

Resource Summary Report

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Segemehl

RRID:SCR_005494

Type: Tool

Proper Citation

Segemehl (RRID:SCR_005494)

Resource Information

URL: <http://www.bioinf.uni-leipzig.de/Software/segemehl/>

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Description: A software to map short sequencer reads to reference genomes. It is able to detect not only mismatches but also insertions and deletions. Furthermore, it is not limited to a specific read length and is able to map primer- or polyadenylation contaminated reads correctly. segemehl implements a matching strategy based on enhanced suffix arrays (ESA). Segemehl now supports the SAM format, reads gzipped queries to save both disk and memory space and allows bisulfite sequencing mapping and split read mapping.

Abbreviations: Segemehl

Synonyms: segemehl - short read mapping with gaps

Resource Type: software resource

Defining Citation: [PMID:24512684](#), [PMID:22581174](#), [PMID:19750212](#), [DOI:10.1371/journal.pcbi.1000502](https://doi.org/10.1371/journal.pcbi.1000502)

Keywords: bio.tools

Availability: Acknowledgement requested, Free, Public

Resource Name: Segemehl

Resource ID: SCR_005494

Alternate IDs: biotools:segemehl, OMICS_00683

Alternate URLs: <https://bio.tools/segemehl>, <https://sources.debian.org/src/segemehl/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260725T190604+0000

Ratings and Alerts

No rating or validation information has been found for Segemehl.

No alerts have been found for Segemehl.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Sailer AL, et al. (2025) Internal in-frame translation generates Cas11b, which is important for effective interference in an archaeal CRISPR-Cas system. *Frontiers in microbiology*, 16, 1543464.

González A, et al. (2025) Multi-omic assessment of mRNA translation dynamics in liver cancer cell lines. *Scientific data*, 12(1), 1520.

Di Cianni N, et al. (2025) Provirus deletion from *Haloferax volcanii* affects motility, stress resistance, and CRISPR RNA expression. *microLife*, 6, uqaf008.

Alcántar-Aguirre FC, et al. (2025) Variable heteroplasmy of the Common 9-bp Deletion in the Human Mitochondrial Genome in Ancient and Present-Day Populations. *microPublication biology*, 2025.

Buratin A, et al. (2023) Systematic benchmarking of statistical methods to assess differential expression of circular RNAs. *Briefings in bioinformatics*, 24(1).

Kolberg T, et al. (2023) Led-Seq: ligation-enhanced double-end sequence-based structure analysis of RNA. *Nucleic acids research*, 51(11), e63.

Feng XY, et al. (2023) New insight into circRNAs: characterization, strategies, and biomedical applications. *Experimental hematology & oncology*, 12(1), 91.

Klassert TE, et al. (2023) Differential Transcriptional Responses of Human Granulocytes to Fungal Infection with *Candida albicans* and *Aspergillus fumigatus*. *Journal of fungi* (Basel, Switzerland), 9(10).

Brümmer A, et al. (2022) Analysis of Eukaryotic lincRNA Sequences Indicates Signatures of Hindered Translation Linked to Selection Pressure. *Molecular biology and evolution*, 39(2).

Mann L, et al. (2022) ECCsplorer: a pipeline to detect extrachromosomal circular DNA (eccDNA) from next-generation sequencing data. *BMC bioinformatics*, 23(1), 40.

Hernandez-Alias X, et al. (2021) Translational adaptation of human viruses to the tissues they infect. *Cell reports*, 34(11), 108872.

Anes J, et al. (2021) Analysis of the Oxidative Stress Regulon Identifies *soxS* as a Genetic Target for Resistance Reversal in Multidrug-Resistant *Klebsiella pneumoniae*. *mBio*, 12(3), e0086721.

Aguilar C, et al. (2021) Reprogramming of microRNA expression via E2F1 downregulation promotes *Salmonella* infection both in infected and bystander cells. *Nature communications*, 12(1), 3392.

Correia Santos S, et al. (2021) MAPS integrates regulation of actin-targeting effector SteC into the virulence control network of *Salmonella* small RNA PinT. *Cell reports*, 34(5), 108722.

Putz EJ, et al. (2021) Distinct transcriptional profiles of *Leptospira borgpetersenii* serovar Hardjo strains JB197 and HB203 cultured at different temperatures. *PLoS neglected tropical diseases*, 15(4), e0009320.

Schäfer RA, et al. (2021) RANue: efficient data analysis for RNA-RNA interactomics. *Nucleic acids research*, 49(10), 5493.

Hoyos M, et al. (2020) Gene autoregulation by 3' UTR-derived bacterial small RNAs. *eLife*, 9.

Hernandez-Alias X, et al. (2020) Translational efficiency across healthy and tumor tissues is proliferation-related. *Molecular systems biology*, 16(3), e9275.

Ankenbauer A, et al. (2020) *Pseudomonas putida* KT2440 is naturally endowed to withstand industrial-scale stress conditions. *Microbial biotechnology*, 13(4), 1145.

Gaffo E, et al. (2019) Circular RNA differential expression in blood cell populations and exploration of circRNA deregulation in pediatric acute lymphoblastic leukemia. *Scientific reports*, 9(1), 14670.