Student Gene Annotation Worksheet

Name______________________________________ Date_______________________

Basic Phage Information	
Phage Name	
Gene #	
Stop Coordinate	
Direction (For/Rev)	
Gap (Overlap) with Previous Gene	
Selected Start Coordinate	
Selected Function	

Annotation Decision #3: What is the Function of the Putative Protein?

Gathering Evidence	Explain Your Rationale
Does this protein align with a protein having a functional assignment in BlastP (phagesDB and/or GenBank) with an alignment of 10^{-4} or smaller with appropriate coverage?	*List the most informative BlastP match from each source PhagesDB:* *NCBI:* *Hint: you may have already found this information from annotation decision #2. Provide the e-value and the Phage/gene#. It is only necessary to provide one match from each database.*
Does this protein align with a protein having a functional assignment in the PDB or other database in HHPred with a probability of 90% or greater with appropriate coverage?	*List the most informative HHPred match, including database source and probability score. It is only necessary to provide the best match.* *Note: If you believe there is not a quality HHPred match, type No Quality Match and list the data for the best match available to affirm the poor quality of the result and to document that HHPred was considered.*
Is this gene a possible transmembrane protein?	*If the answer is YES, indicate supporting data from at least 2 different transmembrane prediction programs. If TMHMM shows 1 transmembrane domain also check SOSUI which is another prediction program. Copy the protein sequence and enter at this website HERE*
Is the proposed function found on the SEA-PHAGES approved function list?	*Indicate a response with a Yes or No response. Once you have arrived at a functional decision, check the SEA-PHAGES Official Function List to ensure that you are following the guidelines for function naming. Functions that are not present on the approved list must be carefully vetted for approval.*
DECISION:	*If you believe this gene should be assigned, please write the name of the function here. If the evidence does not support a functional call, record "NKF" for no known function. 50-70% of phage genes fall into the NKF category.*