Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 26, 2025

4D Genome

RRID:SCR_017489
Type: Tool

Proper Citation

4D Genome (RRID:SCR_017489)

Resource Information

URL: https://4dgenome.research.chop.edu/

Proper Citation: 4D Genome (RRID:SCR_017489)

Description: Repository for chromatin interaction data. Records can be queried by genomic regions, gene names, organism, and detection technology. Database is continuously updated by curators. Contributions from scientific community.

Resource Type: service resource, storage service resource, data or information resource, data repository, database

Keywords: Repository, chromatic, interaction, data, genomic, region, gene, name, detection, technology, curated

Funding:

Availability: Free, Available for download, Freely available

Resource Name: 4D Genome

Resource ID: SCR_017489

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250426T060629+0000

Ratings and Alerts

No rating or validation information has been found for 4D Genome.

No alerts have been found for 4D Genome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Ankill J, et al. (2024) Integrative pan-cancer analysis reveals a common architecture of dysregulated transcriptional networks characterized by loss of enhancer methylation. PLoS computational biology, 20(11), e1012565.

Chen Z, et al. (2024) Fine-mapping analysis including over 254,000 East Asian and European descendants identifies 136 putative colorectal cancer susceptibility genes. Nature communications, 15(1), 3557.

Yang Q, et al. (2021) Ultrasound May Suppress Tumor Growth, Inhibit Inflammation, and Establish Tolerogenesis by Remodeling Innatome via Pathways of ROS, Immune Checkpoints, Cytokines, and Trained Immunity/Tolerance. Journal of immunology research, 2021, 6664453.

Kikutake C, et al. (2021) Pan-cancer analysis of non-coding recurrent mutations and their possible involvement in cancer pathogenesis. NAR cancer, 3(1), zcab008.

Nami B, et al. (2021) Epigenetic Silencing of HER2 Expression during Epithelial-Mesenchymal Transition Leads to Trastuzumab Resistance in Breast Cancer. Life (Basel, Switzerland), 11(9).

Chen YX, et al. (2020) An integrative multi-omics network-based approach identifies key regulators for breast cancer. Computational and structural biotechnology journal, 18, 2826.

Xu S, et al. (2020) regSNPs-ASB: A Computational Framework for Identifying Allele-Specific Transcription Factor Binding From ATAC-seq Data. Frontiers in bioengineering and biotechnology, 8, 886.

Lai B, et al. (2019) Twenty Novel Disease Group-Specific and 12 New Shared Macrophage Pathways in Eight Groups of 34 Diseases Including 24 Inflammatory Organ Diseases and 10 Types of Tumors. Frontiers in immunology, 10, 2612.

Chen Z, et al. (2019) Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers. American journal of human

genetics, 105(3), 477.