

Luke R Lloyd-Jones

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2504308/publications.pdf>

Version: 2024-02-01

23
papers

2,191
citations

516710

16
h-index

610901

24
g-index

31
all docs

31
docs citations

31
times ranked

5313
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	12.8	50
2	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	44
3	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	2.9	23
4	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	12.8	291
5	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. <i>Genetics</i> , 2018, 208, 1397-1408.	2.9	94
6	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
7	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
8	A globally convergent algorithm for lasso-penalized mixture of linear regression models. <i>Computational Statistics and Data Analysis</i> , 2018, 119, 19-38.	1.2	19
9	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. <i>European Journal of Human Genetics</i> , 2018, 26, 1361-1368.	2.8	3
10	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
11	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. <i>Genetics</i> , 2017, 206, 1113-1126.	2.9	30
12	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	6.2	178
13	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, 483.	12.8	22
14	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2533-2544.	1.8	23
15	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.	21.4	119
16	A Block Minorization Maximization Algorithm for Heteroscedastic Regression. <i>IEEE Signal Processing Letters</i> , 2016, 23, 1131-1135.	3.6	1
17	Mixture of Time-Dependent Growth Models with an Application to Blue Swimmer Crab Length-Frequency Data. <i>Biometrics</i> , 2016, 72, 1255-1265.	1.4	3
18	A Universal Approximation Theorem for Mixture-of-Experts Models. <i>Neural Computation</i> , 2016, 28, 2585-2593.	2.2	21

#	ARTICLE	IF	CITATIONS
19	Evidence for mitochondrial genetic control of autosomal gene expression. <i>Human Molecular Genetics</i> , 2016, 25, dww347.	2.9	6
20	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016, 17, 248.	8.8	15
21	Improved estimation of size-transition matrices using tag-recapture data. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2014, 71, 1385-1394.	1.4	8
22	Generalised growth models for aquatic species with an application to blacklip abalone (<i>Haliotis</i>)	2.5	10
23	Latitudinal and seasonal effects on growth of the Australian eastern king prawn (<i>Melicertus</i>)	1.4	19