Bogdan Pasaniuc

List of Publications by Year
in descending order

112	14,233	57681 46	37326 100
papers	citations	h-index	g-index

161	161	161	23026
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Fast estimation of genetic correlation for biobank-scale data. American Journal of Human Genetics, 2022, 109, 24-32.	2.6	11
2	Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification. Nature Genetics, 2022, 54, 30-39.	9.4	63
3	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.	4.1	15
4	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	9.0	35
5	Powerful eQTL mapping through low-coverage RNA sequencing. Human Genetics and Genomics Advances, 2022, 3, 100103.	1.0	2
6	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. American Journal of Human Genetics, 2022, 109, 692-709.	2.6	2
7	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	9.4	61
8	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. Cancer Discovery, 2022, 12, 2074-2097.	7.7	22
9	Transcriptomic Insight Into the Polygenic Mechanisms Underlying Psychiatric Disorders. Biological Psychiatry, 2021, 89, 54-64.	0.7	36
10	CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity. Nature Cancer, 2021, 2, 34-48.	5.7	48
11	PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics. American Journal of Human Genetics, 2021, 108, 36-48.	2.6	22
12	Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors. IScience, 2021, 24, 102188.	1.9	13
13	Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer. Nature Communications, 2021, 12, 1979.	5.8	70
14	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.	1.5	35
15	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.	0.7	10
16	Quantifying the contribution of dominance deviation effects to complex trait variation in biobank-scale data. American Journal of Human Genetics, 2021, 108, 799-808.	2.6	23
17	Leveraging eQTLs to identify individual-level tissue of interest for a complex trait. PLoS Computational Biology, 2021, 17, e1008915.	1.5	3
18	Multitrait transcriptomeâ€wide association study (TWAS) tests. Genetic Epidemiology, 2021, 45, 563-576.	0.6	9

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19	Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization. Nature Communications, 2021, 12, 4569.	5.8	47
20	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
21	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
22	Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. Journal of Computational Biology, 2021, 28, 842-855.	0.8	2
23	Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits. PLoS Computational Biology, 2021, 17, e1009483.	1.5	16
24	A two-step approach to testing overall effect of geneâ€“environment interaction for multiple phenotypes. Bioinformatics, 2021, 36, 5640-5648.	1.8	4
25	Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123.	4.7	30
26	On powerful GWAS in admixed populations. Nature Genetics, 2021, 53, 1631-1633.	9.4	14
27	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300.	2.6	31
28	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, , .	1.4	4
29	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. Nature Genetics, 2020, 52, 790-799.	9.4	174
30	Efficient variance components analysis across millions of genomes. Nature Communications, 2020, 11, 4020.	5.8	31
31	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. Nature Communications, 2020, 11, 5504.	5.8	39
32	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	5.8	53
33	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
34	Localizing Components of Shared Transethnic Genetic Architecture of Complex Traits from GWAS Summary Data. American Journal of Human Genetics, 2020, 106, 805-817.	2.6	71
35	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. Nature Genetics, 2019, 51, 1244-1251.	9.4	69
36	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	13.5	174

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37	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. Nature Medicine, 2019, 25, 1615-1626.	15.2	45
38	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
39	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. Human Genetics, 2019, 138, 1091-1104.	1.8	7
40	RAISS: robust and accurate imputation from summary statistics. Bioinformatics, 2019, 35, 4837-4839.	1.8	14
41	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.	0.4	43
42	Integrative analysis of Dupuytren's disease identifies novel risk locus and reveals a shared genetic etiology with BMI. Genetic Epidemiology, 2019, 43, 629-645.	0.6	13
43	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.	9.4	89
44	Probabilistic fine-mapping of transcriptome-wide association studies. Nature Genetics, 2019, 51, 675-682.	9.4	275
45	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
46	Leveraging Polygenic Functional Enrichment to Improve GWAS Power. American Journal of Human Genetics, 2019, 104, 65-75.	2.6	715
47	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	9.4	406
48	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	1.8	203
49	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
50	Phenotype-Specific Enrichment of Mendelian Disorder Genes near GWAS Regions across 62 Complex Traits. American Journal of Human Genetics, 2018, 103, 535-552.	2.6	90
51	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	5.8	121
52	A unifying framework for joint trait analysis under a non-infinitesimal model. Bioinformatics, 2018, 34, i195-i201.	1.8	5
53	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	0.6	59
54	Methods for fine-mapping with chromatin and expression data. PLoS Genetics, 2018, 14, e1007240.	1.5	5

