

Magda Bienko

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,995
citations

471509

17
h-index

526287

27
g-index

43
all docs

43
docs citations

43
times ranked

5309
citing authors

#	ARTICLE	IF	CITATIONS
1	A Spatiotemporal Organ-Wide Gene Expression and Cell Atlas of the Developing Human Heart. <i>Cell</i> , 2019, 179, 1647-1660.e19.	28.9	470
2	Integrated genome and transcriptome sequencing of the same cell. <i>Nature Biotechnology</i> , 2015, 33, 285-289.	17.5	439
3	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. <i>Nature Methods</i> , 2013, 10, 361-365.	19.0	409
4	Spatially resolved transcriptomics and beyond. <i>Nature Reviews Genetics</i> , 2015, 16, 57-66.	16.3	406
5	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	28.9	399
6	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15058.	12.8	298
7	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. <i>Nature Methods</i> , 2013, 10, 122-124.	19.0	66
8	GPSeq reveals the radial organization of chromatin in the cell nucleus. <i>Nature Biotechnology</i> , 2020, 38, 1184-1193.	17.5	49
9	Human skin long noncoding RNA WAKMAR1 regulates wound healing by enhancing keratinocyte migration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9443-9452.	7.1	48
10	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	44
11	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Nature Communications</i> , 2019, 10, 1636.	12.8	41
12	FuseFISH: Robust Detection of Transcribed Gene Fusions in Single Cells. <i>Cell Reports</i> , 2014, 6, 18-23.	6.4	39
13	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. <i>Frontiers in Oncology</i> , 2021, 11, 700568.	2.8	33
14	Radial Organization in the Mammalian Nucleus. <i>Frontiers in Genetics</i> , 2020, 11, 33.	2.3	32
15	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. <i>Communications Biology</i> , 2018, 1, 209.	4.4	26
16	piRNAs initiate transcriptional silencing of spermatogenic genes during <i>C.Âlegans</i> germline development. <i>Developmental Cell</i> , 2022, 57, 180-196.e7.	7.0	25
17	The era of 3D and spatial genomics. <i>Trends in Genetics</i> , 2022, 38, 1062-1075.	6.7	25
18	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. <i>Oncotarget</i> , 2017, 8, 18680-18698.	1.8	24

#	ARTICLE	IF	CITATIONS
19	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. <i>Nature Communications</i> , 2020, 11, 5445.	12.8	20
20	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. <i>Nature Protocols</i> , 2020, 15, 3894-3941.	12.0	19
21	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. <i>Methods in Molecular Biology</i> , 2018, 1672, 167-194.	0.9	15
22	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. <i>Nature Communications</i> , 2021, 12, 3903.	12.8	14
23	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. <i>Nature Communications</i> , 2019, 10, 4732.	12.8	12
24	RNA gradients: Shapers of 3D genome architecture. <i>Current Opinion in Cell Biology</i> , 2022, 74, 7-12.	5.4	11
25	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. <i>Methods in Molecular Biology</i> , 2018, 1766, 303-333.	0.9	8
26	Breaks Labeling in situ and sequencing (BLISS). <i>Protocol Exchange</i> , 0, , .	0.3	4
27	iFISH:a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Protocol Exchange</i> , 0, , .	0.3	3
28	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. <i>Scientific Data</i> , 2022, 9, .	5.3	3
29	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. <i>Scientific Data</i> , 2022, 9, 47.	5.3	2
30	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
31	Role of UbL Family Modifiers and Their Binding Proteins in Cell Signaling. <i>Methods in Molecular Biology</i> , 2012, 832, 163-171.	0.9	0