

# Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 2026

## NSMAP

RRID:SCR\_005213

Type: Tool

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### Proper Citation

NSMAP (RRID:SCR\_005213)

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### Resource Information

**URL:** <https://sites.google.com/site/nsmapfornaseq/>

**Proper Citation:** NSMAP (RRID:SCR\_005213)

**Description:** Software designed to identify and quantify isoforms from RNA-seq by incorporating a sparsity term into expression level estimation to enable isoform structure prediction and expression estimation simultaneously.

**Abbreviations:** NSMAP

**Synonyms:** Nonnegativity and Sparsity constrained Maximum A Posteriori, NSMAP for RNA-seq, NSMAP: A Method for Spliced Isoforms Identification and Quantification from RNA-Seq

**Resource Type:** software resource

**Defining Citation:** [PMID:21575225](#)

**Availability:** Free, Public

**Resource Name:** NSMAP

**Resource ID:** SCR\_005213

**Alternate IDs:** OMICS\_01282

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260912T195622+0000

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### Ratings and Alerts

No rating or validation information has been found for NSMAP.

No alerts have been found for NSMAP.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Xia Z, et al. (2011) NSMAP: a method for spliced isoforms identification and quantification from RNA-Seq. BMC bioinformatics, 12, 162.