

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## Supersplat

RRID:SCR\_009826

Type: Tool

---

### Proper Citation

Supersplat (RRID:SCR\_009826)

---

### Resource Information

**URL:** <http://mocklerlab.org/tools/1>

**Proper Citation:** Supersplat (RRID:SCR\_009826)

**Description:** An application for discovering potential splice junctions in high throughput sequencing (HTS) data.

**Abbreviations:** Supersplat

**Resource Type:** software resource

**Keywords:** bio.tools

**Resource Name:** Supersplat

**Resource ID:** SCR\_009826

**Alternate IDs:** OMICS\_01256, biotools:supersplat

**Alternate URLs:** <https://bio.tools/supersplat>

**Record Creation Time:** 20220129T080255+0000

**Record Last Update:** 20260903T235012+0000

---

### Ratings and Alerts

No rating or validation information has been found for Supersplat.

No alerts have been found for Supersplat.

---

### Data and Source Information

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

---

## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Uyar B, et al. (2012) RNA-seq analysis of the C. briggsae transcriptome. Genome research, 22(8), 1567.