



## Johns Hopkins Technology Transfer

---

### CisGenome: Software for Genome-wide Chromatin Immunoprecipitation Data Analysis

**ROI Number**

C10237

**Contact**

Andrea Doering, PhD, MBA  
Portfolio Director  
410-516-4565  
adoerin1@jhmi.edu

**Inventors**

Hongkai Ji

**Field**

Research tools

**Patent Status**

Copyright

**Keywords**

CiGenome Browser, Genome analysis, ChIP-seq Analysis, software

**Technology**

Chromatin immunoprecipitation followed by genome tiling array analysis (ChIP-chip) or by massively parallel sequencing (ChIP-seq) is an extremely powerful tool to understand gene regulatory programs in development and disease. CisGenome is a software system for analyzing genome-wide chromatin immunoprecipitation (ChIP) data. Developed by researchers at Johns Hopkins University and Stanford University, CisGenome software is designed to meet all basic needs of ChIP data analyses, including data visualization, data normalization, peak detection, false discovery rate (FDR) computation, gene-peak association, and sequence and motif analysis. CisGenome is a standalone system that bench biologists can use to analyze their own data locally on personal computers, and it has a modular design that allows computational biologists to build large batch jobs for customized analyses on computer servers. This allows researchers to decipher gene regulatory networks by synthesizing multiple sources of information including gene expression, protein-DNA interactions, genome sequences, transcription factor binding motifs and existing knowledge on signaling and metabolic pathways.

**Commercial Use**

ChIP-chip and ChIP-seq Analysis, Genome Information Retrieval

**References**

Ji H et al. (2008) An integrated software system for analyzing ChIP-chip and ChIP-seq data. Nat. Biotechnol. 26(11):1293-300.

Available for download at [www.biostat.jhsph.edu/~hji/cisgenome/](http://www.biostat.jhsph.edu/~hji/cisgenome/)