The Battle Against Antimicrobial Resistance:
ATCC® is your Resource for AMR strains from Drug Discovery to Clinical testing

Victoria Knight-Connoni, PhD
Head of Content Development, ATCC

Joe Petrone, PhD
Senior Bioinformatician, ATCC

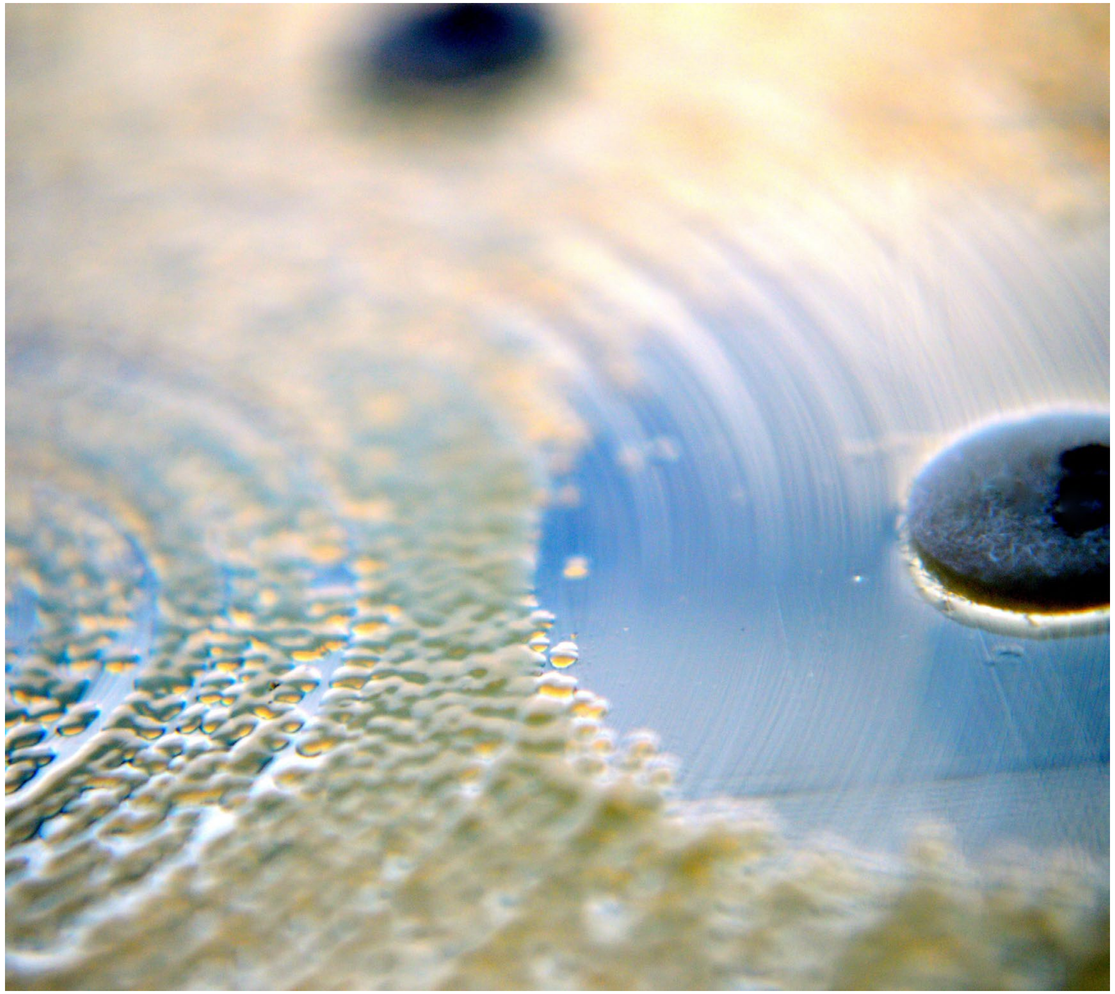
About Us

ATCC is a global leader in providing authenticated, high-quality biological resources and standards for industry, academia, and government.

Founded in 1925, ATCC is a private, nonprofit, global biological resource center and standards organization that provides scientists with the biomaterials and resources they need to conduct critical life science research.

Outline

- The global burden of antimicrobial resistance
- The rise and spread of resistance
- Challenges in antibacterial drug discovery
- ATCC solutions
  - Over 200 multidrug-resistance clinical isolates with source metadata and AST data
  - Complete *de novo* hybrid genome assemblies with annotated antibiotic resistance genes



The Global Burden

- **Global Impact**: At least 1.14 million deaths were directly caused by AMR in 2021, with nearly 5 million associated deaths globally (*Lancet 2024*).
- **U.S. Burden**: Over 2.8 million AMR infections and 48,000 deaths annually (*CDC 2022*).
- **Economic Cost**: Treating the six most common AMR infections in U.S. healthcare costs over $4.6 billion per year (*Nelson et al 2025 Clin Infect Dis 72: S17-S26*).

Factors Increasing Susceptibility to Infection and AMR

Age

- Very young
- Older adults (>65 years)

Illness

- Underlying chronic health conditions
- Compromised immune system
- Recent Infection

Nutrition

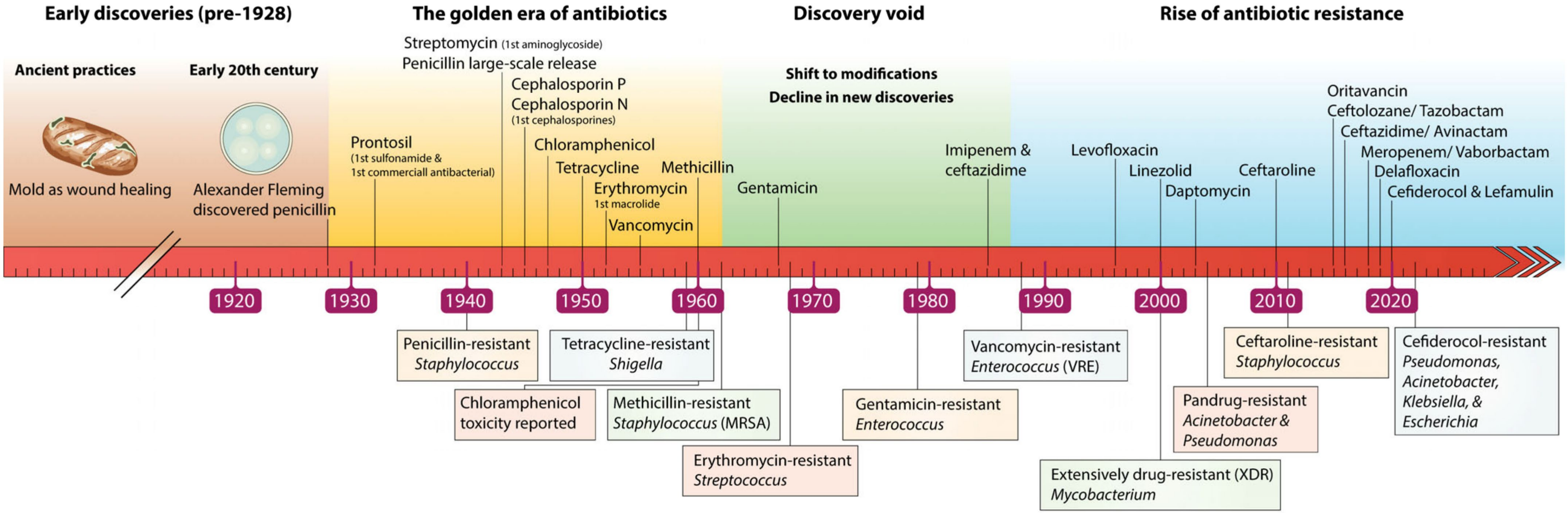
- Malnutrition
- Obesity

Immuno-suppressive drugs or treatments

- Chemotherapy, radiation, and immunosuppressants
- Long-term antibiotic use

The Rise of Resistance

Significant events in antibiotic evolution



Early discoveries (pre-1928)

Ancient practices

Mold as wound healing

Early 20th century

Alexander Fleming discovered penicillin

The golden era of antibiotics

Prontosil (1st sulfonamide & 1st commerciall antibacterial)

Streptomycin (1st aminoglycoside)

Penicillin large-scale release

Cephalosporin P

Cephalosporin N (1st cephalosporines)

Chloramphenicol

Tetracycline

Erythromycin 1st macrolide

Vancomycin

Methicillin

Discovery void

Shift to modifications

Decline in new discoveries

Gentamicin

Imipenem & ceftazidime

Rise of antibiotic resistance

Levofloxacin

Linezolid

Daptomycin

Ceftaroline

Oritavancin

Ceftolozane/ Tazobactam

Ceftazidime/ Avinactam

Meropenem/ Vaborbactam

Delafloxacin

Cefiderocol & Lefamulin

Penicillin-resistant *Staphylococcus*

Chloramphenicol toxicity reported

Tetracycline-resistant *Shigella*

Methicillin-resistant *Staphylococcus* (MRSA)

Erythromycin-resistant *Streptococcus*

Gentamicin-resistant *Enterococcus*

Vancomycin-resistant *Enterococcus* (VRE)

Extensively drug-resistant (XDR) *Mycobacterium*

Pandrug-resistant *Acinetobacter* & *Pseudomonas*

Ceftaroline-resistant *Staphylococcus*

Cefiderocol-resistant *Pseudomonas, Acinetobacter, Klebsiella, & Escherichia*

Tahmasebi H, et al. Biomolecules 15(1): 93, 2025. PubMed: 39858487

Spread of Resistance

Healthcare-acquired infections (HAIs): infections that occur within 30 days of receiving health care

More than a half-million people get health care-associated infections (HAIs)

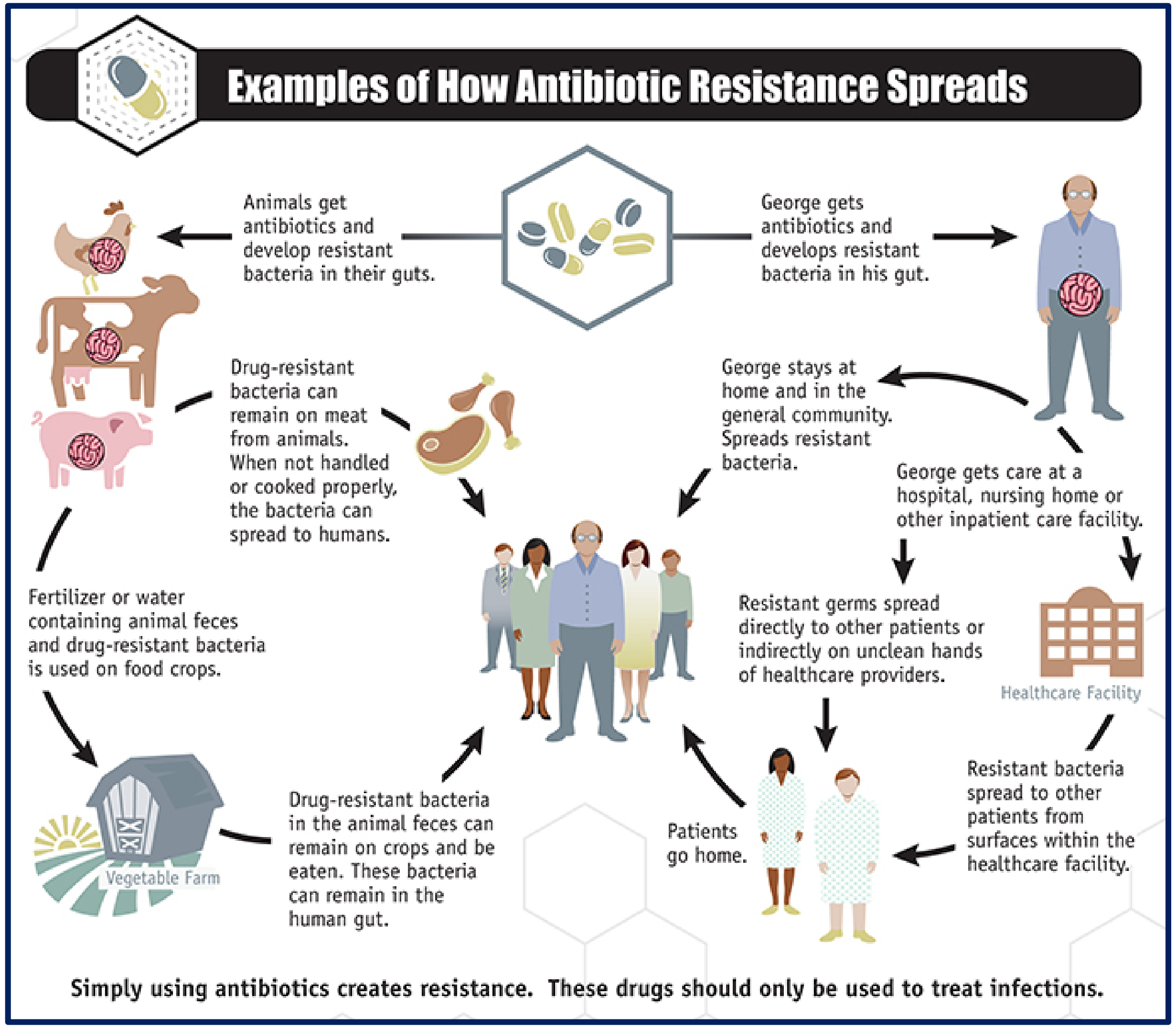
N Engl J Med 379(18): 1732-1744, 2018. PubMed: 30380384

Community-acquired infections (CAIs): infections that cannot be traced to healthcare

A recent study[1] of livestock manure identified:

- > 2000 known antibiotic-resistant genes (ARGs) resistant to 30 antibiotic classes
- ARG levels 2–18 X higher than in human feces, sewage, and soil.

[1] Sci Adv 11(26): eadt8073, 2025. PubMed: 40577477



Examples of How Antibiotic Resistance Spreads

Animals get antibiotics and develop resistant bacteria in their guts.

George gets antibiotics and develops resistant bacteria in his gut.

Drug-resistant bacteria can remain on meat from animals. When not handled or cooked properly, the bacteria can spread to humans.

George stays at home and in the general community. Spreads resistant bacteria.

George gets care at a hospital, nursing home or other inpatient care facility.

Fertilizer or water containing animal feces and drug-resistant bacteria is used on food crops.

Resistant germs spread directly to other patients or indirectly on unclean hands of healthcare providers.

Drug-resistant bacteria in the animal feces can remain on crops and be eaten. These bacteria can remain in the human gut.

Patients go home.

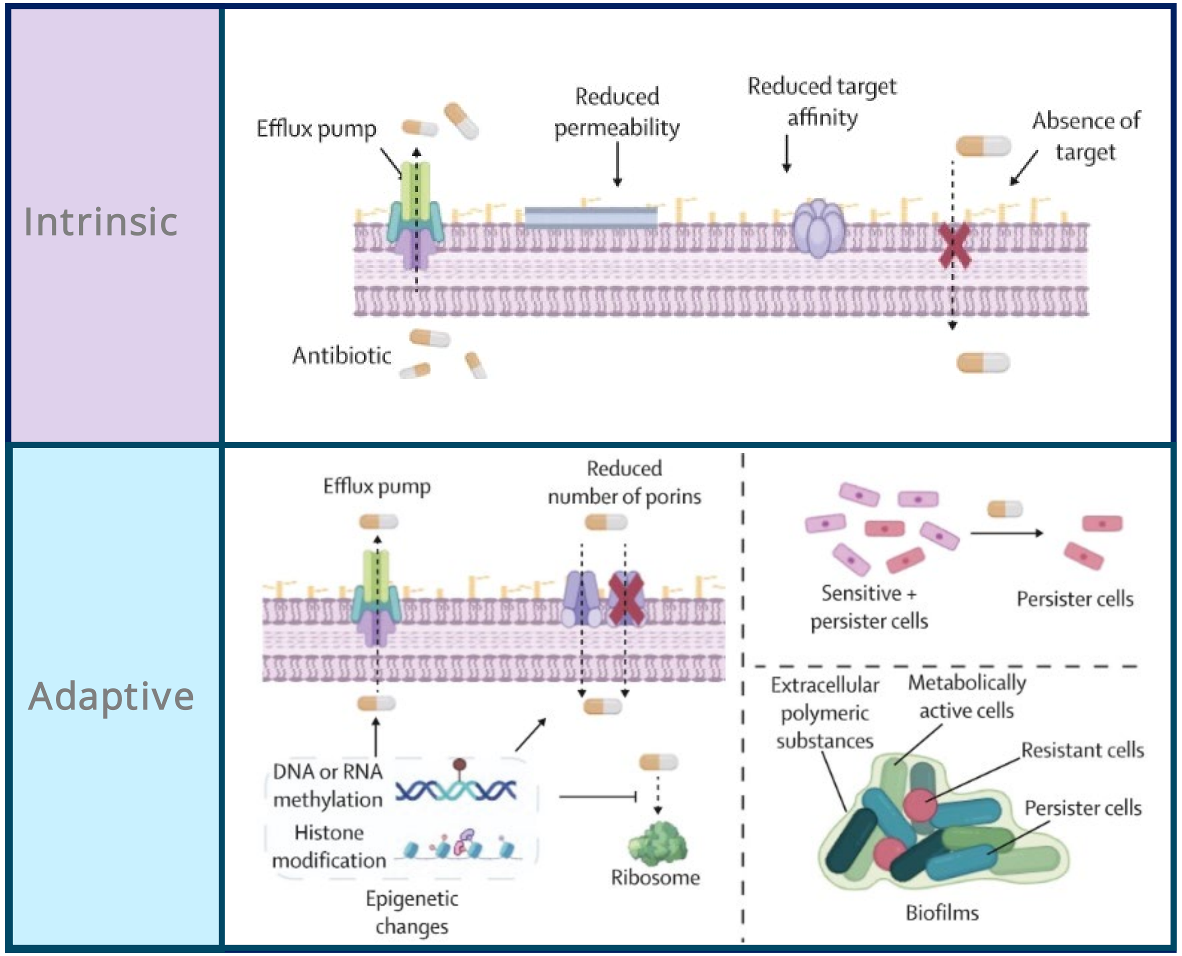
Resistant bacteria spread to other patients from surfaces within the healthcare facility.

Simply using antibiotics creates resistance. These drugs should only be used to treat infections.

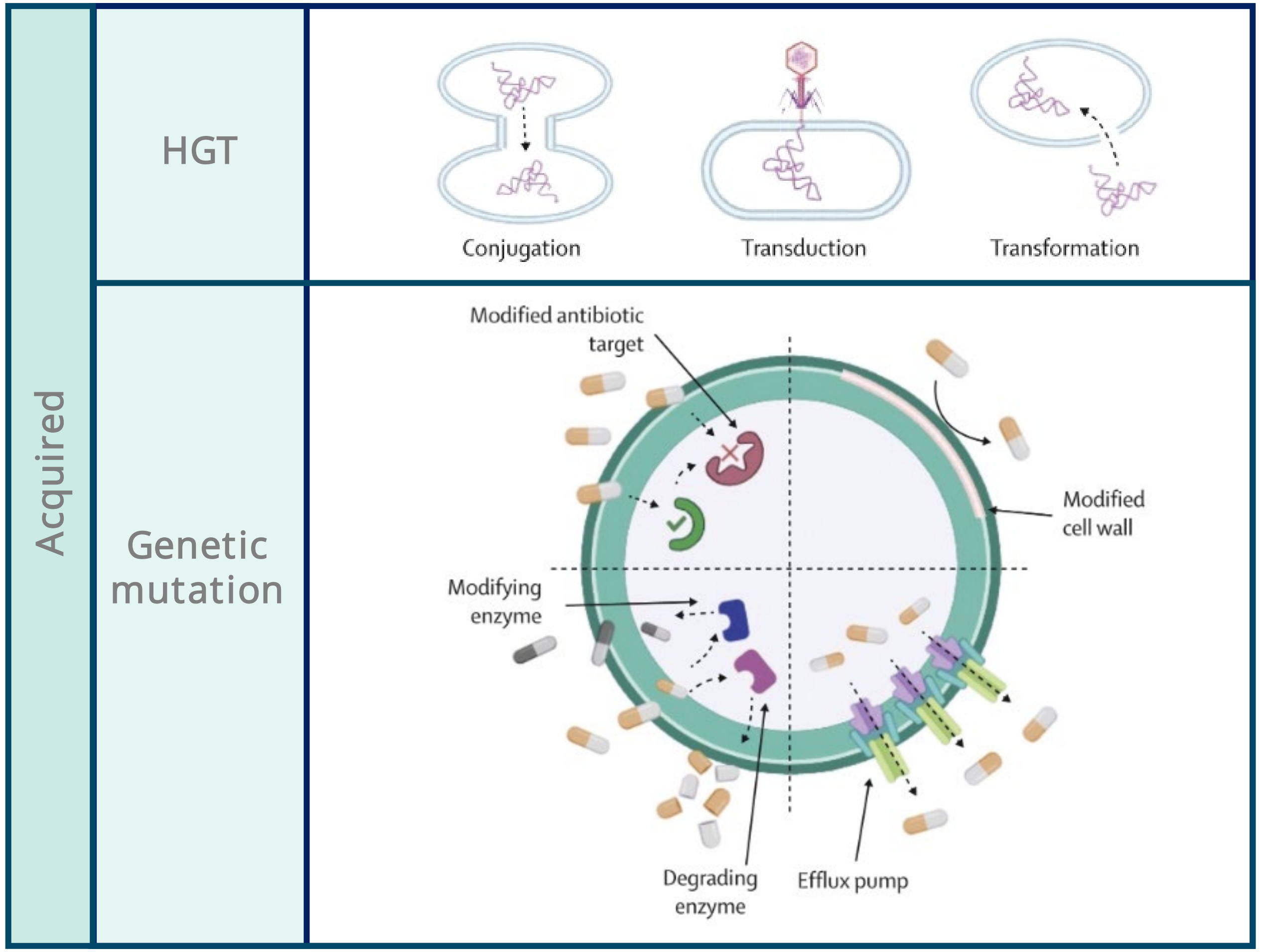
https://www.cdc.gov/narms/resistance/index.html

