Pouya Khankhanian

List of Publications by Year
in descending order

37 papers	2,491 citations	471509 17 h-index	315739 38 g-index
52 all docs	52 docs citations	52 times ranked	5194 citing authors

#	Article	IF	Citations
1	Combined VNS-RNS Neuromodulation for Epilepsy. Journal of Clinical Neurophysiology, 2022, 39, e5-e9.	1.7	3
2	Adverse Childhood Experiences in Patients With Neurologic Disease. Neurology: Clinical Practice, 2022, 12, 60-67.	1.6	4
3	Efficacy and Tolerability of Clobazam in Adults With Drug-Refractory Epilepsy. Neurology: Clinical Practice, 2021, 11, e669-e676.	1.6	7
4	Monitoring the Burden of Seizures and Highly Epileptiform Patterns in Critical Care with a Novel Machine Learning Method. Neurocritical Care, 2021, 34, 908-917.	2.4	17
5	Can antiepileptic efficacy and epilepsy variables be studied from electronic health records? A review of current approaches. Seizure: the Journal of the British Epilepsy Association, 2021, 85, 138-144.	2.0	6
6	The nature of genetic and environmental susceptibility to multiple sclerosis. PLoS ONE, 2021, 16, e0246157.	2.5	29
7	Phenotypic homogeneity in childhood epilepsies evolves in gene-specific patterns across 3251 patient-years of clinical data. European Journal of Human Genetics, 2021, 29, 1690-1700.	2.8	13
8	A longitudinal footprint of genetic epilepsies using automated electronic medical record interpretation. Genetics in Medicine, 2020, 22, 2060-2070.	2.4	22
9	Impact of cervical stenosis on multiple sclerosis lesion distribution in the spinal cord. Multiple Sclerosis and Related Disorders, 2020, 45, 102415.	2.0	7
10	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17â€‰458 subjects. Brain, 2020, 143, 2106-2118.	7.6	47
11	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	1.3	28
12	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. American Journal of Human Genetics, 2019, 105, 267-282.	6.2	237
13	Big data in status epilepticus. Epilepsy and Behavior, 2019, 101, 106457.	1.7	9
14	Cerebrospinal Fluid in Posterior Reversible Encephalopathy Syndrome: Implications of Elevated Protein and Pleocytosis. Neurohospitalist, The, 2019, 9, 58-64.	0.8	20
15	Harnessing electronic medical records to advance research on multiple sclerosis. Multiple Sclerosis Journal, 2019, 25, 408-418.	3.0	21
16	Highly conserved extended haplotypes of the major histocompatibility complex and their relationship to multiple sclerosis susceptibility. PLoS ONE, 2018, 13, e0190043.	2.5	20
17	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. ELife, 2017, 6, .	6.0	333
18	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. International Journal of Epidemiology, 2016, 45, 728-740.	1.9	20

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19	Video Capsule Endoscopy: Is Bowel Preparation Necessary?. Journal of Investigative Medicine, 2016, 64, 1114-1117.	1.6	7
20	Corticosteroidâ€induced morphological changes in cells of the myeloid lineage. American Journal of Hematology, 2015, 90, 679-680.	4.1	2
21	SNP imputation bias reduces effect size determination. Frontiers in Genetics, 2015, 6, 30.	2.3	7
22	An ImmunoChip study of multiple sclerosis risk in African Americans. Brain, 2015, 138, 1518-1530.	7.6	60
23	Pseudo-Pelgerâ€“HuÃ«t anomaly and granulocytic dysplasia associated with human granulocytic anaplasmosis. International Journal of Hematology, 2015, 102, 129-133.	1.6	6
24	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. BMC Medical Genetics, 2015, 16, 55.	2.1	8
25	Haplotype-based approach to known MS-associated regions increases the amount of explained risk. Journal of Medical Genetics, 2015, 52, 587-594.	3.2	22
26	Single Nucleotide Polymorphism (SNP)-Strings: An Alternative Method for Assessing Genetic Associations. PLoS ONE, 2014, 9, e90034.	2.5	10
27	Patients Recovering From Abdominal Surgery Who Walked With Volunteers Had Improved Postoperative Recovery Profiles during Their Hospitalization. World Journal of Surgery, 2014, 38, 1961-1965.	1.6	16
28	HLA Diversity in the 1000 Genomes Dataset. PLoS ONE, 2014, 9, e97282.	2.5	179
29	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. Blood, 2014, 124, 135-135.	1.4	1
30	A genome-wide association study of brain lesion distribution in multiple sclerosis. Brain, 2013, 136, 1012-1024.	7.6	52
31	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. Human Molecular Genetics, 2013, 22, 4194-4205.	2.9	81
32	Sequencing of the IL6 gene in a caseâ€“control study of cerebral palsy in children. BMC Medical Genetics, 2013, 14, 126.	2.1	20
33	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. American Journal of Human Genetics, 2013, 92, 854-865.	6.2	164
34	Genetic variation in the odorant receptors family 13 and the mhc loci influence mate selection in a multiple sclerosis dataset. BMC Genomics, 2010, 11, 626.	2.8	15
35	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. Nature, 2010, 464, 1351-1356.	27.8	463
36	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. Brain, 2010, 133, 2603-2611.	7.6	123

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37	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. Human Molecular Genetics, 2009, 18, 2078-2090.	2.9	371