Bogdan Pasaniuc

List of Publications by Year in descending order

112 papers	14,233 citations	50276 46 h-index	32842 100 g-index
161 all docs	161 docs citations	161 times ranked	20765 citing authors

#	Article	IF	Citations
1	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	21.4	1,618
2	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
3	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. American Journal of Human Genetics, 2019, 104, 65-75.	6.2	715
4	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
5	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	21.4	592
6	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
7	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	6.2	569
8	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	3.5	475
9	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	21.4	406
10	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	2.9	400
11	Dissecting the genetics of complex traits using summary association statistics. Nature Reviews Genetics, 2017, 18, 117-127.	16.3	379
12	Contrasting the Genetic Architecture of 30 Complex Traits from Summary Association Data. American Journal of Human Genetics, 2016, 99, 139-153.	6.2	348
13	Using Extended Genealogy to Estimate Components of Heritability for 23 Quantitative and Dichotomous Traits. PLoS Genetics, 2013, 9, e1003520.	3.5	345
14	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	21.4	275
15	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	6.2	248
16	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	21.4	239
17	Local Genetic Correlation Gives Insights into the Shared Genetic Architecture of Complex Traits. American Journal of Human Genetics, 2017, 101, 737-751.	6.2	220
18	Fast and accurate inference of local ancestry in Latino populations. Bioinformatics, 2012, 28, 1359-1367.	4.1	205

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19	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	4.1	203
20	Leveraging Functional-Annotation Data in Trans-ethnic Fine-Mapping Studies. American Journal of Human Genetics, 2015, 97, 260-271.	6.2	186
21	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	28.9	174
22	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	21.4	174
23	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. Bioinformatics, 2014, 30, 2906-2914.	4.1	173
24	New approaches to disease mapping in admixed populations. Nature Reviews Genetics, 2011, 12, 523-528.	16.3	154
25	Leveraging Genetic Variability across Populations for the Identification of Causal Variants. American Journal of Human Genetics, 2010, 86, 23-33.	6.2	140
26	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	21.4	139
27	Inference of locus-specific ancestry in closely related populations. Bioinformatics, 2009, 25, i213-i221.	4.1	122
28	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	12.8	121
29	Improved methods for multi-trait fine mapping of pleiotropic risk loci. Bioinformatics, 2017, 33, 248-255.	4.1	119
30	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
31	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	3.5	115
32	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	3.5	110
33	Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal. Cell Cycle, 2011, 10, 3016-3030.	2.6	106
34	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	6.2	90
35	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature Genetics, 2019, 51, 815-823.	21.4	89
36	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88

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37	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	12.8	81
38	Genome-wide Comparison of African-Ancestry Populations from CARe and Other Cohorts Reveals Signals of Natural Selection. American Journal of Human Genetics, 2011, 89, 368-381.	6.2	79
39	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	3.5	78
40	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	6.2	74
41	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	4.1	72
42	Localizing Components of Shared Transethnic Genetic Architecture of Complex Traits from GWAS Summary Data. American Journal of Human Genetics, 2020, 106, 805-817.	6.2	71
43	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979.	12.8	70
44	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	21.4	69
45	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. Nature Genetics, 2019, 51, 1244-1251.	21.4	69
46	Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification. Nature Genetics, 2022, 54, 30-39.	21.4	63
47	Using population admixture to help complete maps of the human genome. Nature Genetics, 2013, 45, 406-414.	21.4	61
48	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61
49	Admixture mapping identifies a locus on 6q25 associated with breast cancer risk in US Latinas. Human Molecular Genetics, 2012, 21, 1907-1917.	2.9	60
50	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	1.3	59
51	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	12.8	53
52	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
53	CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity. Nature Cancer, 2021, 2, 34-48.	13.2	48
54	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. Nature Communications, 2021, 12, 4569.	12.8	47

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55	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	30.7	45
56	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. Cancer Research, 2019, 79, 3192-3204.	0.9	43
57	Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments. Journal of Computational Biology, 2011, 18, 459-468.	1.6	41
58	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	3.8	39
59	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. Nature Communications, 2020, 11, 5504.	12.8	39
60	Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation. Bioinformatics, 2013, 29, 1407-1415.	4.1	38
61	Analysis of caseâ€“control association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	4.1	36
62	Transcriptomic Insight Into the Polygenic Mechanisms Underlying Psychiatric Disorders. Biological Psychiatry, 2021, 89, 54-64.	1.3	36
63	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. PLoS Genetics, 2021, 17, e1008973.	3.5	35
64	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	19.0	35
65	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
66	Enhanced Localization of Genetic Samples through Linkage-Disequilibrium Correction. American Journal of Human Genetics, 2013, 92, 882-894.	6.2	31
67	Efficient variance components analysis across millions of genomes. Nature Communications, 2020, 11, 4020.	12.8	31
68	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300.	6.2	31
69	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	10.3	30
70	Enhanced Methods for Local Ancestry Assignment in Sequenced Admixed Individuals. PLoS Computational Biology, 2014, 10, e1003555.	3.2	29
71	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. Human Molecular Genetics, 2016, 25, 5500-5512.	2.9	29
72	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	2.9	26