Spread of Resistance

Resistance can develop in multiple ways


Intrinsic

Adaptive

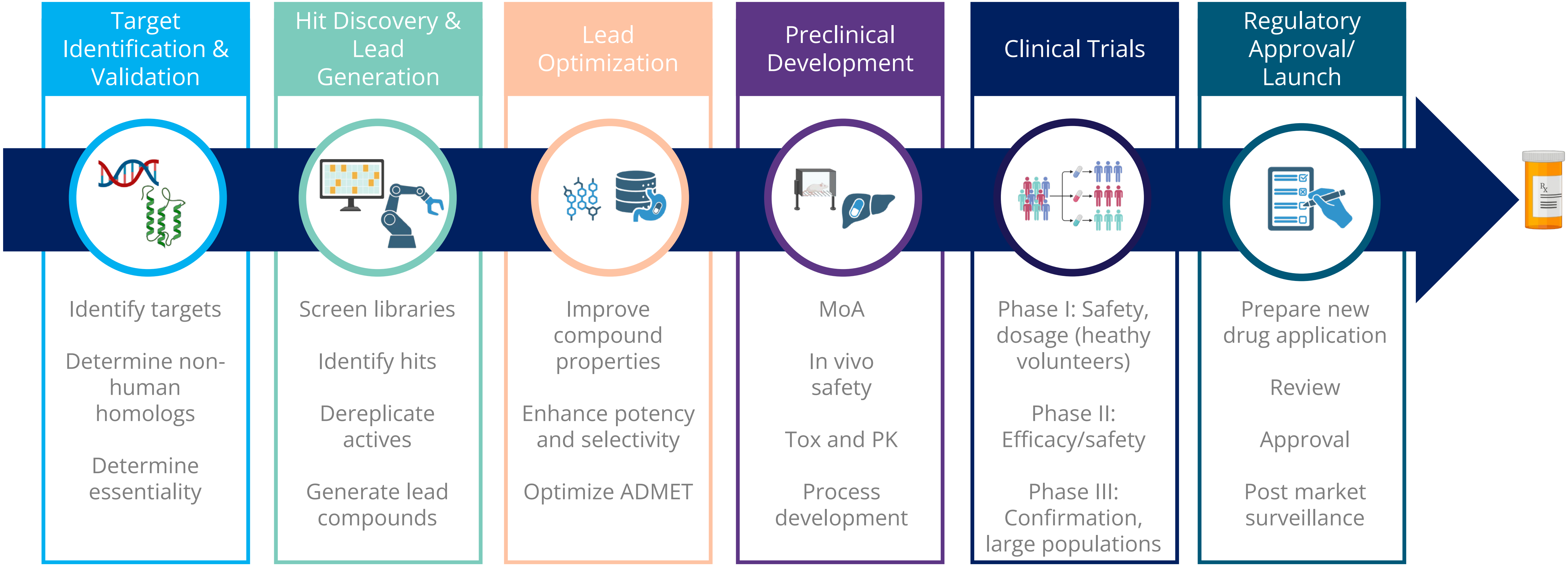

Acquired

HGT

Genetic mutation

Lancet Microbe 6(1): 100947, 2025. PubMed: 39305919

Antibacterial Discovery Pipeline



Target Identification & Validation

- Identify targets
- Determine non-human homologs
- Determine essentiality

Hit Discovery & Lead Generation

- Screen libraries
- Identify hits
- Dereplicate actives
- Generate lead compounds

Lead Optimization

- Improve compound properties
- Enhance potency and selectivity
- Optimize ADMET

Preclinical Development

- MoA
- In vivo safety
- Tox and PK
- Process development

Clinical Trials

- Phase I: Safety, dosage (heathy volunteers)
- Phase II: Efficacy/safety
- Phase III: Confirmation, large populations

Regulatory Approval/ Launch

- Prepare new drug application
- Review
- Approval
- Post market surveillance

2	16	48	64	75	Success (%)
54	18	36	30	12	Time (months)

From Outterson, K. Health Affairs 2021

Meeting the Challenge: Global Efforts

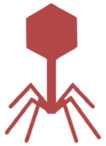
- High-level political commitment
- Evidence-informed policy making
- One Health & multisectoral collaboration

WHO Three Global Priorities for Innovation:

- Severe multidrug-resistant (MDR) gram-negative infections
- Severe gram-positive infections in immunosuppressed and critically ill patients
- Bacterial meningitis, including penicillin- and cephalosporin-resistant community-acquired infections.

INNOVATIVE TECHNOLOGIES

- Novel chemistry
- Antimicrobial peptides
- CRISPR-Cas3
- AI/ML



ALTERNATIVES TO ANTIBIOTICS

- Phage therapy
- Immune modulating agents
- Monoclonal antibodies
- Microbiome

DIAGNOSTICS & SURVEILLANCE

- Rapid phenotypic testing

Meeting the Challenge: ATCC® Offerings

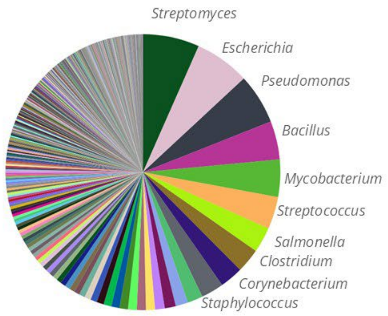
The most comprehensive, fully authenticated collection:

- 80,000+ bacteria, fungi, viruses, and protozoa
- 8,700+ microbial type strains
- 1,000+ derivatives, including genomic and synthetic nucleic acids
- 7,000+ microbial genomes
- 4,000+ cell lines and associated media and reagents

Explore our microbial products

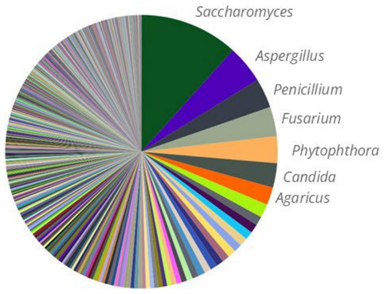
Microbial Diversity

Bacteriology



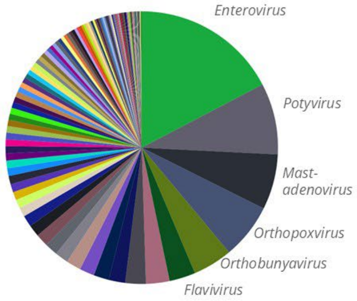
1226 Genera

Mycology



1864 Genera

Virology

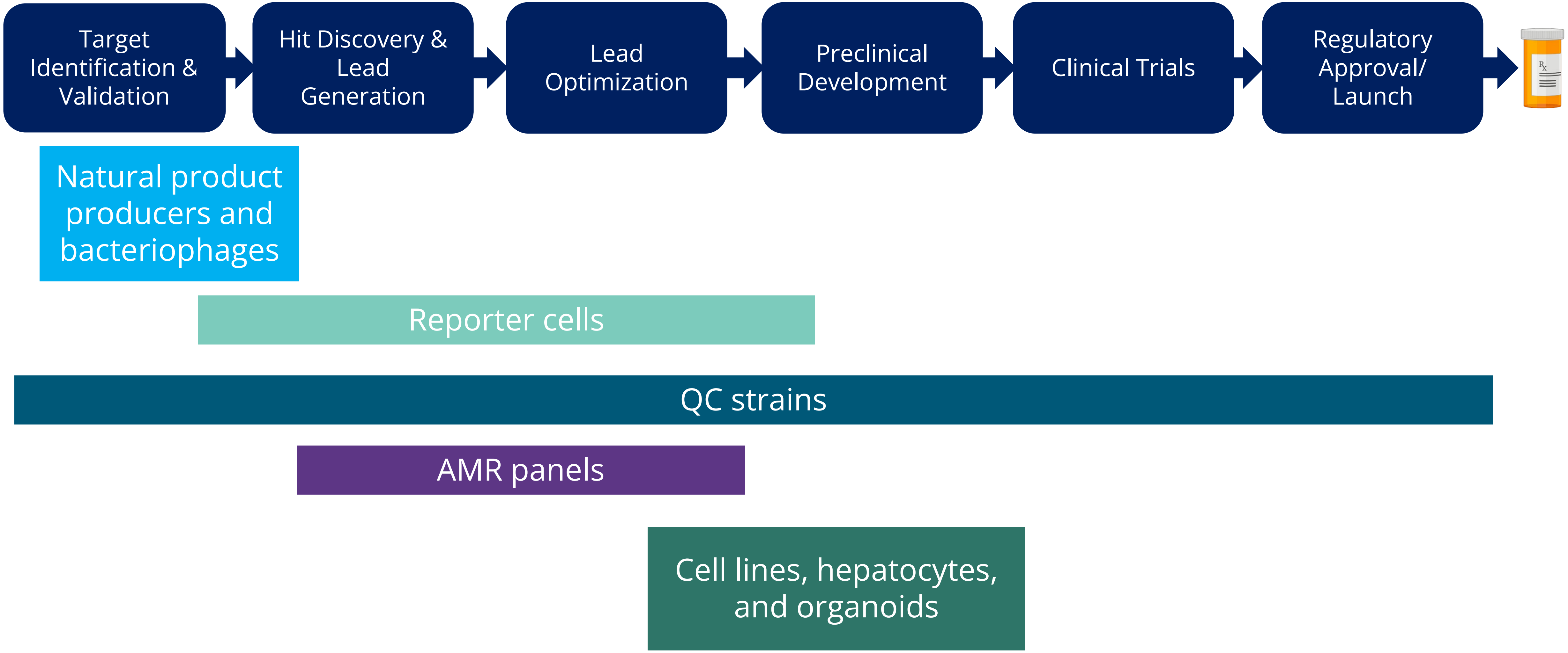


150 Genera

Brand recognition:

- Organizations and regulatory agencies specify ATCC® cultures - USP, ISO, FDA, CLSI, USDA, ASTM, AOAC, etc.
- Over 475 reference strains recommended for use in quality control

ATCC has Tools Supporting the Antibiotic Discovery Pipeline



Target Identification & Validation

Hit Discovery & Lead Generation

Lead Optimization

Preclinical Development

Clinical Trials

Regulatory Approval/ Launch

Natural product producers and bacteriophages

Reporter cells

QC strains

AMR panels

Cell lines, hepatocytes, and organoids

Created using BioRender.com. BioRender is a registered trademark of Science Suite Inc.

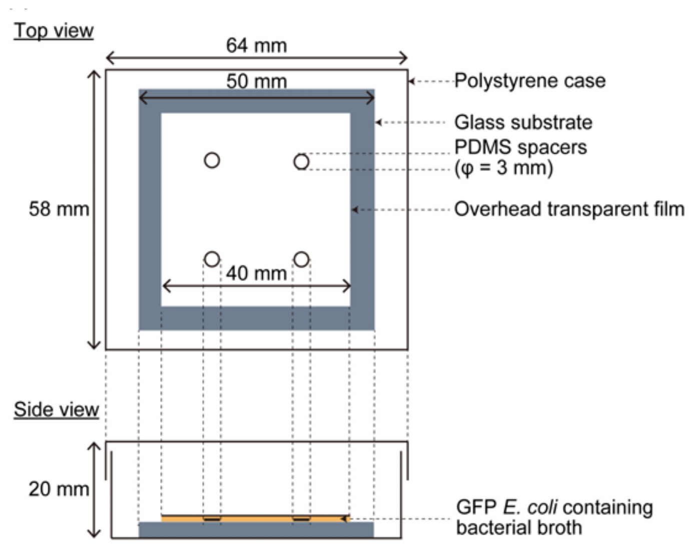
Meeting the Challenge: ATCC® Offerings

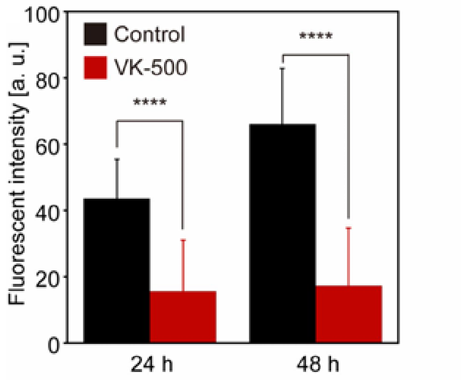
GFP-tagged strains for antibiotic discovery

ATCC ID	Name	Reporter
25922GFP™	*Escherichia coli*	GFP
14028GFP™	*Salmonella enterica* subsp. *enterica* serovar Typhimurium	GFP
12022GFP™	*Shigella flexneri*	GFP
10145GFP™	*Pseudomonas aeruginosa*	GFP
15692GFP™	*Pseudomonas aeruginosa*	GFP

Case Study:

Use of 25922GFP™ to evaluate surface antibacterial activity





Sci Rep 15(1): 1124, 2025. PubMed: 39890805

Meeting the Challenge: ATCC® Offerings

ATCC® strains are cited as QC controls in Clinical and Laboratory and Standards Institute (CLSI) AST methods

CLSI #	Method	ATCC® catalog number																								
		25922™	27853™	29212™	29213™	49619™	25923™	35218™	33186™	29741™	43055™	700057™	750™	6258™	22019™	24433™	90018™	90028™	MYA-3626™	MYA-3629™	MYA-3630™	MYA-3631™	MYA-3633™	MYA-3634™	MYA-4438™	MYA-3349™
M02	Performance standards for disk Susceptibility tests	🟩	🟩	🟩		🟩	🟩	🟩	🟩																	
M07	Methods for Dilution Antimicrobial Susceptibility Tests for Bacteria That Grow Aerobically	🟩	🟩	🟩	🟩	🟩		🟩	🟩	🟩	🟩	🟩														
M11	Methods for Antimicrobial Susceptibility Testing of Anaerobic Bacteria	🟩								🟩	🟩	🟩														
M23	Development of In Vitro Susceptibility Test Methods, Breakpoints, and Quality Control Parameters	🟩	🟩	🟩	🟩		🟩	🟩	🟩																	
M24	Performance Standards for Susceptibility Testing of *Mycobacteria*, *Nocardia* spp., and Other Aerobic Actinomycetes		🟩	🟩	🟩			🟩																		
M27	Performance Standards for Antifungal Susceptibility Testing of Yeasts												🟩	🟩	🟩	🟩	🟩	🟩								
M38	Performance Standards for Antifungal Susceptibility Testing of Filamentous Fungi													🟩	🟩		🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩

Coming soon: Two new CLSI controls for Cefiderocol and Cefiderocol–xeruborbactam combination

Meeting the Challenge: ATCC® Offerings

Priority Antimicrobial-Resistant Strains

Selection

- Recent, clinically relevant isolates
- Prevalent pathogenic species
- Multidrug-resistant and extensively drug-resistant strains

Analysis

- *De novo* genome sequencing and annotation
- Identification of antimicrobial resistance genes
- Evaluation of antimicrobial resistance and susceptibility

Collection

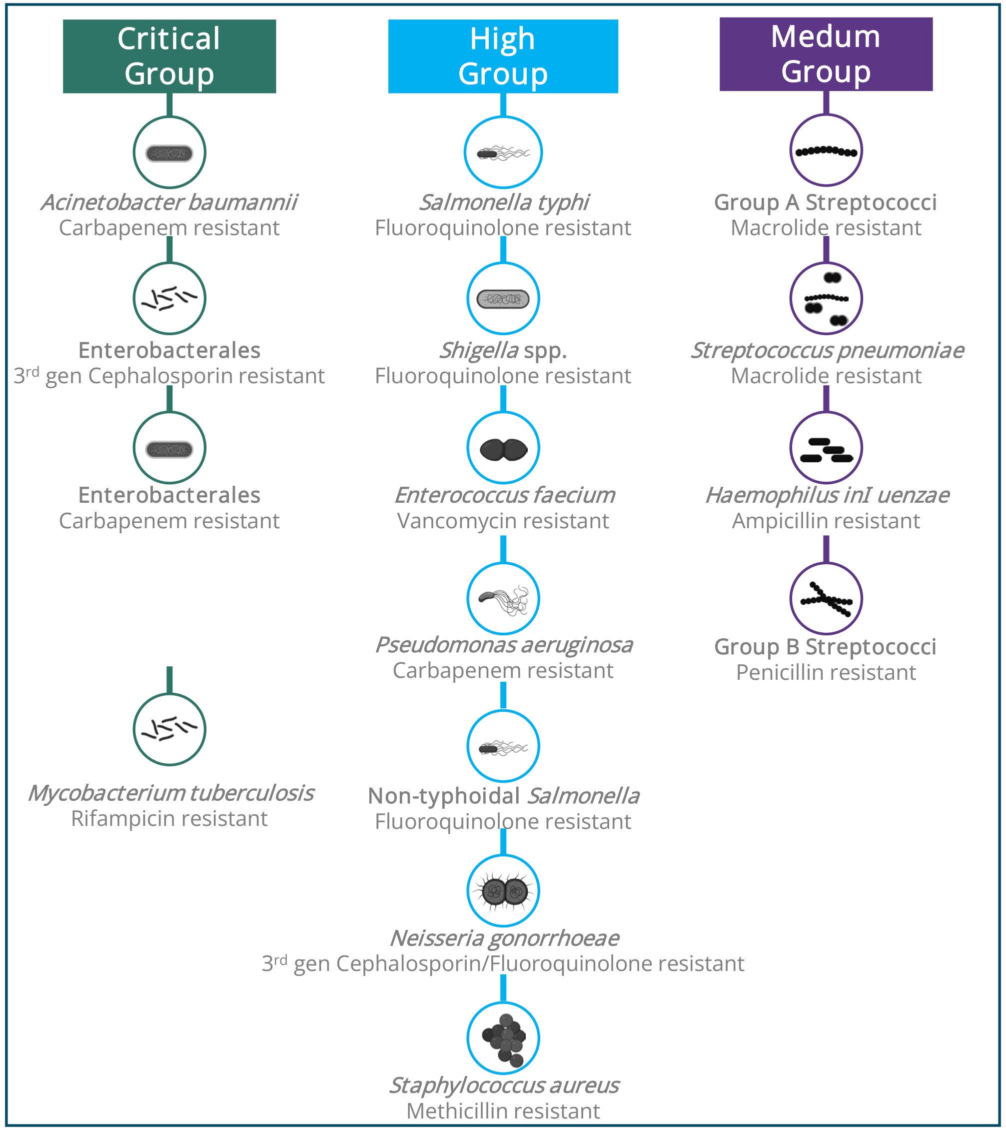
- Strains authenticated and categorized by ATCC
- Genotypically, phenotypically, and functionally characterized

We are sourcing high-priority isolates to add to the collection

Multidrug-resistant *Pseudomonas aeruginosa* from contaminated eye drops
BAA-3443™
BAA-3444™

Meeting the Challenge: ATCC® Offerings

WHO bacterial priority pathogens list, 2024



Critical Group

Acinetobacter baumannii
Carbapenem resistant

Enterobacterales
3rd gen Cephalosporin resistant

Enterobacterales
Carbapenem resistant

Mycobacterium tuberculosis
Rifampicin resistant

High Group

Salmonella typhi
Fluoroquinolone resistant

Shigella spp.
Fluoroquinolone resistant

Enterococcus faecium
Vancomycin resistant

Pseudomonas aeruginosa
Carbapenem resistant

Non-typhoidal *Salmonella*
Fluoroquinolone resistant

Neisseria gonorrhoeae
3rd gen Cephalosporin/Fluoroquinolone resistant

Staphylococcus aureus
Methicillin resistant

Medum Group

Group A Streptococci
Macrolide resistant

Streptococcus pneumoniae
Macrolide resistant

Haemophilus influenzae
Ampicillin resistant

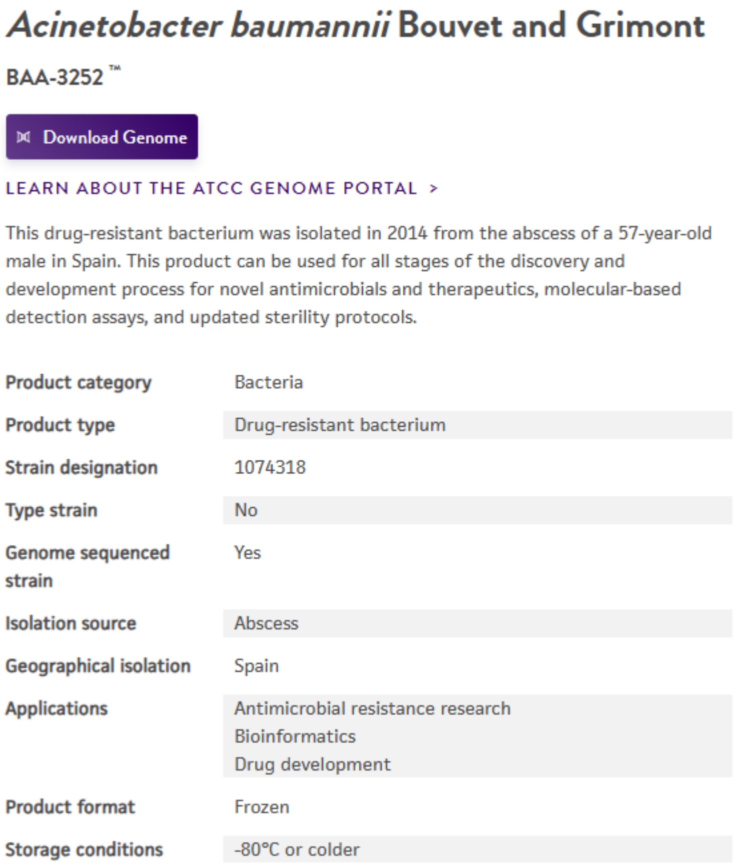
Group B Streptococci
Penicillin resistant

https://www.who.int/publications/i/item/9789240093461

WHO Priority	Species	AMR	No of ATCC® strains
Critical	*Acinetobacter baumannii*	Carbapenem resistant	16
Critical	*Klebsiella pneumoniae*	Third-generation cephalosporin resistant	17
Critical	*Escherichia coli*	Third-generation cephalosporin resistant	19
Critical	*Proteus* spp.	Third-generation cephalosporin resistant	3
Critical	*Citrobacter* spp.	Third-generation cephalosporin resistant	8
Critical	*Serratia* spp.	Third-generation cephalosporin resistant	2
Critical	*Klebsiella pneumoniae*	Carbapenem resistant	6
Critical	*Escherichia coli*	Carbapenem resistant	12
Critical	*Enterobacter* spp.	Carbapenem resistant	7
Critical	*Citrobacter* spp.	Carbapenem resistant	2
Critical	*Mycobacterium tuberculosis*	Rifampicin resistant	2
High	*Enterococcus faecium*	Vancomycin resistant	9
High	*Pseudomonas aeruginosa*	Carbapenem resistant	15
High	*Neisseria gonorrhoeae*	Fluoroquinolone resistant	5
High	*Staphylococcus aureus*	Methicillin resistant	69
Medium	Group A streptococci	Macrolide resistant	5
Medium	*Streptococcus pneumoniae*	Macrolide resistant	28
Medium	*Haemophilus influenzae*	Ampicillin resistant	2

Meeting the Challenge: ATCC® Offerings

Priority antimicrobial-resistant strains



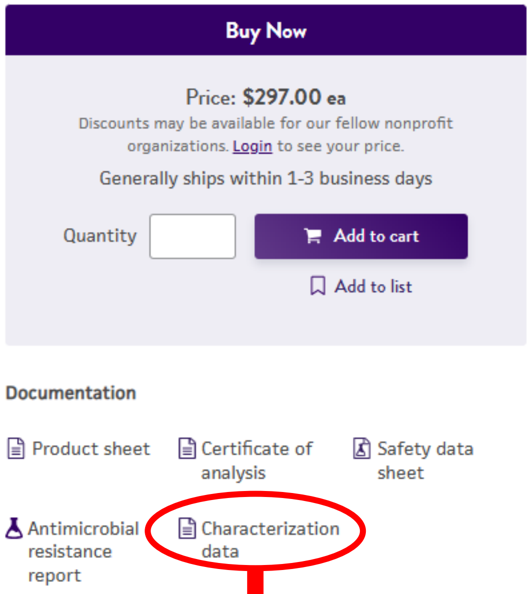
Acinetobacter baumannii Bouvet and Grimont

BAA-3252 ™

LEARN ABOUT THE ATCC GENOME PORTAL >

This drug-resistant bacterium was isolated in 2014 from the abscess of a 57-year-old male in Spain. This product can be used for all stages of the discovery and development process for novel antimicrobials and therapeutics, molecular-based detection assays, and updated sterility protocols.

