

# Resource Summary Report

Generated by [Kravitz](#) on Sep 15, 2026

## 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:** data or information resource, data repository, database, service resource, storage service resource

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

**Availability:** Free, Available for download, Freely available

**Resource Name:** 4D Genome

**Resource ID:** SCR\_017489

**Alternate IDs:** r3d100012282

**Alternate URLs:** <https://doi.org/10.17616/R3SH37>

**Record Creation Time:** 20220129T080335+0000

**Record Last Update:** 20260912T195853+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 11 mentions in open access literature.

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

Xu S, et al. (2025) Artificial intelligence algorithm for preoperative prediction of FIGO stage in ovarian cancer based on clinical features integrated 18F-FDG PET/CT metabolic and radiomics features. *Journal of cancer research and clinical oncology*, 151(2), 87.

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.

Liu Q, et al. (2019) hicGAN infers super resolution Hi-C data with generative adversarial networks. *Bioinformatics (Oxford, England)*, 35(14), i99.

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.