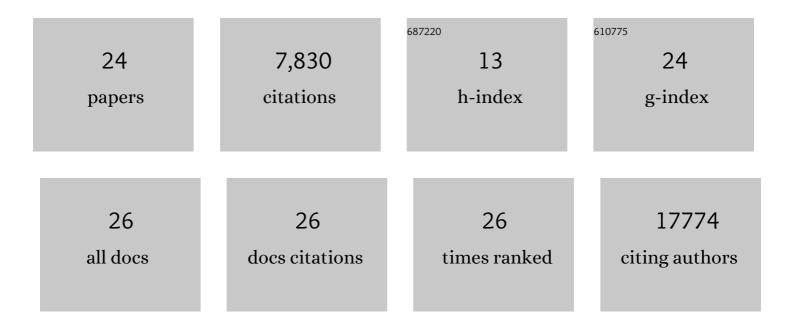
## Jake Lin

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2360066/publications.pdf Version: 2024-02-01



IAVE LIN

#	Article	IF	CITATIONS
1	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. European Journal of Human Genetics, 2021, 29, 309-324.	1.4	19
2	IDARE2â€"Simultaneous Visualisation of Multiomics Data in Cytoscape. Metabolites, 2021, 11, 300.	1.3	2
3	Metagenomics of the faecal virome indicate a cumulative effect of enterovirus and gluten amount on the risk of coeliac disease autoimmunity in genetically at risk children: the TEDDY study. Gut, 2020, 69, 1416-1422.	6.1	82
4	Genetic Adaptation of Coxsackievirus B1 during Persistent Infection in Pancreatic Cells. Microorganisms, 2020, 8, 1790.	1.6	11
5	MetaPhat: Detecting and Decomposing Multivariate Associations From Univariate Genome-Wide Association Statistics. Frontiers in Genetics, 2020, 11, 431.	1.1	12
6	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	1.6	60
7	Data-driven characterization of molecular phenotypes across heterogeneous sample collections. Nucleic Acids Research, 2019, 47, e76-e76.	6.5	23
8	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. Cancer Research, 2019, 79, 2466-2479.	0.4	23
9	Changes in the lung bacteriome in relation to antipseudomonal therapy in children with cystic fibrosis. Folia Microbiologica, 2018, 63, 237-248.	1.1	5
10	Nature-derived microbiota exposure as a novel immunomodulatory approach. Future Microbiology, 2018, 13, 737-744.	1.0	50
11	Bioinformatics Assembling and Assessment of Novel Coxsackievirus B1 Genome. Methods in Molecular Biology, 2018, 1838, 261-272.	0.4	2
12	Imbalance of bacteriome profiles within the Finnish Diabetes Prediction and Prevention study: Parallel use of 16S profiling and virome sequencing in stool samples from children with islet autoimmunity and matched controls. Pediatric Diabetes, 2017, 18, 588-598.	1.2	44
13	Vipie: web pipeline for parallel characterization of viral populations from multiple NGS samples. BMC Genomics, 2017, 18, 378.	1.2	20
14	Quantitative analysis of colony morphology in yeast. BioTechniques, 2014, 56, 18-27.	0.8	21
15	Integrated analysis of transcript-level regulation of metabolism reveals disease-relevant nodes of the human metabolic network. Nucleic Acids Research, 2014, 42, 1474-1496.	6.5	42
16	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. BMC Genomics, 2014, 15, 1154.	1.2	126
17	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	5.8	75
18	Transcriptomics profiling of human SGBS adipogenesis. Genomics Data, 2014, 2, 246-248.	1.3	3

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#	Article	IF	CITATIONS
19	ChIP-seq profiling of the active chromatin marker H3K4me3 and PPARγ, CEBPα and LXR target genes in human SGBS adipocytes. Genomics Data, 2014, 2, 230-236.	1.3	4
20	POMO - Plotting Omics analysis results for Multiple Organisms. BMC Genomics, 2013, 14, 918.	1.2	4
21	High-throughput tetrad analysis. Nature Methods, 2013, 10, 671-675.	9.0	20
22	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
23	Fastbreak: a tool for analysis and visualization of structural variations in genomic data. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 15.	1.4	6
24	EPEPT: A web service for enhanced P-value estimation in permutation tests. BMC Bioinformatics, 2011, 12, 411.	1.2	6