

# Timothy J Peters

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8947807/publications.pdf>

Version: 2024-02-01

20  
papers

2,127  
citations

687363

13  
h-index

794594

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

5167  
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208.	8.8	912
2	De novo identification of differentially methylated regions in the human genome. <i>Epigenetics and Chromatin</i> , 2015, 8, 6.	3.9	684
3	Enduring epigenetic landmarks define the cancer microenvironment. <i>Genome Research</i> , 2018, 28, 625-638.	5.5	74
4	Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. <i>Nature Communications</i> , 2020, 11, 54.	12.8	72
5	Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. <i>Nature Communications</i> , 2019, 10, 416.	12.8	71
6	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. <i>Cancer Cell</i> , 2019, 35, 297-314.e8.	16.8	62
7	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. <i>Scientific Reports</i> , 2019, 9, 8254.	3.3	36
8	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , 2021, 49, e109-e109.	14.5	31
9	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. <i>BMC Genomics</i> , 2017, 18, 250.	2.8	26
10	A multiomics approach to identify host-microbe alterations associated with infection severity in diabetic foot infections: a pilot study. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 29.	6.4	26
11	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	3.3	24
12	Antigen-driven EGR2 expression is required for exhausted CD8+ T cell stability and maintenance. <i>Nature Communications</i> , 2021, 12, 2782.	12.8	20
13	STAT5B restrains human B-cell differentiation to maintain humoral immune homeostasis. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 931-946.	2.9	19
14	Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. <i>Bioinformatics</i> , 2019, 35, 560-570.	4.1	17
15	Transient exposure to miR-203 enhances the differentiation capacity of established pluripotent stem cells. <i>EMBO Journal</i> , 2020, 39, e104324.	7.8	16
16	Uncontrolled CD21 <sup>low</sup> age-associated and B1 B cell accumulation caused by failure of an EGR2/3 tolerance checkpoint. <i>Cell Reports</i> , 2022, 38, 110259.	6.4	15
17	Temporal ordering of omics and multiomic events inferred from time-series data. <i>Npj Systems Biology and Applications</i> , 2020, 6, 22.	3.0	10
18	Host-microbe metatranscriptome reveals differences between acute and chronic infections in diabetes-related foot ulcers. <i>Apmis</i> , 2022, 130, 751-762.	2.0	7

#	ARTICLE	IF	CITATIONS
19	A metatranscriptomic approach to explore longitudinal tissue specimens from non-healing diabetes related foot ulcers. <i>Apmis</i> , 2022, 130, 383-396.	2.0	5
20	Single cell genomics of self-reactive B cells reveals the evolution from benign to pathogenic autoantibody and strategies for early diagnosis and personalised treatment. , 2019, , .		0