Michael F Hammer

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7263162/publications.pdf

Version: 2024-02-01

80	10,928	57758 44	69250 77
papers	citations	h-index	g-index

83	83	83	12593
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
2	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
3	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
4	New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. Genome Research, 2008, 18, 830-838.	5.5	748
5	De Novo Pathogenic SCN8A Mutation Identified by Whole-Genome Sequencing of a Family Quartet Affected by Infantile Epileptic Encephalopathy and SUDEP. American Journal of Human Genetics, 2012, 90, 502-510.	6.2	365
6	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
7	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	27.8	320
8	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
9	Hierarchical Patterns of Global Human Y-Chromosome Diversity. Molecular Biology and Evolution, 2001, 18, 1189-1203.	8.9	275
10	Genetic evidence for archaic admixture in Africa. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15123-15128.	7.1	265
11	Exome sequencing reveals new causal mutations in children with epileptic encephalopathies. Epilepsia, 2013, 54, 1270-1281.	5.1	250
12	Dual origins of the Japanese: common ground for hunter-gatherer and farmer Y chromosomes. Journal of Human Genetics, 2006, 51, 47-58.	2.3	233
13	High-Resolution SNPs and Microsatellite Haplotypes Point to a Single, Recent Entry of Native American Y Chromosomes into the Americas. Molecular Biology and Evolution, 2003, 21, 164-175.	8.9	228
14	Higher Levels of Neanderthal Ancestry in East Asians than in Europeans. Genetics, 2013, 194, 199-209.	2.9	219
15	Contrasting patterns of Y chromosome and mtDNA variation in Africa: evidence for sex-biased demographic processes. European Journal of Human Genetics, 2005, 13, 867-876.	2.8	190
16	A novel multiplex for simultaneous amplification of 20 Y chromosome STR markers. Forensic Science International, 2002, 129, 10-24.	2.2	167
17	A Haplotype at STAT2 Introgressed from Neanderthals and Serves as a Candidate of Positive Selection in Papua New Guinea. American Journal of Human Genetics, 2012, 91, 265-274.	6.2	152
18	The impact of whole-genome sequencing on the reconstruction of human population history. Nature Reviews Genetics, 2014, 15, 149-162.	16.3	147

#	Article	IF	Citations
19	Forensic value of 14 novel STRs on the human Y chromosome. Forensic Science International, 2002, 130, 97-111.	2.2	144
20	Sex-Biased Evolutionary Forces Shape Genomic Patterns of Human Diversity. PLoS Genetics, 2008, 4, e1000202.	3.5	139
21	An Early Divergence of KhoeSan Ancestors from Those of Other Modern Humans Is Supported by an ABC-Based Analysis of Autosomal Resequencing Data. Molecular Biology and Evolution, 2012, 29, 617-630.	8.9	125
22	An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree. American Journal of Human Genetics, 2013, 92, 454-459.	6.2	124
23	Convulsive seizures and SUDEP in a mouse model of SCN8A epileptic encephalopathy. Human Molecular Genetics, 2015, 24, 506-515.	2.9	124
24	High Levels of Y-Chromosome Differentiation among Native Siberian Populations and the Genetic Signature of a Boreal Hunter-Gatherer Way of Life. Human Biology, 2002, 74, 761-789.	0.2	114
25	SCN8A encephalopathy: Research progress and prospects. Epilepsia, 2016, 57, 1027-1035.	5.1	101
26	A novel de novo mutation of SCN8A (Nav1.6) with enhanced channel activation in a child with epileptic encephalopathy. Neurobiology of Disease, 2014, 69, 117-123.	4.4	96
27	The role of the Y chromosome in human evolutionary studies. Evolutionary Anthropology, 1996, 5, 116-134.	3.4	95
28	Characterization of a de novo SCN8A mutation in a patient with epileptic encephalopathy. Epilepsy Research, 2014, 108, 1511-1518.	1.6	92
29	The Time Scale of Recombination Rate Evolution in Great Apes. Molecular Biology and Evolution, 2016, 33, 928-945.	8.9	92
30	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. Nature Genetics, 2010, 42, 830-831.	21.4	90
31	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. Genome Research, 2016, 26, 291-300.	5.5	87
32	Evidence for Archaic Asian Ancestry on the Human X Chromosome. Molecular Biology and Evolution, 2005, 22, 189-192.	8.9	81
33	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	7.1	75
34	A novel DNA sequence database for analyzing human demographic history. Genome Research, 2008, 18, 1354-1361.	5.5	74
35	Global Genetic Variation at OAS1 Provides Evidence of Archaic Admixture in Melanesian Populations. Molecular Biology and Evolution, 2012, 29, 1513-1520.	8.9	74
36	Human Population Structure and Its Effects on Sampling Y Chromosome Sequence Variation. Genetics, 2003, 164, 1495-1509.	2.9	71

