

# Comprehensive analysis of phages



MicroWorldOmics

Blast Alignment Activity PhylogeneticTree TreeVisualization PCR ORF Annotation Plaque **Phage** Tools Helps

**Blast**  
<Default>

**Alignment**  
<Default>

**Phage Lysins/Peptides**  
<Default>

**Phylogenetic tree**  
<Default>

**Tree visualization**  
<Default>

**PCR amplification**  
<Default>

**ORF prediction**  
<Default>

**Annotation**  
<Default>

**Plaque recognition**  
<Default>

**Phage classification**  
<Default>

**Phage deeplearning tools**  
<Default>

**Useful tools**  
<Default>

**Metagenomics/Amplicons**  
<Default>

**Networks**  
<Default>

**Phage**  
Classification  
Deeplearning  
PhaMer  
PhaGCN  
PhaTYP  
CHERRY

**MicroWorldOmics V1.3**  
*Github:*  
<https://github.com/hzaurzli>  
*SourceCodes:*  
<https://github.com/hzaurzli/MicroWorldOmics>  
*Download:*

**MicroWorldOmics Logs**  
**Introduction:** MicroworldOmics(a convenient software for microscopic world analysis and visualization), a desktop software developed based on **PYQT (version-5)**, **R (version-4.0)**, **Python (version-3.6)** and **JavaScript**, which aims to make new exploration and contribution to the development of bioinformatics. **Realizing data**

The logo for MicroWorldOmics, featuring a green shield with a white outline. Inside the shield, there is a stylized illustration of a bacteriophage (virus) with a hexagonal head, a long tail, and a circular base. The text "MicroWorld Omics" is written in white at the bottom of the shield.



PhaMer - Identify the phage sequence

PhaGCN - Species identification

PhaTYP – Life style identification

Cherry – Host prediction

Genomad – Mobile elements identification

# PhaMer - Identify the phage sequence



Input phage/bacterial and fungal genomes (contigs)

The target folder of the output file (user-defined)

The minimum contig length of the filter (contigs shorter than this length are not included in the calculation)

Reject prophage threshold (Default 0.3)

Status

Finished!!!  
example\_prediction.csv is your result!!!

The status bar is completed

PhaMer

Input fasta file  
D:/MicroWorldOmics\_Setup/Example\_data/phamer/phage\_contigs.fa  
Choose

Output folder  
D:/Documents/Desktop/tmp  
Choose

Contig length  
Contig length filter: 3000

Threshold to reject prophage  
Threshold: 0.3

Status  
Running! please wait (5-8mins)  
If no response, never close window!!!

Result table

	Contig	Pred	Score
1	PhaMer1	phage	0.999
2	PhaMer2	phage	1.0

The table results are in the result folder "example\_prediction.csv"

Table

Run

PhaMer

The status bar is running

The results are presented as follows: The first column represents the name of the contigs, the second column shows the discriminant category, and if it is a phage sequence, it is displayed as "phage", and the third column shows the discriminant score. A score close to "1" indicates a higher possibility that it is a phage sequence

Click this button to display the table

# PhaGCN - Species identification



Input phage genomes  
(contigs)

The target folder of the  
output file (user-defined)

The minimum contig length  
of the filter (contigs shorter  
than this length are not  
included in the calculation)

Status

Finished!!!  
phagcn\_prediction.csv is your result!!!

The status bar is completed

PhaGCN

Input fasta file

D:/MicroWorldOmics\_Setup/Example\_data/phagcn/  
phage\_contigs.fa

Choose

Output folder

D:/Documents/Desktop/tmp

Choose

Contig length

Contig length filter: 3000

Status

Running! please wait (15-20mins)  
If no response, never close window!!!

Result table

	Accession	Length	Pred	Score
1	PhaMer2	169936	Straboviridae	1.0
2	PhaMer1	67383	no_family_aval...	1.0

The table results are in the  
result folder  
"phagcn\_prediction.csv"

if the program is finished, click 'Table' to display the result

Table

Run

The status bar is running

The results are shown as  
follows: The first column is  
the name of the contigs, the  
second column is the length  
of the contig, the third  
column is the species  
identification category  
(Family level), and the  
fourth column is the  
discriminant score. A score  
close to "1" indicates a  
higher possibility that it  
belongs to this category

Click this button  
to display the  
table

# PhaTYP – Life style identification



Input phage genomes  
(contigs)

The target folder of the  
output file (user-defined)

The minimum contig length  
of the filter (contigs shorter  
than this length are not  
included in the calculation)

Status

Finished!!!  
lysogen\_prediction.csv is your result!!!

