

[https://www.nlm.nih.gov/ncbi/workshops/2022-08\\_intro-to-pathogen-data/](https://www.nlm.nih.gov/ncbi/workshops/2022-08_intro-to-pathogen-data/)

## Specialty Resources just an introduction

<https://www.ncbi.nlm.nih.gov/pathogens>

<https://www.ncbi.nlm.nih.gov/labs/virus/>

## The NCBI Pathogen Detection resource, it's project & resources

NCBI developed the [Pathogen Detection Program](#) to:

**facilitate the rapid identification and comparison of bacterial pathogen genomic sequences from food, environmental sources, and patients.**

Thereby assisting public health scientists investigate foodborne disease outbreaks by providing insight into potential food contamination sources.

[National Antibiotic Resistance Monitoring System \(NARMS\)](#)  
a unique, publicly available resource that brings together:  
isolate information, AMR phenotypes and genome sequences.

and many others...

<https://www.ncbi.nlm.nih.gov/pathogens>

[https://www.nlm.nih.gov/ncbi/workshops/2022-08\\_intro-to-pathogen-data/](https://www.nlm.nih.gov/ncbi/workshops/2022-08_intro-to-pathogen-data/)

## NCBI's Pathogen Detection Service Outbreak Surveillance

**Pathogen Detection**

To assist the National Database of Antibiotic Resistant Organisms (NDARO), NCBI Pathogen Detection identifies the antimicrobial resistance, stress responses, and virulence genes found in bacterial genomic sequences. This enables scientists to track the spread of resistance genes and to understand the relationships between antimicrobial resistance and virulence.

NCBI Pathogen Detection integrates bi food, environmental sources, and patient sequences to uncover potential food contamination sources, helping public health scientists investigate foodborne disease outbreaks.

Pathogen Detection received the 2020 Federal Laboratory Consortium for Technology Transfer (FLC) [Innovative Agency Award](#). For more info on how this project is transforming food safety, click [here](#).

**Explore the Data**

Species	New Isolates	Total Isolates
<i>Salmonella enterica</i>	122	220,082
<i>E.coli and Shigella</i>	1	137,429
<i>Campylobacter jejuni</i>	21	37,727
<i>Listeria monocytogenes</i>	85	28,888

[See more organisms...](#)

**Contributing Agencies**

Several U.S. health agencies and international partners are currently contributing pathogen sequence data for real-time analysis.

**Centers for Disease Control and Prevention (CDC)**

- CDC Advanced Molecular Detection
- CDC Foodborne Outbreaks

**Food and Drug Administration (FDA)**

- FDA Whole Genome Sequencing Program
- FDA GenomeTrakr
- The National Antimicrobial Resistance Monitoring System

**U.S. Department of Agriculture (USDA)**

- Food Safety Inspection Service (FSIS)
- FSIS Molecular Subtyping

**Public Health England (PHE)**

- PHE Whole Genome Sequencing

**Other Associations**

Many state public health laboratories and others are contributing data. There is a [page that lists the major contributors](#) (note, not every submitter of every genome is listed on that page). [Association of Public Health Laboratories \(APHL\)](#)

<https://www.ncbi.nlm.nih.gov/pathogens>  
**ISOLATES BROWSER**

## NCBI Pathogen Project's Curation Efforts

**National Antibiotic Resistance Monitoring System (NARMS)**  
the NCBI Pathogen Project supports a unique, publicly available resource that brings together: isolate information, AMR phenotypes and genome sequences.

**National Database of Antibiotic Resistant Organisms (NDARO)**  
stored in NCBI's **Biosample database**, isolates with **antibiograms** (measured sensitivity or resistance of a bacterial strain for antibiotic compounds)

**AMRFinderPlus**

Identifies AMR and other genes + resistance-associated mutations  
<https://www.ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/AMRFinder/>

**Isolates with antibiotic resistant phenotypes**  
**Reference Gene Catalog**  
**NEW Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E)**

**Learn More**

- About
- FAQ
- Browser Factsheet
- Antimicrobial Resistance Factsheet**
- Antimicrobial Resistance**
- Contributors
- Help

**Data Resources**

- Isolates Browser
- New Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E)**
- Reference Gene Catalog
- Isolates with antibiotic resistant phenotypes
- Microbiome Analysis Results (EAR)

**Submit**

- How to submit data
- How to submit antibiotic resistance phenotypes
- How to submit beta-lactamases
- NCBI Submission Portal

[https://www.nlm.nih.gov/ncbi/workshops/2022-08\\_intro-to-pathogen-data/](https://www.nlm.nih.gov/ncbi/workshops/2022-08_intro-to-pathogen-data/)

## Pathogen Detection Project Curation Resources

### Isolates Browser: An interactive table with columns for phenotypes & genotypes

- This interactive table contains the results of the AMRFinderPlus analyses for isolates – and link to Biosamples for each isolate – *often* where submitted information is displayed.
- You can also find antibiotic resistance information for isolates by Searching the Biosample database with [antibiogram](#) [filter].

