

# Simon Andrews

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4792252/publications.pdf>

Version: 2024-02-01

25  
papers

5,109  
citations

430874

18  
h-index

580821

25  
g-index

30  
all docs

30  
docs citations

30  
times ranked

8603  
citing authors

#	ARTICLE	IF	CITATIONS
1	Amniogenesis occurs in two independent waves in primates. <i>Cell Stem Cell</i> , 2022, 29, 744-759.e6.	11.1	48
2	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	10.3	15
3	High-resolution three-dimensional chromatin profiling of the Chinese hamster ovary cell genome. <i>Biotechnology and Bioengineering</i> , 2021, 118, 784-796.	3.3	5
4	BioPAN: a web-based tool to explore mammalian lipidome metabolic pathways on LIPID MAPS. <i>F1000Research</i> , 2021, 10, 4.	1.6	44
5	BioPAN: a web-based tool to explore mammalian lipidome metabolic pathways on LIPID MAPS. <i>F1000Research</i> , 2021, 10, 4.	1.6	26
6	The global and promoter-centric 3D genome organization temporally resolved during a circadian cycle. <i>Genome Biology</i> , 2021, 22, 162.	8.8	21
7	TGF $\beta$ 2 signalling is required to maintain pluripotency of human naïve pluripotent stem cells. <i>ELife</i> , 2021, 10, .	6.0	24
8	Reciprocal transcription factor networks govern tissue-resident ILC3 subset function and identity. <i>Nature Immunology</i> , 2021, 22, 1245-1255.	14.5	49
9	A distal enhancer at risk locus 11q13.5 promotes suppression of colitis by Treg cells. <i>Nature</i> , 2020, 583, 447-452.	27.8	40
10	RNA proximity sequencing data and analysis pipeline from a human neuroblastoma nuclear transcriptome. <i>Scientific Data</i> , 2020, 7, 35.	5.3	2
11	RNA proximity sequencing reveals the spatial organization of the transcriptome in the nucleus. <i>Nature Biotechnology</i> , 2019, 37, 793-802.	17.5	30
12	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. <i>Nature Communications</i> , 2018, 9, 1028.	12.8	98
13	FastQ Screen: A tool for multi-genome mapping and quality control. <i>F1000Research</i> , 2018, 7, 1338.	1.6	905
14	FastQ Screen: A tool for multi-genome mapping and quality control. <i>F1000Research</i> , 2018, 7, 1338.	1.6	865
15	Cluster Flow: A user-friendly bioinformatics workflow tool. <i>F1000Research</i> , 2016, 5, 2824.	1.6	18
16	Cluster Flow: A user-friendly bioinformatics workflow tool. <i>F1000Research</i> , 2016, 5, 2824.	1.6	16
17	SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. <i>F1000Research</i> , 2016, 5, 1479.	1.6	149
18	SNPsplit: Allele-specific splitting of alignments between genomes with known SNP genotypes. <i>F1000Research</i> , 2016, 5, 1479.	1.6	109

#	ARTICLE	IF	CITATIONS
19	HiCUP: pipeline for mapping and processing Hi-C data. F1000Research, 2015, 4, 1310.	1.6	485
20	Global Reorganization of the Nuclear Landscape in Senescent Cells. Cell Reports, 2015, 10, 471-483.	6.4	282
21	The pluripotent regulatory circuitry connecting promoters to their long-range interacting elements. Genome Research, 2015, 25, 582-597.	5.5	402
22	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. Nature Genetics, 2015, 47, 598-606.	21.4	857
23	Polycomb repressive complex PRC1 spatially constrains the mouse embryonic stem cell genome. Nature Genetics, 2015, 47, 1179-1186.	21.4	330
24	Epigenetic memory of the first cell fate decision prevents complete ES cell reprogramming into trophoblast. Nature Communications, 2014, 5, 5538.	12.8	68
25	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. Genome Research, 2014, 24, 1854-1868.	5.5	219