Lin S Chen

List of Publications by Year
in descending order

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

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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	CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. Bioinformatics, 2021, 37, 2513-2520.	4.1	4
2	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
3	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
4	Rare, Protein-Altering Variants in AS3MT and Arsenic Metabolism Efficiency: A Multi-Population Association Study. Environmental Health Perspectives, 2021, 129, 47007.	6.0	9
5	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
6	Determinants of telomere length across human tissues. Science, 2020, 369, .	12.6	257
7	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
8	IGREX for quantifying the impact of genetically regulated expression on phenotypes. NAR Genomics and Bioinformatics, 2020, 2, lqaa010.	3.2	15
9	Using multivariate mixed-effects selection models for analyzing batch-processed proteomics data with non-ignorable missingness. Biostatistics, 2019, 20, 648-665.	1.5	3
10	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
11	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
12	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
13	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
14	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. Nature Communications, 2018, 9, 804.	12.8	66
15	A metaâ€analysis approach with filtering for identifying geneâ€level geneâ€“environment interactions. Genetic Epidemiology, 2018, 42, 434-446.	1.3	5
16	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nature Communications, 2018, 9, 4181.	12.8	77
17	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
18	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

#	Article	IF	Citations
19	Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. Genome Research, 2017, 27, 1859-1871.	5.5	72
20	A mixed-effects model for incomplete data from labeling-based quantitative proteomics experiments. Annals of Applied Statistics, 2017, 11, 114-138.	1.1	9
21	The association between telomere length and mortality in Bangladesh. Aging, 2017, 9, 1537-1551.	3.1	12
22	A Unified Set-Based Test with Adaptive Filtering for Geneâ€“Environment Interaction Analyses. Biometrics, 2016, 72, 629-638.	1.4	14
23	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
24	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
25	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
26	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
27	An Exponential Combination Procedure for Set-Based Association Tests in Sequencing Studies. American Journal of Human Genetics, 2012, 91, 977-986.	6.2	34
28	Using eQTLs to Reconstruct Gene Regulatory Networks. Methods in Molecular Biology, 2012, 871, 175-189.	0.9	4
29	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
30	Harnessing naturally randomized transcription to infer regulatory relationships among genes. Genome Biology, 2007, 8, R219.	9.6	109