The status bar is completed

PhaTYP

Input fasta file

D:/MicroWorldOmics\_Setup/Example\_data/phatyp/  
phage\_contigs.fa

Choose

Output folder

D:/Documents/Desktop/tmp

Choose

Contig length

Contig length filter: 3000

Status

Running! please wait (25-30mins)  
If no response, never close window!!!

Result table

	Contig	Pred	Score
1	PhaMer1	virulent	0....
2	PhaMer2	virulent	0....

The table results are in the  
result folder  
"lysogen\_prediction.csv"

If the program is finished, click 'Table' to display the result

Table

Run

The status bar is running

The results are shown as follows: The first column is the name of the contigs, the second column is the discriminant category, and if it is a virulent bacteriophage, it is displayed as "virulent"; otherwise, it is "Lysogen", and the third column is the discriminant score. A score close to "1" indicates a higher possibility that it is "Lysogen", and a score close to "0" indicates a higher possibility that it is "virulent"

Click this button  
to display the  
table

# Cherry – Host prediction



Input phage genomes  
(contigs)

The target folder of the  
output file (user-defined)

The minimum contig length  
of the filter (contigs shorter  
than this length are not  
included in the calculation)

Status

Finished!!!  
cherry\_prediction.csv is your result!!!

The status bar is completed

Cherry

Input fasta file

D:/MicroWorldOmics\_Setup/Example\_data/cherry/  
phage\_contigs.fa

Choose

Output folder

D:/Documents/Desktop/tmp

Choose

Contig length

Contig length filter: 3000

Status

Running! please wait (25-30mins)  
If no response, never close window!!!

Result table

	Accession	Length	Pred	Score	Type
1	PhaMer1	67383	Acinetobacter...	1.0	CRISPR
2	PhaMer2	169936	Pectobacteriu...	1.0	CRISPR

The table results are in the  
result folder  
"cherry\_prediction.csv"

If the program is finished, click 'Table' to display the result

Table

Run

The status bar is running

The results are as follows:  
The first column is the  
contigs name, the second  
column is the contigs length,  
the third column is the host  
identification category  
(family level), and the  
fourth column is the  
discriminant score. A score  
close to "1" indicates a  
higher possibility that it  
belongs to this category. The  
fifth column shows the  
discrimination method,  
where "CRISPR" represents  
the use of crispr for host  
matching

Click this button  
to display the  
table

# Genomad – Mobile elements identification



The status bar is completed

Genomad

Input file (fa, file size less than 20M)

D:\MicroWorldOmicSetup\Example\_data\mlst\fna\GCF\_000014325\_1.fna

Input bacterial genomes (contigs)

Choose

Output folder

D:/Documents/Desktop/tmp

The target folder of the output file (user-defined)

Choose

Status

Finished!!!

Run

GCF_000014325_1_aggregated_classif...	2025/6/26 12:16	文件夹	
GCF_000014325_1_annotate	2025/6/26 12:16	文件夹	
GCF_000014325_1_find_proviruses	2025/6/26 12:16	文件夹	
GCF_000014325_1_marker_classificati...	2025/6/26 12:16	文件夹	
GCF_000014325_1_nn_classification	2025/6/26 12:16	文件夹	
GCF_000014325_1_summary	2025/6/26 12:16	文件夹	
GCF_000014325_1_aggregated_classif...	2025/6/26 12:16	文本文档	4 KB
GCF_000014325_1_annotate.log	2025/6/26 12:16	文本文档	3 KB
GCF_000014325_1_find_proviruses.log	2025/6/26 12:16	文本文档	4 KB
GCF_000014325_1_marker_classificati...	2025/6/26 12:16	文本文档	5 KB
GCF_000014325_1_nn_classification.log	2025/6/26 12:16	文本文档	5 KB
GCF_000014325_1_summary.log	2025/6/26 12:16	文本文档	4 KB

gene	start	end	length	strand	gc_content	genetic_code	rbs_motif	marker	
NZ_CP045018.1_1	1	399	399	1	0.536	11	None	GENOMAD.1	
NZ_CP045018.1_2	401	1111	711	1	0.568	11	AGGAG	GENOMAD.1	
NZ_CP045018.1_3	1143	1493	351	1	0.382	11	AGGAG	GENOMAD.1	
NZ_CP045018.1_4	1509	2120	612	1	0.477	11	GGA/GAG/AGG	GENOMAD.1	
NZ_CP045018.1_5	2183	13516	11334	1	0.566	11	None	GENOMAD.1	
NZ_CP045018.1_6	13585	15084	1500	1	0.550	11	AGGAG	GENOMAD.1	
NZ_CP045018.1_7	15163	16128	966	-1	0.469	11	GGAGG	NA	
...									

Interpretation results can be reference:

<https://github.com/apcamargo/genomad/>