

# Resource Summary Report

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## SCAN.UPC

RRID:SCR\_001334

Type: Tool

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### Proper Citation

SCAN.UPC (RRID:SCR\_001334)

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### Resource Information

**URL:** <http://www.bioconductor.org/packages/release/bioc/html/SCAN.UPC.html>

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**Description:** A microarray normalization software (SCAN) to facilitate personalized-medicine workflows with an extension (UPC) that estimates whether a given gene/transcript is active above background levels in a given sample. Rather than processing microarray samples as groups, which can introduce biases and present logistical challenges, SCAN normalizes each sample individually by modeling and removing probe- and array-specific background noise using only data from within each array. SCAN can be applied to one-channel (e.g., Affymetrix) or two-channel (e.g., Agilent) microarrays. The UPC method can be applied to one-channel or two-channel microarrays as well as to RNA-Seq read counts. Because UPC values are represented on the same scale and have an identical interpretation for each platform, they can be used for cross-platform data integration. A

**Abbreviations:** SCAN.UPC

**Synonyms:** Single-channel array normalization (SCAN) and Universal exPression Codes (UPC), Single-channel array normalization and Universal exPression Codes

**Resource Type:** software resource

**Keywords:** microarray, one channel, preprocessing, rna-seq, two channel

**Availability:** Free, Available for download, Freely available

**Resource Name:** SCAN.UPC

**Resource ID:** SCR\_001334

**Alternate IDs:** OMICS\_02006

**License:** MIT License

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260801T190128+0000

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## Ratings and Alerts

No rating or validation information has been found for SCAN.UPC.

No alerts have been found for SCAN.UPC.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Junet V, et al. (2021) CuBlock: a cross-platform normalization method for gene-expression microarrays. *Bioinformatics* (Oxford, England), 37(16), 2365.

Zogopoulos VL, et al. (2021) Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in *Arabidopsis thaliana*. *iScience*, 24(8), 102848.

Lee J, et al. (2019) Blockade of integrin  $\alpha 3$  attenuates human pancreatic cancer via inhibition of EGFR signalling. *Scientific reports*, 9(1), 2793.

Taroni JN, et al. (2019) MultiPLIER: A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease. *Cell systems*, 8(5), 380.

Lee J, et al. (2019) Scattered DUSP28 is a novel biomarker responsible for aggravating malignancy via the autocrine and paracrine signaling in metastatic pancreatic cancer. *Cancer letters*, 456, 1.

Tang J, et al. (2018) Genome-wide expression profiling of glioblastoma using a large combined cohort. *Scientific reports*, 8(1), 15104.

Kasendra M, et al. (2018) Development of a primary human Small Intestine-on-a-Chip using biopsy-derived organoids. *Scientific reports*, 8(1), 2871.

Boege Y, et al. (2017) A Dual Role of Caspase-8 in Triggering and Sensing Proliferation-Associated DNA Damage, a Key Determinant of Liver Cancer Development. *Cancer cell*, 32(3), 342.

Lee J, et al. (2017) Autocrine DUSP28 signaling mediates pancreatic cancer malignancy via regulation of PDGF-A. *Scientific reports*, 7(1), 12760.

Lee J, et al. (2015) Blockade of dual-specificity phosphatase 28 decreases chemoresistance and migration in human pancreatic cancer cells. *Scientific reports*, 5, 12296.

Forreryd A, et al. (2015) Prediction of chemical respiratory sensitizers using GARD, a novel in vitro assay based on a genomic biomarker signature. *PloS one*, 10(3), e0118808.