Run
Center of Genomic Epidemiology (CGE)
Web-based tools

SpeciesFinder
KmerFinder
MLST
ResFinder

Version: March 2025

Manual to run CGE webtools

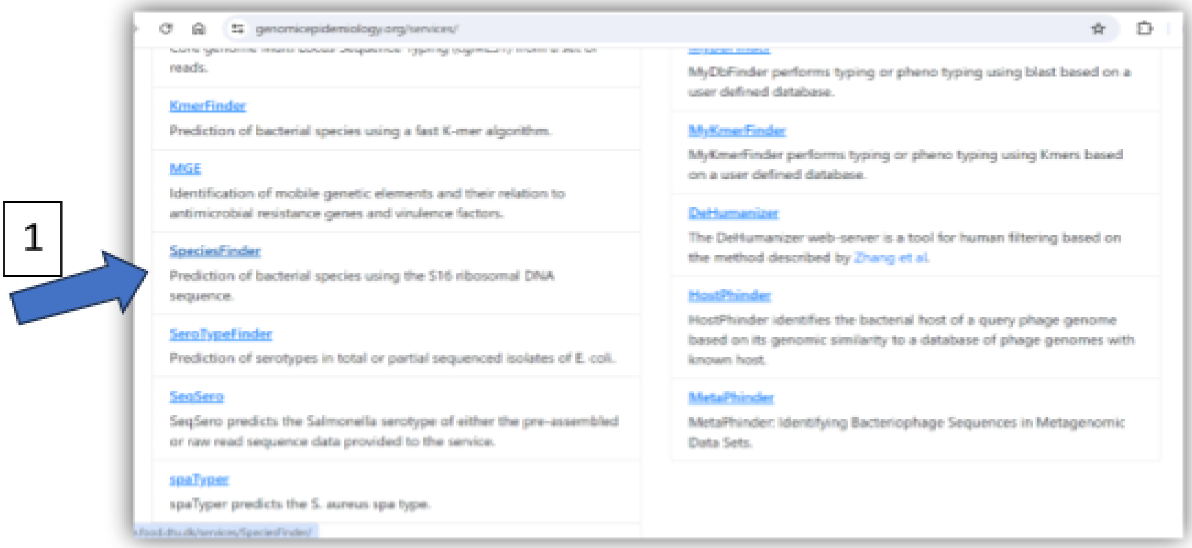
In this manual, we will analyse the genomes with the following tools

A. SpeciesFinder
B. KmerFinder
C. MLST
D. ResFinder

Manual SpeciesFinder

1. Navigate to “Services” webpage of Center for Genomic Epidemiology https://www.genomicepidemiology.org/services/

2. On CGE webpage, navigate to tool “Speciesfinder”



reads.

KmerFinder
Prediction of bacterial species using a fast K-mer algorithm.

MGE
Identification of mobile genetic elements and their relation to antimicrobial resistance genes and virulence factors.

SpeciesFinder
Prediction of bacterial species using the S16 ribosomal DNA sequence.

SeroTypeFinder
Prediction of serotypes in total or partial sequenced isolates of E. coli.

SeqSero
SeqSero predicts the Salmonella serotype of either the pre-assembled or raw read sequence data provided to the service.

spaTyper
spaTyper predicts the S. aureus spa type.

MyDbFinder performs typing or pheno typing using blast based on a user defined database.

MyKmerFinder
MyKmerFinder performs typing or pheno typing using Kmers based on a user defined database.

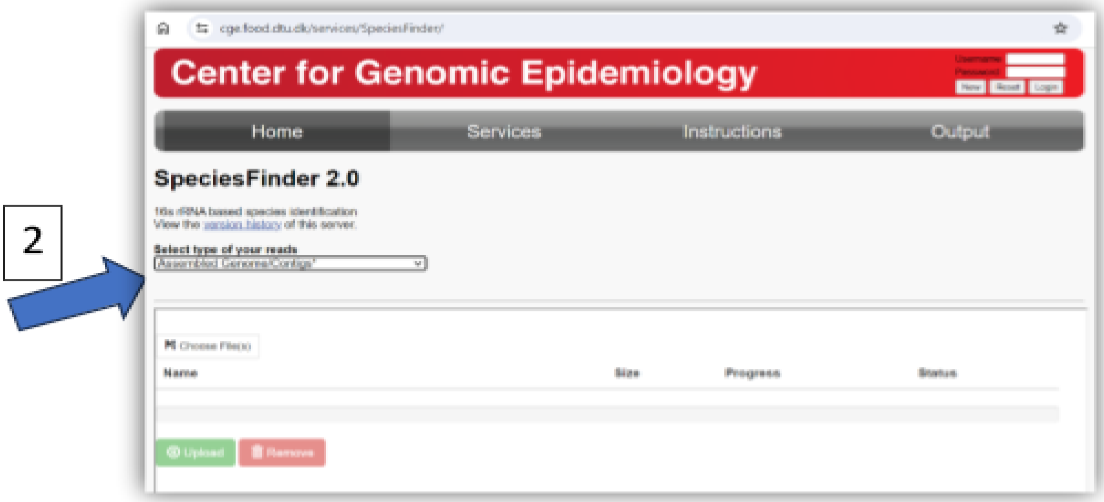
DeHumanizer
The DeHumanizer web-server is a tool for human filtering based on the method described by Zhang et al.

