

Resource Summary Report

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seqMINER

RRID:SCR_013020

Type: Tool

Proper Citation

seqMINER (RRID:SCR_013020)

Resource Information

URL: <http://sourceforge.net/projects/seqminer/>

Proper Citation: seqMINER (RRID:SCR_013020)

Description: Software for a genome wide mapping data interpretation platform for NGS (ChIPSeq).

Abbreviations: seqMINER

Resource Type: software resource

Defining Citation: [PMID:21177645](#)

Keywords: java, bio.tools

Availability: GNU General Public License, v3

Resource Name: seqMINER

Resource ID: SCR_013020

Alternate IDs: biotools:seqminer, OMICS_00460

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260725T190742+0000

Ratings and Alerts

No rating or validation information has been found for seqMINER.

No alerts have been found for seqMINER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 187 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Maestri D, et al. (2025) EBNA leader protein orchestrates chromatin architecture remodeling during Epstein-Barr virus-induced B cell transformation. *Nucleic acids research*, 53(12).

Brulé B, et al. (2025) Accelerated epigenetic aging in Huntington's disease involves polycomb repressive complex 1. *Nature communications*, 16(1), 1550.

Ferrero G, et al. (2025) Nonproteolytic ubiquitination regulates chromatin occupancy by the NCoR/SMRT/HDAC3 corepressor complex in MCF-7 breast cancer cells. *Proceedings of the National Academy of Sciences of the United States of America*, 122(18), e2502805122.

Helleux A, et al. (2025) TFE3 fusions drive oxidative metabolism and ferroptosis resistance in translocation renal cell carcinoma. *EMBO molecular medicine*, 17(5), 1041.

Liakos A, et al. (2025) Cockayne syndrome B protein is implicated in transcription and associated chromatin dynamics in homeostatic and genotoxic conditions. *Aging cell*, 24(1), e14341.

Liu J, et al. (2025) lncRNA-ZFAS1, an Emerging Gate-Keeper in DNA Damage-Dependent Transcriptional Regulation. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(31), e12385.

Cai Q, et al. (2024) LSD1 inhibition circumvents glucocorticoid-induced muscle wasting of male mice. *Nature communications*, 15(1), 3563.

Moreno-Oñate M, et al. (2024) Rewiring of the epigenome and chromatin architecture by exogenously induced retinoic acid signaling during zebrafish embryonic development. *Nucleic acids research*, 52(7), 3682.

Hu M, et al. (2024) PRC1 directs PRC2-H3K27me3 deposition to shield adult spermatogonial stem cells from differentiation. *Nucleic acids research*, 52(5), 2306.

Zhu Y, et al. (2024) CRISPR screening identifies BET and mTOR inhibitor synergy in cholangiocarcinoma through serine glycine one carbon. *JCI insight*, 9(2).

Vladimir de la Rosa J, et al. (2024) Reprogramming of the LXR⁺ Transcriptome Sustains Macrophage Secondary Inflammatory Responses. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(20), e2307201.

Pugacheva EM, et al. (2024) BORIS/CTCF epigenetically reprograms clustered CTCF binding sites into alternative transcriptional start sites. *Genome biology*, 25(1), 40.

Schifferl D, et al. (2023) Genome-wide identification of notochord enhancers comprising the regulatory landscape of the brachyury locus in mouse. *Development (Cambridge, England)*, 150(22).

Wang D, et al. (2023) MOF-mediated histone H4 Lysine 16 acetylation governs mitochondrial and ciliary functions by controlling gene promoters. *Nature communications*, 14(1), 4404.

Kerimov N, et al. (2023) Systematic visualisation of molecular QTLs reveals variant mechanisms at GWAS loci. *bioRxiv : the preprint server for biology*.

Liakos A, et al. (2023) Enhanced frequency of transcription pre-initiation complexes assembly after exposure to UV irradiation results in increased repair activity and reduced probabilities for mutagenesis. *Nucleic acids research*, 51(16), 8575.

Säisä-Borreill S, et al. (2023) General transcription factor TAF4 antagonizes epigenetic silencing by Polycomb to maintain intestine stem cell functions. *Cell death and differentiation*, 30(3), 839.

Kerimov N, et al. (2023) eQTL Catalogue 2023: New datasets, X chromosome QTLs, and improved detection and visualisation of transcript-level QTLs. *PLoS genetics*, 19(9), e1010932.

Osterburg C, et al. (2023) Disease-related p63 DBD mutations impair DNA binding by distinct mechanisms and varying degree. *Cell death & disease*, 14(4), 274.

Offley SR, et al. (2023) A combinatorial approach to uncover an additional Integrator subunit. *Cell reports*, 42(3), 112244.