Hreinn Stefansson

List of Publications by Year
in descending order

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116 papers	41,926 citations	18465 62 h-index	18115 120 g-index
130 all docs	130 docs citations	130 times ranked	41098 citing authors

#	Article	IF	Citations
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
2	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	13.9	2,085
3	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
4	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	9.4	1,685
5	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimerâ€™s disease risk. Nature Genetics, 2019, 51, 404-413.	9.4	1,625
6	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	13.7	1,619
7	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
8	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
9	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	2.6	1,550
10	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
11	Association between Microdeletion and Microduplication at 16p11.2 and Autism. New England Journal of Medicine, 2008, 358, 667-675.	13.9	1,476
12	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	13.7	1,399
13	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
14	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
15	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
16	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
17	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
18	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935

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19	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
20	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
21	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
22	CNVs conferring risk of autism or schizophrenia affect cognition in controls. Nature, 2014, 505, 361-366.	13.7	588
23	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
24	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
25	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. American Journal of Human Genetics, 2003, 72, 83-87.	2.6	518
26	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. Lancet, The, 2010, 376, 1401-1408.	6.3	485
27	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimerâ€™s disease. Nature Genetics, 2021, 53, 1276-1282.	9.4	430
28	Disruption of the neurexin 1 gene is associated with schizophrenia. Human Molecular Genetics, 2009, 18, 988-996.	1.4	424
29	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	9.4	409
30	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	13.7	394
31	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. Nature Neuroscience, 2015, 18, 953-955.	7.1	351
32	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
33	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
34	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
35	Excessive burden of lysosomal storage disorder gene variants in Parkinsonâ€™s disease. Brain, 2017, 140, 3191-3203.	3.7	323
36	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. Nature Genetics, 1997, 17, 84-87.	9.4	288

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37	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	9.4	283
38	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	9.4	248
39	Brain age prediction using deep learning uncovers associated sequence variants. Nature Communications, 2019, 10, 5409.	5.8	238
40	Copy number variations of chromosome 16p13.1 region associated with schizophrenia. Molecular Psychiatry, 2011, 16, 17-25.	4.1	227
41	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
42	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
43	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. Nature Genetics, 2009, 41, 277-279.	9.4	211
44	Genetic factors contribute to the risk of developing endometriosis. Human Reproduction, 2002, 17, 555-559.	0.4	192
45	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	1.4	176
46	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	0.7	175
47	Identification of a novel neuregulin 1 at-risk haplotype in Han schizophrenia Chinese patients, but no association with the Icelandic/Scottish risk haplotype. Molecular Psychiatry, 2004, 9, 698-704.	4.1	149
48	Selection against variants in the genome associated with educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E727-E732.	3.3	149
49	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
50	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	7.1	144
51	A genome-wide scan for preeclampsia in the Netherlands. European Journal of Human Genetics, 2001, 9, 758-764.	1.4	140
52	Multiple novel transcription initiation sites for NRG1. Gene, 2004, 342, 97-105.	1.0	139
53	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	9.4	135
54	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2013, 22, 1039-1049.	1.4	122

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55	Neuregulin 1 and schizophrenia. Annals of Medicine, 2004, 36, 62-71.	1.5	119
56	A Mouse Model that Recapitulates Cardinal Features of the 15q13.3 Microdeletion Syndrome Including Schizophrenia- and Epilepsy-Related Alterations. Biological Psychiatry, 2014, 76, 128-137.	0.7	95
57	Genome-wide association study implicates CHRNA2 in cannabis use disorder. Nature Neuroscience, 2019, 22, 1066-1074.	7.1	94
58	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
59	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. Addiction Biology, 2018, 23, 485-492.	1.4	90
60	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
61	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
62	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
63	Genome-wide common and rare variant analysis provides novel insights into clozapine-associated neutropenia. Molecular Psychiatry, 2017, 22, 1502-1508.	4.1	75
64	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. Translational Psychiatry, 2019, 9, 258.	2.4	75
65	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
66	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. Translational Psychiatry, 2017, 7, e1109-e1109.	2.4	67
67	Truncating mutations in RBM12 are associated with psychosis. Nature Genetics, 2017, 49, 1251-1254.	9.4	63
68	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
69	Genome-Wide Analysis Shows Increased Frequency of Copy Number Variation Deletions in Dutch Schizophrenia Patients. Biological Psychiatry, 2011, 70, 655-662.	0.7	61
70	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
71	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	4.1	58
72	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. Molecular Psychiatry, 2014, 19, 774-783.	4.1	56

