Siddarth Selvaraj

List of Publications by Year
in descending order

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