Hon-Cheong So

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5795005/publications.pdf

Version: 2024-02-01

45 papers	4,826 citations	279487 23 h-index	243296 44 g-index
55 all docs	55 docs citations	55 times ranked	12207 citing authors

#	Article	IF	Citations
1	Prediction of Drug Targets for Specific Diseases Leveraging Gene Perturbation Data: A Machine Learning Approach. Pharmaceutics, 2022, 14, 234.	2.0	6
2	Contributions of common genetic variants to specific languages and to when a language is learned. Scientific Reports, 2022, 12, 580.	1.6	4
3	Causal relationships between blood lipids and depression phenotypes: a Mendelian randomisation analysis. Psychological Medicine, 2021, 51, 2357-2369.	2.7	30
4	Causal associations of short and long sleep durations with 12 cardiovascular diseases: linear and nonlinear Mendelian randomization analyses in UK Biobank. European Heart Journal, 2021, 42, 3349-3357.	1.0	122
5	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
6	A framework to decipher the genetic architecture of combinations of complex diseases: applications in cardiovascular medicine. Bioinformatics, 2021, 37, 4137-4147.	1.8	2
7	Analysis of genetic differences between psychiatric disorders: exploring pathways and cell types/tissues involved and ability to differentiate the disorders by polygenic scores. Translational Psychiatry, 2021, 11, 426.	2.4	1
8	Exploring Drugs and Vaccines Associated with Altered Risks and Severity of COVID-19: A UK Biobank Cohort Study of All ATC Level-4 Drug Categories Reveals Repositioning Opportunities. Pharmaceutics, 2021, 13, 1514.	2.0	16
9	Uncovering Clinical Risk Factors and Predicting Severe COVID-19 Cases Using UK Biobank Data: Machine Learning Approach. JMIR Public Health and Surveillance, 2021, 7, e29544.	1.2	20
10	Genome-wide copy number variation-, validation- and screening study implicates a new copy number polymorphism associated with suicide attempts in major depressive disorder. Gene, 2020, 755, 144901.	1.0	8
11	Pharmacologically reversible zonation-dependent endothelial cell transcriptomic changes with neurodegenerative disease associations in the aged brain. Nature Communications, 2020, 11, 4413.	5.8	59
12	Exploring Diseases/Traits and Blood Proteins Causally Related to Expression of ACE2, the Putative Receptor of SARS-CoV-2: A Mendelian Randomization Analysis Highlights Tentative Relevance of Diabetes-Related Traits. Diabetes Care, 2020, 43, 1416-1426.	4.3	183
13	ASPM -lexical tone association in speakers of a tone language: Direct evidence for the genetic-biasing hypothesis of language evolution. Science Advances, 2020, 6, eaba5090.	4.7	24
14	Epigenetic CRISPR Screens Identify Npm1 as a Therapeutic Vulnerability in Nonâ€“Small Cell Lung Cancer. Cancer Research, 2020, 80, 3556-3567.	0.4	17
15	Turning genome-wide association study findings into opportunities for drug repositioning. Computational and Structural Biotechnology Journal, 2020, 18, 1639-1650.	1.9	21
16	Exploring shared genetic bases and causal relationships of schizophrenia and bipolar disorder with 28 cardiovascular and metabolic traits. Psychological Medicine, 2019, 49, 1286-1298.	2.7	64
17	Drug Repositioning for Schizophrenia and Depression/Anxiety Disorders: A Machine Learning Approach Leveraging Expression Data. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1304-1315.	3.9	60
18	Integrating Clinical Data and Imputed Transcriptome from GWAS to Uncover Complex Disease Subtypes: Applications in Psychiatry and Cardiology. American Journal of Human Genetics, 2019, 105, 1193-1212.	2.6	18

#	Article	IF	Citations
19	Translating GWAS findings into therapies for depression and anxiety disorders: gene-set analyses reveal enrichment of psychiatric drug classes and implications for drug repositioning. Psychological Medicine, 2019, 49, 2692-2708.	2.7	18
20	Using Drug Expression Profiles and Machine Learning Approach for Drug Repurposing. Methods in Molecular Biology, 2019, 1903, 219-237.	0.4	25
21	Implications of de novo mutations in guiding drug discovery: A study of four neuropsychiatric disorders. Journal of Psychiatric Research, 2019, 110, 83-92.	1.5	3
22	Differential associations of depressionâ€related phenotypes with cardiometabolic risks: Polygenic analyses and exploring shared genetic variants and pathways. Depression and Anxiety, 2019, 36, 330-344.	2.0	26
23	Leveraging genome-wide association and clinical data in revealing schizophrenia subgroups. Journal of Psychiatric Research, 2018, 106, 106-117.	1.5	13
24	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
25	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
26	Newspaper coverage of mental illness in <scp>H</scp>ong <scp>K</scp>ong between 2002 and 2012: impact of introduction of a new <scp>C</scp>hinese name of psychosis. Microbial Biotechnology, 2017, 11, 342-345.	0.9	15
27	Exploring the predictive power of polygenic scores derived from genome-wide association studies: a study of 10 complex traits. Bioinformatics, 2017, 33, 886-892.	1.8	39
28	Improving polygenic risk prediction from summary statistics by an empirical Bayes approach. Scientific Reports, 2017, 7, 41262.	1.6	42
29	Analysis of genome-wide association data highlights candidates for drug repositioning in psychiatry. Nature Neuroscience, 2017, 20, 1342-1349.	7.1	135
30	Admission Rates and Psychiatric Beds in Hong Kong, 1999â€“2014: A Population-Based Study. Psychiatric Services, 2016, 67, 579-579.	1.1	3
31	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
32	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	9.4	214
33	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
34	Common Variants on Xq28 Conferring Risk of Schizophrenia in Han Chinese. Schizophrenia Bulletin, 2014, 40, 777-786.	2.3	49
35	No NRG1 V266L in Chinese patients with schizophrenia. Psychiatric Genetics, 2011, 21, 47-49.	0.6	2
36	Multiple Testing and Power Calculations in Genetic Association Studies. Cold Spring Harbor Protocols, 2011, 2011, pdb.top95.	0.2	12

#	Article	IF	Citations
37	Risk Prediction of Complex Diseases from Family History and Known Susceptibility Loci, with Applications for Cancer Screening. American Journal of Human Genetics, 2011, 88, 548-565.	2.6	80
38	Robust Association Tests Under Different Genetic Models, Allowing for Binary or Quantitative Traits and Covariates. Behavior Genetics, 2011, 41, 768-775.	1.4	56
39	Evaluating the heritability explained by known susceptibility variants: a survey of ten complex diseases. Genetic Epidemiology, 2011, 35, 310-317.	0.6	265
40	Uncovering the total heritability explained by all true susceptibility variants in a genome-wide association study. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	67
41	Identification of neuroglycan C and interacting partners as potential susceptibility genes for schizophrenia in a Southern Chinese population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 103-113.	1.1	20
42	Estimating the Total Number of Susceptibility Variants Underlying Complex Diseases from Genome-Wide Association Studies. PLoS ONE, 2010, 5, e13898.	1.1	16
43	A Unifying Framework for Evaluating the Predictive Power of Genetic Variants Based on the Level of Heritability Explained. PLoS Genetics, 2010, 6, e1001230.	1.5	35
44	Effect Size Measures in Genetic Association Studies and Age-Conditional Risk Prediction. Human Heredity, 2010, 70, 205-218.	0.4	10
45	An association study of RGS4 polymorphisms with clinical phenotypes of schizophrenia in a Chinese population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 77-85.	1.1	32