

Barbara J Wold

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8729728/publications.pdf>

Version: 2024-02-01

20
papers

6,229
citations

516710

16
h-index

677142

22
g-index

26
all docs

26
docs citations

26
times ranked

12962
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	6.0	1,547
2	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
4	From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014, 24, 496-510.	5.5	470
5	Sequence census methods for functional genomics. <i>Nature Methods</i> , 2008, 5, 19-21.	19.0	227
6	Oxygen-mediated regulation of skeletal muscle satellite cell proliferation and adipogenesis in culture. <i>Journal of Cellular Physiology</i> , 2001, 189, 189-196.	4.1	204
7	Mapping a multiplexed zoo of mRNA expression. <i>Development (Cambridge)</i> , 2016, 143, 3632-3637.	2.5	198
8	Single-Cell Transcriptome Analysis Reveals Dynamic Changes in lncRNA Expression during Reprogramming. <i>Cell Stem Cell</i> , 2015, 16, 88-101.	11.1	146
9	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	27.8	131
10	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
11	Occupancy maps of 208 chromatin-associated proteins in one human cell type. <i>Nature</i> , 2020, 583, 720-728.	27.8	90
12	Single-Cell Analysis Reveals Regulatory Gene Expression Dynamics Leading to Lineage Commitment in Early T Cell Development. <i>Cell Systems</i> , 2019, 9, 321-337.e9.	6.2	80
13	Evidence for Site-Specific Occupancy of the Mitochondrial Genome by Nuclear Transcription Factors. <i>PLoS ONE</i> , 2014, 9, e84713.	2.5	38
14	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	4.4	30
15	Pitfalls of Mapping High-Throughput Sequencing Data to Repetitive Sequences: Piwi's Genomic Targets Still Not Identified. <i>Developmental Cell</i> , 2015, 32, 765-771.	7.0	26
16	Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. <i>Genome Biology</i> , 2021, 22, 286.	8.8	26
17	Reconstructing a metazoan genetic pathway with transcriptome-wide epistasis measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2930-E2939.	7.1	21
18	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019, 29, 1900-1909.	5.5	21

#	ARTICLE	IF	CITATIONS
19	Dissecting the regulatory activity and sequence content of loci with exceptional numbers of transcription factor associations. <i>Genome Research</i> , 2020, 30, 939-950.	5.5	14
20	A ratiometric-based measure of gene co-expression. <i>BMC Bioinformatics</i> , 2014, 15, 331.	2.6	3