Christopher L Hartl

List of Publications by Year
in descending order

13	16,778	840119 11	1125271 13
papers	citations	h-index	g-index

15	15	15	41693
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolutionary conservation and divergence of the human brain transcriptome. Genome Biology, 2021, 22, 52.	3.8	28
2	Coexpression network architecture reveals the brain-wide and multiregional basis of disease susceptibility. Nature Neuroscience, 2021, 24, 1313-1323.	7.1	44
3	Low Exposure Extended Dosing Mimicking Clinical Exposures of the Oral Formulation of Azacitidine Results in a Sustained Hypomethylation and Targets Leukemic Stem Cells. Blood, 2021, 138, 3355-3355.	0.6	0
4	Clarifying the effect of library batch on extracellular RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1849-1850.	3.3	2
5	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	13.5	174
6	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
7	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
8	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
9	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. Nature, 2016, 540, 423-427.	13.7	603
10	SM a SH: a benchmarking toolkit for human genome variant calling. Bioinformatics, 2014, 30, 2787-2795.	1.8	40
11	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	2.6	24
12	From FastQ Data to Highâ€Confidence Variant Calls: The Genome Analysis Toolkit Best Practices Pipeline. Current Protocols in Bioinformatics, 2013, 43, 11.10.1-11.10.33.	25.8	4,796
13	A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nature Genetics, 2011, 43, 491-498.	9.4	10,018