

Nicholas Mancuso

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6870539/publications.pdf>

Version: 2024-02-01

33
papers

3,271
citations

430874

18
h-index

377865

34
g-index

55
all docs

55
docs citations

55
times ranked

6154
citing authors

#	ARTICLE	IF	CITATIONS
1	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. <i>International Journal of Cancer</i> , 2022, 150, 80-90.	5.1	9
2	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2022, 36, 865-868.	7.2	9
3	Genetically regulated multi-omics study for symptom clusters of posttraumatic stress disorder highlights pleiotropy with hematologic and cardio-metabolic traits. <i>Molecular Psychiatry</i> , 2022, 27, 1394-1404.	7.9	15
4	A genealogical estimate of genetic relationships. <i>American Journal of Human Genetics</i> , 2022, 109, 812-824.	6.2	13
5	Interaction between maternal killer immunoglobulin-like receptors and offspring HLAs and susceptibility of childhood ALL. <i>Blood Advances</i> , 2022, 6, 3756-3766.	5.2	3
6	Investigating DNA methylation as a mediator of genetic risk in childhood acute lymphoblastic leukemia. <i>Human Molecular Genetics</i> , 2022, 31, 3741-3756.	2.9	0
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021, 53, 65-75.	21.4	264
8	A Hierarchical Approach Using Marginal Summary Statistics for Multiple Intermediates in a Mendelian Randomization or Transcriptome Analysis. <i>American Journal of Epidemiology</i> , 2021, 190, 1148-1158.	3.4	3
9	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	6.3	41
10	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. <i>PLoS Genetics</i> , 2021, 17, e1008973.	3.5	35
11	Multitrait transcriptome-wide association study (TWAS) tests. <i>Genetic Epidemiology</i> , 2021, 45, 563-576.	1.3	9
12	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. <i>Nature Communications</i> , 2021, 12, 4569.	12.8	47
13	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. <i>Genome Medicine</i> , 2021, 13, 123.	8.2	23
14	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. <i>American Journal of Human Genetics</i> , 2021, 108, 2284-2300.	6.2	31
15	The Role of Genetically Determined Glycemic Traits in Breast Cancer: A Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2020, 11, 540724.	2.3	3
16	Localizing Components of Shared Transethnic Genetic Architecture of Complex Traits from GWAS Summary Data. <i>American Journal of Human Genetics</i> , 2020, 106, 805-817.	6.2	71
17	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. <i>Nature Genetics</i> , 2019, 51, 1244-1251.	21.4	69
18	Post genome-wide gene-environment interaction study: The effect of genetically driven insulin resistance on breast cancer risk using Mendelian randomization. <i>PLoS ONE</i> , 2019, 14, e0218917.	2.5	8

#	ARTICLE	IF	CITATIONS
19	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. <i>Cell</i> , 2019, 179, 750-771.e22.	28.9	174
20	Integrative analysis of Dupuytren's disease identifies novel risk locus and reveals a shared genetic etiology with BMI. <i>Genetic Epidemiology</i> , 2019, 43, 629-645.	1.3	13
21	Probabilistic fine-mapping of transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 675-682.	21.4	275
22	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
23	Genome-Wide Meta-analysis of Gene-Environment Interaction for Insulin Resistance Phenotypes and Breast Cancer Risk in Postmenopausal Women. <i>Cancer Prevention Research</i> , 2019, 12, 31-42.	1.5	15
24	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	21.4	406
25	Placenta and appetite genes GDF15 and IGFBP7 are associated with hyperemesis gravidarum. <i>Nature Communications</i> , 2018, 9, 1178.	12.8	106
26	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. <i>American Journal of Human Genetics</i> , 2018, 103, 535-552.	6.2	90
27	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	12.8	121
28	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 473-487.	6.2	248
29	Local Genetic Correlation Gives Insights into the Shared Genetic Architecture of Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 101, 737-751.	6.2	220
30	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017, 136, 1363-1373.	3.8	39
31	Targeted mutagenesis in a human-parasitic nematode. <i>PLoS Pathogens</i> , 2017, 13, e1006675.	4.7	104
32	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2016, 48, 30-35.	21.4	139
33	Reconstructing viral quasiespecies from NGS amplicon reads. <i>In Silico Biology</i> , 2011, 11, 237-49.	0.9	15