Patrick May

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

141 papers	5,229 citations	39 h-index	69 g-index
175 ext. papers	7,195 ext. citations	9.6 avg, IF	5.29 L-index

#	Paper	IF	Citations
141	Dairy Intake and Parkinson's Disease: A Mendelian Randomization Study.. *Movement Disorders*, **2022**,	7	2
140	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows.. *Nature Communications*, **2021**, 12, 7305	17.4	8
139	Breast and prostate cancer risk: The interplay of polygenic risk, rare pathogenic germline variants, and family history.. *Genetics in Medicine*, **2021**,	8.1	4
138	Single-cell sequencing of human midbrain reveals glial activation and a Parkinson-specific neuronal state.. *Brain*, **2021**,	11.2	13
137	Mendelian Randomisation Study of Smoking, Alcohol, and Coffee Drinking in Relation to Parkinson's Disease. *Journal of Parkinson's Disease*, **2021**,	5.3	3
136	Genome Sequencing of SARS-CoV-2 Allows Monitoring of Variants of Concern through Wastewater. *Water (Switzerland)*, **2021**, 13, 3018	3	3
135	Persistence of birth mode-dependent effects on gut microbiome composition, immune system stimulation and antimicrobial resistance during the first year of life. *ISME Communications*, **2021**, 1,		7
134	Replication of a Novel Parkinson's Locus in a European Ancestry Population. *Movement Disorders*, **2021**, 36, 1689-1695	7	0
133	Burden of rare variants in synaptic genes in patients with severe tinnitus: An exome based extreme phenotype study. *EBioMedicine*, **2021**, 66, 103309	8.8	10
132	Unification of functional annotation descriptions using text mining. *Biological Chemistry*, **2021**, 402, 983-990	4.3	0
131	Evaluation of the Molecular Pathogenesis of Adrenocortical Tumors by Whole-Genome Sequencing. *Journal of the Endocrine Society*, **2021**, 5, A68-A68	0.4	78
130	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. *Epilepsia*, **2021**, 62, 1518-1527	6.4	1
129	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. *American Journal of Human Genetics*, **2021**, 108, 965-982	11	6
128	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. *Frontiers in Genetics*, **2021**, 12, 666244	4.5	1
127	Mantis: flexible and consensus-driven genome annotation. *GigaScience*, **2021**, 10,	7.6	7
126	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. *Nature Microbiology*, **2021**, 6, 123-135	26.6	16
125	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. *Frontiers in Microbiology*, **2021**, 12, 635781	5.7	18

124	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. *Microbiome*, **2021**, 9, 49	16.6	11
123	Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. *Nature Genetics*, **2021**, 53, 294-303	36.3	31
122	Machine learning-based identification and characterization of 15 novel pathogenic SUOX missense mutations. *Molecular Genetics and Metabolism*, **2021**, 134, 188-194	3.7	3
121	Genotype-phenotype correlations in SCN8A-related disorders reveal prognostic and therapeutic implications. *Brain*, **2021**,	11.2	8
120	Distinct gene-set burden patterns underlie common generalized and focal epilepsies. *EBioMedicine*, **2021**, 72, 103588	8.8	0
119	Systematic characterization of human gut microbiome-secreted molecules by integrated multi-omics.. *ISME Communications*, **2021**, 1, 82		0
118	MISCAST: MIssense variant to protein StruCture Analysis web SuiTe. *Nucleic Acids Research*, **2020**, 48, W132-W139	20.1	4
117	Enrichment of damaging missense variants in genes related with axonal guidance signalling in sporadic Meniere's disease. *Journal of Medical Genetics*, **2020**, 57, 82-88	5.8	11
116	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. *BMC Biology*, **2020**, 18, 62	7.3	50
115	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17 458 subjects. *Brain*, **2020**, 143, 2106-2118	11.2	14
114	Genetic Architecture of Parkinson's Disease in the Indian Population: Harnessing Genetic Diversity to Address Critical Gaps in Parkinson's Disease Research. *Frontiers in Neurology*, **2020**, 11, 524	4.1	7
113	Gene family information facilitates variant interpretation and identification of disease-associated genes in neurodevelopmental disorders. *Genome Medicine*, **2020**, 12, 28	14.4	13
112	Missing heritability in Parkinson's disease: the emerging role of non-coding genetic variation. *Journal of Neural Transmission*, **2020**, 127, 729-748	4.3	11
111	Excess of singleton loss-of-function variants in Parkinson's disease contributes to genetic risk. *Journal of Medical Genetics*, **2020**, 57, 617-623	5.8	4
110	Bi-allelic GAD1 variants cause a neonatal onset syndromic developmental and epileptic encephalopathy. *Brain*, **2020**, 143, 1447-1461	11.2	12
109	Genome-wide linkage analysis of families with primary hyperhidrosis. *PLoS ONE*, **2020**, 15, e0244565	3.7	2
108	Identification of pathogenic variant enriched regions across genes and gene families. *Genome Research*, **2020**, 30, 62-71	9.7	14
107	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. *Nature Communications*, **2020**, 11, 5281	17.4	19

