Yingleong Chan

List of Publications by Year
in descending order

13	2,129	933264 10	1125617 13
papers	citations	h-index	g-index

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

#	Article	IF	Citations
1	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, .	5.8	11
2	Engineering adeno-associated viral vectors to evade innate immune and inflammatory responses. Science Translational Medicine, 2021, 13, .	5.8	99
3	An enhanced CRISPR repressor for targeted mammalian gene regulation. Nature Methods, 2018, 15, 611-616.	9.0	361
4	Enabling multiplexed testing of pooled donor cells through whole-genome sequencing. Genome Medicine, 2018, 10, 31.	3.6	10
5	An unbiased index to quantify participantâ€™s phenotypic contribution to an open-access cohort. Scientific Reports, 2017, 7, 46148.	1.6	6
6	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. Nature Neuroscience, 2017, 20, 1217-1224.	7.1	212
7	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
8	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
9	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.	2.6	67
10	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
11	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.	2.6	29
12	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.	2.6	55
13	Common Variants Show Predicted Polygenic Effects on Height in the Tails of the Distribution, Except in Extremely Short Individuals. PLoS Genetics, 2011, 7, e1002439.	1.5	49