Resource Summary Report

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University of North Carolina at Chapel Hill Biospecimen Processing Core Facility

RRID:SCR_021290
Type: Tool

Proper Citation

University of North Carolina at Chapel Hill Biospecimen Processing Core Facility (RRID:SCR_021290)

Resource Information

URL: https://bsp.web.unc.edu/

Proper Citation: University of North Carolina at Chapel Hill Biospecimen Processing Core Facility (RRID:SCR_021290)

Description: Centralized, quality controlled facility and biorepository for processing, storage and disbursement of human specimens.Offers high throughput processing of human biospecimens, with specific emphasis on DNA and RNA isolation and purification.Provides laboratory support for investigator initiated large scale clinical, epidemiologic, and other studies.Functions as human specimen biorepository resource for clinicians who wish to store and study samples from unusual or potentially important patients.Biorepository is managed by custom LIMS, with sample accessioning, tracking and audits at each step.Provides scientific resource for investigators seeking advice or consultation on study design including specimen collection and storage methods, and human subject issues. Core staff act as liaison to other UNC core facilities and outside collaborators.

Abbreviations: BSP, UNC BSP

Synonyms: UNC Biospecimen Processing Facility

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

Keywords: USEDit, ABRF

Availability: open

Resource Name: University of North Carolina at Chapel Hill Biospecimen Processing Core Facility

Resource ID: SCR_021290

Alternate IDs: ABRF_1186

Alternate URLs: https://coremarketplace.org/?FacilityID=1186

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260904T000836+0000

Ratings and Alerts

No rating or validation information has been found for University of North Carolina at Chapel Hill Biospecimen Processing Core Facility.

No alerts have been found for University of North Carolina at Chapel Hill Biospecimen Processing Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Kaczmarzyk JR, et al. (2026) Towards interpretable prediction of recurrence risk in breast cancer using pathology foundation models. NPJ digital medicine, 9(1), 149.

Wang Q, et al. (2026) Molecular and socioeconomic characteristics of inflammatory breast cancer in the Carolina Breast Cancer Study. Breast cancer research and treatment, 215(2), 61.

Chiles JW, et al. (2026) Whole Genome Sequence Analysis of Weight Loss in 16 972 Participants With COPD Reveals Novel Risk Loci in DRAIC and RFX3. Journal of cachexia, sarcopenia and muscle, 17(3), e70293.

Hickman E, et al. (2026) Similarity of sputum mediator signatures between e-cigarette users and COPD depends on GOLD stage and type of e-cigarette: a pilot study. PloS one, 21(3), e0343940.

Orchard P, et al. (2026) Cross-cohort analysis of expression and splicing quantitative trait loci in TOPMed. Science (New York, N.Y.), 393(6808), eadx2989.

Suri R, et al. (2025) Reply to Currow et al.: Geographic Variation in Prevalence of Breathlessness: Latitude. American journal of respiratory and critical care medicine, 211(6), 1093.

Wilson AC, et al. (2025) Novel risk loci encompassing genes influencing STAT3, GPCR, and oxidative stress signaling are associated with co-morbid GERD and COPD. PLoS

genetics, 21(2), e1011531.

Azad Rabby AS, et al. (2025) Light Convolutional Neural Network to Detect Chronic Obstructive Pulmonary Disease (COPDxNet): A Multicenter Model Development and External Validation Study. medRxiv : the preprint server for health sciences.

Guzman DE, et al. (2025) Proteomic discovery analysis of quantitatively assessed emphysema in the general population. The MESA Lung Study. Respiratory research, 26(1), 236.

Orchard P, et al. (2025) Cross-cohort analysis of expression and splicing quantitative trait loci in TOPMed. medRxiv : the preprint server for health sciences.

Niu H, et al. (2025) Spatial Clustering for Carolina Breast Cancer Study. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 30, 346.

Walker AE, et al. (2025) Prognostic significance of CD8+ T cell Spatial Biomarkers in ER+ and ER- breast cancer: A retrospective cohort study. PLoS medicine, 22(10), e1004647.

Konigsberg IR, et al. (2025) Omic Risk Scores are Associated with COPD-related Traits Across Three Cohorts. medRxiv : the preprint server for health sciences.

Zhang YH, et al. (2025) Proteomic biomarkers of emphysema-predominant and non-emphysema-predominant chronic obstructive pulmonary disease. EBioMedicine, 117, 105800.

Lang JD, et al. (2025) Super-enhancers and efficacy of triptolide in small cell carcinoma of the ovary hypercalcemic type. iScience, 28(2), 111770.

Tejwani V, et al. (2025) Associations of serum and bronchoalveolar immunoglobulins with lung microbiota diversity, B-cell memory phenotypes, and COPD morbidity and exacerbations. Respiratory research, 26(1), 250.

Walker AE, et al. (2025) Prognostic Significance of CD8 T-cell Spatial Biomarkers in ER+ and ER- Breast Cancer. medRxiv : the preprint server for health sciences.

Broadaway KA, et al. (2025) Genomic loci and molecular genetic mechanisms for hidradenitis suppurativa. The British journal of dermatology, 193(5), 948.

Cao S, et al. (2025) Epigenomic study of the lower airway reveals COPD-associated methylation patterns and potential microbiota links. BMJ open respiratory research, 12(1).

Buschur KL, et al. (2025) Hair follicle gene expression profiling in the SubPopulations and InteRmediate Outcome Measures in COPD Study (SPIROMICS). BMC medical genomics, 18(1), 192.