

# 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	RNA gradients: Shapers of 3D genome architecture. <i>Current Opinion in Cell Biology</i> , 2022, 74, 7-12.	5.4	11
2	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
3	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. <i>Scientific Data</i> , 2022, 9, 47.	5.3	2
4	The era of 3D and spatial genomics. <i>Trends in Genetics</i> , 2022, 38, 1062-1075.	6.7	25
5	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. <i>Scientific Data</i> , 2022, 9, .	5.3	3
6	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. <i>Nature Communications</i> , 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. <i>Frontiers in Oncology</i> , 2021, 11, 700568.	2.8	33
8	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. <i>Nature Communications</i> , 2020, 11, 5445.	12.8	20
9	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. <i>Nature Protocols</i> , 2020, 15, 3894-3941.	12.0	19
10	Radial Organization in the Mammalian Nucleus. <i>Frontiers in Genetics</i> , 2020, 11, 33.	2.3	32
11	GPSseq reveals the radial organization of chromatin in the cell nucleus. <i>Nature Biotechnology</i> , 2020, 38, 1184-1193.	17.5	49
12	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
13	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
14	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. <i>Nature Communications</i> , 2019, 10, 1636.	12.8	41
15	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
16	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. <i>Methods in Molecular Biology</i> , 2018, 1766, 303-333.	0.9	8
17	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
18	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

#	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