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Understanding similarities and differences between membrane proteins in mycobacteriophage Izajani

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The mycobacteriophage Izajani, discovered in 2018 at Purdue University, is included in the 10% of phages classified in the Myoviridae family in the C1 cluster. The beginning of the genome, from 15-16456 bp, was annotated using PECAAN. In this base pair range, all of the genes faced forward and five functions were identified—membrane protein, nucleotidyl transferase, histidine triad nucleotide binding protein, band-7-like membrane protein, and ribbon-helix-helix DNA binding domain. Out of these 51 genes, six were classified as a membrane protein using TmHmm and SOSUI.  
  
The membrane protein function is identified only when the rest of the annotation programs (NCBI, PhagesDB, Phamerator, HHPred) call the gene function as “NKF”. TmHmm, a transmembrane helix prediction software, uses a hidden Markov model to predict membrane proteins. SOSUI is the second program that is used to identify membrane proteins by classifying the secondary structure of the gene to determine if it is a transmembrane or soluble protein. Membrane proteins, a type of protein found in the cell wall, are integral to the overall purpose of a genome. The more membrane proteins identified in a genome, the greater the chances that other molecules can be used with the phage. Because “membrane protein” is a classification of function, this project will focus on similarities and differences between membrane proteins identified in Izajani to see whether further classification could be possible in hopes of determining a more specific function call or classification.