### Reference Gene Catalog: A table of identified key genes with links to sequences & isolates

- An interactive table with a non-redundant list bacterial genes related to antimicrobial resistance, biocide and stress resistance, efflux potential, virulence, and antigenicity.
- Links to RefSeq and GenBank nucleotide and protein sequences are available. The Gene Family link will retrieve all isolates assessed to have this particular annotation.

### MicroBIGG-E: Microbial Browser for Identification of Genetic and Genomic Elements

- An interactive table that contains genetic and genomic elements that have been found in GenBank genomic isolates as a result of AMRFinderPlus analyses.
- Each row represents an antimicrobial resistance (AMR), stress response or virulence element with information about the method used to identify it, supporting evidence, and the element's type, subtype, class, subclass, and more.
- This initial release includes genes, alleles, and point mutations. In the future, the plan is to add larger genetic elements such as transposons, plasmids, etc.

NIH National Library of Medicine  
National Center for Biotechnology Information
Log in

Health > Pathogen Detection > Success Stories

## Success Stories

Some examples of how scientists are using NCBI Pathogen Detection resources to promote public health and further their research goals.

### Outbreak analysis

- FDA GenomeTrakr network has used Pathogen Detection Isolates Browser for 837 actions intended to protect consumers from foodborne illness.

2022

- Scientists from an international collaboration used NCBI Pathogen Detection to link [Salmonella in Trinidad and Tobago to an emergent, widespread, multidrug resistance clone of Salmonella Infantis](#).
- Scientists at Cornell University used NCBI Pathogen Detection to [cluster isolates from wildlife with known foodborne isolates and provide detailed descriptions of Listeria monocytogenes](#).
- Scientists use the Pathogen Detection System to [link isolates from Southeast Asia to clinical cases in England and the US](#), some of which had a history of travel.

2021

- Pro Publica used NCBI Pathogen Detection to track an ongoing multi-drug resistant [Salmonella outbreak](#).
- FDA economists examine the [impact of the switch to whole genome sequencing for three foodborne bacterial pathogens in the US and the use of the Pathogen Detection browser with significant impacts economically and for public health](#).
- Scientists in Oregon public health institutions use [NCBI Pathogen Detection Browser to identify pathogenic Escherichia coli O157:H7 from venison from harvested deer and clinical cases from hunters in the same area](#).
- Scientists at New York State Department of Health use NCBI Pathogen Detection Browser for a [retrospective analysis of Clostridium difficile outbreaks](#).
- Scientists at multiple institutions use NCBI Pathogen Detection Browser for [evaluation of Shigella isolates](#). Analysis includes evaluation of macrolide resistance, plasmid structure, and identified multiple outbreaks in the United States and evidence of intercontinental transmission.

### Antimicrobial resistance, point mutations, virulence, and stress response genes and genotypes

2022

- Scientists used output from the Pathogen Detection Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E) to [identify conserved functional regions in erythromycin resistance methyltransferases](#).
- Scientists from the University of Liege, Belgium used class D beta-lactamase sequences from the Reference Gene Catalog to [identify possible class D beta-lactamase sequences in non-clinical bacterial strains](#).
- Scientists used AMR and virulence factor data from NCBI Pathogen Detection to [characterize Klebsiella pneumoniae from Low and Middle Income Countries \(LMICs\)](#).
- A diverse set of Shigella in Africa and Southeast Asia are [examined using AMRFinderPlus to examine AMR genotypes in multi-drug resistant Shigella spp. and to guide policy on treatments and vaccination](#).
- Cornell uses Pathogen Detection Isolates Browser as a framework leveraging WGS data to [identify Salmonella subtypes over- and underrepresented among human clinical cases and then examine genotypes for potential contribution](#). A particular known virulence gene in Salmonella Saintpaul was confirmed using this method.

