

## 2022 Phage Genomics Workshop Resources December 5 – 9, 2022

*This document provides quick links to Bioinformatic Guide Entries and Video Tutorials on various topics.*

Annotation Topics	Readings	<a href="#">Short Videos</a>	Associated Tasks
<ul style="list-style-type: none"> <li>• Overview</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Introduction</a></li> <li>• <a href="#">Annotation Outline</a></li> <li>• <a href="#">Genome annotation Overview</a></li> <li>• <a href="#">Decision Trees</a></li> <li>• <a href="#">Mechanics: Part 1(through "Generating a rough draft...)</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Auto-annotation</a></li> <li>• <a href="#">BLASTing your genome in DNA Master</a></li> <li>• <a href="#">Saving your DNA Master file</a></li> </ul>	<ul style="list-style-type: none"> <li>• Auto-annotate and then BLAST your phage genome in DNA Master</li> <li>• Save File</li> </ul>
<ul style="list-style-type: none"> <li>• Genome Overview</li> <li>• Compare genomes using Phamerator</li> <li>• Compare using BLASTN on phagesdb.org</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Guiding principles</a></li> <li>• <a href="#">Mechanics: Phamerator</a></li> <li>• <a href="#">Mechanics: Other</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Phagesdb tour</a></li> <li>• <a href="#">Phamerator overview</a></li> <li>• <a href="#">GeneMark output</a></li> <li>• <a href="#">Aragorn output</a></li> <li>• <a href="#">tRNAscanSE output</a></li> </ul>	<ul style="list-style-type: none"> <li>• Generate GeneMark S and GeneMark host files</li> <li>• Generate Aragorn and tRNAscanSE outputs.</li> <li>• Phamerator map your phage and others</li> </ul>
<ul style="list-style-type: none"> <li>• Choosing starts</li> <li>• Record keeping</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Evaluating gene predictions</a></li> <li>• <a href="#">Evaluating gene starts</a></li> <li>• <a href="#">Mechanics: DNA Master</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Using Starterator</a></li> <li>• <a href="#">GeneMark output overview</a></li> <li>• <a href="#">Other how-to DNA Master videos</a></li> </ul>	<ul style="list-style-type: none"> <li>• Call more genes in DNA Master.</li> </ul>
<ul style="list-style-type: none"> <li>• tRNAs</li> <li>• Programmed frameshift</li> <li>• Call more genes</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Predicting tRNAs</a></li> <li>• <a href="#">Frameshift</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Frameshift</a></li> <li>• <a href="#">tRNAs</a></li> </ul>	<ul style="list-style-type: none"> <li>• Call more genes</li> </ul>
<ul style="list-style-type: none"> <li>• Bacteriophage Biology (what genes to expect)</li> <li>• Functions</li> <li>• Documenting gene calls</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Bacteriophage Biology</a></li> <li>• <a href="#">Predicting Phage Gene Functions</a></li> <li>• <a href="#">Case Studies</a></li> <li>• <a href="#">Cluster specific forums</a></li> <li>• <a href="#">Official Function List</a></li> <li>• <a href="#">Databases</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Using HHPred</a></li> </ul>	<ul style="list-style-type: none"> <li>• Call more genes</li> <li>• Assign functions</li> </ul>

<ul style="list-style-type: none"> <li>• Holistic approaches</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Reviewing Gaps</a></li> <li>• <a href="#">Quality control</a></li> <li>• <a href="#">Bioinformatics Basics</a></li> <li>• <a href="#">Programs</a></li> </ul>	<ul style="list-style-type: none"> <li>• Make genome profile</li> </ul>	<ul style="list-style-type: none"> <li>• Make genome profile &amp; map</li> </ul>
<ul style="list-style-type: none"> <li>• Check gaps</li> <li>• Difficult genes/features</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Checking gaps</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Checking the gaps</a></li> </ul>	<ul style="list-style-type: none"> <li>• Keeping working on the genome, review the first genes that you called</li> </ul>
<ul style="list-style-type: none"> <li>• File submissions</li> <li>• Annotation QC— behind the scenes</li> <li>• Review to Improve</li> <li>• Where and when to ask questions</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Submitting your files to phagesdb</a></li> <li>• <a href="#">SEA-PHAGES forums</a></li> <li>• <a href="#">Review to Improve</a></li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">Making your submission files</a></li> <li>• <a href="#">Submitting your annotation</a></li> <li>• <a href="#">Review to Improve</a></li> </ul>	<ul style="list-style-type: none"> <li>• Generate the files for file submission</li> <li>• Review to Improve</li> </ul>
<ul style="list-style-type: none"> <li>• Investigating clusters</li> <li>• PECAAN</li> <li>• Pedagogy</li> </ul>	<ul style="list-style-type: none"> <li>• <a href="#">PECAAN</a></li> </ul>		<ul style="list-style-type: none"> <li>• Recording Notes</li> <li>• Storing data</li> </ul>