



PRODUCT SPOTLIGHT

GENOME PORTAL

SETTING NEW STANDARDS FOR AUTHENTICATION

Reproducible research starts with credible biological materials. As part of our commitment to advancing authentication, we started the Enhanced Authentication Initiative to provide researchers with authenticated biological materials paired with reference-quality, whole-genome sequences. This initiative not only enriches the characterization of our biological collections by using next-generation sequencing and state-of-the-art bioinformatics methods, but also includes making those data available to everyone through the ATCC Genome Portal.

LEARN MORE ABOUT OUR ENHANCED AUTHENTICATION INITIATIVE AT WWW.ATCC.ORG/EAI



PROTECT YOUR RESEARCH WITH AUTHENTICATED DATA



Current publicly available, consensus-driven genomic sequences often lack data authenticity, quality, completeness, or traceability, which can compromise your research. Without the ability to confidently compare and correlate data between different bodies of work, research cannot be expanded upon and scientific progress stalls. This could result in retracted publications or wasted time and effort.

For scientists to make insightful correlations, they need access to rigorously validated reference genomes tied back to credible biological materials. That's why we developed a standardized genome sequencing, assembly, and genome annotation pipeline to provide researchers with the whole-genome sequences of the specific, authenticated materials needed to generate credible data.

VISIT THE ATCC GENOME PORTAL AT GENOMES.ATCC.ORG TO GET STARTED

SHIFT FROM CONSENSUS TO DISCERNABLE

It is time to shift life science research from the consensus to the discernible. The ATCC Genome Portal offers more than just a collection of reference-quality genomes originating from authenticated ATCC materials. It is a cloud-based platform where you can easily browse genomic data and metadata by simply logging into the portal. You can:

-  Download whole-genome sequences and annotations of ATCC materials
-  Search for nucleotide sequences or genes within genomes
-  View genome assembly metadata and quality metrics

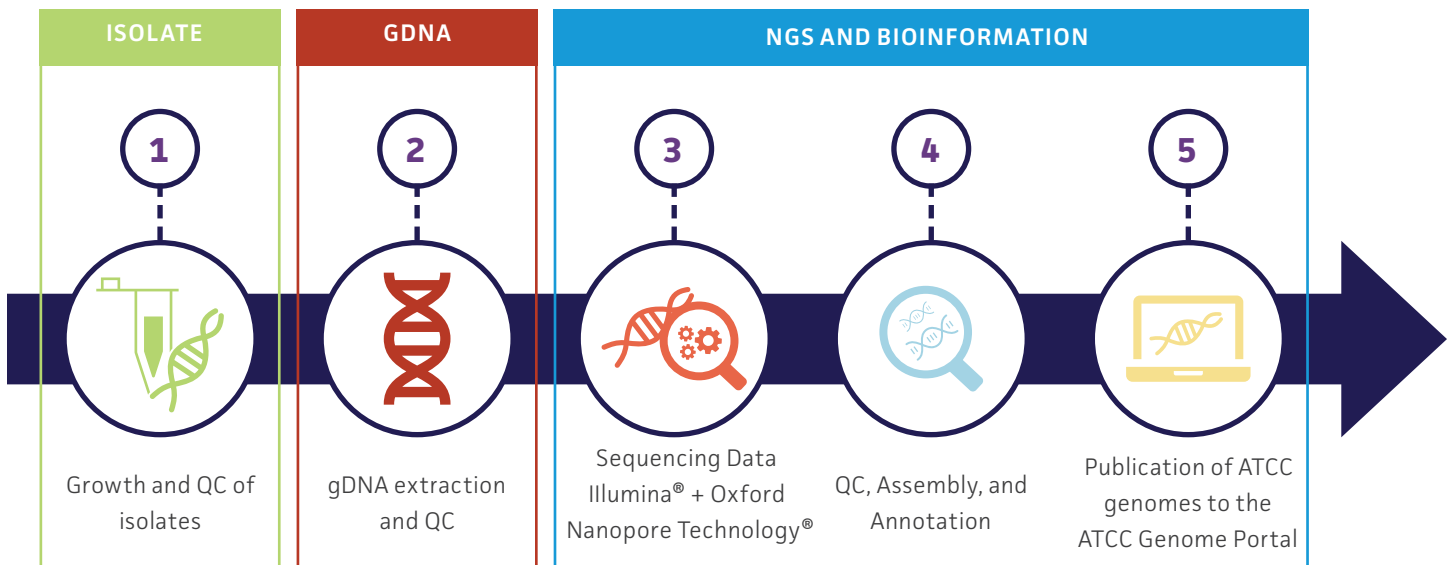
With high-quality, annotated data at your fingertips, you can confidently perform bioinformatics analyses on your materials! Visit the ATCC Genome Portal today to explore our growing collection of reference-quality genome sequences.

GET STARTED AT GENOMES.ATCC.ORG



UNDERSTAND OUR APPROACH

Our optimized methodology is designed to achieve complete, circularized (when biologically appropriate), and contiguous genomic elements by using short-read (virology collection) and hybrid (bacteriology and mycology collections) assembly techniques. We then take our workflow one step further by accompanying each stage of the process with rigorous quality control analyses that ensure the highest quality data.



Only the data that passes all quality control criteria are published to the ATCC Genome Portal.

GET ALL THE DETAILS ABOUT OUR APPROACH AT WWW.ATCC.ORG/GENOMEPORTALTECHDOC

WEBINAR: THE IMPORTANCE OF USING NEXT-GENERATION SEQUENCING TO FURTHER AUTHENTICATE THE ATCC MICROBIAL COLLECTIONS

Despite the availability of consensus-driven genome sequences in public databases, the quality, completeness, authenticity, accuracy, and traceability of genomic data are inadequate. ATCC addressed these problems by implementing a robust NGS and genome assembly workflow to enrich the characterization of the biological materials in our collection. We then made the reference genomes and corresponding metadata publicly available through the ATCC Genome Portal.

Watch our on-demand webinar at www.atcc.org/genomeportalwebinar to learn more about our standardized NGS and genome assembly workflow and to explore the features of the ATCC Genome Portal.

PRESERVE YOUR BIOMATERIALS FOR FUTURE RESEARCH

Want to make your strains available to the global scientific community? Deposit them at ATCC! Visit us online at www.atcc.org/Deposit to learn more about our deposit process. When you fill out the deposit request form, be sure to inquire about including whole-genome sequencing and analysis as part of your submission to our collection.

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