#	Article	IF	Citations
37	Extended Y chromosome haplotypes resolve multiple and unique lineages of the Jewish priesthood. Human Genetics, 2009, 126, 707-717.	3.8	70
38	The spectrum of intermediate <scp>SCN</scp>8Aâ€related epilepsy. Epilepsia, 2019, 60, 830-844.	5.1	70
39	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. Human Biology, 2013, 85, 859-900.	0.2	68
40	Deep Haplotype Divergence and Long-Range Linkage Disequilibrium at Xp21.1 Provide Evidence That Humans Descend From a Structured Ancestral Population. Genetics, 2005, 170, 1849-1856.	2.9	67
41	Evidence for Increased Levels of Positive and Negative Selection on the X Chromosome versus Autosomes in Humans. Molecular Biology and Evolution, 2014, 31, 2267-2282.	8.9	59
42	Heterogeneous Patterns of Variation Among Multiple Human X-Linked Loci. Genetics, 2004, 167, 1841-1853.	2.9	56
43	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2015, 32, 600-612.	8.9	55
44	Clinical implications of <scp>SCN</scp>1A missense and truncation variants in a large Japanese cohort with Dravet syndrome. Epilepsia, 2017, 58, 282-290.	5.1	55
45	Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. Genome Research, 2016, 26, 279-290.	5.5	54
46	Population structure of Y chromosome SNP haplogroups in the United States and forensic implications for constructing Y chromosome STR databases. Forensic Science International, 2006, 164, 45-55.	2.2	53
47	Machine-Learning Approaches for Classifying Haplogroup from Y Chromosome STR Data. PLoS Computational Biology, 2008, 4, e1000093.	3.2	49
48	Autosomal Resequence Data Reveal Late Stone Age Signals of Population Expansion in Sub-Saharan African Foraging and Farming Populations. PLoS ONE, 2009, 4, e6366.	2.5	45
49	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. Genetics, 2015, 200, 295-308.	2.9	44
50	Genomic Evidence of Local Adaptation to Climate and Diet in Indigenous Siberians. Molecular Biology and Evolution, 2019, 36, 315-327.	8.9	41
51	Multistate Structural Modeling and Voltage-Clamp Analysis of Epilepsy/Autism Mutation Kv10.2â€“R327H Demonstrate the Role of This Residue in Stabilizing the Channel Closed State. Journal of Neuroscience, 2013, 33, 16586-16593.	3.6	39
52	Joint match probabilities for Y chromosomal and autosomal markers. Forensic Science International, 2008, 174, 234-238.	2.2	35
53	Exome Sequencing Provides Evidence of Polygenic Adaptation to a Fat-Rich Animal Diet in Indigenous Siberian Populations. Molecular Biology and Evolution, 2017, 34, 2913-2926.	8.9	31
54	The KCNJ8-S422L variant previously associated with J-wave syndromes is found at an increased frequency in Ashkenazi Jews. European Journal of Human Genetics, 2014, 22, 94-98.	2.8	28

