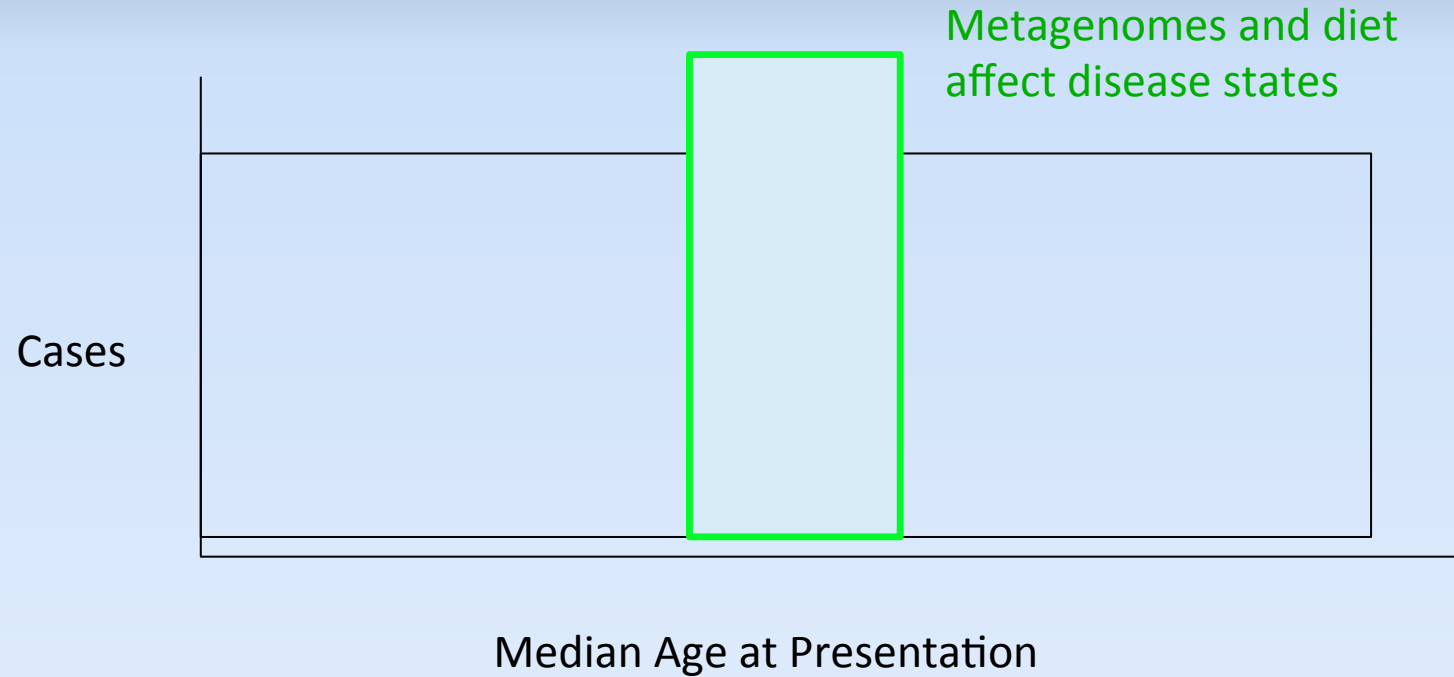


Rethinking Disease



*A completely hypothetical example to
illustrate a point*

Metagenomics

We have ~10 trillion human cells in and on our bodies



We have ~100 trillion bacterial cells in and on our bodies

Antibiotic Resistance

CDC Home

CDC Centers for Disease Control and Prevention
CDC 24/7: Saving Lives. Protecting People.™

A-Z Index [A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [X](#) [Y](#) [Z](#) <#>

Antibiotic / Antimicrobial Resistance

Antibiotic / Antimicrobial Resistance

- About Antimicrobial Resistance
- Diseases/Pathogens Associated with Antimicrobial Resistance
- Education Campaigns
- Interagency Task Force on Antimicrobial Resistance
- Public Health Action Plan
- Annual Reports
- Strategic Priorities Workshop
- Surveillance Systems
- Glossary
- References & Resources
- Laboratory Testing & Training Resources
- Threat Report 2013**

[Antibiotic / Antimicrobial Resistance](#)

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Threat Report 2013


This report, *Antibiotic resistance threats in the United States, 2013* gives a first-ever snapshot of the burden and threats posed by the antibiotic-resistant germs having the most impact on human health.

