Priit Palta

List of Publications by Year
in descending order

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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	Primary ageâ€related tauopathy in a Finnish populationâ€based study of the oldest old (Vantaa 85+). Neuropathology and Applied Neurobiology, 2022, 48, .	1.8	6
2	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
3	High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. European Journal of Human Genetics, 2021, 29, 615-624.	1.4	17
4	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. European Respiratory Journal, 2021, 57, 2003091.	3.1	85
5	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. European Journal of Human Genetics, 2021, 29, 309-324.	1.4	19
6	Association of the MYOC p.(Gln368Ter) Variant With Glaucoma in a Finnish Population. JAMA Ophthalmology, 2021, 139, 762.	1.4	7
7	Familial hypercholesterolaemia and LDL-C polygenic risk in patients with severe carotid artery stenosis. Atherosclerosis, 2021, 331, e48.	0.4	0
8	Systematic evaluation of NIPT aneuploidy detection software tools with clinically validated NIPT samples. PLoS Computational Biology, 2021, 17, e1009684.	1.5	6
9	The role of polygenic risk and susceptibility genes in breast cancer over the course of life. Nature Communications, 2020, 11, 6383.	5.8	101
10	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
11	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. Circulation Genomic and Precision Medicine, 2020, 13, e002725.	1.6	60
12	Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. Nature Medicine, 2020, 26, 549-557.	15.2	281
13	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
14	Computational framework for targeted high-coverage sequencing based NIPT. PLoS ONE, 2019, 14, e0209139.	1.1	11
15	Polygenic Hyperlipidemia Increases Coronary Artery Disease Risk In The Uk Biobank. Atherosclerosis, 2019, 287, e92.	0.4	0
16	Genetics of human plasma lipidome and its link to diseases susceptibility. Atherosclerosis, 2019, 287, e14-e15.	0.4	2
17	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	5.8	120
18	A molecular tool for menstrual cycle phase dating of endometrial samples in endometriosis transcriptome studiesâ€. Biology of Reproduction, 2019, 101, 1-3.	1.2	7

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19	POLYGENIC HYPERLIPIDEMIAS AND CORONARY ARTERY DISEASE RISK. Journal of the American College of Cardiology, 2019, 73, 1690.	1.2	0
20	Migraine polygenic risk score associates with efficacy of migraine-specific drugs. Neurology: Genetics, 2019, 5, e364.	0.9	28
21	NIPTmer: rapid k-mer-based software package for detection of fetal aneuploidies. Scientific Reports, 2018, 8, 5616.	1.6	12
22	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
23	Epigenetic DNA methylation changes associated with headache chronification: A retrospective case-control study. Cephalalgia, 2018, 38, 312-322.	1.8	25
24	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180.	4.1	32
25	Nordic Exome Variant Catalogue a Web Resource for Genomic Data Browsing. , 2018, , .		0
26	TAC-seq: targeted DNA and RNA sequencing for precise biomarker molecule counting. Npj Genomic Medicine, 2018, 3, 34.	1.7	26
27	Differences in the commonly used genotype imputation algorithms and their imputation accuracy estimates. , 2018, , .		0
28	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
29	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	1.4	60
30	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. European Journal of Human Genetics, 2017, 25, 869-876.	1.4	181
31	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E327-E336.	3.3	39
32	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	5.8	64
33	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
34	Haplotype Phasing and Inheritance of Copy Number Variants in Nuclear Families. PLoS ONE, 2015, 10, e0122713.	1.1	9
35	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
36	Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. Translational Psychiatry, 2015, 5, e607-e607.	2.4	35

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37	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
38	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351
39	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
40	Structural Genomic Variation as Risk Factor for Idiopathic Recurrent Miscarriage. Human Mutation, 2014, 35, 972-982.	1.1	33
41	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
42	Genome-wide methylation analyses of primary human leukocyte subsets identifies functionally important cell-typeâ€“specific hypomethylated regions. Blood, 2013, 122, e52-e60.	0.6	63
43	No evidence of somatic DNA copy number alterations in eutopic and ectopic endometrial tissue in endometriosis. Human Reproduction, 2012, 27, 1857-1864.	0.4	15
44	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChipÂ® for Methylome Profiling. PLoS ONE, 2012, 7, e50233.	1.1	83
45	A parallel SNP array study of genomic aberrations associated with mental retardation in patients and general population in Estonia. European Journal of Medical Genetics, 2011, 54, 136-143.	0.7	8
46	The GENCODE exome: sequencing the complete human exome. European Journal of Human Genetics, 2011, 19, 827-831.	1.4	58
47	Detection of NASBA amplified bacterial tmRNA molecules on SLICSel designed microarray probes. BMC Biotechnology, 2011, 11, 17.	1.7	12
48	Comparison of DNA extraction methods for multiplex polymerase chain reaction. Analytical Biochemistry, 2010, 398, 260-262.	1.1	16
49	Detection of tmRNA molecules on microarrays at low temperatures using helper oligonucleotides. BMC Biotechnology, 2010, 10, 34.	1.7	7
50	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. Nature, 2010, 463, 671-675.	13.7	476
51	Fluorescent labeling of NASBA amplified tmRNA molecules for microarray applications. BMC Biotechnology, 2009, 9, 45.	1.7	10
52	Evaluation of the 124-plex SNP typing microarray for forensic testing. Forensic Science International: Genetics, 2009, 4, 43-48.	1.6	29
53	Array-MAPH: a methodology for the detection of locus copy-number changes in complex genomes. Nature Protocols, 2008, 3, 849-865.	5.5	8
54	Application of two different microarray-based copy-number detection methodologies â€“ array-comparative genomic hybridization and array-multiplex amplifiable probe hybridization â€“ with identical amplifiable target sequences. Clinical Chemistry and Laboratory Medicine, 2008, 46, 722-4.	1.4	1

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55	Screening of 20 patients with X-linked mental retardation using chromosome X-specific array-MAPH. European Journal of Medical Genetics, 2007, 50, 399-410.	0.7	8
56	Detection of small genomic imbalances using microarray-based multiplex amplifiable probe hybridization. European Journal of Human Genetics, 2007, 15, 162-172.	1.4	13