**MRA Faculty Checklist**

**This document is designed to assist faculty in completing the final check of an MRA prior to submission. Please ensure each listed element is included in the MRA to be submitted.**

* **Title:** MRA contains an appropriate title that includes the name of the isolation host and the name of the phage(s) described in the MRA
* **Author List:** All co-authors are represented in the author list with their corresponding department and institution
* **Corresponding Author:** A corresponding author is indicated with an email address
* **Abstract:** An abstract that is 50 words or fewer is present. Please use word count to confirm the length of the abstract.
* **Background Information:** The first paragraph of the MRA includes background information relevant to the host/phages included in the MRA
* **Phage Isolation and Characterization:** Each item indicated below must be present in the text of the MRA for each phage included in the MRA.
	+ Host
	+ Sample Type
	+ Sample Location
	+ Enriched vs Direct Plate
	+ Media Type
	+ Isolation Temperature
	+ Plaque Assay Incubation Time
	+ Rounds of Purification
	+ Plaque Morphology
	+ Plaque Size
	+ Phage Morphotype
	+ Capsid Size
	+ Tail Length
* **Genome Isolation and Characterization:** Each item indicated below must be present in the text of the MRA for each phage included in the MRA. Sequencing Method, Sequencing Kit, Assembly software, do not need to be repeated if they were the same for all phages included in the MRA.
	+ Sequencing Method
	+ Sequencing Kit
	+ Number of Reads
	+ Length of Reads
	+ Sequencing Coverage
	+ Software Used for Assembly
		- Consed (version must be included)
		- Newbler (version must be included)
	+ Genome Length
	+ GC% content
	+ Genome End Type
	+ Cluster Assignment
	+ Character of genome ends
* **Software Used for Annotation:** All software used for annotation of the complete genome should be included in the text of the MRA and in the reference list. *Please check that all listed software includes a version number.* Potential software to be included are listed below:
	+ DNA Master
	+ PECAAN
	+ Glimmer
	+ GeneMark
	+ Starterator
	+ Phamerator
	+ BLASTp
	+ HHPred
	+ Aragorn
	+ tRNAscanSE
	+ TMHMM
	+ TOPCONS
* **Genome Annotation:** The information in this section can vary depending on phages included in the MRA. At a minimum, the information listed below must be included.
	+ Number of genes
	+ Number and type of tRNAs
* **Nucleotide Sequence Accession Numbers:** Please check that the following information is present for each phage included in the MRA, and that both accession numbers are hyperlinked.
	+ GenBank Accession Number
	+ Sequence Read Archive (SRA) No.
* **References:** Below is a list of software that may have been used during sequencing/annotation for which a proper reference should be included.Other cited sources should also be included in the reference list.
	+ Newbler
	+ Consed
	+ DNA Master
	+ PECAAN
	+ Glimmer
	+ GeneMark
	+ Starterator
	+ Phamerator
	+ BLASTp
	+ HHPred
	+ Aragorn
	+ tRNAscanSE
	+ TMHMM
	+ TOPCONS