William W Greenwald

List of Publications by Year
in descending order

10 papers	583 citations	1040056 9 h-index	1372567 10 g-index
12 all docs	12 docs citations	12 times ranked	1765 citing authors

#	Article	IF	Citations
1	iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. Stem Cell Reports, 2017, 8, 1086-1100.	4.8	147
2	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. Nature Communications, 2019, 10, 1054.	12.8	100
3	Insights into the Mutational Burden of Human Induced Pluripotent Stem Cells from an Integrative Multi-Omics Approach. Cell Reports, 2018, 24, 883-894.	6.4	85
4	Updated and standardized genome-scale reconstruction of Mycobacterium tuberculosis H37Rv, iEK1011, simulates flux states indicative of physiological conditions. BMC Systems Biology, 2018, 12, 25.	3.0	63
5	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	6.2	60
6	Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. BMC Bioinformatics, 2017, 18, 207.	2.6	35
7	Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. Stem Cell Reports, 2019, 12, 1342-1353.	4.8	32
8	Identification of Common and Rare Genetic Variation Associated With Plasma Protein Levels Using Whole-Exome Sequencing and Mass Spectrometry. Circulation Genomic and Precision Medicine, 2018, 11, e002170.	3.6	26
9	Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. BMC Genomics, 2017, 18, 296.	2.8	21
10	Efficient Prioritization of Multiple Causal eQTL Variants via Sparse Polygenic Modeling. Genetics, 2017, 207, 1301-1312.	2.9	10