Peter Ebert

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1168784/publications.pdf

Version: 2024-02-01

21 papers	2,004 citations	623734 14 h-index	713466 21 g-index
30 all docs	30 docs citations	30 times ranked	4731 citing authors

#	Article	IF	Citations
1	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
2	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
3	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell Stem Cell, 2016, 19, 808-822.	11.1	216
4	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. Immunity, 2016, 45, 1148-1161.	14.3	174
5	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
6	Combining transcription factor binding affinities with open-chromatin data for accurate gene expression prediction. Nucleic Acids Research, 2017, 45, 54-66.	14.5	112
7	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	21.4	92
8	Epigenetic dynamics of monocyte-to-macrophage differentiation. Epigenetics and Chromatin, 2016, 9, 33.	3.9	73
9	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. Genome Biology, 2018, 19, 150.	8.8	71
10	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
11	Ten Simple Rules for Developing Usable Software in Computational Biology. PLoS Computational Biology, 2017, 13, e1005265.	3.2	58
12	TEPIC 2â€"an extended framework for transcription factor binding prediction and integrative epigenomic analysis. Bioinformatics, 2019, 35, 1608-1609.	4.1	34
13	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	14.5	31
14	BiQ Analyzer HiMod: an interactive software tool for high-throughput locus-specific analysis of 5-methylcytosine and its oxidized derivatives. Nucleic Acids Research, 2014, 42, W501-W507.	14.5	21
15	Temporal enhancer profiling of parallel lineages identifies AHR and GLIS1 as regulators of mesenchymal multipotency. Nucleic Acids Research, 2019, 47, 1141-1163.	14.5	16
16	An environment for sustainable research software in Germany and beyond: current state, open challenges, and call for action. F1000Research, 2020, 9, 295.	1.6	16
17	A general concept for consistent documentation of computational analyses. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav050.	3.0	9
18	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	4.1	9

#	Article	IF	Citations
19	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. Epigenetics and Chromatin, 2018, 11, 66.	3.9	6
20	Fast detection of differential chromatin domains with SCIDDO. Bioinformatics, 2021, 37, 1198-1205.	4.1	6
21	Improving reference epigenome catalogs by computational prediction. Nature Biotechnology, 2015, 33, 354-355.	17.5	5