Resource Summary Report

Generated by <u>NIF</u> on May 16, 2025

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

Funding:

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: 20250420T014401+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: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.