

Michael F Hammer

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

10,928
citations

57758

44
h-index

69250

77
g-index

83
all docs

83
docs citations

83
times ranked

12593
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical characteristics and treatment experience of individuals with SCN8A developmental and epileptic encephalopathy (SCN8A-DEE): Findings from an online caregiver survey. <i>Seizure: the Journal of the British Epilepsy Association</i> , 2022, 97, 50-57.	2.0	3
2	Whole exome sequencing and co-expression analysis identify an <i>SCN1A</i> variant that modifies pathogenicity in a family with genetic epilepsy and febrile seizures plus. <i>Epilepsia</i> , 2022, 63, 1970-1980.	5.1	2
3	SCN8A Epilepsy, Developmental Encephalopathy, and Related Disorders. <i>Pediatric Neurology</i> , 2021, 122, 76-83.	2.1	25
4	Variable patterns of mutation density among NaV1.1, NaV1.2 and NaV1.6 point to channel-specific functional differences associated with childhood epilepsy. <i>PLoS ONE</i> , 2020, 15, e0238121.	2.5	11
5	Title is missing!. , 2020, 15, e0238121.		0
6	Title is missing!. , 2020, 15, e0238121.		0
7	Title is missing!. , 2020, 15, e0238121.		0
8	Title is missing!. , 2020, 15, e0238121.		0
9	Influence of age at seizure onset on the acquisition of neurodevelopmental skills in an SCN8A cohort. <i>Epilepsia</i> , 2019, 60, 1711-1720.	5.1	10
10	Altered expression of signaling pathways regulating neuronal excitability in hippocampal tissue of temporal lobe epilepsy patients with low and high seizure frequency. <i>Epilepsy Research</i> , 2019, 155, 106145.	1.6	7
11	Substructured Population Growth in the Ashkenazi Jews Inferred with Approximate Bayesian Computation. <i>Molecular Biology and Evolution</i> , 2019, 36, 1162-1171.	8.9	11
12	The spectrum of intermediate <i>SCN8A</i> -related epilepsy. <i>Epilepsia</i> , 2019, 60, 830-844.	5.1	70
13	Leukocyte expression profiles reveal gene sets with prognostic value for seizure-free outcome following stereotactic laser amygdalohypocampotomy. <i>Scientific Reports</i> , 2019, 9, 1086.	3.3	4
14	Genomic Evidence of Local Adaptation to Climate and Diet in Indigenous Siberians. <i>Molecular Biology and Evolution</i> , 2019, 36, 315-327.	8.9	41
15	Siberian genetic diversity reveals complex origins of the Samoyedic-speaking populations. <i>American Journal of Human Biology</i> , 2018, 30, e23194.	1.6	15
16	A novel variant in <i>TAF1</i> affects gene expression and is associated with X-linked <i>TAF1</i> intellectual disability syndrome. <i>Neuronal Signaling</i> , 2018, 2, NS20180141.	3.2	16
17	The Role of Phylogenetically Conserved Elements in Shaping Patterns of Human Genomic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 2284-2295.	8.9	5
18	Modeling SNP array ascertainment with Approximate Bayesian Computation for demographic inference. <i>Scientific Reports</i> , 2018, 8, 10209.	3.3	12

