Christopher P Nelson

List of Publications by Year
in descending order

135 papers	21,847 citations	16411 64 h-index	11288 136 g-index
150 all docs	150 docs citations	150 times ranked	30765 citing authors

#	Article	IF	Citations
1	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
2	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
3	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
4	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
5	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
6	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	6.3	686
7	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
8	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	6.3	668
9	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
10	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
11	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	1.2	557
12	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
13	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
14	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
15	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
16	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
17	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
18	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286

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19	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. Epigenetics, 2014, 9, 1382-1396.	1.3	285
20	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
21	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
22	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
23	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
24	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	2.6	222
25	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
26	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
27	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	3.3	208
28	Flexible parametric models for relative survival, with application in coronary heart disease. Statistics in Medicine, 2007, 26, 5486-5498.	0.8	202
29	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
30	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
31	Inheritance of coronary artery disease in men: an analysis of the role of the Y chromosome. Lancet, The, 2012, 379, 915-922.	6.3	179
32	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
33	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	2.0	166
34	Common genetic loci influencing plasma homocysteine concentrations and their effect on risk of coronary artery disease. American Journal of Clinical Nutrition, 2013, 98, 668-676.	2.2	161
35	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
36	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159

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37	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
38	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
39	Polygenic basis and biomedical consequences of telomere length variation. Nature Genetics, 2021, 53, 1425-1433.	9.4	145
40	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
41	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
42	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
43	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
44	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
45	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
46	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
47	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115
48	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
49	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
50	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	1.2	109
51	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	3.1	103
52	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
53	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	3.9	95
54	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94

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55	Galactosylation of IgA1 Is Associated with Common Variation in C1GALT1. Journal of the American Society of Nephrology: JASN, 2017, 28, 2158-2166.	3.0	93
56	Heritability of Early Repolarization. Circulation: Cardiovascular Genetics, 2011, 4, 134-138.	5.1	89
57	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
58	Longer genotypically-estimated leukocyte telomere length is associated with increased adult glioma risk. Oncotarget, 2015, 6, 42468-42477.	0.8	87
59	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
60	Longer Leukocyte Telomeres Are Associated with Ultra-Endurance Exercise Independent of Cardiovascular Risk Factors. PLoS ONE, 2013, 8, e69377.	1.1	84
61	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
62	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
63	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
64	Systems Genetics Analysis of Genome-Wide Association Study Reveals Novel Associations Between Key Biological Processes and Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1712-1722.	1.1	72
65	Dense Genotyping of Candidate Gene Loci Identifies Variants Associated With High-Density Lipoprotein Cholesterol. Circulation: Cardiovascular Genetics, 2011, 4, 145-155.	5.1	71
66	Genetic Predisposition to Higher Blood Pressure Increases Coronary Artery Disease Risk. Hypertension, 2013, 61, 995-1001.	1.3	70
67	The Relationship Between Plasma Angiopoietin-like Protein 4 Levels, Angiopoietin-like Protein 4 Genotype, and Coronary Heart Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2277-2282.	1.1	64
68	Genetic Architecture of Ambulatory Blood Pressure in the General Population. Hypertension, 2010, 56, 1069-1076.	1.3	64
69	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
70	Genetic Variation Associated with Longer Telomere Length Increases Risk of Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1043-1049.	1.1	61
71	Retinal Layer Abnormalities as Biomarkers of Schizophrenia. Schizophrenia Bulletin, 2018, 44, 876-885.	2.3	60
72	Adult height and risk of 50 diseases: a combined epidemiological and genetic analysis. BMC Medicine, 2018, 16, 187.	2.3	60

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73	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
74	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. Journal of the American College of Cardiology, 2013, 61, 957-970.	1.2	58
75	Male-Specific Region of the Y Chromosome and Cardiovascular Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1722-1727.	1.1	57
76	Identifying Novel Gene Variants in Coronary Artery Disease and Shared Genes With Several Cardiovascular Risk Factors. Circulation Research, 2016, 118, 83-94.	2.0	52
77	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
78	Relative survival: what can cardiovascular disease learn from cancer?. European Heart Journal, 2008, 29, 941-947.	1.0	48
79	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
80	Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. American Journal of Human Genetics, 2015, 97, 228-237.	2.6	37
81	Shorter leukocyte telomere length is associated with adverse COVID-19 outcomes: A cohort study in UK Biobank. EBioMedicine, 2021, 70, 103485.	2.7	36
82	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
83	Polymorphisms in Catechol- O -Methyltransferase Modify Treatment Effects of Aspirin on Risk of Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2160-2167.	1.1	35
84	Large-Scale Analysis of Determinants, Stability, and Heritability of High-Density Lipoprotein Cholesterol Efflux Capacity. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1956-1962.	1.1	33
85	Large-Scale Candidate Gene Analysis of HDL Particle Features. PLoS ONE, 2011, 6, e14529.	1.1	32
86	A flexible and parallelizable approach to genomeâ€wide polygenic risk scores. Genetic Epidemiology, 2019, 43, 730-741.	0.6	32
87	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
88	The shared allelic architecture of adiponectin levels and coronary artery disease. Atherosclerosis, 2013, 229, 145-148.	0.4	30
89	Novel Loci Associated with Increased Risk of Sudden Cardiac Death in the Context of Coronary Artery Disease. PLoS ONE, 2013, 8, e59905.	1.1	30
90	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29