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55	Integrating Gene Expression with Summary Association Statistics to Identify Genes Associated with 30 Complex Traits. American Journal of Human Genetics, 2017, 100, 473-487.	2.6	248
56	Widespread Allelic Heterogeneity in Complex Traits. American Journal of Human Genetics, 2017, 100, 789-802.	2.6	74
57	Enhanced methods to detect haplotypic effects on gene expression. Bioinformatics, 2017, 33, 2307-2313.	1.8	5
58	Local Genetic Correlation Gives Insights into the Shared Genetic Architecture of Complex Traits. American Journal of Human Genetics, 2017, 101, 737-751.	2.6	220
59	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	1.8	39
60	Improved methods for multi-trait fine mapping of pleiotropic risk loci. Bioinformatics, 2017, 33, 248-255.	1.8	119
61	Dissecting the genetics of complex traits using summary association statistics. Nature Reviews Genetics, 2017, 18, 117-127.	7.7	379
62	A Genetic Population Isolate in The Netherlands Showing Extensive Haplotype Sharing and Long Regions of Homozygosity. Genes, 2017, 8, 133.	1.0	7
63	Colocalization of GWAS and eQTL Signals Detects Target Genes. American Journal of Human Genetics, 2016, 99, 1245-1260.	2.6	569
64	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
65	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.	1.4	29
66	Contrasting the Genetic Architecture of 30 Complex Traits from Summary Association Data. American Journal of Human Genetics, 2016, 99, 139-153.	2.6	348
67	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	9.4	139
68	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	9.4	1,618
69	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	1.4	26
70	Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders. European Journal of Human Genetics, 2016, 24, 113-119.	1.4	3
71	Leveraging local ancestry to detect gene-gene interactions in genome-wide data. BMC Genetics, 2015, 16, 124.	2.7	14
72	A Spatial Haplotype Copying Model with Applications to Genotype Imputation. Journal of Computational Biology, 2015, 22, 451-462.	0.8	0

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73	Identification of causal genes for complex traits. Bioinformatics, 2015, 31, i206-i213.	1.8	72
74	Leveraging Functional-Annotation Data in Trans-ethnic Fine-Mapping Studies. American Journal of Human Genetics, 2015, 97, 260-271.	2.6	186
75	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
76	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. Bioinformatics, 2015, 31, 3514-3521.	1.8	2
77	Fast and accurate imputation of summary statistics enhances evidence of functional enrichment. Bioinformatics, 2014, 30, 2906-2914.	1.8	173
78	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
79	Enhanced Methods for Local Ancestry Assignment in Sequenced Admixed Individuals. PLoS Computational Biology, 2014, 10, e1003555.	1.5	29
80	Spatial Localization of Recent Ancestors for Admixed Individuals. G3: Genes, Genomes, Genetics, 2014, 4, 2505-2518.	0.8	19
81	Identifying causal variants at loci with multiple signals of association. , 2014, , .		7
82	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	5.8	81
83	IBD Genetics: Focus on (Dys) Regulation in Immune Cells and the Epithelium. Gastroenterology, 2014, 146, 896-899.	0.6	10
84	Identifying Causal Variants at Loci with Multiple Signals of Association. Genetics, 2014, 198, 497-508.	1.2	400
85	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
86	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
87	A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation. Lecture Notes in Computer Science, 2014, , 371-384.	1.0	1
88	Leveraging reads that span multiple single nucleotide polymorphisms for haplotype inference from sequencing data. Bioinformatics, 2013, 29, 2245-2252.	1.8	23
89	Using population admixture to help complete maps of the human genome. Nature Genetics, 2013, 45, 406-414.	9.4	61
90	Enhanced Localization of Genetic Samples through Linkage-Disequilibrium Correction. American Journal of Human Genetics, 2013, 92, 882-894.	2.6	31

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91	Using Extended Genealogy to Estimate Components of Heritability for 23 Quantitative and Dichotomous Traits. PLoS Genetics, 2013, 9, e1003520.	1.5	345
92	Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation. Bioinformatics, 2013, 29, 1407-1415.	1.8	38
93	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	1.5	115
94	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	1.5	78
95	Analysis of caseâ€“control association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	1.8	36
96	Admixture mapping identifies a locus on 6q25 associated with breast cancer risk in US Latinas. Human Molecular Genetics, 2012, 21, 1907-1917.	1.4	60
97	Fast and accurate inference of local ancestry in Latino populations. Bioinformatics, 2012, 28, 1359-1367.	1.8	205
98	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	9.4	239
99	Optimal Testing of Digital Microfluidic Biochips. INFORMS Journal on Computing, 2011, 23, 518-529.	1.0	13
100	New approaches to disease mapping in admixed populations. Nature Reviews Genetics, 2011, 12, 523-528.	7.7	154
101	Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal. Cell Cycle, 2011, 10, 3016-3030.	1.3	106
102	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.	2.6	79
103	Genotyping common and rare variation using overlapping pool sequencing. BMC Bioinformatics, 2011, 12, S2.	1.2	5
104	Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments. Journal of Computational Biology, 2011, 18, 459-468.	0.8	41
105	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	1.5	110
106	Leveraging Genetic Variability across Populations for the Identification of Causal Variants. American Journal of Human Genetics, 2010, 86, 23-33.	2.6	140
107	A generic coalescentâ€based framework for the selection of a reference panel for imputation. Genetic Epidemiology, 2010, 34, 773-782.	0.6	22
108	Inference of locus-specific ancestry in closely related populations. Bioinformatics, 2009, 25, i213-i221.	1.8	122

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109	Imputation-Based Local Ancestry Inference in Admixed Populations. Lecture Notes in Computer Science, 2009, , 221-233.	1.0	11
110	Highly Scalable Genotype Phasing by Entropy Minimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 252-261.	1.9	17
111	Genotype Error Detection Using Hidden Markov Models of Haplotype Diversity. Journal of Computational Biology, 2008, 15, 1155-1171.	0.8	16
112	Highly Scalable Genotype Phasing by Entropy Minimization. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0