HostPhinder
HostPhinder identifies the bacterial host of a query phage genome based on its genomic similarity to a database of phage genomes with known host.

MetaPhinder
MetaPhinder: Identifying Bacteriophage Sequences in Metagenomic Data Sets.

food.dtu.dk/services/SpeciesFinder/

2. On SpeciesFinder page, select type of your reads “Assembled Genomes/Contigs”



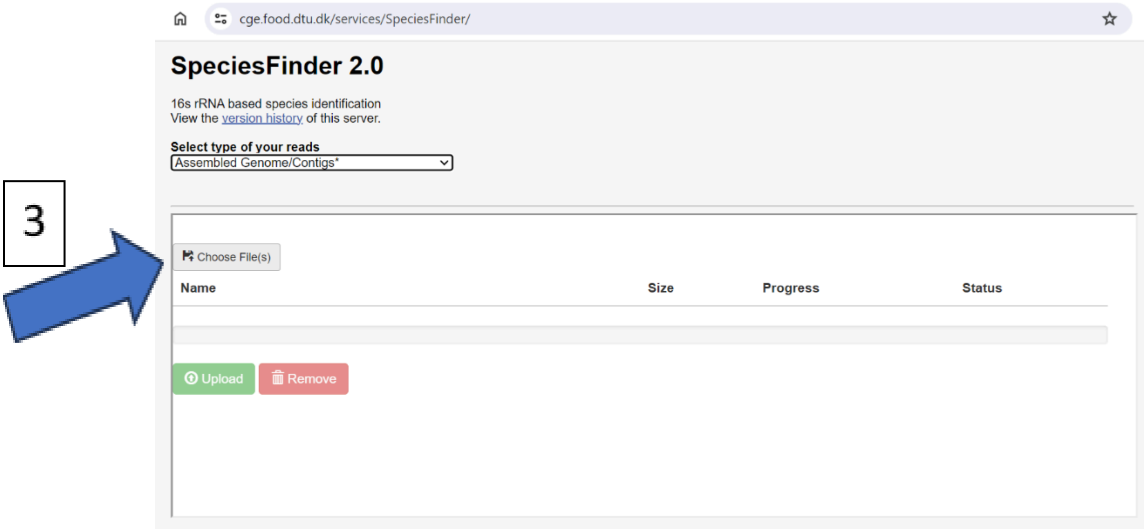
SpeciesFinder 2.0

16s rRNA based species identification
View the version history of this server.

Select type of your reads
Assembled Genomes/Contigs*

Name	Size	Progress	Status

3. Select "Choose File(s)"



cge.food.dtu.dk/services/SpeciesFinder/

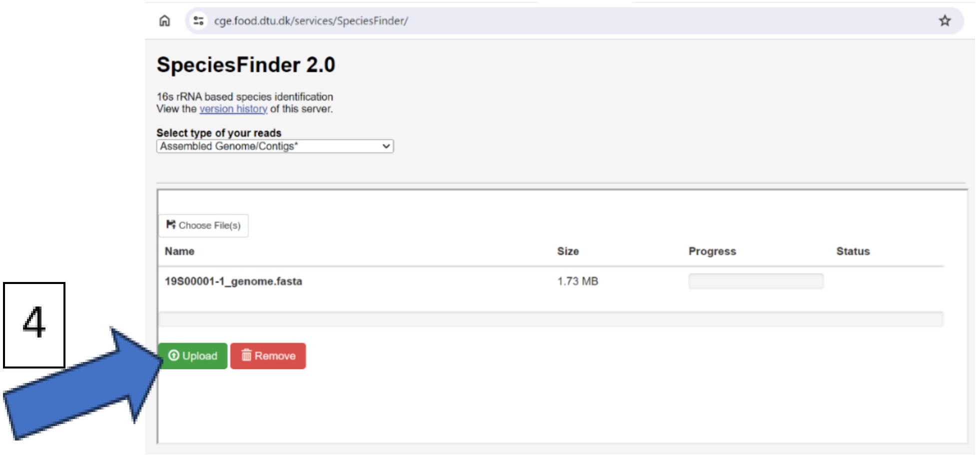
SpeciesFinder 2.0

16s rRNA based species identification
View the version history of this server.

