

Resource Summary Report

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Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility

RRID:SCR_028602

Type: Tool

Proper Citation

Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility (RRID:SCR_028602)

Resource Information

URL: <https://cores.research.asu.edu/genomics>

Proper Citation: Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility (RRID:SCR_028602)

Description: Sequencing facility offers to perform a full range of genomic applications, such as Whole Genome Sequencing (WGS), RNA sequencing (including options for poly(A) selection, ribosomal depletion, and degraded/FFPE RNA), library preparation of ChIP samples, de novo sequencing, metagenomics sequencing, single-cell sequencing and PacBio long read sequencing applications. All next generation sequencing applications are performed on the Illumina platform with the NextSeq and NovaSeq instruments. Long-read sequencing applications are performed on the PacBio Revio using Single-Molecule, Real-Time (SMRT) Sequencing. The Revio is ideal for high-quality de novo whole genome assemblies, full-length transcriptomes, cell-type specific isoforms, and targeted long-read amplicon sequencing. Provides 10X genomics instrument for sample partitioning and molecular barcoding prior to sequencing. For metagenomics sequencing, 16S, 18S, or ITS regions can be isolated and sequenced as relevant and are sequenced on the NextSeq instrument, allowing researchers to characterize and study microbial communities from various environments such as soils, freshwater, seawater, wastewater, and host-microbe associations. Offers expertise of facility staff is available for researchers at any point in the experimental process.

Synonyms: , Arizona State University Knowledge Enterprise Desert Southwest Genomics Center, Desert Southwest Genomics Facility

Resource Type: access service resource, core facility, service resource

Keywords: ABRF, sequencing services, Whole Genome Sequencing (WGS), RNA sequencing (including options for poly(A) selection, ribosomal depletion, and degraded/FFPE RNA), library preparation of ChIP samples, de novo sequencing,

metagenomics sequencing, single-cell sequencing and PacBio long read sequencing,

Availability: Open

Resource Name: Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility

Resource ID: SCR_028602

Alternate IDs: ABRF_6006

Alternate URLs: https://coremarketplace.org/RRID:SCR_028602/?citation=1

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Record Last Update: 20260905T133615+0000

Ratings and Alerts

No rating or validation information has been found for Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility.

No alerts have been found for Arizona State University Knowledge Enterprise Desert Southwest Genomics Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.