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19	Clinical implications of <i>SCN1A</i> missense and truncation variants in a large Japanese cohort with Dravet syndrome. <i>Epilepsia</i> , 2017, 58, 282-290.	5.1	55
20	Altered gene expression profile in a mouse model of SCN8A encephalopathy. <i>Experimental Neurology</i> , 2017, 288, 134-141.	4.1	27
21	Exome Sequencing Provides Evidence of Polygenic Adaptation to a Fat-Rich Animal Diet in Indigenous Siberian Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2913-2926.	8.9	31
22	Rare variants of small effect size in neuronal excitability genes influence clinical outcome in Japanese cases of SCN1A truncation-positive Dravet syndrome. <i>PLoS ONE</i> , 2017, 12, e0180485.	2.5	18
23	<i>SCN8A</i> encephalopathy: Research progress and prospects. <i>Epilepsia</i> , 2016, 57, 1027-1035.	5.1	101
24	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
25	Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. <i>Genome Research</i> , 2016, 26, 279-290.	5.5	54
26	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. <i>Genome Research</i> , 2016, 26, 291-300.	5.5	87
27	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	8.9	92
28	Coevolution of genes and languages and high levels of population structure among the highland populations of Daghestan. <i>Journal of Human Genetics</i> , 2016, 61, 181-191.	2.3	27
29	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
30	Convulsive seizures and SUDEP in a mouse model of SCN8A epileptic encephalopathy. <i>Human Molecular Genetics</i> , 2015, 24, 506-515.	2.9	124
31	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 600-612.	8.9	55
32	Reconstructing Past Admixture Processes from Local Genomic Ancestry Using Wavelet Transformation. <i>Genetics</i> , 2015, 200, 469-481.	2.9	24
33	Extensive genome-wide autozygosity in the population isolates of Daghestan. <i>European Journal of Human Genetics</i> , 2015, 23, 1405-1412.	2.8	21
34	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	12.6	293
35	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. <i>Genetics</i> , 2015, 200, 295-308.	2.9	44
36	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	5.5	348

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37	Improved phylogenetic resolution and rapid diversification of Y-chromosome haplogroup K-M526 in Southeast Asia. <i>European Journal of Human Genetics</i> , 2015, 23, 369-373.	2.8	22
38	Reply to "The "extremely ancient" chromosome that isn't" by Elhaik et al. <i>European Journal of Human Genetics</i> , 2015, 23, 564-567.	2.8	2
39	Isolation, contact and social behavior shaped genetic diversity in West Timor. <i>Journal of Human Genetics</i> , 2014, 59, 494-503.	2.3	17
40	The KCNJ8-S422L variant previously associated with J-wave syndromes is found at an increased frequency in Ashkenazi Jews. <i>European Journal of Human Genetics</i> , 2014, 22, 94-98.	2.8	28
41	The impact of whole-genome sequencing on the reconstruction of human population history. <i>Nature Reviews Genetics</i> , 2014, 15, 149-162.	16.3	147
42	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
43	Evidence for Increased Levels of Positive and Negative Selection on the X Chromosome versus Autosomes in Humans. <i>Molecular Biology and Evolution</i> , 2014, 31, 2267-2282.	8.9	59
44	Characterization of a de novo SCN8A mutation in a patient with epileptic encephalopathy. <i>Epilepsy Research</i> , 2014, 108, 1511-1518.	1.6	92
45	A novel de novo mutation of SCN8A (Nav1.6) with enhanced channel activation in a child with epileptic encephalopathy. <i>Neurobiology of Disease</i> , 2014, 69, 117-123.	4.4	96
46	Exome sequencing reveals new causal mutations in children with epileptic encephalopathies. <i>Epilepsia</i> , 2013, 54, 1270-1281.	5.1	250
47	Higher Levels of Neanderthal Ancestry in East Asians than in Europeans. <i>Genetics</i> , 2013, 194, 199-209.	2.9	219
48	An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree. <i>American Journal of Human Genetics</i> , 2013, 92, 454-459.	6.2	124
49	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
50	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. <i>Human Biology</i> , 2013, 85, 859-900.	0.2	68
51	Multistate Structural Modeling and Voltage-Clamp Analysis of Epilepsy/Autism Mutation Kv10.2 "R327H Demonstrate the Role of This Residue in Stabilizing the Channel Closed State. <i>Journal of Neuroscience</i> , 2013, 33, 16586-16593.	3.6	39
52	An Early Divergence of KhoeSan Ancestors from Those of Other Modern Humans Is Supported by an ABC-Based Analysis of Autosomal Resequencing Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 617-630.	8.9	125
53	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
54	A Haplotype at STAT2 Introgressed from Neanderthals and Serves as a Candidate of Positive Selection in Papua New Guinea. <i>American Journal of Human Genetics</i> , 2012, 91, 265-274.	6.2	152

