Timothy J Peters

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Uncontrolled CD21low age-associated and B1 B cell accumulation caused by failure of an EGR2/3 tolerance checkpoint. Cell Reports, 2022, 38, 110259.	6.4	15
2	A metatranscriptomic approach to explore longitudinal tissue specimens from nonâ€healing diabetes related foot ulcers. Apmis, 2022, 130, 383-396.	2.0	5
3	Hostâ€microbe metatranscriptome reveals differences between acute and chronic infections in diabetesâ€related foot ulcers. Apmis, 2022, 130, 751-762.	2.0	7
4	STAT5B restrains human B-cell differentiation to maintain humoral immune homeostasis. Journal of Allergy and Clinical Immunology, 2022, 150, 931-946.	2.9	19
5	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. Nucleic Acids Research, 2021, 49, e109-e109.	14.5	31
6	A multiomics approach to identify host-microbe alterations associated with infection severity in diabetic foot infections: a pilot study. Npj Biofilms and Microbiomes, 2021, 7, 29.	6.4	26
7	Antigen-driven EGR2 expression is required for exhausted CD8+ T cell stability and maintenance. Nature Communications, 2021, 12, 2782.	12.8	20
8	Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. Nature Communications, 2020, 11, 54.	12.8	72
9	Temporal ordering of omics and multiomic events inferred from time-series data. Npj Systems Biology and Applications, 2020, 6, 22.	3.0	10
10	Transient exposure to miRâ€⊋03 enhances the differentiation capacity of established pluripotent stem cells. EMBO Journal, 2020, 39, e104324.	7.8	16
11	Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. Bioinformatics, 2019, 35, 560-570.	4.1	17
12	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. Scientific Reports, 2019, 9, 9511.	3.3	24
13	Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. Nature Communications, 2019, 10, 416.	12.8	71
14	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. Scientific Reports, 2019, 9, 8254.	3.3	36
15	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. Cancer Cell, 2019, 35, 297-314.e8.	16.8	62
16	241â€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
17	Enduring epigenetic landmarks define the cancer microenvironment. Genome Research, 2018, 28, 625-638.	5.5	74
18	Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. BMC Genomics, 2017, 18, 250.	2.8	26

#	Article	lF	CITATIONS
19	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. Genome Biology, 2016, 17, 208.	8.8	912
20	De novo identification of differentially methylated regions in the human genome. Epigenetics and Chromatin, 2015, 8, 6.	3.9	684