# MRA Rubric

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| Section Points | Section Criteria | Points | Comments |
| Title Page (2 points) | The title page includes:* Well-constructed, descriptive title
* Name of isolation host
* Name of the phage(s) in the MRA
 |  |  |
| Author List(2 points) | * All co-authors are listed
* Every co-author has a corresponding department and institution
 |  |  |
| Corresponding Author(1 point) | * A corresponding author is indicated with an email address
 |  |  |
| Abstract(5 points) | * The Abstract has 50 words or fewer. (Use word count to confirm the length of the abstract).
 |  |  |
| Background Information(5 points) | * This section of the paper describes the relevance of the investigation (e.g., why is this topic of interest).
 |  |  |
| Phage Isolation and Characterization(10 points) | Each item indicated below MUST be present in the text of the MRA for EACH phage included in the MRA

|  |  |
| --- | --- |
| * Bacteria Host
 | * Rounds of Purification
 |
| * Sample Type
 | * Plaque Morphology
 |
| * Sample Location
 | * Plaque Size
 |
| * Enriched vs Direct Plate
 | * Phage

Morphotype |
| * Media Type
 | * Capsid Size
 |
| * Isolation Temperature
 | * Tail Length
 |
| * Plaque Assay Incubation Time
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| Genome Isolation and Characterization(10 points) | Each item below must be present in the text of the MRA for each phage included in the MRA.

|  |  |
| --- | --- |
| * Sequencing Method
 | * Genome Length
 |
| * Sequencing Kit
 | * GC% Content
 |
| * Number of Reads
 | * Genome End Type
 |
| * Length of Reads
 | * Cluster Assignment
 |
| * Sequencing Coverage
 | * Character of genome ends
 |
| * Consed (version included)
* Newbler (version included)
 | * Tail Length
 |

 |  |  |
| Software Used for Annotation(5 points) | All software used for annotation of the complete genome should be included in the text of the MRA. All listed software must include a version number.

|  |  |
| --- | --- |
| * DNA Master
 | * BLASTp
 |
| * PECAAN
 | * HHPred
 |
| * Glimmer
 | * Aragorn
 |
| * GeneMark
 | * tRNAscanSE
 |
| * Starterator
 | * TMHMM
 |
| * Phamerator
 | * TOPCONS
 |

 |  |  |
| Genome Annotation(5 points) | The information in this section can very depending on phages included in the MRA. The information below must be included in the text of the MRA. * Number of genes
* Number and type of tRNAs
 |  |  |
| Nucleotide Sequence Accession Numbers(2 points) | Please check that the following information is present for each phage in the MRA.* GenBank Accession Number
* Sequence Read Archive (SRA) No.
 |  |  |
| References (3 points) | List of references cited for this paper.

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| --- | --- |
| * Newbler
 | * Consed
 |
| * DNA Master
 | * BLASTp
 |
| * PECAAN
 | * HHPred
 |
| * Glimmer
 | * Aragorn
 |
| * GeneMark
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