

Resource Summary Report

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SeqMonk

RRID:SCR_001913

Type: Tool

Proper Citation

SeqMonk (RRID:SCR_001913)

Resource Information

URL: <https://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

Availability: Free, Available for download, Freely available

Resource Name: SeqMonk

Resource ID: SCR_001913

Alternate IDs: OMICS_01936

Old URLs: <http://www.bioinformatics.babraham.ac.uk/projects/seqmonk/>

License: GNU General Public License, v3 or later

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260725T190512+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 594 mentions in open access literature.

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

Kuroha K, et al. (2025) Abnormal H3K27me3 underlies degenerative spermatogonial stem cells in cryptorchid testis. *Development (Cambridge, England)*, 152(2).

Joung J, et al. (2025) Cell enlargement modulated by GATA4 and YAP instructs the senescence-associated secretory phenotype. *Nature communications*, 16(1), 1696.

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.

Campos-León K, et al. (2025) Repression of CADM1 transcription by HPV type 18 is mediated by three-dimensional rearrangement of promoter-enhancer interactions. *PLoS pathogens*, 21(1), e1012506.

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

Khader N, et al. (2025) JUND plays a genome-wide role in the quiescent to contractile switch in the pregnant human myometrium. *PLoS genetics*, 21(6), e1011261.

Myers JM, et al. (2025) Discovery of giant viruses as past and present infections of zoosporic fungi. *bioRxiv : the preprint server for biology*.

Robertson K, et al. (2025) Gpr37 modulates the severity of inflammation-induced GI dysmotility by regulating enteric reactive gliosis. *iScience*, 28(7), 112885.

Samo N, et al. (2025) Polycomb repressive complex 2 facilitates the transition from heterotrophy to photoautotrophy during seedling emergence. *The Plant cell*, 37(7).

Krala A, et al. (2025) Phospholipid flippase ATP11A brokers uterine epithelial integrity and function. *Proceedings of the National Academy of Sciences of the United States of America*, 122(17), e2420617122.

Sáenz-Narciso B, et al. (2025) ZFP36-family RNA-binding proteins in regulatory T cells reinforce immune homeostasis. *Nature communications*, 16(1), 4192.

Ingham A, et al. (2025) CRAMP1-dependent histone H1 biogenesis is essential for topoisomerase II inhibitor tolerance. *Molecular cell*, 85(13), 2487.

Joudi AM, et al. (2025) Maintenance DNA methylation is required for induced regulatory T cell reparative function following viral pneumonia. *bioRxiv : the preprint server for biology*.

Kao SH, et al. (2025) The application of cell-free DNA methylation patterns in critical illnesses: A protocol paper. PloS one, 20(5), e0321626.

Gimeno-Valiente F, et al. (2025) DNA methylation cooperates with genomic alterations during non-small cell lung cancer evolution. Nature genetics, 57(9), 2226.

Ramage DE, et al. (2025) Loss-of-function mutations in the dystonia gene THAP1 impair proteasome function by inhibiting PSMB5 expression. Nature communications, 16(1), 1511.

Roson-Calero N, et al. (2025) In vitro potentiation of tetracyclines in *Pseudomonas aeruginosa* by RW01, a new cyclic peptide. Antimicrobial agents and chemotherapy, 69(2), e0145924.

Zakarya R, et al. (2025) Developmental air pollution exposure augments airway hyperreactivity, alters transcriptome, and DNA methylation in female adult progeny. Communications biology, 8(1), 400.

Kugler BA, et al. (2025) Aerobic Capacity and Exercise Mediate Protection Against Hepatic Steatosis via Enhanced Bile Acid Metabolism. Function (Oxford, England), 6(3).

Misel-Wuchter KM, et al. (2025) Developmental epigenetic programming by Tet1/3 determines peripheral CD8 T cell fate. EMBO reports, 26(10), 2494.