Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility

RRID:SCR_022606
Type: Tool

Proper Citation

Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility (RRID:SCR_022606)

Resource Information

URL: https://www.fredhutch.org/en/research/shared-resources/core-facilities/genomics-bioinformatics.html

Proper Citation: Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility (RRID:SCR_022606)

Description: Provides set of services that encompass experimental design, data generation and data interpretation. Expert genomics and bioinformatics teams are available to consult and collaborate at every step of process and work closely together to develop optimized experimental strategies to ensure that appropriate technology and data analysis tools are used to address each unique scientific question.

Synonyms: Fred Hutchinson Cancer Center Genomics and Bioinformatics Shared Resource Core

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

Keywords: experimental design, data generation and data interpretation, genomics and bioinformatics, ABRF, USEDit, NACCSR

Availability: Open

Resource Name: Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility

Resource ID: SCR_022606

Alternate IDs: ABRF_1540

Alternate URLs: https://coremarketplace.org/RRID:SCR_022606/?citation=1

Record Creation Time: 20220802T050144+0000

Record Last Update: 20260905T133427+0000

Ratings and Alerts

No rating or validation information has been found for Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility.

No alerts have been found for Fred Hutchinson Cancer Center Genomics and Bioinformatics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 111 mentions in open access literature.

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

Ahn JJ, et al. (2026) Influenza hemagglutinin subtypes have different sequence constraints despite sharing extremely similar structures. Virus evolution, 12(1), veag018.

Hamm DC, et al. (2026) KLF18 is a necessary component of the DUX4-initiated transcriptional network and a candidate locus for phenotypic diversity. Genes & development, 40(11-12), 873.

Murray J, et al. (2026) Engraftment of gene-edited hematopoietic stem cells after antibody-drug conjugate conditioning in nonhuman primates. Blood advances, 10(4), 1094.

Ahn JJ, et al. (2026) Influenza hemagglutinin subtypes have different sequence constraints despite sharing extremely similar structures. bioRxiv : the preprint server for biology.

Larsen BB, et al. (2026) Functional and antigenic constraints on the Nipah virus fusion protein. bioRxiv : the preprint server for biology.

Patton RD, et al. (2026) Deep learning-based non-invasive profiling of tumor transcriptomes from cell-free DNA for precision oncology. bioRxiv : the preprint server for biology.

Chhan CB, et al. (2026) Transgenic mouse-derived human monoclonal antibodies targeting EBV gp350 and gp42 provide basis for therapeutic development. Cell reports. Medicine, 7(2), 102618.

Harari S, et al. (2026) Mutations to the HCoV-229E spike have counterbalancing effects on serum antibody neutralization and receptor binding. bioRxiv : the preprint server for

biology.

Kelly KP, et al. (2026) Atg8 orchestrates stress-responsive chromatin programs across immunity and metabolism. bioRxiv : the preprint server for biology.

Kikawa C, et al. (2026) Near real-time data on the human neutralizing antibody landscape to influenza virus as of early 2026 to inform vaccine-strain selection. bioRxiv : the preprint server for biology.

Hagen MW, et al. (2026) The bone marrow niche and hematopoietic system are distinctly remodeled by CD45-targeted astatine-211 radioimmunotherapy. Blood advances, 10(7), 2452.

Yu TC, et al. (2026) Pleiotropic mutational effects on function and stability constrain the antigenic evolution of influenza haemagglutinin. Nature ecology & evolution, 10(3), 452.

Zhang S, et al. (2026) A CD8?? co-receptor modified to contain an intracellular CD28 signaling tail enhances TCR-engineered T cell function independent of solid-tumor-associated co-stimulatory ligands. Nature communications, 17(1), 753.

Kikawa C, et al. (2026) High-throughput neutralization measurements correlate strongly with evolutionary success of human influenza strains. eLife, 14.

Loes AN, et al. (2026) Strain-specific differences in the response to egg-derived versus recombinant protein influenza vaccines. bioRxiv : the preprint server for biology.

Liu Y, et al. (2026) Therapeutic scheduling of WEE1 inhibition preserves T cell function and promotes immune control of HPV+ tumors. bioRxiv : the preprint server for biology.

Loes AN, et al. (2026) Strain-specific differences in the response to egg-derived versus recombinant protein influenza vaccines. Journal of virology, 100(6), e0031726.

Romero EV, et al. (2026) Recurrent mutations drive rapid HIV escape from two broadly neutralizing antibodies in vivo. Proceedings of the National Academy of Sciences of the United States of America, 123(16), e2524021123.

Avanessian SC, et al. (2026) IL2/IL15 Signaling Induces NK Cell Production of FLT3LG, Augmenting Anti-PD-1 Immunotherapy. Cancer immunology research, 14(1), 122.

Loroña NC, et al. (2026) Site- and age-dependent associations between Fusobacterium nucleatum and colorectal cancer mortality. Cancer, 132(12), e70484.