Product category	Bacteria
Product type	Drug-resistant bacterium
Strain designation	1074318
Type strain	No
Genome sequenced strain	Yes
Isolation source	Abscess
Geographical isolation	Spain
Applications	Antimicrobial resistance research Bioinformatics Drug development
Product format	Frozen
Storage conditions	-80°C or colder



Price: **$297.00** ea

Discounts may be available for our fellow nonprofit organizations. Login to see your price.

Generally ships within 1-3 business days

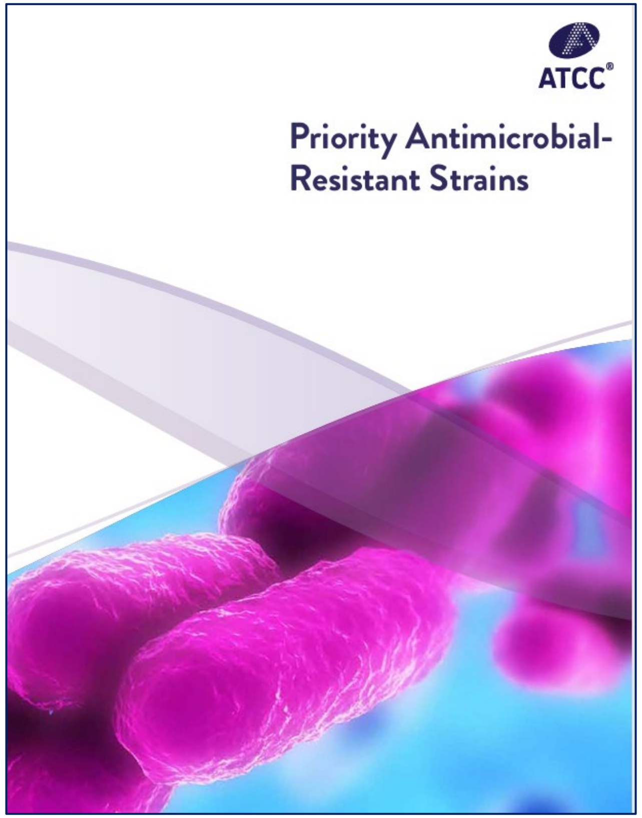
Quantity

Documentation

- Product sheet
- Certificate of analysis
- Safety data sheet
- Antimicrobial resistance report
- Characterization data

Priority AMR Strains Brochure

www.atcc.org/AMR-brochure



Meeting the Challenge: ATCC® Offerings

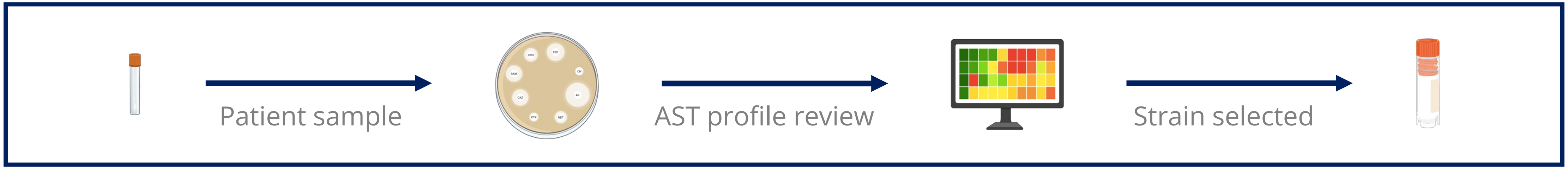
Acinetobacter baumannii: Priority Antimicrobial-Resistant Strains

Antibiotics	Class	Antibiotic target	BAA-3278™	BAA-3301™	BAA-3275™	BAA-3320™	BAA-3257™	BAA-3276™	BAA-3300™	BAA-3302™	BAA-3252™	BAA-3282™	BAA-3283™	BAA-3338™	BAA-3311™
Gentamicin	Aminoglycosides	30S	≥16 (R)	≥16 (R)	≤1 (S)	≤1 (S)	≥16 (R)	4 (S)	≥16 (R)	8 (I)	≤1(S)	4 (S)	≤1 (S)	≥16 (R)	≤1 (S)
Tobramycin			≥16 (R)	≥16 (R)	≤1 (S)	≤1 (S)	≥16 (R)	2 (S)	≥16 (R)	8 (I)	≤1 (S)	8 (I)	2 (S)	8 (I)	≤1 (S)
Imipenem	Carbapenems	Cell wall	8 (I)	8 (I)	8 (I)	≥16 (R)	8 (I)	≥16 (R)	8 (I)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	0.25 (S)
Meropenem			≥16 (R)	4 (S)	≥16 (R)	≥16 (R)	4 (S)	≥16 (R)	≥16 (R)	8 (I)	≥16 (R)	≥16 (R)	≥16 (R)	≥16 (R)	0.25 (S)
Cefazolin	Third Generation Cephalosporin		≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)
Cefepime			≥64 (R)	16 (I)	32 (R)	≥64 (R)	8 (S)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	32 (R)	≥64 (R)	2 (S)
Cefotaxime			≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	16 (I)
Ceftazidime			≥64 (R)	≥64 (R)	≥64 (R)	16 (I)	16 (I)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	4 (S)
Ceftriaxone			≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	≥64 (R)	16 (I)
TMP-sulfamethoxazole	Diaminopyrimidines	Folic acid metabolism	160 (R)	160 (R)	≥320 (R)	≤20 (S)	≥320 (R)	160 (R)	≤20 (S)	≥320 (R)	≥320 (R)	≥320 (R)	≥320 (R)	≥320 (R)	≤20 (S)
Ciprofloxacin	Fluoroquinolones	DNA gyrase	≥4 (R)	≥4 (R)	2 (I)	1 (S)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	≥4 (R)	0.25 (S)
Levofloxacin			≥8 (R)	≥8 (R)	1 (S)	0.5 (S)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	≥8 (R)	0.12 (S)
Ampicilin/Sultbactam	Penicillin/BLI	Cell wall	16 (I)	4 (S)	8 (S)	16 (I)	16 (I)	8 (S)	16 (I)	≥32 (R)	8 (S)	≤2 (S)	16 (I)	≥32 (R)	≤2 (S)
Piperacillin/Tazaobactam			≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	≥128 (R)	8 (I)
Tetracycline	Tetracyclines	30S	2 (S)	2 (S)	≥16 (R)	2 (S)	2 (S)	4 (S)	2 (S)	2 (S)	≥16 (R)	≥16 (R)	≥16 (R)	4 (S)	≤1 (S)
	Metadata	Isolation country	Honduras	Italy	France	Venezuela	Spain	USA	Singapore	Italy	Spain	USA	Taiwan	USA	Korea
		Year of isolation	2006	2006	2006	2006	2004	2014	2004	2015	2014	2004	2006	2004	2006
		Source of isolation	Catheters	Blood	Blood	Blood	Blood	Sputum	Trachea	Blood	Abscess	Wound	Sputum	Blood	Blood
		Patient Gender	Female	Female	Male	Male	Female	Male	Male	Male	Male	Female	Female	Female	Female
		Patient Age (Yr)	<1	53	84	19	68	75	71	41	57	51	80	764	73

Priority AMR Strains Brochure
www.atcc.org/AMR-brochure

Meeting the Challenge: ATCC® Offerings

New bacterial isolates coming soon


Patient sample

AST profile review

Strain selected

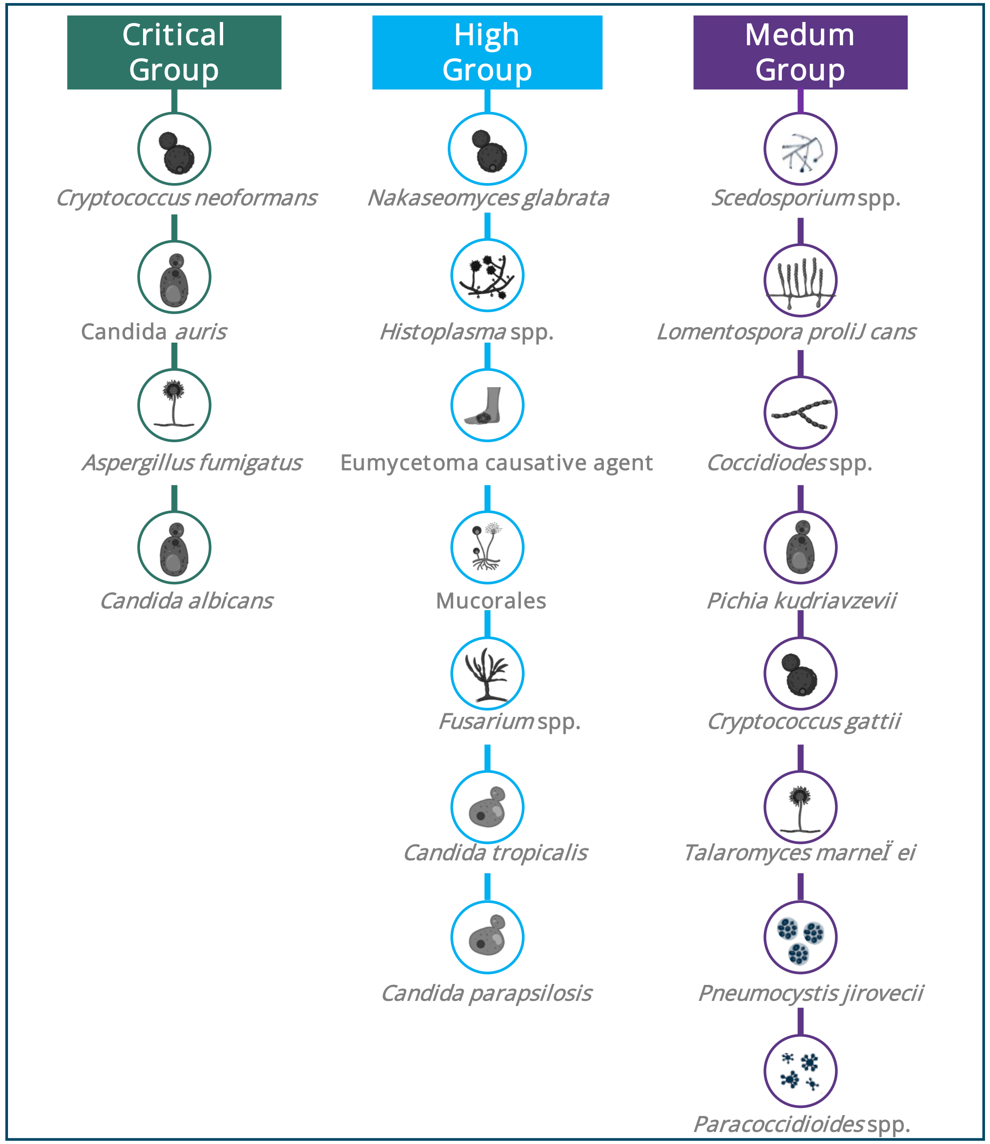
WHO Priority	Species	AMR	No of ATCC® strains	Why
Critical	*Enterobacter* spp.	Third-generation cephalosporin resistant	8	Recent isolates
Critical	*Escherichia coli*	Third-generation cephalosporin resistant	3	Recent isolates
Critical	*Morganella morganii*	Third-generation cephalosporin resistant	3	Gap
Critical	*Pluralibacter* spp.	Third-generation cephalosporin resistant	1	Gap
Critical	*Enterobacter* spp.	Carbapenem resistant	3	Recent isolates
Critical	*Morganella morganii*	Carbapenem resistant	2	Gap
Critical	*Klebsiella pneumoniae*	Carbapenem resistant	1	Recent isolates
Critical	*Shigella* spp.	Fluoroquinolone resistant	1	Gap

- *Mycobacterium* strains resistant to known treatments developed in an attenuated mycobacterial strain (TB vaccine strain Bacillus Calmette-Guérin, or BCG) containing defined drug resistance mutations.

- New two new CLSI reference materials for Cefiderocol and Cefiderocol–xeruborbactam

Meeting the Challenge: ATCC® Offerings

WHO fungal priority pathogens 2022 list



Critical Group
- *Cryptococcus neoformans*
- Candida *auris*
- *Aspergillus fumigatus*
- *Candida albicans*

High Group
- *Nakaseomyces glabrata*
- *Histoplasma* spp.
- Eumycetoma causative agent
- Mucorales
- *Fusarium* spp.
- *Candida tropicalis*
- *Candida parapsilosis*

Medum Group
- *Scedosporium* spp.
- *Lomentospora prolificans*
- *Coccidiodes* spp.
- *Pichia kudriavzevii*
- *Cryptococcus gattii*
- *Talaromyces marneffei*
- *Pneumocystis jirovecii*
- *Paracoccidioides* spp.

WHO Priority	Species	No of ATCC® strains
Critical	*Cryptococcus neoformans*	134
Critical	*Candida auris*	8
Critical	*Aspergillus fumigatus*	101
Critical	*Candida albicans*	227
High	*Nakaseomyces glabrata*	30
High	*Histoplamsa* spp.	62
High	Eumycetoma causing agents	59
High	*Mucorales*	287
High	*Fusarium* spp.	1125
High	*Candida tropicalis*	67
High	*Candida parapsilosis*	41
Medium	*Paracoccioides* spp.	31
Medium	*Cryptococcus gatti*	26
Medium	*Pichia kudriavzvii*	20
Medium	*Talaomyces marneffei*	19
Medium	*Scedosporium* spp.	18
Medium	*Cocciodioides* spp.	11
Medium	*Lomentospora prolificans*	7
Medium	*Pneumocystis jirovici*	1

Meeting the Challenge: ATCC® Offerings

New fungal pathogens coming soon

Strain	# of Isolates	Amphotericin B	Anidulafungin	Caspofungin	Fluconazole	Micafungin	Itraconazole	Terbinafine	Gap in Collection
Candida auris	5	🟥	🟩	🟥	🟥	🟩			Gap, fill caspofungin and amphotericin resistance
Candida auris	15	🟥	🟩	🟩	🟥	🟩			Gap, fill caspofungin resistance
Candida auris	11	🟩	🟩	🟩	🟥	🟩			New isolates
Candida auris	1	🟩	🟥	🟥	🟥	🟥			Gap, fill Anidulafungin resistance
T. indotineae[1]	5						🟩	🟥	Gap, new species
T. indotineae	2						🟥	🟩	Gap, new species
T. indotineae	2						🟥	🟥	Gap, new species
T. indotineae	3						🟩	🟩	Gap, new species

[1] *Trichophyton indotineae*

ATCC® Genome Portal

The only authenticated reference genome database for ATCC microbes

The ATCC® Genome Portal (AGP) is a rapidly growing ISO 9001–compliant database of high-quality reference genomes from authenticated microbial strains in the ATCC collection. Customers can easily access and download meticulously curated whole-genome assemblies for purchased strains and *Supporting Members* have full access to the AGP.

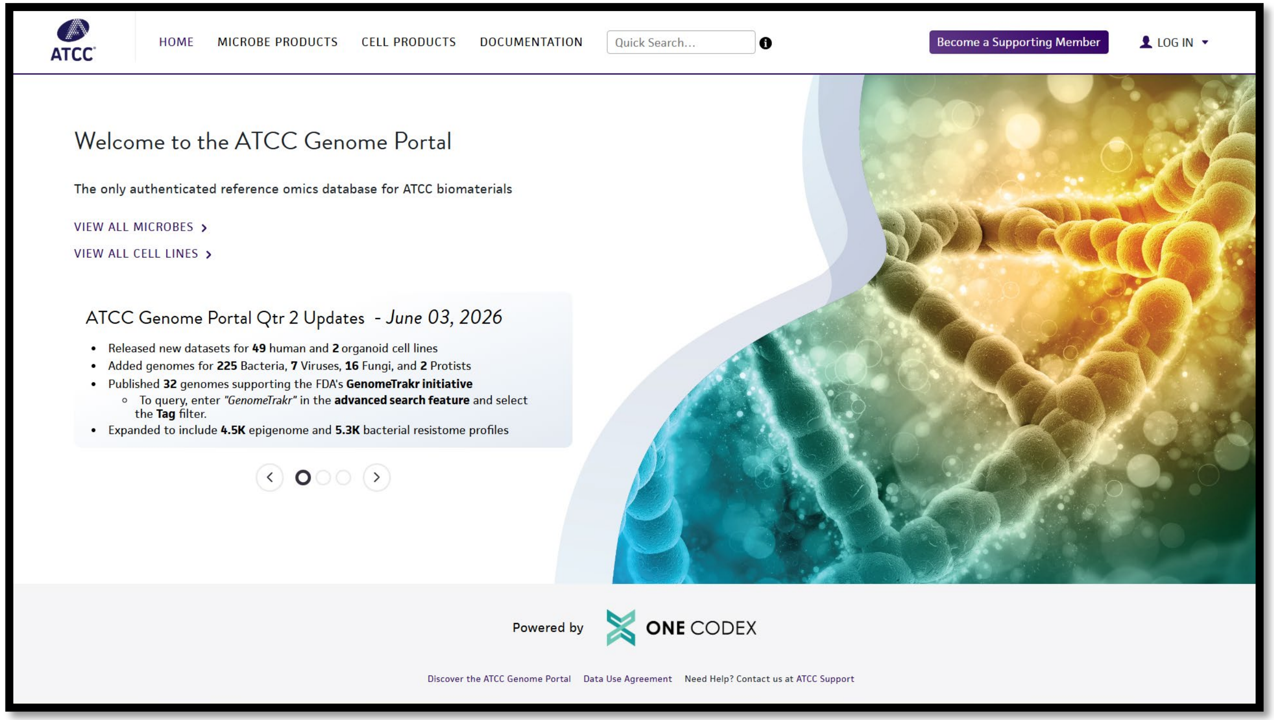
7,000+

Available microbial reference genomes

as of June 2026

- Download ATCC® microbial genomes.
- View ClinVar variants for ATCC ® cell-lines.
- Search by sequence and annotations.
- Stratify taxonomy, isolation source, catalog number, type strain status, strain name, biosafety level, etc.
- View genome assembly statistics and quality metrics.
- Find relatedness of ATCC® genomes.

New genomes are released at the end of every quarter.



Welcome to the ATCC Genome Portal

The only authenticated reference omics database for ATCC biomaterials

VIEW ALL MICROBES ›

VIEW ALL CELL LINES ›

ATCC Genome Portal Qtr 2 Updates - *June 03, 2026*

- Released new datasets for **49** human and **2** organoid cell lines
- Added genomes for **225** Bacteria, **7** Viruses, **16** Fungi, and **2** Protists
- Published **32** genomes supporting the FDA's **GenomeTrakr initiative**
  - To query, enter *"GenomeTrakr"* in the **advanced search feature** and select the **Tag** filter.
- Expanded to include **4.5K** epigenome and **5.3K** bacterial resistome profiles

Powered by ONE CODEX

Discover the ATCC Genome Portal   Data Use Agreement   Need Help? Contact us at ATCC Support

Learn more about the ATCC® Genome Portal

Vial to File

Physical Repository

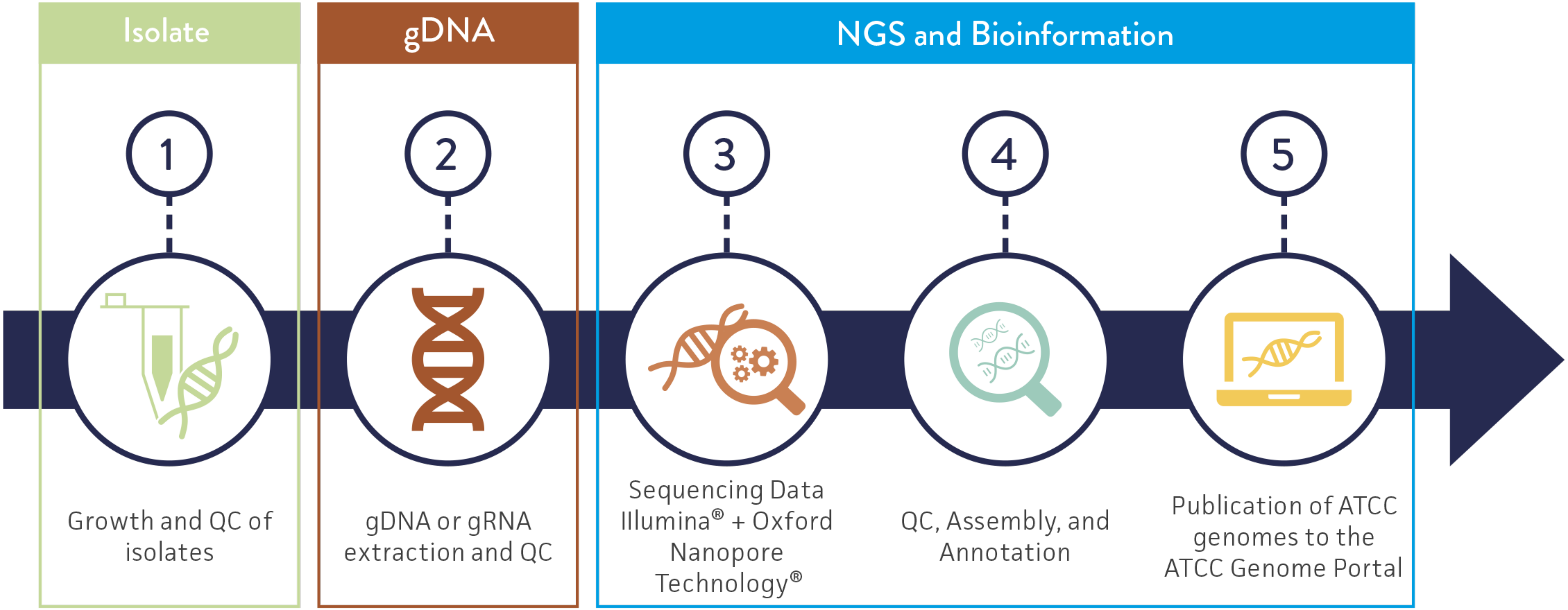
- Strains
- Derivatives
- Standards
- Reference materials

Authenticated Reference Data

- Sequencing data
- Assembled genomes
- Annotated genes

Drive scientific advancement by providing the scientific community with high-quality, annotated whole-genome sequence (WGS) information to complement ATCC's biological materials.

