Bjarni J Vilhjalmsson

List of Publications by Year
in descending order

59 papers	11,595 citations	126858 33 h-index	155592 55 g-index
80 all docs	80 docs citations	80 times ranked	18672 citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature, 2010, 465, 627-631.	13.7	1,651
2	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	9.4	1,285
3	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
4	An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. Nature Genetics, 2012, 44, 825-830.	9.4	884
5	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
6	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
7	Genome-wide patterns of genetic variation in worldwide Arabidopsis thaliana accessions from the RegMap panel. Nature Genetics, 2012, 44, 212-216.	9.4	476
8	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ELife, 2015, 4, e05255.	2.8	457
9	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. Nature Genetics, 2012, 44, 1066-1071.	9.4	380
10	Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. Nature Genetics, 2013, 45, 884-890.	9.4	371
11	Genome-wide association study of Arabidopsis thaliana leaf microbial community. Nature Communications, 2014, 5, 5320.	5.8	322
12	Association between Mental Disorders and Subsequent Medical Conditions. New England Journal of Medicine, 2020, 382, 1721-1731.	13.9	258
13	LDpred2: better, faster, stronger. Bioinformatics, 2021, 36, 5424-5431.	1.8	257
14	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia. JAMA Psychiatry, 2015, 72, 635.	6.0	242
15	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. American Journal of Human Genetics, 2015, 96, 329-339.	2.6	230
16	Conditions Under Which Genome-Wide Association Studies Will be Positively Misleading. Genetics, 2010, 186, 1045-1052.	1.2	178
17	The nature of confounding in genome-wide association studies. Nature Reviews Genetics, 2013, 14, 1-2.	7.7	169
18	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis Â. Plant Cell, 2013, 24, 4793-4805.	3.1	162

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19	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	2.6	149
20	Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. PLoS Genetics, 2013, 9, e1003372.	1.5	137
21	Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. American Journal of Human Genetics, 2022, 109, 12-23.	2.6	136
22	Performing Highly Efficient Genome Scans for Local Adaptation with R Package pcadapt Version 4. Molecular Biology and Evolution, 2020, 37, 2153-2154.	3.5	133
23	Making the Most of Clumping and Thresholding for Polygenic Scores. American Journal of Human Genetics, 2019, 105, 1213-1221.	2.6	123
24	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	1.5	115
25	Efficient toolkit implementing best practices for principal component analysis of population genetic data. Bioinformatics, 2020, 36, 4449-4457.	1.8	76
26	Improved genetic prediction of complex traits from individual-level data or summary statistics. Nature Communications, 2021, 12, 4192.	5.8	76
27	Nature and prevalence of combinations of mental disorders and their association with excess mortality in a populationâ€based cohortÂstudy. World Psychiatry, 2020, 19, 339-349.	4.8	72
28	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
29	Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification. Nature Genetics, 2022, 54, 30-39.	9.4	63
30	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
31	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. Genetics, 2016, 204, 711-722.	1.2	54
32	Effect of Genetic Variation in a *Drosophila* Model of Diabetes-Associated Misfolded Human Proinsulin. Genetics, 2014, 196, 557-567.	1.2	52
33	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 2018, 7, .	3.3	46
34	Polygenic Risk and Progression to Bipolar or Psychotic Disorders Among Individuals Diagnosed With Unipolar Depression in Early Life. American Journal of Psychiatry, 2020, 177, 936-943.	4.0	40
35	Risk of Early-Onset Depression Associated With Polygenic Liability, Parental Psychiatric History, and Socioeconomic Status. JAMA Psychiatry, 2021, 78, 387.	6.0	33
36	Symbiosis genes show a unique pattern of introgression and selection within a Rhizobium leguminosarum species complex. Microbial Genomics, 2020, 6, .	1.0	31

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37	Linking the association between circRNAs and Alzheimer's disease progression by multi-tissue circular RNA characterization. RNA Biology, 2020, 17, 1789-1797.	1.5	30
38	Extreme genetic signatures of local adaptation during Lotus japonicus colonization of Japan. Nature Communications, 2020, 11, 253.	5.8	30
39	Association of Childhood Exposure to Nitrogen Dioxide and Polygenic Risk Score for Schizophrenia With the Risk of Developing Schizophrenia. JAMA Network Open, 2019, 2, e1914401.	2.8	29
40	Genome-wide association study of febrile seizures implicates fever response and neuronal excitability genes. Brain, 2022, 145, 555-568.	3.7	29
41	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27
42	Leveraging both individual-level genetic data and GWAS summary statistics increases polygenic prediction. American Journal of Human Genetics, 2021, 108, 1001-1011.	2.6	22
43	Multitrait GWAS to connect disease variants and biological mechanisms. PLoS Genetics, 2021, 17, e1009713.	1.5	16
44	Accounting for age of onset and family history improves power in genome-wide association studies. American Journal of Human Genetics, 2022, 109, 417-432.	2.6	16
45	JAWAMix5: an out-of-core HDF5-based java implementation of whole-genome association studies using mixed models. Bioinformatics, 2013, 29, 1220-1222.	1.8	15
46	JASS: command line and web interface for the joint analysis of GWAS results. NAR Genomics and Bioinformatics, 2020, 2, lqaa003.	1.5	11
47	Polygenic Risk Score–Enhanced Risk Stratification of Coronary Artery Disease in Patients With Stable Chest Pain. Circulation Genomic and Precision Medicine, 2021, 14, e003298.	1.6	9
48	Analysis and visualization of Arabidopsis thaliana GWAS using web 2.0 technologies. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar014-bar014.	1.4	8
49	Polygenic liability, stressful life events and risk for secondary-treated depression in early life: a nationwide register-based case-cohort study. Psychological Medicine, 2023, 53, 217-226.	2.7	7
50	Evaluating the interrelations between the autism polygenic score and psychiatric family history in risk for autism. Autism Research, 2022, 15, 171-182.	2.1	7
51	Polygenic Liability and Recurrence of Depression in Patients With First-Onset Depression Treated in Hospital-Based Settings. JAMA Psychiatry, 2021, 78, 792.	6.0	6
52	Transgenerational effects of inter-ploidy cross direction on reproduction and F2 seed development of Arabidopsis thaliana F1 hybrid triploids. Plant Reproduction, 2019, 32, 275-289.	1.3	5
53	Genetic liability to major depression and risk of childhood asthma. Brain, Behavior, and Immunity, 2020, 89, 433-439.	2.0	5
54	Finding hidden treasures in summary statistics from genome-wide association studies. Nature Genetics, 2021, 53, 431-432.	9.4	3

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55	Families, Health Registers, and Biobanks: Making the Unmeasurable Measurable. Biological Psychiatry, 2020, 88, 440-441.	0.7	2
56	Response to Day etÂal.. American Journal of Human Genetics, 2016, 98, 394-395.	2.6	1
57	Association Mapping and Disease: Evolutionary Perspectives. Methods in Molecular Biology, 2019, 1910, 533-553.	0.4	0
58	Headaches and polygenic scores. Neurology: Genetics, 2019, 5, e368.	0.9	0
59	Early-Life Injuries and the Development of Attention-Deficit/Hyperactivity Disorder. Journal of Clinical Psychiatry, 2022, 83, .	1.1	0