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| **PhagesDB** | |
| PhagesDB home | http://phagesdb.org/ |
| PhagesDB BLAST | http://phagesdb.org/blast/ |
| DNAMaster Quick Start | http://phagesdb.org/media/docs/DNAMasterQuickStartGuide_1.pdf |
| DNAMaster Annotation Guide, 2015 | http://phagesdb.org/media/docs/Annotation_Guide_12.01.2015.pdf |
| Local BLAST in DNAMaster How-to | http://phagesdb.org/media/docs/BLASTable_Database_2013.pdf |
| Annotated genome maps by cluster, 2013 | http://phagesdb.org/media/docs/Genome_Maps_1.2013.pdf |
| Starterator Guide, 2014 | http://phagesdb.org/media/docs/Starterator_Guide_2014_2.pdf |
| Etude annotation by Welkin | http://phagesdb.org/media/docs/Case_Study_Etude_Annotation.pdf |
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| **SEA-PHAGES** | |
| Videos, how-to and from symposia | http://seaphages.org/videos/ |
| Forums | http://seaphages.org/forums/ |
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| **BLAST** | |
| BLAST: Basic Local Alignment Search Tool | http://blast.ncbi.nlm.nih.gov/Blast.cgi |
| PhagesDB BLAST | http://phagesdb.org/blast/ |
| BLAST Ring Image Generator (BRIG) | http://brig.sourceforge.net |
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| **DNAMaster** | |
| Download DNAMaster | http://cobamide2.bio.pitt.edu/ |
| Running DNAMaster on a Mac using WINE | https://baylor.box.com/s/295to06pr1cpztqiu2jn0h77iy3vkanz |
| DNAMaster Quick Start | http://phagesdb.org/media/docs/DNAMasterQuickStartGuide_1.pdf |
| DNAMaster Annotation Guide, 2015 | http://phagesdb.org/media/docs/Annotation_Guide_12.01.2015.pdf |
| Local BLAST in DNAMaster How-to | http://phagesdb.org/media/docs/BLASTable_Database_2013.pdf |
| DNAMaster how-to videos | http://seaphages.org/videos/ |
| Etude annotation by Welkin | http://phagesdb.org/media/docs/Case_Study_Etude_Annotation.pdf |
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| **Dotplot** | |
| Gepard: Institute of Computational Biology | http://www.helmholtz-muenchen.de/icb/software/gepard/index.html |
| (To make a multigenome plot: Using phamerator, select several phage and create a fasta file to make one containing several genomes) | |
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| **GeneMark** | |
| GeneMark | http://exon.gatech.edu/GeneMark/gm.cgi |
| GeneMark.hmm prokaryotic | http://exon.gatech.edu/GeneMark/gmhmmp.cgi |
| GeneMarkS | http://exon.gatech.edu/GeneMark/genemarks.cgi |
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| **Phylogeny Prediction** | |
| SPLITSTREE | http://www.splitstree.org |
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| **Protein Structure and Function Prediction** | |
| HHpred - Homology detection & structure prediction by HMM-HMM comparison | http://toolkit.tuebingen.mpg.de/hhpred |
| I-TASSER server for protein structure and function prediction | http://zhanglab.ccmb.med.umich.edu/I-TASSER/ |
| PHYRE2 Protein Fold Recognition Server | http://www.sbg.bio.ic.ac.uk/~phyre2/html/page.cgi?id=index |
| PredictProtein - Protein Sequence Analysis, Prediction of Structural and Functional Features | https://www.predictprotein.org |
| RCSB Protein Data Bank | http://www.rcsb.org/pdb/home/home.do |
| UCSF Chimera Home Page | https://www.cgl.ucsf.edu/chimera/ |
| FATCAT protein structure alignment | http://fatcat.burnham.org/ |
| COILS/PCOILS | http://toolkit.tuebingen.mpg.de/pcoils |
| hey nick!!!! | |
| **Repetitive Elements** | |
| MEME Suite - Introduction | http://meme.nbcr.net/meme/ |
| WebLogo - Create Sequence Logos | http://weblogo.berkeley.edu/logo.cgi |
| Skylign - Interactive logos for alignments and profile HMM's | http://skylign.org |
| WebLogo is a web based application designed to make the generation of sequence logos | http://weblogo.threeplusone.com |
| LogOddsLogo - Creates logos with proper statistical basis | http://www.ncbi.nlm.nih.gov/CBBresearch/Yu/logoddslogo/index.html |
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| **RNA Structure Prediction** | |
| RNAfold web server | http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi |
| RNAStructure Web | http://rna.urmc.rochester.edu/RNAstructureWeb/ |
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| **Sequence Alignment and Viewing** | |

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| MUSCLE Multiple Sequence Alignment | http://www.ebi.ac.uk/Tools/msa/muscle/ |
| CLC Sequence Viewer - CLC bio | http://www.clcbio.com/products/clc-sequence-viewer/ |
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| **Terminators** | |
| ARNold, finding terminators at IGM - Web Server | http://rna.igmors.u-psud.fr/toolbox/arnold/ |
| FindTerm | http://www.softberry.com/berry.phtml?topic=findterm&group=programs&subgroup=gfindb |
| WebGeSTer, a transcription terminator database | http://pallab.serc.iisc.ernet.in/gester/rungester.html |
| phiSITE, database of gene regulation in bacteriophages | http://www.phisite.org/main/index.php?nav=home |
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| **Transmembrane Domains** | |
| TMHMM Server, v. 2.0 | http://www.cbs.dtu.dk/services/TMHMM/ |
| TMpred Server | http://www.ch.embnet.org/software/TMPRED_form.html |
| TopPred at Mobyle portal @Pasteur | http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::toppred |
| SOSUI | http://harrier.nagahama-i-bio.ac.jp/sosui/ |
| (Use phamerator to make a protein fasta file, a single file with all of a phage's predicted protein sequences) | |
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| **tRNA** | |
| ARAGORN, tRNA (and tmRNA) detection | http://mbio-serv2.mbioekol.lu.se/ARAGORN/ |
| | http://130.235.46.10/ARAGORN/ |
| tRNAscan-SE | http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::trnascan |
| | http://lowelab.ucsc.edu/tRNAscan-SE/ |
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| **Other** | |
| R: The R Project for Statistical Computing | https://www.r-project.org |
| PECAAN | https://pecaan.kbrinsgd.org/ |
| Galaxy - an open source, web-based platform for data intensive biomedical research | https://usegalaxy.org |
| Broad Institute Software - covers lots of applications | https://www.broadinstitute.org/scientific-community/software |
| NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 & BLAST). | http://www.ncbi.nlm.nih.gov/tools/primer-blast/ |
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| **Other Lists** | |
| Bioinformatics Links Directory | https://bioinformatics.ca/links_directory/ |