# 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 | LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295. | 9.4 | 3,905 |
| 2 | Fast, sensitive and accurate integration of single-cell data with Harmony. Nature Methods, 2019, 16, 1289-1296. | 9.0 | 3,494 |
| 3 | An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241. | 9.4 | 3,145 |
| 4 | Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287. | 9.4 | 2,828 |
| 5 | Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235. | 9.4 | 2,045 |
| 6 | Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448. | 9.4 | 1,357 |
| 7 | Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290. | 9.4 | 1,285 |
| 8 | Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592. | 2.6 | 1,098 |
| 9 | Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629. | 9.4 | 807 |
| 10 | Leveraging Polygenic Functional Enrichment to Improve GWAS Power. American Journal of Human Genetics, 2019, 104, 65-75. | 2.6 | 715 |
| 11 | Mixed-model association for biobank-scale datasets. Nature Genetics, 2018, 50, 906-908. | 9.4 | 521 |
| 12 | Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. Genetics, 2013, 193, 1233-1254. | 1.2 | 445 |
| 13 | Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392. | 9.4 | 431 |
| 14 | 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 |
| 15 | Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252. | 13.7 | 406 |
| 16 | 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 |
| 17 | Linkage disequilibriumâ€“dependent architecture of human complex traits shows action of negative selection. Nature Genetics, 2017, 49, 1421-1427. | 9.4 | 400 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Fast and accurate long-range phasing in a UK Biobank cohort. Nature Genetics, 2016, 48, 811-816. | 9.4 | 290 |
| 20 | Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355. | 13.7 | 279 |
| 21 | Multiethnic polygenic risk scores improve risk prediction in diverse populations. Genetic Epidemiology, 2017, 41, 811-823. | 0.6 | 248 |
| 22 | 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 |
| 23 | Genetic Evidence for Recent Population Mixture in India. American Journal of Human Genetics, 2013, 93, 422-438. | 2.6 | 234 |
| 24 | Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657. | 13.7 | 198 |
| 25 | 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 |
| 26 | Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623. | 9.4 | 158 |
| 27 | Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. Nature Genetics, 2018, 50, 1041-1047. | 9.4 | 154 |
| 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 | Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. Molecular Biology and Evolution, 2013, 30, 1788-1802. | 3.5 | 121 |
| 30 | Monogenic and polygenic inheritance become instruments for clonal selection. Nature, 2020, 584, 136-141. | 13.7 | 119 |
| 31 | Prize-based contests can provide solutions to computational biology problems. Nature Biotechnology, 2013, 31, 108-111. | 9.4 | 116 |
| 32 | Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024. | 15.2 | 109 |
| 33 | Chromosomal alterations among age-related haematopoietic clones in Japan. Nature, 2020, 584, 130-135. | 13.7 | 102 |
| 34 | Compressive genomics. Nature Biotechnology, 2012, 30, 627-630. | 9.4 | 99 |
| 35 | Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. Nature Communications, 2019, 10, 790. | 5.8 | 98 |
| 36 | Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. Science, 2021, 373, 1499-1505. | 6.0 | 96 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | A Robust Example of Collider Bias in a Genetic Association Study. American Journal of Human Genetics, 2016, 98, 392-393. | 2.6 | 95 |
| 38 | Whole-exome imputation within UK Biobank powers rare coding variant association and fine-mapping analyses. Nature Genetics, 2021, 53, 1260-1269. | 9.4 | 88 |
| 39 | Heritability of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2017, 10, . | 5.1 | 72 |
| 40 | Estimating crossâ€population genetic correlations of causal effect sizes. Genetic Epidemiology, 2019, 43, 180-188. | 0.6 | 70 |
| 41 | Reconstructing Roma History from Genome-Wide Data. PLoS ONE, 2013, 8, e58633. | 1.1 | 61 |
| 42 | Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730. | 2.6 | 60 |
| 43 | Liability threshold modeling of caseâ€“control status and family history of disease increases association power. Nature Genetics, 2020, 52, 541-547. | 9.4 | 60 |
| 44 | Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493. | 9.4 | 55 |
| 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 | Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. Nature Communications, 2021, 12, 6052. | 5.8 | 52 |
| 47 | GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719. | 5.8 | 50 |
| 48 | Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. Nature Communications, 2019, 10, 569. | 5.8 | 50 |
| 49 | Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. PLoS Genetics, 2015, 11, e1005550. | 1.5 | 49 |
| 50 | Genes with High Network Connectivity Are Enriched for Disease Heritability. American Journal of Human Genetics, 2019, 104, 896-913. | 2.6 | 46 |
| 51 | Large mosaic copy number variations confer autism risk. Nature Neuroscience, 2021, 24, 197-203. | 7.1 | 36 |
| 52 | Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. American Journal of Human Genetics, 2015, 97, 677-690. | 2.6 | 26 |
| 53 | A spectrum of recessiveness among Mendelian disease variants in UK Biobank. American Journal of Human Genetics, 2022, 109, 1298-1307. | 2.6 | 26 |
| 54 | Genome-wide mapping of somatic mutation rates uncovers drivers of cancer. Nature Biotechnology, 2022, 40, 1634-1643. | 9.4 | 23 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. Nature Communications, 2021, 12, 4178. | 5.8 | 20 |
| 56 | Incorporating family history of disease improves polygenic risk scores in diverse populations. Cell Genomics, 2022, 2, 100152. | 3.0 | 17 |
| 57 | Phenotype Prediction Using Regularized Regression on Genetic Data in the DREAM5 Systems Genetics B Challenge. PLoS ONE, 2011, 6, e29095. | 1.1 | 16 |
| 58 | Stepwise Distributed Open Innovation Contests for Software Development: Acceleration of Genome-Wide Association Analysis. GigaScience, 2017, 6, 1-10. | 3.3 | 16 |
| 59 | Annotations capturing cell type-specific TF binding explain a large fraction of disease heritability. Human Molecular Genetics, 2020, 29, 1057-1067. | 1.4 | 16 |
| 60 | 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 |
| 61 | Mixed Model Association with Family-Biased Case-Control Ascertainment. American Journal of Human Genetics, 2017, 100, 31-39. | 2.6 | 14 |
| 62 | Genetically predicted telomere length is associated with clonal somatic copy number alterations in peripheral leukocytes. PLoS Genetics, 2020, 16, e1009078. | 1.5 | 14 |
| 63 | 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 |
| 64 | Estimating the effective sample size in association studies of quantitative traits. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 12 |
| 65 | Chromosomal phase improves aneuploidy detection in non-invasive prenatal testing at low fetal DNA fractions. Scientific Reports, 2022, 12, . | 1.6 | 1 |
| 66 | Response to Shen etÂal.. American Journal of Human Genetics, 2016, 99, 1220-1221. | 2.6 | 0 |