Patrick Deelen

List of Publications by Year
in descending order

65 papers	9,717 citations	87888 38 h-index	102487 66 g-index
91 all docs	91 docs citations	91 times ranked	21023 citing authors

#	Article	IF	Citations
1	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
2	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	21.4	672
3	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
4	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
5	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
6	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
7	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
8	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	3.5	324
9	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. Nature Genetics, 2018, 50, 493-497.	21.4	289
10	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	28.9	275
11	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
12	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
13	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. BMJ Open, 2015, 5, e006772.	1.9	207
14	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	3.5	194
15	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
16	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	30.7	148
17	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. Nature Genetics, 2022, 54, 143-151.	21.4	132
18	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. BMC Genomics, 2014, 15, 860.	2.8	124

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19	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	1.4	122
20	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
21	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116
22	Improving the diagnostic yield of exome- sequencing by predicting geneâ€“phenotype associations using large-scale gene expression analysis. Nature Communications, 2019, 10, 2837.	12.8	107
23	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
24	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
25	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature Genetics, 2018, 50, 1524-1532.	21.4	97
26	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
27	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. Genome Medicine, 2015, 7, 30.	8.2	91
28	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
29	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
30	A Proteomics and Transcriptomics Approach to Identify Leukemic Stem Cell (LSC) Markers. Molecular and Cellular Proteomics, 2013, 12, 626-637.	3.8	79
31	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
32	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	6.5	64
33	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
34	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	12.0	62
35	RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture. Stroke, 2016, 47, 1286-1293.	2.0	55
36	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. SSM - Population Health, 2021, 15, 100878.	2.7	53

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37	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. BMJ Open, 2021, 11, e044474.	1.9	49
38	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
39	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
40	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. Frontiers in Genetics, 2020, 11, 613.	2.3	45
41	Functional and Genomic Architecture of Borrelia burgdorferi -Induced Cytokine Responses in Humans. Cell Host and Microbe, 2016, 20, 822-833.	11.0	44
42	TMEM258 Is a Component of the Oligosaccharyltransferase Complex Controlling ER Stress and Intestinal Inflammation. Cell Reports, 2016, 17, 2955-2965.	6.4	42
43	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	2.6	38
44	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
45	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
46	Lessons Learned from Whole Exome Sequencing in Multiplex Families Affected by a Complex Genetic Disorder, Intracranial Aneurysm. PLoS ONE, 2015, 10, e0121104.	2.5	32
47	Runningâ€wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a postâ€transcriptional mechanism. Aging Cell, 2018, 17, e12700.	6.7	31
48	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	8.2	30
49	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
50	RNA-Sequencing Highlights Inflammation and Impaired Integrity of the Vascular Wall in Brain Arteriovenous Malformations. Stroke, 2020, 51, 268-274.	2.0	22
51	Immunochip meta-analysis in European and Argentinian populations identifies two novel genetic loci associated with celiac disease. European Journal of Human Genetics, 2020, 28, 313-323.	2.8	21
52	Pooled Resequencing of 122 Ulcerative Colitis Genes in a Large Dutch Cohort Suggests Population-Specific Associations of Rare Variants in MUC2. PLoS ONE, 2016, 11, e0159609.	2.5	21
53	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. Journal of Women's Health, 2021, 30, 1686-1692.	3.3	20
54	TAB2 deletions and variants cause a highly recognisable syndrome with mitral valve disease, cardiomyopathy, short stature and hypermobility. European Journal of Human Genetics, 2021, 29, 1669-1676.	2.8	19

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55	Exome sequencing in a family segregating for celiac disease. Clinical Genetics, 2011, 80, 138-147.	2.0	16
56	A GWAS meta-analysis suggests roles for xenobiotic metabolism and ion channel activity in the biology of stool frequency. Gut, 2017, 66, 756-758.	12.1	14
57	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	1.3	14
58	Occupational exposure to gases/fumes and mineral dust affect DNA methylation levels of genes regulating expression. Human Molecular Genetics, 2019, 28, 2477-2485.	2.9	9
59	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
60	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	2.5	6
61	A pipelineâ€friendly software tool for genome diagnostics to prioritize genes by matching patient symptoms to literature. Genetics & Genomics Next, 2020, 1, e10023.	1.5	3
62	Increased genetic contribution to wellbeing during the COVID-19 pandemic. PLoS Genetics, 2022, 18, e1010135.	3.5	3
63	Targeted RNA-Sequencing Enables Detection of Relevant Translocations and Single Nucleotide Variants and Provides a Method for Classification of Hematological Malignanciesâ€“RANKING. Clinical Chemistry, 2020, 66, 1521-1530.	3.2	2
64	IdÃ©fix: identifying accidental sample mix-ups in biobanks using polygenic scores. Bioinformatics, 2022, 38, 1059-1066.	4.1	1
65	FC 011KIDNEYNETWORK: USING KIDNEY DERIVED GENE EXPRESSION DATA TO PREDICT AND PRIORITIZE NOVEL GENES INVOLVED IN KIDNEY DISEASE. Nephrology Dialysis Transplantation, 2021, 36, .	0.7	0