

# Christina Kendziorski

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/2730265/christina-kendziorski-publications-by-citations.pdf>  
**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48 papers	2,658 citations	20 h-index	51 g-index
52 ext. papers	3,536 ext. citations	8 avg, IF	5.17 L-index

#	Paper	IF	Citations
48	EBSeq: an empirical Bayes hierarchical model for inference in RNA-seq experiments. <i>Bioinformatics</i> , <b>2013</b> , 29, 1035-43	7.2	805
47	Design and computational analysis of single-cell RNA-sequencing experiments. <i>Genome Biology</i> , <b>2016</b> , 17, 63	18.3	301
46	A gene expression network model of type 2 diabetes links cell cycle regulation in islets with diabetes susceptibility. <i>Genome Research</i> , <b>2008</b> , 18, 706-16	9.7	269
45	Single-cell RNA-seq reveals novel regulators of human embryonic stem cell differentiation to definitive endoderm. <i>Genome Biology</i> , <b>2016</b> , 17, 173	18.3	195
44	SCnorm: robust normalization of single-cell RNA-seq data. <i>Nature Methods</i> , <b>2017</b> , 14, 584-586	21.6	189
43	A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. <i>Genome Biology</i> , <b>2016</b> , 17, 222	18.3	133
42	Oscope identifies oscillatory genes in unsynchronized single-cell RNA-seq experiments. <i>Nature Methods</i> , <b>2015</b> , 12, 947-950	21.6	116
41	A review of statistical methods for expression quantitative trait loci mapping. <i>Mammalian Genome</i> , <b>2006</b> , 17, 509-17	3.2	83
40	Single-cell RNA sequencing reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. <i>PLoS Biology</i> , <b>2017</b> , 15, e2004050	9.7	72
39	Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions. <i>Journal of the American Statistical Association</i> , <b>2006</b> , 101, 1323-1332	2.8	58
38	EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. <i>Bioinformatics</i> , <b>2015</b> , 31, 2614-22	7.2	49
37	Regionally specified human pluripotent stem cell-derived astrocytes exhibit different molecular signatures and functional properties. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	30
36	Collaborative rewiring of the pluripotency network by chromatin and signalling modulating pathways. <i>Nature Communications</i> , <b>2015</b> , 6, 6188	17.4	29
35	Genetic Drivers of Pancreatic Islet Function. <i>Genetics</i> , <b>2018</b> , 209, 335-356	4	26
34	Gene loci associated with insulin secretion in islets from non-diabetic mice. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 4419-4432	15.9	26
33	Mutations in GFAP Disrupt the Distribution and Function of Organelles in Human Astrocytes. <i>Cell Reports</i> , <b>2018</b> , 25, 947-958.e4	10.6	26
32	Histone chaperone ASF1B promotes human Ecell proliferation via recruitment of histone H3.3. <i>Cell Cycle</i> , <b>2016</b> , 15, 3191-3202	4.7	25

31	Tissue specific human fibroblast differential expression based on RNAsequencing analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 308	4.5	22
30	The Transcription Factor Nfatc2 Regulates ECell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006466	6	22
29	An In Vitro Human Segmentation Clock Model Derived from Embryonic Stem Cells. <i>Cell Reports</i> , <b>2019</b> , 28, 2247-2255.e5	10.6	21
28	OEFinder: a user interface to identify and visualize ordering effects in single-cell RNA-seq data. <i>Bioinformatics</i> , <b>2016</b> , 32, 1408-10	7.2	17
27	The Dissection of Expression Quantitative Trait Locus Hotspots. <i>Genetics</i> , <b>2016</b> , 202, 1563-74	4	16
26	Trendy: segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 380	3.6	16
25	Identification of the Bile Acid Transporter Slco1a6 as a Candidate Gene That Broadly Affects Gene Expression in Mouse Pancreatic Islets. <i>Genetics</i> , <b>2015</b> , 201, 1253-62	4	15
24	Fungal Morphology, Iron Homeostasis, and Lipid Metabolism Regulated by a GATA Transcription Factor in <i>Blastomyces dermatitidis</i> . <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004959	7.6	14
23	Human induced pluripotent stem cell-derived vocal fold mucosa mimics development and responses to smoke exposure. <i>Nature Communications</i> , <b>2019</b> , 10, 4161	17.4	13
22	Discordance between histologic and visual assessment of tissue viability in excised burn wound tissue. <i>Wound Repair and Regeneration</i> , <b>2019</b> , 27, 150-161	3.6	12
21	Identification and Correction of Sample Mix-Ups in Expression Genetic Data: A Case Study. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 2177-86	3.2	11
20	Identification of a serum-induced transcriptional signature associated with metastatic cervical cancer. <i>PLoS ONE</i> , <b>2017</b> , 12, e0181242	3.7	8
19	CB2 improves power of cell detection in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , <b>2020</b> , 21, 137	18.3	6
18	Comparing gene expression data from formalin-fixed, paraffin embedded tissues and qPCR with that from snap-frozen tissue and microarrays for modeling outcomes of patients with ovarian carcinoma. <i>BMC Clinical Pathology</i> , <b>2015</b> , 15, 17	3	6
17	Automated minute scale RNA-seq of pluripotent stem cell differentiation reveals early divergence of human and mouse gene expression kinetics. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007543	5	4
16	Mechanotransduction of vocal fold fibroblasts and mesenchymal stromal cells in the context of the vocal fold mechanome. <i>Journal of Biomechanics</i> , <b>2019</b> , 83, 227-234	2.9	3
15	Interspecies chimeric conditions affect the developmental rate of human pluripotent stem cells. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008778	5	3
14	CHARTS: a web application for characterizing and comparing tumor subpopulations in publicly available single-cell RNA-seq data sets. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 83	3.6	3

13	Extending information retrieval methods to personalized genomic-based studies of disease. <i>Cancer Informatics</i> , <b>2014</b> , 13, 85-95	2.4	2
12	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239711	3.7	2
11	A Compositional Model to Assess Expression Changes from Single-Cell Rna-Seq Data		2
10	Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	2
9	The Anna Karenina Model of $\beta$ Cell Maturation in Development and Their Dedifferentiation in Type 1 and Type 2 Diabetes. <i>Diabetes</i> , <b>2021</b> , 70, 2058-2066	0.9	2
8	Combined Expression Trait Correlations and Expression Quantitative Trait Locus Mapping. <i>PLoS Genetics</i> , <b>2005</b> , preprint, e6	6	1
7	Novel immortalized human vocal fold epithelial cell line: In vitro tool for mucosal biology. <i>FASEB Journal</i> , <b>2021</b> , 35, e21243	0.9	1
6	Identification of direct transcriptional targets of NFATC2 that promote $\beta$ cell proliferation. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,	15.9	1
5	Statistical Methods for Latent Class Quantitative Trait Loci Mapping. <i>Genetics</i> , <b>2017</b> , 206, 1309-1317	4	
4	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis <b>2020</b> , 15, e0239711		
3	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis <b>2020</b> , 15, e0239711		
2	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis <b>2020</b> , 15, e0239711		
1	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis <b>2020</b> , 15, e0239711		