**Subread**

RRID:SCR_009803  
Type: Tool

**Proper Citation**

Subread (RRID:SCR_009803)

**Resource Information**

**URL:** http://subread.sourceforge.net/

**Proper Citation:** Subread (RRID:SCR_009803)

**Description:** Software package for high-performance read alignment, quantification and mutation discovery. General purpose read aligner which can be used to map both genomic DNA-seq reads and RNA-seq reads. Subread aligner as fast, accurate and scalable read mapping by seed-and-vote. These programs were also implemented in Bioconductor R package Rsubread.

**Resource Type:** Resource, software resource, software application, data processing software

**References:** PMID:23558742

**Keywords:** read alignment, DNA-seq reads mapping, RNA-seq reads mapping, mutation discovery, , bio.tools

**Parent Organization:** University of Melbourne; Victoria; Australia

**Funding Agency:** Australian Government, Australian National Health and Medical Research Council, Victorian State Government Operational Infrastructure Support

**Related resources:** Rsubread

**Availability:** Free, Freely available

**Website Status:** Last checked up
Resource Name: Subread
Resource ID: SCR_009803
Alternate IDs: OMICS_01255, biotools:subread
Alternate URLs: https://bio.tools/subread

Ratings and Alerts
No rating or validation information has been found for Subread.
No alerts have been found for Subread.

Data and Source Information
Source: SciCrunch Registry

Usage and Citation Metrics
We found 395 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://www.fdi-lab.org).

Russell JP, et al. (2021) Pituitary stem cells produce paracrine WNT signals to control the expansion of their descendant progenitor cells. eLife, 10.


Biotechnology reports (Amsterdam, Netherlands), 27, e00521.