Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

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: 20260912T195530+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 found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Allbee AW, et al. (2023) PD-L1+ diffuse large B-cell lymphoma with extremely high mutational burden and microsatellite instability due to acquired PMS2 mutation. Cold Spring Harbor molecular case studies, 9(4).

Landsburg DJ, et al. (2023) TP53 mutations predict for poor outcomes in patients with newly diagnosed aggressive B-cell lymphomas in the current era. Blood advances, 7(23), 7243.

Landsburg DJ, et al. (2022) Mutation analysis performed on tumor biopsies from patients with newly-diagnosed germinal center aggressive B cell lymphomas. Oncotarget, 13, 1237.

Tuerk A, et al. (2017) Mixture models reveal multiple positional bias types in RNA-Seq data and lead to accurate transcript concentration estimates. PLoS computational biology, 13(5), e1005515.