# Resource Summary Report

Generated by RRID on Apr 17, 2025

# PEAR

RRID:SCR_003776
Type: Tool

## Proper Citation

PEAR (RRID:SCR_003776)

## Resource Information

**URL:** http://www.exelixis-lab.org/software.html

**Proper Citation:** PEAR (RRID:SCR_003776)

**Description:** Software for an ultrafast, memory-efficient and highly accurate pair-end read merger. It is fully parallelized and can run with as low as just a few kilobytes of memory.

**Abbreviations:** PEAR

**Synonyms:** Pair-end read merger, PEAR: Pair-end read merger

**Resource Type:** software resource

**Defining Citation:** PMID:24142950

**Keywords:** next-generation sequencing, sequence analysis

**Funding:**

**Resource Name:** PEAR

**Resource ID:** SCR_003776

**Alternate IDs:** OMICS_00674

**Record Creation Time:** 20220129T080220+0000

**Record Last Update:** 20250410T065039+0000

## Ratings and Alerts

No rating or validation information has been found for PEAR.

No alerts have been found for PEAR.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 770 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.

Nakano Y, et al. (2025) Genome-wide profiling of tRNA modifications by Induro-tRNAseq reveals coordinated changes. Nature communications, 16(1), 1047.

Becker J, et al. (2025) Molecular age prediction using skull bone samples from individuals with and without signs of decomposition: a multivariate approach combining analysis of posttranslational protein modifications and DNA methylation. International journal of legal medicine, 139(1), 157.

Yu Y, et al. (2025) RPA and Rad27 limit templated and inverted insertions at DNA breaks. Nucleic acids research, 53(1).

Obi LU, et al. (2025) Dynamics and Insights into the Unique Ecological Guild of Fungi in Bacteria-Bioaugmented Anaerobic Digesters. Journal of fungi (Basel, Switzerland), 11(1).

Llanos-Lizcano A, et al. (2025) Intra-individual variability in ancient plasmodium DNA recovery highlights need for enhanced sampling. Scientific reports, 15(1), 757.

Traversa D, et al. (2025) De Novo Assembly of the Polyhydroxybutyrate (PHB) Producer Azohydromonas lata Strain H1 Genome and Genomic Analysis of PHB Production Machinery. Microorganisms, 13(1).

Häkkinen L, et al. (2025) Fungal communities in boreal soils are influenced by land use, agricultural soil management, and depth. FEMS microbiology ecology, 101(2).

Xu Y, et al. (2025) The Dynamics of Symbiodiniaceae and Photosynthetic Bacteria Under High-Temperature Conditions. Microbial ecology, 87(1), 169.

Neha SA, et al. (2025) Impacts of host phylogeny, diet, and geography on the gut microbiome of rodents. PloS one, 20(1), e0316101.

Malas J, et al. (2025) Impact of antibiotics, iron oxide, and sodium sulfate on microbial community composition in laboratory-built municipal solid waste microcosms. PloS one, 20(1), e0318351.

Adams CS, et al. (2025) De novo design of protein minibinder agonists of TLR3. Nature communications, 16(1), 1234.

Zhai Z, et al. (2024) Long-Term Exposure to Polystyrene Microspheres and High-Fat Diet-Induced Obesity in Mice: Evaluating a Role for Microbiota Dysbiosis. Environmental health perspectives, 132(9), 97002.

Li X, et al. (2024) The changes of rhizosphere microbial communities in pepper varieties with different capsaicinoids. Frontiers in microbiology, 15, 1430682.

Castillo-Hair S, et al. (2024) Optimizing 5'UTRs for mRNA-delivered gene editing using deep learning. Nature communications, 15(1), 5284.

Wang J, et al. (2024) Electroacupuncture regulates gut microbiota to reduce depressive-like behavior in rats. Frontiers in microbiology, 15, 1327630.

Hara S, et al. (2024) Does Rhizobial Inoculation Change the Microbial Community in Field Soils? A? ?Comparison with Agricultural Land-use Changes. Microbes and environments, 39(3).

Broman E, et al. (2024) Biotic interactions between benthic infauna and aerobic methanotrophs mediate methane fluxes from coastal sediments. The ISME journal, 18(1).

Romdhane S, et al. (2024) Manipulating the physical distance between cells during soil colonization reveals the importance of biotic interactions in microbial community assembly. Environmental microbiome, 19(1), 18.

Zhang L, et al. (2024) Multi-dimensional niche differentiation of two sympatric breeding secondary cave-nesting birds in Northeast China using DNA metabarcoding. Ecology and evolution, 14(7), e11709.

Yin R, et al. (2024) Gra-CRC-miRTar: The pre-trained nucleotide-to-graph neural networks to identify potential miRNA targets in colorectal cancer. bioRxiv : the preprint server for biology.