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	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
2	Left ventricular hypertrophy and other cardiac risk factors in migraineurs. Acta Neurologica Scandinavica, 2021, 143, 661-665.	1.0	1
3	Electrocardiographic findings in migraineurs: results of the Finnish Health 2000 survey. Acta Neurologica Scandinavica, 2021, 144, 730-735.	1.0	0
4	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
5	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
6	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
7	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
8	Novel hypotheses emerging from GWAS in migraine?. Journal of Headache and Pain, 2019, 20, 5.	2.5	39
9	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
10	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
11	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
12	Genetics of migraine. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 148, 493-503.	1.0	25
13	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
14	Statistical power and utility of meta-analysis methods for cross-phenotype genome-wide association studies. PLoS ONE, 2018, 13, e0193256.	1.1	28
15	Serum calcium and risk of migraine: a Mendelian randomization study. Human Molecular Genetics, 2017, 26, ddw416.	1.4	26
16	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
17	Heterogeneous contribution of microdeletions in the development of common generalised and focal epilepsies. Journal of Medical Genetics, 2017, 54, 598-606.	1.5	22
18	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

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19	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
20	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. PLoS ONE, 2017, 12, e0185663.	1.1	44
21	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
22	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
23	Involvement of astrocyte and oligodendrocyte gene sets in migraine. Cephalalgia, 2016, 36, 640-647.	1.8	15
24	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
25	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
26	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
27	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
28	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. PLoS ONE, 2016, 11, e0163877.	1.1	23
29	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
30	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
31	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
32	In silico phenotyping via co-training for improved phenotype prediction from genotype. Bioinformatics, 2015, 31, i303-i310.	1.8	9
33	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
34	An atlas of genetic correlations across human diseases and traits. Nature Genetics, 2015, 47, 1236-1241.	9.4	3,145
35	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
36	Selectivity in Genetic Association with Sub-classified Migraine in Women. PLoS Genetics, 2014, 10, e1004366.	1.5	45

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37	High Risk Population Isolate Reveals Low Frequency Variants Predisposing to Intracranial Aneurysms. PLoS Genetics, 2014, 10, e1004134.	1.5	55
38	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
39	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
40	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
41	Probing the Brain of Comorbidity. Science Translational Medicine, 2013, 5, 183fs15, 1-3.	5.8	2
42	IFITM3 restricts the morbidity and mortality associated with influenza. Nature, 2012, 484, 519-523.	13.7	668
43	Novel mutations consolidateKCTD7as a progressive myoclonus epilepsy gene. Journal of Medical Genetics, 2012, 49, 391-399.	1.5	69
44	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
45	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	9.4	294
46	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
47	Towards an understanding of genetic predisposition to migraine. Genome Medicine, 2011, 3, 17.	3.6	11
48	Genome-wide association study reveals three susceptibility loci for common migraine in the general population. Nature Genetics, 2011, 43, 695-698.	9.4	355
49	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
50	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
51	European lactase persistence genotype shows evidence of association with increase in body mass index. Human Molecular Genetics, 2010, 19, 1129-1136.	1.4	58
52	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
53	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
54	Consistently Replicating Locus Linked to Migraine on 10q22-q23. American Journal of Human Genetics, 2008, 82, 1051-1063.	2.6	40

#	Article	IF	Citations
55	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