

How To: Download a list of human, clinical *E. faecalis* isolates

NCBI Pathogen Detection

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



U.S. National Library of Medicine
National Center for Biotechnology Information

How do I find only human, clinical *E. faecalis* isolates?

- Use the [Isolates Browser](#)
- Use filters or search to select Organism Group “Enterococcus faecalis”
- Use filters or search to select Isolation Type “clinical”
- Download table

Pathogen Detection BETA



To assist the National Database of Antibiotic Resistant Organisms (NDARO), NCBI Pathogen Detection identifies the antimicrobial resistance, stress response, 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 bacterial pathogen genomic sequences originating in food, environmental sources, and patients. It quickly clusters and identifies related sequences to uncover potential food contamination sources, helping public health scientists investigate foodborne disease outbreaks.



There has been a change to the *Isolation type / epi_type* attribute that affects *min-same/min-diff* computation. Now where an isolate has no information to support the setting *environmental/other* the Browser will no longer default to that value but instead present as *NULL*. This means that the *min-same/min-diff* values for this isolate will present as *n/a*, and other *min-same/min-diff* values for isolates clustered with this isolate may change. Please see the [Help](#) text for more details.

Learn More

[About](#)

[FAQ](#)

[Browser Factsheet](#)

[Antimicrobial Resistance Factsheet](#)

[Antimicrobial Resistance](#)

[Contributors](#)

[Help](#)

1. Click Isolate Browser

Data Resources

[Isolates Browser](#)

[Microbial Browser for Identification of Genetic and Genomic Elements \(MicroBIGG-E\)](#)

[Reference Gene Catalog](#)

NEW [Reference HMM Catalog](#)

3. Click Organism Group and Isolation Type to show organism group and isolation type filters

2. Click Filters bar to show filters

6. Select clinical

5. NOTE: some Organism groups contain multiple species. You can use Scientific name to further refine your search

4. Select Enterococcus faecalis.

Filters 2

Available filters

- Ref Gene Catalog version
- Organism Group
- Isolation type
- Scientific name
- AMR genotypes core
- Stress genotypes
- AMRFinderPlus analysis type
- Host
- SNP cluster
- Virulence genotypes
- BioProject
- Run
- AST phenotypes
- Isolate identifiers
- Serovar
- Isolate

1 Organism group

Organism group	Count
<input type="checkbox"/> Listeria monocytogenes	14964
<input type="checkbox"/> Clostridioides difficile	14223
<input type="checkbox"/> Neisseria	869
<input type="checkbox"/> Enterococcus	94
<input type="checkbox"/> Acinetobacter	0
<input type="checkbox"/> Pseudomonas	2
<input type="checkbox"/> Mycobacterium	1
<input type="checkbox"/> Enterobacter	4239
<input type="checkbox"/> Vibrio paranaemolyticus	2165
<input checked="" type="checkbox"/> Enterococcus faecalis	2105
<input type="checkbox"/> Vibrio cholerae	2015
<input type="checkbox"/> Serratia marcescens	1200

Total unique values: 34

1 Isolation type

Isolation type	Count
<input checked="" type="checkbox"/> clinical	2105
<input type="checkbox"/> environmental/other	1490
<input type="checkbox"/> <empty>	3659

Total unique values: 2

Matched Clusters

#	Organism groups	SNP cluster	Matched isolates	Matched clinical isolates	Matched environmental isolates	Total isolates	Minimal min-diff	Mir
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Available filters ↻

Filter
<input type="checkbox"/> PD Ref Gene Catalog version
<input checked="" type="checkbox"/> Organism Group
<input checked="" type="checkbox"/> Isolation type
<input type="checkbox"/> Scientific name
<input type="checkbox"/> AMR genotypes core
<input type="checkbox"/> Stress genotypes
<input type="checkbox"/> AMRFinderPlus analysis type
<input type="checkbox"/> Host
<input type="checkbox"/> SNP cluster
<input type="checkbox"/> Virulence genotypes
<input type="checkbox"/> BioProject
<input type="checkbox"/> Run
<input type="checkbox"/> AST phenotypes
<input type="checkbox"/> Isolate identifiers
<input type="checkbox"/> Serovar
<input type="checkbox"/> Isolate

