

Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

Peakzilla

RRID:SCR_007471

Type: Tool

Proper Citation

Peakzilla (RRID:SCR_007471)

Resource Information

URL: <https://github.com/steinmann/peakzilla>

Proper Citation: Peakzilla (RRID:SCR_007471)

Description: An algorithm to identify transcription factor binding sites from ChIP-seq data.

Abbreviations: Peakzilla

Resource Type: software resource

Keywords: bio.tools

Resource Name: Peakzilla

Resource ID: SCR_007471

Alternate IDs: biotools:peakzilla, OMICS_00454

Alternate URLs: <https://bio.tools/peakzilla>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260829T182253+0000

Ratings and Alerts

No rating or validation information has been found for Peakzilla.

No alerts have been found for Peakzilla.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Kamat A, et al. (2025) Variability in intrinsic promoter strength underlies the temporal hierarchy of the *Caulobacter* SOS response induction. *PLoS biology*, 23(12), e3003557.

Dahlet T, et al. (2021) E2F6 initiates stable epigenetic silencing of germline genes during embryonic development. *Nature communications*, 12(1), 3582.

Sharma V, et al. (2020) Comparative analysis of ChIP-exo peak-callers: impact of data quality, read duplication and binding subtypes. *BMC bioinformatics*, 21(1), 65.

Hartl D, et al. (2019) CG dinucleotides enhance promoter activity independent of DNA methylation. *Genome research*, 29(4), 554.

Pinter N, et al. (2019) Signal peptide peptidase activity connects the unfolded protein response to plant defense suppression by *Ustilago maydis*. *PLoS pathogens*, 15(4), e1007734.

Gaiti F, et al. (2017) Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. *eLife*, 6.