Authenticated Physical Material Coupled with Reference-Quality Genome Sequences



Growth and QC of isolates

gDNA or gRNA extraction and QC

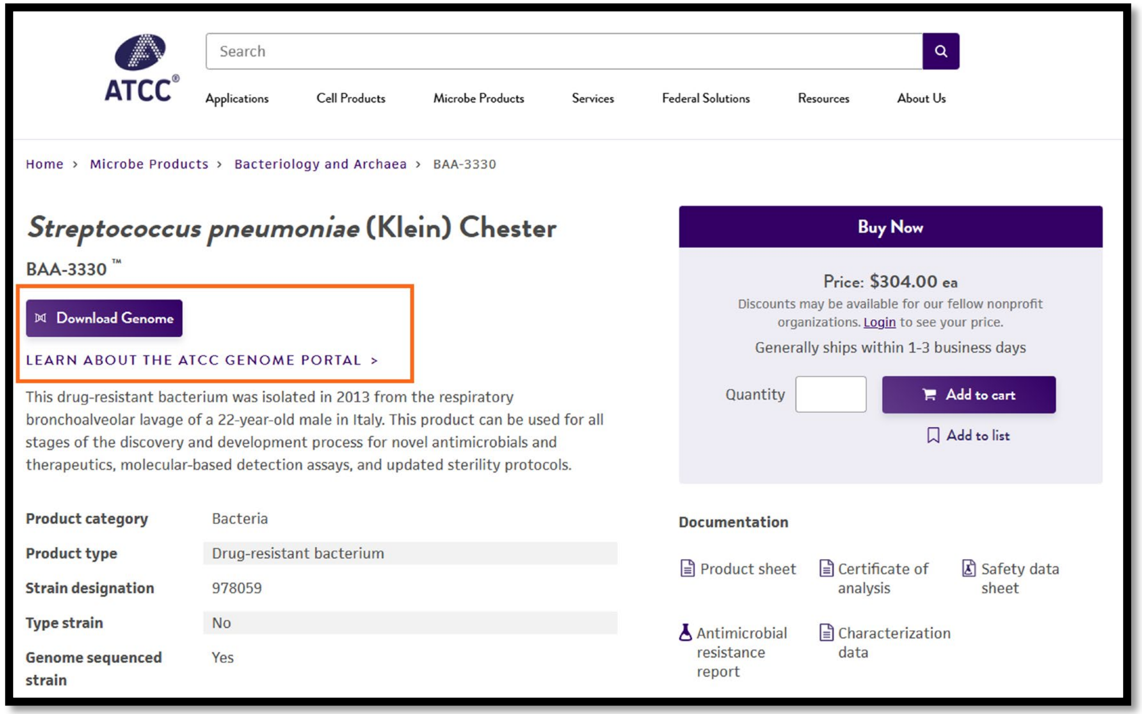
Sequencing Data Illumina® + Oxford Nanopore Technology®

QC, Assembly, and Annotation

Publication of ATCC genomes to the ATCC Genome Portal

- Fully traceable and authenticated to ATCC® materials.
- All genome assemblies produced in-house at ATCC® in an ISO certified laboratory.

ATCC® Genome Portal – Ways to visit the AGP



Streptococcus pneumoniae (Klein) Chester

BAA-3330™

This drug-resistant bacterium was isolated in 2013 from the respiratory bronchoalveolar lavage of a 22-year-old male in Italy. This product can be used for all stages of the discovery and development process for novel antimicrobials and therapeutics, molecular-based detection assays, and updated sterility protocols.

Product category	Bacteria
Product type	Drug-resistant bacterium
Strain designation	978059
Type strain	No
Genome sequenced strain	Yes

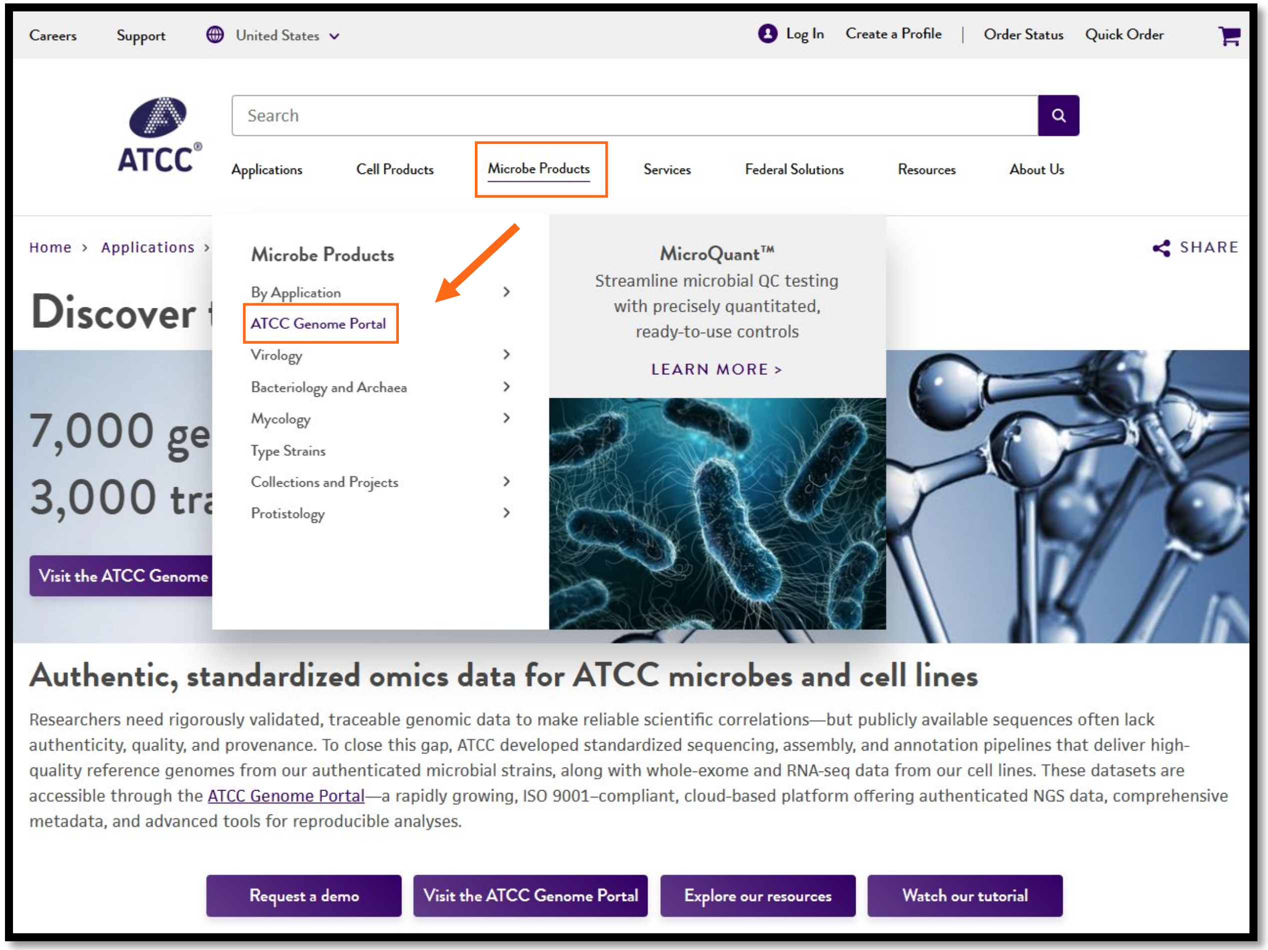
Buy Now

Price: $304.00 ea

Discounts may be available for our fellow nonprofit organizations. Login to see your price.

Generally ships within 1-3 business days

Documentation



MicroQuant™

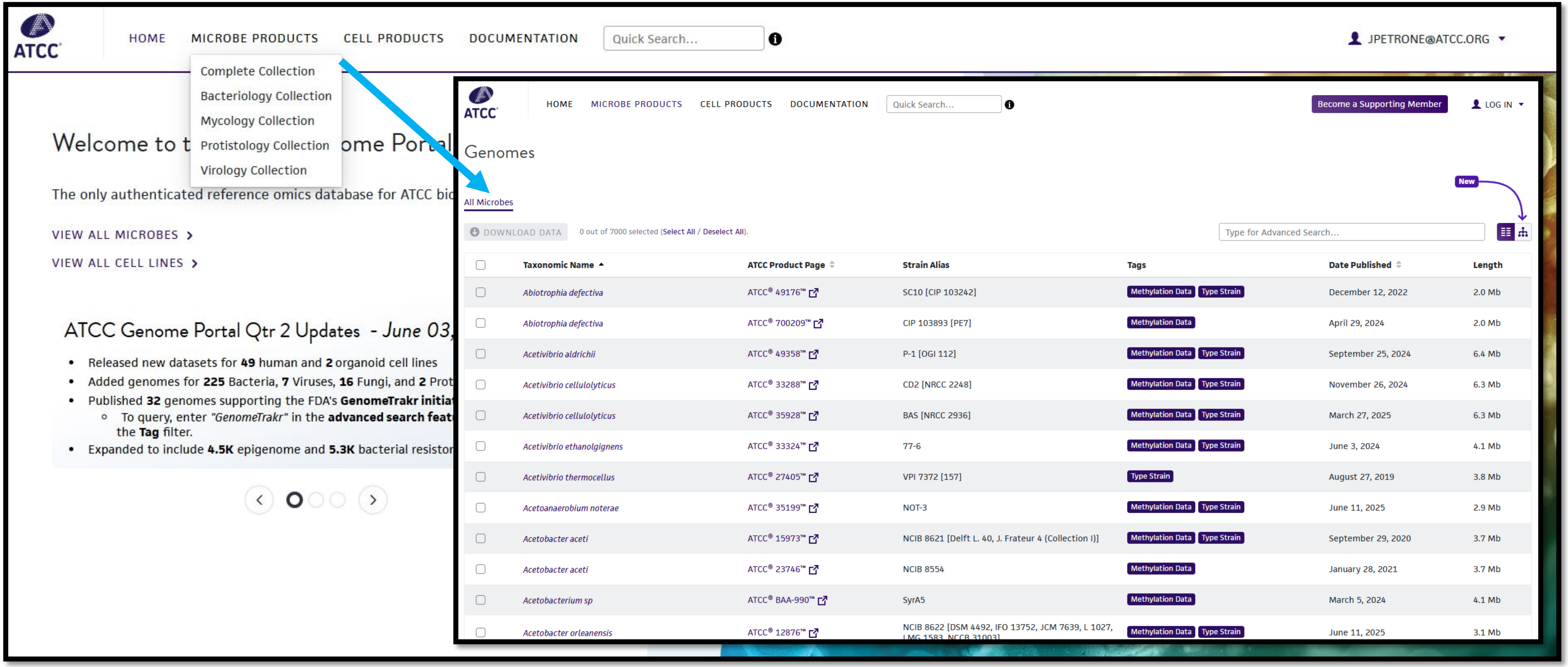
Streamline microbial QC testing with precisely quantitated, ready-to-use controls

Authentic, standardized omics data for ATCC microbes and cell lines

Researchers need rigorously validated, traceable genomic data to make reliable scientific correlations—but publicly available sequences often lack authenticity, quality, and provenance. To close this gap, ATCC developed standardized sequencing, assembly, and annotation pipelines that deliver high-quality reference genomes from our authenticated microbial strains, along with whole-exome and RNA-seq data from our cell lines. These datasets are accessible through the ATCC Genome Portal—a rapidly growing, ISO 9001–compliant, cloud-based platform offering authenticated NGS data, comprehensive metadata, and advanced tools for reproducible analyses.

ATCC® Genome Portal
www.atcc.org/genomeportal

ATCC® Genome Portal – Browse for Strains / Data



Welcome to t … ome Portal

The only authenticated reference omics database for ATCC bio

VIEW ALL MICROBES >

VIEW ALL CELL LINES >

ATCC Genome Portal Qtr 2 Updates - *June 03,*

- Released new datasets for **49** human and **2** organoid cell lines
- Added genomes for **225** Bacteria, **7** Viruses, **16** Fungi, and **2** Prot
- Published **32** genomes supporting the FDA's **GenomeTrakr initia**
  - To query, enter *"GenomeTrakr"* in the **advanced search feat** the **Tag** filter.
- Expanded to include **4.5K** epigenome and **5.3K** bacterial resistor

Genomes

All Microbes

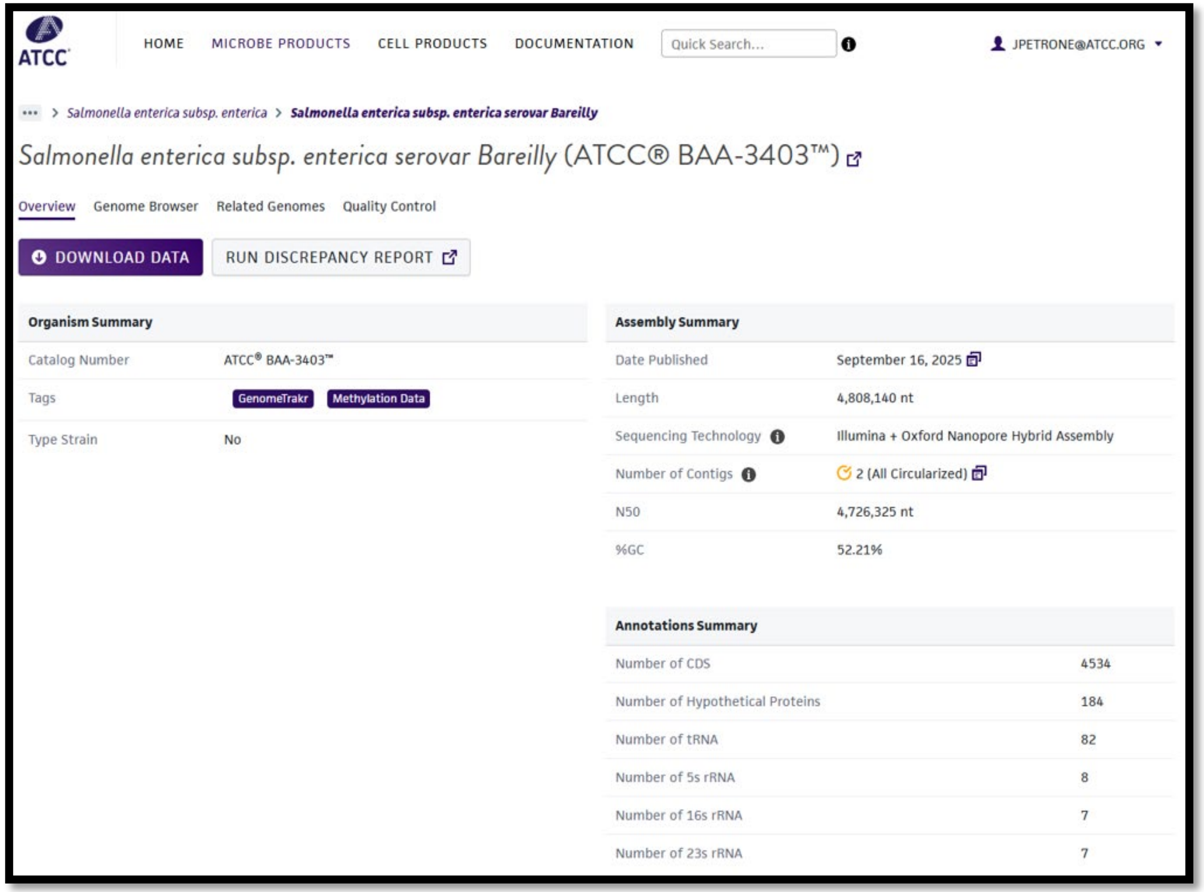
0 out of 7000 selected (Select All / Deselect All).

☐	Taxonomic Name ▲	ATCC Product Page	Strain Alias	Tags	Date Published	Length
☐	*Abiotrophia defectiva*	ATCC® 49176™	SC10 [CIP 103242]	Methylation Data Type Strain	December 12, 2022	2.0 Mb
☐	*Abiotrophia defectiva*	ATCC® 700209™	CIP 103893 [PE7]	Methylation Data	April 29, 2024	2.0 Mb
☐	*Acetivibrio aldrichii*	ATCC® 49358™	P-1 [OGI 112]	Methylation Data Type Strain	September 25, 2024	6.4 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 33288™	CD2 [NRCC 2248]	Methylation Data Type Strain	November 26, 2024	6.3 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 35928™	BAS [NRCC 2936]	Methylation Data Type Strain	March 27, 2025	6.3 Mb
☐	*Acetivibrio ethanolgignens*	ATCC® 33324™	77-6	Methylation Data Type Strain	June 3, 2024	4.1 Mb
☐	*Acetivibrio thermocellus*	ATCC® 27405™	VPI 7372 [157]	Type Strain	August 27, 2019	3.8 Mb
☐	*Acetoanaerobium noterae*	ATCC® 35199™	NOT-3	Methylation Data Type Strain	June 11, 2025	2.9 Mb
☐	*Acetobacter aceti*	ATCC® 15973™	NCIB 8621 [Delft L. 40, J. Frateur 4 (Collection I)]	Methylation Data Type Strain	September 29, 2020	3.7 Mb
☐	*Acetobacter aceti*	ATCC® 23746™	NCIB 8554	Methylation Data	January 28, 2021	3.7 Mb
☐	*Acetobacterium sp*	ATCC® BAA-990™	SyrA5	Methylation Data	March 5, 2024	4.1 Mb
☐	*Acetobacter orleanensis*	ATCC® 12876™	NCIB 8622 [DSM 4492, IFO 13752, JCM 7639, L 1027, LMG 1583, NCCB 31003]	Methylation Data Type Strain	June 11, 2025	3.1 Mb

ATCC® Genome Portal – Reference Genome Pages

Salmonella enterica subsp. *enterica* serovar Bareilly (ATCC® BAA-3403™)

Overview page



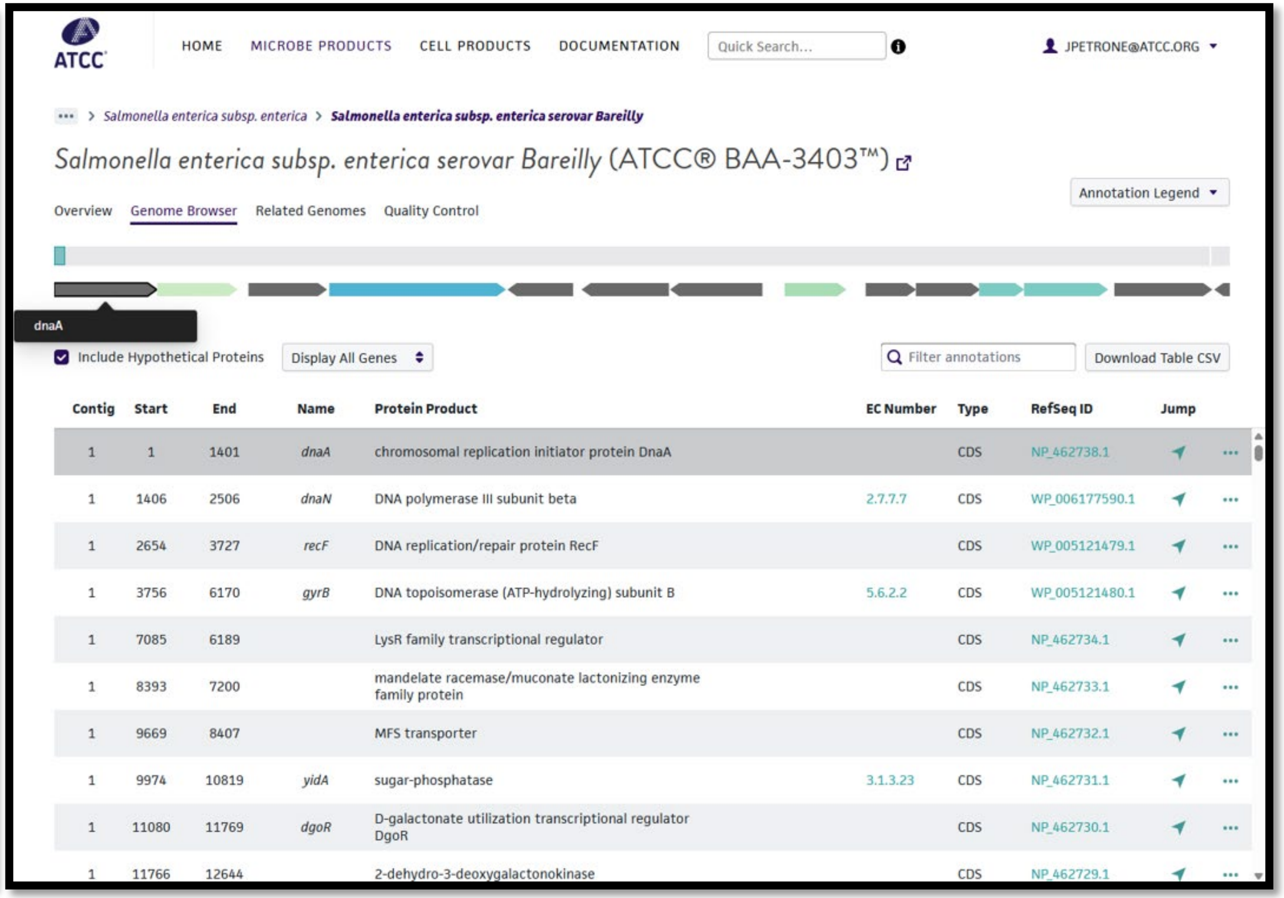
Salmonella enterica subsp. enterica serovar Bareilly (ATCC® BAA-3403™)

Organism Summary	
Catalog Number	ATCC® BAA-3403™
Tags	GenomeTrakr Methylation Data
Type Strain	No

Assembly Summary	
Date Published	September 16, 2025
Length	4,808,140 nt
Sequencing Technology	Illumina + Oxford Nanopore Hybrid Assembly
Number of Contigs	2 (All Circularized)
N50	4,726,325 nt
%GC	52.21%

Annotations Summary	
Number of CDS	4534
Number of Hypothetical Proteins	184
Number of tRNA	82
Number of 5s rRNA	8
Number of 16s rRNA	7
Number of 23s rRNA	7

Genome Annotations Browser



Salmonella enterica subsp. enterica serovar Bareilly (ATCC® BAA-3403™)

