

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

pyDNase

RRID:SCR_005406

Type: Tool

Proper Citation

pyDNase (RRID:SCR_005406)

Resource Information

URL: <http://pythonhosted.org/pyDNase/>

Proper Citation: pyDNase (RRID:SCR_005406)

Description: A software library for analyzing DNase-seq data.

Abbreviations: pyDNase

Resource Type: software resource

Resource Name: pyDNase

Resource ID: SCR_005406

Alternate IDs: OMICS_00518

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260801T190251+0000

Ratings and Alerts

No rating or validation information has been found for pyDNase.

No alerts have been found for pyDNase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Wang D, et al. (2025) Deciphering the epigenomic regulatory variations reveals function diversity in adipose lineage among different adipose depots of pigs. *Cell & bioscience*, 15(1), 170.

Hu M, et al. (2025) Myogenic enhancer snatching promotes adipogenic differentiation during epigenetic reprogramming mediated by lineage-specific transcription factors. *Cellular and molecular life sciences : CMLS*, 82(1), 412.

Chen XF, et al. (2024) Integrative high-throughput enhancer surveying and functional verification divulges a YY2-condensed regulatory axis conferring risk for osteoporosis. *Cell genomics*, 4(3), 100501.

Pastore SF, et al. (2023) Neuronal transcription of autism gene PTCHD1 is regulated by a conserved downstream enhancer sequence. *Scientific reports*, 13(1), 20391.

Madrigal P, et al. (2023) Epigenetic and transcriptional regulations prime cell fate before division during human pluripotent stem cell differentiation. *Nature communications*, 14(1), 405.

Noonan ML, et al. (2023) Osteocyte EglN1/Phd2 links oxygen sensing and biomineralization via FGF23. *Bone research*, 11(1), 7.

Schleussner N, et al. (2023) Transcriptional reprogramming by mutated IRF4 in lymphoma. *Nature communications*, 14(1), 6947.

Hu M, et al. (2022) Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues. *Genomics*, 114(2), 110276.

Coda DM, et al. (2022) A network of transcription factors governs the dynamics of NODAL/Activin transcriptional responses. *Journal of cell science*, 135(8).

Yadav S, et al. (2022) Lipid exposure activates gene expression changes associated with estrogen receptor negative breast cancer. *NPJ breast cancer*, 8(1), 59.

Sobel J, et al. (2021) Scrt1, a transcriptional regulator of β -cell proliferation identified by differential chromatin accessibility during islet maturation. *Scientific reports*, 11(1), 8800.

Éliás S, et al. (2021) Gene Regulatory Network of Human GM-CSF-Secreting T Helper Cells. *Journal of immunology research*, 2021, 8880585.

King AJ, et al. (2021) Reactivation of a developmentally silenced embryonic globin gene. *Nature communications*, 12(1), 4439.

Huang L, et al. (2021) Profiling of chromatin accessibility identifies transcription factor binding sites across the genome of *Aspergillus* species. *BMC biology*, 19(1), 189.

Morral N, et al. (2021) Aberrant gene expression induced by a high fat diet is linked to H3K9 acetylation in the promoter-proximal region. *Biochimica et biophysica acta. Gene*

regulatory mechanisms, 1864(3), 194691.

Clapes T, et al. (2021) Chemotherapy-induced transposable elements activate MDA5 to enhance haematopoietic regeneration. *Nature cell biology*, 23(7), 704.

Bevington SL, et al. (2021) Stable Epigenetic Programming of Effector and Central Memory CD4 T Cells Occurs Within 7 Days of Antigen Exposure In Vivo. *Frontiers in immunology*, 12, 642807.

Guerrero-Martínez JA, et al. (2020) TGF β promotes widespread enhancer chromatin opening and operates on genomic regulatory domains. *Nature communications*, 11(1), 6196.

Liu J, et al. (2020) Genome-wide studies reveal the essential and opposite roles of ARID1A in controlling human cardiogenesis and neurogenesis from pluripotent stem cells. *Genome biology*, 21(1), 169.

Zhu T, et al. (2020) ATAC-seq with unique molecular identifiers improves quantification and footprinting. *Communications biology*, 3(1), 675.