Select type of your reads
Assembled Genome/Contigs*

4. Browse to downloaded genome file (*.fasta), select file and choose "Open".

Click "Upload" button.



cge.food.dtu.dk/services/SpeciesFinder/

SpeciesFinder 2.0

16s rRNA based species identification
View the version history of this server.

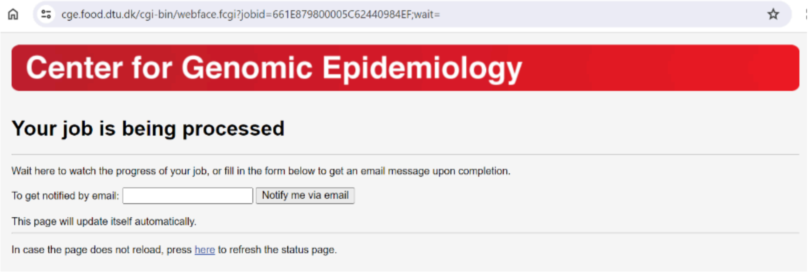
Select type of your reads
Assembled Genome/Contigs*

Name	Size	Progress	Status
19S00001-1_genome.fasta	1.73 MB		

Wait till the progress bar is filled (complete blue)

Page will continue automatically to new page “your job is being processed”

You can fill in your email address to receive an email with the results, or you can wait till the analysis is finished. When the analysis is finished, the page will refresh itself with the results.



Your job is being processed

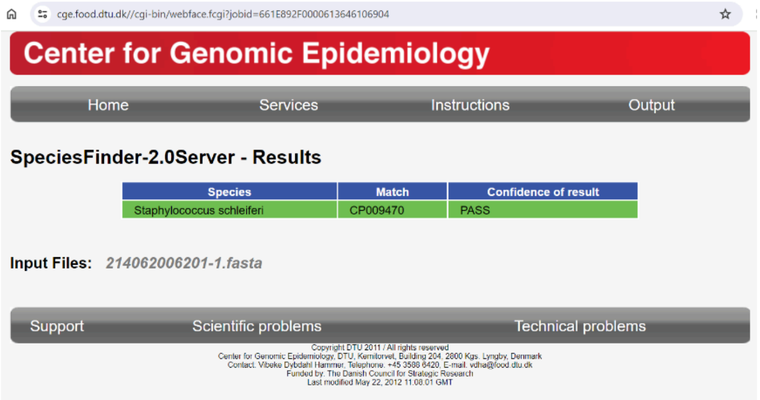
Wait here to watch the progress of your job, or fill in the form below to get an email message upon completion.

To get notified by email:

This page will update itself automatically.

In case the page does not reload, press here to refresh the status page.

Screen with result is as follows. If the result fail (red), probably your fasta file is not correct uploaded.



SpeciesFinder-2.0Server - Results

Species	Match	Confidence of result
Staphylococcus schleiferi	CP009470	PASS

Input Files: 214062006201-1.fasta

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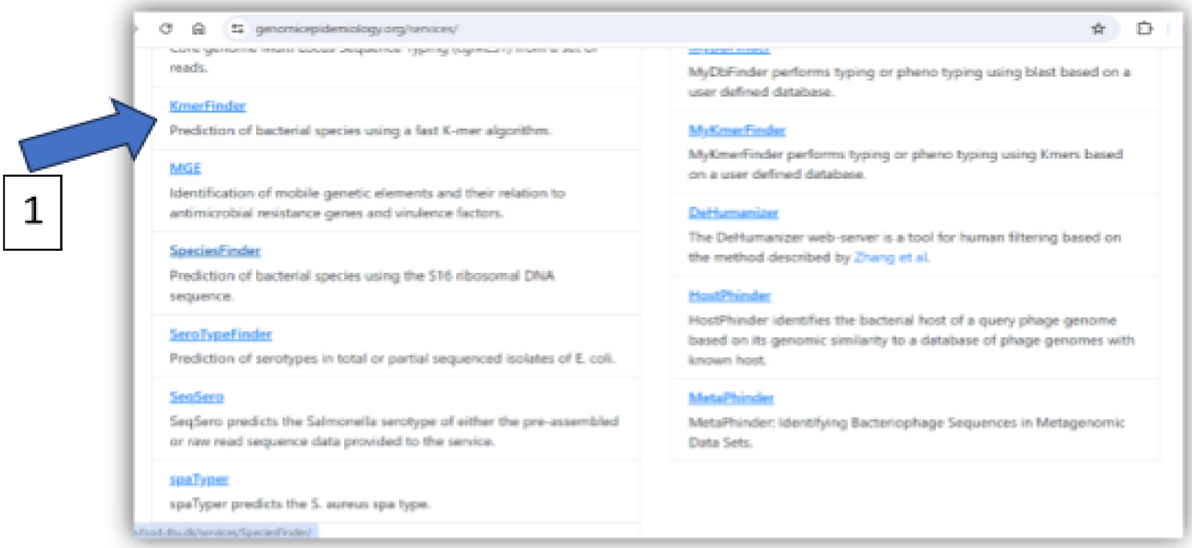
Center for Genomic Epidemiology, DTU, Kemitorvet, Building 204, 2800 Kgs. Lyngby, Denmark
Contact: Vibeke Dybdahl Hammer, Telephone: +45 3588 6420, E-mail: vdha@food.dtu.dk
Funded by: The Danish Council for Strategic Research
Last modified May 22, 2012 11:08:01 GMT

