

Resource Summary Report

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

Scotty

RRID:SCR_011889

Type: Tool

Proper Citation

Scotty (RRID:SCR_011889)

Resource Information

URL: <http://euler.bc.edu/marthlab/scotty/scotty.php/>

Proper Citation: Scotty (RRID:SCR_011889)

Description: A tool to assist in the designing of RNA Seq experiments that have adequate power to detect differential expression at the level required to achieve experimental aims.

Abbreviations: Scotty

Synonyms: Scotty - Power Analysis for RNA Seq Experiments

Resource Type: software resource

Resource Name: Scotty

Resource ID: SCR_011889

Alternate IDs: OMICS_01315

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T195741+0000

Ratings and Alerts

No rating or validation information has been found for Scotty.

No alerts have been found for Scotty.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Strey K, et al. (2026) Computational identification of novel therapeutic candidates for Streptococcus pyogenes and influenza A coinfections through transcriptomic-based drug repositioning. BMC microbiology, 26(1).

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. Genomics & informatics, 23(1), 13.

Suárez-Vega A, et al. (2019) Conjugated linoleic acid (CLA)-induced milk fat depression: application of RNA-Seq technology to elucidate mammary gene regulation in dairy ewes. Scientific reports, 9(1), 4473.

Wieck MM, et al. (2017) Prolonged Absence of Mechanoluminal Stimulation in Human Intestine Alters the Transcriptome and Intestinal Stem Cell Niche. Cellular and molecular gastroenterology and hepatology, 3(3), 367.

Moisiadis VG, et al. (2017) Prenatal Glucocorticoid Exposure Modifies Endocrine Function and Behaviour for 3 Generations Following Maternal and Paternal Transmission. Scientific reports, 7(1), 11814.

Suárez-Vega A, et al. (2016) Comprehensive RNA-Seq profiling to evaluate lactating sheep mammary gland transcriptome. Scientific data, 3, 160051.

Leshkowitz D, et al. (2016) Using Synthetic Mouse Spike-In Transcripts to Evaluate RNA-Seq Analysis Tools. PloS one, 11(4), e0153782.

DeVecchia AG, et al. (2016) Ancient and methane-derived carbon subsidizes contemporary food webs. Nature communications, 7, 13163.

Resnyk CW, et al. (2015) RNA-Seq Analysis of Abdominal Fat in Genetically Fat and Lean Chickens Highlights a Divergence in Expression of Genes Controlling Adiposity, Hemostasis, and Lipid Metabolism. PloS one, 10(10), e0139549.