

# Johanna Klughammer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4133252/publications.pdf>

Version: 2024-02-01

16  
papers

4,712  
citations

516710

16  
h-index

940533

16  
g-index

19  
all docs

19  
docs citations

19  
times ranked

9339  
citing authors

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