Verneri Anttila

List of Publications by Year
in descending order

55	18,788	117453	155451
papers	citations	34 h-index	55 g-index

59	59	59	28264
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	9.4	3,145
2	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
3	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
4	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
5	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
6	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
7	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	1.8	822
8	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
9	IFITM3 restricts the morbidity and mortality associated with influenza. Nature, 2012, 484, 519-523.	13.7	668
10	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
11	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
12	Genome-wide association study reveals three susceptibility loci for common migraine in the general population. Nature Genetics, 2011, 43, 695-698.	9.4	355
13	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
14	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
15	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
16	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
17	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	9.4	294
18	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204

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19	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	1.4	188
20	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
21	A high-density association screen of 155 ion transport genes for involvement with common migraine. Human Molecular Genetics, 2008, 17, 3318-3331.	1.4	90
22	Novel mutations consolidateKCTD7as a progressive myoclonus epilepsy gene. Journal of Medical Genetics, 2012, 49, 391-399.	1.5	69
23	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
24	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
25	European lactase persistence genotype shows evidence of association with increase in body mass index. Human Molecular Genetics, 2010, 19, 1129-1136.	1.4	58
26	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	1.5	55
27	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. Genome Research, 2010, 20, 1344-1351.	2.4	52
28	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
29	Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. Human Genetics, 2016, 135, 425-439.	1.8	47
30	Selectivity in Genetic Association with Sub-classified Migraine in Women. PLoS Genetics, 2014, 10, e1004366.	1.5	45
31	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. PLoS ONE, 2017, 12, e0185663.	1.1	44
32	Systematic re-evaluation of genes from candidate gene association studies in migraine using a large genome-wide association data set. Cephalalgia, 2016, 36, 604-614.	1.8	41
33	Consistently Replicating Locus Linked to Migraine on 10q22-q23. American Journal of Human Genetics, 2008, 82, 1051-1063.	2.6	40
34	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	1.8	40
35	Novel hypotheses emerging from GWAS in migraine?. Journal of Headache and Pain, 2019, 20, 5.	2.5	39
36	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

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37	A Potential Novel Spontaneous Preterm Birth Gene, AR, Identified by Linkage and Association Analysis of X Chromosomal Markers. PLoS ONE, 2012, 7, e51378.	1.1	32
38	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
39	SNP Variants in Major Histocompatibility Complex Are Associated with Sarcoidosis Susceptibilityâ€"A Joint Analysis in Four European Populations. Frontiers in Immunology, 2017, 8, 422.	2.2	31
40	Statistical power and utility of meta-analysis methods for cross-phenotype genome-wide association studies. PLoS ONE, 2018, 13, e0193256.	1.1	28
41	Serum calcium and risk of migraine: a Mendelian randomization study. Human Molecular Genetics, 2017, 26, ddw416.	1.4	26
42	Genetics of migraine. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 148, 493-503.	1.0	25
43	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. PLoS ONE, 2016, 11, e0163877.	1.1	23
44	Heterogeneous contribution of microdeletions in the development of common generalised and focal epilepsies. Journal of Medical Genetics, 2017, 54, 598-606.	1.5	22
45	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
46	Genome wide association study identifies variants in NBEA associated with migraine in bipolar disorder. Journal of Affective Disorders, 2015, 172, 453-461.	2.0	15
47	Involvement of astrocyte and oligodendrocyte gene sets in migraine. Cephalalgia, 2016, 36, 640-647.	1.8	15
48	Towards an understanding of genetic predisposition to migraine. Genome Medicine, 2011, 3, 17.	3.6	11
49	In silico phenotyping via co-training for improved phenotype prediction from genotype. Bioinformatics, 2015, 31, i303-i310.	1.8	9
50	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
51	Valsalva Maneuver as Migraine Inducer: A Case Report of a Woman With Patent Foramen Ovale and an Ischemic Stroke. Headache, 2009, 49, 146-147.	1.8	5
52	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	1.1	3
53	Probing the Brain of Comorbidity. Science Translational Medicine, 2013, 5, 183fs15, 1-3.	5.8	2
54	Left ventricular hypertrophy and other cardiac risk factors in migraineurs. Acta Neurologica Scandinavica, 2021, 143, 661-665.	1.0	1

#	Article	IF	Citations
55	Electrocardiographic findings in migraineurs: results of the Finnish Health 2000 survey. Acta Neurologica Scandinavica, 2021, 144, 730-735.	1.0	0