# Christina Kendziorski

## List of Publications by Year in Descending Order

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|---|---|---|---|
| 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 | Interspecies chimeric conditions affect the developmental rate of human pluripotent stem cells. *PLoS Computational Biology*, **2021**, 17, e1008778 | 5 | 3 |
| 47 | Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. *Bioinformatics*, **2021**, | 7.2 | 2 |
| 46 | The Anna Karenina Model of Cell Maturation in Development and Their Dedifferentiation in Type 1 and Type 2 Diabetes. *Diabetes*, **2021**, 70, 2058-2066 | 0.9 | 2 |
| 45 | Novel immortalized human vocal fold epithelial cell line: In vitro tool for mucosal biology. *FASEB Journal*, **2021**, 35, e21243 | 0.9 | 1 |
| 44 | CHARTS: a web application for characterizing and comparing tumor subpopulations in publicly available single-cell RNA-seq data sets. *BMC Bioinformatics*, **2021**, 22, 83 | 3.6 | 3 |
| 43 | Identification of direct transcriptional targets of NFATC2 that promote cell proliferation. *Journal of Clinical Investigation*, **2021**, 131, | 15.9 | 1 |
| 42 | CB2 improves power of cell detection in droplet-based single-cell RNA sequencing data. *Genome Biology*, **2020**, 21, 137 | 18.3 | 6 |
| 41 | Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. *PLoS ONE*, **2020**, 15, e0239711 | 3.7 | 2 |
| 40 | Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis **2020**, 15, e0239711 | | |
| 39 | Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis **2020**, 15, e0239711 | | |
| 38 | Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis **2020**, 15, e0239711 | | |
| 37 | Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis **2020**, 15, e0239711 | | |
| 36 | An In Vitro Human Segmentation Clock Model Derived from Embryonic Stem Cells. *Cell Reports*, **2019**, 28, 2247-2255.e5 | 10.6 | 21 |
| 35 | Human induced pluripotent stem cell-derived vocal fold mucosa mimics development and responses to smoke exposure. *Nature Communications*, **2019**, 10, 4161 | 17.4 | 13 |
| 34 | Mechanotransduction of vocal fold fibroblasts and mesenchymal stromal cells in the context of the vocal fold mechanome. *Journal of Biomechanics*, **2019**, 83, 227-234 | 2.9 | 3 |
| 33 | Regionally specified human pluripotent stem cell-derived astrocytes exhibit different molecular signatures and functional properties. *Development (Cambridge)*, **2019**, 146, | 6.6 | 30 |
| 32 | Tissue specific human fibroblast differential expression based on RNAsequencing analysis. *BMC Genomics*, **2019**, 20, 308 | 4.5 | 22 |

