

# Magda Bienko

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28

papers

1,912

citations

14

h-index

43

g-index

43

ext. papers

2,563

ext. citations

16.4

avg, IF

4.79

L-index

#	Paper	IF	Citations
28	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH.. <i>Scientific Data</i> , <b>2022</b> , 9, 47	8.2	0
27	RNA gradients: Shapers of 3D genome architecture.. <i>Current Opinion in Cell Biology</i> , <b>2022</b> , 74, 7-12	9	1
26	piRNAs initiate transcriptional silencing of spermatogenic genes during <i>C. elegans</i> germline development.. <i>Developmental Cell</i> , <b>2021</b> ,	10.2	2
25	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. <i>Nature Communications</i> , <b>2021</b> , 12, 3903	17.4	4
24	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 700568	5.3	5
23	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. <i>Nature Protocols</i> , <b>2020</b> , 15, 3894-3941	18.8	7
22	Radial Organization in the Mammalian Nucleus. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 33	4.5	14
21	GPSeq reveals the radial organization of chromatin in the cell nucleus. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1184-1193	44.5	21
20	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. <i>Nature Communications</i> , <b>2020</b> , 11, 5445	17.4	8
19	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> , <b>2019</b> , 116, 9443-9452	11.5	24
18	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Nature Communications</i> , <b>2019</b> , 10, 1636	17.4	20
17	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. <i>Nature Communications</i> , <b>2019</b> , 10, 4732	17.4	8
16	A Spatiotemporal Organ-Wide Gene Expression and Cell Atlas of the Developing Human Heart. <i>Cell</i> , <b>2019</b> , 179, 1647-1660.e19	56.2	188
15	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1766, 303-333	1.4	6
14	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1672, 167-194	1.4	13
13	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. <i>Communications Biology</i> , <b>2018</b> , 1, 209	6.7	15
12	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. <i>Nature Communications</i> , <b>2017</b> , 8, 15058	17.4	203

11	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. <i>Oncotarget</i> , <b>2017</b> , 8, 18680-18698	3.3	15
10	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , <b>2016</b> , 7, 13182	17.4	33
9	Integrated genome and transcriptome sequencing of the same cell. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 285-289	44.9	326
8	Genome-wide maps of nuclear lamina interactions in single human cells. <i>Cell</i> , <b>2015</b> , 163, 134-47	56.2	291
7	Spatially resolved transcriptomics and beyond. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 57-66	30.1	299
6	FuseFISH: robust detection of transcribed gene fusions in single cells. <i>Cell Reports</i> , <b>2014</b> , 6, 18-23	10.6	32
5	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. <i>Nature Methods</i> , <b>2013</b> , 10, 122-124	21.6	48
4	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. <i>Nature Methods</i> , <b>2013</b> , 10, 361-5	21.6	320
3	Role of UbL family modifiers and their binding proteins in cell signaling. <i>Methods in Molecular Biology</i> , <b>2012</b> , 832, 163-71	1.4	
2	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. <i>SSRN Electronic Journal</i> ,	1	1
1	Breaks Labeling in situ and sequencing (BLISS). <i>Protocol Exchange</i> ,		4