Elizabeth Purdom

List of Publications by Year
in descending order

36 papers	18,954 citations	218381 26 h-index	360668 35 g-index
44 all docs	44 docs citations	44 times ranked	31572 citing authors

#	Article	IF	Citations
1	Diversity of the Human Intestinal Microbial Flora. Science, 2005, 308, 1635-1638.	6.0	6,617
2	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
3	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. BMC Genomics, 2018, 19, 477.	1.2	1,562
4	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. Science Advances, 2020, 6, .	4.7	865
5	Drought and host selection influence bacterial community dynamics in the grass root microbiome. ISME Journal, 2017, 11, 2691-2704.	4.4	464
6	Subtype and pathway specific responses to anticancer compounds in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2724-2729.	3.3	417
7	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	13.7	316
8	Temporal Dissection of Tumorigenesis in Primary Cancers. Cancer Discovery, 2011, 1, 137-143.	7.7	240
9	Transcriptional Programming of Normal and Inflamed Human Epidermis at Single-Cell Resolution. Cell Reports, 2018, 25, 871-883.	2.9	206
10	Fungal community assembly in drought-stressed sorghum shows stochasticity, selection, and universal ecological dynamics. Nature Communications, 2020, 11, 34.	5.8	176
11	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	13.7	166
12	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. Cell Stem Cell, 2017, 20, 817-830.e8.	5.2	164
13	Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10995-11000.	3.3	146
14	Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 27124-27132.	3.3	129
15	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. Molecular Cancer Research, 2010, 8, 961-974.	1.5	121
16	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. Cell Systems, 2019, 8, 315-328.e8.	2.9	117
17	Transcription Restores DNA Repair to Heterochromatin, Determining Regional Mutation Rates in Cancer Genomes. Cell Reports, 2014, 9, 1228-1234.	2.9	104
18	A Tetrahymena Piwi Bound to Mature tRNA 3â€² Fragments Activates the Exonuclease Xrn2 for RNA Processing in the Nucleus. Molecular Cell, 2012, 48, 509-520.	4.5	98

#	Article	IF	Citations
19	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. Nature Communications, 2021, 12, 3209.	5.8	93
20	APOBEC mutation drives early-onset squamous cell carcinomas in recessive dystrophic epidermolysis bullosa. Science Translational Medicine, 2018, 10, .	5.8	91
21	Strong succession in arbuscular mycorrhizal fungal communities. ISME Journal, 2019, 13, 214-226.	4.4	86
22	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. Cell Stem Cell, 2017, 21, 775-790.e9.	5.2	67
23	Cobolt: integrative analysis of multimodal single-cell sequencing data. Genome Biology, 2021, 22, 351.	3.8	62
24	Co-occurrence networks reveal more complexity than community composition in resistance and resilience of microbial communities. Nature Communications, 2022, 13, .	5.8	58
25	Classification of human chronic inflammatory skin disease based on single-cell immune profiling. Science Immunology, 2022, 7, eabl9165.	5.6	53
26	clusterExperiment and RSEC: A Bioconductor package and framework for clustering of single-cell and other large gene expression datasets. PLoS Computational Biology, 2018, 14, e1006378.	1.5	48
27	mbkmeans: Fast clustering for single cell data using mini-batch k-means. PLoS Computational Biology, 2021, 17, e1008625.	1.5	36
28	Methods and challenges in timing chromosomal abnormalities within cancer samples. Bioinformatics, 2013, 29, 3113-3120.	1.8	26
29	Microarray Analysis Reveals Differences in Gene Expression of Circulating CD8+ T Cells in Melanoma Patients and Healthy Donors. Cancer Research, 2004, 64, 3661-3667.	0.4	24
30	A20 and ABIN1 Suppression of a Keratinocyte Inflammatory Program with a Shared Single-Cell Expression Signature in Diverse Human Rashes. Journal of Investigative Dermatology, 2019, 139, 1264-1273.	0.3	16
31	Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference. F1000Research, 2017, 6, 1158.	0.8	13
32	Unifying Gene Expression Measures from Multiple Platforms Using Factor Analysis. PLoS ONE, 2011, 6, e17691.	1.1	12
33	Successional adaptive strategies revealed by correlating arbuscular mycorrhizal fungal abundance with host plant gene expression. Molecular Ecology, 2023, 32, 2674-2687.	2.0	11
34	Clustering of mRNA-Seq data based on alternative splicing patterns. Biostatistics, 2017, 18, 295-307.	0.9	7
35	A pipeline to analyse time-course gene expression data. F1000Research, 0, 9, 1447.	0.8	6
36	Cell Wall Compositions of Sorghum bicolor Leaves and Roots Remain Relatively Constant Under Drought Conditions. Frontiers in Plant Science, 2021, 12, 747225.	1.7	5