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73	Leveraging reads that span multiple single nucleotide polymorphisms for haplotype inference from sequencing data. Bioinformatics, 2013, 29, 2245-2252.	4.1	23
74	Quantifying the contribution of dominance deviation effects to complex trait variation in biobank-scale data. American Journal of Human Genetics, 2021, 108, 799-808.	6.2	23
75	A generic coalescentâ€based framework for the selection of a reference panel for imputation. Genetic Epidemiology, 2010, 34, 773-782.	1.3	22
76	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. American Journal of Human Genetics, 2021, 108, 36-48.	6.2	22
77	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. Cancer Discovery, 2022, 12, 2074-2097.	9.4	22
78	Spatial Localization of Recent Ancestors for Admixed Individuals. G3: Genes, Genomes, Genetics, 2014, 4, 2505-2518.	1.8	19
79	Highly Scalable Genotype Phasing by Entropy Minimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 252-261.	3.0	17
80	Genotype Error Detection Using Hidden Markov Models of Haplotype Diversity. Journal of Computational Biology, 2008, 15, 1155-1171.	1.6	16
81	Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits. PLoS Computational Biology, 2021, 17, e1009483.	3.2	16
82	Genetically regulated multi-omics study for symptom clusters of posttraumatic stress disorder highlights pleiotropy with hematologic and cardio-metabolic traits. Molecular Psychiatry, 2022, 27, 1394-1404.	7.9	15
83	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. BMC Genetics, 2015, 16, 124.	2.7	14
84	RAISS: robust and accurate imputation from summary statistics. Bioinformatics, 2019, 35, 4837-4839.	4.1	14
85	On powerful GWAS in admixed populations. Nature Genetics, 2021, 53, 1631-1633.	21.4	14
86	Optimal Testing of Digital Microfluidic Biochips. INFORMS Journal on Computing, 2011, 23, 518-529.	1.7	13
87	Integrative analysis of Dupuytren's disease identifies novel risk locus and reveals a shared genetic etiology with BMI. Genetic Epidemiology, 2019, 43, 629-645.	1.3	13
88	Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors. IScience, 2021, 24, 102188.	4.1	13
89	Imputation-Based Local Ancestry Inference in Admixed Populations. Lecture Notes in Computer Science, 2009, , 221-233.	1.3	11
90	Fast estimation of genetic correlation for biobank-scale data. American Journal of Human Genetics, 2022, 109, 24-32.	6.2	11

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91	IBD Genetics: Focus on (Dys) Regulation in Immune Cells and the Epithelium. Gastroenterology, 2014, 146, 896-899.	1.3	10
92	Gene Expression Imputation Across Multiple Tissue Types Provides Insight Into the Genetic Architecture of Frontotemporal Dementia and Its Clinical Subtypes. Biological Psychiatry, 2021, 89, 825-835.	1.3	10
93	Multitrait transcriptomeâ€wide association study (TWAS) tests. Genetic Epidemiology, 2021, 45, 563-576.	1.3	9
94	Identifying causal variants at loci with multiple signals of association. , 2014, , .		7
95	A Genetic Population Isolate in The Netherlands Showing Extensive Haplotype Sharing and Long Regions of Homozygosity. Genes, 2017, 8, 133.	2.4	7
96	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. Human Genetics, 2019, 138, 1091-1104.	3.8	7
97	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.7	6
98	Genotyping common and rare variation using overlapping pool sequencing. BMC Bioinformatics, 2011, 12, S2.	2.6	5
99	Enhanced methods to detect haplotypic effects on gene expression. Bioinformatics, 2017, 33, 2307-2313.	4.1	5
100	A unifying framework for joint trait analysis under a non-infinitesimal model. Bioinformatics, 2018, 34, i195-i201.	4.1	5
101	Methods for fine-mapping with chromatin and expression data. PLoS Genetics, 2018, 14, e1007240.	3.5	5
102	A two-step approach to testing overall effect of geneâ€“environment interaction for multiple phenotypes. Bioinformatics, 2021, 36, 5640-5648.	4.1	4
103	A summary-statistics-based approach to examine the role of serotonin transporter promoter tandem repeat polymorphism in psychiatric phenotypes. European Journal of Human Genetics, 2021, , .	2.8	4
104	Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. European Journal of Human Genetics, 2016, 24, 113-119.	2.8	3
105	Leveraging eQTLs to identify individual-level tissue of interest for a complex trait. PLoS Computational Biology, 2021, 17, e1008915.	3.2	3
106	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. Bioinformatics, 2015, 31, 3514-3521.	4.1	2
107	Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. Journal of Computational Biology, 2021, 28, 842-855.	1.6	2
108	Powerful eQTL mapping through low-coverage RNA sequencing. Human Genetics and Genomics Advances, 2022, 3, 100103.	1.7	2

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109	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. American Journal of Human Genetics, 2022, 109, 692-709.	6.2	2
110	A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation. Lecture Notes in Computer Science, 2014, , 371-384.	1.3	1
111	A Spatial Haplotype Copying Model with Applications to Genotype Imputation. Journal of Computational Biology, 2015, 22, 451-462.	1.6	0
112	Highly Scalable Genotype Phasing by Entropy Minimization. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0