

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

JETTA

RRID:SCR_003091

Type: Tool

Proper Citation

JETTA (RRID:SCR_003091)

Resource Information

URL: <http://igenomed.stanford.edu/~junhee/JETTA/rnaseq.html>

Proper Citation: JETTA (RRID:SCR_003091)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented July 6, 2017. Software to detect alternatively spliced exons between two conditions, for example, between two groups of treated and untreated patients in a typical clinical study.

Abbreviations: JETTA

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

Defining Citation: [PMID:22433281](#)

Keywords: exon, exon splicing

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: JETTA

Resource ID: SCR_003091

Alternate IDs: OMICS_01334

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132457+0000

Ratings and Alerts

No rating or validation information has been found for JETTA.

No alerts have been found for JETTA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Zang C, et al. (2016) High-dimensional genomic data bias correction and data integration using MANCIE. Nature communications, 7, 11305.

Jiang P, et al. (2015) Network analysis of gene essentiality in functional genomics experiments. Genome biology, 16, 239.

Joo JH, et al. (2014) Role of Pnn in alternative splicing of a specific subset of lncRNAs of the corneal epithelium. Molecular vision, 20, 1629.