

Integrated database for epigenomics

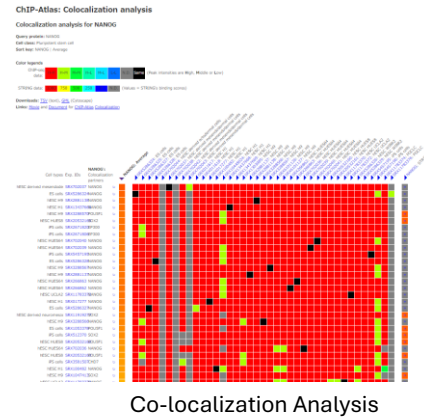
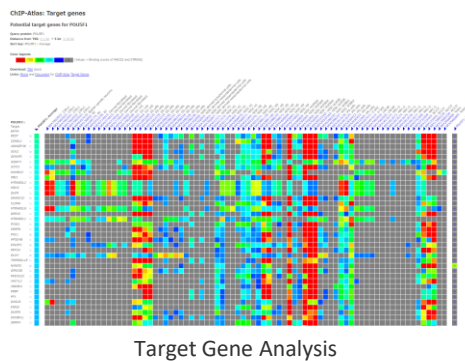
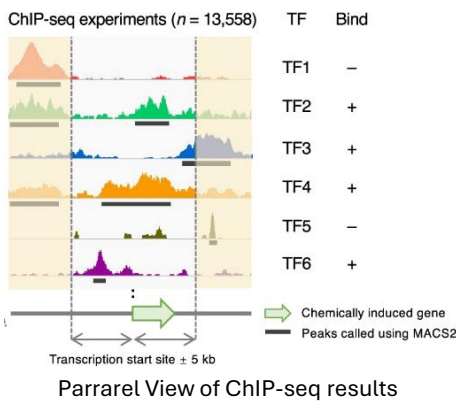
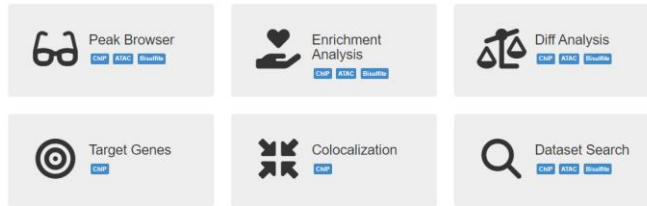
ChIP-Atlas 3.0

<https://chip-atlas.org/>



ChIP-Atlas

A data-mining suite for exploring epigenomic landscapes by fully integrating 425,000 ChIP-seq, ATAC-seq and Bisulfite-seq experiments.



ChIP-Atlas is an integrated database of epigenomics. It contains genome-protein interactions (ChIP-seq), open chromatin information (DNase-seq, ATAC-seq), and methylome information (Bisulfite-seq) for human and five model organisms (mouse, rat, Drosophila, nematode, and budding yeast).

In ChIP-Atlas 3.0 which was released in October 2023, it integrates annotated information such as the three-dimensional structure of the genome (Hi-C) and genomic variation for disease susceptibility, and adds Diff Analysis, a comparative analysis tool that detects changes in epigenomic states related to gene expression regulation.

In the seven years since its release in 2018, ChIP-Atlas has been cited in more than 1,000 papers, primarily in the life and medical sciences. ChIP-Atlas Version 3.0 has become the infrastructure for epigenomic information with the largest number of data in the world and equipped with advanced analysis capabilities. It is expected to further contribute to the elucidation of pathogenic mechanisms of genetic diseases and drug action mechanisms, as well as to the efficiency of research on cellular differentiation and transformation.

<Data in ChIP-Atlas Data> (May 2025)

ChIP-seq (genome-protein interactions)	262,635 entries
ATAC-seq (open chromatin information)	97,673 entries
DNase-seq (open chromatin information)	6,495 entries
Bisulfite-seq (methylome information)	65,516 entries
Total	432,319 entries

ChIP-Atlas is developed by Prof. Shinya Oki at Kumamoto University, as a part of JST Database Integration Coordination Program (DICP), "Construction of an integrative data platform for transcriptional regulations (PI: Takeya Kasukawa, Team Leader, RIKEN)".

Examples of studies using ChIP-Atlas

ChIP-Atlas 3.0

<https://chip-atlas.org/>



ChIP-Atlas is used by many researchers, and has been cited in many papers.