If SpeciesFinder does not give a result; try KmerFinder

Manual KmerFinder

1. On CGE webpage, navigate to tool “KmerFinder”



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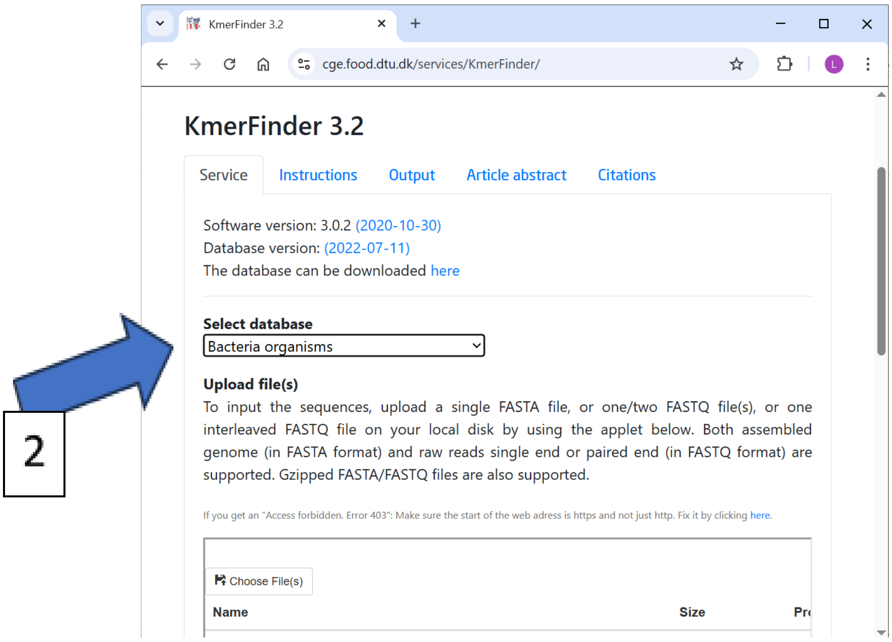
HostPhinder
HostPhinder identifies the bacterial host of a query phage genome based on its genomic similarity to a database of phage genomes with known host.

MetaPhinder
MetaPhinder: Identifying Bacteriophage Sequences in Metagenomic Data Sets.

2. On KmerFinder page, select database “Bacteria organisms”



KmerFinder 3.2

Software version: 3.0.2 (2020-10-30)
Database version: (2022-07-11)
The database can be downloaded here