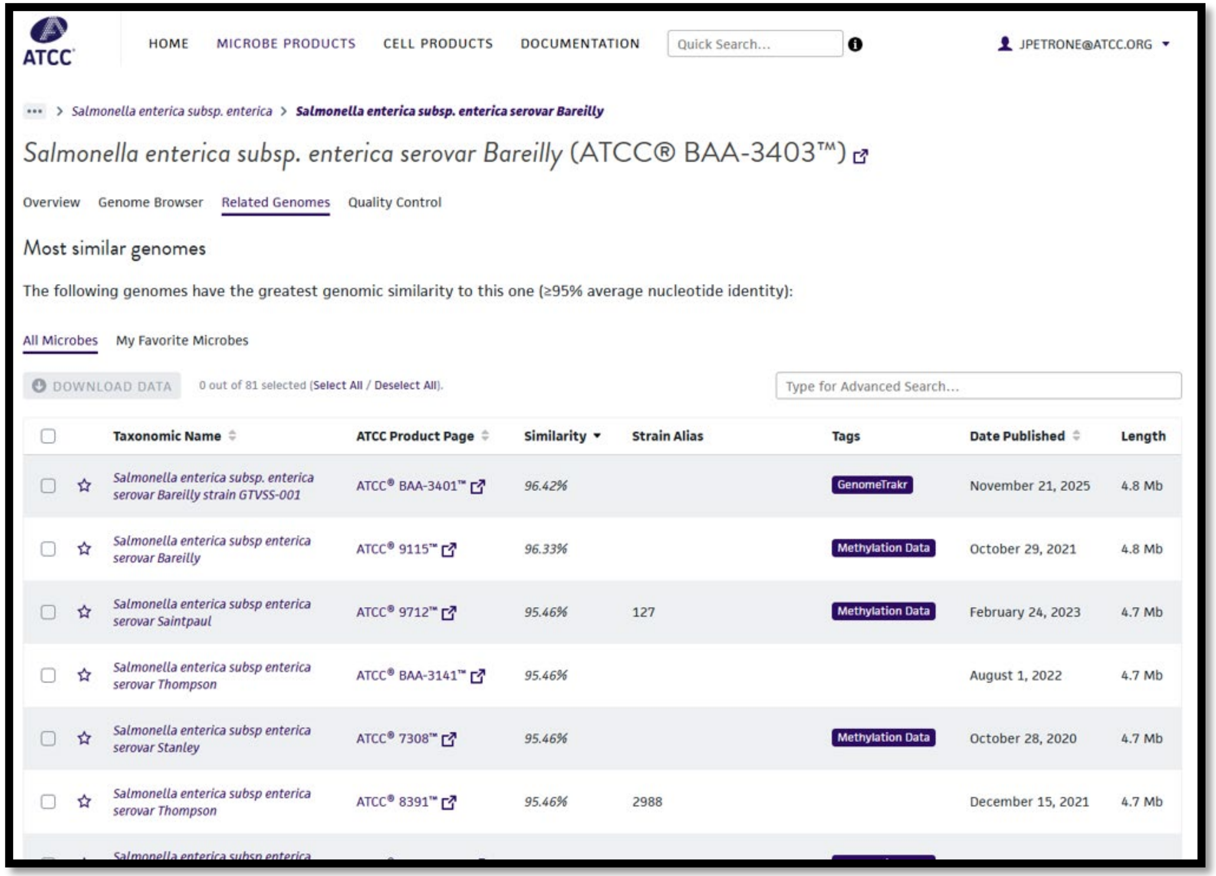
☑ Include Hypothetical Proteins

Contig	Start	End	Name	Protein Product	EC Number	Type	RefSeq ID	Jump
1	1	1401	*dnaA*	chromosomal replication initiator protein DnaA		CDS	NP_462738.1	
1	1406	2506	*dnaN*	DNA polymerase III subunit beta	2.7.7.7	CDS	WP_006177590.1	
1	2654	3727	*recF*	DNA replication/repair protein RecF		CDS	WP_005121479.1	
1	3756	6170	*gyrB*	DNA topoisomerase (ATP-hydrolyzing) subunit B	5.6.2.2	CDS	WP_005121480.1	
1	7085	6189		LysR family transcriptional regulator		CDS	NP_462734.1	
1	8393	7200		mandelate racemase/muconate lactonizing enzyme family protein		CDS	NP_462733.1	
1	9669	8407		MFS transporter		CDS	NP_462732.1	
1	9974	10819	*yidA*	sugar-phosphatase	3.1.3.23	CDS	NP_462731.1	
1	11080	11769	*dgoR*	D-galactonate utilization transcriptional regulator DgoR		CDS	NP_462730.1	
1	11766	12644		2-dehydro-3-deoxygalactonokinase		CDS	NP_462729.1	

ATCC® Genome Portal – Reference Genome Pages

Salmonella enterica subsp. *enterica* serovar Bareilly (ATCC® BAA-3403™)

Related Genomes



Salmonella enterica subsp. enterica serovar Bareilly (ATCC® BAA-3403™)

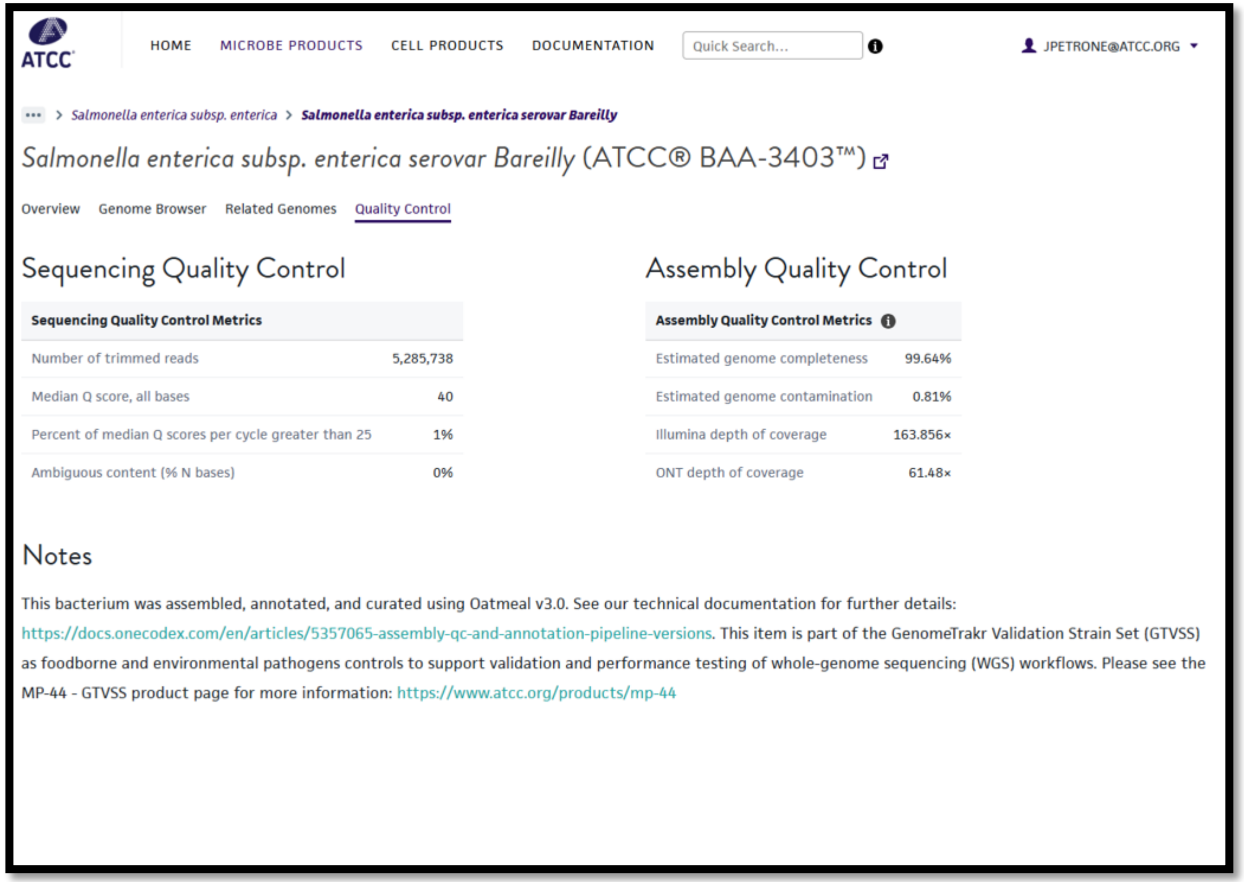
Most similar genomes

The following genomes have the greatest genomic similarity to this one (≥95% average nucleotide identity):

0 out of 81 selected (Select All / Deselect All).

☐		Taxonomic Name	ATCC Product Page	Similarity	Strain Alias	Tags	Date Published	Length
☐	☆	*Salmonella enterica subsp. enterica serovar Bareilly strain GTVSS-001*	ATCC® BAA-3401™	*96.42%*		GenomeTrakr	November 21, 2025	4.8 Mb
☐	☆	*Salmonella enterica subsp enterica serovar Bareilly*	ATCC® 9115™	*96.33%*		Methylation Data	October 29, 2021	4.8 Mb
☐	☆	*Salmonella enterica subsp enterica serovar Saintpaul*	ATCC® 9712™	*95.46%*	127	Methylation Data	February 24, 2023	4.7 Mb
☐	☆	*Salmonella enterica subsp enterica serovar Thompson*	ATCC® BAA-3141™	*95.46%*			August 1, 2022	4.7 Mb
☐	☆	*Salmonella enterica subsp enterica serovar Stanley*	ATCC® 7308™	*95.46%*		Methylation Data	October 28, 2020	4.7 Mb
☐	☆	*Salmonella enterica subsp enterica serovar Thompson*	ATCC® 8391™	*95.46%*	2988		December 15, 2021	4.7 Mb

Quality Control



Salmonella enterica subsp. enterica serovar Bareilly (ATCC® BAA-3403™)

Sequencing Quality Control

Sequencing Quality Control Metrics	
Number of trimmed reads	5,285,738
Median Q score, all bases	40
Percent of median Q scores per cycle greater than 25	1%
Ambiguous content (% N bases)	0%

Assembly Quality Control

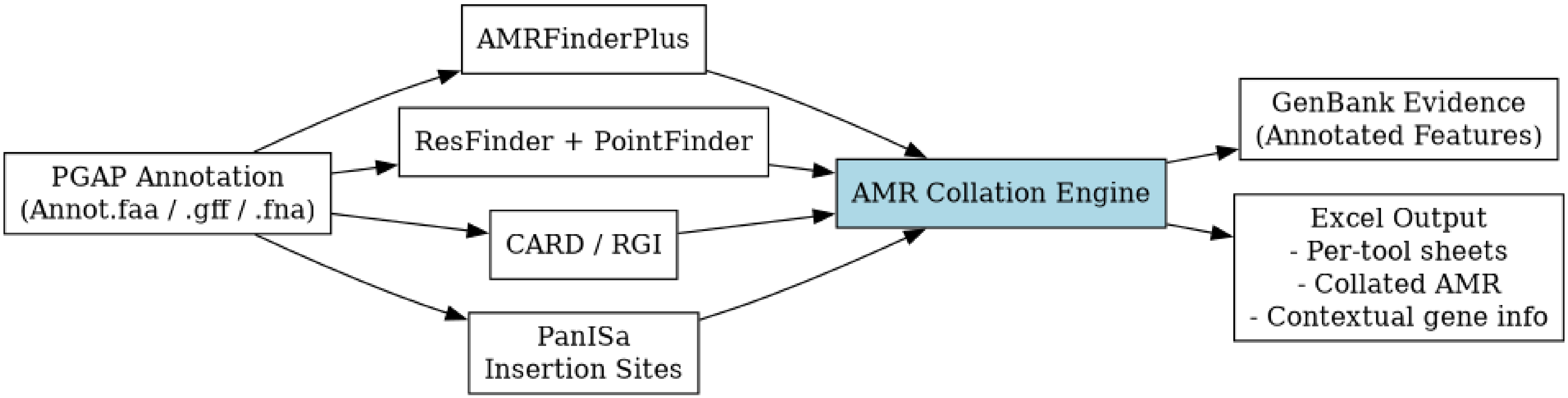
Assembly Quality Control Metrics	
Estimated genome completeness	99.64%
Estimated genome contamination	0.81%
Illumina depth of coverage	163.856×
ONT depth of coverage	61.48×

Notes

This bacterium was assembled, annotated, and curated using Oatmeal v3.0. See our technical documentation for further details: https://docs.onecodex.com/en/articles/5357065-assembly-qc-and-annotation-pipeline-versions. This item is part of the GenomeTrakr Validation Strain Set (GTVSS) as foodborne and environmental pathogens controls to support validation and performance testing of whole-genome sequencing (WGS) workflows. Please see the MP-44 - GTVSS product page for more information: https://www.atcc.org/products/mp-44

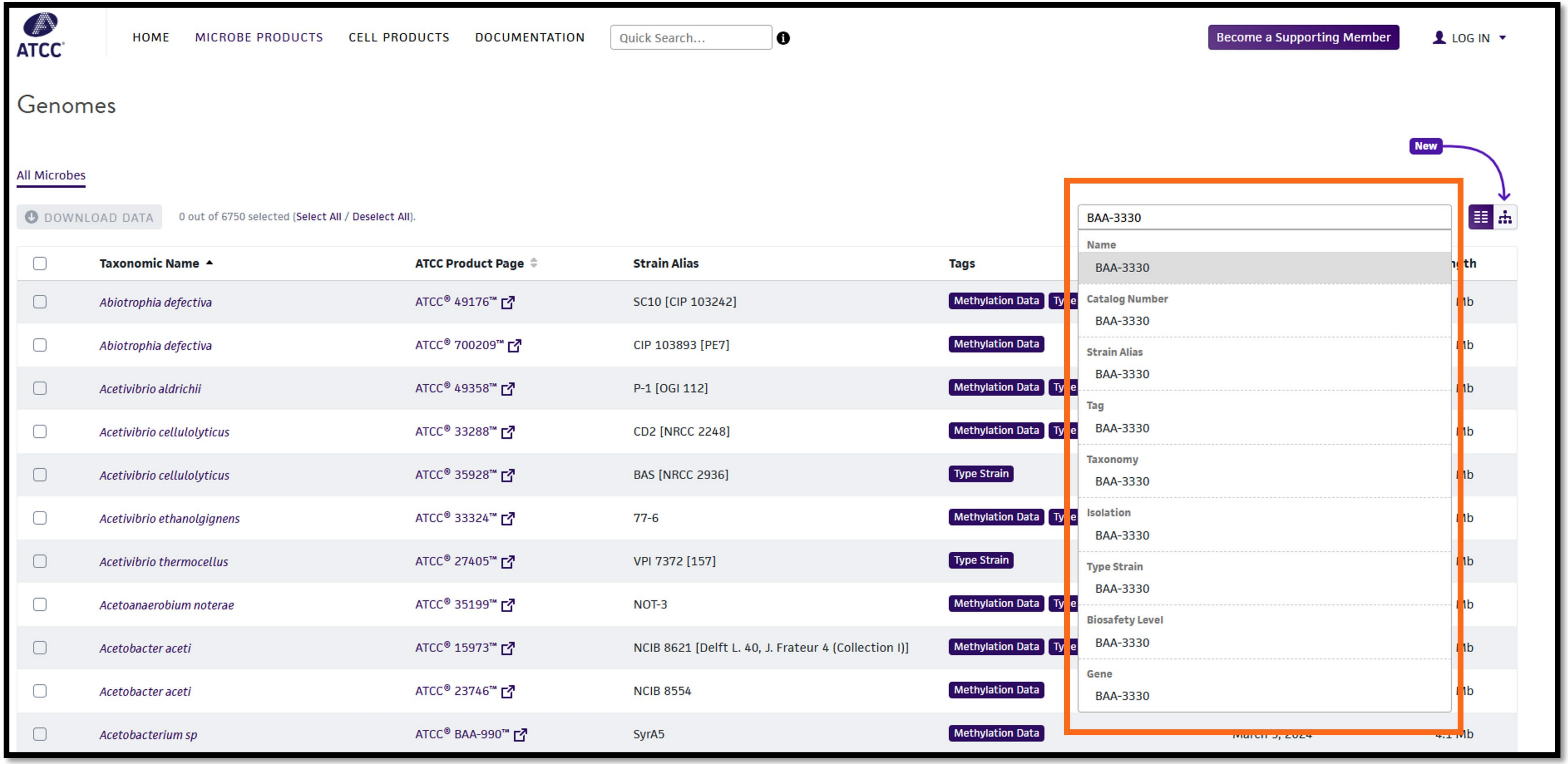
ATCC® Genome Portal – Bacterial Resistome Pipeline

- Hybrid assembly and ILM polishing gives confidence to SNP-based AMR.
- Resistome datasets are uploaded with every new bacterial genome deposition.
- Resistome packages also updated yearly with PGAP and AMR tool updates.
- VITEK 2 and Antibiogram data also made available from AGP and JSON format.



ATCC® Genome Portal – Ways to view AMR

Via Product page / GUI



Genomes

All Microbes

DOWNLOAD DATA   0 out of 6750 selected (Select All / Deselect All).

BAA-3330

Name
BAA-3330

Catalog Number
BAA-3330

Strain Alias
BAA-3330

Tag
BAA-3330

Taxonomy
BAA-3330

Isolation
BAA-3330

Type Strain
BAA-3330

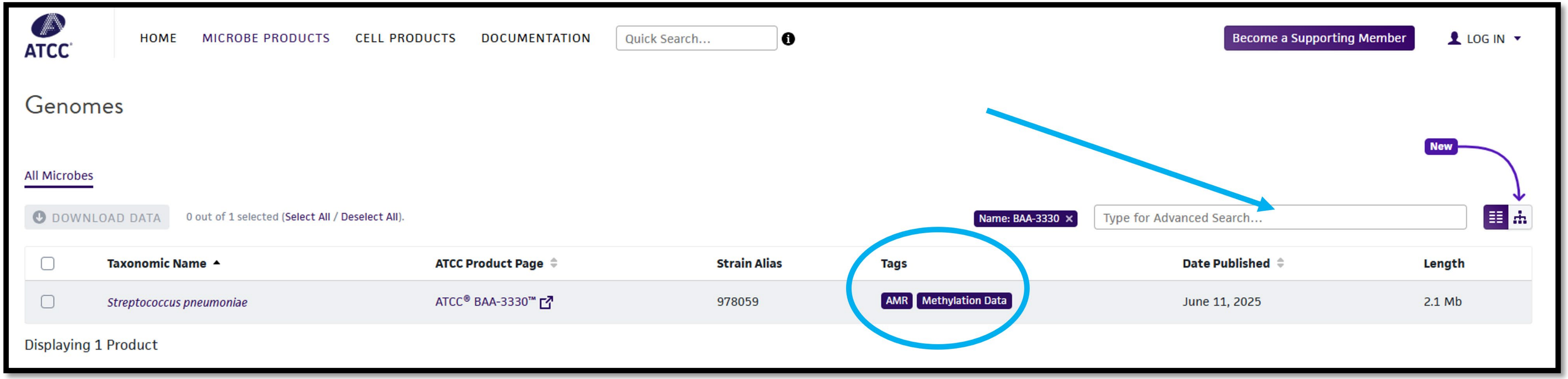
Biosafety Level
BAA-3330

Gene
BAA-3330

☐	Taxonomic Name ▲	ATCC Product Page	Strain Alias	Tags
☐	*Abiotrophia defectiva*	ATCC® 49176™	SC10 [CIP 103242]	Methylation Data
☐	*Abiotrophia defectiva*	ATCC® 700209™	CIP 103893 [PE7]	Methylation Data
☐	*Acetivibrio aldrichii*	ATCC® 49358™	P-1 [OGI 112]	Methylation Data
☐	*Acetivibrio cellulolyticus*	ATCC® 33288™	CD2 [NRCC 2248]	Methylation Data
☐	*Acetivibrio cellulolyticus*	ATCC® 35928™	BAS [NRCC 2936]	Type Strain
☐	*Acetivibrio ethanolgignens*	ATCC® 33324™	77-6	Methylation Data
☐	*Acetivibrio thermocellus*	ATCC® 27405™	VPI 7372 [157]	Type Strain
☐	*Acetoanaerobium noterae*	ATCC® 35199™	NOT-3	Methylation Data
☐	*Acetobacter aceti*	ATCC® 15973™	NCIB 8621 [Delft L. 40, J. Frateur 4 (Collection I)]	Methylation Data
☐	*Acetobacter aceti*	ATCC® 23746™	NCIB 8554	Methylation Data
☐	*Acetobacterium sp*	ATCC® BAA-990™	SyrA5	Methylation Data

ATCC® Genome Portal – Ways to view AMR

Via Product page / GUI



Genomes

All Microbes

0 out of 1 selected (Select All / Deselect All).

