

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 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:** 20260725T190726+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 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.