Vinicius Tragante Do O

List of Publications by Year
in descending order

68 papers	4,841 citations	136885 32 h-index	110317 64 g-index
70 all docs	70 docs citations	70 times ranked	11238 citing authors

#	Article	IF	Citations
1	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
2	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
3	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
4	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
5	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
6	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
7	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
8	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
9	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
10	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
11	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
12	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
13	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
14	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
15	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
16	Relations between lipoprotein(a) concentrations, LPA genetic variants, and the risk of mortality in patients with established coronary heart disease: a molecular and genetic association study. Lancet Diabetes and Endocrinology,the, 2017, 5, 534-543.	5.5	84
17	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
18	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83

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19	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	13.7	81
20	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
21	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
22	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
23	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. European Heart Journal, 2021, 42, 1742-1756.	1.0	63
24	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
25	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59
26	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	5.8	59
27	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	3.6	49
28	The ENCODE Project and Perspectives on Pathways. Genetic Epidemiology, 2014, 38, 275-280.	0.6	47
29	Genetic Variants at Chromosome 9p21 and RiskÂof First Versus Subsequent Coronary HeartÂDisease Events. Journal of the American College of Cardiology, 2014, 63, 2234-2245.	1.2	44
30	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	5.8	44
31	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	1.6	43
32	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
33	Distinction between the effects of parental and fetal genomes on fetal growth. Nature Genetics, 2021, 53, 1135-1142.	9.4	41
34	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
35	Assessing thyroid cancer risk using polygenic risk scores. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5997-6002.	3.3	39
36	The impact of susceptibility loci for coronary artery disease on other vascular domains and recurrence risk. European Heart Journal, 2013, 34, 2896-2904.	1.0	32

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37	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
38	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. JAMA Cardiology, 2020, 5, 13.	3.0	29
39	Sequence variants with large effects on cardiac electrophysiology and disease. Nature Communications, 2019, 10, 4803.	5.8	28
40	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
41	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
42	Comprehensive pathway analyses of schizophrenia risk loci point to dysfunctional postsynaptic signaling. Schizophrenia Research, 2018, 199, 195-202.	1.1	26
43	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
44	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
45	Impact of carotid atherosclerosis loci on cardiovascular events. Atherosclerosis, 2015, 243, 466-468.	0.4	18
46	Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. Circulation: Cardiovascular Genetics, 2015, 8, 327-333.	5.1	17
47	Instance-level accuracy versus bag-level accuracy in multi-instance learning. Data Mining and Knowledge Discovery, 2016, 30, 313-341.	2.4	17
48	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	1.6	17
49	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
50	Estudo espacial e temporal da hansenÃase no estado de SÃ£o Paulo, 2004-2006. Revista De Saude Publica, 2008, 42, 1012-1020.	0.7	15
51	Harnessing publicly available genetic data to prioritize lipid modifying therapeutic targets for prevention of coronary heart disease based on dysglycemic risk. Human Genetics, 2016, 135, 453-467.	1.8	15
52	Association of the coronary artery disease risk gene GUCY1A3 with ischaemic events after coronary intervention. Cardiovascular Research, 2019, 115, 1512-1518.	1.8	15
53	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. Communications Biology, 2021, 4, 655.	2.0	12
54	Genetic meta-analysis of 15,901 African Americans identifies variation in EXOC3L1 is associated with HDL concentration. Journal of Lipid Research, 2015, 56, 1781-1786.	2.0	11

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55	Identifying geneâ€“gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. Human Genetics, 2017, 136, 165-178.	1.8	11
56	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
57	rs41291957 controls miRâ€143 and miRâ€145 expression and impacts coronary artery disease risk. EMBO Molecular Medicine, 2021, 13, e14060.	3.3	11
58	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
59	Integrative Functional Annotation of 52 Genetic Loci Influencing Myocardial Mass Identifies Candidate Regulatory Variants and Target Genes. Circulation Genomic and Precision Medicine, 2019, 12, e002328.	1.6	7
60	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	2.0	7
61	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
62	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. European Heart Journal, 2022, 43, 4707-4718.	1.0	5
63	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Mining, 2017, 10, 18.	2.2	4
64	Comment on â€œEvaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human geneticsâ€. Science Translational Medicine, 2021, 13, eabe8497.	5.8	4
65	Integrative Bioinformatics Approaches for Identification of Drug Targets in Hypertension. Frontiers in Cardiovascular Medicine, 2018, 5, 25.	1.1	3
66	Mendelian randomization: A powerful method to determine causality of biomarkers in diseases. International Journal of Cardiology, 2018, 268, 227-228.	0.8	2
67	A comparison of two workflows for regulome and transcriptomeâ€based prioritization of genetic variants associated with myocardial mass. Genetic Epidemiology, 2019, 43, 717-726.	0.6	1
68	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1