Select database
Bacteria organisms

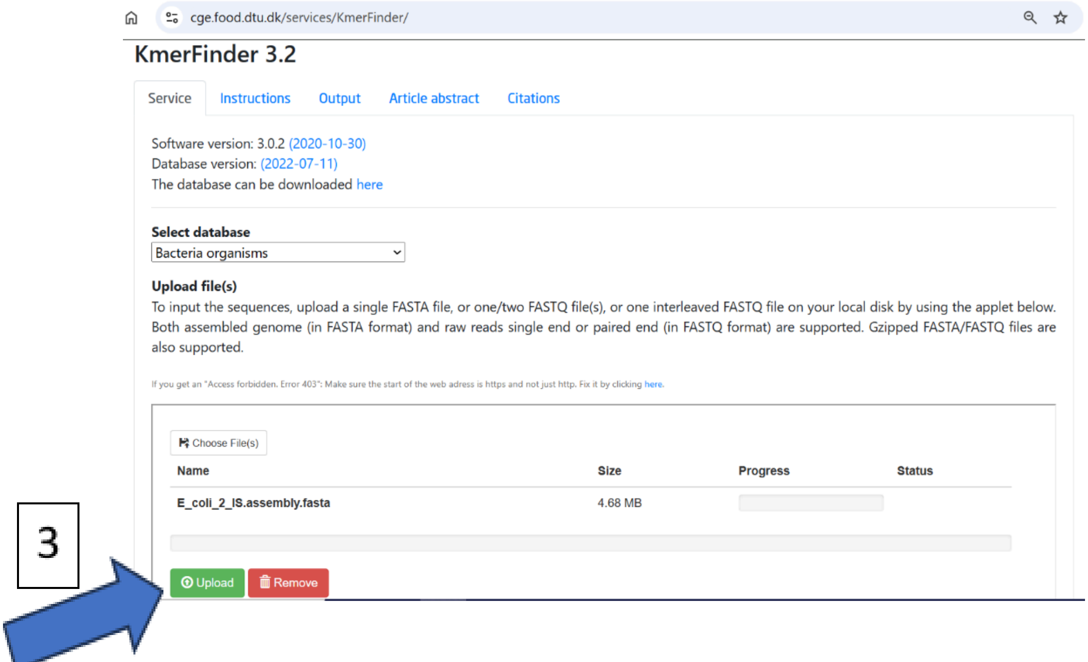
Upload file(s)
To input the sequences, upload a single FASTA file, or one/two FASTQ file(s), or one interleaved FASTQ file on your local disk by using the applet below. Both assembled genome (in FASTA format) and raw reads single end or paired end (in FASTQ format) are supported. Gzipped FASTA/FASTQ files are also supported.

If you get an "Access forbidden. Error 403": Make sure the start of the web adress is https and not just http. Fix it by clicking here.

3. Browse to downloaded genome file (*.fasta), select file and choose “Open”.

Click “Upload” button.

Wait till the progress bar is filled (complete blue)



KmerFinder 3.2

Service | Instructions | Output | Article abstract | Citations

Software version: 3.0.2 (2020-10-30)
Database version: (2022-07-11)
The database can be downloaded here

Select database
Bacteria organisms

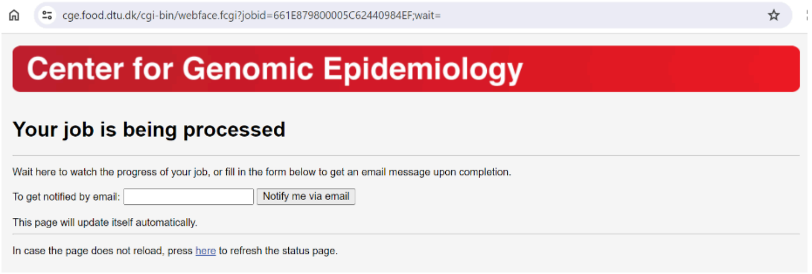
Upload file(s)
To input the sequences, upload a single FASTA file, or one/two FASTQ file(s), or one interleaved FASTQ file on your local disk by using the applet below. Both assembled genome (in FASTA format) and raw reads single end or paired end (in FASTQ format) are supported. Gzipped FASTA/FASTQ files are also supported.

If you get an "Access forbidden. Error 403": Make sure the start of the web adress is https and not just http. Fix it by clicking here.

Name	Size	Progress	Status
E_coli_2_IS.assembly.fasta	4.68 MB		

Page will continue automatically to new page “your job is being processed”

You can fill in your email address to receive an email with the results, or you can wait till the analysis is finished. When the analysis is finished, the page will refresh itself with the results.



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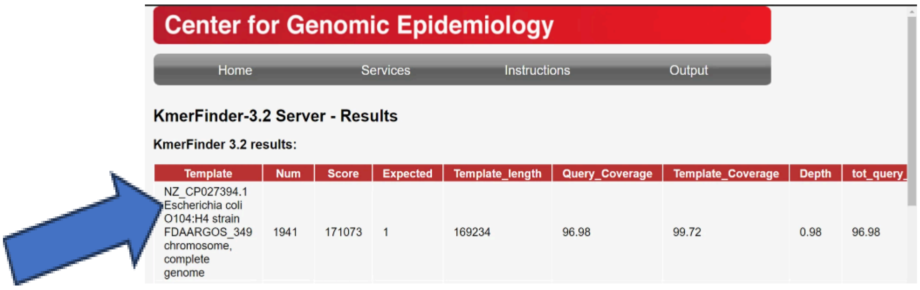


