

Resource Summary Report

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SeqPrep

RRID:SCR_013004

Type: Tool

Proper Citation

SeqPrep (RRID:SCR_013004)

Resource Information

URL: <https://github.com/jstjohn/SeqPrep>

Proper Citation: SeqPrep (RRID:SCR_013004)

Description: A program to merge paired end Illumina reads that are overlapping into a single longer read.

Abbreviations: SeqPrep

Synonyms: SeqPrep - Tool for stripping adaptors and/or merging paired reads with overlap into single reads

Resource Type: software resource

Keywords: bio.tools

Resource Name: SeqPrep

Resource ID: SCR_013004

Alternate IDs: biotools:seqprep, OMICS_01092

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260801T190443+0000

Ratings and Alerts

No rating or validation information has been found for SeqPrep.

No alerts have been found for SeqPrep.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 977 mentions in open access literature.

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

Zhang Q, et al. (2026) Integrated analysis of DNA methylation and transcriptome profiles in broiler heart and lung tissues reveals epigenetic regulatory mechanisms underlying ascites syndrome. *Poultry science*, 105(1), 106034.

Fiorica PN, et al. (2025) Germline Pathogenic DROSHA Variants Are Linked to Pineoblastoma and Wilms Tumor Predisposition. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(8), 1491.

Liu Q, et al. (2025) Transcriptomics combined with physiological analysis provides insights into the mechanism of resistance to *Coleosporium bletiae* in *Bletilla striata*. *Frontiers in plant science*, 16, 1604512.

Feng B, et al. (2025) Short-Term Fertilization with the Nitrogen-Fixing Bacterium (NFB) *Kosakonia radicincitans* GXGL-4A Agent Can Modify the Transcriptome Expression Profiling of Cucumber (*Cucumis sativus* L.) Root. *Microorganisms*, 13(3).

Troshin K, et al. (2025) *Pseudomonas* Phage Lydia and the Evolution of the Mesyzhinoviridae Family. *Viruses*, 17(3).

Garc  s-Pastor S, et al. (2025) Wild and domesticated animal abundance is associated with greater late-Holocene alpine plant diversity. *Nature communications*, 16(1), 3924.

Sun H, et al. (2025) Multi-omics reveals the inhibition of asexual reproduction in the jellyfish *Aurelia coerulea* polyp by *Bacillus pacificus*. *Environmental microbiome*, 20(1), 78.

Qiu YS, et al. (2025) Improved gut microbiota by selenium-enriched *Bifidobacterium longum* DD98 alleviates chemotherapy-induced intestinal mucositis via inhibiting the STING pathway. *NPJ science of food*, 9(1), 107.

Liu Q, et al. (2025) Identification and characterization of the TmSnRK2 family proteins related to chicoric acid biosynthesis in *Taraxacum mongolicum*. *BMC genomics*, 26(1), 276.

Liu J, et al. (2025) The splicing auxiliary factor OsU2AF35a enhances thermotolerance via protein separation and promoting proper splicing of OsHSA32 pre-mRNA in rice. *Plant biotechnology journal*, 23(4), 1308.

Shu L, et al. (2025) Comparative Transcriptomic Analysis Reveals New Insights into Spawn Aging in *Agaricus bisporus*: Mitochondrial Dysfunction. *International journal of molecular sciences*, 26(2).

Woo I, et al. (2025) Saturation genome editing of BARD1 resolves VUS and provides insight into BRCA1-BARD1 tumor suppression. medRxiv : the preprint server for health sciences.

Xu Z, et al. (2025) Creeping Stem 1 regulates directional auxin transport for lodging resistance in soybean. Plant biotechnology journal, 23(2), 377.

Zhang N, et al. (2025) Integration of multi-omics data accelerates molecular analysis of common wheat traits. Nature communications, 16(1), 2200.

Lord E, et al. (2025) Genome analyses suggest recent speciation and postglacial isolation in the Norwegian lemming. Proceedings of the National Academy of Sciences of the United States of America, 122(28), e2424333122.

Zhang YH, et al. (2025) Bacterial community composition and function in different habitats in Antarctic Fildes region revealed by high-throughput sequencing. Frontiers in microbiology, 16, 1524681.

Zhao T, et al. (2025) GPAT4 sustains endoplasmic reticulum homeostasis in endocardial cells and safeguards heart development. Nature communications, 16(1), 3345.

Luo M, et al. (2025) Pathogenicity and host-interacting mechanisms of enterogenic Enterobacter cancerogenus in silkworm. Frontiers in microbiology, 16, 1548808.

Guo Y, et al. (2025) Two sexually compatible monokaryons from a heterokaryotic Lentinula edodes strain respond differently to heat stress. Frontiers in microbiology, 16, 1522075.

Ringbauer H, et al. (2025) Punic people were genetically diverse with almost no Levantine ancestors. Nature, 643(8070), 139.