Niek Verweij

List of Publications by Year
in descending order

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134 papers	27,925 citations	20759 60 h-index	11288 136 g-index
161 all docs	161 docs citations	161 times ranked	35122 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
5	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
6	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
7	Identification of 64 Novel Genetic Loci Provides an Expanded View on the Genetic Architecture of Coronary Artery Disease. Circulation Research, 2018, 122, 433-443.	2.0	850
8	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
9	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
10	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
11	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
12	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
13	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
14	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
15	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
16	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
17	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
18	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383

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19	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
20	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
21	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.	1.5	331
22	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
23	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
24	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
25	Associations of Combined Genetic and Lifestyle Risks With Incident Cardiovascular Disease and Diabetes in the UK Biobank Study. JAMA Cardiology, 2018, 3, 693.	3.0	310
26	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
27	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
28	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
29	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
30	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
31	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
32	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
33	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
34	Incidence of Atrial Fibrillation and Relationship With Cardiovascular Events, Heart Failure, and Mortality. Journal of the American College of Cardiology, 2015, 66, 1000-1007.	1.2	218
35	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
36	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

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37	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
38	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
39	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
40	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
41	Relationship of Arterial Stiffness Index and Pulse Pressure With Cardiovascular Disease and Mortality. Journal of the American Heart Association, 2018, 7, .	1.6	142
42	Normal values of the electrocardiogram for ages 16â€“90years. Journal of Electrocardiology, 2014, 47, 914-921.	0.4	136
43	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
44	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. Nature Genetics, 2016, 48, 1557-1563.	9.4	131
45	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
46	Sequencing of 640,000 exomes identifies GPR75 variants associated with protection from obesity. Science, 2021, 373, .	6.0	130
47	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
48	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
49	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.	2.6	109
50	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	1.5	105
51	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96
52	Genetic Obesity and the Risk of Atrial Fibrillation. Circulation, 2017, 135, 741-754.	1.6	96
53	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
54	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91

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55	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
56	Genetic Risk Prediction of Atrial Fibrillation. Circulation, 2017, 135, 1311-1320.	1.6	87
57	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
58	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
59	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
60	Identification of 15 novel risk loci for coronary artery disease and genetic risk of recurrent events, atrial fibrillation and heart failure. Scientific Reports, 2017, 7, 2761.	1.6	81
61	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
62	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
63	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
64	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
65	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
66	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	9.4	68
67	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	9.4	68
68	Genome-wide association studies and Mendelian randomization analyses for leisure sedentary behaviours. Nature Communications, 2020, 11, 1770.	5.8	66
69	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation. JAMA Cardiology, 2019, 4, 144.	3.0	64
70	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
71	Genetic study links components of the autonomous nervous system to heart-rate profile during exercise. Nature Communications, 2018, 9, 898.	5.8	60
72	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59

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73	The Genetic Makeup of the Electrocardiogram. Cell Systems, 2020, 11, 229-238.e5.	2.9	55
74	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
75	Genetic Determinants of P Wave Duration and PR Segment. Circulation: Cardiovascular Genetics, 2014, 7, 475-481.	5.1	45
76	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	5.8	45
77	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	2.7	43
78	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	2.6	42
79	A Genome-Wide Association Study of Circulating Galectin-3. PLoS ONE, 2012, 7, e47385.	1.1	41
80	Hydrogel embedding of precisionâ€œcut liver slices in a microfluidic device improves drug metabolic activity. Biotechnology and Bioengineering, 2011, 108, 1404-1412.	1.7	38
81	Erythropoietin in the General Population: Reference Ranges and Clinical, Biochemical and Genetic Correlates. PLoS ONE, 2015, 10, e0125215.	1.1	38
82	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	5.8	35
83	Genome-Wide Association Study on Plasma Levels of Midregional-Proadrenomedullin and C-Terminal-Pro-Endothelin-1. Hypertension, 2013, 61, 602-608.	1.3	34
84	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	1.5	34
85	Genetics and the heart rate response to exercise. Cellular and Molecular Life Sciences, 2019, 76, 2391-2409.	2.4	34
86	Heart Rate Recovery 10 Seconds After Cessation of Exercise Predicts Death. Journal of the American Heart Association, 2018, 7, .	1.6	33
87	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	5.8	30
88	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
89	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
90	Genome-Wide Association Study and Identification of a Protective Missense Variant on Lipoprotein(a) Concentration. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1792-1800.	1.1	29