Each year in the United States, at least 2 million people become infected with bacteria that are resistant to antibiotics and at least 23,000 people die each year as a direct result of these infections. Many more people die from other conditions that were complicated by an antibiotic-resistant infection.

Antibiotic-resistant infections can happen anywhere. Data show that most happen in the general community; however, most deaths related to antibiotic resistance happen in healthcare settings such as hospitals and nursing homes.

What's in the Report

- [Foreword](#)
- [Executive Summary](#)
- [Section 1: The Threat of Antibiotic Resistance](#)
- [Introduction](#)



ANTIBIOTIC RESISTANCE THREATS
in the United States, 2013

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Antibiotic Resistance



Pathogen Detection

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.

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Related Projects

[National Database for Antimicrobial Resistant Organisms \(NDARO\)](#)

[Submitting antibiotic resistance phenotypes](#)

[Submitting beta lactamases](#)

[Beta lactamase resources](#)

[List of samples with antibiotic resistant phenotypes](#)

Clostridium difficile

ACOI 2008 – Marco Island – Oct 31, 2008
**EMERGING INFECTIOUS DISEASES
OF THE 21st CENTURY**
Clostridium difficile
Antibiotic-associated Colitis

Dennis G. Maki, MD

Section of Infectious Diseases
Department of Medicine

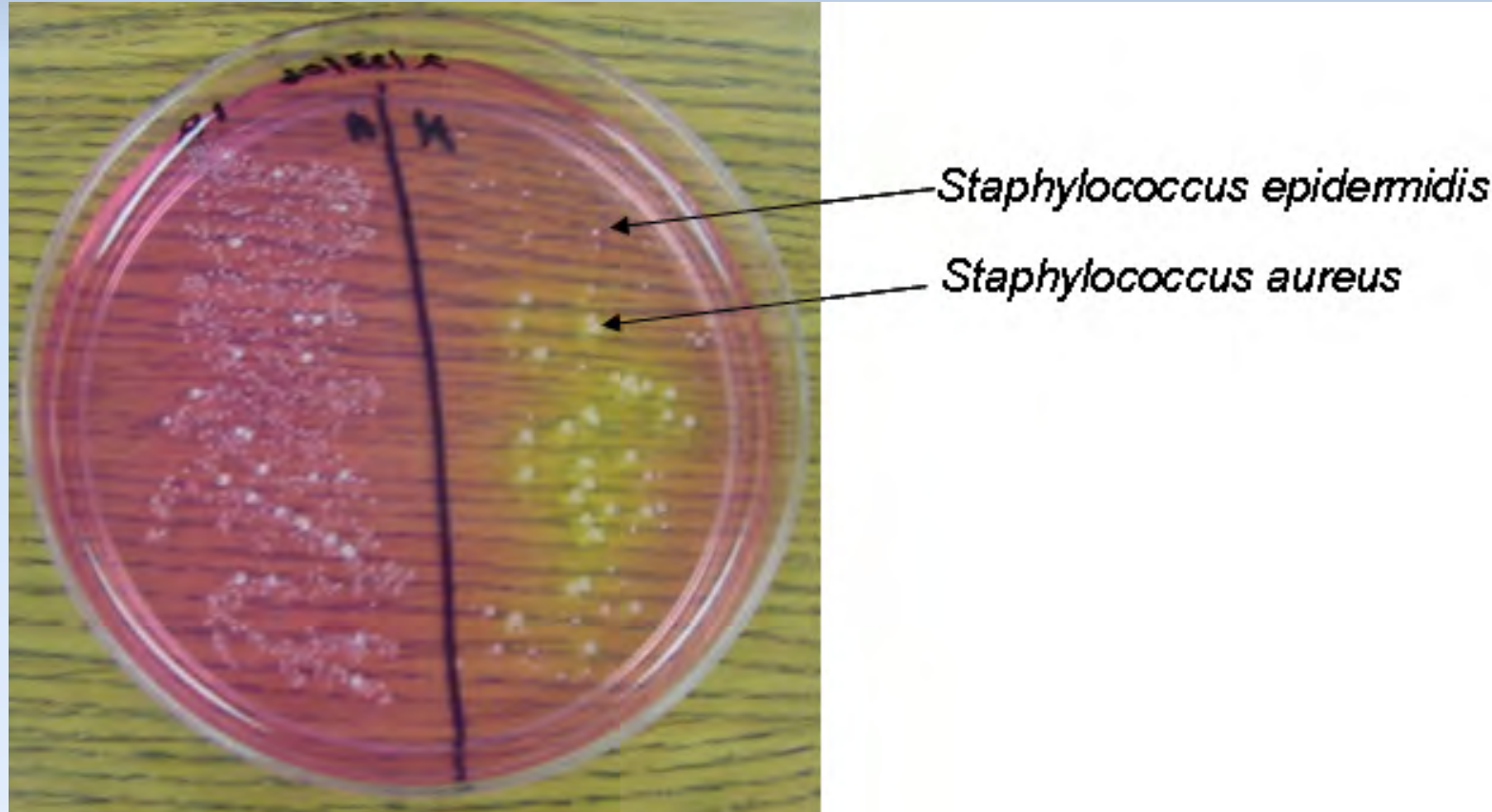
Center for Trauma and Life Support

University of Wisconsin
Hospital & Clinics
Madison, WI

dgmaki@medicine.wisc.edu



Staphylococcus epidermidis



Where to Get the Genomes

NCBI Resources How To busbybr@ncbi.nlm.nih.gov My NCBI Sign Out

Assembly Assembly Search Advanced Browse by organism Help

Display Settings: Full Report Send to:

ASM19595v2

Organism name: [Mycobacterium tuberculosis H37Rv](#)

Infraspecific name: Strain: H37Rv

Submitter: Sanger Institute

Date: 2013/02/01

Assembly level: Gapless Chromosome

Genome representation: full

RefSeq category: reference-genome

GenBank Assembly ID: GCA_000195955.2 (latest)

RefSeq Assembly ID: GCF_000195955.2 (latest)

RefSeq Assembly and GenBank Assembly Identical: yes

IDs: 538048 [JGI] 538028 [GenBank] 538048 [RefSeq]

History ([Show revision history](#))

Global statistics

Total sequence length	4,411,532
Total assembly gap length	0
Total number of chromosomes and plasmids	1

Access the data

- Download the full sequence report
- Download the statistics report
- GenBank FTP site
- RefSeq FTP site

Assembly Information

- Assembly Help
- Assembly Basics
- NCBI Assembly Data Model

Related Information

- BioProject
- Genome
- Nucleotide INSDC
- Nucleotide RefSeq
- PubMed
- Taxonomy

PubMed articles for this assembly

TubercuList—10 years after.

Re-annotation of the genome sequence of *Mycobacterium tuberculosis* H37Rv.

Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.

See [Genome](#) information for *Mycobacterium tuberculosis*

There are 1765 assemblies for this organism. [See more](#)

