

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: 20260905T132731+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 190 mentions in open access literature.

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

Hanna R, et al. (2026) BMI1 represses G-quadruplex DNA formation to maintain genomic stability during replication. The Journal of biological chemistry, 302(3), 111172.

Magri MS, et al. (2026) Deep conservation of cis-regulatory elements and chromatin organization in echinoderms uncover ancestral regulatory features of animal genomes. Nature ecology & evolution, 10(2), 355.

Riley DM, et al. (2026) Functional genomics analysis of developing zebrafish and human endoderm reveals highly conserved cis-regulatory modules acting during vertebrate organogenesis. Genome research, 36(4), 695.

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.

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.

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

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

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

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.

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).

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.

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

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.