Magda Bienko

List of Publications by Citations

28	1,912	14	43
papers	citations	h-index	g-index

43	2,563	16.4	4.79
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
28	Integrated genome and transcriptome sequencing of the same cell. *Nature Biotechnology*, **2015**, 33, 285-289	44.5	326
27	Nucleotide-resolution DNA double-strand break mapping by next-generation sequencing. *Nature Methods*, **2013**, 10, 361-5	21.6	320
26	Spatially resolved transcriptomics and beyond. *Nature Reviews Genetics*, **2015**, 16, 57-66	30.1	299
25	Genome-wide maps of nuclear lamina interactions in single human cells. *Cell*, **2015**, 163, 134-47	56.2	291
24	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. *Nature Communications*, **2017**, 8, 15058	17.4	203
23	A Spatiotemporal Organ-Wide Gene Expression and Cell Atlas of the Developing Human Heart. *Cell*, **2019**, 179, 1647-1660.e19	56.2	188
22	A versatile genome-scale PCR-based pipeline for high-definition DNA FISH. *Nature Methods*, **2013**, 10, 122-124	21.6	48
21	Massive and parallel expression profiling using microarrayed single-cell sequencing. *Nature Communications*, **2016**, 7, 13182	17.4	33
20	FuseFISH: robust detection of transcribed gene fusions in single cells. *Cell Reports*, **2014**, 6, 18-23	10.6	32
19	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	11.5	24
18	GPSeq reveals the radial organization of chromatin in the cell nucleus. *Nature Biotechnology*, **2020**, 38, 1184-1193	44.5	21
17	iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. *Nature Communications*, **2019**, 10, 1636	17.4	20
16	Quantification of HER2 and estrogen receptor heterogeneity in breast cancer by single-molecule RNA fluorescence in situ hybridization. *Oncotarget*, **2017**, 8, 18680-18698	3.3	15
15	RollFISH achieves robust quantification of single-molecule RNA biomarkers in paraffin-embedded tumor tissue samples. *Communications Biology*, **2018**, 1, 209	6.7	15
14	Radial Organization in the Mammalian Nucleus. *Frontiers in Genetics*, **2020**, 11, 33	4.5	14
13	Genome-Wide Profiling of DNA Double-Strand Breaks by the BLESS and BLISS Methods. *Methods in Molecular Biology*, **2018**, 1672, 167-194	1.4	13
12	CUTseq is a versatile method for preparing multiplexed DNA sequencing libraries from low-input samples. *Nature Communications*, **2019**, 10, 4732	17.4	8

List of Publications

11	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. *Nature Communications*, **2020**, 11, 5445	17.4	8
10	Genome-wide detection of DNA double-strand breaks by in-suspension BLISS. *Nature Protocols*, **2020**, 15, 3894-3941	18.8	7
9	An Application-Directed, Versatile DNA FISH Platform for Research and Diagnostics. *Methods in Molecular Biology*, **2018**, 1766, 303-333	1.4	6
8	Somatic Copy Number Alterations in Human Cancers: An Analysis of Publicly Available Data From The Cancer Genome Atlas. *Frontiers in Oncology*, **2021**, 11, 700568	5.3	5
7	Breaks Labeling in situ and sequencing (BLISS). *Protocol Exchange*,		4
6	COVseq is a cost-effective workflow for mass-scale SARS-CoV-2 genomic surveillance. *Nature Communications*, **2021**, 12, 3903	17.4	4
5	piRNAs initiate transcriptional silencing of spermatogenic genes during C. elegans germline development.. *Developmental Cell*, **2021**,	10.2	2
4	RNA gradients: Shapers of 3D genome architecture.. *Current Opinion in Cell Biology*, **2022**, 74, 7-12	9	1
3	An Organ-Wide Gene Expression Atlas of the Developing Human Heart. *SSRN Electronic Journal*,	1	1
2	Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH.. *Scientific Data*, **2022**, 9, 47	8.2	0
1	Role of UbL family modifiers and their binding proteins in cell signaling. *Methods in Molecular Biology*, **2012**, 832, 163-71	1.4	