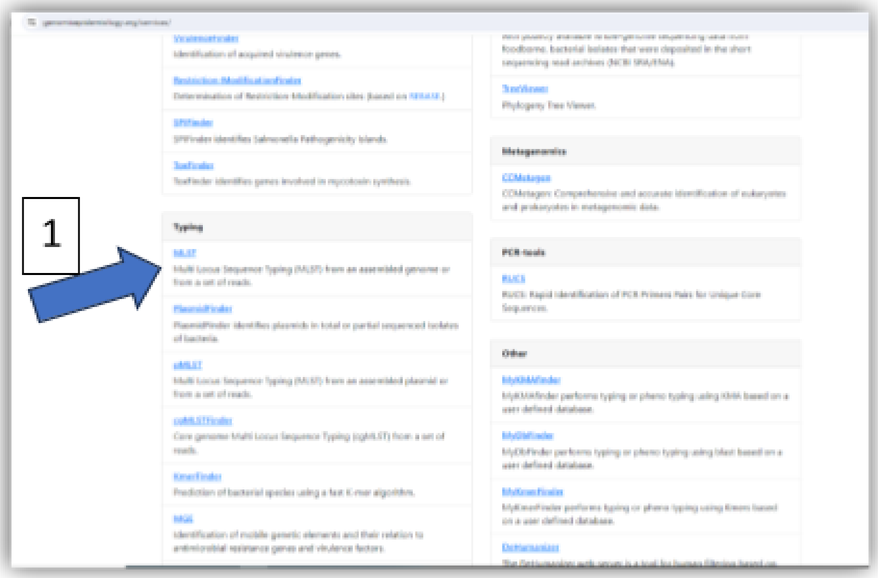
KmerFinder-3.2 Server - Results

KmerFinder 3.2 results:

Template	Num	Score	Expected	Template_length	Query_Coverage	Template_Coverage	Depth	tot_query_
NZ_CP027394.1 Escherichia coli O104:H4 strain FDAARGOS_349 chromosome, complete genome	1941	171073	1	169234	96.98	99.72	0.98	96.98

Manual MLST

1. On CGE webpage, navigate to tool "MLST"



2. At "select MLST configuration", select the species of your genome, for example "Staphylococcus aureus"

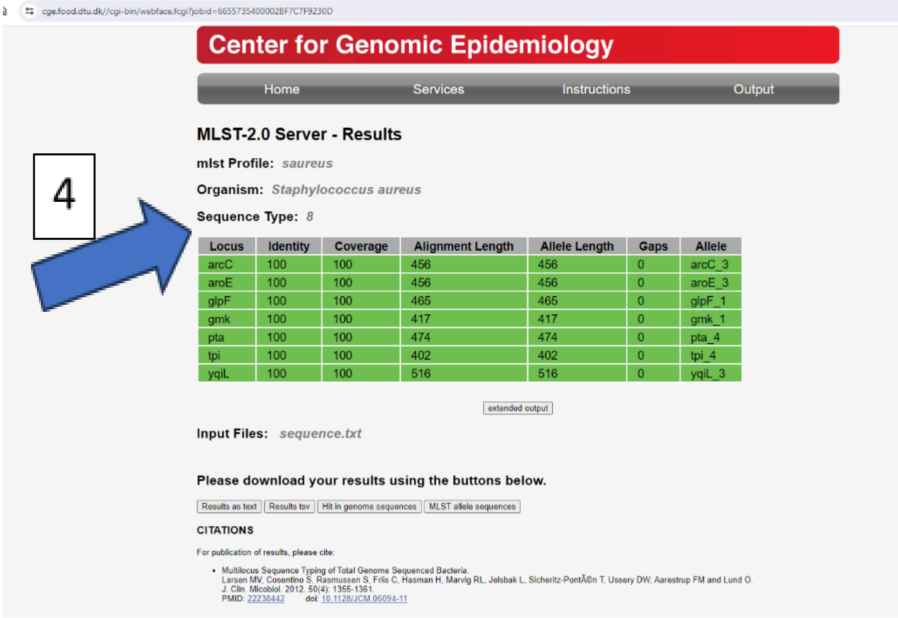
Use default parameters:

Select min. depth for an allele: 5x

Select type of data input: Assembled or Draft Genome/Contigs

3. Upload your genome file, you know how to do it now

4. Please fill in the Sequence Type (ST) of your genome in the Google docs sheet



MLST-2.0 Server - Results

mlst Profile: *saureus*

Organism: *Staphylococcus aureus*

Sequence Type: *8*

Locus	Identity	Coverage	Alignment Length	Allele Length	Gaps	Allele
arcC	100	100	456	456	0	arcC_3
aroE	100	100	456	456	0	aroE_3
glpF	100	100	465	465	0	glpF_1
gmk	100	100	417	417	0	gmk_1
pta	100	100	474	474	0	pta_4
tpi	100	100	402	402	0	tpi_4
yqiL	100	100	516	516	0	yqiL_3

Input Files: *sequence.txt*

Please download your results using the buttons below.

