

# Lukas M Weber

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3967127/publications.pdf>

Version: 2024-02-01

22  
papers

2,993  
citations

567281

15  
h-index

794594

19  
g-index

38  
all docs

38  
docs citations

38  
times ranked

5966  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy. <i>Nature Medicine</i> , 2018, 24, 144-153.	30.7	564
2	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. <i>Nature Neuroscience</i> , 2021, 24, 425-436.	14.8	418
3	Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 1084-1096.	1.5	321
4	CytoF workflow: Differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017, 6, 748.	1.6	312
5	Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes. <i>Development (Cambridge)</i> , 2016, 143, 2025-37.	2.5	244
6	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017, 6, 748.	1.6	244
7	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	4.4	162
8	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125.	8.8	114
9	High-dimensional single-cell analysis reveals the immune signature of narcolepsy. <i>Journal of Experimental Medicine</i> , 2016, 213, 2621-2633.	8.5	106
10	Statistical methods for detecting differentially methylated loci and regions. <i>Frontiers in Genetics</i> , 2014, 5, 324.	2.3	99
11	Circulating neutrophil subsets in advanced lung cancer patients exhibit unique immune signature and relate to prognosis. <i>FASEB Journal</i> , 2020, 34, 4204-4218.	0.5	70
12	SpatialExperiment: infrastructure for spatially-resolved transcriptomics data in R using Bioconductor. <i>Bioinformatics</i> , 2022, 38, 3128-3131.	4.1	48
13	An updated guide for the perplexed: cytometry in the high-dimensional era. <i>Nature Immunology</i> , 2021, 22, 1190-1197.	14.5	39
14	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1009290.	3.2	38
15	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 0, 6, 748.	1.6	36
16	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. <i>GigaScience</i> , 2021, 10, .	6.4	17
17	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 0, 6, 748.	1.6	16
18	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. <i>F1000Research</i> , 2019, 8, 1459.	1.6	13

#	ARTICLE	IF	CITATIONS
19	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	1.6	8
20	A Retrospective Study of the Effectiveness of Four Different Treatments of Periodontal Disease in Equine Cheek Teeth. Journal of Veterinary Dentistry, 2016, 33, 83-89.	0.3	3
21	HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats. F1000Research, 0, 8, 1459.	1.6	3
22	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	1.6	0