Search ↻ ✕ »

Organism Group	Count
<input type="checkbox"/> Klebsiella pneumoniae	30071
<input type="checkbox"/> Campylobacter jejuni	29536
<input type="checkbox"/> Staphylococcus aureus	20588
<input type="checkbox"/> Listeria monocytogenes	14964
<input type="checkbox"/> Clostridioides difficile	14223
<input type="checkbox"/> Neisseria	12869
<input type="checkbox"/> Enterococcus faecium	11794
<input type="checkbox"/> Acinetobacter baumannii	9340
<input type="checkbox"/> Pseudomonas aeruginosa	8362
<input type="checkbox"/> Mycobacterium tuberculosis	8071
<input type="checkbox"/> Enterobacter	4239
<input type="checkbox"/> Vibrio parahaemolyticus	2165
<input checked="" type="checkbox"/> Enterococcus faecalis	2105
<input type="checkbox"/> Vibrio cholerae	2015
<input type="checkbox"/> Serratia marcescens	1200

1 Organism Group « Total unique values: 34

Search ↻ ✕

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1 Isolation type « Total unique values: 2

Matched Clusters

#	Organism groups	SNP cluster	Matched isolates	Matched clinical isolates	Matched environmental isolates	Total isolates	Minimal min-diff	Mir
1	Enterococcus faecalis	PDS000063124.1	5	5	0	16	2	
2	Enterococcus faecalis	PDS000058807.1	10	10	0	91	12	
3	Enterococcus faecalis	PDS000090158.1	1	1		2	12	
4	Enterococcus faecalis	PDS000058712.4	33	33		48	17	
5	Enterococcus faecalis	PDS000065397.5	7	7		8	17	
6	Enterococcus faecalis	PDS000058725.1	2	2		6	18	
7	Enterococcus faecalis	PDS000093530.1	2	2		3	19	

7. Click Download button

Matched Isolates

6

<input type="checkbox"/>	Run	<input type="checkbox"/>	Vibrio parahaemolyticus	2165
<input type="checkbox"/>	AST phenotypes	<input checked="" type="checkbox"/>	Enterococcus faecalis	2105
<input type="checkbox"/>	Isolate identifiers	<input type="checkbox"/>	Vibrio cholerae	2015
<input type="checkbox"/>	Serovar	<input type="checkbox"/>	Serratia marcescens	1200
<input type="checkbox"/>	Isolate	Total unique values: 34		Total unique values: 2

Matched Clusters

#	Organism groups	SNP cluster	Matched isolates	Matched clinical isolates	Matched environmental isolates	Total isolates
1	Enterococcus faecalis	PDS000063124.1	5	5	0	16
2	Enterococcus faecalis	PDS000058807.1	10	10	0	91
3	Enterococcus faecalis	PDS000090158.1	1	1	0	2
4	Enterococcus faecalis	PDS000058712.4	33	33	0	
5	Enterococcus faecalis	PDS000065397.5	7	7	0	
6	Enterococcus faecalis	PDS000058725.1	2	2	0	
7	Enterococcus faecalis	PDS000093530.1	2	2	0	

9. Can edit the name of the download file

Matched Isolates

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Choose columns Download Show all AMR genotypes and all Cross-browser selection

8. Click Download to get data in tab-delimited format

Download [X]

Data type: Table

Type: Tab-delimited (.tsv)

Name: isolates.tsv

2105 isolate record(s)

Download Cancel

#	Strain	AMRFin	Organis	Stress genoty...	AMRFinderPlus ...	Host
1	K48_3	3.10.11	2021-08-11.1 Enteroc	(10) NONE	NUCLEOTIDE	Homc
2	K52_2	3.10.11	2021-08-11.1 Enteroc	(11) NONE	NUCLEOTIDE	Homc

More information

- For full help documentation of the Reference Gene Catalog see:
https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#reference-gene-catalog
- For details about filters see:
https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#refgene-filters
- For details about the table downloads see:
https://www.ncbi.nlm.nih.gov/pathogens/pathogens_help/#refgene-access-download

Questions and further help: email pd-help@ncbi.nlm.nih.gov