**STAR**

**RRID:** SCR_015899  
**Type:** Tool

**Proper Citation**

STAR (RRID:SCR_015899)

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**Resource Information**

**URL:** [https://github.com/alexdobin/STAR](https://github.com/alexdobin/STAR)

**Description:** Software performing alignment of high-throughput RNA-seq data. STAR is based on a previously undescribed RNA-seq alignment algorithm that uses sequential maximum mappable seed search in uncompressed suffix arrays followed by seed clustering and stitching procedure.

**Resource Name:** STAR

**Proper Citation:** STAR (RRID:SCR_015899)

**Resource Type:** Resource, algorithm resource, standalone software, data processing software, software application, sequence analysis software, data analysis software, software resource

**Keywords:** alignment, rna, rna-seq, reference, aligner, algorithm, short read, suffix, array, cluster, stitch

**Resource ID:** SCR_015899

**Funding Agency:** NHGRI

**References:** PMID:23104886

**Availability:** Open source, Free, Available for download, Runs on Linux, Runs on MAC OS

**Website Status:** Last checked up

**Abbreviations:** STAR
Mentions Count: 399

Ratings and Alerts

No rating or validation information has been found for STAR.

No alerts have been found for STAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 399 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](https://scicrunch.org).


Han D, et al. (2019) NEIL1 and NEIL2 DNA glycosylases protect neural crest development against mitochondrial oxidative stress. eLife, 8.