<Number of papers published in major scientific journals (since 2022)>

- 5 papers in Nature, and its sister journals (5 papers in Nat Genet, 3 papers in Nat Aging, 18 papers in Nat Commun, and Nat Biotechnol, Nat Immunol, Nat Methods, Nat Neurosci etc.)
- 1 paper in Science, and its sister journals (4 papers in Sci Adv, 3 papers in Sci Signal, etc.)
- Cell sister journals (1 paper in Cancer Cell, 3 papers in Dev Cell, etc.)

<Examples of papers using ChIP-Atlas>

1. Rader, AE., et al. Combined inactivation of RB and Hippo converts differentiating Drosophila photoreceptors into eye progenitor cells through derepression of homothorax. *Dev Cell*, 2023. (DOI: 10.1016/J.DEVCEL.2023.09.003)
Using ChIP-Atlas Enrichment Analysis tool, the authors searched for transcription factors that bind around the transcription start sites of important genes expressed in males in sex determination in *C. elegans*, and found that these transcription factors are also related to the lifespan of males.
2. Zhang, T., et al. ADAR1 masks the cancer immunotherapeutic promise of ZBP1-driven necroptosis. *Nature*, 2022. (DOI: 10.1038/S41586-022-04753-7)
ChIP-Atlas data were used to identify genomic regions where the transcription factor ZBP1 binds. This revealed that a small molecular compound (CBL0137) that induces Z-DNA formation activates ZBP1, resulting in necroptosis.
3. Mannens, CCA, et al. Chromatin accessibility during human first-trimester neurodevelopment. *Nature*, 2024. (DOI: 10.1038/S41586-024-07234-1)
ChIP-seq data from plasma B cells in ChIP-Atlas reveal Purkinje cell gene regulatory network.
4. Oguchi, A., et al. An atlas of transcribed enhancers across helper T cell diversity for decoding human diseases. *Science*, 2024. (DOI: 10.1126/SCIENCE.ADD8394)
Using Enrichment Analysis tool of ChIP-Atlas, transcription factors and histone modification states bound to enhancer regions involved in helper T cell diversity were identified.
5. Deng, Q., et al. SMARCA4 is a haploinsufficient B cell lymphoma tumor suppressor that fine-tunes centrocyte cell fate decisions. *Cancer Cell*, 2024. (DOI: 10.1016/J.CCELL.2024.02.011)
Using ChIP-Atlas, the authors elucidated that chromatin remodeling by SMARCA4 affects the binding sites of transcription factors such as PU.1 and IRF, and that partial loss of function of SMARCA4 is associated with epigenetic changes and tumorigenesis in B cells.
6. Kamimoto, K., et al. Dissecting cell identity via network inference and in silico gene perturbation. *Nature*, 2023. (DOI: 10.1038/S41586-022-05688-9)
The 1,298 ChIP-seq datasets in ChIP-Atlas were integrated to construct a comprehensive gene regulatory network (GRN) for 80 regulatory factors across five different tissues. This data was used as a benchmark to evaluate the performance of different GRN estimation algorithms and to validate the accuracy of GRN modeling with CellOracle.
7. Zhang, W., et al. FOXP3 recognizes microsatellites and bridges DNA through multimerization. *Nature*, 2023. (DOI: 10.1038/S41586-023-06793-Z)
Peak call data of FOXP family members were downloaded from ChIP-Atlas and motif analysis revealed that microsatellite repeats, especially TnG repeats, are recognized by FOXP3. This reveals a mechanism for transcriptional regulation of immune function by regulatory T cells.
8. Badia-i-Mompel, P., et al. Gene regulatory network inference in the era of single-cell multi-omics. *Nat Rev Genet*, 2023. (DOI: 10.1038/S41576-023-00618-5)
In a review of gene regulatory network (GRN) estimation, ChIP-Atlas was introduced as a tool to construct GRNs based on transcription factor binding site information.
9. Frenkel, M., et al. Large-scale discovery of chromatin dysregulation induced by oncofusions and other protein-coding variants. *Nat Biotechnol*, 2024. (DOI: 10.1038/S41587-024-02347-4)
The open chromatin regions induced by cancer-inducing fusion proteins were analyzed to determine the extent to which they coincide with the ATAC peaks of various cell types registered in ChIP-Atlas, with a particularly strong correlation with rhabdomyosarcoma.
10. Maity, AK., et al. Inference of age-associated transcription factor regulatory activity changes in single cells. *Nat Aging*, 2022. (DOI: 10.1038/s43587-022-00233-9)
This paper constructed cell type-specific transcription factor regulons from mouse scRNA-seq data and estimated their regulatory activity, and validated the transcription factor regulons using ChIP-Atlas.