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91	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	1.6	27
92	Contributions of Interactions Between Lifestyle and Genetics on Coronary Artery Disease Risk. Current Cardiology Reports, 2019, 21, 89.	1.3	27
93	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
94	Circulating total bilirubin and risk of non-alcoholic fatty liver disease in the PREVEND study: observational findings and a Mendelian randomization study. European Journal of Epidemiology, 2020, 35, 123-137.	2.5	26
95	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms. Nature Communications, 2021, 12, 4571.	5.8	26
96	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
97	Gene-level analysis of rare variants in 379,066 whole exome sequences identifies an association of GIGYF1 loss of function with type 2 diabetes. Scientific Reports, 2021, 11, 21565.	1.6	25
98	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	1.4	24
99	Effect of Systolic Blood Pressure on Left Ventricular Structure and Function. Hypertension, 2019, 74, 826-832.	1.3	23
100	Telomere Length and Risk of Cardiovascular Disease and Cancer. Journal of the American College of Cardiology, 2017, 70, 506-507.	1.2	22
101	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	0.7	22
102	Genomic insights in ascending aortic size and distensibility. EBioMedicine, 2022, 75, 103783.	2.7	22
103	Associations of Observational and Genetically Determined Caffeine Intake With Coronary Artery Disease and Diabetes Mellitus. Journal of the American Heart Association, 2020, 9, e016808.	1.6	21
104	Human genetic determinants of the gut microbiome and their associations with health and disease: a phenome-wide association study. Scientific Reports, 2020, 10, 14771.	1.6	20
105	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19
106	Genome-wide studies of heart failure and endophenotypes: lessons learned and future directions. Cardiovascular Research, 2018, 114, 1209-1225.	1.8	18
107	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	2.6	18
108	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

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109	Twenty-Five Novel Loci for Carotid Intima-Media Thickness: A Genome-Wide Association Study in >45â€‰000 Individuals and Meta-Analysis of >100â€‰000 Individuals. Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, 484-501.	1.1	17
110	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
111	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	1.6	16
112	Gene-gene Interaction Analyses for Atrial Fibrillation. Scientific Reports, 2016, 6, 35371.	1.6	15
113	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	1.6	15
114	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	2.3	15
115	Genetic and functional evidence links a missense variant in B4GALT1 to lower LDL and fibrinogen. Science, 2021, 374, 1221-1227.	6.0	14
116	Identifying Genetic Variants for Heart Rate Variability in the Acetylcholine Pathway. PLoS ONE, 2014, 9, e112476.	1.1	13
117	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
118	The impact of coronary artery disease risk loci on ischemic heart failure severity and prognosis: association analysis in the COntrolled ROsuvastatin multiNAtional trial in heart failure (CORONA). BMC Medical Genetics, 2014, 15, 140.	2.1	9
119	Lipidomics, Atrial Conduction, and Body Mass Index. Circulation Genomic and Precision Medicine, 2019, 12, e002384.	1.6	9
120	A Bidirectional Mendelian Randomization Study to evaluate the causal role of reduced blood vitamin D levels with type 2 diabetes risk in South Asians and Europeans. Nutrition Journal, 2021, 20, 71.	1.5	9
121	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
122	Interactions between uncoupling protein 2 gene polymorphisms, obesity and alcohol intake on liver function: a large meta-analysed population-based study. European Journal of Endocrinology, 2015, 173, 863-872.	1.9	7
123	ukbpheno v1.0: An R package for phenotyping health-related outcomes in the UK Biobank. STAR Protocols, 2022, 3, 101471.	0.5	6
124	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	1.6	5
125	Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. American Journal of Nephrology, 2019, 49, 193-202.	1.4	5
126	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 753.	2.6	4

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127	Genetically Determined Physical Activity and Its Association with Circulating Blood Cells. Genes, 2019, 10, 908.	1.0	4
128	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. Journal of Nutrition, 2020, 150, 2635-2645.	1.3	4
129	Search for a Functional Genetic Variant Mimicking the Effect of SGLT2 Inhibitor Treatment. Genes, 2021, 12, 1174.	1.0	3
130	Meta-GWAS and Meta-Analysis of Exome Array Studies Do Not Reveal Genetic Determinants of Serum Hepcidin. PLoS ONE, 2016, 11, e0166628.	1.1	2
131	Genetically Determined High Levels of Iron Parameters Are Protective for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002544.	1.6	2
132	Causal Pathways from Blood Pressure to Larger QRS Amplitudes: a Mendelian Randomization Study. Scientific Reports, 2018, 8, 5817.	1.6	1
133	Refining Thromboembolic Risk in the GeneralÂPopulation. Journal of the American College of Cardiology, 2017, 70, 403-404.	1.2	0
134	An Erythropoietin-Independent Mechanism of Erythrocytic Precursor Proliferation Underlies Hypoxia Tolerance in Sea Nomads. Frontiers in Physiology, 2021, 12, 760851.	1.3	0