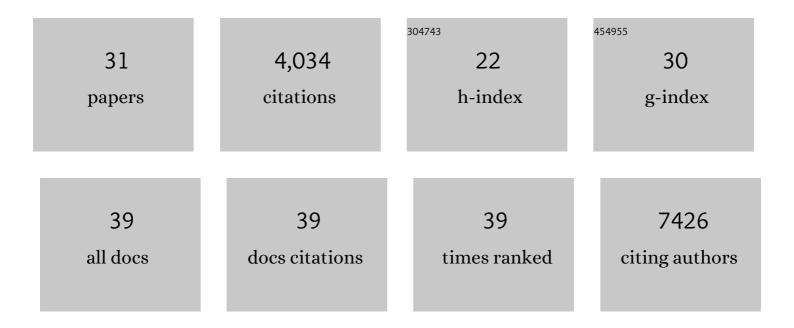
## **Christoph Lippert**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/652246/publications.pdf Version: 2024-02-01



CHRISTORN LIDDERT

#	Article	IF	CITATIONS
1	Self-Supervised Learning Methods for Label-Efficient Dental Caries Classification. Diagnostics, 2022, 12, 1237.	2.6	8
2	transferGWAS: GWAS of images using deep transfer learning. Bioinformatics, 2022, 38, 3621-3628.	4.1	15
3	Multimodal Self-supervised Learning for Medical Image Analysis. Lecture Notes in Computer Science, 2021, , 661-673.	1.3	40
4	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
5	Time to reality check the promises of machine learning-powered precision medicine. The Lancet Digital Health, 2020, 2, e677-e680.	12.3	126
6	Deep learning of genomic variation and regulatory network data. Human Molecular Genetics, 2018, 27, R63-R71.	2.9	64
7	Ensembles of Lasso Screening Rules. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2018, 40, 2841-2852.	13.9	12
8	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. Plant Cell, 2017, 29, 5-19.	6.6	98
9	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
10	Identification of individuals by trait prediction using whole-genome sequencing data. Proceedings of the United States of America, 2017, 114, 10166-10171.	7.1	118
11	Sparse probit linear mixed model. Machine Learning, 2017, 106, 1621-1642.	5.4	4
12	Accurate liability estimation improves power in ascertained case-control studies. Nature Methods, 2015, 12, 332-334.	19.0	36
13	Efficient set tests for the genetic analysis of correlated traits. Nature Methods, 2015, 12, 755-758.	19.0	97
14	Computational and statistical issues in personalized medicine. Xrds, 2015, 21, 24-27.	0.3	0
15	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	12.8	47
16	Quantifying the uncertainty in heritability. Journal of Human Genetics, 2014, 59, 269-275.	2.3	21
17	Greater power and computational efficiency for kernel-based association testing of sets of genetic variants. Bioinformatics, 2014, 30, 3206-3214.	4.1	35
18	Epigenome-wide association studies without the need for cell-type composition. Nature Methods, 2014, 11, 309-311.	19.0	205

CHRISTOPH LIPPERT

#	Article	IF	CITATIONS
19	Further Improvements to Linear Mixed Models for Genome-Wide Association Studies. Scientific Reports, 2014, 4, 6874.	3.3	61
20	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	4.1	99
21	FaST-LMM-Select for addressing confounding from spatial structure and rare variants. Nature Genetics, 2013, 45, 470-471.	21.4	88
22	An Exhaustive Epistatic SNP Association Analysis on Expanded Wellcome Trust Data. Scientific Reports, 2013, 3, 1099.	3.3	59
23	Patterns of methylation heritability in a genome-wide analysis of four brain regions. Nucleic Acids Research, 2013, 41, 2095-2104.	14.5	44
24	The benefits of selecting phenotype-specific variants for applications of mixed models in genomics. Scientific Reports, 2013, 3, 1815.	3.3	43
25	A powerful and efficient set test for genetic markers that handles confounders. Bioinformatics, 2013, 29, 1526-1533.	4.1	72
26	Detecting regulatory gene–environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	4.1	12
27	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
28	Improved linear mixed models for genome-wide association studies. Nature Methods, 2012, 9, 525-526.	19.0	292
29	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	21.4	910
30	FaST linear mixed models for genome-wide association studies. Nature Methods, 2011, 8, 833-835.	19.0	1,021
31	Gene function prediction from synthetic lethality networks via ranking on demand. Bioinformatics, 2010, 26, 912-918.	4.1	23