

## PhagesDB

PhagesDB home

<http://phagesdb.org/>

PhagesDB BLAST

<http://phagesdb.org/blast/>

DNAMaster Quick Start

[http://phagesdb.org/media/docs/DNAMasterQuickStartGuide\\_1.pdf](http://phagesdb.org/media/docs/DNAMasterQuickStartGuide_1.pdf)

DNAMaster Annotation Guide, 2015

[http://phagesdb.org/media/docs/Annotation\\_Guide\\_12.01.2015.pdf](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](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](http://phagesdb.org/media/docs/Genome_Maps_1.2013.pdf)

Starterator Guide, 2014

[http://phagesdb.org/media/docs/Starterator\\_Guide\\_2014\\_2.pdf](http://phagesdb.org/media/docs/Starterator_Guide_2014_2.pdf)

Etude annotation by Welkin

[http://phagesdb.org/media/docs/Case\\_Study\\_Etude\\_Annotation.pdf](http://phagesdb.org/media/docs/Case_Study_Etude_Annotation.pdf)

## SEA-PHAGES

Videos, how-to and from symposia

<http://seaphages.org/videos/>

Forums

<http://seaphages.org/forums/>

## 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>

## DNAMaster

Download DNAMaster

<http://cobamide2.bio.pitt.edu/>

Running DNAMaster on a Mac using WINE

<https://baylor.box.com/s/295to06pr1cpztqiu2jn0h77iy3vkanz>

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DNAMaster how-to videos

<http://seaphages.org/videos/>

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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)

## GeneMark

GeneMark

<http://exon.gatech.edu/GeneMark/gm.cgi>

GeneMark.hmm prokaryotic

<http://exon.gatech.edu/GeneMark/gmhmm.cgi>

GeneMarkS

<http://exon.gatech.edu/GeneMark/genemarks.cgi>

## Phylogeny Prediction

SPLITSTREE

<http://www.splittree.org>

## Protein Structure and Function Prediction

HHpred - Homology detection & structure prediction by HMM-HI <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 Structure <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>

## Repetitive Elements

MEME Suite - Introduction

<http://meme.nbcr.net/meme/>

WebLogo - Create Sequence Logos

<http://weblogo.berkeley.edu/logo.cgi>

## RNA Structure Prediction

RNAfold web server

<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>

RNAstructure Web

<http://rna.urmc.rochester.edu/RNAstructureWeb/>

## Sequence Alignment and Viewing

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/>

## 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>

## 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](http://www.ch.embnet.org/software/TMPRED_form.html)

TopPred at Mobyly portal @Pasteur

<http://mobyly.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)

## tRNA

ARAGORN, tRNA (and tmRNA) detection

<http://mbio-serv2.mbioekol.lu.se/ARAGORN/>

<http://130.235.46.10/ARAGORN/>

tRNAscan-SE

<http://mobyly.pasteur.fr/cgi-bin/portal.py#forms::trnscan>

<http://lowelab.ucsc.edu/tRNAscan-SE/>

## Other

SPLITSTREE

<http://www.splitstree.org>

R: The R Project for Statistical Computing

<https://www.r-project.org>

WebLogo - Create Sequence Logos

<http://weblogo.berkeley.edu/logo.cgi>

PECAAN

<https://pecaan.kbrinsgd.org/>

## Online at

[https://docs.google.com/spreadsheets/d/15dToev8nCF\\_sZMfuYmQo-uKat05m-CMwKsLQj3XGDA8/edit?usp=sharing](https://docs.google.com/spreadsheets/d/15dToev8nCF_sZMfuYmQo-uKat05m-CMwKsLQj3XGDA8/edit?usp=sharing)