| 31 | Discordance between histologic and visual assessment of tissue viability in excised burn wound tissue. *Wound Repair and Regeneration*, **2019**, 27, 150-161 | 3.6 | 12 |
| 30 | Gene loci associated with insulin secretion in islets from non-diabetic mice. *Journal of Clinical Investigation*, **2019**, 129, 4419-4432 | 15.9 | 26 |
| 29 | Automated minute scale RNA-seq of pluripotent stem cell differentiation reveals early divergence of human and mouse gene expression kinetics. *PLoS Computational Biology*, **2019**, 15, e1007543 | 5 | 4 |
| 28 | Genetic Drivers of Pancreatic Islet Function. *Genetics*, **2018**, 209, 335-356 | 4 | 26 |
| 27 | Mutations in GFAP Disrupt the Distribution and Function of Organelles in Human Astrocytes. *Cell Reports*, **2018**, 25, 947-958.e4 | 10.6 | 26 |
| 26 | Trendy: segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments. *BMC Bioinformatics*, **2018**, 19, 380 | 3.6 | 16 |
| 25 | SCnorm: robust normalization of single-cell RNA-seq data. *Nature Methods*, **2017**, 14, 584-586 | 21.6 | 189 |
| 24 | Statistical Methods for Latent Class Quantitative Trait Loci Mapping. *Genetics*, **2017**, 206, 1309-1317 | 4 | |
| 23 | Single-cell RNA sequencing reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. *PLoS Biology*, **2017**, 15, e2004050 | 9.7 | 72 |
| 22 | Identification of a serum-induced transcriptional signature associated with metastatic cervical cancer. *PLoS ONE*, **2017**, 12, e0181242 | 3.7 | 8 |
| 21 | Single-cell RNA-seq reveals novel regulators of human embryonic stem cell differentiation to definitive endoderm. *Genome Biology*, **2016**, 17, 173 | 18.3 | 195 |
| 20 | A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. *Genome Biology*, **2016**, 17, 222 | 18.3 | 133 |
| 19 | Histone chaperone ASF1B promotes human β-cell proliferation via recruitment of histone H3.3. *Cell Cycle*, **2016**, 15, 3191-3202 | 4.7 | 25 |
| 18 | OEFinder: a user interface to identify and visualize ordering effects in single-cell RNA-seq data. *Bioinformatics*, **2016**, 32, 1408-10 | 7.2 | 17 |
| 17 | The Transcription Factor Nfatc2 Regulates β-Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. *PLoS Genetics*, **2016**, 12, e1006466 | 6 | 22 |
| 16 | Design and computational analysis of single-cell RNA-sequencing experiments. *Genome Biology*, **2016**, 17, 63 | 18.3 | 301 |
| 15 | The Dissection of Expression Quantitative Trait Locus Hotspots. *Genetics*, **2016**, 202, 1563-74 | 4 | 16 |
| 14 | Identification of the Bile Acid Transporter Slco1a6 as a Candidate Gene That Broadly Affects Gene Expression in Mouse Pancreatic Islets. *Genetics*, **2015**, 201, 1253-62 | 4 | 15 |

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|---|---|---|---|
| 13 | Oscope identifies oscillatory genes in unsynchronized single-cell RNA-seq experiments. *Nature Methods*, **2015**, 12, 947-950 | 21.6 | 116 |
| 12 | 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. *BMC Clinical Pathology*, **2015**, 15, 17 | 3 | 6 |
| 11 | Fungal Morphology, Iron Homeostasis, and Lipid Metabolism Regulated by a GATA Transcription Factor in Blastomyces dermatitidis. *PLoS Pathogens*, **2015**, 11, e1004959 | 7.6 | 14 |
| 10 | Identification and Correction of Sample Mix-Ups in Expression Genetic Data: A Case Study. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2177-86 | 3.2 | 11 |
| 9 | EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. *Bioinformatics*, **2015**, 31, 2614-22 | 7.2 | 49 |
| 8 | Collaborative rewiring of the pluripotency network by chromatin and signalling modulating pathways. *Nature Communications*, **2015**, 6, 6188 | 17.4 | 29 |
| 7 | Extending information retrieval methods to personalized genomic-based studies of disease. *Cancer Informatics*, **2014**, 13, 85-95 | 2.4 | 2 |
| 6 | EBSeq: an empirical Bayes hierarchical model for inference in RNA-seq experiments. *Bioinformatics*, **2013**, 29, 1035-43 | 7.2 | 805 |
| 5 | A gene expression network model of type 2 diabetes links cell cycle regulation in islets with diabetes susceptibility. *Genome Research*, **2008**, 18, 706-16 | 9.7 | 269 |
| 4 | Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions. *Journal of the American Statistical Association*, **2006**, 101, 1323-1332 | 2.8 | 58 |
| 3 | A review of statistical methods for expression quantitative trait loci mapping. *Mammalian Genome*, **2006**, 17, 509-17 | 3.2 | 83 |
| 2 | Combined Expression Trait Correlations and Expression Quantitative Trait Locus Mapping. *PLoS Genetics*, **2005**, preprint, e6 | 6 | 1 |
| 1 | A Compositional Model to Assess Expression Changes from Single-Cell Rna-Seq Data | | 2 |