

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: 20260801T190154+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 [ASWG](#).

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.

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.

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

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.