

# Aleksandra A Kolodziejczyk

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3786035/publications.pdf>

Version: 2024-02-01

22  
papers

6,721  
citations

361413

20  
h-index

610901

24  
g-index

30  
all docs

30  
docs citations

30  
times ranked

11490  
citing authors

#	ARTICLE	IF	CITATIONS
1	The spatiotemporal program of zonal liver regeneration following acute injury. <i>Cell Stem Cell</i> , 2022, 29, 973-989.e10.	11.1	60
2	Commensal inter-bacterial interactions shaping the microbiota. <i>Current Opinion in Microbiology</i> , 2021, 63, 158-171.	5.1	30
3	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021, 599, 684-691.	27.8	112
4	Gut microbiota modulates weight gain in mice after discontinued smoke exposure. <i>Nature</i> , 2021, 600, 713-719.	27.8	35
5	Acute liver failure is regulated by MYC- and microbiome-dependent programs. <i>Nature Medicine</i> , 2020, 26, 1899-1911.	30.7	95
6	Diet-microbiota interactions and personalized nutrition. <i>Nature Reviews Microbiology</i> , 2019, 17, 742-753.	28.6	514
7	The role of the microbiome in <sc>NAFLD</sc> and <sc>NASH</sc>. <i>EMBO Molecular Medicine</i> , 2019, 11, .	6.9	368
8	Global and targeted approaches to single-cell transcriptome characterization. <i>Briefings in Functional Genomics</i> , 2018, 17, 209-219.	2.7	28
9	Bile acids in glucose metabolism in health and disease. <i>Journal of Experimental Medicine</i> , 2018, 215, 383-396.	8.5	275
10	Dysbiosis and the immune system. <i>Nature Reviews Immunology</i> , 2017, 17, 219-232.	22.7	1,102
11	Ageing increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	12.6	265
12	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017, 550, 393-397.	27.8	223
13	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	12.8	62
14	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 66-76.	3.3	17
15	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 29.	8.8	572
16	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	9.7	1,014
17	Single-cell transcriptomic reconstruction reveals cell cycle and multi-lineage differentiation defects in Bcl11a-deficient hematopoietic stem cells. <i>Genome Biology</i> , 2015, 16, 178.	8.8	86
18	#ASemCellScientistBecause. <i>Cell Stem Cell</i> , 2015, 17, 381-384.	11.1	0

#	ARTICLE	IF	CITATIONS
19	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015, 6, 8687.	12.8	213
20	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	11.1	505
21	Single-Cell RNA Sequencing Reveals T Helper Cells Synthesizing Steroids De Novo to Contribute to Immune Homeostasis. <i>Cell Reports</i> , 2014, 7, 1130-1142.	6.4	198
22	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	19.0	929