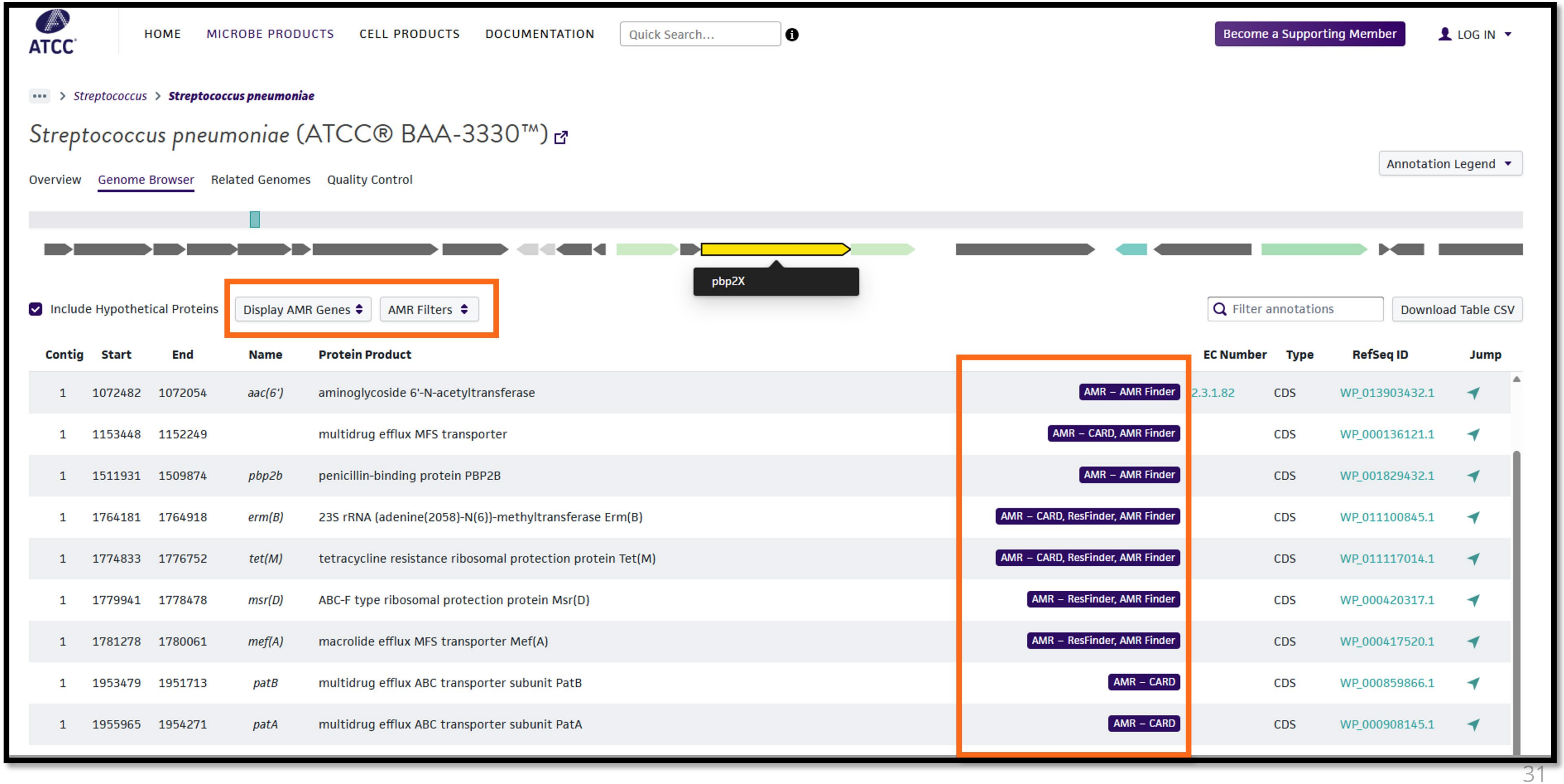
Name: BAA-3330 ×

☐	Taxonomic Name	ATCC Product Page	Strain Alias	Tags	Date Published	Length
☐	*Streptococcus pneumoniae*	ATCC® BAA-3330™	978059	AMR Methylation Data	June 11, 2025	2.1 Mb

Displaying 1 Product

ATCC® Genome Portal – Ways to view AMR

Via Product page / GUI



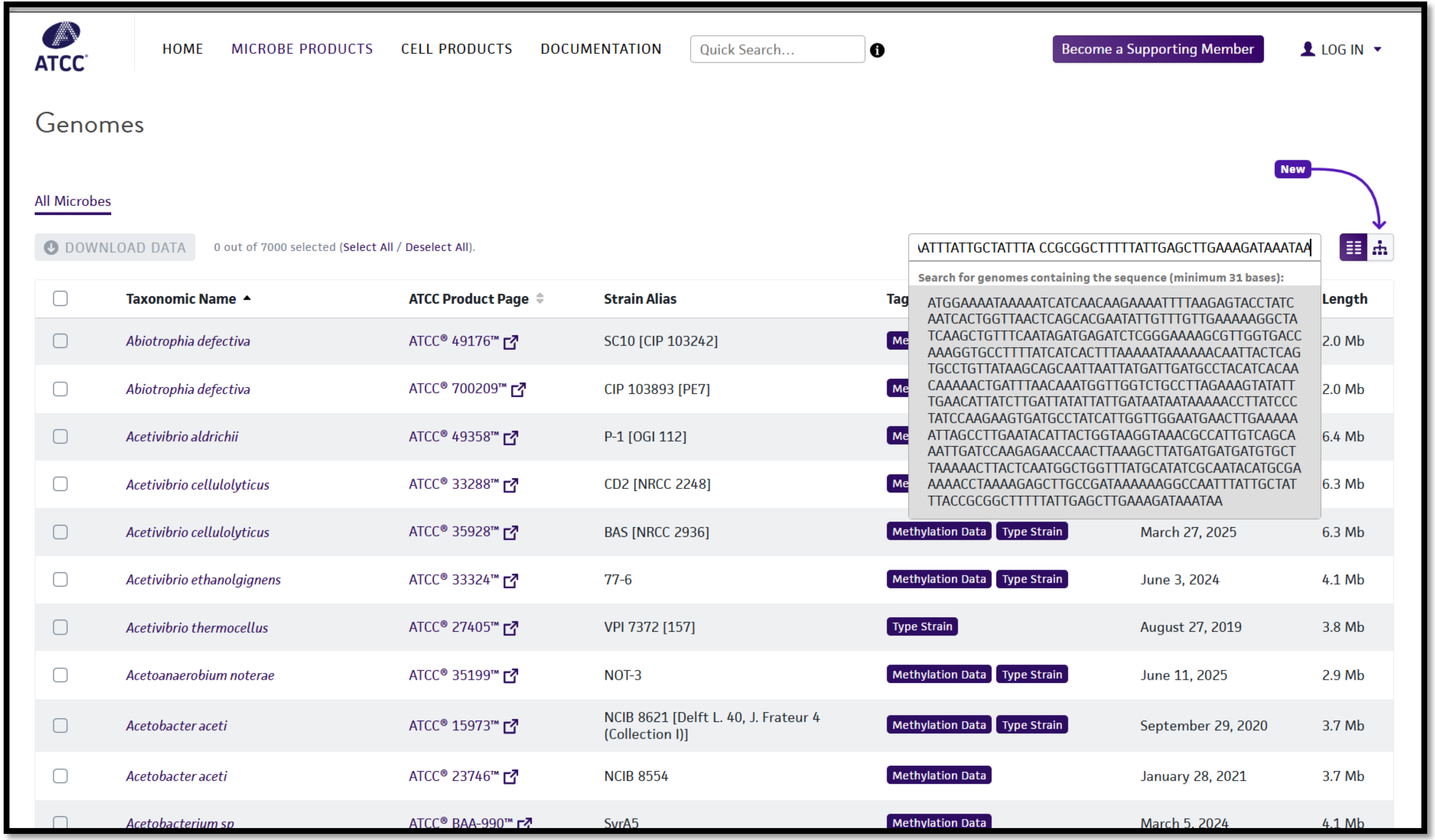
Streptococcus pneumoniae (ATCC® BAA-3330™)

Contig	Start	End	Name	Protein Product		EC Number	Type	RefSeq ID	Jump
1	1072482	1072054	*aac(6')*	aminoglycoside 6'-N-acetyltransferase	AMR – AMR Finder	2.3.1.82	CDS	WP_013903432.1	➤
1	1153448	1152249		multidrug efflux MFS transporter	AMR – CARD, AMR Finder		CDS	WP_000136121.1	➤
1	1511931	1509874	*pbp2b*	penicillin-binding protein PBP2B	AMR – AMR Finder		CDS	WP_001829432.1	➤
1	1764181	1764918	*erm(B)*	23S rRNA (adenine(2058)-N(6))-methyltransferase Erm(B)	AMR – CARD, ResFinder, AMR Finder		CDS	WP_011100845.1	➤
1	1774833	1776752	*tet(M)*	tetracycline resistance ribosomal protection protein Tet(M)	AMR – CARD, ResFinder, AMR Finder		CDS	WP_011117014.1	➤
1	1779941	1778478	*msr(D)*	ABC-F type ribosomal protection protein Msr(D)	AMR – ResFinder, AMR Finder		CDS	WP_000420317.1	➤
1	1781278	1780061	*mef(A)*	macrolide efflux MFS transporter Mef(A)	AMR – ResFinder, AMR Finder		CDS	WP_000417520.1	➤
1	1953479	1951713	*patB*	multidrug efflux ABC transporter subunit PatB	AMR – CARD		CDS	WP_000859866.1	➤
1	1955965	1954271	*patA*	multidrug efflux ABC transporter subunit PatA	AMR – CARD		CDS	WP_000908145.1	➤

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence

Sequence Searching

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence



Genomes

All Microbes

0 out of 7000 selected (Select All / Deselect All).

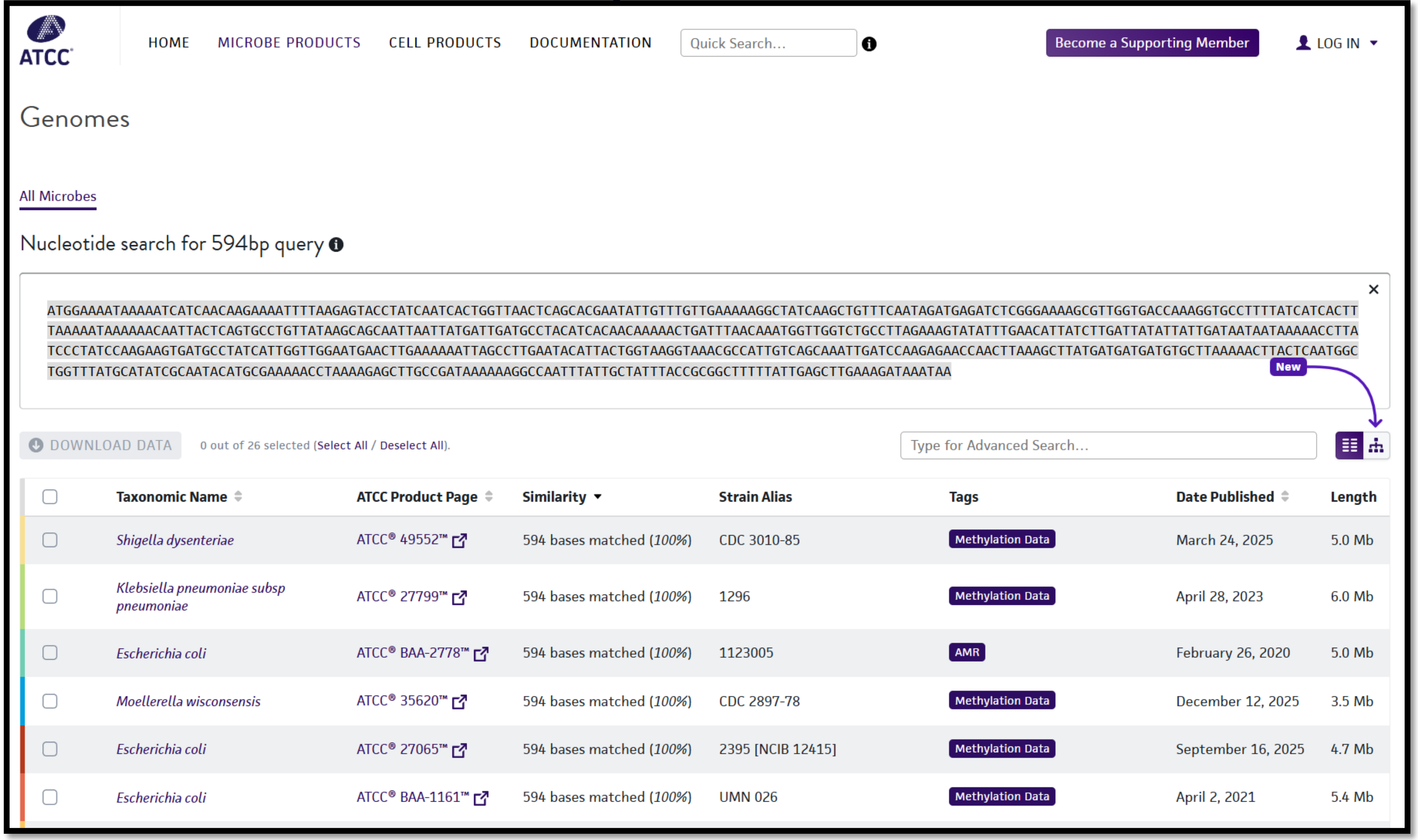
ATTTATTGCTATTTA CCGCGGCTTTTTATTGAGCTTGAAAGATAAATAA

Search for genomes containing the sequence (minimum 31 bases):

```
ATGGAAAATAAAAATCATCAACAAGAAAATTTTAAGAGTACCTATC
AATCACTGGTTAACTCAGCACGAATATTGTTTGTTGAAAAAGGCTA
TCAAGCTGTTTCAATAGATGAGATCTCGGGAAAAGCGTTGGTGACC
AAAGGTGCCTTTTATCATCACTTTAAAAATAAAAAACAATTACTCAG
TGCCTGTTATAAGCAGCAATTAATTATGATTGATGCCTACATCACAA
CAAAAACTGATTTAACAAATGGTTGGTCTGCCTTAGAAAGTATATT
TGAACATTATCTTGATTATATTATTGATAATAATAAAAACCTTATCCC
TATCCAAGAAGTGATGCCTATCATTGGTTGGAATGAACTTGAAAAA
ATTAGCCTTGAATACATTACTGGTAAGGTAAACGCCATTGTCAGCA
AATTGATCCAAGAGAACCAACTTAAAGCTTATGATGATGATGTGCT
TAAAAACTTACTCAATGGCTGGTTTATGCATATCGCAATACATGCGA
AAAACCTAAAAGAGCTTGCCGATAAAAAAGGCCAATTTATTGCTAT
TTACCGCGGCTTTTTATTGAGCTTGAAAGATAAATAA
```

☐	Taxonomic Name	ATCC Product Page	Strain Alias	Tag		Length
☐	*Abiotrophia defectiva*	ATCC® 49176™	SC10 [CIP 103242]	Me		2.0 Mb
☐	*Abiotrophia defectiva*	ATCC® 700209™	CIP 103893 [PE7]	Me		2.0 Mb
☐	*Acetivibrio aldrichii*	ATCC® 49358™	P-1 [OGI 112]	Me		6.4 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 33288™	CD2 [NRCC 2248]	Me		6.3 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 35928™	BAS [NRCC 2936]	Methylation Data Type Strain	March 27, 2025	6.3 Mb
☐	*Acetivibrio ethanolgignens*	ATCC® 33324™	77-6	Methylation Data Type Strain	June 3, 2024	4.1 Mb
☐	*Acetivibrio thermocellus*	ATCC® 27405™	VPI 7372 [157]	Type Strain	August 27, 2019	3.8 Mb
☐	*Acetoanaerobium noterae*	ATCC® 35199™	NOT-3	Methylation Data Type Strain	June 11, 2025	2.9 Mb
☐	*Acetobacter aceti*	ATCC® 15973™	NCIB 8621 [Delft L. 40, J. Frateur 4 (Collection I)]	Methylation Data Type Strain	September 29, 2020	3.7 Mb
☐	*Acetobacter aceti*	ATCC® 23746™	NCIB 8554	Methylation Data	January 28, 2021	3.7 Mb
☐	*Acetobacterium sp*	ATCC® BAA-990™	SyrA5	Methylation Data	March 5, 2024	4.1 Mb

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence



Genomes

All Microbes

Nucleotide search for 594bp query

```
ATGGAAAATAAAAATCATCAACAAGAAAATTTTAAGAGTACCTATCAATCACTGGTTAACTCAGCACGAATATTGTTTGTTGAAAAAGGCTATCAAGCTGTTTCAATAGATGAGATCTCGGGAAAAGCGTTGGTGACCAAAGGTGCCTTTTATCATCACTT
TAAAAATAAAAAACAATTACTCAGTGCCTGTTATAAGCAGCAATTAATTATGATTGATGCCTACATCACAACAAAAACTGATTTAACAAATGGTTGGTCTGCCTTAGAAAGTATATTTGAACATTATCTTGATTATATTATTGATAATAATAAAAACCTTA
TCCCTATCCAAGAAGTGATGCCTATCATTGGTTGGAATGAACTTGAAAAAATTAGCCTTGAATACATTACTGGTAAGGTAAACGCCATTGTCAGCAAATTGATCCAAGAGAACCAACTTAAAGCTTATGATGATGATGTGCTTAAAAACTTACTCAATGGC
TGGTTTATGCATATCGCAATACATGCGAAAAACCTAAAAGAGCTTGCCGATAAAAAAGGCCAATTTATTGCTATTTACCGCGGCTTTTTATTGAGCTTGAAAGATAAATAA
```

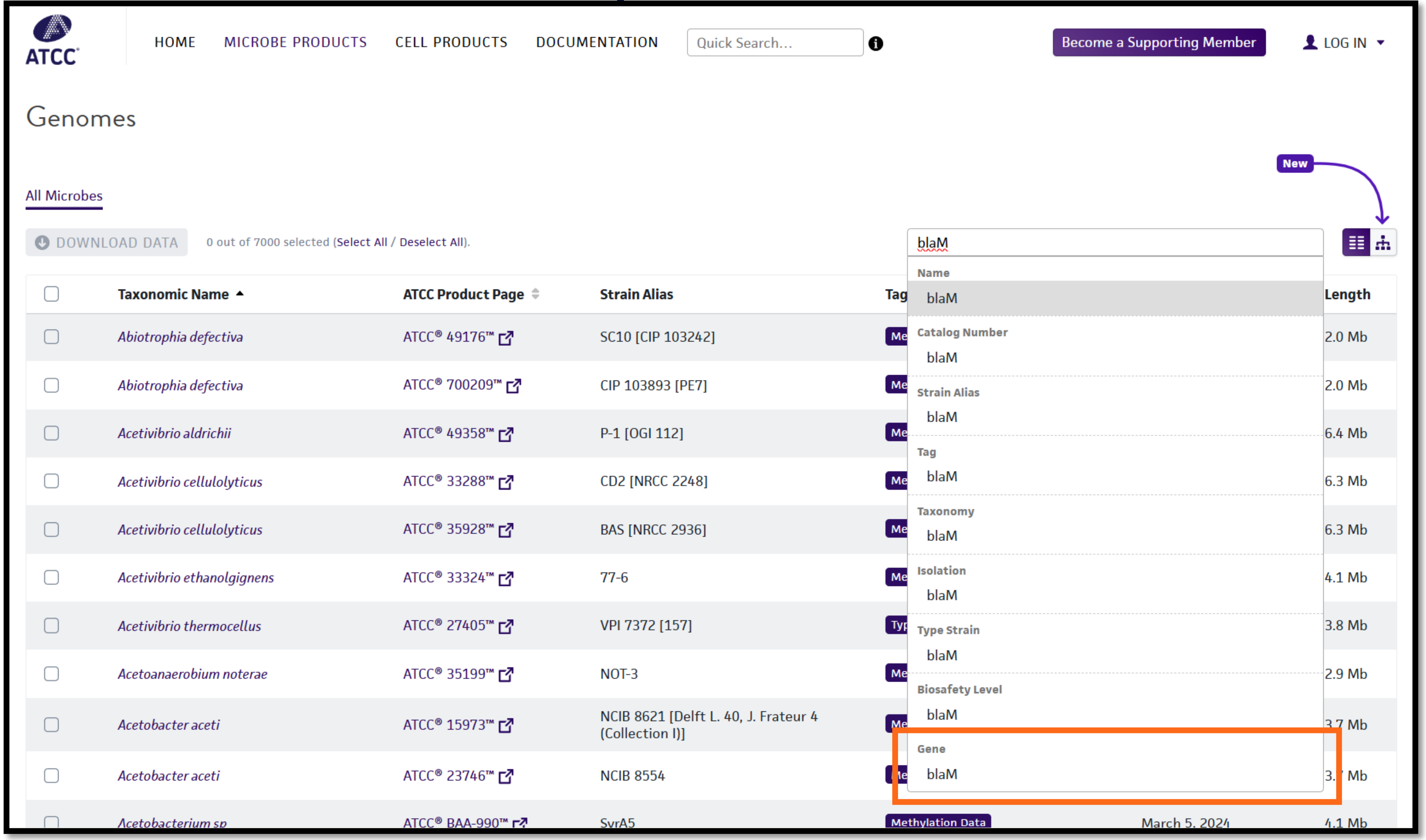
0 out of 26 selected (Select All / Deselect All).

☐	Taxonomic Name	ATCC Product Page	Similarity	Strain Alias	Tags	Date Published	Length
☐	*Shigella dysenteriae*	ATCC® 49552™	594 bases matched (*100%*)	CDC 3010-85	Methylation Data	March 24, 2025	5.0 Mb
☐	*Klebsiella pneumoniae subsp pneumoniae*	ATCC® 27799™	594 bases matched (*100%*)	1296	Methylation Data	April 28, 2023	6.0 Mb
☐	*Escherichia coli*	ATCC® BAA-2778™	594 bases matched (*100%*)	1123005	AMR	February 26, 2020	5.0 Mb
☐	*Moellerella wisconsensis*	ATCC® 35620™	594 bases matched (*100%*)	CDC 2897-78	Methylation Data	December 12, 2025	3.5 Mb
☐	*Escherichia coli*	ATCC® 27065™	594 bases matched (*100%*)	2395 [NCIB 12415]	Methylation Data	September 16, 2025	4.7 Mb
☐	*Escherichia coli*	ATCC® BAA-1161™	594 bases matched (*100%*)	UMN 026	Methylation Data	April 2, 2021	5.4 Mb

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence

Annotation Searching

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence



Genomes

All Microbes

DOWNLOAD DATA

0 out of 7000 selected (Select All / Deselect All).

