

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

BBSeq

RRID:SCR_011877

Type: Tool

Proper Citation

BBSeq (RRID:SCR_011877)

Resource Information

URL: http://www.bios.unc.edu/research/genomic_software/BBSeq/

Proper Citation: BBSeq (RRID:SCR_011877)

Description: A Powerful and Flexible Approach to the Analysis of RNA Sequence Count Data.

Abbreviations: BBSeq

Resource Type: software resource

Keywords: bio.tools

Resource Name: BBSeq

Resource ID: SCR_011877

Alternate IDs: biotools:bbseq, OMICS_01300

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

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260808T190001+0000

Ratings and Alerts

No rating or validation information has been found for BBSeq.

No alerts have been found for BBSeq.

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 [NIF](#) .

Mate-Kole EM, et al. (2024) Machine learning-enhanced stochastic uncertainty and sensitivity analysis of the ICRP human respiratory tract model for an inhaled radionuclide. Journal of radiological protection : official journal of the Society for Radiological Protection, 44(4).

Sun S, et al. (2017) Differential expression analysis for RNAseq using Poisson mixed models. Nucleic acids research, 45(11), e106.

Fang Z, et al. (2012) Statistical methods for identifying differentially expressed genes in RNA-Seq experiments. Cell & bioscience, 2(1), 26.