

# Resource Summary Report

Generated by T1D on Aug 5, 2026

## QPALMA

RRID:SCR\_008791

Type: Tool

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### Proper Citation

QPALMA (RRID:SCR\_008791)

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### Resource Information

**URL:** <http://www.raetschlab.org/suppl/qpalma>

**Proper Citation:** QPALMA (RRID:SCR\_008791)

**Description:** An alignment tool targeted to align spliced reads produced by Next Generation sequencing platforms such as Illumina Solexa or 454.

**Abbreviations:** QPALMA

**Synonyms:** QPALMA: Optimal Spliced Alignments of Short Sequence Reads

**Resource Type:** software resource

**Resource Name:** QPALMA

**Resource ID:** SCR\_008791

**Alternate IDs:** OMICS\_01248

**Record Creation Time:** 20220129T080249+0000

**Record Last Update:** 20260801T190353+0000

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### Ratings and Alerts

No rating or validation information has been found for QPALMA.

No alerts have been found for QPALMA.

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### Data and Source Information

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

## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. Genome biology, 22(1), 249.