106	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. *Acta Neuropathologica*, **2020**, 140, 919-949	14.3	24
105	Semantic Similarity Analysis Reveals Robust Gene-Disease Relationships in Developmental and Epileptic Encephalopathies. *American Journal of Human Genetics*, **2020**, 107, 683-697	11	8
104	Predicting functional effects of missense variants in voltage-gated sodium and calcium channels. *Science Translational Medicine*, **2020**, 12,	17.5	27
103	Comprehensive characterization of amino acid positions in protein structures reveals molecular effect of missense variants. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 28201-28211	11.5	22
102	Non-Coding RNAs in the Brain-Heart Axis: The Case of Parkinson's Disease. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	12
101	A patient-based model of RNA mis-splicing uncovers treatment targets in Parkinson's disease. *Science Translational Medicine*, **2020**, 12,	17.5	10
100	A rare loss-of-function variant of ADAM17 is associated with late-onset familial Alzheimer disease. *Molecular Psychiatry*, **2020**, 25, 629-639	15.1	27
99	BSA4Yeast: Web-based quantitative trait locus linkage analysis and bulk segregant analysis of yeast sequencing data. *GigaScience*, **2019**, 8,	7.6	2
98	Simple ClinVar: an interactive web server to explore and retrieve gene and disease variants aggregated in ClinVar database. *Nucleic Acids Research*, **2019**, 47, W99-W105	20.1	21
97	A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. *American Journal of Human Genetics*, **2019**, 104, 1060-1072	11	39
96	Intestinal-Cell Kinase and Juvenile Myoclonic Epilepsy. *New England Journal of Medicine*, **2019**, 380, e24	59.2	4
95	Variant Score Ranker-a web application for intuitive missense variant prioritization. *Bioinformatics*, **2019**, 35, 4478-4479	7.2	5
94	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. *Cancer Research*, **2019**, 79, 2466-2479	10.1	14
93	Clinical spectrum of -related epileptic disorders. *Neurology*, **2019**, 92, e1238-e1249	6.5	25
92	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	11	104
91	Mutations in Disrupt Endoplasmic Reticulum-Mitochondria Contact Sites Interfering with Calcium Homeostasis and Mitochondrial Dynamics in Parkinson's Disease. *Antioxidants and Redox Signaling*, **2019**, 31, 1213-1234	8.4	33
90	Assessment of genetic variant burden in epilepsy-associated brain lesions. *European Journal of Human Genetics*, **2019**, 27, 1738-1744	5.3	4
89	Polygenic burden in focal and generalized epilepsies. *Brain*, **2019**, 142, 3473-3481	11.2	38