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73	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
74	GBA and APOE Îµ4 associate with sporadic dementia with Lewy bodies in European genome wide association study. Scientific Reports, 2019, 9, 7013.	1.6	53
75	Parental Origin of Interstitial Duplications at 15q11.2-q13.3 in Schizophrenia and Neurodevelopmental Disorders. PLoS Genetics, 2016, 12, e1005993.	1.5	51
76	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
77	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
78	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
79	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
80	Meta-analysis of Alzheimerâ€™s disease on 9,751 samples from Norway and IGAP study identifies four risk loci. Scientific Reports, 2018, 8, 18088.	1.6	47
81	Association of AADAC Deletion and Gilles de la Tourette Syndrome in a Large European Cohort. Biological Psychiatry, 2016, 79, 383-391.	0.7	41
82	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. Communications Biology, 2020, 3, 703.	2.0	40
83	Neuregulin 1 in schizophrenia: out of Iceland. Molecular Psychiatry, 2003, 8, 639-640.	4.1	36
84	The influence of genetic constitution on migraine drug responses. Cephalalgia, 2016, 36, 624-639.	1.8	34
85	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
86	The Adult Reading History Questionnaire (ARHQ) in Icelandic. Journal of Learning Disabilities, 2014, 47, 532-542.	1.5	33
87	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
88	Identification of genetic overlap and novel risk loci for attention-deficit/hyperactivity disorder and bipolar disorder. Molecular Psychiatry, 2021, 26, 4055-4065.	4.1	31
89	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
90	Reproductive fitness and genetic risk of psychiatric disorders in the general population. Nature Communications, 2017, 8, 15833.	5.8	30

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91	Effects of copy number variations on brain structure and risk for psychiatric illness: Largeâ€scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	1.9	30
92	Reciprocal White Matter Changes Associated With Copy Number Variation at 15q11.2 BP1-BP2: A Diffusion Tensor Imaging Study. Biological Psychiatry, 2019, 85, 563-572.	0.7	29
93	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.5	26
94	Endometriosis is not associated with or linked to the GALT gene. Fertility and Sterility, 2001, 76, 1019-1022.	0.5	24
95	The association between candidate migraine susceptibility loci and severe migraine phenotype in a clinical sample. Cephalalgia, 2016, 36, 615-623.	1.8	24
96	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
97	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). International Journal of Epidemiology, 2021, 50, 719-720e.	0.9	23
98	Addictions and their familiality in Iceland. Annals of the New York Academy of Sciences, 2010, 1187, 208-217.	1.8	22
99	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	9.4	22
100	MAP1B mutations cause intellectual disability and extensive white matter deficit. Nature Communications, 2018, 9, 3456.	5.8	21
101	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
102	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
103	Identification of Genetic Loci Shared Between Attention-Deficit/Hyperactivity Disorder, Intelligence, and Educational Attainment. Biological Psychiatry, 2020, 87, 1052-1062.	0.7	13
104	Comparing migraine with and without aura to healthy controls using RNA sequencing. Cephalalgia, 2019, 39, 1435-1444.	1.8	12
105	HLA-DQB1 6672G>C (rs113332494) is associated with clozapine-induced neutropenia and agranulocytosis in individuals of European ancestry. Translational Psychiatry, 2021, 11, 214.	2.4	12
106	Predicting facial characteristics from complex polygenic variations. Forensic Science International: Genetics, 2015, 19, 263-268.	1.6	11
107	Analysis of Diffusion Tensor Imaging Data From the UK Biobank Confirms Dosage Effect of 15q11.2 Copy Number Variation on White Matter and Shows Association With Cognition. Biological Psychiatry, 2021, 90, 307-316.	0.7	11
108	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	2.0	10

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109	Neuroimaging findings in neurodevelopmental copy number variants: identifying molecular pathways to convergent phenotypes. Biological Psychiatry, 2022, , .	0.7	9
110	Elevated common variant genetic risk for tourette syndrome in a densely-affected pedigree. Molecular Psychiatry, 2021, 26, 7522-7529.	4.1	8
111	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
112	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	5.8	7
113	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. BMJ Open, 2021, 11, e049709.	0.8	7
114	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2013, 22, 1696-1696.	1.4	3
115	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. Intelligence, 2021, 88, 101565.	1.6	2
116	Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 4-5.	0.7	0