

Resource Summary Report

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PennSeq

RRID:SCR_001763

Type: Tool

Proper Citation

PennSeq (RRID:SCR_001763)

Resource Information

URL: <http://sourceforge.net/projects/pennseq/>

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Description: Software for isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. Instead of making parametric assumptions, they give adequate weight to the underlying data by the use of a non-parametric approach. The rationale is that regardless what factors lead to non-uniformity, whether it is due to hexamer priming bias, local sequence bias, positional bias, RNA degradation, mapping bias or other unknown reasons, the probability that a fragment is sampled from a particular region will be reflected in the aligned data. This empirical approach thus maximally reflects the true underlying non-uniform read distribution.

Abbreviations: PennSeq

Resource Type: software resource

Defining Citation: [PMID:24362841](#)

Keywords: isoform, gene expression, rna-seq, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: PennSeq

Resource ID: SCR_001763

Alternate IDs: biotools:pennseq, OMICS_01946

Alternate URLs: <https://bio.tools/pennseq>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20261017T202500+0000

Ratings and Alerts

No rating or validation information has been found for PennSeq.

No alerts have been found for PennSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.