88	Biallelic VARS variants cause developmental encephalopathy with microcephaly that is recapitulated in vars knockout zebrafish. *Nature Communications*, **2019**, 10, 708	17.4	27
87	Spectrum of GABAA receptor variants in epilepsy. *Current Opinion in Neurology*, **2019**, 32, 183-190	7.1	24
86	Understanding the role of genetic variability in LRRK2 in Indian population. *Movement Disorders*, **2019**, 34, 496-505	7	6
85	Extraction and Analysis of RNA Isolated from Pure Bacteria-Derived Outer Membrane Vesicles. *Methods in Molecular Biology*, **2018**, 1737, 213-230	1.4	10
84	Reply: No evidence for rare TRAP1 mutations influencing the risk of idiopathic Parkinson's disease. *Brain*, **2018**, 141, e17	11.2	2
83	Exome-wide analysis of mutational burden in patients with typical and atypical Rolandic epilepsy. *European Journal of Human Genetics*, **2018**, 26, 258-264	5.3	12
82	Insufficient evidence for pathogenicity of SNCA His50Gln (H50Q) in Parkinson's disease. *Neurobiology of Aging*, **2018**, 64, 159.e5-159.e8	5.6	23
81	Rare variants in 2 German families with Alzheimer disease. *Neurology: Genetics*, **2018**, 4, e224	3.8	9
80	Small RNA profiling of low biomass samples: identification and removal of contaminants. *BMC Biology*, **2018**, 16, 52	7.3	38
79	Frequency of Loss of Function Variants in LRRK2 in Parkinson Disease. *JAMA Neurology*, **2018**, 75, 1416-1422	14.2	50
78	Rare coding variants in genes encoding GABA receptors in genetic generalised epilepsies: an exome-based case-control study. *Lancet Neurology, The*, **2018**, 17, 699-708	24.1	44
77	Natural variation of chronological aging in the species reveals diet-dependent mechanisms of life span control. *Npj Aging and Mechanisms of Disease*, **2018**, 4, 3	5.5	16
76	The RNA Complement of Outer Membrane Vesicles From Serovar Typhimurium Under Distinct Culture Conditions. *Frontiers in Microbiology*, **2018**, 9, 2015	5.7	31
75	Major changes of cell function and toxicant sensitivity in cultured cells undergoing mild, quasi-natural genetic drift. *Archives of Toxicology*, **2018**, 92, 3487-3503	5.8	12
74	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. *Nature Communications*, **2018**, 9, 5091	17.4	112
73	Guideline-based and bioinformatic reassessment of lesion-associated gene and variant pathogenicity in focal human epilepsies. *Epilepsia*, **2018**, 59, 2145-2152	6.4	6
72	Rare gene deletions in genetic generalized and Rolandic epilepsies. *PLoS ONE*, **2018**, 13, e0202022	3.7	3
71	De novo variants in neurodevelopmental disorders with epilepsy. *Nature Genetics*, **2018**, 50, 1048-1053	36.3	139