Assembly Definition Assembly Statistics

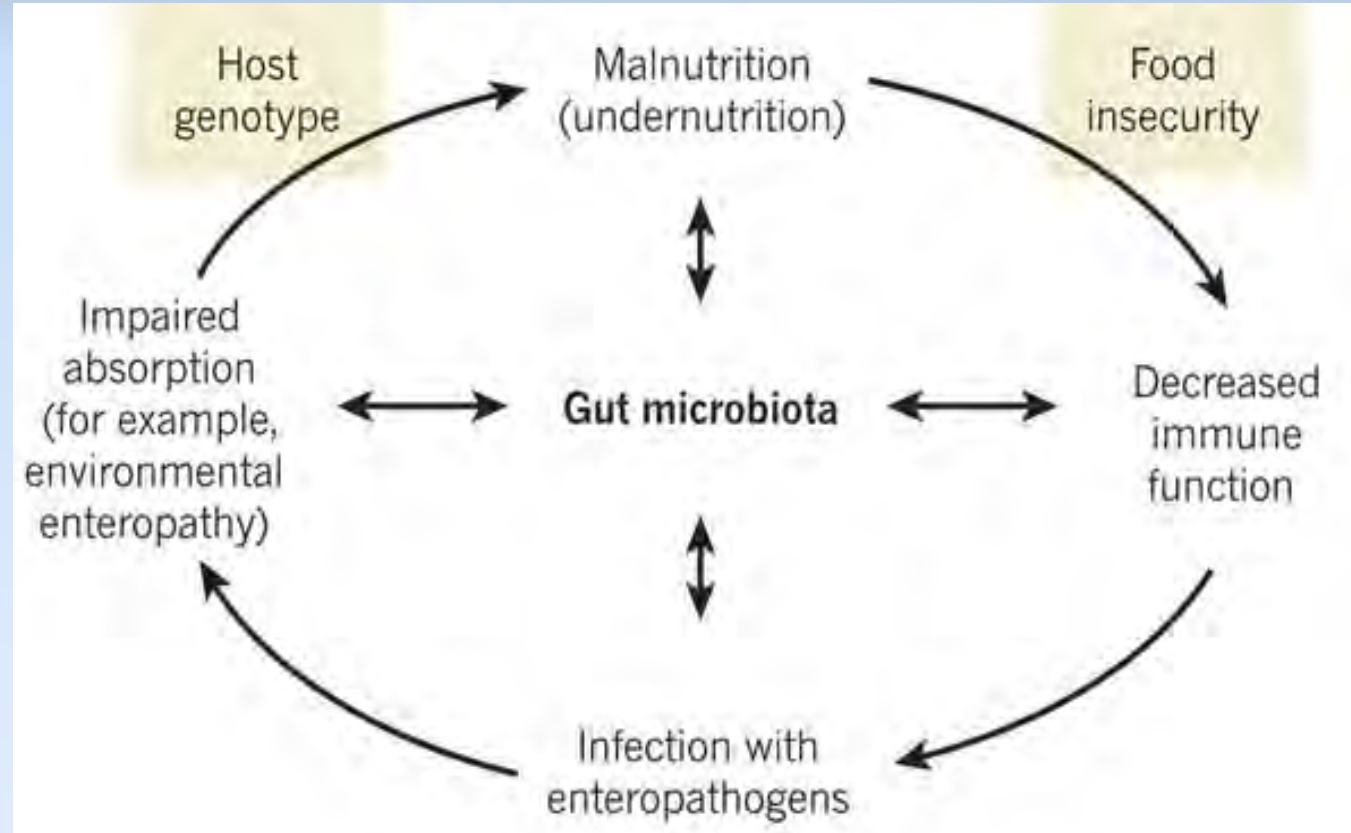
Global assembly definition [Download the full sequence report](#)

Assembly Unit: Primary Assembly (GCF_000195955.2)