#	Article	IF	Citations
55	Testing for Archaic Hominin Admixture on the X Chromosome: Model Likelihoods for the Modern Human RRM2P4 Region From Summaries of Genealogical Topology Under the Structured Coalescent. Genetics, 2008, 178, 427-437.	2.9	27
56	Coevolution of genes and languages and high levels of population structure among the highland populations of Daghestan. Journal of Human Genetics, 2016, 61, 181-191.	2.3	27
57	Altered gene expression profile in a mouse model of SCN8A encephalopathy. Experimental Neurology, 2017, 288, 134-141.	4.1	27
58	SCN8A Epilepsy, Developmental Encephalopathy, and Related Disorders. Pediatric Neurology, 2021, 122, 76-83.	2.1	25
59	Reconstructing Past Admixture Processes from Local Genomic Ancestry Using Wavelet Transformation. Genetics, 2015, 200, 469-481.	2.9	24
60	Genetic Structure Among 38 Populations from the United States Based on 11 U.S. Core Y Chromosome STRs*. Journal of Forensic Sciences, 2006, 51, 580-585.	1.6	22
61	Improved phylogenetic resolution and rapid diversification of Y-chromosome haplogroup K-M526 in Southeast Asia. European Journal of Human Genetics, 2015, 23, 369-373.	2.8	22
62	Extensive genome-wide autozygosity in the population isolates of Daghestan. European Journal of Human Genetics, 2015, 23, 1405-1412.	2.8	21
63	Rare variants of small effect size in neuronal excitability genes influence clinical outcome in Japanese cases of SCN1A truncation-positive Dravet syndrome. PLoS ONE, 2017, 12, e0180485.	2.5	18
64	Isolation, contact and social behavior shaped genetic diversity in West Timor. Journal of Human Genetics, 2014, 59, 494-503.	2.3	17
65	A novel variant in TAF1 affects gene expression and is associated with X-linked TAF1 intellectual disability syndrome. Neuronal Signaling, 2018, 2, NS20180141.	3.2	16
66	Siberian genetic diversity reveals complex origins of the Samoyedicâ€speaking populations. American Journal of Human Biology, 2018, 30, e23194.	1.6	15
67	Modeling SNP array ascertainment with Approximate Bayesian Computation for demographic inference. Scientific Reports, 2018, 8, 10209.	3.3	12
68	Substructured Population Growth in the Ashkenazi Jews Inferred with Approximate Bayesian Computation. Molecular Biology and Evolution, 2019, 36, 1162-1171.	8.9	11
69	Variable patterns of mutation density among NaV1.1, NaV1.2 and NaV1.6 point to channel-specific functional differences associated with childhood epilepsy. PLoS ONE, 2020, 15, e0238121.	2.5	11
70	Influence of age at seizure onset on the acquisition of neurodevelopmental skills in an SCN8A cohort. Epilepsia, 2019, 60, 1711-1720.	5.1	10
71	Altered expression of signaling pathways regulating neuronal excitability in hippocampal tissue of temporal lobe epilepsy patients with low and high seizure frequency. Epilepsy Research, 2019, 155, 106145.	1.6	7
72	The Role of Phylogenetically Conserved Elements in Shaping Patterns of Human Genomic Diversity. Molecular Biology and Evolution, 2018, 35, 2284-2295.	8.9	5

#	Article	IF	Citations
73	Leukocyte expression profiles reveal gene sets with prognostic value for seizure-free outcome following stereotactic laser amygdalohippocampotomy. Scientific Reports, 2019, 9, 1086.	3.3	4
74	Clinical characteristics and treatment experience of individuals with SCN8A developmental and epileptic encephalopathy (SCN8A-DEE): Findings from an online caregiver survey. Seizure: the Journal of the British Epilepsy Association, 2022, 97, 50-57.	2.0	3
75	Reply to â€˜The â€˜extremely ancientâ€™ chromosome that isnâ€™tâ€™ by Elhaik et al. European Journal of Human Genetics, 2015, 23, 564-567.	2.8	2
76	Whole exome sequencing and coâ€expression analysis identify an SCN1A variant that modifies pathogenicity in a family with genetic epilepsy and febrile seizures plus. Epilepsia, 2022, 63, 1970-1980.	5.1	2
77	Title is missing!. , 2020, 15, e0238121.		0
78	Title is missing!. , 2020, 15, e0238121.		0
79	Title is missing!. , 2020, 15, e0238121.		0
80	Title is missing!. , 2020, 15, e0238121.		0