Po-Ru Loh

List of Publications by Year in descending order

66 papers	28,474 citations	70961 41 h-index	98622 67 g-index
95 all docs	95 docs citations	95 times ranked	34289 citing authors

#	Article	IF	Citations
1	A spectrum of recessiveness among Mendelian disease variants in UK Biobank. American Journal of Human Genetics, 2022, 109, 1298-1307.	2.6	26
2	Genome-wide mapping of somatic mutation rates uncovers drivers of cancer. Nature Biotechnology, 2022, 40, 1634-1643.	9.4	23
3	Incorporating family history of disease improves polygenic risk scores in diverse populations. Cell Genomics, 2022, 2, 100152.	3.0	17
4	Chromosomal phase improves aneuploidy detection in non-invasive prenatal testing at low fetal DNA fractions. Scientific Reports, 2022, 12, .	1.6	1
5	Large mosaic copy number variations confer autism risk. Nature Neuroscience, 2021, 24, 197-203.	7.1	36
6	Estimating the effective sample size in association studies of quantitative traits. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	12
7	A model and test for coordinated polygenic epistasis in complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
8	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
9	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. Nature Communications, 2021, 12, 4178.	5.8	20
10	Whole-exome imputation within UK Biobank powers rare coding variant association and fine-mapping analyses. Nature Genetics, 2021, 53, 1260-1269.	9.4	88
11	Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. Science, 2021, 373, 1499-1505.	6.0	96
12	Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. Nature Communications, 2021, 12, 6052.	5.8	52
13	Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067.	1.4	16
14	Chromosomal alterations among age-related haematopoietic clones in Japan. Nature, 2020, 584, 130-135.	13.7	102
15	Monogenic and polygenic inheritance become instruments for clonal selection. Nature, 2020, 584, 136-141.	13.7	119
16	Liability threshold modeling of caseâ€“control status and family history of disease increases association power. Nature Genetics, 2020, 52, 541-547.	9.4	60
17	Genetically predicted telomere length is associated with clonal somatic copy number alterations in peripheral leukocytes. PLoS Genetics, 2020, 16, e1009078.	1.5	14
18	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719.	5.8	50

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19	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
20	Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913.	2.6	46
21	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. Nature Communications, 2019, 10, 569.	5.8	50
22	Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790.	5.8	98
23	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
24	Fast, sensitive and accurate integration of single-cell data with Harmony. Nature Methods, 2019, 16, 1289-1296.	9.0	3,494
25	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. American Journal of Human Genetics, 2019, 104, 65-75.	2.6	715
26	Estimating crossâ€population genetic correlations of causal effect sizes. Genetic Epidemiology, 2019, 43, 180-188.	0.6	70
27	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
28	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. Nature Genetics, 2018, 50, 1600-1607.	9.4	132
29	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
30	A genome-wide cross-trait analysis from UK Biobank highlights the shared genetic architecture of asthma and allergic diseases. Nature Genetics, 2018, 50, 857-864.	9.4	191
31	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047.	9.4	154
32	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	13.7	279
33	Mixed-model association for biobank-scale datasets. Nature Genetics, 2018, 50, 906-908.	9.4	521
34	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
35	Stepwise Distributed Open Innovation Contests for Software Development: Acceleration of Genome-Wide Association Analysis. GigaScience, 2017, 6, 1-10.	3.3	16
36	Mixed Model Association with Family-Biased Case-Control Ascertainment. American Journal of Human Genetics, 2017, 100, 31-39.	2.6	14

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37	Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427.	9.4	400
38	Multiethnic polygenic risk scores improve risk prediction in diverse populations. Genetic Epidemiology, 2017, 41, 811-823.	0.6	248
39	Heritability of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	72
40	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	9.4	158
41	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
42	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
43	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	9.4	2,828
44	Response to Shen etÂal.. American Journal of Human Genetics, 2016, 99, 1220-1221.	2.6	0
45	Population Structure of UK Biobank and Ancient Eurasians Reveals Adaptation at Genes Influencing Blood Pressure. American Journal of Human Genetics, 2016, 99, 1130-1139.	2.6	53
46	Fast and accurate long-range phasing in a UK Biobank cohort. Nature Genetics, 2016, 48, 811-816.	9.4	290
47	A Robust Example of Collider Bias in a Genetic Association Study. American Journal of Human Genetics, 2016, 98, 392-393.	2.6	95
48	Fast Principal-Component Analysis Reveals Convergent Evolution of ADH1B in Europe and East Asia. American Journal of Human Genetics, 2016, 98, 456-472.	2.6	335
49	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. PLoS Genetics, 2015, 11, e1005550.	1.5	49
50	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
51	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	9.4	1,285
52	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
53	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
54	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045

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55	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	9.4	3,145
56	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	9.4	431
57	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. American Journal of Human Genetics, 2015, 97, 677-690.	2.6	26
58	Ancient west Eurasian ancestry in southern and eastern Africa. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2632-2637.	3.3	246
59	Genetic Evidence for Recent Population Mixture in India. American Journal of Human Genetics, 2013, 93, 422-438.	2.6	234
60	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. Genetics, 2013, 193, 1233-1254.	1.2	445
61	Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. Molecular Biology and Evolution, 2013, 30, 1788-1802.	3.5	121
62	Prize-based contests can provide solutions to computational biology problems. Nature Biotechnology, 2013, 31, 108-111.	9.4	116
63	Reconstructing Roma History from Genome-Wide Data. PLoS ONE, 2013, 8, e58633.	1.1	61
64	Compressive genomics. Nature Biotechnology, 2012, 30, 627-630.	9.4	99
65	Building Quantitative Prediction Models for Tissue Residue of Two Explosives Compounds in Earthworms from Microarray Gene Expression Data. Environmental Science & Technology, 2012, 46, 19-26.	4.6	13
66	Phenotype Prediction Using Regularized Regression on Genetic Data in the DREAM5 Systems Genetics B Challenge. PLoS ONE, 2011, 6, e29095.	1.1	16