Georg B Ehret

List of Publications by Year
in descending order

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135 papers	28,448 citations	22153 59 h-index	12597 132 g-index
142 all docs	142 docs citations	142 times ranked	34476 citing authors

#	Article	IF	Citations
1	Silent brain infarcts impact on cognitive function in atrial fibrillation. European Heart Journal, 2022, 43, 2127-2135.	2.2	50
2	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
3	Blood Pressure and Brain Lesions in Patients With Atrial Fibrillation. Hypertension, 2021, 77, 662-671.	2.7	8
4	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. Scientific Reports, 2021, 11, 3100.	3.3	15
5	Heritability and association with distinct genetic loci of erythropoietin levels in the general population. Haematologica, 2021, 106, 2499-2501.	3.5	3
6	Reduced adrenal stress response in patients on PCSK9 inhibitor therapy. Atherosclerosis, 2021, 325, 63-68.	0.8	3
7	Hypertension and heart failure with preserved ejection fraction: position paper by the European Society of Hypertension. Journal of Hypertension, 2021, 39, 1522-1545.	0.5	47
8	Sex- and age-specific reference intervals for diagnostic ratios reflecting relative activity of steroidogenic enzymes and pathways in adults. PLoS ONE, 2021, 16, e0253975.	2.5	2
9	Assessment of a strategy combining ambulatory blood pressure, adherence monitoring and a standardised triple therapy in resistant hypertension. Blood Pressure, 2021, 30, 332-340.	1.5	1
10	Investigating the Relations Between Caffeine-Derived Metabolites and Plasma Lipids in 2 Population-Based Studies. Mayo Clinic Proceedings, 2021, 96, 3071-3085.	3.0	2
11	Changes of lipoprotein(a) levels with endogenous steroid hormones. European Journal of Clinical Investigation, 2021, , e13699.	3.4	1
12	Parathyroid Hormone and Plasma Phosphate Are Predictors of Soluble Î±-Klotho Levels in Adults of European Descent. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e1135-e1143.	3.6	8
13	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
14	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	2.9	7
15	Feasibility and safety of high-intensity interval training for the rehabilitation of geriatric inpatients (HIITERGY) a pilot randomized study. BMC Geriatrics, 2020, 20, 197.	2.7	13
16	Ambulatory Blood Pressure in Relation to Plasma and Urinary Manganese. Hypertension, 2020, 75, 1133-1139.	2.7	8
17	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	28.9	152
18	In the Age of Genomics, Is it Still Worth it to Investigate Individual Loci?. Hypertension, 2019, 74, 495-496.	2.7	0

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19	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
20	Measured and Genotyped Differences in Blood Pressure and the Usefulness of Precise Extreme Phenotypes Based on Cardiovascular Magnetic Resonance. Hypertension, 2019, 74, 747-748.	2.7	0
21	Renal Resistive Index Is Associated With Inactive Matrix Gla (Î³â€Carboxyglutamate) Protein in an Adult Populationâ€Based Study. Journal of the American Heart Association, 2019, 8, e013558.	3.7	5
22	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
23	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
24	Urinary Sex Steroid and Glucocorticoid Hormones Are Associated With Muscle Mass and Strength in Healthy Adults. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 2195-2215.	3.6	14
25	Association of FMO3 Variants with Blood Pressure in the Atherosclerosis Risk in Communities Study. International Journal of Hypertension, 2019, 2019, 1-8.	1.3	3
26	Relationships of Overt and Silent Brain Lesions With Cognitive Function in Patients With Atrial Fibrillation. Journal of the American College of Cardiology, 2019, 73, 989-999.	2.8	148
27	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.	2.9	31
28	Reference intervals for the urinary steroid metabolome: The impact of sex, age, day and night time on human adult steroidogenesis. PLoS ONE, 2019, 14, e0214549.	2.5	38
29	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	2.8	5
30	Urinary Cadmium Excretion Is Associated With Increased Synthesis of Cortico- and Sex Steroids in a Population Study. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 748-758.	3.6	18
31	Association of 24-Hour Blood Pressure With Urinary Sodium Excretion in Healthy Adults. American Journal of Hypertension, 2018, 31, 784-791.	2.0	9
32	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.	6.2	123
33	Associations of Urinary Caffeine and Caffeine Metabolites With Arterial Stiffness in a Large Population-Based Study. Mayo Clinic Proceedings, 2018, 93, 586-596.	3.0	17
34	Genome-Wide Meta-Analysis Unravels Interactions between Magnesium Homeostasis and Metabolic Phenotypes. Journal of the American Society of Nephrology: JASN, 2018, 29, 335-348.	6.1	34
35	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
36	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924

