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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11922255/publications.pdf

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20 papers	1,848 citations	516710 16 h-index	713466 21 g-index
27 all docs	27 docs citations	27 times ranked	5794 citing authors

#	Article	IF	Citations
1	FOXO1 mitigates the SMAD3/FOXL2C134W transcriptomic effect in a model of human adult granulosa cell tumor. Journal of Translational Medicine, 2021, 19, 90.	4.4	5
2	Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. PLoS Genetics, 2021, 17, e1009531.	3.5	13
3	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402.	27.8	170
4	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	27.8	89
5	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
6	Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. Nature Communications, 2019, 10, 1054.	12.8	100
7	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517.	21.4	35
8	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
9	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 533-546.e7.	11.1	157
10	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
11	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
12	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
13	Sequencing and characterizing the genome of Estrella lausannensis as an undergraduate project: training students and biological insights. Frontiers in Microbiology, 2015, 6, 101.	3.5	32
14	Comparative genome analysis of <scp>P</scp>seudomonas knackmussiiâ€...<scp>B</scp>13, the first bacterium known to degrade chloroaromatic compounds. Environmental Microbiology, 2015, 17, 91-104.	3.8	52
15	Mutational screening of splicing factor genes in cases with autosomal dominant retinitis pigmentosa. Molecular Vision, 2014, 20, 843-51.	1.1	11
16	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
17	Target Sequencing, Cell Experiments, and a Population Study Establish Endothelial Nitric Oxide Synthase (eNOS) Gene as Hypertension Susceptibility Gene. Hypertension, 2013, 62, 844-852.	2.7	48
18	Genomewide Association Study Using a High-Density Single Nucleotide Polymorphism Array and Case-Control Design Identifies a Novel Essential Hypertension Susceptibility Locus in the Promoter Region of Endothelial NO Synthase. Hypertension, 2012, 59, 248-255.	2.7	144

#	Article	IF	Citations
19	Next generation sequencing of pooled samples reveals new SNRNP200 mutations associated with retinitis pigmentosa. Human Mutation, 2011, 32, E2246-E2258.	2.5	42
20	Ultra High Throughput Sequencing in Human DNA Variation Detection: A Comparative Study on the NDUFA3-PRPF31 Region. PLoS ONE, 2010, 5, e13071.	2.5	11