Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

Johns Hopkins University School of Medicine Genetic Resources Core Facility

RRID:SCR_018669
Type: Tool

Proper Citation

Johns Hopkins University School of Medicine Genetic Resources Core Facility (RRID:SCR_018669)

Resource Information

URL: https://grcf.jhmi.edu/

Proper Citation: Johns Hopkins University School of Medicine Genetic Resources Core Facility (RRID:SCR_018669)

Description: Established to produce immortalized cell lines from human blood (EBV transformations). Offers genomics applications for single cells, including RNA-seq, gene expression profiling by qPCR and DNA amplification for whole-genome or targeted (exome or PCR-based analysis) through 10x Genomics Chromium platform (similar to Drop Seq). Offers custom genotyping to analyze short tandem repeats, variable number tandem repeats and single nucleotide polymorphisms.

Abbreviations: GRCF

Synonyms: GRCF Cell Center, Genetic Resources Core Facility, JHU-NAT, GRCF Biorepository and Cell Center, GRCF DNA Services, Genetic Resources Core Facility (GRCF) BioRepository and Cell Center, JHU Nucleic Acid Technologies, JHU BioBank

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

Keywords: USEDit, immortalized cell line production, human blood, RNAseq, gene expression profiling, qPCR, DNA amplification, exome, genome, PCR, analysis, ABRF

Resource Name: Johns Hopkins University School of Medicine Genetic Resources Core Facility

Resource ID: SCR_018669

Alternate IDs: ABRF_344

Alternate URLs: https://grcf.jhmi.edu/grcf-services/

Old URLs: https://grcf.jhmi.edu/biorepository-cell-center/

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260905T133417+0000

Ratings and Alerts

No rating or validation information has been found for Johns Hopkins University School of Medicine Genetic Resources Core Facility.

No alerts have been found for Johns Hopkins University School of Medicine Genetic Resources Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Hatch K, et al. (2026) ??-Radiation Induces Long-Term Dose-Related Proteomic and Phosphorylated-Tau Species Changes in Non-Human Primate Hippocampus. Research square.

Olson MV, et al. (2026) Institutional Biobanking as shared public health infrastructure: a financially sustainable service center model. Frontiers in health services, 6, 1778446.

Scott AF, et al. (2026) A Nanopore-Only Assembly of a Nuclear and Mitochondrial Genome of a Red Coachwhip (Masticophis flagellum piceus). Genes, 17(3).

Sun J, et al. (2026) Mitochondrial DNA Fragment Dynamics in Acute and Chronic Human Immunodeficiency Virus: Insights From Human and Nonhuman Primate Models. The Journal of infectious diseases, 233(4), 652.

Heinsberg LW, et al. (2026) Differential DNA Methylation of the Brain-Derived Neurotrophic Factor Gene is Observed after Pediatric Traumatic Brain Injury Compared with Orthopedic Injury. Journal of neurotrauma, 43(7-8), 575.

Mace JW, et al. (2026) Autoimmune neuroinflammation leads to neuronal death via MIF nuclease-mediated parthanatos. Nature neuroscience, 29(4), 796.

Hatch K, et al. (2026) Long-term molecular effects of 16O-ion exposure in rat brain and implications for space radiation risk. NPJ microgravity.

Sofowora I, et al. (2025) Regulation of the promoter for capsular polysaccharide synthesis in Neisseria meningitidis serogroup B by HTH_XRE family transcription factor.

Microbiology spectrum, 13(6), e0330124.

Seluzicki CM, et al. (2025) Regulation of translation elongation and integrated stress response in heat-shocked neurons. Cell reports, 44(5), 115639.

Grossman NT, et al. (2025) Three annotated chromosome-level de novo genome assemblies of Lomentospora prolificans provide evidence for a chromosomal translocation event. G3 (Bethesda, Md.), 15(6).

Randighieri M, et al. (2025) The impact of brain-derived neurotrophic factor gene polymorphisms on post-stroke naming in aphasia. PloS one, 20(7), e0327320.

Zhang W, et al. (2025) Complete CD16A Deficiency and Defective NK Cell Function in a Man Living with HIV. Journal of clinical immunology, 45(1), 98.

Saini T, et al. (2025) Insulin-Like Growth Factor 2 mRNA-Binding Protein 2 (IGF2BP2) Promotes Castration-Resistant Prostate Cancer Progression by Regulating AR-V7 mRNA Stability. Cancer reports (Hoboken, N.J.), 8(2), e70096.

Fernandez RF, et al. (2025) Dysregulated hippocampal fatty acid metabolism following intermittent hypoxemia-induced neonatal brain injury is rescued by treatment with acetate. Nature communications.

Lai M, et al. (2025) Epigenome-wide association study of nuclear DNA methylation in relation to mitochondrial heteroplasmy. Nature communications, 16(1), 10962.

Jacobs E, et al. (2025) A method for authenticating the fidelity of Cryptococcus neoformans knockout collections. bioRxiv : the preprint server for biology.

Heinsberg LW, et al. (2025) Differential DNA Methylation of the Brain-Derived Neurotrophic Factor Gene is Observed after Pediatric Traumatic Brain Injury Compared to Orthopedic Injury. medRxiv : the preprint server for health sciences.

Catterson PJ, et al. (2025) Indicator Tubes: A Novel Solution for Monitoring Temperature Excursions in Biobank Storage. Methods and protocols, 8(5).

Dragotakes Q, et al. (2025) A conserved enzymatic toolkit targeting host cell metabolism is associated with Cryptococcus neoformans intracellular survival in protozoal and mammalian phagocytic cells. PLoS pathogens, 21(12), e1013787.

Jacobs E, et al. (2025) A method for authenticating the fidelity of Cryptococcus neoformans knockout collections. Microbiology spectrum, 13(10), e0050125.