

# Elizabeth Purdom

## List of Publications by Year in descending order

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36  
papers

18,954  
citations

218677  
26  
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361022  
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44  
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44  
docs citations

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times ranked

31572  
citing authors

#	ARTICLE	IF	CITATIONS
1	Successional adaptive strategies revealed by correlating arbuscular mycorrhizal fungal abundance with host plant gene expression. <i>Molecular Ecology</i> , 2023, 32, 2674-2687.	3.9	11
2	Classification of human chronic inflammatory skin disease based on single-cell immune profiling. <i>Science Immunology</i> , 2022, 7, eabl9165.	11.9	53
3	Co-occurrence networks reveal more complexity than community composition in resistance and resilience of microbial communities. <i>Nature Communications</i> , 2022, 13, .	12.8	58
4	mbkmeans: Fast clustering for single cell data using mini-batch k-means. <i>PLoS Computational Biology</i> , 2021, 17, e1008625.	3.2	36
5	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. <i>Nature Communications</i> , 2021, 12, 3209.	12.8	93
6	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
7	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	27.8	316
8	Cell Wall Compositions of Sorghum bicolor Leaves and Roots Remain Relatively Constant Under Drought Conditions. <i>Frontiers in Plant Science</i> , 2021, 12, 747225.	3.6	5
9	Cobolt: integrative analysis of multimodal single-cell sequencing data. <i>Genome Biology</i> , 2021, 22, 351.	8.8	62
10	Fungal community assembly in drought-stressed sorghum shows stochasticity, selection, and universal ecological dynamics. <i>Nature Communications</i> , 2020, 11, 34.	12.8	176
11	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , 2020, 6, .	10.3	865
12	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	6.2	117
13	A20 and ABIN1 Suppression of a Keratinocyte Inflammatory Program with a Shared Single-Cell Expression Signature in Diverse Human Rashes. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1264-1273.	0.7	16
14	Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27124-27132.	7.1	129
15	Strong succession in arbuscular mycorrhizal fungal communities. <i>ISME Journal</i> , 2019, 13, 214-226.	9.8	86
16	Transcriptional Programming of Normal and Inflamed Human Epidermis at Single-Cell Resolution. <i>Cell Reports</i> , 2018, 25, 871-883.	6.4	206
17	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. <i>PLoS Computational Biology</i> , 2018, 14, e1006378.	3.2	48
18	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. <i>BMC Genomics</i> , 2018, 19, 477.	2.8	1,562

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19	APOBEC mutation drives early-onset squamous cell carcinomas in recessive dystrophic epidermolysis bullosa. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	91
20	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. <i>Cell Stem Cell</i> , 2017, 20, 817-830.e8.	11.1	164
21	Drought and host selection influence bacterial community dynamics in the grass root microbiome. <i>ISME Journal</i> , 2017, 11, 2691-2704.	9.8	464
22	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. <i>Cell Stem Cell</i> , 2017, 21, 775-790.e9.	11.1	67
23	Clustering of mRNA-Seq data based on alternative splicing patterns. <i>Biostatistics</i> , 2017, 18, 295-307.	1.5	7
24	Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. <i>F1000Research</i> , 2017, 6, 1158.	1.6	13
25	Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10995-11000.	7.1	146
26	Transcription Restores DNA Repair to Heterochromatin, Determining Regional Mutation Rates in Cancer Genomes. <i>Cell Reports</i> , 2014, 9, 1228-1234.	6.4	104
27	Methods and challenges in timing chromosomal abnormalities within cancer samples. <i>Bioinformatics</i> , 2013, 29, 3113-3120.	4.1	26
28	A Tetrahymena Piwi Bound to Mature tRNA 3' Fragments Activates the Exonuclease Xrn2 for RNA Processing in the Nucleus. <i>Molecular Cell</i> , 2012, 48, 509-520.	9.7	98
29	Subtype and pathway specific responses to anticancer compounds in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2724-2729.	7.1	417
30	Unifying Gene Expression Measures from Multiple Platforms Using Factor Analysis. <i>PLoS ONE</i> , 2011, 6, e17691.	2.5	12
31	Temporal Dissection of Tumorigenesis in Primary Cancers. <i>Cancer Discovery</i> , 2011, 1, 137-143.	9.4	240
32	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	16.8	6,138
33	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	3.4	121
34	Diversity of the Human Intestinal Microbial Flora. <i>Science</i> , 2005, 308, 1635-1638.	12.6	6,617
35	Microarray Analysis Reveals Differences in Gene Expression of Circulating CD8+ T Cells in Melanoma Patients and Healthy Donors. <i>Cancer Research</i> , 2004, 64, 3661-3667.	0.9	24
36	A pipeline to analyse time-course gene expression data. <i>F1000Research</i> , 0, 9, 1447.	1.6	6