

Resource Summary Report

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SeqMap

RRID:SCR_005495

Type: Tool

Proper Citation

SeqMap (RRID:SCR_005495)

Resource Information

URL: <http://www-personal.umich.edu/~jianghui/seqmap/>

Proper Citation: SeqMap (RRID:SCR_005495)

Description: A software tool for mapping large amount of oligonucleotide to the genome. It is designed for finding all the places in a genome where an oligonucleotide could potentially come from. SeqMap can efficiently map as many as dozens of millions of short sequences to a genome of several billions of nucleotides. While doing the mapping, several mutations as well as insertions / deletions of the nucleotide bases in the sequences can be tolerated and furthermore detected. Various input and output formats are supported, as well as many command line options for tuning almost every steps in the mapping process. A typical mapping can be done in a few hours on an ordinary PC.

Abbreviations: SeqMap

Synonyms: SeqMap - A Tool For Mapping Millions Of Short Sequences To The Genome

Resource Type: software resource

Defining Citation: [PMID:18697769](#)

Keywords: bio.tools

Availability: Free, Non-commercial, Commercial use requires permission

Resource Name: SeqMap

Resource ID: SCR_005495

Alternate IDs: biotools:seqmap, OMICS_00684

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

Record Creation Time: 20220129T080230+0000

Ratings and Alerts

No rating or validation information has been found for SeqMap.

No alerts have been found for SeqMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Liu Y, et al. (2025) Machine learning combined with multi-omics to identify immune-related LncRNA signature as biomarkers for predicting breast cancer prognosis. Scientific reports, 15(1), 23863.

Rasheed MA, et al. (2025) An ensemble strategy for piRNA identification through hybrid moment-based feature modeling. Scientific reports, 15(1), 30157.

Xu D, et al. (2025) SPDEv3.0: A multidisciplinary integrated data analysis platform. Plant physiology, 199(3).

Yu W, et al. (2025) A novel defined risk signature of ferroptosis-related lncRNAs for predicting prognosis, immune infiltration, and chemotherapy response in multiple myeloma. Discover oncology, 16(1), 160.

Huang K, et al. (2025) Construction of a lncRNA-miRNA-mRNA Network for Biomarker Identification in Intervertebral Disc Degeneration. Journal of musculoskeletal & neuronal interactions, 25(3), 316.

Jehn J, et al. (2024) miR-Blood - a small RNA atlas of human blood components. Scientific data, 11(1), 164.

Gawlitt S, et al. (2024) Expanding the flexibility of base editing for high-throughput genetic screens in bacteria. Nucleic acids research, 52(7), 4079.

Corell-Sierra J, et al. (2024) SARS-CoV-2 remodels the landscape of small non-coding RNAs with infection time and symptom severity. NPJ systems biology and applications, 10(1), 41.

Cao X, et al. (2024) ncRNADrug: a database for validated and predicted ncRNAs associated with drug resistance and targeted by drugs. Nucleic acids research, 52(D1), D1393.

Amoroso CG, et al. (2024) SiMul-db: a database of single and multi-target Cas9 guides for hazelnut editing. *Frontiers in genetics*, 15, 1467316.

Naeem P, et al. (2023) Anticarcinogenic impact of extracellular vesicles (exosomes) from cord blood stem cells in malignant melanoma: A potential biological treatment. *Journal of cellular and molecular medicine*, 27(2), 222.

Wang H, et al. (2023) An exosome-based specific transcriptomic signature for profiling regulation patterns and modifying tumor immune microenvironment infiltration in triple-negative breast cancer. *Frontiers in immunology*, 14, 1295558.

Jung J, et al. (2023) Design and off-target prediction for antisense oligomers targeting bacterial mRNAs with the MASON web server. *RNA (New York, N.Y.)*, 29(5), 570.

Zhou Q, et al. (2023) Tumor-derived exosomes RNA expression profiling identifies the prognosis, immune characteristics, and treatment in HR+/HER2-breast cancer. *Aging*, 15(16), 8471.

Shi ZL, et al. (2022) Identification of a Prognostic Colorectal Cancer Model Including LncRNA FOXP4-AS1 and LncRNA BBOX1-AS1 Based on Bioinformatics Analysis. *Cancer biotherapy & radiopharmaceuticals*, 37(10), 893.

Su Z, et al. (2022) TRMT6/61A-dependent base methylation of tRNA-derived fragments regulates gene-silencing activity and the unfolded protein response in bladder cancer. *Nature communications*, 13(1), 2165.

Liao Y, et al. (2022) Downregulation of LNMAS orchestrates partial EMT and immune escape from macrophage phagocytosis to promote lymph node metastasis of cervical cancer. *Oncogene*, 41(13), 1931.

H??r J, et al. (2022) INRI-seq enables global cell-free analysis of translation initiation and off-target effects of antisense inhibitors. *Nucleic acids research*, 50(22), e128.

Xu Y, et al. (2022) A novel classification of HCC basing on fatty-acid-associated lncRNA. *Scientific reports*, 12(1), 18863.

Li Y, et al. (2021) Transcriptomics based multi-dimensional characterization and drug screen in esophageal squamous cell carcinoma. *EBioMedicine*, 70, 103510.