

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## Maq

RRID:SCR\_005485

Type: Tool

### Proper Citation

Maq (RRID:SCR\_005485)

### Resource Information

**URL:** <http://maq.sourceforge.net/>

**Proper Citation:** Maq (RRID:SCR\_005485)

**Description:** A set of programs that map and assemble fixed-length Solexa/SOLiD reads in a fast and accurate way.

**Abbreviations:** Maq

**Synonyms:** mapass2, Mapping and Assembly with Quality, Mapping and Assembly with Qualities, Maq: Mapping and Assembly with Qualities

**Resource Type:** software resource

**Defining Citation:** [DOI:10.1101/gr.078212.108](https://doi.org/10.1101/gr.078212.108)

**Keywords:** command-line, curses/ncurses, opengl, c, c++, perl, bio.tools

**Availability:** GNU General Public License, v2

**Resource Name:** Maq

**Resource ID:** SCR\_005485

**Alternate IDs:** OMICS\_00668, biotools:maq

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

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260821T193744+0000

### Ratings and Alerts

No rating or validation information has been found for Maq.

No alerts have been found for Maq.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 74 mentions in open access literature.

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

Li Q, et al. (2026) Revealing the Potential Associations of Mutation-Related Genes with Lymph Node Metastasis in Gallbladder Cancer Through Transcriptome and Exome Sequencing. *Biomedicines*, 14(5).

Blazyte A, et al. (2026) Fifteen Years of the Genome Analysis Toolkit as the De Facto Standard in Short-Read Variant Calling. *International journal of molecular sciences*, 27(9).

Wu Y, et al. (2025) Integrated metagenomic and metabolomic analysis reveals microbial metabolite interactions involved in the quality formation of *Codonopsis Radix*. *Scientific reports*, 15(1), 40278.

Kalyesubula M, et al. (2025) Stearoyl-CoA desaturase 1 deficiency drives saturated lipid accumulation and increases liver and plasma acylcarnitines. *Journal of lipid research*, 66(6), 100824.

Chen XH, et al. (2025) YTHDF3 recognizes DNA N6-methyladenine and recruits ALKBH1 for 6mA removal from genomic DNA. *The EMBO journal*, 44(17), 4899.

Meng Y, et al. (2025) Research on the mining of candidate genes for pepper fruit color and development of SNP markers based on SLAF-seq technology. *Scientific reports*, 15(1), 11392.

Wang C, et al. (2025) Enrichment of the commensal microbiome in the lower respiratory tract is associated with improved outcomes following lung transplantation. *Chinese medical journal pulmonary and critical care medicine*, 3(4), 308.

Armani-Tourret M, et al. (2024) Selection of epigenetically privileged HIV-1 proviruses during treatment with panobinostat and interferon- $\gamma$ 2a. *Cell*, 187(5), 1238.

Xing Y, et al. (2024) Multi-omics approach to improve patient-tailored therapy using immune checkpoint blockade and cytokine-induced killer cell infusion in an elderly patient with lung cancer: A case report and literature review. *Oncology letters*, 27(5), 203.

Shi M, et al. (2024) Genetic and microenvironmental evolution of colorectal liver metastases under chemotherapy. *Cell reports. Medicine*, 5(12), 101838.

You S, et al. (2024) Thermal acclimation uncovers a simple genetic basis of adaptation to high temperature in a cosmopolitan pest. *iScience*, 27(3), 109242.

Lian X, et al. (2023) Progressive transformation of the HIV-1 reservoir cell profile over two decades of antiviral therapy. *Cell host & microbe*, 31(1), 83.

Liu Z, et al. (2023) Absence of Lugol staining indicates initiation of esophageal squamous cell carcinoma: A combined genomic and epidemiologic study. *Cell reports. Medicine*, 4(9), 101168.

Han S, et al. (2023) Whole-genome sequencing analysis of suicide deaths integrating brain-regulatory eQTLs data to identify risk loci and genes. *Molecular psychiatry*, 28(9), 3909.

Viesná ?, et al. (2022) FastContext: A tool for identification of adapters and other sequence patterns in next generation sequencing (NGS) data. *Vavilovskii zhurnal genetiki i selektsii*, 26(8), 806.

Einkauf KB, et al. (2022) Parallel analysis of transcription, integration, and sequence of single HIV-1 proviruses. *Cell*, 185(2), 266.

Kamata T, et al. (2022) Statins mediate anti- and pro-tumourigenic functions by remodelling the tumour microenvironment. *Disease models & mechanisms*, 15(2).

Nin DS, et al. (2021) GAGE mediates radio resistance in cervical cancers via the regulation of chromatin accessibility. *Cell reports*, 36(9), 109621.

Han X, et al. (2021) Targeted sequencing of NOTCH signaling pathway genes and association analysis of variants correlated with mandibular prognathism. *Head & face medicine*, 17(1), 17.

Rother N, et al. (2020) Hydroxychloroquine Inhibits the Trained Innate Immune Response to Interferons. *Cell reports. Medicine*, 1(9), 100146.