REFERENCES

Akhter, S., Aziz, R. K., & Edwards, R. A. (2012). PhiSpy: A novel algorithm for finding PROPHAGES in bacterial genomes that combines similarity- and Composition-based strategies. *Nucleic Acids Research, 40*(16). doi:10.1093/nar/gks406

Arndt, D., Grant, J. R., Marcu, A., Sajed, T., Pon, A., Liang, Y., & Wishart, D. S. (2016). PHASTER: A better, faster version of the PHAST phage search tool. *Nucleic Acids Research, 44*(W1). doi:10.1093/nar/gkw387

Danovaro, R., Corinaldesi, C., Dell'Anno, A., Fuhrman, J. A., Middelburg, J. J., Noble, R. T., & Suttle, C. A. (2011). Marine viruses and global climate change. *FEMS Microbiology Reviews, 35*(6), 993-1034. doi:10.1111/j.1574-6976.2010.00258.x

Dunivin, T. K., Choi, J., Howe, A., & Shade, A. (2019). Refsoil+: A reference database for genes and traits of soil plasmids. *MSystems, 4*(1). doi:10.1128/msystems.00349-18

Gan, R., Zhou, F., Si, Y., Yang, H., Chen, C., Wu, J., . . . Huang, Z. (2020). DBSCAN-SWA: An integrated tool for rapid PROPHAGE detection and annotation. doi:10.1101/2020.07.12.199018

Klemetsen, T., Raknes, I. A., Fu, J., Agafonov, A., Balasundaram, S. V., Tartari, G., . . . Willassen, N. P. (2017). The mar databases: Development and implementation of databases specific for MARINE METAGENOMICS. *Nucleic Acids Research, 46*(D1). doi:10.1093/nar/gkx1036

Lin, H., & Lin, D. (2019). Faculty opinions recommendation of genetic and life-history traits associated with the distribution Of PROPHAGES in bacteria. *Faculty Opinions – Post-Publication Peer Review of the Biomedical Literature*. doi:10.3410/f.726236908.793561066

Malmstroem, L. (2020). Faculty opinions recommendation of 1,520 reference genomes from CULTIVATED human gut bacteria enable functional MICROBIOME ANALYSES. *Faculty Opinions – Post-Publication Peer Review of the Biomedical Literature*. doi:10.3410/f.734998228.793570170

Ondov, B. D., Bergman, N. H., & Phillippy, A. M. (2015). Krona: Interactive METAGENOMIC visualization in a web browser. *Encyclopedia of Metagenomics*, 339-346. doi:10.1007/978-1-4899-7478-5_802

Paez-Espino, D., Eloe-Fadrosh, E. A., Pavlopoulos, G. A., Thomas, A. D., Huntemann, M., Mikhailova, N., . . . Kyrpides, N. C. (2016). Uncovering EARTH'S virome. *Nature, 536*(7617), 425-430. doi:10.1038/nature19094

Roux, S., Enault, F., Hurwitz, B. L., & Sullivan, M. B. (2015). VirSorter: Mining viral signal from microbial genomic data. *PeerJ, 3*. doi:10.7717/peerj.985