

Resource Summary Report

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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

Resource Name: PEAR

Resource ID: SCR_003776

Alternate IDs: OMICS_00674

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260905T132508+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

Usage and Citation Metrics

We found 914 mentions in open access literature.

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

McFarland LN, et al. (2026) The dilution effect of stocking and the loss of wildness among North American mallards. *Current biology : CB*.

Lobel L, et al. (2026) Dietary sulfur amino acids enhance anti-tumor immunity in colon cancer via an NKT cell-XCL1-cDC1 circuit. *Immunity*, 59(6), 1708.

Kim S, et al. (2026) Gut microbiota transfer from autoimmune dry eye mice imprints stereotypic B cell receptor repertoires in the lacrimal gland and induces disease. *Frontiers in immunology*, 17, 1827057.

Buddle S, et al. (2026) Contaminating plasmid sequences and disrupted vector genomes in the liver following adeno-associated virus gene therapy. *Nature medicine*, 32(2), 472.

van de Guchte M, et al. (2026) Improving ulcerative colitis prospects through fecal microbiota transfer: atypical donor microbiota can boost success rate. *Gut microbes*, 18(1), 2609457.

Peng Z, et al. (2026) Association between weaning stress and rumen microbiota in goat kids: evidence from granger causality and randomized controlled trial validation. *Animal bioscience*, 39(1), 250092.

Kato H, et al. (2026) Higher-dimensional ordination analysis teases out impacts of *Bradyrhizobium* bioaugmentation on native soil microbial communities. *Microbiology spectrum*, 14(4), e0288025.

LeBlanc CJ, et al. (2026) Evolutionary turnover of key amino acids explains conservation of function without conservation of sequence in transcriptional activation domains. *PLoS genetics*, 22(3), e1012069.

Santos R, et al. (2026) Multi-Kingdom Fecal Microbiota Alterations in Horses with Severe Equine Asthma. *Microorganisms*, 14(2).

Tao M, et al. (2026) Microbially driven methane and sulfur cycling processes and coupling mechanisms in mangrove sediments. *Environmental microbiome*, 21(1).

Mahajna A, et al. (2026) Linking composition and function: a two-year metatranscriptomic study of microbial adaptation in an industrial wastewater treatment plant. *FEMS microbiology ecology*, 102(7).

Wang X, et al. (2026) Contrasting salinity regimes reshape microbe-DOM coupling and reduce recalcitrant dissolved organic carbon preservation in a salt lake. *The ISME journal*, 20(1).

Wu L, et al. (2026) Comparative Analysis of Lepidopteran Community Structure Using DNA Metabarcoding: Warm-Temperate Forest Versus Grass-Shrub Ecotones in Pangquangou National Nature Reserve. *Ecology and evolution*, 16(6), e73738.

Lin Y, et al. (2026) Butyrylated Starch Attenuates Antibiotic-Exacerbated Allergic Rhinitis by Restoring the Gut Microbiota and Barrier Function in Mice. *Food science & nutrition*, 14(6), e72000.

Zhang H, et al. (2026) Effect of Dietary Postbiotics Derived from *Lactiplantibacillus plantarum* and *Pediococcus lactis* on Lipid Metabolism, Blood Biochemistry, and Fecal Microbiota in Cats: A Pilot Study. *Veterinary sciences*, 13(6).

Aga AM, et al. (2026) Development of an aptamer-based rapid diagnostic assay for *Salmonella* detection using whole-cell SELEX technique. *Microbiology spectrum*, 14(4), e0331925.

Chen J, et al. (2026) De Novo Assembly and Characterization of Venom Gland Transcriptome for *Rhabdophis lateralis*. *Toxins*, 18(4).

Zhao X, et al. (2026) *Leuconostoc mesenteroides* AA001: A High-Efficiency Nitrite Degradar Facilitating Controlled and Safe Traditional Vegetable Fermentation. *Microorganisms*, 14(2).

Thom?? CC, et al. (2026) Distinct steps of nuclear maturation of human pre-60S complexes require the activity of GTPases including GNL3L. *Nucleic acids research*, 54(5).

Cai T, et al. (2026) Intermolecular 3'UTR-3'UTR interactions drive Wnt gene activation through heteromeric protein assembly. *bioRxiv : the preprint server for biology*.