

Lisette J A Kogelman

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

1,290
citations

471371

17
h-index

395590

33
g-index

40
all docs

40
docs citations

40
times ranked

2843
citing authors

#	ARTICLE	IF	CITATIONS
1	Smooth muscle ATP-sensitive potassium channels mediate migraine-relevant hypersensitivity in mouse models. <i>Cephalalgia</i> , 2022, 42, 93-107.	1.8	11
2	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. <i>Nature Genetics</i> , 2022, 54, 152-160.	9.4	135
3	Population-based prevalence of cranial autonomic symptoms in migraine and proposed diagnostic appendix criteria. <i>Cephalalgia</i> , 2022, 42, 1160-1171.	1.8	7
4	Chronic migraine: Genetics or environment?. <i>European Journal of Neurology</i> , 2021, 28, 1726-1736.	1.7	10
5	Twenty-five years of triptans – a nationwide population study. <i>Cephalalgia</i> , 2021, 41, 894-904.	1.8	9
6	Changes in the gene expression profile during spontaneous migraine attacks. <i>Scientific Reports</i> , 2021, 11, 8294.	1.6	10
7	Genetic Susceptibility Loci in Genomewide Association Study of Cluster Headache. <i>Annals of Neurology</i> , 2021, 90, 203-216.	2.8	22
8	Functional gene networks reveal distinct mechanisms segregating in migraine families. <i>Brain</i> , 2020, 143, 2945-2956.	3.7	15
9	Familial analysis reveals rare risk variants for migraine in regulatory regions. <i>Neurogenetics</i> , 2020, 21, 149-157.	0.7	11
10	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson’s disease. <i>Nature Genetics</i> , 2020, 52, 482-493.	9.4	216
11	Prevalence and socio-demographic characteristics of persons who have never had a headache among healthy voluntary blood donors – a population-based study. <i>Cephalalgia</i> , 2020, 40, 1055-1062.	1.8	4
12	Characterization of eQTLs associated with androstenone by RNA sequencing in porcine testis. <i>Physiological Genomics</i> , 2019, 51, 488-499.	1.0	14
13	Characterization of Familial and Sporadic Migraine. <i>Headache</i> , 2019, 59, 1802-1807.	1.8	5
14	Comparing migraine with and without aura to healthy controls using RNA sequencing. <i>Cephalalgia</i> , 2019, 39, 1435-1444.	1.8	12
15	Predicting treatment response using pharmacy register in migraine. <i>Journal of Headache and Pain</i> , 2019, 20, 31.	2.5	8
16	Migraine polygenic risk score associates with efficacy of migraine-specific drugs. <i>Neurology: Genetics</i> , 2019, 5, e364.	0.9	28
17	Transcriptomic profiling of trigeminal nucleus caudalis and spinal cord dorsal horn. <i>Brain Research</i> , 2018, 1692, 23-33.	1.1	5
18	Systems genetics analysis of pharmacogenomics variation during antidepressant treatment. <i>Pharmacogenomics Journal</i> , 2018, 18, 144-152.	0.9	6

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19	Transcription Factor Co-expression Networks of Adipose RNA-Seq Data Reveal Regulatory Mechanisms of Obesity. <i>Current Genomics</i> , 2018, 19, 289-299.	0.7	9
20	Comorbidity of migraine with ADHD in adults. <i>BMC Neurology</i> , 2018, 18, 147.	0.8	24
21	WISH-Râ€“ a fast and efficient tool for construction of epistatic networks for complex traits and diseases. <i>BMC Bioinformatics</i> , 2018, 19, 277.	1.2	14
22	Differential expression and co-expression gene networks reveal candidate biomarkers of boar taint in non-castrated pigs. <i>Scientific Reports</i> , 2017, 7, 12205.	1.6	46
23	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. <i>PLoS ONE</i> , 2016, 11, e0167519.	1.1	21
24	Multi-omic data integration and analysis using systems genomics approaches: methods and applications in animal production, health and welfare. <i>Genetics Selection Evolution</i> , 2016, 48, 38.	1.2	144
25	Applications of Systems Genetics and Biology for Obesity Using Pig Models. , 2016, , 25-42.		7
26	Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. <i>BMC Genomics</i> , 2015, 16, 1073.	1.2	161
27	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. <i>Genome Medicine</i> , 2015, 7, 105.	3.6	30
28	Potential role of lncRNA cyp2c91â€™ protein interactions on diseases of the immune system. <i>Frontiers in Genetics</i> , 2015, 6, 255.	1.1	30
29	Comparative Analyses of QTLs Influencing Obesity and Metabolic Phenotypes in Pigs and Humans. <i>PLoS ONE</i> , 2015, 10, e0137356.	1.1	21
30	Systems Genetics of Complex Diseases Using RNA-Sequencing Methods. <i>International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB)</i> , 2015, 5, 264-279.	0.2	6
31	Systems genetics of obesity in an F2 pig model by genome-wide association, genetic network, and pathway analyses. <i>Frontiers in Genetics</i> , 2014, 5, 214.	1.1	25
32	Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model. <i>BMC Medical Genomics</i> , 2014, 7, 57.	0.7	96
33	Weighted Interaction SNP Hub (WISH) network method for building genetic networks for complex diseases and traits using whole genome genotype data. <i>BMC Systems Biology</i> , 2014, 8, S5.	3.0	42
34	An F2 Pig Resource Population as a Model for Genetic Studies of Obesity and Obesity-Related Diseases in Humans: Design and Genetic Parameters. <i>Frontiers in Genetics</i> , 2013, 4, 29.	1.1	42
35	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	1.2	18