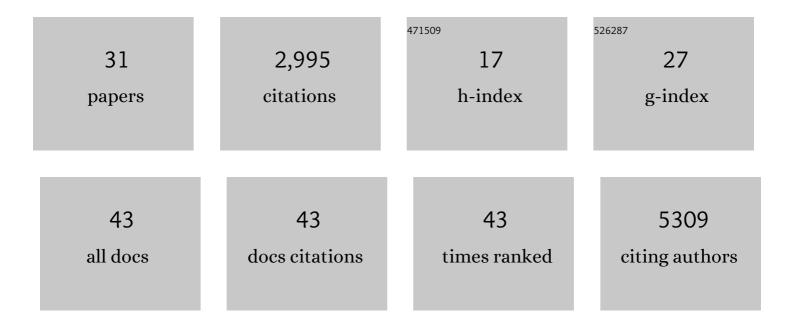
Magda Bienko

List of Publications by Year in descending order

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MACDA RIENKO

#	Article	IF	CITATIONS
1	RNA gradients: Shapers of 3D genome architecture. Current Opinion in Cell Biology, 2022, 74, 7-12.	5.4	11
2	piRNAs initiate transcriptional silencing of spermatogenic genes during C.Âelegans germline development. Developmental Cell, 2022, 57, 180-196.e7.	7.0	25
3	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. Scientific Data, 2022, 9, 47.	5.3	2
4	The era of 3D and spatial genomics. Trends in Genetics, 2022, 38, 1062-1075.	6.7	25
5	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. Scientific Data, 2022, 9, .	5.3	3
6	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. Nature Communications, 2021, 12, 3903.	12.8	14
7	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. Frontiers in Oncology, 2021, 11, 700568.	2.8	33
8	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. Nature Communications, 2020, 11, 5445.	12.8	20
9	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. Nature Protocols, 2020, 15, 3894-3941.	12.0	19
10	Radial Organization in the Mammalian Nucleus. Frontiers in Genetics, 2020, 11, 33.	2.3	32
11	GPSeq reveals the radial organization of chromatin in the cell nucleus. Nature Biotechnology, 2020, 38, 1184-1193.	17.5	49
12	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. Nature Communications, 2019, 10, 4732.	12.8	12
13	Human skin long noncoding RNA WAKMAR1 regulates wound healing by enhancing keratinocyte migration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9443-9452.	7.1	48
14	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. Nature Communications, 2019, 10, 1636.	12.8	41
15	A Spatiotemporal Organ-Wide Gene Expression and Cell Atlas of the Developing Human Heart. Cell, 2019, 179, 1647-1660.e19.	28.9	470
16	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. Methods in Molecular Biology, 2018, 1766, 303-333.	0.9	8
17	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. Methods in Molecular Biology, 2018, 1672, 167-194.	0.9	15
18	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. Communications Biology, 2018, 1, 209.	4.4	26

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#	Article	IF	CITATIONS
19	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. Nature Communications, 2017, 8, 15058.	12.8	298
20	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. Oncotarget, 2017, 8, 18680-18698.	1.8	24
21	Massive and parallel expression profiling using microarrayed single-cell sequencing. Nature Communications, 2016, 7, 13182.	12.8	44
22	Integrated genome and transcriptome sequencing of the same cell. Nature Biotechnology, 2015, 33, 285-289.	17.5	439
23	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. Cell, 2015, 163, 134-147.	28.9	399
24	Spatially resolved transcriptomics and beyond. Nature Reviews Genetics, 2015, 16, 57-66.	16.3	406
25	FuseFISH: Robust Detection of Transcribed Gene Fusions in Single Cells. Cell Reports, 2014, 6, 18-23.	6.4	39
26	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. Nature Methods, 2013, 10, 122-124.	19.0	66
27	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. Nature Methods, 2013, 10, 361-365.	19.0	409
28	Role of UbL Family Modifiers and Their Binding Proteins in Cell Signaling. Methods in Molecular Biology, 2012, 832, 163-171.	0.9	0
29	Breaks Labeling in situ and sequencing (BLISS). Protocol Exchange, 0, , .	0.3	4
30	iFISH:a publically available resource enabling versatile DNA FISH to study genome architecture. Protocol Exchange, 0, , .	0.3	3
31	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. SSRN Electronic Journal, 0, , .	0.4	1