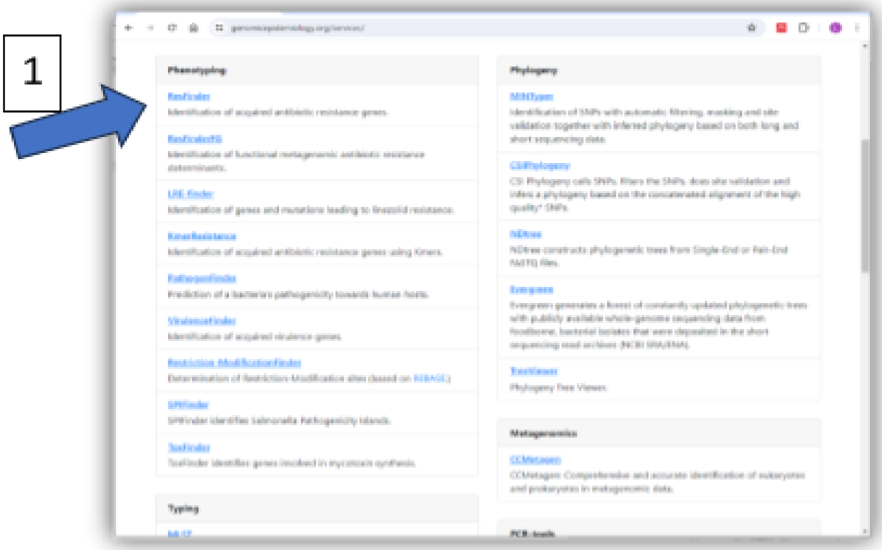
CITATIONS

For publication of results, please cite:

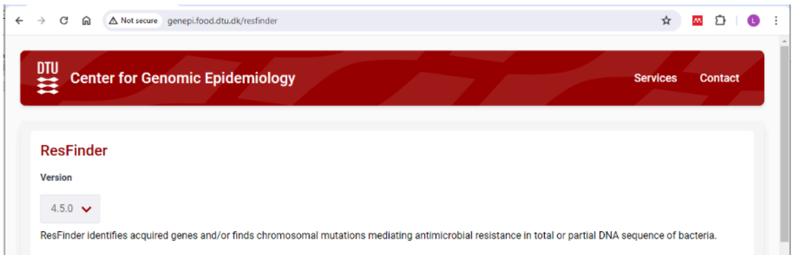
- Multilocus Sequence Typing of Total Genome Sequenced Bacteria.
  Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-PontÃ©n T, Ussery DW, Aarestrup FM and Lund O.
  J. Clin. Micobiol. 2012. 50(4): 1355-1361.
  PMID: 22238442 doi: 10.1128/JCM.06094-11

Manual ResFinder

1. On CGE webpage, navigate to tool "ResFinder"



2. On ResFinder page:
    - Chromosomal point mutations:
        i. Treshold for %ID: 90%
        ii. Minimum length: 60%
    - Acquired antimicrobial resistance genes:
        i. Treshold for %ID: 90%
        ii. Minimum length: 60%
    - Species and input data type:
        i. Select species of your genome: for example "*Staphylococcus aureus*"
        ii. Select input type: Fasta (Assembled genome/contigs)
    - Desinfectant: keep switch off
    - Upload and submit job:
        i. Fill in your emailadress to get result in your emailbox
        ii. Choose file: upload your genome



