

# Resource Summary Report

Generated by [T1D](#) on Aug 1, 2026

## GEM

RRID:SCR\_005339

Type: Tool

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### Proper Citation

GEM (RRID:SCR\_005339)

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### Resource Information

**URL:** <http://cgs.csail.mit.edu/gem/>

**Proper Citation:** GEM (RRID:SCR\_005339)

**Description:** Java software for studying protein-DNA interaction using ChIP-seq / ChIP-exo data. It links binding event discovery and motif discovery with positional priors in the context of a generative probabilistic model of ChIP data and genome sequence, resolves ChIP data into explanatory motifs and binding events at unsurpassed spatial resolution. GEM reciprocally improves motif discovery using binding event locations, and binding event predictions using discovered motifs.

**Abbreviations:** GEM

**Synonyms:** Genome wide Event finding and Motif discovery, GEM: ChIP-Seq and ChIP-exo analysis tool

**Resource Type:** software resource

**Defining Citation:** [PMID:22912568](#)

**Keywords:** chip-seq, chip-exo, genome, event, motif, protein-dna interaction, java, transcription factor, genome sequence, motif discovery, binding event calling

**Resource Name:** GEM

**Resource ID:** SCR\_005339

**Alternate IDs:** OMICS\_00441

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260801T190258+0000

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### Ratings and Alerts

No rating or validation information has been found for GEM.

No alerts have been found for GEM.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 12 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Gonzalez-Teran B, et al. (2022) Transcription factor protein interactomes reveal genetic determinants in heart disease. *Cell*, 185(5), 794.

Landeras-Bueno S, et al. (2021) Cellular mRNA triggers structural transformation of Ebola virus matrix protein VP40 to its essential regulatory form. *Cell reports*, 35(2), 108986.

Kluge M, et al. (2020) Watchdog 2.0: New developments for reusability, reproducibility, and workflow execution. *GigaScience*, 9(6).

Morgulis A, et al. (2020) SRPRISM (Single Read Paired Read Indel Substitution Minimizer): an efficient aligner for assemblies with explicit guarantees. *GigaScience*, 9(4).

Kurylo CM, et al. (2018) Endogenous rRNA Sequence Variation Can Regulate Stress Response Gene Expression and Phenotype. *Cell reports*, 25(1), 236.

Iwata S, et al. (2017) The Transcription Factor T-bet Limits Amplification of Type I IFN Transcriptome and Circuitry in T Helper 1 Cells. *Immunity*, 46(6), 983.

Mak SST, et al. (2017) Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. *GigaScience*, 6(8), 1.

He BZ, et al. (2017) Evolution of reduced co-activator dependence led to target expansion of a starvation response pathway. *eLife*, 6.

Gould GM, et al. (2016) Identification of new branch points and unconventional introns in *Saccharomyces cerevisiae*. *RNA (New York, N.Y.)*, 22(10), 1522.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. *Biology direct*, 9, 4.

Chung D, et al. (2013) dPeak: high resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. *PLoS computational biology*, 9(10), e1003246.

Guo Y, et al. (2012) High resolution genome wide binding event finding and motif discovery reveals transcription factor spatial binding constraints. *PLoS computational biology*, 8(8), e1002638.