Christoph Lippert

List of Publications by Year
in descending order

31	4,034	304743 22	454955 30
papers	citations	h-index	g-index

39	39	39	7426
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	FaST linear mixed models for genome-wide association studies. Nature Methods, 2011, 8, 833-835.	19.0	1,021
2	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	21.4	910
3	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	19.0	292
4	Epigenome-wide association studies without the need for cell-type composition. Nature Methods, 2014, 11, 309-311.	19.0	205
5	Profiling of Short-Tandem-Repeat Disease Alleles in 12,632 Human Whole Genomes. American Journal of Human Genetics, 2017, 101, 700-715.	6.2	142
6	Time to reality check the promises of machine learning-powered precision medicine. The Lancet Digital Health, 2020, 2, e677-e680.	12.3	126
7	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	6.0	126
8	Identification of individuals by trait prediction using whole-genome sequencing data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10166-10171.	7.1	118
9	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	4.1	99
10	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. Plant Cell, 2017, 29, 5-19.	6.6	98
11	Efficient set tests for the genetic analysis of correlated traits. Nature Methods, 2015, 12, 755-758.	19.0	97
12	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. Nature Genetics, 2013, 45, 470-471.	21.4	88
13	A powerful and efficient set test for genetic markers that handles confounders. Bioinformatics, 2013, 29, 1526-1533.	4.1	72
14	Deep learning of genomic variation and regulatory network data. Human Molecular Genetics, 2018, 27, R63-R71.	2.9	64
15	Further Improvements to Linear Mixed Models for Genome-Wide Association Studies. Scientific Reports, 2014, 4, 6874.	3.3	61
16	An Exhaustive Epistatic SNP Association Analysis on Expanded Wellcome Trust Data. Scientific Reports, 2013, 3, 1099.	3.3	59
17	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	12.8	47
18	Patterns of methylation heritability in a genome-wide analysis of four brain regions. Nucleic Acids Research, 2013, 41, 2095-2104.	14.5	44

#	Article	IF	Citations
19	The benefits of selecting phenotype-specific variants for applications of mixed models in genomics. Scientific Reports, 2013, 3, 1815.	3.3	43
20	Multimodal Self-supervised Learning for Medical Image Analysis. Lecture Notes in Computer Science, 2021, , 661-673.	1.3	40
21	Accurate liability estimation improves power in ascertained case-control studies. Nature Methods, 2015, 12, 332-334.	19.0	36
22	Greater power and computational efficiency for kernel-based association testing of sets of genetic variants. Bioinformatics, 2014, 30, 3206-3214.	4.1	35
23	Gene function prediction from synthetic lethality networks via ranking on demand. Bioinformatics, 2010, 26, 912-918.	4.1	23
24	Quantifying the uncertainty in heritability. Journal of Human Genetics, 2014, 59, 269-275.	2.3	21
25	Predicting the SARS-CoV-2 effective reproduction number using bulk contact data from mobile phones. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
26	transferGWAS: GWAS of images using deep transfer learning. Bioinformatics, 2022, 38, 3621-3628.	4.1	15
27	Detecting regulatory geneâ€“environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	4.1	12
28	Ensembles of Lasso Screening Rules. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2018, 40, 2841-2852.	13.9	12
29	Self-Supervised Learning Methods for Label-Efficient Dental Caries Classification. Diagnostics, 2022, 12, 1237.	2.6	8
30	Sparse probit linear mixed model. Machine Learning, 2017, 106, 1621-1642.	5.4	4
31	Computational and statistical issues in personalized medicine. Xrds, 2015, 21, 24-27.	0.3	0