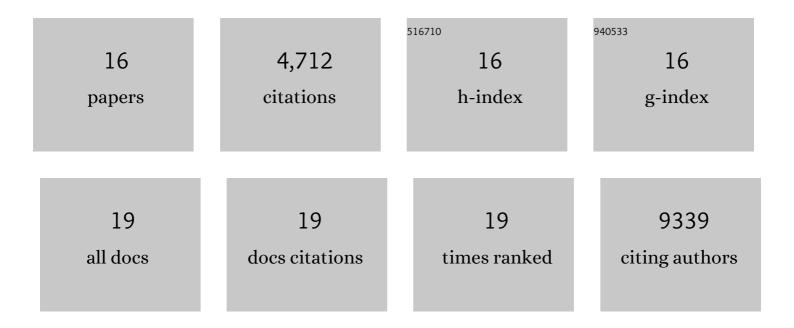
## Johanna Klughammer

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4133252/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Pooled CRISPR screening with single-cell transcriptome readout. Nature Methods, 2017, 14, 297-301.	19.0	749
2	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	19.0	708
3	Specification of tissue-resident macrophages during organogenesis. Science, 2016, 353, .	12.6	609
4	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	30.7	381
5	Single-Cell DNA Methylome Sequencing and Bioinformatic Inference of Epigenomic Cell-State Dynamics. Cell Reports, 2015, 10, 1386-1397.	6.4	378
6	Artemisinins Target GABAA Receptor Signaling and Impair α Cell Identity. Cell, 2017, 168, 86-100.e15.	28.9	330
7	The DNA methylation landscape of glioblastoma disease progression shows extensive heterogeneity in time and space. Nature Medicine, 2018, 24, 1611-1624.	30.7	229
8	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
9	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell Stem Cell, 2016, 19, 808-822.	11.1	216
10	Singleâ€cell transcriptomes reveal characteristic features of human pancreatic islet cell types. EMBO Reports, 2016, 17, 178-187.	4.5	206
11	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	12.6	197
12	DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma. Nature Medicine, 2017, 23, 386-395.	30.7	193
13	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. Nature Genetics, 2021, 53, 1469-1479.	21.4	100
14	SM-Omics is an automated platform for high-throughput spatial multi-omics. Nature Communications, 2022, 13, 795.	12.8	73
15	Divergent Expression Regulation of Gonad Development Genes in Medaka Shows Incomplete Conservation of the Downstream Regulatory Network of Vertebrate Sex Determination. Molecular Biology and Evolution, 2013, 30, 2328-2346.	8.9	65
16	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in Neisseria meningitidis during Invasive Disease. PLoS ONE, 2017, 12, e0169892.	2.5	26