

# Siddarth Selvaraj

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11386981/publications.pdf>

Version: 2024-02-01

17  
papers

12,665  
citations

623188

14  
h-index

887659

17  
g-index

23  
all docs

23  
docs citations

23  
times ranked

17229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	13.7	5,786
2	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
4	A high-resolution map of the three-dimensional chromatin interactome in human cells. <i>Nature</i> , 2013, 503, 290-294.	13.7	1,074
5	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	13.7	605
6	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
7	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. <i>PLoS Computational Biology</i> , 2019, 15, e1007273.	1.5	509
8	5mC Oxidation by Tet2 Modulates Enhancer Activity and Timing of Transcriptome Reprogramming during Differentiation. <i>Molecular Cell</i> , 2014, 56, 286-297.	4.5	285
9	Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. <i>Nature Biotechnology</i> , 2013, 31, 1111-1118.	9.4	257
10	HiCNorm: removing biases in Hi-C data via Poisson regression. <i>Bioinformatics</i> , 2012, 28, 3131-3133.	1.8	228
11	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
12	Bayesian Inference of Spatial Organizations of Chromosomes. <i>PLoS Computational Biology</i> , 2013, 9, e1002893.	1.5	188
13	CRISPR Reveals a Distal Super-Enhancer Required for Sox2 Expression in Mouse Embryonic Stem Cells. <i>PLoS ONE</i> , 2014, 9, e114485.	1.1	168
14	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. <i>Nature Communications</i> , 2019, 10, 1054.	5.8	100
15	Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. <i>BMC Genomics</i> , 2015, 16, 900.	1.2	10
16	InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. <i>Nucleic Acids Research</i> , 2016, 44, e111-e111.	6.5	1
17	3D chromosome rendering from Hi-C data using virtual reality. , 2015, , .		0