

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

University of Massachusetts Amherst Genomics Resource Laboratory Core Facility

RRID:SCR_017907

Type: Tool

Proper Citation

University of Massachusetts Amherst Genomics Resource Laboratory Core Facility
(RRID:SCR_017907)

Resource Information

URL: <http://www.umass.edu/ials/genomics>

Proper Citation: University of Massachusetts Amherst Genomics Resource Laboratory Core Facility (RRID:SCR_017907)

Description: Core provides services and advanced instrumentation support for nucleic acid (DNA and RNA) analysis, high-throughput next-generation sequencing, including solutions for sample processing such as nucleic-acid isolation, nucleic-acid quantitative and qualitative analysis, NGS library preparation, quantitative-PCR analysis, etc. Provides sample processing and library preparation such as whole genome sequencing, shotgun metagenomics, metatranscriptomics, targeted amplicon sequencing, RNA-Seq, ChIP-Seq, Exome Sequencing, Methyl-seq, Single Cell Genomics, etc. Facility accepts samples and will perform requested analysis. Offers training to users to conduct experimentation.

Abbreviations: GRL

Synonyms: Genomics Resource Laboratory

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

Keywords: ABRF

Resource Name: University of Massachusetts Amherst Genomics Resource Laboratory Core Facility

Resource ID: SCR_017907

Alternate IDs: ABRF_789

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260919T195933+0000

Ratings and Alerts

No rating or validation information has been found for University of Massachusetts Amherst Genomics Resource Laboratory Core Facility.

No alerts have been found for University of Massachusetts Amherst Genomics Resource Laboratory Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Martin KR, et al. (2026) Major Histocompatibility Complex Immunogenetic Diversity Differs Substantially Across Sea Turtle Species and Genomic Regions. *Genome biology and evolution*, 18(2).

Bermudez Y, et al. (2025) Virally encoded interleukin-6 (vIL-6) coordinates with human IL-6 to modulate cytokine expression during KSHV infection. *bioRxiv : the preprint server for biology*.

Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *bioRxiv : the preprint server for biology*.

Sarsani V, et al. (2025) Discovering genetic modulators of the protein homeostasis system through multilevel analysis. *PNAS nexus*, 4(1), pgae574.

Fan R, et al. (2025) Effects of Fish Oil with Heat Treatment on Obesity, Inflammation, and Gut Microbiota in Ovariectomized Mice. *Nutrients*, 17(3).

Fan R, et al. (2025) Heat treatment activates futile calcium cycling in brown adipose tissue to modulate energy metabolism and alters gut microbiota in C57BL/6 mice. *Acta physiologica (Oxford, England)*, 241(4), e70025.

Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *Current biology : CB*, 35(23), 5696.

Kennard AS, et al. (2025) Tubulin sequence divergence is associated with the use of distinct microtubule regulators. *Current biology : CB*, 35(2), 233.

Satbhai KM, et al. (2025) Single-cell RNA sequencing reveals tissue-specific transcriptomic changes induced by perfluorooctanesulfonic acid (PFOS) in larval zebrafish (*Danio rerio*). *Journal of hazardous materials*, 489, 137515.

Pavon N, et al. (2024) Patterning ganglionic eminences in developing human brain organoids using a morphogen-gradient-inducing device. *Cell reports methods*, 4(1), 100689.

Kennard AS, et al. (2024) An internally controlled system to study microtubule network diversification links tubulin evolution to the use of distinct microtubule regulators. *bioRxiv* : the preprint server for biology.

Shinfuku MS, et al. (2024) Seasonal effects of long-term warming on ecosystem function and bacterial diversity. *PloS one*, 19(10), e0311364.

He XD, et al. (2024) TATA-binding associated factors have distinct roles during early mammalian development. *Developmental biology*, 511, 53.

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, *Berghia stephanieae*. *The Journal of comparative neurology*, 532(6), e25628.

He XD, et al. (2024) Overlapping peri-implantation phenotypes of ZNHIT1 and ZNHIT2 despite distinct functions during early mouse development???. *Biology of reproduction*, 111(5), 1017.

Sarsani V, et al. (2024) Discovering Genetic Modulators of the Protein Homeostasis System through Multilevel Analysis. *bioRxiv* : the preprint server for biology.

Kim M, et al. (2023) Mutation of the polyadenylation complex subunit CstF77 reveals that mRNA 3' end formation and HSP101 levels are critical for a robust heat stress response. *The Plant cell*, 35(2), 924.

Leonard ER, et al. (2023) Dietary exposure to the food preservative tert-Butylhydroquinone (tBHQ) impairs zebrafish (*Danio rerio*) survival, growth, organ development, and gene expression in Nrf2a-dependent and independent ways. *Food and chemical toxicology* : an international journal published for the British Industrial Biological Research Association, 176, 113788.

Kim M, et al. (2021) mTERF18 and ATAD3 are required for mitochondrial nucleoid structure and their disruption confers heat tolerance in *Arabidopsis thaliana*. *The New phytologist*, 232(5), 2026.