

# Priit Palta

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

6,449  
citations

249298

26  
h-index

162838

57  
g-index

81  
all docs

81  
docs citations

81  
times ranked

16019  
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
2	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
3	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	9.4	520
4	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. <i>Nature</i> , 2010, 463, 671-675.	13.7	476
5	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351
6	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	9.4	338
7	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. <i>Nature Medicine</i> , 2020, 26, 549-557.	15.2	281
8	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. <i>European Journal of Human Genetics</i> , 2017, 25, 869-876.	1.4	181
9	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4329.	5.8	120
10	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. <i>Nature Communications</i> , 2020, 11, 6383.	5.8	101
11	Shared genetic basis for migraine and ischemic stroke. <i>Neurology</i> , 2015, 84, 2132-2145.	1.5	91
12	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. <i>European Respiratory Journal</i> , 2021, 57, 2003091.	3.1	85
13	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChip® for Methyloome Profiling. <i>PLoS ONE</i> , 2012, 7, e50233.	1.1	83
14	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	5.8	64
15	Genome-wide methylation analyses of primary human leukocyte subsets identifies functionally important cell-type-specific hypomethylated regions. <i>Blood</i> , 2013, 122, e52-e60.	0.6	63
16	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. <i>Neuron</i> , 2018, 98, 743-753.e4.	3.8	63
17	Genetic analysis for a shared biological basis between migraine and coronary artery disease. <i>Neurology: Genetics</i> , 2015, 1, e10.	0.9	61
18	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. <i>European Journal of Human Genetics</i> , 2017, 25, 477-484.	1.4	60

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19	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002725.	1.6	60
20	The GENCODE exome: sequencing the complete human exome. <i>European Journal of Human Genetics</i> , 2011, 19, 827-831.	1.4	58
21	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E327-E336.	3.3	39
22	Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. <i>Translational Psychiatry</i> , 2015, 5, e607-e607.	2.4	35
23	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	0.9	34
24	Structural Genomic Variation as Risk Factor for Idiopathic Recurrent Miscarriage. <i>Human Mutation</i> , 2014, 35, 972-982.	1.1	33
25	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. <i>Molecular Psychiatry</i> , 2018, 23, 1169-1180.	4.1	32
26	Evaluation of the 124-plex SNP typing microarray for forensic testing. <i>Forensic Science International: Genetics</i> , 2009, 4, 43-48.	1.6	29
27	Migraine polygenic risk score associates with efficacy of migraine-specific drugs. <i>Neurology: Genetics</i> , 2019, 5, e364.	0.9	28
28	TAC-seq: targeted DNA and RNA sequencing for precise biomarker molecule counting. <i>Npj Genomic Medicine</i> , 2018, 3, 34.	1.7	26
29	Epigenetic DNA methylation changes associated with headache chronification: A retrospective case-control study. <i>Cephalalgia</i> , 2018, 38, 312-322.	1.8	25
30	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. <i>European Journal of Human Genetics</i> , 2021, 29, 309-324.	1.4	19
31	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2370-2380.	1.7	18
32	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. <i>European Journal of Human Genetics</i> , 2021, 29, 615-624.	1.4	17
33	Comparison of DNA extraction methods for multiplex polymerase chain reaction. <i>Analytical Biochemistry</i> , 2010, 398, 260-262.	1.1	16
34	No evidence of somatic DNA copy number alterations in eutopic and ectopic endometrial tissue in endometriosis. <i>Human Reproduction</i> , 2012, 27, 1857-1864.	0.4	15
35	Detection of small genomic imbalances using microarray-based multiplex amplifiable probe hybridization. <i>European Journal of Human Genetics</i> , 2007, 15, 162-172.	1.4	13
36	Detection of NASBA amplified bacterial tmRNA molecules on SLICSel designed microarray probes. <i>BMC Biotechnology</i> , 2011, 11, 17.	1.7	12

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37	NIPTmer: rapid k-mer-based software package for detection of fetal aneuploidies. <i>Scientific Reports</i> , 2018, 8, 5616.	1.6	12
38	Computational framework for targeted high-coverage sequencing based NIPT. <i>PLoS ONE</i> , 2019, 14, e0209139.	1.1	11
39	Fluorescent labeling of NASBA amplified tmRNA molecules for microarray applications. <i>BMC Biotechnology</i> , 2009, 9, 45.	1.7	10
40	Haplotype Phasing and Inheritance of Copy Number Variants in Nuclear Families. <i>PLoS ONE</i> , 2015, 10, e0122713.	1.1	9
41	Screening of 20 patients with X-linked mental retardation using chromosome X-specific array-MAPH. <i>European Journal of Medical Genetics</i> , 2007, 50, 399-410.	0.7	8
42	Array-MAPH: a methodology for the detection of locus copy-number changes in complex genomes. <i>Nature Protocols</i> , 2008, 3, 849-865.	5.5	8
43	A parallel SNP array study of genomic aberrations associated with mental retardation in patients and general population in Estonia. <i>European Journal of Medical Genetics</i> , 2011, 54, 136-143.	0.7	8
44	Detection of tmRNA molecules on microarrays at low temperatures using helper oligonucleotides. <i>BMC Biotechnology</i> , 2010, 10, 34.	1.7	7
45	A molecular tool for menstrual cycle phase dating of endometrial samples in endometriosis transcriptome studies. <i>Biology of Reproduction</i> , 2019, 101, 1-3.	1.2	7
46	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. <i>JAMA Ophthalmology</i> , 2021, 139, 762.	1.4	7
47	Elucidating the relationship between migraine risk and brain structure using genetic data. <i>Brain</i> , 2022, 145, 3214-3224.	3.7	7
48	Primary age-related tauopathy in a Finnish population-based study of the oldest old (Vantaa 85+). <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	1.8	6
49	Systematic evaluation of NIPT aneuploidy detection software tools with clinically validated NIPT samples. <i>PLoS Computational Biology</i> , 2021, 17, e1009684.	1.5	6
50	Genetics of human plasma lipidome and its link to diseases susceptibility. <i>Atherosclerosis</i> , 2019, 287, e14-e15.	0.4	2
51	Application of two different microarray-based copy-number detection methodologies "array-comparative genomic hybridization and array-multiplex amplifiable probe hybridization" with identical amplifiable target sequences. <i>Clinical Chemistry and Laboratory Medicine</i> , 2008, 46, 722-4.	1.4	1
52	Nordic Exome Variant Catalogue a Web Resource for Genomic Data Browsing. , 2018, , .		0
53	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0
54	Polygenic Hyperlipidemia Increases Coronary Artery Disease Risk In The Uk Biobank. <i>Atherosclerosis</i> , 2019, 287, e92.	0.4	0

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55	POLYGENIC HYPERLIPIDEMIAS AND CORONARY ARTERY DISEASE RISK. <i>Journal of the American College of Cardiology</i> , 2019, 73, 1690.	1.2	0
56	Familial hypercholesterolaemia and LDL-C polygenic risk in patients with severe carotid artery stenosis. <i>Atherosclerosis</i> , 2021, 331, e48.	0.4	0