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37	Genes for Preeclampsia. Hypertension, 2018, 72, 285-286.	2.7	5
38	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
39	Uromodulin and Nephron Mass. Clinical Journal of the American Society of Nephrology: CJASN, 2018, 13, 1556-1557.	4.5	44
40	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
41	Epidemiological and histological findings implicate matrix Gla protein in diastolic left ventricular dysfunction. PLoS ONE, 2018, 13, e0193967.	2.5	10
42	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
43	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. European Journal of Preventive Cardiology, 2017, 24, 492-504.	1.8	22
44	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
45	Rare coding variants associated with blood pressure variation in 15â€Š914 individuals of African ancestry. Journal of Hypertension, 2017, 35, 1381-1389.	0.5	15
46	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
47	A population-based approach to assess the heritability and distribution of renal handling of electrolytes. Kidney International, 2017, 92, 1536-1543.	5.2	20
48	Next Steps for Gene Identification in Primary Hypertension Genomics. Hypertension, 2017, 70, 695-697.	2.7	3
49	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
50	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	21.4	281
51	Molecular pathways associated with blood pressure and hexadecanedioate levels. PLoS ONE, 2017, 12, e0175479.	2.5	8
52	Design of the Swiss Atrial Fibrillation Cohort Study (Swiss-AF): structural brain damage and cognitive decline among patients with atrial fibrillation. Swiss Medical Weekly, 2017, 147, w14467.	1.6	46
53	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. PLoS ONE, 2016, 11, e0164132.	2.5	24
54	Fibroblast growth factor 23 and markers of mineral metabolism in individuals with preserved renalÂfunction. Kidney International, 2016, 90, 648-657.	5.2	51

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55	The role of GRIP1 and ephrin B3 in blood pressure control and vascular smooth muscle cell contractility. Scientific Reports, 2016, 6, 38976.	3.3	13
56	Relation of 24-hour urinary caffeine and caffeine metabolite excretions with self-reported consumption of coffee and other caffeinated beverages in the general population. Nutrition and Metabolism, 2016, 13, 81.	3.0	19
57	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. Human Molecular Genetics, 2016, 25, ddw334.	2.9	107
58	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
59	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
60	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
61	Protocol of the Swiss Longitudinal Cohort Study (SWICOS) in rural Switzerland. BMJ Open, 2016, 6, e013280.	1.9	6
62	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
63	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
64	Association Analysis ofFOXO3Longevity Variants With Blood Pressure and Essential Hypertension. American Journal of Hypertension, 2016, 29, 1292-1300.	2.0	21
65	Sociodemographic, behavioral and genetic determinants of allostatic load in a Swiss population-based study. Psychoneuroendocrinology, 2016, 67, 76-85.	2.7	50
66	Associations of Urinary Uromodulin with Clinical Characteristics and Markers of Tubular Function in the General Population. Clinical Journal of the American Society of Nephrology: CJASN, 2016, 11, 70-80.	4.5	87
67	CYP17A1 Enzyme Activity Is Linked to Ambulatory Blood Pressure in a Family-Based Population Study. American Journal of Hypertension, 2016, 29, 484-493.	2.0	13
68	Heritability of ambulatory and office blood pressure in the Swiss population. Journal of Hypertension, 2015, 33, 2061-2067.	0.5	12
69	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
70	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
71	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
72	Associations of Ambulatory Blood Pressure With Urinary Caffeine and Caffeine Metabolite Excretions. Hypertension, 2015, 65, 691-696.	2.7	36

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73	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
74	Post-Transcriptional Regulation of Renalase Gene by miR-29 and miR-146 MicroRNAs: Implications for Cardiometabolic Disorders. Journal of Molecular Biology, 2015, 427, 2629-2646.	4.2	17
75	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
76	PÂ<Â5ÂÃ—Â10â˜’8 has emerged as a standard of statistical significance for genome-wide association studies. Journal of Clinical Epidemiology, 2015, 68, 460-465.	5.0	42
77	Inactive Matrix Gla-Protein Is Associated With Arterial Stiffness in an Adult Populationâ€“Based Study. Hypertension, 2015, 66, 85-92.	2.7	85
78	Copeptin Is Associated with Kidney Length, Renal Function, and Prevalence of Simple Cysts in a Population-Based Study. Journal of the American Society of Nephrology: JASN, 2015, 26, 1415-1425.	6.1	48
79	Epidemiology of Masked and White-Coat Hypertension: The Family-Based SKIPOGH Study. PLoS ONE, 2014, 9, e92522.	2.5	56
80	Eligibility for Renal Denervation. Hypertension, 2014, 63, 1319-1325.	2.7	61
81	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
82	Genetic Evidence for a Normal-Weight â€œMetabolically Obeseâ€•Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. Diabetes, 2014, 63, 4369-4377.	0.6	185
83	Reference Values and Factors Associated With Renal Resistive Index in a Family-Based Population Study. Hypertension, 2014, 63, 136-142.	2.7	97
84	Predicting Stroke Through Genetic Risk Functions. Stroke, 2014, 45, 403-412.	2.0	62
85	Meeting highlights from the 2013 <scp>E</scp>uropean <scp>S</scp>ociety of <scp>C</scp>ardiology <scp>H</scp>eart <scp>F</scp>ailure <scp>A</scp>ssociation <scp>W</scp>inter <scp>M</scp>eeting on <scp>T</scp>ranslational <scp>H</scp>eart <scp>F</scp>ailure <scp>R</scp>esearch. European Journal of Heart Failure, 2014, 16, 6-14.	7.1	1
86	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
87	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
88	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
89	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
90	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	2.8	36