Molecule name	GenBank ID		RefSeq ID
Chromosome	AL123456.3	=	NC_000962.3

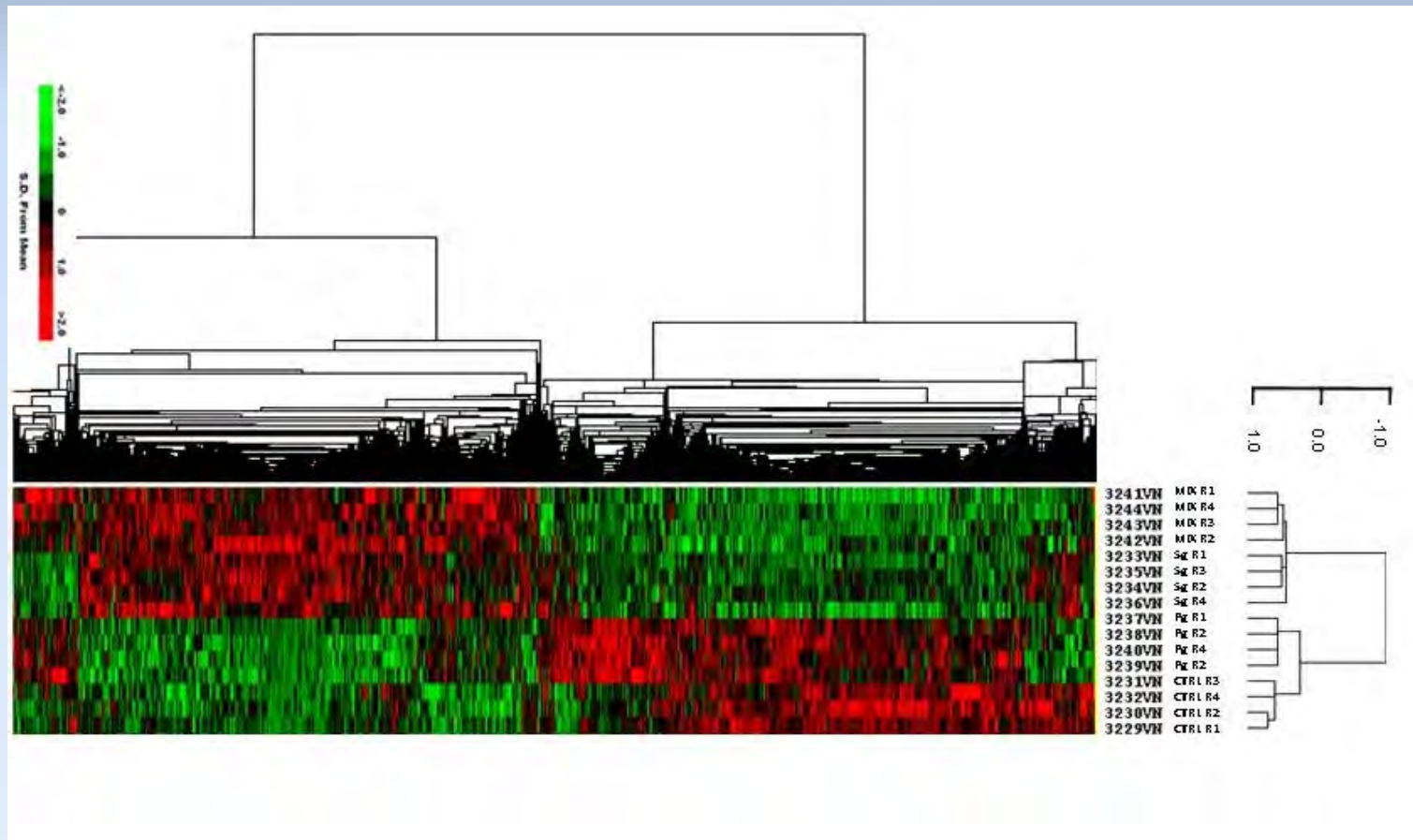


Metagenomics



Metagenomics

Affects transcription in gut epithelia



<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2736203/figure/F1/>

MOLE-BLAST: BLAST for Metagenomics

← → × blast.ncbi.nlm.nih.gov/moleblast/moleblast.cgi ☆ ☰

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Nucleotide

