

Noah A Zaitlen

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

7,783
citations

623734

14
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

14130
citing authors

#	ARTICLE	IF	CITATIONS
1	Disentangling selection on genetically correlated polygenic traits via whole-genome genealogies. <i>American Journal of Human Genetics</i> , 2021, 108, 219-239.	6.2	48
2	Race and Genetic Ancestry in Medicine – A Time for Reckoning with Racism. <i>New England Journal of Medicine</i> , 2021, 384, 474-480.	27.0	371
3	Toward a fine-scale population health monitoring system. <i>Cell</i> , 2021, 184, 2068-2083.e11.	28.9	78
4	Admixed Populations Improve Power for Variant Discovery and Portability in Genome-Wide Association Studies. <i>Frontiers in Genetics</i> , 2021, 12, 673167.	2.3	22
5	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. <i>Cell Reports</i> , 2020, 31, 107489.	6.4	91
6	An evolutionary compass for detecting signals of polygenic selection and mutational bias. <i>Evolution Letters</i> , 2019, 3, 69-79.	3.3	29
7	Mixed Model Association with Family-Biased Case-Control Ascertainment. <i>American Journal of Human Genetics</i> , 2017, 100, 31-39.	6.2	14
8	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. <i>Genome Research</i> , 2016, 26, 863-873.	5.5	63
9	The landscape of genomic imprinting across diverse adult human tissues. <i>Genome Research</i> , 2015, 25, 927-936.	5.5	216
10	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	6.2	60
11	Assessing allele-specific expression across multiple tissues from RNA-seq read data. <i>Bioinformatics</i> , 2015, 31, 2497-2504.	4.1	90
12	Advantages and pitfalls in the application of mixed-model association methods. <i>Nature Genetics</i> , 2014, 46, 100-106.	21.4	876
13	Response to Sul and Eskin. <i>Nature Reviews Genetics</i> , 2013, 14, 300-300.	16.3	14
14	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 348-354.	21.4	2,287
15	New approaches to population stratification in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 459-463.	16.3	1,047
16	EMINIM: An Adaptive and Memory-Efficient Algorithm for Genotype Imputation. <i>Journal of Computational Biology</i> , 2010, 17, 547-560.	1.6	16
17	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009, 41, 35-46.	21.4	676
18	An Adaptive and Memory Efficient Algorithm for Genotype Imputation. <i>Lecture Notes in Computer Science</i> , 2009, , 482-495.	1.3	2

#	ARTICLE	IF	CITATIONS
19	Efficient Control of Population Structure in Model Organism Association Mapping. Genetics, 2008, 178, 1709-1723.	2.9	1,752