

Jake Lin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2360066/publications.pdf>

Version: 2024-02-01

24
papers

7,830
citations

686830

13
h-index

610482

24
g-index

26
all docs

26
docs citations

26
times ranked

17774
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
2	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. <i>BMC Genomics</i> , 2014, 15, 1154.	1.2	126
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. <i>Gut</i> , 2020, 69, 1416-1422.	6.1	82
4	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	5.8	75
5	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002725.	1.6	60
6	Nature-derived microbiota exposure as a novel immunomodulatory approach. <i>Future Microbiology</i> , 2018, 13, 737-744.	1.0	50
7	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. <i>Pediatric Diabetes</i> , 2017, 18, 588-598.	1.2	44
8	Integrated analysis of transcript-level regulation of metabolism reveals disease-relevant nodes of the human metabolic network. <i>Nucleic Acids Research</i> , 2014, 42, 1474-1496.	6.5	42
9	Data-driven characterization of molecular phenotypes across heterogeneous sample collections. <i>Nucleic Acids Research</i> , 2019, 47, e76-e76.	6.5	23
10	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. <i>Cancer Research</i> , 2019, 79, 2466-2479.	0.4	23
11	Quantitative analysis of colony morphology in yeast. <i>BioTechniques</i> , 2014, 56, 18-27.	0.8	21
12	High-throughput tetrad analysis. <i>Nature Methods</i> , 2013, 10, 671-675.	9.0	20
13	Vipie: web pipeline for parallel characterization of viral populations from multiple NGS samples. <i>BMC Genomics</i> , 2017, 18, 378.	1.2	20
14	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. <i>European Journal of Human Genetics</i> , 2021, 29, 309-324.	1.4	19
15	MetaPhat: Detecting and Decomposing Multivariate Associations From Univariate Genome-Wide Association Statistics. <i>Frontiers in Genetics</i> , 2020, 11, 431.	1.1	12
16	Genetic Adaptation of Coxsackievirus B1 during Persistent Infection in Pancreatic Cells. <i>Microorganisms</i> , 2020, 8, 1790.	1.6	11
17	EPEPT: A web service for enhanced P-value estimation in permutation tests. <i>BMC Bioinformatics</i> , 2011, 12, 411.	1.2	6
18	Fastbreak: a tool for analysis and visualization of structural variations in genomic data. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2012, 2012, 15.	1.4	6

#	ARTICLE	IF	CITATIONS
19	Changes in the lung bacteriome in relation to antipseudomonal therapy in children with cystic fibrosis. <i>Folia Microbiologica</i> , 2018, 63, 237-248.	1.1	5
20	POMO - Plotting Omics analysis results for Multiple Organisms. <i>BMC Genomics</i> , 2013, 14, 918.	1.2	4
21	ChIP-seq profiling of the active chromatin marker H3K4me3 and PPAR α , CEBP β and LXR target genes in human SGBS adipocytes. <i>Genomics Data</i> , 2014, 2, 230-236.	1.3	4
22	Transcriptomics profiling of human SGBS adipogenesis. <i>Genomics Data</i> , 2014, 2, 246-248.	1.3	3
23	Bioinformatics Assembling and Assessment of Novel Coxsackievirus B1 Genome. <i>Methods in Molecular Biology</i> , 2018, 1838, 261-272.	0.4	2
24	IDARE2â€™ Simultaneous Visualisation of Multiomics Data in Cytoscape. <i>Metabolites</i> , 2021, 11, 300.	1.3	2