MOLE-BLAST searches for closest neighbors... [Reset page](#)

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Enter nucleotide accessions, gis, or FASTA sequences (up to 200 input sequences with up to 5000 bases each) [Clear](#)

Or, upload FASTA file No file chosen

Job Title

Choose Search Set

Database

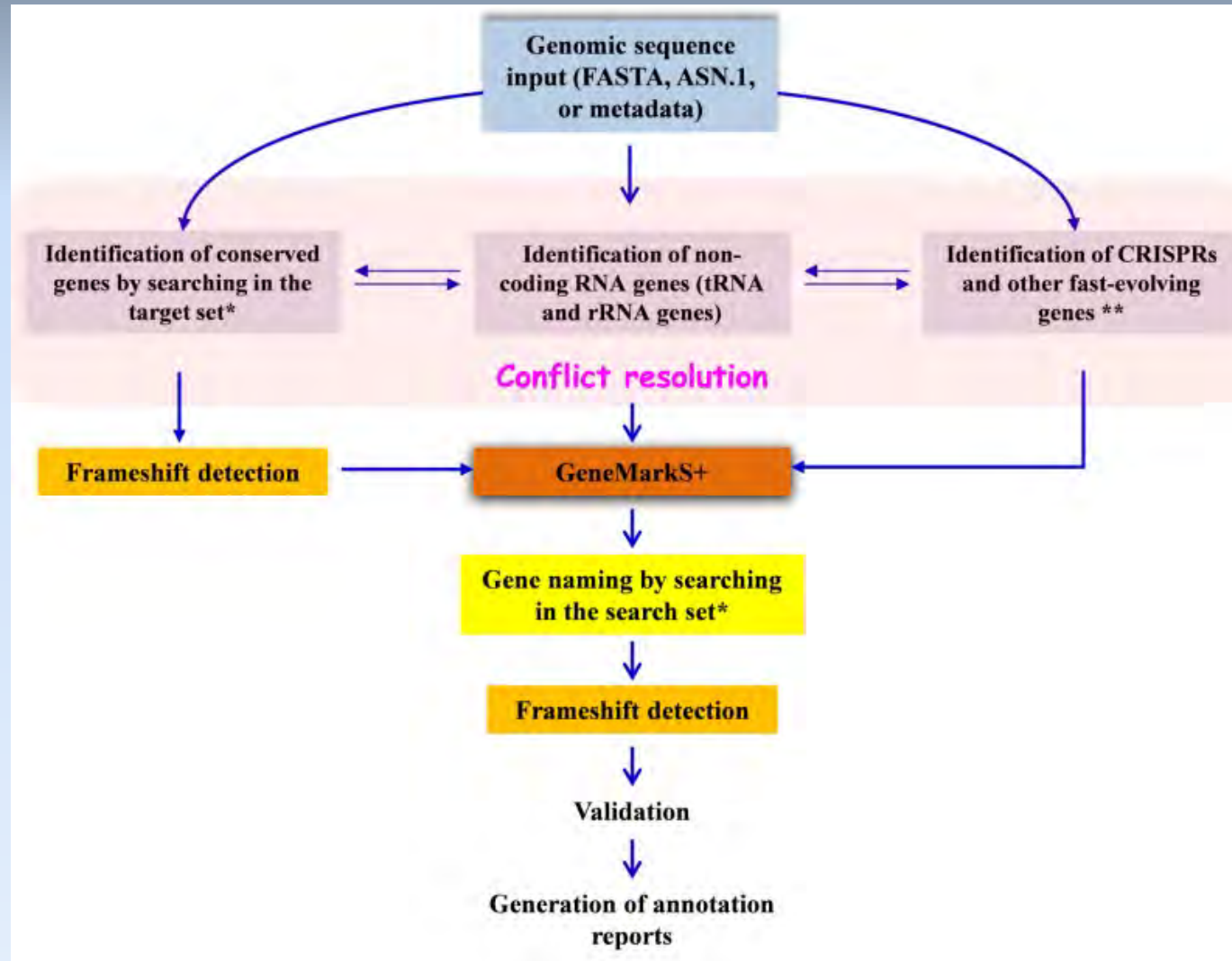
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How Prokaryotic Genomes are Annotated at NCBI



