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