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91	Sequence Analysis of Six Blood Pressure Candidate Regions in 4,178 Individuals: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. PLoS ONE, 2014, 9, e109155.	2.5	19
92	Heritability, determinants and reference values of renal length: a family-based population study. European Radiology, 2013, 23, 2899-2905.	4.5	47
93	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
94	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	6.2	77
95	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
96	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
97	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
98	Genes for blood pressure: an opportunity to understand hypertension. European Heart Journal, 2013, 34, 951-961.	2.2	163
99	A Systematic Mapping Approach of 16q12.2/FTO and BMI in More Than 20,000 African Americans Narrows in on the Underlying Functional Variation: Results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2013, 9, e1003171.	3.5	63
100	Effects of Rare and Common Blood Pressure Gene Variants on Essential Hypertension. Circulation Research, 2013, 112, 318-326.	4.5	24
101	Framinghamâ€™s Contribution to Gene Identification for CV Risk Factors and Coronary Disease. Global Heart, 2013, 8, 59.	2.3	3
102	Influence of CYP2D6 activity on pre-emptive analgesia by the N-methyl-D-aspartate antagonist dextromethorphan in a randomized controlled trial of acute pain. Pain Physician, 2013, 16, 45-56.	0.4	9
103	Genome-Wide Profiling of Blood Pressure in Adults and Children. Hypertension, 2012, 59, 241-247.	2.7	31
104	Next-Generation Sequencing of Human Mitochondrial Reference Genomes Uncovers High Heteroplasmy Frequency. PLoS Computational Biology, 2012, 8, e1002737.	3.2	61
105	Caffeine intake and CYP1A2 variants associated with high caffeine intake protect non-smokers from hypertension. Human Molecular Genetics, 2012, 21, 3283-3292.	2.9	55
106	Integrated Computational and Experimental Analysis of the Neuroendocrine Transcriptome in Genetic Hypertension Identifies Novel Control Points for the Cardiometabolic Syndrome. Circulation: Cardiovascular Genetics, 2012, 5, 430-440.	5.1	6
107	A Multi-SNP Locus-Association Method Reveals a Substantial Fraction of the Missing Heritability. American Journal of Human Genetics, 2012, 91, 863-871.	6.2	47
108	KLHL3 mutations cause familial hyperkalemic hypertension by impairing ion transport in the distal nephron. Nature Genetics, 2012, 44, 456-460.	21.4	281

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109	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
110	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
111	SNPs and Other Features as They Predispose to Complex Disease: Genome-Wide Predictive Analysis of a Quantitative Phenotype for Hypertension. PLoS ONE, 2011, 6, e27891.	2.5	4
112	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
113	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
114	Five Blood Pressure Loci Identified by an Updated Genome-Wide Linkage Scan: Meta-Analysis of the Family Blood Pressure Program. American Journal of Hypertension, 2011, 24, 347-354.	2.0	17
115	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
116	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. PLoS Genetics, 2011, 7, e1002158.	3.5	117
117	Variation in the checkpoint kinase 2 gene is associated with type 2 diabetes in multiple populations. Acta Diabetologica, 2010, 47, 199-207.	2.5	6
118	Genome-Wide Association Studies: Contribution of Genomics to Understanding Blood Pressure and Essential Hypertension. Current Hypertension Reports, 2010, 12, 17-25.	3.5	186
119	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
120	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
121	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. PLoS Genetics, 2010, 6, e1001045.	3.5	185
122	Positional identification of variants of Adamts16 linked to inherited hypertension. Human Molecular Genetics, 2009, 18, 2825-2838.	2.9	57
123	Follow-up of a major linkage peak on chromosome 1 reveals suggestive QTLs associated with essential hypertension: GenNet study. European Journal of Human Genetics, 2009, 17, 1650-1657.	2.8	52
124	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
125	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	21.4	553
126	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224

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127	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	21.4	363
128	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	21.4	324
129	Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. European Journal of Human Genetics, 2008, 16, 1507-1511.	2.8	64
130	An ancestral variant of Secretogranin II confers regulation by PHOX2 transcription factors and association with hypertension. Human Molecular Genetics, 2007, 16, 1752-1764.	2.9	29
131	Methadone-associated long QT syndrome: improving pharmacotherapy for dependence on illegal opioids and lessons learned for pharmacology. Expert Opinion on Drug Safety, 2007, 6, 289-303.	2.4	48
132	Genome-Wide Association Scan Shows Genetic Variants in the FTO Gene Are Associated with Obesity-Related Traits. PLoS Genetics, 2007, 3, e115.	3.5	1,446
133	Drug-Induced Long QT Syndrome in Injection Drug Users Receiving Methadone. Archives of Internal Medicine, 2006, 166, 1280.	3.8	200
134	QT Interval Prolongation in Patients on Methadone With Concomitant Drugs. Journal of Clinical Psychopharmacology, 2004, 24, 446-448.	1.4	49
135	DNA Binding Specificity of Different STAT Proteins. Journal of Biological Chemistry, 2001, 276, 6675-6688.	3.4	330