**Student tRNA Annotation Worksheet**

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| **Basic Phage Information** | |
| **Phage Name** |  |
| **Start Coordinate of tRNA** |  |
| **Stop Coordinate of tRNA (trimmed for CCA)** |  |
| **Direction (For/Rev)** |  |
| **Gap (Overlap) with Previous Gene** |  |
| **Anticodon** |  |
| **Amino Acid (three letter abbreviation)** |  |

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| **Gathering Evidence** | **Explain Your Rationale** |
| Was the tRNA called by web-based Aragorn, tRNAScan-SE, or both? | *Examine the data for the tRNA calling programs and indicate (YES BOTH, YES Aragorn only, YES tRNAScan-SE only, Neither)* |
| Does the infernal score of the tRNA meet [appropriate criteria](https://seaphagesbioinformatics.helpdocsonline.com/article-41)? | *List the infernal score of the tRNA provided by tRNAScan-SE. Indicate whether or not this score passes the scoring threshold specified in the* [*Bioinformatics Guide*](https://seaphagesbioinformatics.helpdocsonline.com/article-41)*.* |
| Does the tRNA meet appropriate inclusion criteria? | *tRNAs are usually less than 90 bp in length, are not found significantly overlapping protein encoding genes, and if present in the middle of a cluster of other tRNAs, are not found on the opposite strand within this cluster. Specify how the proposed tRNA meets or does not meet the above inclusion criteria.* |
| Does the acceptor stem loop have 7 base pairs? | *Respond with YES or NO* |
| Does the 3’ end of the tRNA contain the sequence CCA? | *Web-based Aragorn correctly trims the ends of the tRNA to meet this criterion. If the proposed tRNA was not called by Aragorn, trimming must be manually performed. The 3’ end of any tRNA that does not contain the CCA sequence should be trimmed at the first deviation from the CCA sequence.* |
| **DECISION:** | *Respond here with INCLUDED or NOT INCLUDED after reviewing the evidence gathered above. Specify the anticodon and amino acid of the tRNA in the table at the top of this document.* |