Vincenzo Forgetta

List of Publications by Year
in descending order

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67 papers	5,731 citations	172207 29 h-index	95083 68 g-index
84 all docs	84 docs citations	84 times ranked	10474 citing authors

#	Article	IF	Citations
1	Clinically Relevant Circulating Protein Biomarkers for Type 1 Diabetes: Evidence From a Two-Sample Mendelian Randomization Study. Diabetes Care, 2022, 45, 169-177.	4.3	18
2	An effector index to predict target genes at GWAS loci. Human Genetics, 2022, 141, 1431-1447.	1.8	28
3	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA). BMJ Open, 2022, 12, e059021.	0.8	17
4	Polygenic risk score as a possible tool for identifying familial monogenic causes of complex diseases. Genetics in Medicine, 2022, 24, 1545-1555.	1.1	12
5	Capturing additional genetic risk from family history for improved polygenic risk prediction. Communications Biology, 2022, 5, .	2.0	6
6	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. Diabetes Care, 2021, 44, 556-562.	4.3	21
7	The effect of angiotensin-converting enzyme levels on COVID-19 susceptibility and severity: a Mendelian randomization study. International Journal of Epidemiology, 2021, 50, 75-86.	0.9	10
8	Individuals with common diseases but with a low polygenic risk score could be prioritized for rare variant screening. Genetics in Medicine, 2021, 23, 508-515.	1.1	39
9	Vitamin D levels and risk of type 1 diabetes: A Mendelian randomization study. PLoS Medicine, 2021, 18, e1003536.	3.9	42
10	Improved prediction of fracture risk leveraging a genome-wide polygenic risk score. Genome Medicine, 2021, 13, 16.	3.6	35
11	A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity. Nature Medicine, 2021, 27, 659-667.	15.2	188
12	Polygenic Risk Score for Low-Density Lipoprotein Cholesterol Is Associated With Risk of Ischemic Heart Disease and Enriches for Individuals With Familial Hypercholesterolemia. Circulation Genomic and Precision Medicine, 2021, 14, e003106.	1.6	21
13	Childhood obesity and multiple sclerosis: A Mendelian randomization study. Multiple Sclerosis Journal, 2021, 27, 2150-2158.	1.4	30
14	A Polygenic Risk Score to Predict Future Adult Short Stature Among Children. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1918-1928.	1.8	19
15	Genetically increased circulating FUT3 level leads to reduced risk of Idiopathic Pulmonary Fibrosis: a Mendelian Randomisation Study. European Respiratory Journal, 2021, , 2003979.	3.1	9
16	Vitamin D and COVID-19 susceptibility and severity in the COVID-19 Host Genetics Initiative: A Mendelian randomization study. PLoS Medicine, 2021, 18, e1003605.	3.9	91
17	Rare loss-of-function variants in type I IFN immunity genes are not associated with severe COVID-19. Journal of Clinical Investigation, 2021, 131, .	3.9	56
18	Health Effects of Calcium: Evidence From Mendelian Randomization Studies. JBMR Plus, 2021, 5, e10542.	1.3	8

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19	Utility of Genetically Predicted Lp(a) (Lipoprotein [a]) and ApoB Levels for Cardiovascular Risk Assessment. Circulation Genomic and Precision Medicine, 2021, 14, e003312.	1.6	6
20	Block coordinate descent algorithm improves variable selection and estimation in errorâ€inâ€variables regression. Genetic Epidemiology, 2021, 45, 874-890.	0.6	5
21	Increased Burden of Common Risk Alleles in Children With a Significant Fracture History. Journal of Bone and Mineral Research, 2020, 35, 875-882.	3.1	6
22	Genetically Decreased Circulating Vascular Endothelial Growth Factor and Osteoporosis Outcomes: A Mendelian Randomization Study. Journal of Bone and Mineral Research, 2020, 35, 649-656.	3.1	9
23	Genetic Determinants of Antibody-Mediated Immune Responses to Infectious Diseases Agents: A Genome-Wide and HLA Association Study. Open Forum Infectious Diseases, 2020, 7, ofaa450.	0.4	12
24	The undiagnosed disease burden associated with alpha-1 antitrypsin deficiency genotypes. European Respiratory Journal, 2020, 56, 2001441.	3.1	40
25	A Polygenic Risk Score as a Risk Factor for Medicationâ€Associated Fractures. Journal of Bone and Mineral Research, 2020, 35, 1935-1941.	3.1	5
26	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study. PLoS Medicine, 2020, 17, e1003152.	3.9	45
27	Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. American Journal of Human Genetics, 2020, 106, 327-337.	2.6	144
28	Polygenic risk for coronary heart disease acts through atherosclerosis in type 2 diabetes. Cardiovascular Diabetology, 2020, 19, 12.	2.7	23
29	Rare Genetic Variants of Large Effect Influence Risk of Type 1 Diabetes. Diabetes, 2020, 69, 784-795.	0.3	69
30	Title is missing!. , 2020, 17, e1003152.		0
31	Title is missing!. , 2020, 17, e1003152.		0
32	Title is missing!. , 2020, 17, e1003152.		0
33	Title is missing!. , 2020, 17, e1003152.		0
34	Title is missing!. , 2020, 17, e1003152.		0
35	Title is missing!. , 2020, 17, e1003152.		0
36	Identifying Causes of Fracture Beyond Bone Mineral Density: Evidence From Human Genetics. Journal of Bone and Mineral Research, 2020, 37, 1592-1602.	3.1	5

