

Resource Summary Report

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Medical College of Wisconsin Mellowes Center for Genomic Sciences and Precision Medicine Core Facility

RRID:SCR_022926

Type: Tool

Proper Citation

Medical College of Wisconsin Mellowes Center for Genomic Sciences and Precision Medicine Core Facility (RRID:SCR_022926)

Resource Information

URL: <https://www.mcw.edu/departments/genomic-sciences-and-precision-medicine-center-gspmc>

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Description: Core for advancing genomic sciences and precision medicine in fields of Omics, Data Science, and Systems Biology. Provides whole genome sequencing technologies to investigate how gene variants impact gene expression and to define genetic variants associated with rare and common disease, embryonic development, and effects of environmental factors and drugs upon gene expression and disease.

Synonyms: MC-Mellowes Center for Genomic Sciences and Precision Medicine, Medical College of Wisconsin Mellowes Center for Genomic Sciences and Precision Medicine

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

Keywords: USEDit, ABRF, genomic sciences and precision medicine, Omics, Data Science, Systems Biology

Resource Name: Medical College of Wisconsin Mellowes Center for Genomic Sciences and Precision Medicine Core Facility

Resource ID: SCR_022926

Alternate IDs: ABRF_1606

Alternate URLs: <https://coremarketplace.org/?FacilityID=1606&citation=1>

Record Creation Time: 20221026T050203+0000

Record Last Update: 20260801T191253+0000

Ratings and Alerts

No rating or validation information has been found for Medical College of Wisconsin Mellows Center for Genomic Sciences and Precision Medicine Core Facility.

No alerts have been found for Medical College of Wisconsin Mellows Center for Genomic Sciences and Precision Medicine Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Veluri R, et al. (2025) An Integrative Multitiered Computational Analysis for Better Understanding the Structure and Function of 85 Miniproteins. bioRxiv : the preprint server for biology.

Zenga J, et al. (2025) Radiation therapy results in preferential tumor antigen-specific lymphodepletion in head and neck cancer. Nature communications, 16(1), 5660.

Rousseau H, et al. (2025) Decreased endothelial cell retinoic acid signaling accelerates progression of single ventricle pulmonary arteriovenous malformations. bioRxiv : the preprint server for biology.

Veluri R, et al. (2025) An integrative multitiered computational analysis for better understanding the structure and function of 85 miniproteins. NAR genomics and bioinformatics, 7(4), lqaf178.

Ergun P, et al. (2025) Amprenavir Mitigates Pepsin-Induced Transcriptomic Changes in Normal and Precancerous Esophageal Cells. International journal of molecular sciences, 26(13).

Edderkaoui M, et al. (2025) HDAC4/MybL1/YAP novel signaling axis is required for pancreatic cancer metastasis to the liver. International journal of biological sciences, 21(15), 6907.

Cantarero L, et al. (2024) Abnormal redox balance at membrane contact sites causes axonopathy in GDAP1-related Charcot-Marie-Tooth disease. Research square.

Kim J, et al. (2024) Transcriptional Profiling Underscores the Role of Preprocurement Allograft Metabolism and Innate Immune Status on Outcomes in Human Liver

Transplantation. Annals of surgery open : perspectives of surgical history, education, and clinical approaches, 5(2), e444.

Slick RA, et al. (2024) High mobility group box??1 (HMGB1) is a potential disease biomarker in cell and mouse models of Duchenne muscular dystrophy. Biology open, 13(9).

Ergun P, et al. (2024) Global Transcriptomic Analysis of Topical Sodium Alginate Protection against Peptic Damage in an In Vitro Model of Treatment-Resistant Gastroesophageal Reflux Disease. International journal of molecular sciences, 25(19).

Pollin G, et al. (2024) EHMT2 Inactivation in Pancreatic Epithelial Cells Shapes the Transcriptional Landscape and Inflammation Response of the Whole Pancreas. bioRxiv : the preprint server for biology.

Pollin G, et al. (2024) Ehmt2 inactivation in pancreatic epithelial cells shapes the transcriptional landscape and inflammation response of the whole pancreas. Frontiers in genetics, 15, 1412767.

Ratnasinghe BD, et al. (2023) Beyond structural bioinformatics for genomics with dynamics characterization of an expanded KRAS mutational landscape. Computational and structural biotechnology journal, 21, 4790.

Ratnasinghe BD, et al. (2023) Beyond Structural Bioinformatics for Genomics with Dynamics Characterization of an Expanded KRAS Mutational Landscape. bioRxiv : the preprint server for biology.