2021

- AMRFinderPlus and MicroBIGG-E output help to [identify health risks of antibiotic resistance genes](#).

[https://www.ncbi.nlm.nih.gov/pathogens/success\\_stories/](https://www.ncbi.nlm.nih.gov/pathogens/success_stories/)

NIH National Library of Medicine  
National Center for Biotechnology Information
NCBI Workshop  
NCBI

[https://www.nlm.nih.gov/ncbi/workshops/2022-08\\_intro-to-pathogen-data/](https://www.nlm.nih.gov/ncbi/workshops/2022-08_intro-to-pathogen-data/)

# NCBI Virus: a great place to find viral metadata and sequences

A group effort integrating Viral Genome & Taxonomy Experts and a team of Product Managers & Developers.

Their goals:

- improve the quality, accessibility and usefulness of viral resources
- create a helpful and unified set of resources
- and work on priorities with the assistance of the viral research community!



This is an NCBI Labs Experiment. Learn more

NIH National Library of Medicine National Center for Biotechnology Information

COVID-19 is an emerging, rapidly evolving situation. Get the latest public health information from CDC: <https://www.cdc.gov/covid19/>. Get the latest research from NIH: <https://www.nih.gov/covid19/>. Find NCBI SARS-CoV-2 literature, sequence, and clinical data: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

NCBI Virus

<https://www.ncbi.nlm.nih.gov/labs/virus>

Quick Access to SARS-CoV-2 Data!

- Novel Severe acute respiratory syndrome
- View our new SARS-CoV-2 interactive
- A new page to submit SARS-CoV-2 sequences

NCBI Visual Data Dashboard

13,274 RefSeq Nucleotides | 7,204,041 All Proteins | 3,517,612 All Nucleotides

183,915 Complete Nucleotides | 477,628 RefSeq Proteins

Taxonomy of viruses | Host distribution

Search by sequence

Geographic and Time Distribution



# NCBI Virus

NIH National Library of Medicine National Center for Biotechnology Information

NCBI Virus

SARS-CoV-2 Data Hub

1 Refine Results

2 Download

3 Select Columns

4 Build Phylogenetic Tree

Accession	Submitters	Release Date	Genotype	Isolate	Species	Molecule Type	Length	Geo Location	USA?
NC_025512	Wu, F., et al.	2020-01-13	B	Wuhan Hu-1	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29883	China	
OM58882	Jung, J.-H., et al.	2022-05-31	undiscovered	Omicron Variant	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	3816	United Kingdom: Norfolk...	
OM58321	Raychoudhury, S.	2022-05-31	Unassigned	WA-UW 22050772358	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29375	USA: Washington	WA
OM58322	Raychoudhury, S.	2022-05-31	Unassigned	WA-UW 22050815363	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29376	USA: Washington	WA
OM58323	Raychoudhury, S.	2022-05-31	BA.2	WA-UW 22042025214	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58324	Raychoudhury, S.	2022-05-31	BA.2.3	WA-UW 22042446564	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58325	Raychoudhury, S.	2022-05-31	BA.2.1.1	WA-UW 22042417778	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58326	Raychoudhury, S.	2022-05-31	BA.2.3	WA-UW 22042037352	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58327	Raychoudhury, S.	2022-05-31	BA.2.1.1	WA-UW 22042435165	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58328	Raychoudhury, S.	2022-05-31	BA.2	WA-UW 22042074335	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58329	Raychoudhury, S.	2022-05-31	BA.2.1.2	WA-UW 22042449289	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29376	USA: Washington	WA
OM58330	Raychoudhury, S.	2022-05-31	BA.2.3	WA-UW 22042428591	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29365	USA: Washington	WA
OM58331	Raychoudhury, S.	2022-05-31	Unassigned	WA-UW 22050840819	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29375	USA: Washington	WA
OM58332	Raychoudhury, S.	2022-05-31	BA.2	WA-UW 22042403756	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29376	USA: Washington	WA
OM58333	Raychoudhury, S.	2022-05-31	BA.2	WA-UW 22050747062	Severe acute respiratory syndrome coronavirus 2	ssRNA(+)	29376	USA: Washington	WA

2 Download

Download Results

Step 1 of 3: Select Data Type

Sequence data (FASTA format)

Accession List

Current table view result

Nucleotide

CDS format

Coding Region

Protein

XML format

Protein

Assembly

3 Align

4 Build Phylogenetic Tree