Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 28, 2024

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/

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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: core facility, access service resource, service resource

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

Availability: Open

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/

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 19 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hart WS, et al. (2024) Divergent transcriptomic signatures from putative mesenchymal stimuli in glioblastoma cells. Cancer gene therapy.

Liu S, et al. (2023) A longitudinal epigenome-wide association study of preeclamptic and normotensive pregnancy. Epigenetics communications, 3(1).

Wilson JL, et al. (2023) The Influenza B Virus Victoria and Yamagata Lineages Display Distinct Cell Tropism and Infection Induced Host Gene Expression in Human Nasal Epithelial Cell Cultures. bioRxiv : the preprint server for biology.

Resnick JD, et al. (2023) Early Transcriptional Responses of Human Nasal Epithelial Cells to Infection with Influenza A and SARS-CoV-2 Virus Differ and Are Influenced by Physiological Temperature. Pathogens (Basel, Switzerland), 12(3).

Wilson JL, et al. (2023) The Influenza B Virus Victoria and Yamagata Lineages Display Distinct Cell Tropism and Infection-Induced Host Gene Expression in Human Nasal Epithelial Cell Cultures. Viruses, 15(9).

Resnick JD, et al. (2023) Growth media affects susceptibility of air-lifted human nasal epithelial cell cultures to SARS-CoV2, but not Influenza A, virus infection. bioRxiv : the preprint server for biology.

Resnick JD, et al. (2023) Early transcriptional responses of human nasal epithelial cells to infection with Influenza A and SARS-CoV-2 virus differ and are influenced by physiological temperature. bioRxiv : the preprint server for biology.

Yeung-Luk BH, et al. (2023) SARS-CoV-2 infection alters mitochondrial and cytoskeletal function in human respiratory epithelial cells mediated by expression of spike protein. mBio, 14(4), e0082023.

Killian JT, et al. (2023) Alloreactivity and autoreactivity converge to support B cell epitope targeting in transplant rejection. bioRxiv : the preprint server for biology.

Edwardson MA, et al. (2023) Expansion of plasma MicroRNAs over the first month following human stroke. Journal of cerebral blood flow and metabolism : official journal of the International Society of Cerebral Blood Flow and Metabolism, 43(12), 2130.

Halasz L, et al. (2023) An Atlas of Promoter Chromatin Modifications and HiChIP Regulatory Interactions in Human Subcutaneous Adipose-Derived Stem Cells. International journal of molecular sciences, 25(1).

Veltri AJ, et al. (2022) Distinct elongation stalls during translation are linked with distinct pathways for mRNA degradation. eLife, 11.

Melendez JH, et al. (2022) Retrospective Analysis of Ugandan Men with Urethritis Reveals Mycoplasma genitalium and Associated Macrolide Resistance. Microbiology spectrum, 10(2), e0230421.

Romero JC, et al. (2022) Oligodendrogenesis and myelination tracing in a CRISPR/Cas9-engineered brain microphysiological system. Frontiers in cellular neuroscience, 16, 1094291.

Song AY, et al. (2022) Associations between accelerated parental biologic age, autism spectrum disorder, social traits, and developmental and cognitive outcomes in their children. Autism research : official journal of the International Society for Autism Research, 15(12), 2359.

Creisher PS, et al. (2022) Downregulation of transcriptional activity, increased inflammation, and damage in the placenta following in utero Zika virus infection is associated with adverse pregnancy outcomes. Frontiers in virology, 2.

Castiglione GM, et al. (2021) Evolutionary pathways to SARS-CoV-2 resistance are opened and closed by epistasis acting on ACE2. PLoS biology, 19(12), e3001510.

Shifera AS, et al. (2021) Identification of microbial agents in tissue specimens of ocular and periocular sarcoidosis using a metagenomics approach. F1000Research, 10, 820.

Christodoulou I, et al. (2021) Glycoprotein Targeted CAR-NK Cells for the Treatment of SARS-CoV-2 Infection. Frontiers in immunology, 12, 763460.