

Resource Summary Report

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Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility

RRID:SCR_024905

Type: Tool

Proper Citation

Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility
(RRID:SCR_024905)

Resource Information

URL: <http://www.spatialtechnology.org>

Proper Citation: Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility (RRID:SCR_024905)

Description: Core for spatial and single cell technologies provides expertise, training, education and equipment. Supports projects, starting from consultation with matching right technologies to project needs, budget, and timeline. Provided services include single cell and spatial assays, tissue preparations, staining, sequencing, bioinformatic analyses. Equipment include 10x Genomics Visium, 10x Genomics Xenium, Akoya Phenomager HT whole slide scanner, Akoya Phenocycler Fusion, Bruker Vutara VXL, Nanostring GeoMX DSP, Vizgen MERSCOPE, Eppendorf TMA Grandmaster and more.

Synonyms: Spatial Technologies Unit

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

Keywords: ABRF, spatial and single cell technologies services, single cell and spatial assays, tissue preparations, staining, sequencing, bioinformatic services, ,

Availability: Open

Resource Name: Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility

Resource ID: SCR_024905

Alternate IDs: ABRF_2608

Alternate URLs: <https://coremarketplace.org/?FacilityID=2608&citation=1>

Record Creation Time: 20240120T050237+0000

Record Last Update: 20260905T133444+0000

Ratings and Alerts

No rating or validation information has been found for Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility.

No alerts have been found for Beth Israel Deaconess Medical Center Spatial Technologies Unit Core Facility.

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 [Kravitz](#) .

Pilcher WC, et al. (2026) A single-cell atlas characterizes dysregulation of the bone marrow immune microenvironment associated with outcomes in multiple myeloma. *Nature cancer*, 7(1), 224.

Neyazi M, et al. (2026) Integrative Molecular Analyses of Inflammatory and Autoimmune Signals in Cardiac Sarcoidosis. *Circulation*, 153(25), 2011.

Rai A, et al. (2026) Aging-related Transcriptomic Changes with Spatial Resolution in the Human Prefrontal Cortex. *bioRxiv : the preprint server for biology*.

Valenzuela-Arzeta IE, et al. (2026) A microRNA atlas of the human prefrontal cortex across the adult lifespan. *bioRxiv : the preprint server for biology*.

Cheloni G, et al. (2025) Durable response to CAR T is associated with elevated activation and clonotypic expansion of the cytotoxic native T cell repertoire. *Nature communications*, 16(1), 4819.

Liegel J, et al. (2025) Vaccine-educated T cells and a CD123 bispecific T-cell engager for treatment of acute myeloid leukemia. *Blood advances*, 9(21), 5585.

Castanho I, et al. (2025) Molecular hallmarks of excitatory and inhibitory neuronal resilience and resistance to Alzheimer's disease. *bioRxiv : the preprint server for biology*.

Castanho I, et al. (2025) Molecular hallmarks of excitatory and inhibitory neuronal resilience to Alzheimer's disease. *Molecular neurodegeneration*, 20(1), 103.

Pita-Juarez Y, et al. (2025) A single-nucleus and spatial transcriptomic atlas of the COVID-19 liver reveals topological, functional, and regenerative organ disruption in

patients. *Genome biology*, 26(1), 56.

Wang S, et al. (2024) FixNCut: A Practical Guide to Sample Preservation by Reversible Fixation for Single Cell Assays. *Bio-protocol*, 14(17), e5063.

Pilcher WC, et al. (2024) A single-cell atlas characterizes dysregulation of the bone marrow immune microenvironment associated with outcomes in multiple myeloma. *bioRxiv* : the preprint server for biology.

Izumi M, et al. (2024) Integrative single-cell RNA-seq and spatial transcriptomics analyses reveal diverse apoptosis-related gene expression profiles in EGFR-mutated lung cancer. *Cell death & disease*, 15(8), 580.