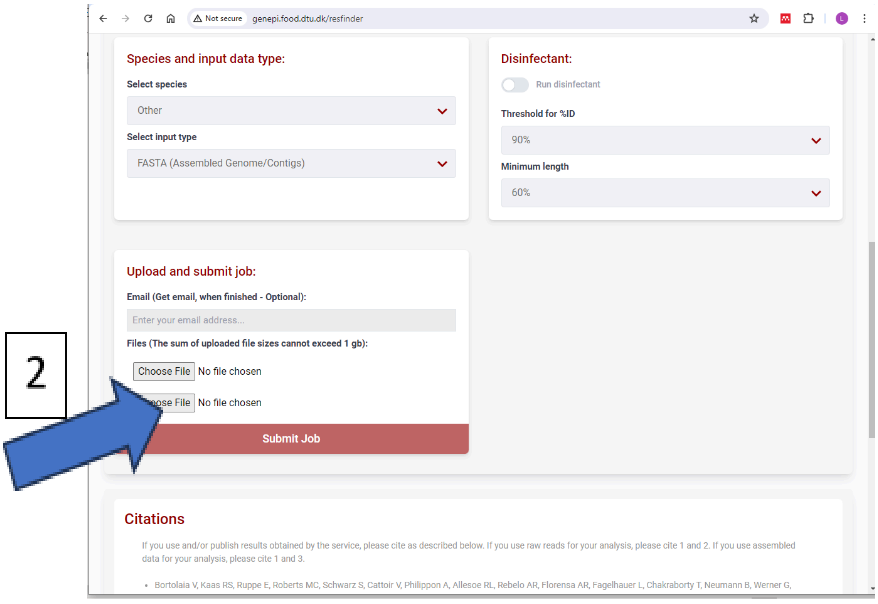
ResFinder

Version

4.5.0

ResFinder identifies acquired genes and/or finds chromosomal mutations mediating antimicrobial resistance in total or partial DNA sequence of bacteria.

2



Not secure genepi.food.dtu.dk/resfinder

Species and input data type:

Select species: Other

Select input type: FASTA (Assembled Genome/Contigs)

Disinfectant:

Run disinfectant

Threshold for %ID: 90%

Minimum length: 60%

Upload and submit job:

Email (Get email, when finished - Optional): Enter your email address...

Files (The sum of uploaded file sizes cannot exceed 1 gb):

Choose File No file chosen

Choose File No file chosen

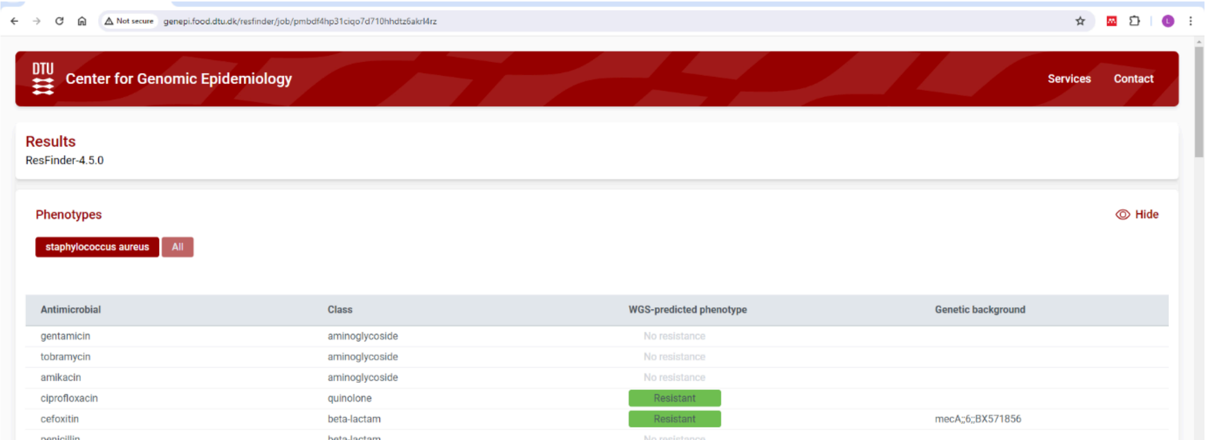
Submit Job

Citations

If you use and/or publish results obtained by the service, please cite as described below. If you use raw reads for your analysis, please cite 1 and 2. If you use assembled data for your analysis, please cite 1 and 3.

- Bortolaia V, Kaas RS, Ruppe E, Roberts MC, Schwarz S, Cattoir V, Philippon A, Allesoe RL, Rebelo AR, Florensa AR, Fagelhauer L, Chakraborty T, Neumann B, Werner G,

3. ResFinder will show which AMR genes are present in your genome, including the predicted phenotype



Not secure genepi.food.dtu.dk/resfinder/job/pmbdf4hp31ciqo7d710hhdtz6akrl4rz

Results

ResFinder-4.5.0

Phenotypes

Antimicrobial	Class	WGS-predicted phenotype	Genetic background
gentamicin	aminoglycoside	No resistance	
tobramycin	aminoglycoside	No resistance	
amikacin	aminoglycoside	No resistance	
ciprofloxacin	quinolone	Resistant	
cefoxitin	beta-lactam	Resistant	mecA;;6;;BX571856
penicillin	beta-lactam	No resistance	