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	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
2	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
3	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
4	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
5	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
6	Neuroimaging findings in neurodevelopmental copy number variants: identifying molecular pathways to convergent phenotypes. Biological Psychiatry, 2022, , .	0.7	9
7	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
8	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
9	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	4.1	58
10	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
11	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). International Journal of Epidemiology, 2021, 50, 719-720e.	0.9	23
12	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
13	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
14	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
15	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
16	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
17	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	2.0	10
18	Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 4-5.	0.7	0

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19	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
20	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
21	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
22	Elevated common variant genetic risk for tourette syndrome in a densely-affected pedigree. Molecular Psychiatry, 2021, 26, 7522-7529.	4.1	8
23	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
24	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
25	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
26	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
27	Identification of Genetic Loci Shared Between Attention-Deficit/Hyperactivity Disorder, Intelligence, and Educational Attainment. Biological Psychiatry, 2020, 87, 1052-1062.	0.7	13
28	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
29	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. Communications Biology, 2020, 3, 703.	2.0	40
30	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
31	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
32	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
33	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. Translational Psychiatry, 2019, 9, 258.	2.4	75
34	Comparing migraine with and without aura to healthy controls using RNA sequencing. Cephalalgia, 2019, 39, 1435-1444.	1.8	12
35	Genome-wide association study implicates CHRNA2 in cannabis use disorder. Nature Neuroscience, 2019, 22, 1066-1074.	7.1	94
36	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	5.8	7

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37	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
38	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
39	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	9.4	22
40	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
41	Brain age prediction using deep learning uncovers associated sequence variants. Nature Communications, 2019, 10, 5409.	5.8	238
42	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
43	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
44	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
45	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
46	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
47	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
48	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
49	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
50	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. Addiction Biology, 2018, 23, 485-492.	1.4	90
51	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
52	MAP1B mutations cause intellectual disability and extensive white matter deficit. Nature Communications, 2018, 9, 3456.	5.8	21
53	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
54	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

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55	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
56	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. Translational Psychiatry, 2017, 7, e1109-e1109.	2.4	67
57	Truncating mutations in RBM12 are associated with psychosis. Nature Genetics, 2017, 49, 1251-1254.	9.4	63
58	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
59	Reproductive fitness and genetic risk of psychiatric disorders in the general population. Nature Communications, 2017, 8, 15833.	5.8	30
60	Genome-wide common and rare variant analysis provides novel insights into clozapine-associated neutropenia. Molecular Psychiatry, 2017, 22, 1502-1508.	4.1	75
61	Excessive burden of lysosomal storage disorder gene variants in Parkinsonâ€™s disease. Brain, 2017, 140, 3191-3203.	3.7	323
62	Parental Origin of Interstitial Duplications at 15q11.2-q13.3 in Schizophrenia and Neurodevelopmental Disorders. PLoS Genetics, 2016, 12, e1005993.	1.5	51
63	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
64	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
65	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
66	Association of AADAC Deletion and Gilles de la Tourette Syndrome in a Large European Cohort. Biological Psychiatry, 2016, 79, 383-391.	0.7	41
67	The influence of genetic constitution on migraine drug responses. Cephalalgia, 2016, 36, 624-639.	1.8	34
68	The association between candidate migraine susceptibility loci and severe migraine phenotype in a clinical sample. Cephalalgia, 2016, 36, 615-623.	1.8	24
69	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
70	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. Nature Neuroscience, 2015, 18, 953-955.	7.1	351
71	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
72	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	9.4	283

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73	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
74	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
75	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
76	Predicting facial characteristics from complex polygenic variations. Forensic Science International: Genetics, 2015, 19, 263-268.	1.6	11
77	The Adult Reading History Questionnaire (ARHQ) in Icelandic. Journal of Learning Disabilities, 2014, 47, 532-542.	1.5	33
78	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
79	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. Molecular Psychiatry, 2014, 19, 774-783.	4.1	56
80	CNVs conferring risk of autism or schizophrenia affect cognition in controls. Nature, 2014, 505, 361-366.	13.7	588
81	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
82	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
83	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
84	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
85	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	7.1	144
86	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	13.9	2,085
87	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
88	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2013, 22, 1696-1696.	1.4	3
89	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
90	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	1.4	176

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91	Genome-Wide Analysis Shows Increased Frequency of Copy Number Variation Deletions in Dutch Schizophrenia Patients. Biological Psychiatry, 2011, 70, 655-662.	0.7	61
92	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	13.7	394
93	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
94	Copy number variations of chromosome 16p13.1 region associated with schizophrenia. Molecular Psychiatry, 2011, 16, 17-25.	4.1	227
95	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
96	Addictions and their familiality in Iceland. Annals of the New York Academy of Sciences, 2010, 1187, 208-217.	1.8	22
97	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. Lancet, The, 2010, 376, 1401-1408.	6.3	485
98	Disruption of the neurexin 1 gene is associated with schizophrenia. Human Molecular Genetics, 2009, 18, 988-996.	1.4	424
99	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
100	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. Nature Genetics, 2009, 41, 277-279.	9.4	211
101	Association between Microdeletion and Microduplication at 16p11.2 and Autism. New England Journal of Medicine, 2008, 358, 667-675.	13.9	1,476
102	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	13.7	1,399
103	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	13.7	1,619
104	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	9.4	409
105	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
106	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
107	Neuregulin 1 and schizophrenia. Annals of Medicine, 2004, 36, 62-71.	1.5	119
108	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

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109	Multiple novel transcription initiation sites for NRG1. Gene, 2004, 342, 97-105.	1.0	139
110	Neuregulin 1 in schizophrenia: out of Iceland. Molecular Psychiatry, 2003, 8, 639-640.	4.1	36
111	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. American Journal of Human Genetics, 2003, 72, 83-87.	2.6	518
112	Genetic factors contribute to the risk of developing endometriosis. Human Reproduction, 2002, 17, 555-559.	0.4	192
113	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	2.6	1,550
114	Endometriosis is not associated with or linked to the GALT gene. Fertility and Sterility, 2001, 76, 1019-1022.	0.5	24
115	A genome-wide scan for preeclampsia in the Netherlands. European Journal of Human Genetics, 2001, 9, 758-764.	1.4	140
116	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. Nature Genetics, 1997, 17, 84-87.	9.4	288