

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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: 20260725T190741+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 [kravitz2](#) .

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.

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).

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.

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 Mesyanzhinoviridae Family. Viruses, 17(3).

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.

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.

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.

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.

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.

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.

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.

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

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.

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

Wu F, et al. (2025) Transcriptional analysis of *Camellia Huana* under low-phosphorus stress. Scientific reports, 15(1), 15796.

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.