Yingleong Chan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9323820/publications.pdf

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13	2,129	933447	1125743
papers	citations	10 h-index	13 g-index

14	14	14	9064
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	12.8	706
2	An enhanced CRISPR repressor for targeted mammalian gene regulation. Nature Methods, 2018, 15, 611-616.	19.0	361
3	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
4	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. Nature Neuroscience, 2017, 20, 1217-1224.	14.8	212
5	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
6	Engineering adeno-associated viral vectors to evade innate immune and inflammatory responses. Science Translational Medicine, 2021, 13, .	12.4	99
7	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. American Journal of Human Genetics, 2015, 96, 695-708.	6.2	67
8	An Excess of Risk-Increasing Low-Frequency Variants Can Be a Signal of Polygenic Inheritance in Complex Diseases. American Journal of Human Genetics, 2014, 94, 437-452.	6.2	55
9	Common Variants Show Predicted Polygenic Effects on Height in the Tails of the Distribution, Except in Extremely Short Individuals. PLoS Genetics, 2011, 7, e1002439.	3.5	49
10	A Novel Test for Recessive Contributions to Complex Diseases Implicates Bardet-Biedl Syndrome Gene BBS10 in Idiopathic Type 2 Diabetes and Obesity. American Journal of Human Genetics, 2014, 95, 509-520.	6.2	29
11	Orgo-Seq integrates single-cell and bulk transcriptomic data to identify cell type specific-driver genes associated with autism spectrum disorder. Nature Communications, 2022, 13, .	12.8	11
12	Enabling multiplexed testing of pooled donor cells through whole-genome sequencing. Genome Medicine, 2018, 10, 31.	8.2	10
13	An unbiased index to quantify participantâ€™s phenotypic contribution to an open-access cohort. Scientific Reports, 2017, 7, 46148.	3.3	6