

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

NSMAP

RRID:SCR_005213

Type: Tool

Proper Citation

NSMAP (RRID:SCR_005213)

Resource Information

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

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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: 20260919T195049+0000

Ratings and Alerts

No rating or validation information has been found for NSMAP.

No alerts have been found for NSMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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