Foodborne Pathogens

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- [Beta lactamase resources](#)
- [List of samples with antibiotic resistant phenotypes](#)

Foodborne Pathogens

NCBI Resources How To

BioSample BioSample ▾ antibiogram[filter]

Create alert Advanced

Organism Customize ...

Attribute name
collection date
geographic location
host
isolate
strain
tissue
Customize ...

Sample type
Pathogen.cl (570)
Pathogen.env (665)

Access
Public (1,525)

Other
Used by SRA (1,165)

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Items: 1 to 20 of 1525

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☐ [Enterobacter cloacae MRSN17626: clinical isolate carrying the blaVIM-1 gene](#)

1. Identifiers: BioSample: SAMN03316841; Sample name: MRSN17626
Organism: Enterobacter cloacae
strain: MRSN 17626
Package: Pathogen: clinical or host-associated; version 1.0
Accession: SAMN03316841 ID: 3316841
[BioProject](#) [Nucleotide](#)

☐ [Acinetobacter baumannii isolate MRSN7828 collected within the U.S. military healthcare system](#)

2. Identifiers: BioSample: SAMN04525209; SRA: SRS1317396; WRAIR-MRSN: MRSN7828
Organism: Acinetobacter baumannii
strain: MRSN7828
Package: Pathogen: clinical or host-associated; version 1.0
Accession: SAMN04525209 ID: 4525209
[BioProject](#) [SRA](#)

☐ [Acinetobacter baumannii isolate MRSN7818 collected within the U.S. military healthcare system](#)

3. Identifiers: BioSample: SAMN04525208; SRA: SRS1317397; WRAIR-MRSN: MRSN7818
Organism: Acinetobacter baumannii

Foodborne Pathogens

List of Pathogens

Currently the collaborative project is focusing on sequencing and analyzing the four bacterial groups that are the major causes of foodborne illness in the US:

- Campylobacter
- Escherichia coli and Shigella
- Listeria
- Salmonella

Several other clinically relevant pathogens have been added with more expected to follow:

- Acinetobacter
- Klebsiella pneumoniae

 NCBI

Resources  How To 

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Pathogen Detection Submit Pathogen Detection FAQ About NDARO_About Beta Lactamase Submissions Beta Lactamase Data Resources

Beta-Lactamase Data Resources

Along with assigning new allele numbers to [certain beta-lactamase families](#), NCBI is providing [downloadable protein sequence files](#), [nucleotide sequence files](#), and [a table providing accessions and curated gene product names](#). These files contain those beta-lactamases from the [Lahey Beta-Lactamase site](#) through to July 1, 2015 for which there were either nucleotide or protein accessions in Genbank. Additional information about these resources is provided in the [Read Me file](#), and the parent directory of these files is found at <http://ftp.ncbi.nlm.nih.gov/pathogen/betalactamases/>.