blaM

Name
blaM

Catalog Number
blaM

Strain Alias
blaM

Tag
blaM

Taxonomy
blaM

Isolation
blaM

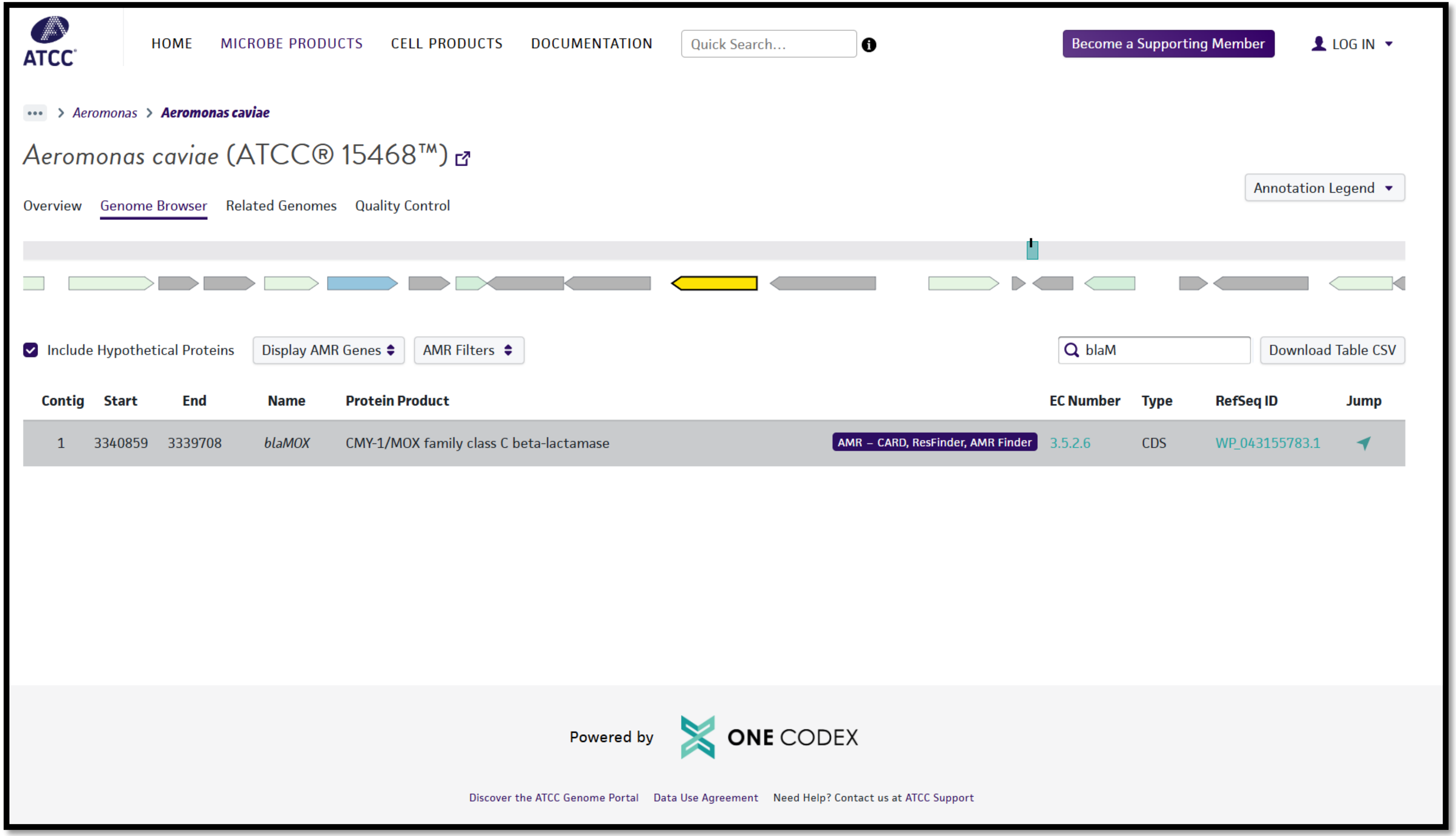
Type Strain
blaM

Biosafety Level
blaM

Gene
blaM

☐	Taxonomic Name	ATCC Product Page	Strain Alias	Tag		Length
☐	*Abiotrophia defectiva*	ATCC® 49176™	SC10 [CIP 103242]	Me		2.0 Mb
☐	*Abiotrophia defectiva*	ATCC® 700209™	CIP 103893 [PE7]	Me		2.0 Mb
☐	*Acetivibrio aldrichii*	ATCC® 49358™	P-1 [OGI 112]	Me		6.4 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 33288™	CD2 [NRCC 2248]	Me		6.3 Mb
☐	*Acetivibrio cellulolyticus*	ATCC® 35928™	BAS [NRCC 2936]	Me		6.3 Mb
☐	*Acetivibrio ethanolgignens*	ATCC® 33324™	77-6	Me		4.1 Mb
☐	*Acetivibrio thermocellus*	ATCC® 27405™	VPI 7372 [157]	Typ		3.8 Mb
☐	*Acetoanaerobium noterae*	ATCC® 35199™	NOT-3	Me		2.9 Mb
☐	*Acetobacter aceti*	ATCC® 15973™	NCIB 8621 [Delft L. 40, J. Frateur 4 (Collection I)]	Me		3.7 Mb
☐	*Acetobacter aceti*	ATCC® 23746™	NCIB 8554	Me		3. Mb
☐	*Acetobacterium sp*	ATCC® BAA-990™	SyrA5	Methylation Data	March 5, 2024	4.1 Mb

ATCC® Genome Portal – AMR Gene Search: Gene Name and/or Sequence



Aeromonas caviae (ATCC® 15468™)

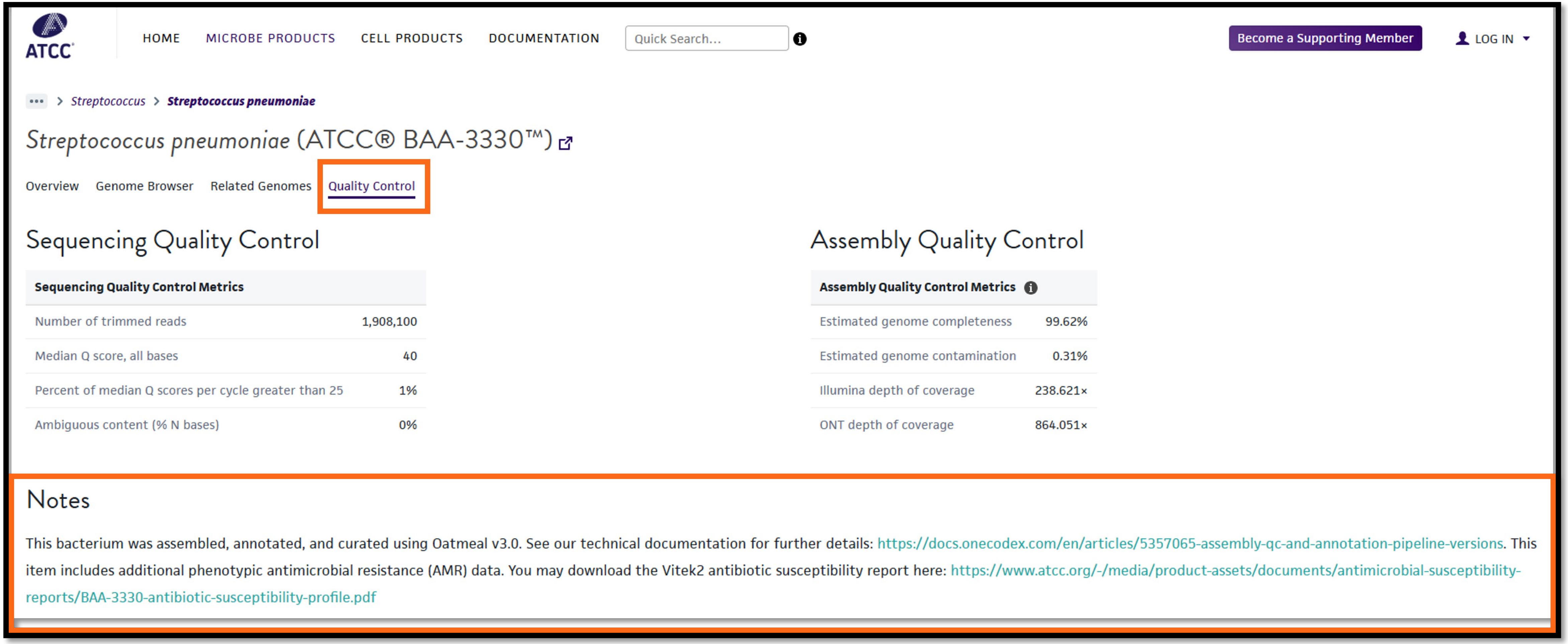
☑ Include Hypothetical Proteins

Search: blaM

Contig	Start	End	Name	Protein Product		EC Number	Type	RefSeq ID	Jump
1	3340859	3339708	*blaMOX*	CMY-1/MOX family class C beta-lactamase	AMR – CARD, ResFinder, AMR Finder	3.5.2.6	CDS	WP_043155783.1	

ATCC® Genome Portal – Ways to view AMR

View / Download Phenotypical Data



Streptococcus pneumoniae (ATCC® BAA-3330™)

Sequencing Quality Control

Sequencing Quality Control Metrics	
Number of trimmed reads	1,908,100
Median Q score, all bases	40
Percent of median Q scores per cycle greater than 25	1%
Ambiguous content (% N bases)	0%

Assembly Quality Control

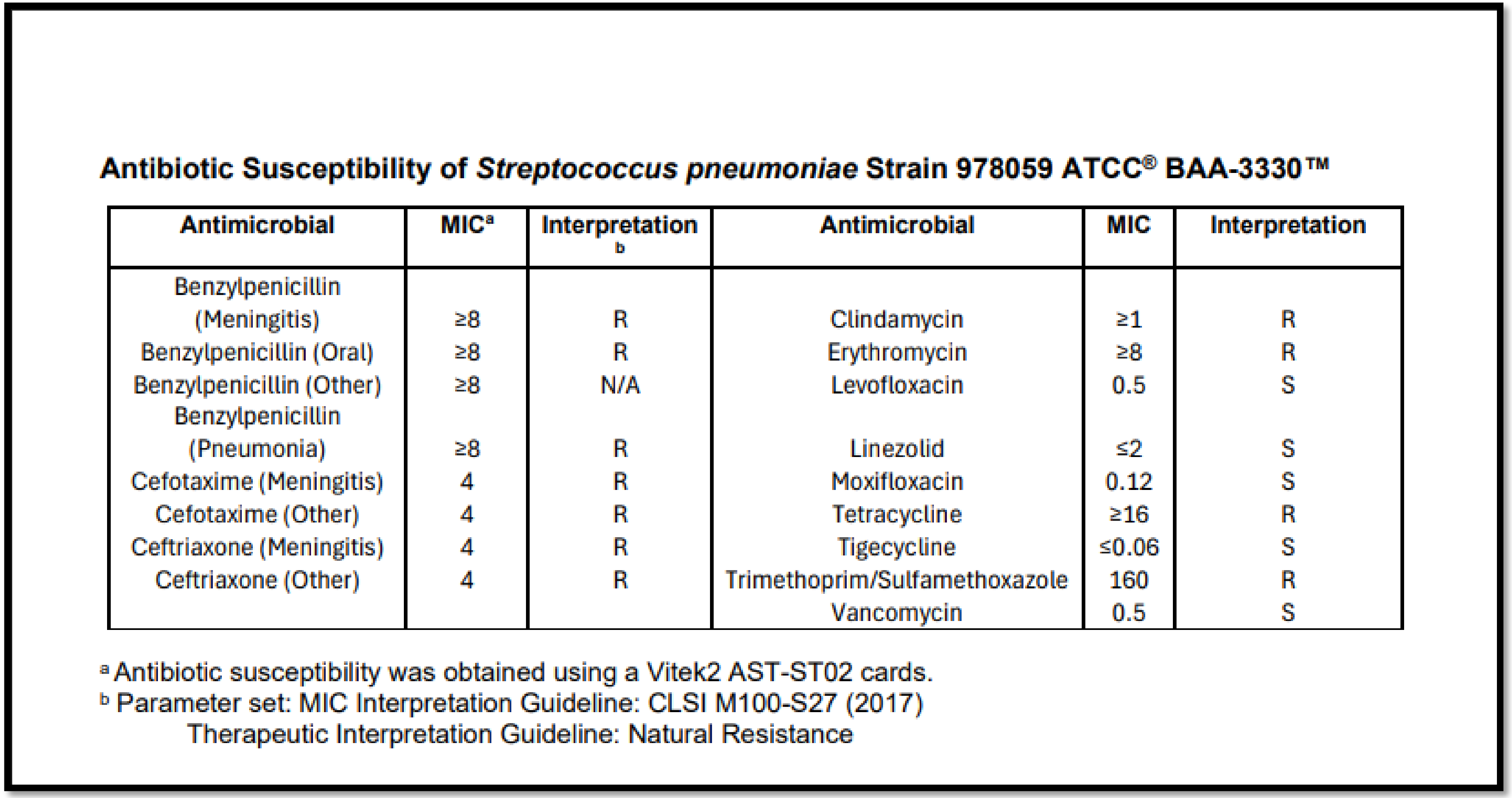
Assembly Quality Control Metrics	
Estimated genome completeness	99.62%
Estimated genome contamination	0.31%
Illumina depth of coverage	238.621×
ONT depth of coverage	864.051×

Notes

This bacterium was assembled, annotated, and curated using Oatmeal v3.0. See our technical documentation for further details: https://docs.onecodex.com/en/articles/5357065-assembly-qc-and-annotation-pipeline-versions. This item includes additional phenotypic antimicrobial resistance (AMR) data. You may download the Vitek2 antibiotic susceptibility report here: https://www.atcc.org/-/media/product-assets/documents/antimicrobial-susceptibility-reports/BAA-3330-antibiotic-susceptibility-profile.pdf

ATCC® Genome Portal – Ways to view AMR

View / Download Phenotypical Data



Antibiotic Susceptibility of *Streptococcus pneumoniae* Strain 978059 ATCC® BAA-3330™

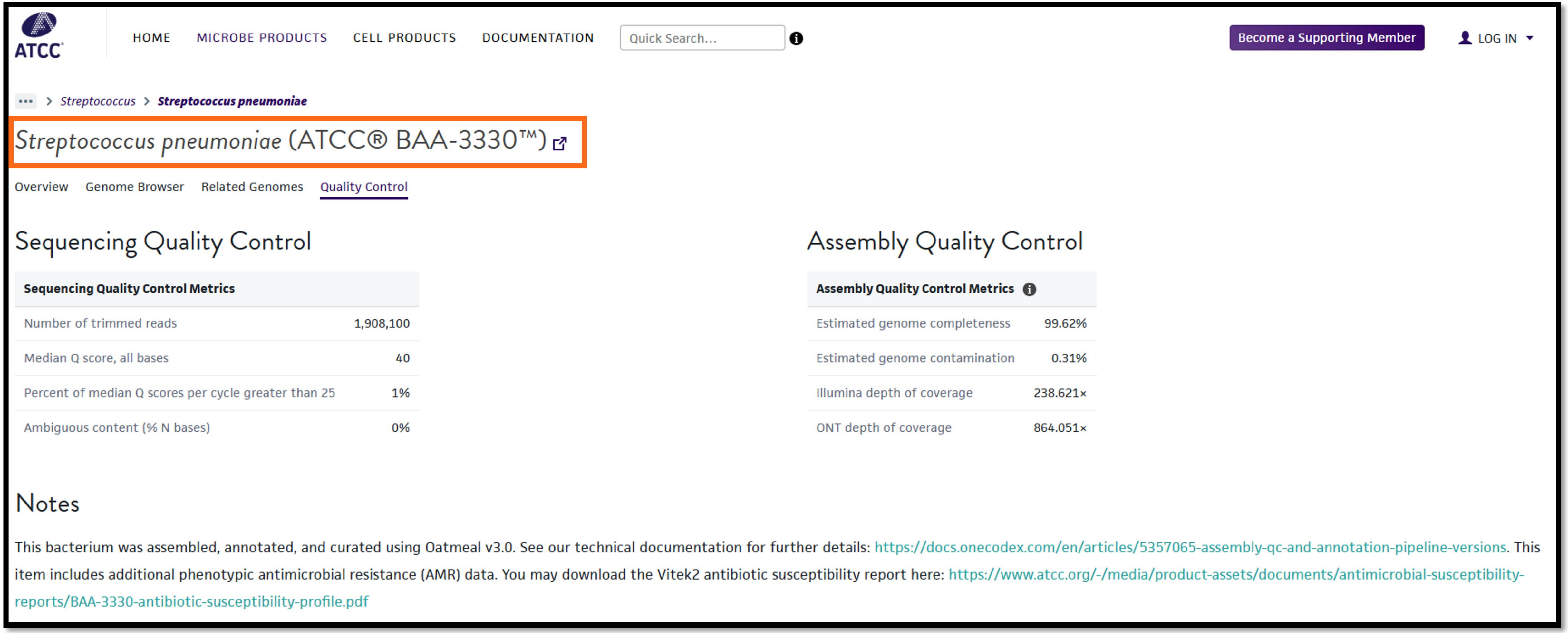
Antimicrobial	MIC[a]	Interpretation[b]	Antimicrobial	MIC	Interpretation
Benzylpenicillin (Meningitis)	≥8	R	Clindamycin	≥1	R
Benzylpenicillin (Oral)	≥8	R	Erythromycin	≥8	R
Benzylpenicillin (Other)	≥8	N/A	Levofloxacin	0.5	S
Benzylpenicillin (Pneumonia)	≥8	R	Linezolid	≤2	S
Cefotaxime (Meningitis)	4	R	Moxifloxacin	0.12	S
Cefotaxime (Other)	4	R	Tetracycline	≥16	R
Ceftriaxone (Meningitis)	4	R	Tigecycline	≤0.06	S
Ceftriaxone (Other)	4	R	Trimethoprim/Sulfamethoxazole	160	R
			Vancomycin	0.5	S

[a] Antibiotic susceptibility was obtained using a Vitek2 AST-ST02 cards.

[b] Parameter set: MIC Interpretation Guideline: CLSI M100-S27 (2017)
Therapeutic Interpretation Guideline: Natural Resistance

ATCC® Genome Portal – Ways to view AMR

View / Download Phenotypical Data



Streptococcus pneumoniae (ATCC® BAA-3330™)

Sequencing Quality Control

Sequencing Quality Control Metrics	
Number of trimmed reads	1,908,100
Median Q score, all bases	40
Percent of median Q scores per cycle greater than 25	1%
Ambiguous content (% N bases)	0%

Assembly Quality Control

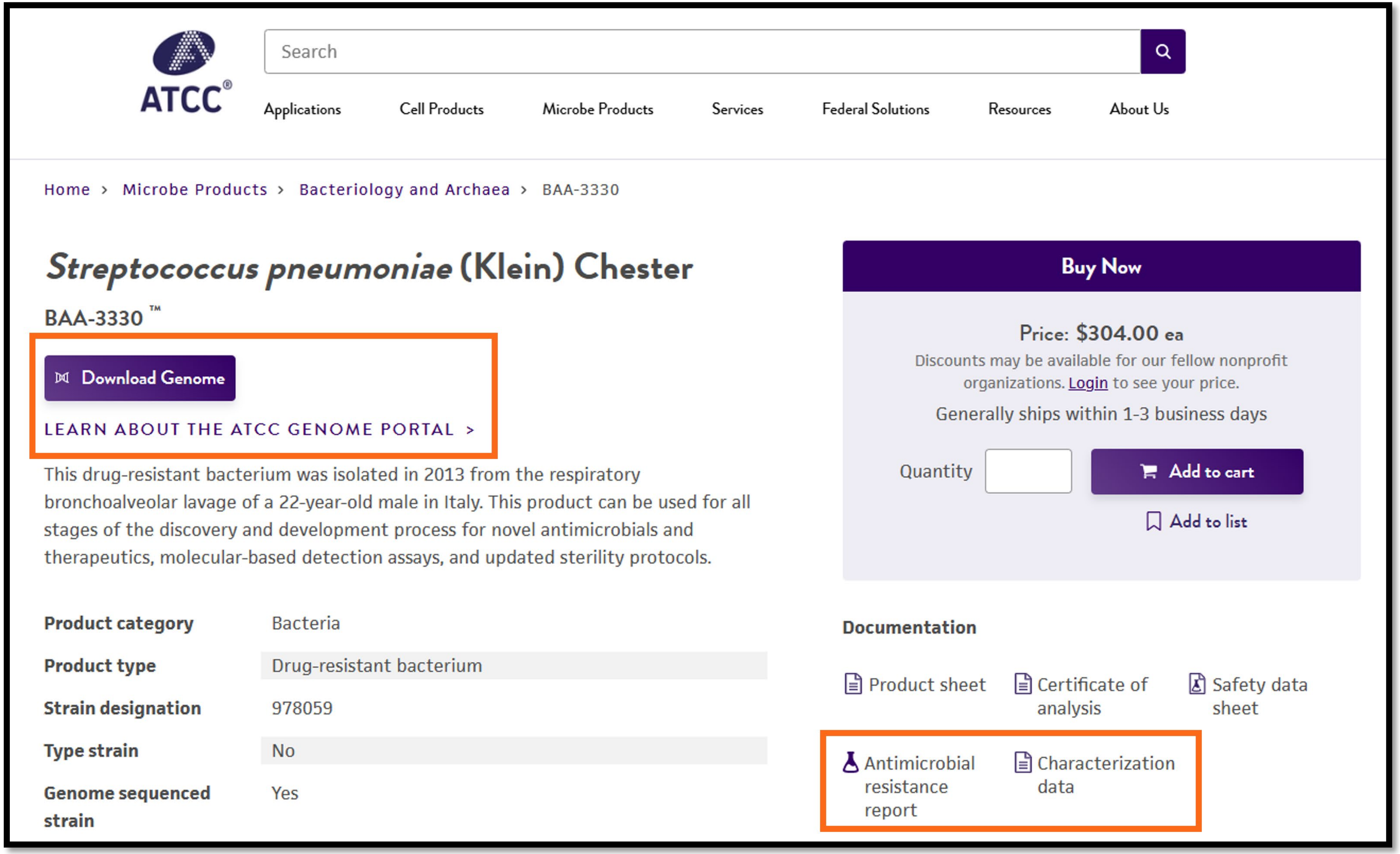
Assembly Quality Control Metrics	
Estimated genome completeness	99.62%
Estimated genome contamination	0.31%
Illumina depth of coverage	238.621×
ONT depth of coverage	864.051×

Notes

This bacterium was assembled, annotated, and curated using Oatmeal v3.0. See our technical documentation for further details: https://docs.onecodex.com/en/articles/5357065-assembly-qc-and-annotation-pipeline-versions. This item includes additional phenotypic antimicrobial resistance (AMR) data. You may download the Vitek2 antibiotic susceptibility report here: https://www.atcc.org/-/media/product-assets/documents/antimicrobial-susceptibility-reports/BAA-3330-antibiotic-susceptibility-profile.pdf

ATCC® Genome Portal – Ways to view AMR

View / Download Phenotypical Data



Search

Home › Microbe Products › Bacteriology and Archaea › BAA-3330

Streptococcus pneumoniae (Klein) Chester

BAA-3330 ™

This drug-resistant bacterium was isolated in 2013 from the respiratory bronchoalveolar lavage of a 22-year-old male in Italy. This product can be used for all stages of the discovery and development process for novel antimicrobials and therapeutics, molecular-based detection assays, and updated sterility protocols.

Product category	Bacteria
Product type	Drug-resistant bacterium
Strain designation	978059
Type strain	No
Genome sequenced strain	Yes

Buy Now

Price: $304.00 ea

Discounts may be available for our fellow nonprofit organizations. Login to see your price.

