we chose to investigate gene twenty-two due to its complex protein structure. SWISS-MODEL also defined the protein’s local and global quality estimates, coverage, and possible ligands. We ran the amino acid sequence through protein structure prediction programs InterPro, Phyre2, and ProFunc. We then identified domains, repeats, detailed signature matches, predicted GO terms, cellular components, and identified portions of gene twenty-two for which one protein function had been determined with 99.9%-100% confidence. Using these tools, we determined that the product of gene twenty-two in the Makai genome is involved in general catalytic activity as a function of hydrolase enzymes. Evidence supports that the function of gene twenty-two’s product in the Makai bacteriophage genome is that of a hydrolase enzyme. Based on the data available for other bacteriophages, we determined that this catalytic activity involving hydrolase enzymes occurs in the tail region of bacteriophage Makai and aids in the transference of DNA between virus and host.