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91	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	1.4	29
92	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
93	Genetic associations with lipoprotein subfractions provide information on their biological nature. Human Molecular Genetics, 2012, 21, 1433-1443.	1.4	28
94	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	1.4	28
95	Pathway Analysis Shows Association between FGFBP1 and Hypertension. Journal of the American Society of Nephrology: JASN, 2011, 22, 947-955.	3.0	27
96	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	1.2	27
97	Modifiable traits, healthy behaviours, and leukocyte telomere length: a population-based study in UK Biobank. The Lancet Healthy Longevity, 2022, 3, e321-e331.	2.0	27
98	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. Atherosclerosis, 2015, 241, 419-426.	0.4	26
99	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	1.6	25
100	Geographical location affects the levels and association of trimethylamine Nâ€oxide with heart failure mortality in BIOSTATâ€CHF: a postâ€hoc analysis. European Journal of Heart Failure, 2019, 21, 1291-1294.	2.9	25
101	Resuscitated cardiac arrest and prognosis following myocardial infarction. Heart, 2014, 100, 1125-1132.	1.2	23
102	Novel Genetic Approach to Investigate the Role of Plasma Secretory Phospholipase A2 (sPLA) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 144-150.	5.1	22
103	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. Circulation Genomic and Precision Medicine, 2019, 12, e002471.	1.6	22
104	Coronary artery disease predisposing haplogroup I of the YÂchromosome, aggression and sex steroids â€“ Genetic associationÂanalysis. Atherosclerosis, 2014, 233, 160-164.	0.4	21
105	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
106	Renal Mechanisms of Association between Fibroblast Growth Factor 1 and Blood Pressure. Journal of the American Society of Nephrology: JASN, 2015, 26, 3151-3160.	3.0	20
107	The Prevalence and Significance of the Early Repolarization Pattern in Sudden Arrhythmic Death Syndrome Families. Circulation: Arrhythmia and Electrophysiology, 2016, 9, .	2.1	19
108	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19

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109	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
110	Hypothesis-Based Analysis of Gene-Gene Interactions and Risk of Myocardial Infarction. PLoS ONE, 2012, 7, e41730.	1.1	17
111	Investigation of a UK biobank cohort reveals causal associations of self-reported walking pace with telomere length. Communications Biology, 2022, 5, 381.	2.0	17
112	Genetic Associations With Plasma Angiotensin Converting Enzyme 2 Concentration. Circulation, 2020, 142, 1117-1119.	1.6	16
113	The Relation of Rapid Changes in Obesity Measures to Lipid Profile - Insights from a Nationwide Metabolic Health Survey in 444 Polish Cities. PLoS ONE, 2014, 9, e86837.	1.1	15
114	Genetic risk and atrial fibrillation in patients with heart failure. European Journal of Heart Failure, 2020, 22, 519-527.	2.9	15
115	Genetic determinants of telomere length and cancer risk. Current Opinion in Genetics and Development, 2020, 60, 63-68.	1.5	15
116	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	2.3	15
117	Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102.	1.8	14
118	Association of shorter leucocyte telomere length with risk of frailty. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 1741-1751.	2.9	13
119	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. Circulation: Cardiovascular Genetics, 2012, 5, 630-638.	5.1	12
120	Genetic Analysis of Leukocyte Type-I Interferon Production and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1456-1462.	1.1	11
121	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
122	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
123	Elucidation of the genetic causes of bicuspid aortic valve disease. Cardiovascular Research, 2023, 119, 857-866.	1.8	11
124	Effects of the coronary artery disease associated LPA and 9p21 loci on risk of aortic valve stenosis. International Journal of Cardiology, 2019, 276, 212-217.	0.8	9
125	Analysis of Gene-Gene Interactions among Common Variants in Candidate Cardiovascular Genes in Coronary Artery Disease. PLoS ONE, 2015, 10, e0117684.	1.1	8
126	Cumulative effects of common genetic variants on risk of sudden cardiac death. IJC Heart and Vasculature, 2015, 7, 88-91.	0.6	7

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127	The narrow-sense and common single nucleotide polymorphism heritability of early repolarization. International Journal of Cardiology, 2019, 279, 135-140.	0.8	7
128	The importance of previous lifetime trauma in stroke-induced PTSD symptoms and mental health outcomes. Journal of Psychiatric Research, 2021, 136, 589-594.	1.5	7
129	Whole blood transcriptomic profiling identifies molecular pathways related to cardiovascular mortality in heart failure. European Journal of Heart Failure, 2022, 24, 1009-1019.	2.9	6
130	Characterization and Discovery of a Selective Small-Molecule Modulator of Mitochondrial Complex I Targeting a Unique Binding Site. Journal of Medicinal Chemistry, 2020, 63, 11819-11830.	2.9	5
131	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	1.6	5
132	Telomere length is independently associated with all-cause mortality in chronic heart failure. Heart, 2022, 108, 124-129.	1.2	5
133	Are toll-like receptors potential drug targets for atherosclerosis? Evidence from genetic studies to date. Immunogenetics, 2019, 71, 1-11.	1.2	4
134	Exome Sequencing Analysis Identifies Rare Variants in ATM and RPL8 That Are Associated With Shorter Telomere Length. Frontiers in Genetics, 2020, 11, 337.	1.1	4
135	Reply to the Letter by Hayashi et al. Circulation: Cardiovascular Genetics, 2011, 4, .	5.1	0