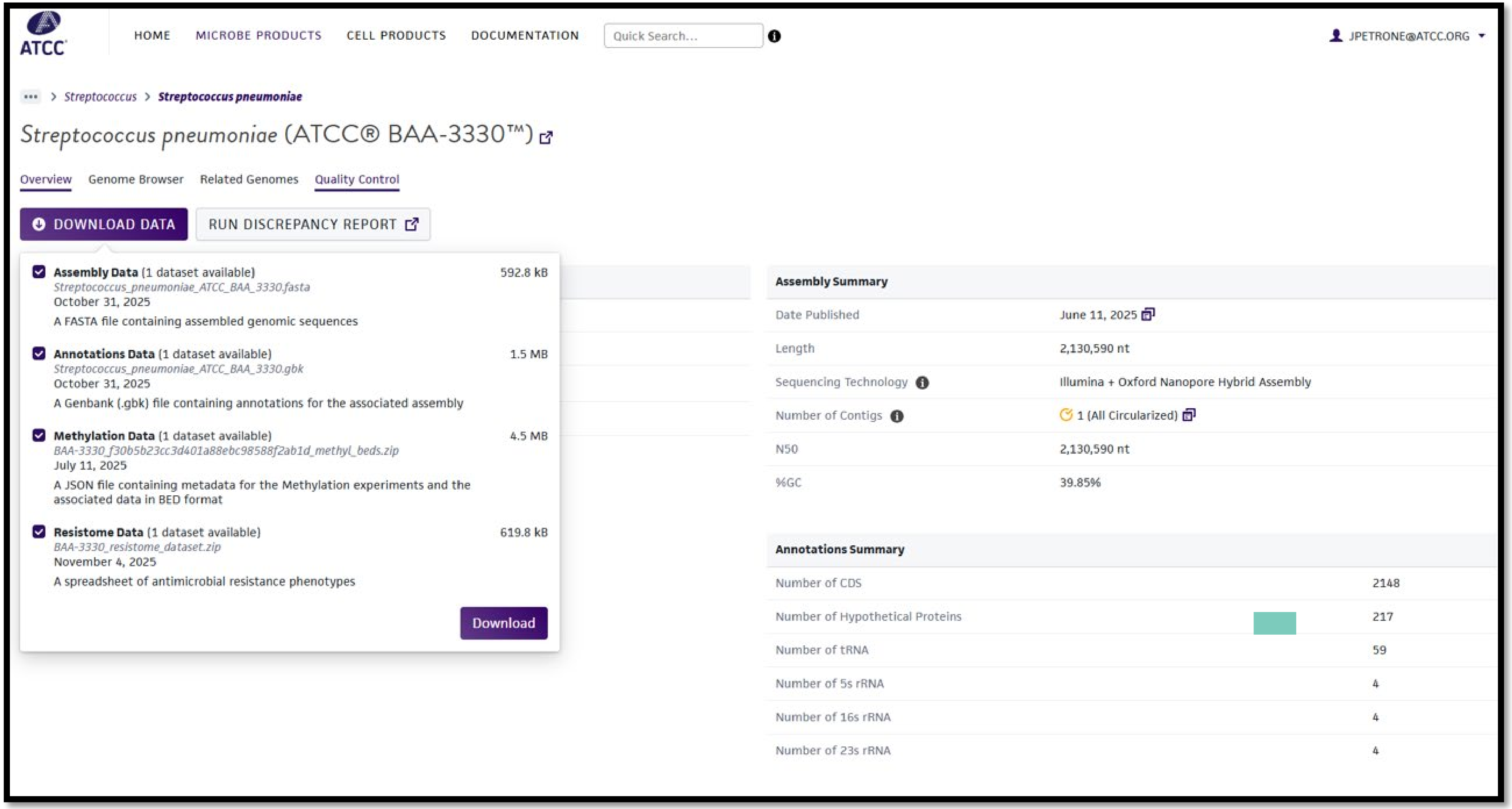
Generally ships within 1-3 business days

Quantity

Documentation

ATCC® Genome Portal – Ways to view AMR

Download Resistome Dataset - GUI



Streptococcus pneumoniae (ATCC® BAA-3330™)

☑ **Assembly Data** (1 dataset available) 592.8 kB
Streptococcus_pneumoniae_ATCC_BAA_3330.fasta
October 31, 2025
A FASTA file containing assembled genomic sequences

☑ **Annotations Data** (1 dataset available) 1.5 MB
Streptococcus_pneumoniae_ATCC_BAA_3330.gbk
October 31, 2025
A Genbank (.gbk) file containing annotations for the associated assembly

☑ **Methylation Data** (1 dataset available) 4.5 MB
BAA-3330_f30b5b23cc3d401a88ebc98588f2ab1d_methyl_beds.zip
July 11, 2025
A JSON file containing metadata for the Methylation experiments and the associated data in BED format

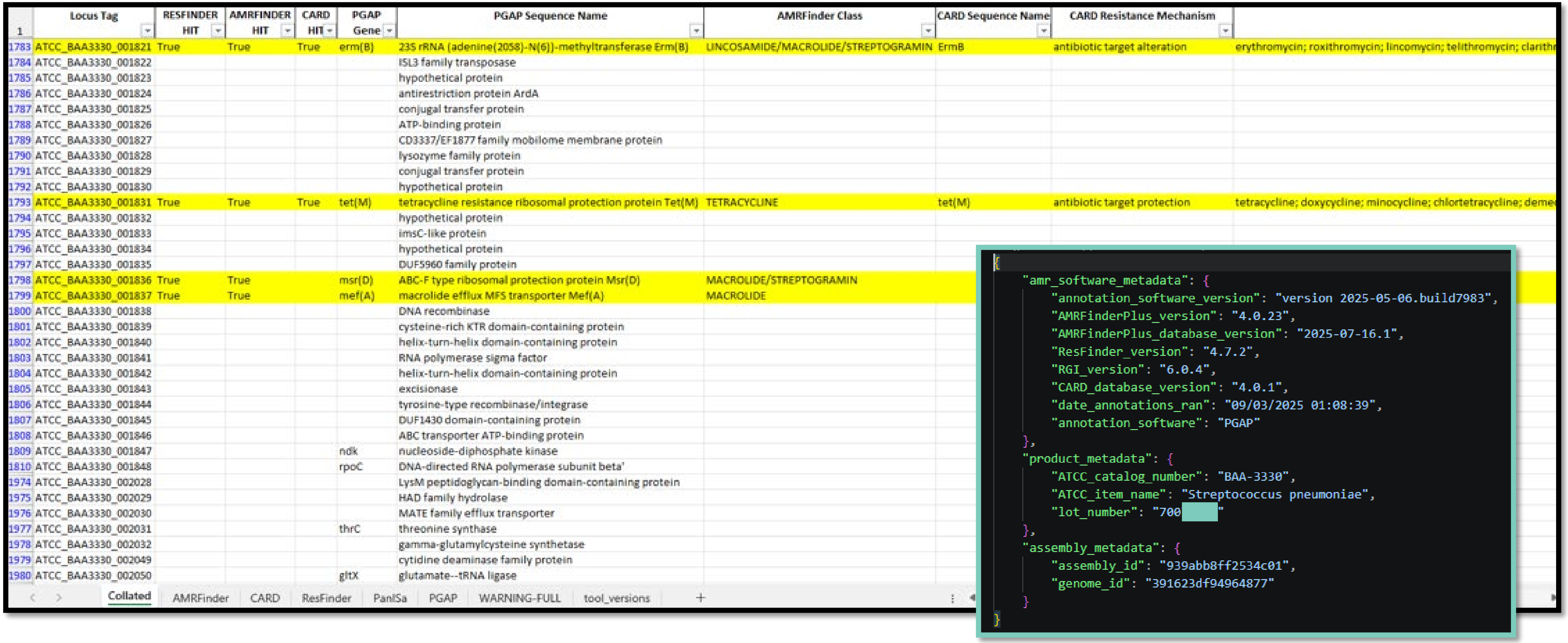
☑ **Resistome Data** (1 dataset available) 619.8 kB
BAA-3330_resistome_dataset.zip
November 4, 2025
A spreadsheet of antimicrobial resistance phenotypes

Assembly Summary	
Date Published	June 11, 2025
Length	2,130,590 nt
Sequencing Technology	Illumina + Oxford Nanopore Hybrid Assembly
Number of Contigs	1 (All Circularized)
N50	2,130,590 nt
%GC	39.85%

Annotations Summary	
Number of CDS	2148
Number of Hypothetical Proteins	217
Number of tRNA	59
Number of 5s rRNA	4
Number of 16s rRNA	4
Number of 23s rRNA	4

ATCC® Genome Portal – Ways to view AMR

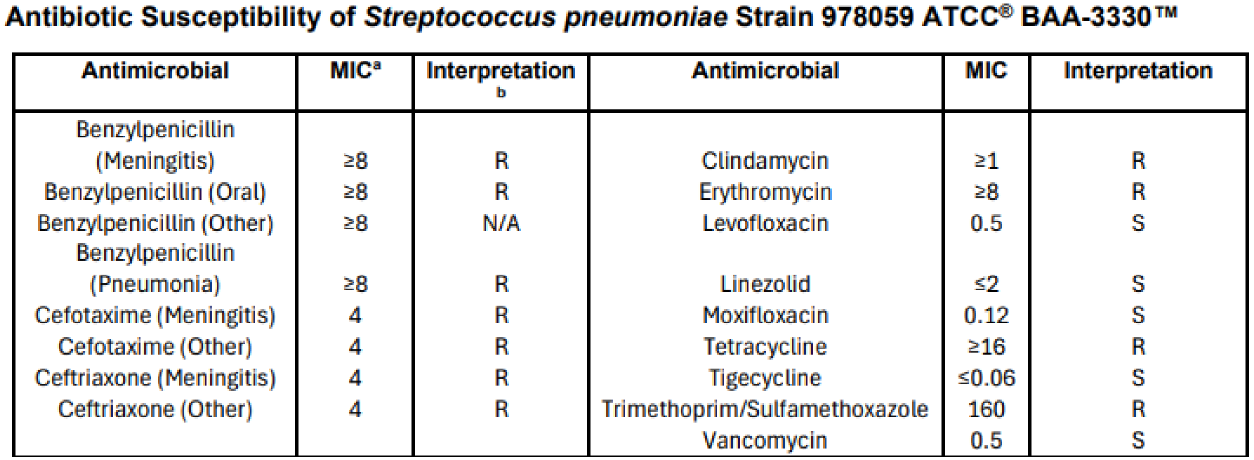
Download Resistome Dataset - GUI



1	Locus Tag	RESFINDER HIT	AMRFINDER HIT	CARD HIT	PGAP Gene	PGAP Sequence Name	AMRFinder Class	CARD Sequence Name	CARD Resistance Mechanism	
1783	ATCC_BAA3330_001821	True	True	True	erm(B)	23S rRNA (adenine(2058)-N(6))-methyltransferase Erm(B)	LINCOSAMIDE/MACROLIDE/STREPTOGRAMIN	ErmB	antibiotic target alteration	erythromycin; roxithromycin; lincomycin; telithromycin; clarithr
1784	ATCC_BAA3330_001822					ISL3 family transposase				
1785	ATCC_BAA3330_001823					hypothetical protein				
1786	ATCC_BAA3330_001824					antirestriction protein ArdA				
1787	ATCC_BAA3330_001825					conjugal transfer protein				
1788	ATCC_BAA3330_001826					ATP-binding protein				
1789	ATCC_BAA3330_001827					CD3337/EF1877 family mobilome membrane protein				
1790	ATCC_BAA3330_001828					lysozyme family protein				
1791	ATCC_BAA3330_001829					conjugal transfer protein				
1792	ATCC_BAA3330_001830					hypothetical protein				
1793	ATCC_BAA3330_001831	True	True	True	tet(M)	tetracycline resistance ribosomal protection protein Tet(M)	TETRACYCLINE	tet(M)	antibiotic target protection	tetracycline; doxycycline; minocycline; chlortetracycline; deme
1794	ATCC_BAA3330_001832					hypothetical protein				
1795	ATCC_BAA3330_001833					imsC-like protein				
1796	ATCC_BAA3330_001834					hypothetical protein				
1797	ATCC_BAA3330_001835					DUF5960 family protein				
1798	ATCC_BAA3330_001836	True	True		msr(D)	ABC-F type ribosomal protection protein Msr(D)	MACROLIDE/STREPTOGRAMIN			
1799	ATCC_BAA3330_001837	True	True		mef(A)	macrolide efflux MFS transporter Mef(A)	MACROLIDE			
1800	ATCC_BAA3330_001838					DNA recombinase				
1801	ATCC_BAA3330_001839					cysteine-rich KTR domain-containing protein				
1802	ATCC_BAA3330_001840					helix-turn-helix domain-containing protein				
1803	ATCC_BAA3330_001841					RNA polymerase sigma factor				
1804	ATCC_BAA3330_001842					helix-turn-helix domain-containing protein				
1805	ATCC_BAA3330_001843					excisionase				
1806	ATCC_BAA3330_001844					tyrosine-type recombinase/integrase				
1807	ATCC_BAA3330_001845					DUF1430 domain-containing protein				
1808	ATCC_BAA3330_001846					ABC transporter ATP-binding protein				
1809	ATCC_BAA3330_001847				ndk	nucleoside-diphosphate kinase				
1810	ATCC_BAA3330_001848				rpoC	DNA-directed RNA polymerase subunit beta'				
1974	ATCC_BAA3330_002028					LysM peptidoglycan-binding domain-containing protein				
1975	ATCC_BAA3330_002029					HAD family hydrolase				
1976	ATCC_BAA3330_002030					MATE family efflux transporter				
1977	ATCC_BAA3330_002031				thrC	threonine synthase				
1978	ATCC_BAA3330_002032					gamma-glutamylcysteine synthetase				
1979	ATCC_BAA3330_002049					cytidine deaminase family protein				
1980	ATCC_BAA3330_002050				gltX	glutamate--tRNA ligase				

```
{
    "amr_software_metadata": {
        "annotation_software_version": "version 2025-05-06.build7983",
        "AMRFinderPlus_version": "4.0.23",
        "AMRFinderPlus_database_version": "2025-07-16.1",
        "ResFinder_version": "4.7.2",
        "RGI_version": "6.0.4",
        "CARD_database_version": "4.0.1",
        "date_annotations_ran": "09/03/2025 01:08:39",
        "annotation_software": "PGAP"
    },
    "product_metadata": {
        "ATCC_catalog_number": "BAA-3330",
        "ATCC_item_name": "Streptococcus pneumoniae",
        "lot_number": "700[redacted]"
    },
    "assembly_metadata": {
        "assembly_id": "939abb8ff2534c01",
        "genome_id": "391623df94964877"
    }
}
```

Linking Phenotype and Genotype of ATCC Strains



Antibiotic Susceptibility of *Streptococcus pneumoniae* Strain 978059 ATCC® BAA-3330™

Antimicrobial	MIC[a]	Interpretation [b]	Antimicrobial	MIC	Interpretation
Benzylpenicillin (Meningitis)	≥8	R	Clindamycin	≥1	R
Benzylpenicillin (Oral)	≥8	R	Erythromycin	≥8	R
Benzylpenicillin (Other)	≥8	N/A	Levofloxacin	0.5	S
Benzylpenicillin (Pneumonia)	≥8	R	Linezolid	≤2	S
Cefotaxime (Meningitis)	4	R	Moxifloxacin	0.12	S
Cefotaxime (Other)	4	R	Tetracycline	≥16	R
Ceftriaxone (Meningitis)	4	R	Tigecycline	≤0.06	S
Ceftriaxone (Other)	4	R	Trimethoprim/Sulfamethoxazole	160	R
			Vancomycin	0.5	S

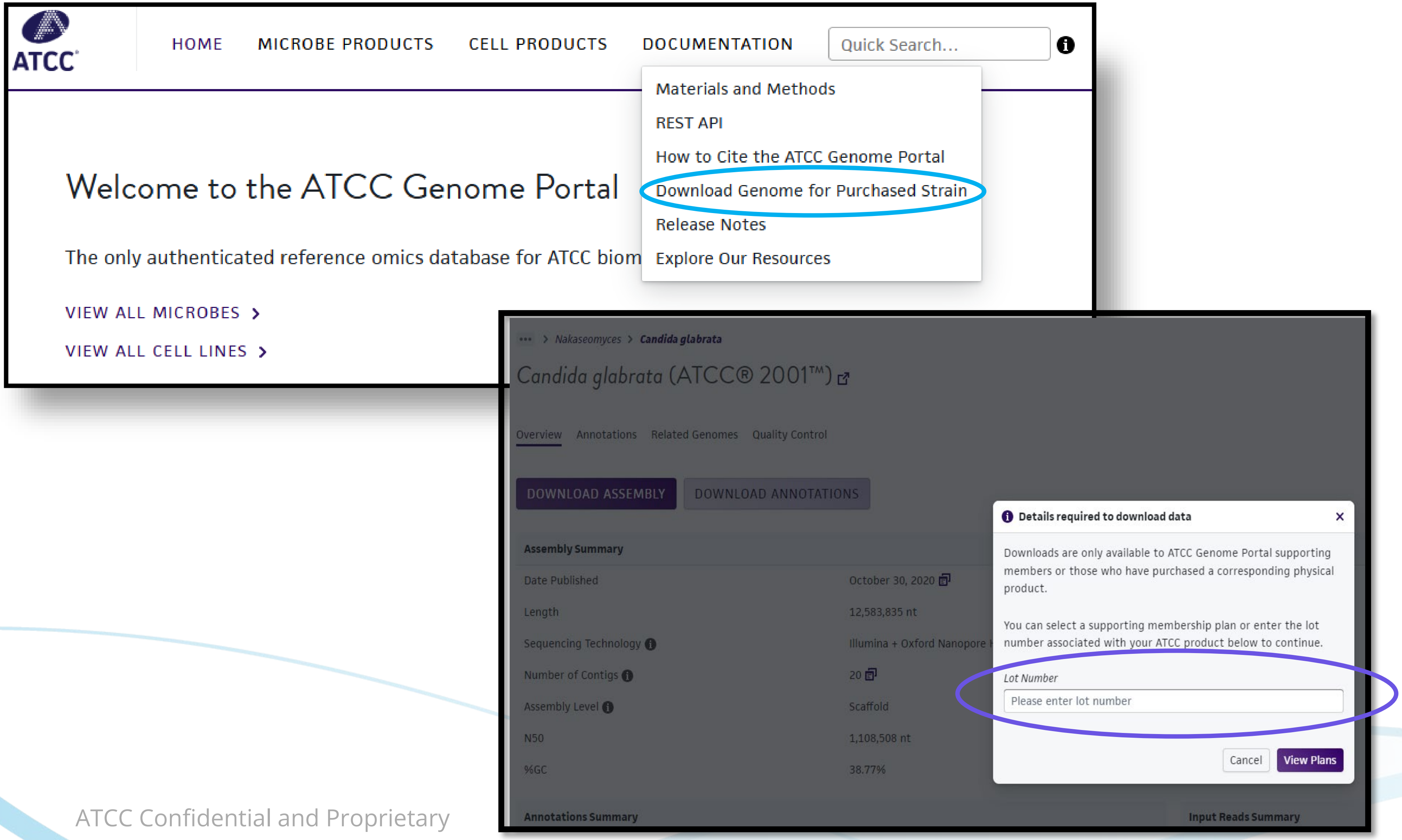
VITEK Phenotype

[a] Antibiotic susceptibility was obtained using a Vitek2 AST-ST02 cards.
[b] Parameter set: MIC Interpretation Guideline: CLSI M100-S27 (2017)
Therapeutic Interpretation Guideline: Natural Resistance

Resistome Genotype

Locus Tag	RESFINDER HIT	AMRFINDER HIT	CARD HIT	PGAP Gene symbol	AMRFinder Subclass	CARD Sequence Name	CARD Resistance Mechanism	CARD Antibiotic	RESFINDER Phenotype
ATCC_BAA3330_000368		True		pbp2X	BETA-LACTAM				
ATCC_BAA3330_000624			True	ldcB		vanY gene in vanB cluster	antibiotic target alteration	vancomycin	
ATCC_BAA3330_001083		True		aac(6')	AMINOGLYCOSIDE				
ATCC_BAA3330_001167		True	True		QUINOLONE	pmrA	antibiotic efflux	ciprofloxacin; norfloxacin	
ATCC_BAA3330_001533		True		pbp2b	BETA-LACTAM				
ATCC_BAA3330_001821	True	True	True	erm(B)	CLINDAMYCIN/ERYTHROMYCIN/STREPTOGRAMIN B	ErmB	antibiotic target alteration	erythromycin; roxithromycin; lincomycin; telithromycin; clarithromycin; clindamycin; tylosin; spiramycin; azithromycin; dirithromycin; pristinamycin IA; quinupristin; virginiamycin M1; madumycin II; griseoviridin; dalfopristin; pristinamycin IB; virginiamycin S2; pristinamycin IC; vernamycin C; patricin A; patricin B; ostreogrycin B3; oleandomycin	Erythromycin, Lincomycin, Clindamycin, Quinupristin, Pristinamycin IA, Virginiamycin S
ATCC_BAA3330_001831	True	True	True	tet(M)	TETRACYCLINE	tet(M)	antibiotic target protection	tetracycline; doxycycline; minocycline; chlortetracycline; demeclocycline; oxytetracycline	Doxycycline, Tetracycline, Minocycline
ATCC_BAA3330_001836	True	True		msr(D)	AZITHROMYCIN/ERYTHROMYCIN/STREPTOGRAMIN B				Erythromycin, Azithromycin, Telithromycin, Quinupristin, Pristinamycin IA, Virginiamycin S
ATCC_BAA3330_001837	True	True		mef(A)	AZITHROMYCIN/ERYTHROMYCIN				Erythromycin, Azithromycin
ATCC_BAA3330_002054			True	patB		patB	antibiotic efflux	ciprofloxacin; norfloxacin	
ATCC_BAA3330_002056			True	patA		patA	antibiotic efflux	ciprofloxacin; norfloxacin	
ATCC_BAA3330_002083			True			RlmA(II)	antibiotic target alteration	tylosin; mycinamicin	

ATCC® Genome Portal – Download with Lot Number (All Users)



Welcome to the ATCC Genome Portal

The only authenticated reference omics database for ATCC biom

Candida glabrata (ATCC® 2001™)

Assembly Summary

Date Published	October 30, 2020
Length	12,583,835 nt
Sequencing Technology	Illumina + Oxford Nanopore
Number of Contigs	20
Assembly Level	Scaffold
N50	1,108,508 nt
%GC	38.77%

Annotations Summary

Input Reads Summary

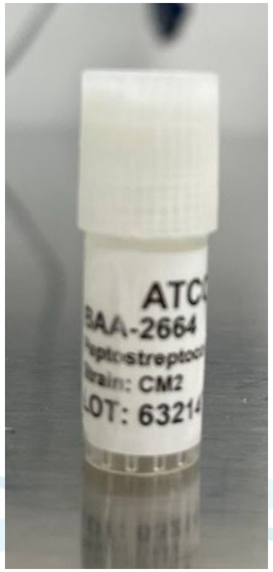
Details required to download data

Downloads are only available to ATCC Genome Portal supporting members or those who have purchased a corresponding physical product.

You can select a supporting membership plan or enter the lot number associated with your ATCC product below to continue.

Lot Number

Please enter lot number



Access to the entire database… …..purchase an annual *Supporting Membership*

	Free	Individual	Research Group	Institution
View organism and genome metadata, assemblies, and annotations	✓	✓	✓	✓
Search for genomes of interest	✓	✓	✓	✓
Purchase the corresponding authenticated ATCC source materials	✓	✓	✓	✓
Download genome assemblies and annotations	Only for purchased products	All products	All products	All products
Access our REST-API	Not available	✓	✓	✓
Analyze isolates with Discrepancy Reports	Fee for each report	12 free reports per year	60 free reports per year	Inquire
Members with full access	0	1	5	Unlimited
		$600/$1,800 NFP / Profit	$2,400/$7,200 NFP / Profit	Inquire

Meet ATCC Scientists at ASM Microbe

Discover trusted microbial standards, reference genomes, and expert guidance for reproducible results

ATCC®

Visit us at
booth #1724

Check out our 10
scientific posters

Explore our
resources

See our full agenda for ASM Microbe 2026