Lin S Chen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5576029/publications.pdf

Version: 2024-02-01

30 papers	2,108 citations	471509 17 h-index	434195 31 g-index
33 all docs	33 docs citations	33 times ranked	4423 citing authors

#	Article	IF	Citations
1	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
2	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
3	Determinants of telomere length across human tissues. Science, 2020, 369, .	12.6	257
4	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
5	Insights into Colon Cancer Etiology via a Regularized Approach to Gene Set Analysis of GWAS Data. American Journal of Human Genetics, 2010, 86, 860-871.	6.2	130
6	Harnessing naturally randomized transcription to infer regulatory relationships among genes. Genome Biology, 2007, 8, R219.	9.6	109
7	Mediation Analysis Demonstrates That Trans-eQTLs Are Often Explained by Cis-Mediation: A Genome-Wide Analysis among 1,800 South Asians. PLoS Genetics, 2014, 10, e1004818.	3.5	88
8	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nature Communications, 2018, 9, 4181.	12.8	77
9	Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
10	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. Nature Communications, 2018, 9, 804.	12.8	66
11	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
12	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. Human Molecular Genetics, 2016, 25, ddw305.	2.9	50
13	An Exponential Combination Procedure for Set-Based Association Tests in Sequencing Studies. American Journal of Human Genetics, 2012, 91, 977-986.	6.2	34
14	Genome-wide association study of telomere length among South Asians identifies a second RTEL1 association signal. Journal of Medical Genetics, 2018, 55, 64-71.	3.2	33
15	Primo: integration of multiple GWAS and omics QTL summary statistics for elucidation of molecular mechanisms of trait-associated SNPs and detection of pleiotropy in complex traits. Genome Biology, 2020, 21, 236.	8.8	26
16	The contribution of parent-to-offspring transmission of telomeres to the heritability of telomere length in humans. Human Genetics, 2019, 138, 49-60.	3.8	24
17	Insights into Impact of DNA Copy Number Alteration and Methylation on the Proteogenomic Landscape of Human Ovarian Cancer via a Multi-omics Integrative Analysis. Molecular and Cellular Proteomics, 2019, 18, S52-S65.	3.8	23
18	IGREX for quantifying the impact of genetically regulated expression on phenotypes. NAR Genomics and Bioinformatics, 2020, 2, lqaa010.	3.2	15

#	Article	IF	Citations
19	A Unified Set-Based Test with Adaptive Filtering for Geneâ€“Environment Interaction Analyses. Biometrics, 2016, 72, 629-638.	1.4	14
20	The association between telomere length and mortality in Bangladesh. Aging, 2017, 9, 1537-1551.	3.1	12
21	Breast cancer risk after fullâ€term pregnancies among A frican women from N igeria, C ameroon, and U ganda. Cancer, 2015, 121, 2237-2243.	4.1	11
22	A robust twoâ€sample transcriptomeâ€wide Mendelian randomization method integrating GWAS with multiâ€tissue eQTL summary statistics. Genetic Epidemiology, 2021, 45, 353-371.	1.3	11
23	A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. Annals of Applied Statistics, 2017, 11, 114-138.	1.1	9
24	Germline Variation and Breast Cancer Incidence: A Gene-Based Association Study and Whole-Genome Prediction of Early-Onset Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1057-1064.	2.5	9
25	Rare, Protein-Altering Variants in AS3MT and Arsenic Metabolism Efficiency: A Multi-Population Association Study. Environmental Health Perspectives, 2021, 129, 47007.	6.0	9
26	Integrative Proteo-genomic Analysis to Construct CNA-protein Regulatory Map in Breast and Ovarian Tumors. Molecular and Cellular Proteomics, 2019, 18, S66-S81.	3.8	6
27	A metaâ€analysis approach with filtering for identifying geneâ€level geneâ€“environment interactions. Genetic Epidemiology, 2018, 42, 434-446.	1.3	5
28	Using eQTLs to Reconstruct Gene Regulatory Networks. Methods in Molecular Biology, 2012, 871, 175-189.	0.9	4
29	CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. Bioinformatics, 2021, 37, 2513-2520.	4.1	4
30	Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. Biostatistics, 2019, 20, 648-665.	1.5	3