**Writing a Microbiology Resource Announcement**

**General Instructions**

You will write a **Microbiology Resource Announcement (MRA)** for the phage(s) that you annotated this semester (or quarter). This is a short paper (limit of 500 words) in which you will describe the details on the process and results of sequencing the genome(s), what software and databases were used to annotate the genome(s), and highlight interesting, unusual, exciting, or otherwise noteworthy findings from your genome or group of genomes. You will have no problem writing 500 words of text about your phage(s); in fact, the challenge will be for you to describe your phage(s) in *only* 500 words!

**Writing Resources**

A **Microbiology Resource Announcement** template will be provided to guide you through the various sections of the paper and what should be included in each one. We will provide a few published genome announcements but you may also visit the journal’s website at

 <https://mra.asm.org/> if you want to look at more writing samples.

Here is some helpful information for each section:

*Title page*: The title should be concise and usually includes the name of the host bacteria and name of the phage or phages being described (**not to exceed 54 characters and spaces**). Make sure to properly italicize species names. Manuscript titles are traditionally typed in **bold** font. Here’s an example: “Genome sequences of bacteriophages KaiHaiDragon and OneinaGillian isolated from *Microbacterium foliorum* in Riverside, California”. A few blank lines will separate the title from the manuscript authors. Here you would normally list all the paper’s authors and their affiliations in order, but you should list **only** your own name here for now.

*Abstract*: The abstract is **50 words or less** and summarizes the entire work. Here you should describe the host bacterium and the phage, and its general relationship to other phages. Because this is a summary of the rest of the paper, this section is usually written last.

Rest of paper/references (not including acknowledgments) = **500 words or less**

\*\*since the full MRA is 500 words, it is typically written **WITHOUT any headers**, see the examples. This does not mean that the paper does not have follow the sections below and the best ones “tell a story”.

*Introduction*: Like any paper, the genome announcement starts off with an introduction. Briefly, provide background information about the topic at large and the importance/relevance of said topic. For example, you must communicate why anyone should care that you have sequenced this genome, and we typically begin by talking about the bacterial host.

*Methods*: An important aspect of any scientific paper is that the methods are clearly outlined. The idea is that someone could follow exactly what you did. Since you were likely not involved in the isolation or sequencing of the phage you are annotating, we will provide you with all the information you need to write this section. Important information about the phage is also available on the website www.phagesdb.org. You will also need to include the programs/software used to annotate the genome. It will be up to you to arrange this information into prose. Please look at published genome announcement papers to see how other authors have done this.

*Genome content*: This section will include general information on your genome(s), such as genome length, number of protein coding genes and tRNA, genomic termini (if known), G+C content, cluster, general genome architecture, and relatedness to other genomes. **The last part of a genome announcement highlights interesting, unusual, exciting, or otherwise noteworthy findings from your genome or group of genomes.**

*Nucleotide sequence accession numbers and SRA information*: Before a Genome Announcement can be submitted to the journal, we must have an accession number for the genome and the SRA (Sequence Read Archive) information. This means that the annotation must be complete and sent off to NCBI for approval and University of Pittsburgh submits the SRA data. Typically, it takes 8-12 weeks from the initial submission date for a genome to appear in the database. We will add your genome’s accession number to your manuscript.

*References*: The References section (bibliography) is found at the end of papers and contains the complete reference for each of the in-text citations used in the paper. Generally, a citation includes the name of the author(s), year of publication, article title, name of the journal in which it was published, journal volume and page numbers. In the reference list, references are numbered in the order in which they are cited in the article. In the text, references are cited parenthetically by number in sequential order.

**Formatting:**

1. 12 point font; standard typeface like Times New Roman, Arial or Cambria.
2. 1 inch margin, double-spaced
3. Page numbering and line numbering for the manuscript should be turned on. Line numbers are controlled under the *Layout* tab in newer versions of MS Word.

**Submission Guidelines**:

1. Upload digital submissions to the Learning Management System (Blackboard, CANVAS, etc.) by the stated due dates (refer to the course syllabus). Late submissions are not accepted.
2. Please edit your work and confirm the file name before uploading.
3. Submission access ends at **X time** on the due date listed in the **Syllabus**