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55	Global Genetic Variation at OAS1 Provides Evidence of Archaic Admixture in Melanesian Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 1513-1520.	8.9	74
56	De Novo Pathogenic SCN8A Mutation Identified by Whole-Genome Sequencing of a Family Quartet Affected by Infantile Epileptic Encephalopathy and SUDEP. <i>American Journal of Human Genetics</i> , 2012, 90, 502-510.	6.2	365
57	Genetic evidence for archaic admixture in Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15123-15128.	7.1	265
58	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. <i>Nature Genetics</i> , 2010, 42, 830-831.	21.4	90
59	Autosomal Resequencing Data Reveal Late Stone Age Signals of Population Expansion in Sub-Saharan African Foraging and Farming Populations. <i>PLoS ONE</i> , 2009, 4, e6366.	2.5	45
60	Extended Y chromosome haplotypes resolve multiple and unique lineages of the Jewish priesthood. <i>Human Genetics</i> , 2009, 126, 707-717.	3.8	70
61	Joint match probabilities for Y chromosomal and autosomal markers. <i>Forensic Science International</i> , 2008, 174, 234-238.	2.2	35
62	Testing for Archaic Hominin Admixture on the X Chromosome: Model Likelihoods for the Modern Human <i>RRM2P4</i> Region From Summaries of Genealogical Topology Under the Structured Coalescent. <i>Genetics</i> , 2008, 178, 427-437.	2.9	27
63	New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. <i>Genome Research</i> , 2008, 18, 830-838.	5.5	748
64	A novel DNA sequence database for analyzing human demographic history. <i>Genome Research</i> , 2008, 18, 1354-1361.	5.5	74
65	Sex-Biased Evolutionary Forces Shape Genomic Patterns of Human Diversity. <i>PLoS Genetics</i> , 2008, 4, e1000202.	3.5	139
66	Machine-Learning Approaches for Classifying Haplogroup from Y Chromosome STR Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000093.	3.2	49
67	Genetic Structure Among 38 Populations from the United States Based on 11 U.S. Core Y Chromosome STRs*. <i>Journal of Forensic Sciences</i> , 2006, 51, 580-585.	1.6	22
68	Population structure of Y chromosome SNP haplogroups in the United States and forensic implications for constructing Y chromosome STR databases. <i>Forensic Science International</i> , 2006, 164, 45-55.	2.2	53
69	Dual origins of the Japanese: common ground for hunter-gatherer and farmer Y chromosomes. <i>Journal of Human Genetics</i> , 2006, 51, 47-58.	2.3	233
70	Contrasting patterns of Y chromosome and mtDNA variation in Africa: evidence for sex-biased demographic processes. <i>European Journal of Human Genetics</i> , 2005, 13, 867-876.	2.8	190
71	Deep Haplotype Divergence and Long-Range Linkage Disequilibrium at Xp21.1 Provide Evidence That Humans Descend From a Structured Ancestral Population. <i>Genetics</i> , 2005, 170, 1849-1856.	2.9	67
72	Evidence for Archaic Asian Ancestry on the Human X Chromosome. <i>Molecular Biology and Evolution</i> , 2005, 22, 189-192.	8.9	81

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73	Heterogeneous Patterns of Variation Among Multiple Human X-Linked Loci. <i>Genetics</i> , 2004, 167, 1841-1853.	2.9	56
74	High-Resolution SNPs and Microsatellite Haplotypes Point to a Single, Recent Entry of Native American Y Chromosomes into the Americas. <i>Molecular Biology and Evolution</i> , 2003, 21, 164-175.	8.9	228
75	Human Population Structure and Its Effects on Sampling Y Chromosome Sequence Variation. <i>Genetics</i> , 2003, 164, 1495-1509.	2.9	71
76	High Levels of Y-Chromosome Differentiation among Native Siberian Populations and the Genetic Signature of a Boreal Hunter-Gatherer Way of Life. <i>Human Biology</i> , 2002, 74, 761-789.	0.2	114
77	A novel multiplex for simultaneous amplification of 20 Y chromosome STR markers. <i>Forensic Science International</i> , 2002, 129, 10-24.	2.2	167
78	Forensic value of 14 novel STRs on the human Y chromosome. <i>Forensic Science International</i> , 2002, 130, 97-111.	2.2	144
79	Hierarchical Patterns of Global Human Y-Chromosome Diversity. <i>Molecular Biology and Evolution</i> , 2001, 18, 1189-1203.	8.9	275
80	The role of the Y chromosome in human evolutionary studies. <i>Evolutionary Anthropology</i> , 1996, 5, 116-134.	3.4	95