Resource Summary Report

Generated by <u>NIF</u> on May 25, 2025

<u>SeqMonk</u>

RRID:SCR_001913 Type: Tool

Proper Citation

SeqMonk (RRID:SCR_001913)

Resource Information

URL: http://www.bioinformatics.babraham.ac.uk/projects/seqmonk/

Proper Citation: SeqMonk (RRID:SCR_001913)

Description: Software tool to visualize and analyse high throughput mapped sequence data.

Abbreviations: SeqMonk

Resource Type: software resource

Keywords: java, high throughput sequencing, mapped, visualization, analysis

Funding:

Availability: GNU General Public License, v3 or later

Resource Name: SeqMonk

Resource ID: SCR_001913

Alternate IDs: OMICS_01936

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250525T030645+0000

Ratings and Alerts

No rating or validation information has been found for SeqMonk.

No alerts have been found for SeqMonk.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 542 mentions in open access literature.

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

Humphries S, et al. (2025) Hypoxia impairs decitabine-induced expression of HLA-DR in acute myeloid leukaemia cell lines. Clinical epigenetics, 17(1), 8.

Xypolita ME, et al. (2025) The zinc-finger transcription factor Blimp1/Prdm1 is required for uterine remodelling and repair in the mouse. Nature communications, 16(1), 1220.

Brewis HT, et al. (2025) Characterizing the regulatory effects of H2A.Z and SWR1-C on gene expression during hydroxyurea exposure in Saccharomyces cerevisiae. PLoS genetics, 21(1), e1011566.

Maezawa S, et al. (2025) Site-specific DNA demethylation during spermatogenesis presets the sites of nucleosome retention in mouse sperm. bioRxiv : the preprint server for biology.

Demond H, et al. (2025) Transcriptome and DNA methylation profiling during the NSN to SN transition in mouse oocytes. BMC molecular and cell biology, 26(1), 2.

Bryan E, et al. (2025) Nucleosomal asymmetry shapes histone mark binding and promotes poising at bivalent domains. Molecular cell, 85(3), 471.

Liu Z, et al. (2024) Epigenomic tomography for probing spatially defined chromatin state in the brain. Cell reports methods, 4(3), 100738.

Barceló IM, et al. (2024) Transferable AmpCs in Klebsiella pneumoniae: interplay with peptidoglycan recycling, mechanisms of hyperproduction, and virulence implications. Antimicrobial agents and chemotherapy, 68(5), e0131523.

Orcel E, et al. (2024) A single workflow for multi-species blood transcriptomics. BMC genomics, 25(1), 282.

Porbahaie M, et al. (2024) Dietary Intervention with Whey Protein Concentrate Does Not Affect Toll-like Receptor Responses and Gene Expression Patterns in Peripheral Blood Mononuclear Cells of Healthy Volunteers. Nutrients, 16(5).

Daly AE, et al. (2024) Selective regulation of a defined subset of inflammatory and immunoregulatory genes by an NF-?B p50-I?B? pathway. Genes & development, 38(11-12),

536.

Conn VM, et al. (2024) Use of synthetic circular RNA spike-ins (SynCRS) for normalization of circular RNA sequencing data. Nature protocols.

Seneviratne JA, et al. (2024) A low-input high resolution sequential chromatin immunoprecipitation method captures genome-wide dynamics of bivalent chromatin. Epigenetics & chromatin, 17(1), 3.

Screen M, et al. (2024) RNA helicase EIF4A1-mediated translation is essential for the GC response. Life science alliance, 7(2).

Badel C, et al. (2024) Chromosome architecture in an archaeal species naturally lacking structural maintenance of chromosomes proteins. Nature microbiology, 9(1), 263.

Luu LDW, et al. (2024) Profiling the colonic mucosal response to fecal microbiota transplantation identifies a role for GBP5 in colitis in humans and mice. Nature communications, 15(1), 2645.

Picco G, et al. (2024) Novel WRN Helicase Inhibitors Selectively Target Microsatellite-Unstable Cancer Cells. Cancer discovery, 14(8), 1457.

Petkau G, et al. (2024) Zfp36l1 establishes the high-affinity CD8 T-cell response by directly linking TCR affinity to cytokine sensing. European journal of immunology, 54(2), e2350700.

Wang C, et al. (2024) Constructing eRNA-mediated gene regulatory networks to explore the genetic basis of muscle and fat-relevant traits in pigs. Genetics, selection, evolution : GSE, 56(1), 28.

Senkpeil L, et al. (2024) Innate immune activation restricts priming and protective efficacy of the radiation-attenuated PfSPZ malaria vaccine. JCI insight, 9(11).