70	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. *Neurobiology of Aging*, **2017**, 57, 247.e9-247.e13	5.6	54
69	Recessive mutations in SLC35A3 cause early onset epileptic encephalopathy with skeletal defects. *American Journal of Medical Genetics, Part A*, **2017**, 173, 1119-1123	2.5	10
68	Biallelic Variants in OTUD6B Cause an Intellectual Disability Syndrome Associated with Seizures and Dysmorphic Features. *American Journal of Human Genetics*, **2017**, 100, 676-688	11	36
67	Metformin reverses TRAP1 mutation-associated alterations in mitochondrial function in Parkinson's disease. *Brain*, **2017**, 140, 2444-2459	11.2	59
66	Variant-DB: A Tool for Efficiently Exploring Millions of Human Genetic Variants and Their Annotations. *Lecture Notes in Computer Science*, **2017**, 22-28	0.9	1
65	[P2108]: IDENTIFICATION OF A RARE GENE VARIANT THAT IS ASSOCIATED WITH FAMILIAL ALZHEIMER DISEASE AND REGULATES APP EXPRESSION **2017**, 13, P648-P648		
64	Confronting the catalytic dark matter encoded by sequenced genomes. *Nucleic Acids Research*, **2017**, 45, 11495-11514	20.1	38
63	Rare GABRA3 variants are associated with epileptic seizures, encephalopathy and dysmorphic features. *Brain*, **2017**, 140, 2879-2894	11.2	24
62	The new protein topology graph library web server. *Bioinformatics*, **2016**, 32, 474-6	7.2	4
61	Targeted sequencing of 351 candidate genes for epileptic encephalopathy in a large cohort of patients. *Molecular Genetics & Genomic Medicine*, **2016**, 4, 568-80	2.3	60
60	Loss of SYNJ1 dual phosphatase activity leads to early onset refractory seizures and progressive neurological decline. *Brain*, **2016**, 139, 2420-30	11.2	49
59	Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. *Nature Microbiology*, **2016**, 2, 16180	26.6	166
58	Evaluation of Presumably Disease Causing SCN1A Variants in a Cohort of Common Epilepsy Syndromes. *PLoS ONE*, **2016**, 11, e0150426	3.7	10
57	Identification, Recovery, and Refinement of Hitherto Undescribed Population-Level Genomes from the Human Gastrointestinal Tract. *Frontiers in Microbiology*, **2016**, 7, 884	5.7	8
56	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. *Genome Biology*, **2016**, 17, 260	18.3	81
55	CHD2 variants are a risk factor for photosensitivity in epilepsy. *Brain*, **2015**, 138, 1198-207	11.2	81
54	De novo loss- or gain-of-function mutations in KCNA2 cause epileptic encephalopathy. *Nature Genetics*, **2015**, 47, 393-399	36.3	162
53	Recessive loss-of-function mutations in AP4S1 cause mild fever-sensitive seizures, developmental delay and spastic paraplegia through loss of AP-4 complex assembly. *Human Molecular Genetics*, **2015**, 24, 2218-27	5.6	37

52	Recessive mutations in SLC13A5 result in a loss of citrate transport and cause neonatal epilepsy, developmental delay and teeth hypoplasia. *Brain*, **2015**, 138, 3238-50	11.2	57
51	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. *Npj Biofilms and Microbiomes*, **2015**, 1, 15007	8.2	59
50	Proteomic Analysis of Dhh1 Complexes Reveals a Role for Hsp40 Chaperone Ydj1 in Yeast P-Body Assembly. *G3: Genes, Genomes, Genetics*, **2015**, 5, 2497-511	3.2	11
49	A novel Fanconi anaemia subtype associated with a dominant-negative mutation in RAD51. *Nature Communications*, **2015**, 6, 8829	17.4	93
48	Molecular and clinical evidence for an ARMC5 tumor syndrome: concurrent inactivating germline and somatic mutations are associated with both primary macronodular adrenal hyperplasia and meningioma. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E119-28	5.6	61
47	Evaluation of Cell Line Suitability for Disease Specific Perturbation Experiments. *Studies in Classification, Data Analysis, and Knowledge Organization*, **2015**, 297-307	0.2	
46	Mapping the Gene Expression Diversity Across Hematological and Lymphoid Malignancies. *Blood*, **2015**, 126, 4805-4805	2.2	
45	Mercator: a fast and simple web server for genome scale functional annotation of plant sequence data. *Plant, Cell and Environment*, **2014**, 37, 1250-8	8.4	373
44	Mutations in STX1B, encoding a presynaptic protein, cause fever-associated epilepsy syndromes. *Nature Genetics*, **2014**, 46, 1327-32	36.3	138
43	De novo mutations in synaptic transmission genes including DNM1 cause epileptic encephalopathies. *American Journal of Human Genetics*, **2014**, 95, 360-70	11	299
42	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. *BMC Genomics*, **2014**, 15, 1154	4.5	87
41	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. *Nature Communications*, **2014**, 5, 5603	17.4	56
40	Condensing the omics fog of microbial communities. *Trends in Microbiology*, **2013**, 21, 325-33	12.4	62
39	The effects of carbon dioxide and temperature on microRNA expression in Arabidopsis development. *Nature Communications*, **2013**, 4, 2145	17.4	92
38	POMO--Plotting Omics analysis results for Multiple Organisms. *BMC Genomics*, **2013**, 14, 918	4.5	3
37	Hierarchical representation of supersecondary structures using a graph-theoretical approach. *Methods in Molecular Biology*, **2013**, 932, 7-33	1.4	
36	New insights into Chlamydomonas reinhardtii hydrogen production processes by combined microarray/RNA-seq transcriptomics. *Plant Biotechnology Journal*, **2013**, 11, 717-33	11.6	42
35	High-throughput tetrad analysis. *Nature Methods*, **2013**, 10, 671-5	21.6	13

