

# Nicholas Mancuso

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

3,271  
citations

430442

18  
h-index

377514

34  
g-index

55  
all docs

55  
docs citations

55  
times ranked

6154  
citing authors

#	ARTICLE	IF	CITATIONS
1	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	9.4	592
2	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	9.4	406
3	Probabilistic fine-mapping of transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 675-682.	9.4	275
4	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.	9.4	264
5	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.	2.6	248
6	Local Genetic Correlation Gives Insights into the Shared Genetic Architecture of Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 101, 737-751.	2.6	220
7	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. <i>Cell</i> , 2019, 179, 750-771.e22.	13.5	174
8	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2016, 48, 30-35.	9.4	139
9	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	5.8	121
10	Placenta and appetite genes GDF15 and IGFBP7 are associated with hyperemesis gravidarum. <i>Nature Communications</i> , 2018, 9, 1178.	5.8	106
11	Targeted mutagenesis in a human-parasitic nematode. <i>PLoS Pathogens</i> , 2017, 13, e1006675.	2.1	104
12	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.	2.6	90
13	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.	2.6	71
14	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. <i>Nature Genetics</i> , 2019, 51, 1244-1251.	9.4	69
15	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. <i>Nature Communications</i> , 2021, 12, 4569.	5.8	47
16	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	3.0	41
17	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017, 136, 1363-1373.	1.8	39
18	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.	1.5	35

#	ARTICLE	IF	CITATIONS
19	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. <i>American Journal of Human Genetics</i> , 2021, 108, 2284-2300.	2.6	31
20	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. <i>Genome Medicine</i> , 2021, 13, 123.	3.6	23
21	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.	0.7	15
22	Reconstructing viral quasispecies from NGS amplicon reads. <i>In Silico Biology</i> , 2011, 11, 237-49.	0.4	15
23	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.	4.1	15
24	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.	0.6	13
25	A genealogical estimate of genetic relationships. <i>American Journal of Human Genetics</i> , 2022, 109, 812-824.	2.6	13
26	Multitrait transcriptome-wide association study (TWAS) tests. <i>Genetic Epidemiology</i> , 2021, 45, 563-576.	0.6	9
27	A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. <i>International Journal of Cancer</i> , 2022, 150, 80-90.	2.3	9
28	Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2022, 36, 865-868.	3.3	9
29	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.	1.1	8
30	The Role of Genetically Determined Glycemic Traits in Breast Cancer: A Mendelian Randomization Study. <i>Frontiers in Genetics</i> , 2020, 11, 540724.	1.1	3
31	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.	1.6	3
32	Interaction between maternal killer immunoglobulin-like receptors and offspring HLAs and susceptibility of childhood ALL. <i>Blood Advances</i> , 2022, 6, 3756-3766.	2.5	3
33	Investigating DNA methylation as a mediator of genetic risk in childhood acute lymphoblastic leukemia. <i>Human Molecular Genetics</i> , 2022, 31, 3741-3756.	1.4	0