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	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1
2	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
3	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
4	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
5	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. European Heart Journal, 2021, 42, 1742-1756.	1.0	63
6	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. Communications Biology, 2021, 4, 655.	2.0	12
7	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
8	Distinction between the effects of parental and fetal genomes on fetal growth. Nature Genetics, 2021, 53, 1135-1142.	9.4	41
9	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	2.0	7
10	rs41291957 controls miRâ€143 and miRâ€145 expression and impacts coronary artery disease risk. EMBO Molecular Medicine, 2021, 13, e14060.	3.3	11
11	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
12	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
13	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
14	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. JAMA Cardiology, 2020, 5, 13.	3.0	29
15	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
16	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
17	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
18	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

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19	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
20	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	13.7	81
21	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
22	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
23	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	5.8	59
24	Sequence variants with large effects on cardiac electrophysiology and disease. Nature Communications, 2019, 10, 4803.	5.8	28
25	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
26	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
27	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	1.6	17
28	Association of the coronary artery disease risk gene GUCY1A3 with ischaemic events after coronary intervention. Cardiovascular Research, 2019, 115, 1512-1518.	1.8	15
29	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
30	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
31	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
32	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
33	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	1.6	43
34	Comprehensive pathway analyses of schizophrenia risk loci point to dysfunctional postsynaptic signaling. Schizophrenia Research, 2018, 199, 195-202.	1.1	26
35	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	5.8	44
36	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	1.0	59

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37	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
38	Mendelian randomization: A powerful method to determine causality of biomarkers in diseases. International Journal of Cardiology, 2018, 268, 227-228.	0.8	2
39	Integrative Bioinformatics Approaches for Identification of Drug Targets in Hypertension. Frontiers in Cardiovascular Medicine, 2018, 5, 25.	1.1	3
40	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
41	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
42	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
43	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
44	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Mining, 2017, 10, 18.	2.2	4
45	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
46	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	2.2	7
47	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
48	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
49	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
50	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
51	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
52	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
53	Instance-level accuracy versus bag-level accuracy in multi-instance learning. Data Mining and Knowledge Discovery, 2016, 30, 313-341.	2.4	17
54	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	3.6	49

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55	Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. Circulation: Cardiovascular Genetics, 2015, 8, 327-333.	5.1	17
56	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
57	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
58	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
59	Impact of carotid atherosclerosis loci on cardiovascular events. Atherosclerosis, 2015, 243, 466-468.	0.4	18
60	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
61	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
62	The ENCODE Project and Perspectives on Pathways. Genetic Epidemiology, 2014, 38, 275-280.	0.6	47
63	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
64	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
65	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
66	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
67	Gene-Centric Meta-Analysis of Lipid Traits in African, East Asian and Hispanic Populations. PLoS ONE, 2012, 7, e50198.	1.1	40
68	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