Resource Summary Report

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3D Genome

RRID:SCR_017525
Type: Tool

Proper Citation

3D Genome (RRID:SCR_017525)

Resource Information

URL: http://promoter.bx.psu.edu/hi-c/

Proper Citation: 3D Genome (RRID:SCR_017525)

Description: Genome Browser for study of 3D genome organization and gene regulation and data visualization. Used to visualizing chromatin interaction data, browse other omics data such as ChIP-Seq or RNA-Seq for same genomic region, and gain complete view of both regulatory landscape and 3D genome structure for any given gene.

Resource Type: service resource

Keywords: 3D, genome, organization, gene, regulation, data, visualization, chromatin, interaction, omic, ChIPseq, RNAseq, regulatory, structure

Funding:

Availability: Free, Freely available

Resource Name: 3D Genome

Resource ID: SCR_017525

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250420T014839+0000

Ratings and Alerts

No rating or validation information has been found for 3D Genome.

No alerts have been found for 3D Genome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Li Z, et al. (2022) ESR1 mutant breast cancers show elevated basal cytokeratins and immune activation. Nature communications, 13(1), 2011.

Choi J, et al. (2021) Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. eLife, 10.

Su G, et al. (2021) CTCF-binding element regulates ESC differentiation via orchestrating long-range chromatin interaction between enhancers and HoxA. The Journal of biological chemistry, 296, 100413.

Li F, et al. (2021) Interplay of m6 A and histone modifications contributes to temozolomide resistance in glioblastoma. Clinical and translational medicine, 11(9), e553.

Ray D, et al. (2021) Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. PLoS genetics, 17(7), e1009584.

Errichiello E, et al. (2021) RB1CC1 duplication and aberrant overexpression in a patient with schizophrenia: further phenotype delineation and proposal of a pathogenetic mechanism. Molecular genetics & genomic medicine, 9(1), e1561.

Jain Y, et al. (2021) Convergent evolution of a genomic rearrangement may explain cancer resistance in hystrico- and sciuromorpha rodents. NPJ aging and mechanisms of disease, 7(1), 20.

Su G, et al. (2021) Enhancer architecture-dependent multilayered transcriptional regulation orchestrates RA signaling-induced early lineage differentiation of ESCs. Nucleic acids research, 49(20), 11575.

Si N, et al. (2020) Duplications involving the long range HMX1 enhancer are associated with human isolated bilateral concha-type microtia. Journal of translational medicine, 18(1), 244.

Seo W, et al. (2020) Runx-mediated regulation of CCL5 via antagonizing two enhancers influences immune cell function and anti-tumor immunity. Nature communications, 11(1),

1562.

Choi J, et al. (2020) Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature communications, 11(1), 2718.

Zhou S, et al. (2020) Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. Nature communications, 11(1), 441.

Jiang K, et al. (2020) Broadening our understanding of the genetics of Juvenile Idiopathic Arthritis (JIA): Interrogation of three dimensional chromatin structures and genetic regulatory elements within JIA-associated risk loci. PloS one, 15(7), e0235857.

Tang C, et al. (2020) DC-SCRIPT affects mammary organoids branching morphogenesis by modulating the FGFR1-pERK signaling axis. Developmental biology, 463(2), 101.

Muranen TA, et al. (2020) Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. NPJ breast cancer, 6, 44.

Ainsworth HC, et al. (2020) Intrinsic DNA topology as a prioritization metric in genomic fine-mapping studies. Nucleic acids research, 48(20), 11304.

Laisk T, et al. (2020) The genetic architecture of sporadic and multiple consecutive miscarriage. Nature communications, 11(1), 5980.

Bansal P, et al. (2019) Forged by DXZ4, FIRRE, and ICCE: How Tandem Repeats Shape the Active and Inactive X Chromosome. Frontiers in cell and developmental biology, 7, 328.

Ritter N, et al. (2019) The lncRNA Locus Handsdown Regulates Cardiac Gene Programs and Is Essential for Early Mouse Development. Developmental cell, 50(5), 644.

Huang L, et al. (2019) Genetic factors define CPO and CLO subtypes of nonsyndromicorofacial cleft. PLoS genetics, 15(10), e1008357.