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37	Laboratory-developed test for detection of acute Clostridium difficile infections with the capacity for quantitative sample normalization. Diagnostic Microbiology and Infectious Disease, 2019, 95, 113-118.	0.8	4
38	Effect of age at puberty on risk of multiple sclerosis. Neurology, 2019, 92, e1803-e1810.	1.5	23
39	Genetic predisposition to increased serum calcium, bone mineral density, and fracture risk in individuals with normal calcium levels: mendelian randomisation study. BMJ: British Medical Journal, 2019, 366, l4410.	2.4	32
40	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
41	Exome-wide rare variant analyses of two bone mineral density phenotypes: the challenges of analyzing rare genetic variation. Scientific Reports, 2018, 8, 220.	1.6	2
42	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	2.6	252
43	Genome-wide association study of extreme high bone mass: Contribution of common genetic variation to extreme BMD phenotypes and potential novel BMD-associated genes. Bone, 2018, 114, 62-71.	1.4	43
44	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. Journal of Bone and Mineral Research, 2017, 32, 1644-1650.	3.1	49
45	Large differences in adiponectin levels have no clear effect on multiple sclerosis risk: A Mendelian randomization study. Multiple Sclerosis Journal, 2017, 23, 1461-1468.	1.4	11
46	A Mendelian Randomization Study of the Effect of Type-2 Diabetes and Glycemic Traits on Bone Mineral Density. Journal of Bone and Mineral Research, 2017, 32, 1072-1081.	3.1	44
47	Low-Frequency Synonymous Coding Variation in CYP2R1 Has Large Effects on Vitamin D Levels and Risk of Multiple Sclerosis. American Journal of Human Genetics, 2017, 101, 227-238.	2.6	112
48	Effect of Fixed-Bolus (5,000 Units) Unfractionated Heparin Before Primary Percutaneous Coronary Intervention on Activated Clotting Time, Time Flow, and All-Cause Mortality. American Journal of Cardiology, 2017, 119, 178-185.	0.7	4
49	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	9.4	391
50	Software Application Profiles: useful and novel software for epidemiological data analysis. International Journal of Epidemiology, 2016, 45, 309-310.	0.9	2
51	Genetically decreased vitamin D and risk of Alzheimer disease. Neurology, 2016, 87, 2567-2574.	1.5	92
52	A method for analyzing multiple continuous phenotypes in rare variant association studies allowing for flexible correlations in variant effects. European Journal of Human Genetics, 2016, 24, 1344-1351.	1.4	21
53	Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS ONE, 2015, 10, e0128773.	1.1	53
54	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75

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55	A Mendelian randomization study of the effect of type-2 diabetes on coronary heart disease. Nature Communications, 2015, 6, 7060.	5.8	111
56	Assay for estimating total bacterial load: relative qPCR normalisation of bacterial load with associated clinical implications. Diagnostic Microbiology and Infectious Disease, 2015, 83, 1-6.	0.8	22
57	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
58	Mendelian randomisation applied to drug development in cardiovascular disease: a review. Journal of Medical Genetics, 2015, 52, 71-79.	1.5	52
59	Vitamin D and Risk of Multiple Sclerosis: A Mendelian Randomization Study. PLoS Medicine, 2015, 12, e1001866.	3.9	380
60	Duplex PCR Methods for the Molecular Detection of Escherichia fergusonii Isolates from Broiler Chickens. Applied and Environmental Microbiology, 2014, 80, 1941-1948.	1.4	13
61	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	9.4	1,084
62	Pathway analysis for genetic association studies: to do, or not to do? That is the question. BMC Proceedings, 2014, 8, S103.	1.8	2
63	Sequencing of the Dutch Elm Disease Fungus Genome Using the Roche/454 GS-FLX Titanium System in a Comparison of Multiple Genomics Core Facilities. Journal of Biomolecular Techniques, 2013, 24, jbt.12-2401-005.	0.8	47
64	Fourteen-Genome Comparison Identifies DNA Markers for Severe-Disease-Associated Strains of Clostridium difficile. Journal of Clinical Microbiology, 2011, 49, 2230-2238.	1.8	43
65	Identification of the gene responsible for methylmalonic aciduria and homocystinuria, cblC type. Nature Genetics, 2006, 38, 93-100.	9.4	331
66	Loss of heterozygosity and transcriptome analyses of a 1.2 Mb candidate ovarian cancer tumor suppressor locus region at 17q25.1-q25.2. Molecular Carcinogenesis, 2005, 43, 141-154.	1.3	46
67	Allelic Variation in TLR4 Is Linked to Susceptibility to Salmonella enterica Serovar Typhimurium Infection in Chickens. Infection and Immunity, 2003, 71, 1116-1124.	1.0	215