Luke R Lloyd-Jones

List of Publications by Year
in descending order

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	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
2	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	21.4	304
3	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	12.8	291
4	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
5	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
6	Genotype–covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	21.4	119
7	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. Genetics, 2018, 208, 1397-1408.	2.9	94
8	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	12.8	50
9	The effect of X-linked dosage compensation on complex trait variation. Nature Communications, 2019, 10, 3009.	12.8	44
10	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. Genetics, 2017, 206, 1113-1126.	2.9	30
11	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2533-2544.	1.8	23
12	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	2.9	23
13	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	12.8	22
14	A Universal Approximation Theorem for Mixture-of-Experts Models. Neural Computation, 2016, 28, 2585-2593.	2.2	21
15	Latitudinal and seasonal effects on growth of the Australian eastern king prawn (<i>Melicertus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	19
16	A globally convergent algorithm for lasso-penalized mixture of linear regression models. Computational Statistics and Data Analysis, 2018, 119, 19-38.	1.2	19
17	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	15
18	Improved estimation of size-transition matrices using tag–recapture data. Canadian Journal of Fisheries and Aquatic Sciences, 2014, 71, 1385-1394.	1.4	8

#	Article	IF	Citations
19	Generalised growth models for aquatic species with an application to blacklip abalone (Haliotis) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	8
20	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	2.9	6
21	Mixture of Time-Dependent Growth Models with an Application to Blue Swimmer Crab Length-Frequency Data. Biometrics, 2016, 72, 1255-1265.	1.4	3
22	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. European Journal of Human Genetics, 2018, 26, 1361-1368.	2.8	3
23	A Block Minorization–Maximization Algorithm for Heteroscedastic Regression. IEEE Signal Processing Letters, 2016, 23, 1131-1135.	3.6	1