Resource Summary Report

Generated by NIF on Apr 20, 2025

GenomeStudio

RRID:SCR_010973
Type: Tool

Proper Citation

GenomeStudio (RRID:SCR_010973)

Resource Information

URL: http://www.illumina.com/software/genomestudio_software.ilmn

Proper Citation: GenomeStudio (RRID:SCR_010973)

Description: Visualize and analyze data generated by all of Illumina''s platforms.

Abbreviations: GenomeStudio

Resource Type: software resource

Funding:

Resource Name: GenomeStudio

Resource ID: SCR_010973

Alternate IDs: OMICS_00854

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014517+0000

Ratings and Alerts

No rating or validation information has been found for GenomeStudio.

No alerts have been found for GenomeStudio.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2780 mentions in open access literature.

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

Shi Q, et al. (2025) Correlation analysis of key genes and immune infiltration in visceral adipose tissue and subcutaneous adipose tissue of patients with type 2 diabetes in women. Adipocyte, 14(1), 2442419.

King SE, et al. (2025) Prenatal maternal stress in rats alters the epigenetic and transcriptomic landscape of the maternal-fetal interface across four generations. Communications biology, 8(1), 38.

Huang Y, et al. (2025) Genetic factors shaping the plasma lipidome and the relations to cardiometabolic risk in children and adolescents. EBioMedicine, 112, 105537.

Stevens H, et al. (2025) TAS1R2 rs35874116 Associations with Taste, Diet, and Health in an Italian Population. Nutrients, 17(2).

Mangini G, et al. (2025) Genome-wide association study identifies QTL and candidate genes for grain size and weight in a Triticum turgidum collection. The plant genome, 18(1), e20562.

Gianno F, et al. (2025) MicroRNAs Expression Profile in MN1-Altered Astroblastoma. Biomedicines, 13(1).

Sekita T, et al. (2025) Early separation and parallel clonal selection of dedifferentiated and well-differentiated components in dedifferentiated liposarcoma. Neoplasia (New York, N.Y.), 59, 101074.

Crine V, et al. (2025) Associations between inflammation and striatal dopamine D2-receptor availability in aging. Journal of neuroinflammation, 22(1), 24.

Stroupe S, et al. (2025) Genetic reassessment of population subdivision in Yellowstone National Park bison. The Journal of heredity, 116(1), 1.

Wang X, et al. (2025) Construction of functional tissue-engineered microvasculatures using circulating fibrocytes as mural cells. Journal of tissue engineering, 16, 20417314251315523.

Silva ACD, et al. (2025) Genetic diversity, population structure in a historical panel of Brazilian soybean cultivars. PloS one, 20(1), e0313151.

Kessler AL, et al. (2025) HLA I immunopeptidome of synthetic long peptide pulsed human dendritic cells for therapeutic vaccine design. NPJ vaccines, 10(1), 12.

Chaubal R, et al. (2024) Surgical Tumor Resection Deregulates Hallmarks of Cancer in

Resected Tissue and the Surrounding Microenvironment. Molecular cancer research : MCR, 22(6), 572.

Nevado JB, et al. (2024) Transcriptional profiles associated with coronary artery disease in type 2 diabetes mellitus. Frontiers in endocrinology, 15, 1323168.

Venu V, et al. (2024) Fine-scale contemporary recombination variation and its fitness consequences in adaptively diverging stickleback fish. Nature ecology & evolution, 8(7), 1337.

Bandres-Ciga S, et al. (2024) NeuroBooster Array: A Genome-Wide Genotyping Platform to Study Neurological Disorders Across Diverse Populations. Movement disorders : official journal of the Movement Disorder Society.

Knauer C, et al. (2024) Preclinical evaluation of CRISPR-based therapies for Noonan syndrome caused by deep-intronic LZTR1 variants. Molecular therapy. Nucleic acids, 35(1), 102123.

Jiang F, et al. (2024) A landscape of gene expression regulation for synovium in arthritis. Nature communications, 15(1), 1409.

Fan S, et al. (2024) Mapping QTLs for blight resistance and morpho-phenological traits in inter-species hybrid families of chestnut (Castanea spp.). Frontiers in plant science, 15, 1365951.

Wei H, et al. (2024) DNA Hyper-methylation Associated With Schizophrenia May Lead to Increased Levels of Autoantibodies. Schizophrenia bulletin open, 5(1), sgac047.