**Student Gene Annotation Worksheet**

|  |  |
| --- | --- |
| **Basic Phage Information** | |
| **Phage Name** | **Wardwill** |
| **Gene #** | **xx** |
| **Stop Coordinate** | **27218** |
| **Direction (For/Rev)** | **Rev** |
| **Gap (Overlap) with Previous Gene** | **-54** |
| **Selected Start Coordinate** | **27287** |
| **Selected Function** | **tRNA-OTHER** |

**Annotation Decision**

tRNAscan-SE v.2.0.12 (Nov 2022) scan results

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sequence  Name | tRNA # | tRNA  Begin | Bounds  End | tRNA  Type | Anti  Codon | Intron  Begin | Bounds  End | Inf  Score | Note |
| -------- | ------ | ----- | ------ | ---- | ----- | ----- | ---- | ------ | ------ |
| Microbacterium | 1 | 27287 | 27218 | Undet | NNN | 0 | 0 | 56.1 |  |

Microbacterium.trna1 (27287-27218) Length: 70 bp

Type: Undet Anticodon: NNN at 0-0 (0-0) Score: 56.1

\* | \* | \* | \* | \* | \* | \*

Seq: GGGCCGGTAGTTCAATTGGCTGAACACCATTGCGCGGGAGtTGTAGGTTCGAGTCCTACCCGGTCCACCA

Str: >>>>>>>..>>>>........<<<<.>>........<<....>>>>>.......<<<<<<<<<<<<....

RNAfold web server prediction of secondary structures

Imagen que contiene aire, tabla, collar, grande

El contenido generado por IA puede ser incorrecto.

Synteny conserved and present in other related phages:

Escala de tiempo

El contenido generado por IA puede ser incorrecto.