

# Angelika N Christ

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11517072/publications.pdf>

Version: 2024-02-01

16  
papers

7,924  
citations

623188

14  
h-index

887659

17  
g-index

19  
all docs

19  
docs citations

19  
times ranked

14476  
citing authors

#	ARTICLE	IF	CITATIONS
1	Absence of Batf3 reveals a new dimension of cell state heterogeneity within conventional dendritic cells. <i>IScience</i> , 2021, 24, 102402.	1.9	16
2	Acquisition of murine splenic myeloid cells for protein and gene expression profiling by advanced flow cytometry and CITE-seq. <i>STAR Protocols</i> , 2021, 2, 100842.	0.5	2
3	Single-Cell Transcriptomic Analysis of Cardiac Differentiation from Human PSCs Reveals HOPX-Dependent Cardiomyocyte Maturation. <i>Cell Stem Cell</i> , 2018, 23, 586-598.e8.	5.2	215
4	Single-cell RNA-seq of human induced pluripotent stem cells reveals cellular heterogeneity and cell state transitions between subpopulations. <i>Genome Research</i> , 2018, 28, 1053-1066.	2.4	102
5	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	13.7	716
6	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	0.6	174
7	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	13.7	2,700
8	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	2.1	98
9	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	13.7	1,206
10	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	13.7	2,132
11	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , 2014, 57, 31-38.	0.8	0
12	Genome-wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLIT-ROBO, ITGA2 and MET signaling. <i>International Journal of Cancer</i> , 2014, 135, 1110-1118.	2.3	192
13	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	5.8	236
14	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	1.1	67
15	Identification and characterisation of new inhibitors for the human hematopoietic prostaglandin D <sub>2</sub> synthase. <i>European Journal of Medicinal Chemistry</i> , 2010, 45, 447-454.	2.6	15
16	Development and Characterization of New Inhibitors of the Human and Mouse Hematopoietic Prostaglandin D <sub>2</sub> Synthases. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 5536-5548.	2.9	19