An Announcement is a brief report (limit of 500 words exclusive of the abstract and acknowledgments) stating that the genome of a particular organism (prokaryote, eukaryote, or virus) has been sequenced and providing a citable record of the corresponding GenBank submission.

I think we need some specific details about what technology was utilized to get the base pair sequence?

After reviewing a couple, the following list appears to be the general information that should / can be covered.

- Very brief overview of what’s going down with the gene banks (SEA-PHAGES project).

- Name and location of discovery of the mycobacteriophage.

- Method of isolation (enrichment vs direct plating), also host bacteria used.

- Morphology of plaques and virus.

- Sequencing tool, analysis, type of genetic material (double stranded DNA vs. single etc.), something about # fold coverage (not sure what that is)

- Length of genome in bp, % G&C, overhang if applicable

- GeneMark and Glimmer use and the number of predicted genes. Mention manual evaluation.

- Number of added or deleted genes and total.

- Discuss function determination and software.

- Number of tRNA’s and the software used.

- % identical to another mycobacteriophage with % span and use this to support cluster.

- Can do number of forward vs. backward transcribed genes if unusual (I think ours is a typical case)

- Comparison to other mycobacteriophages in the same cluster in terms of function, special features, and anything related to special features.

- Unique characteristics of the cluster.