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	IdÃ©fix: identifying accidental sample mix-ups in biobanks using polygenic scores. Bioinformatics, 2022, 38, 1059-1066.	4.1	1
2	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
3	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
4	Increased genetic contribution to wellbeing during the COVID-19 pandemic. PLoS Genetics, 2022, 18, e1010135.	3.5	3
5	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
6	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
7	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
8	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
9	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	2.5	6
10	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
11	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
12	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
13	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
14	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
15	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
16	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
17	RNA-Sequencing Highlights Inflammation and Impaired Integrity of the Vascular Wall in Brain Arteriovenous Malformations. Stroke, 2020, 51, 268-274.	2.0	22
18	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

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19	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
20	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	8.2	30
21	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
22	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
23	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	2.6	38
24	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
25	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
26	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
27	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
28	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
29	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. Nature Genetics, 2018, 50, 493-497.	21.4	289
30	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
31	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. Nature Genetics, 2018, 50, 1524-1532.	21.4	97
32	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
33	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	12.6	103
34	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
35	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
36	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64

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37	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	30.7	148
38	TMEM258 Is a Component of the Oligosaccharyltransferase Complex Controlling ER Stress and Intestinal Inflammation. Cell Reports, 2016, 17, 2955-2965.	6.4	42
39	RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture. Stroke, 2016, 47, 1286-1293.	2.0	55
40	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
41	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
42	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
43	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	21.4	672
44	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
45	Functional and Genomic Architecture of Borrelia burgdorferi -Induced Cytokine Responses in Humans. Cell Host and Microbe, 2016, 20, 822-833.	11.0	44
46	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	28.9	275
47	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
48	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
49	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
50	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
51	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
52	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
53	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116
54	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8

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55	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
56	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. BMC Genomics, 2014, 15, 860.	2.8	124
57	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
58	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	1.4	122
59	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
60	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
61	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
62	A Proteomics and Transcriptomics Approach to Identify Leukemic Stem Cell (LSC) Markers. Molecular and Cellular Proteomics, 2013, 12, 626-637.	3.8	79
63	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	3.5	194
64	Exome sequencing in a family segregating for celiac disease. Clinical Genetics, 2011, 80, 138-147.	2.0	16
65	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