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	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
2	Genome-wide association study of febrile seizures implicates fever response and neuronal excitability genes. Brain, 2022, 145, 555-568.	3.7	29
3	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
4	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
5	Early-Life Injuries and the Development of Attention-Deficit/Hyperactivity Disorder. Journal of Clinical Psychiatry, 2022, 83, .	1.1	0
6	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
7	Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification. Nature Genetics, 2022, 54, 30-39.	9.4	63
8	LDpred2: better, faster, stronger. Bioinformatics, 2021, 36, 5424-5431.	1.8	257
9	Finding hidden treasures in summary statistics from genome-wide association studies. Nature Genetics, 2021, 53, 431-432.	9.4	3
10	Risk of Early-Onset Depression Associated With Polygenic Liability, Parental Psychiatric History, and Socioeconomic Status. JAMA Psychiatry, 2021, 78, 387.	6.0	33
11	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
12	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
13	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
14	Improved genetic prediction of complex traits from individual-level data or summary statistics. Nature Communications, 2021, 12, 4192.	5.8	76
15	Multitrait GWAS to connect disease variants and biological mechanisms. PLoS Genetics, 2021, 17, e1009713.	1.5	16
16	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
17	Genetic liability to major depression and risk of childhood asthma. Brain, Behavior, and Immunity, 2020, 89, 433-439.	2.0	5
18	Nature and prevalence of combinations of mental disorders and their association with excess mortality in a population‐based cohort study. World Psychiatry, 2020, 19, 339-349.	4.8	72

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19	Families, Health Registers, and Biobanks: Making the Unmeasurable Measurable. Biological Psychiatry, 2020, 88, 440-441.	0.7	2
20	Efficient toolkit implementing best practices for principal component analysis of population genetic data. Bioinformatics, 2020, 36, 4449-4457.	1.8	76
21	JASS: command line and web interface for the joint analysis of GWAS results. NAR Genomics and Bioinformatics, 2020, 2, lqaa003.	1.5	11
22	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
23	Extreme genetic signatures of local adaptation during Lotus japonicus colonization of Japan. Nature Communications, 2020, 11, 253.	5.8	30
24	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
25	Association between Mental Disorders and Subsequent Medical Conditions. New England Journal of Medicine, 2020, 382, 1721-1731.	13.9	258
26	Symbiosis genes show a unique pattern of introgression and selection within a Rhizobium leguminosarum species complex. Microbial Genomics, 2020, 6, .	1.0	31
27	Association Mapping and Disease: Evolutionary Perspectives. Methods in Molecular Biology, 2019, 1910, 533-553.	0.4	0
28	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
29	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
30	Headaches and polygenic scores. Neurology: Genetics, 2019, 5, e368.	0.9	0
31	Making the Most of Clumping and Thresholding for Polygenic Scores. American Journal of Human Genetics, 2019, 105, 1213-1221.	2.6	123
32	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
33	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 2018, 7, .	3.3	46
34	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27
35	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. Genetics, 2016, 204, 711-722.	1.2	54
36	Response to Day et Âal.. American Journal of Human Genetics, 2016, 98, 394-395.	2.6	1

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37	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
38	Efficient Bayesian mixed-model analysis increases association power in large cohorts. Nature Genetics, 2015, 47, 284-290.	9.4	1,285
39	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
40	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia. JAMA Psychiatry, 2015, 72, 635.	6.0	242
41	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
42	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ELife, 2015, 4, e05255.	2.8	457
43	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
44	Leveraging population admixture to characterize the heritability of complex traits. Nature Genetics, 2014, 46, 1356-1362.	9.4	69
45	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
46	Genome-wide association study of Arabidopsis thaliana leaf microbial community. Nature Communications, 2014, 5, 5320.	5.8	322
47	Effect of Genetic Variation in a *Drosophila* Model of Diabetes-Associated Misfolded Human Proinsulin. Genetics, 2014, 196, 557-567.	1.2	52
48	The nature of confounding in genome-wide association studies. Nature Reviews Genetics, 2013, 14, 1-2.	7.7	169
49	GWAPP: A Web Application for Genome-Wide Association Mapping in Arabidopsis Â. Plant Cell, 2013, 24, 4793-4805.	3.1	162
50	Quantifying Missing Heritability at Known GWAS Loci. PLoS Genetics, 2013, 9, e1003993.	1.5	115
51	Genetic Architecture of Skin and Eye Color in an African-European Admixed Population. PLoS Genetics, 2013, 9, e1003372.	1.5	137
52	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
53	Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. Nature Genetics, 2013, 45, 884-890.	9.4	371
54	Genome-wide patterns of genetic variation in worldwide Arabidopsis thaliana accessions from the RegMap panel. Nature Genetics, 2012, 44, 212-216.	9.4	476

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55	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. Nature Genetics, 2012, 44, 1066-1071.	9.4	380
56	An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. Nature Genetics, 2012, 44, 825-830.	9.4	884
57	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
58	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature, 2010, 465, 627-631.	13.7	1,651
59	Conditions Under Which Genome-Wide Association Studies Will be Positively Misleading. Genetics, 2010, 186, 1045-1052.	1.2	178