

Resource Summary Report

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University of Virginia Bioinformatics Core

RRID:SCR_012718

Type: Tool

Proper Citation

University of Virginia Bioinformatics Core (RRID:SCR_012718)

Resource Information

URL: <https://med.virginia.edu/bioinformatics-core/>

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Description: Core serves as a centralized resource for providing expert and timely bioinformatics consulting and data analysis solutions. The core offers services to investigators both within and outside UVA on both grant-funded and chargeback-based projects for management and analysis of large-scale biological datasets produced by high-throughput genomics experiments. The Core's mission is to build and maintain an infrastructure that enables the application of strong bioinformatics analysis with a measurable impact on the ability of UVA investigators to both publish their work and obtain new funding.

Abbreviations: UVA Bioinformatics Core

Synonyms: , UVA, University of Virginia, core facility, School of Medicine, Bioinformatics

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

Keywords: core facility, data analysis, infrastructure,

Availability: Available to external user

Resource Name: University of Virginia Bioinformatics Core

Resource ID: SCR_012718

Alternate IDs: SciEx_8923

Old URLs: <http://www.scienceexchange.com/facilities/bioinformatics-core-virginia>

Record Creation Time: 20220129T080311+0000

Record Last Update: 20260829T183307+0000

Ratings and Alerts

No rating or validation information has been found for University of Virginia Bioinformatics Core.

No alerts have been found for University of Virginia Bioinformatics Core.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Hinson S, et al. (2026) Non-uniform chromosomal SNP density biases sites of meiotic crossovers in *Drosophila melanogaster*. *G3* (Bethesda, Md.), 16(6).

Genetta TL, et al. (2026) ZEB1 Promotes Alternate Lengthening of Telomeres at Multiple Levels. *Cancers*, 18(3).

Ahmed K, et al. (2026) Decoding the circRNA-miRNA-mRNA regulatory network in hepatitis B virus-driven hepatocellular carcinoma. *Cell communication and signaling : CCS*, 24(1).

Ali MS, et al. (2026) A Post-GWAS Analysis of the Shared Genetic Architecture Between COVID-19 and Coronary Artery Disease. *International journal of molecular sciences*, 27(9).

Boulton A, et al. (2026) The MLLT3 YEATS domain binds histone marks (H3K9/18/27ac/cr) and ncRNA (7SK), linking transcription and RNA signaling to regulate hematopoiesis. *Cell reports*, 45(6), 117540.

Cook SR, et al. (2025) A 3D-printed multi-compartment organ-on-chip platform with a tubing-free pump models communication with the lymph node. *Lab on a chip*, 25(2), 155.

Hinson S, et al. (2025) Non-uniform chromosomal SNP density biases sites of meiotic crossovers in *Drosophila melanogaster*: SNP density and sites of meiotic crossovers. *bioRxiv : the preprint server for biology*.

Boulton A, et al. (2025) The MLLT3 YEATS domain is a dual reader of histone marks (H3K9/18/27ac/cr) and ncRNA (7SK), linking epigenetic and RNA signaling to regulate hematopoiesis. *bioRxiv : the preprint server for biology*.

Uddin MJ, et al. (2024) Investigating the impact of antibiotic-induced dysbiosis on protection from *Clostridium difficile* colitis by mouse colonic innate lymphoid cells. *mBio*, 15(3), e0333823.

Pierce R, et al. (2024) Persistent dysbiosis of duodenal microbiota in patients with controlled pediatric Crohn's disease after resolution of inflammation. *Scientific reports*, 14(1), 12668.

Cook SR, et al. (2024) A 3D-printed multi-compartment organ-on-chip platform with a tubing-free pump models communication with the lymph node. *bioRxiv : the preprint server for biology*.

Bingham GC, et al. (2023) High-dimensional comparison of monocytes and T cells in post-COVID and idiopathic pulmonary fibrosis. *Frontiers in immunology*, 14, 1308594.