34	Genomic sequence diversity and population structure of Saccharomyces cerevisiae assessed by RAD-seq. *G3: Genes, Genomes, Genetics*, **2013**, 3, 2163-71	3.2	96
33	A protein prioritization approach tailored for the FA/BRCA pathway. *PLoS ONE*, **2013**, 8, e62017	3.7	8
32	Give It AGO: The Search for miRNA-Argonaute Sorting Signals in Arabidopsis thaliana Indicates a Relevance of Sequence Positions Other than the 5SPosition Alone. *Frontiers in Plant Science*, **2012**, 3, 272	6.2	20
31	Comparative analysis of miRNAs and their targets across four plant species. *BMC Research Notes*, **2011**, 4, 483	2.3	18
30	Distribution pattern of small RNA and degradome reads provides information on miRNA gene structure and regulation. *Plant Signaling and Behavior*, **2011**, 6, 1609-11	2.5	30
29	Stars and symbiosis: microRNA- and microRNA*-mediated transcript cleavage involved in arbuscular mycorrhizal symbiosis. *Plant Physiology*, **2011**, 156, 1990-2010	6.6	164
28	Integration of proteomic and metabolomic profiling as well as metabolic modeling for the functional analysis of metabolic networks. *Methods in Molecular Biology*, **2011**, 694, 341-63	1.4	8
27	Modeling RNA loops using sequence homology and geometric constraints. *Bioinformatics*, **2010**, 26, 1671-2	7.2	4
26	Sequence-structure relationships in RNA loops: establishing the basis for loop homology modeling. *Nucleic Acids Research*, **2010**, 38, 970-80	20.1	30
25	PTGL: a database for secondary structure-based protein topologies. *Nucleic Acids Research*, **2010**, 38, D326-30	20.1	10
24	Targeted proteomics for Chlamydomonas reinhardtii combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. *Molecular BioSystems*, **2010**, 6, 1018-31		81
23	Expression pattern suggests a role of MiR399 in the regulation of the cellular response to local Pi increase during arbuscular mycorrhizal symbiosis. *Molecular Plant-Microbe Interactions*, **2010**, 23, 915-26	3.6	121
22	Algebraic connectivity may explain the evolution of gene regulatory networks. *Journal of Theoretical Biology*, **2010**, 267, 7-14	2.3	3
21	Identification and classification of ncRNA molecules using graph properties. *Nucleic Acids Research*, **2009**, 37, e66	20.1	29
20	JAIL: a structure-based interface library for macromolecules. *Nucleic Acids Research*, **2009**, 37, D338-41	20.1	7
19	Identification of nutrient-responsive Arabidopsis and rapeseed microRNAs by comprehensive real-time polymerase chain reaction profiling and small RNA sequencing. *Plant Physiology*, **2009**, 150, 1541-55	6.6	352
18	ChlamyCyc: an integrative systems biology database and web-portal for Chlamydomonas reinhardtii. *BMC Genomics*, **2009**, 10, 209	4.5	72
17	An integrative approach towards completing genome-scale metabolic networks. *Molecular BioSystems*, **2009**, 5, 1889-903		56

16	Metabolomics- and proteomics-assisted genome annotation and analysis of the draft metabolic network of Chlamydomonas reinhardtii. *Genetics*, **2008**, 179, 157-66	4	128
15	Metabolic networks are NP-hard to reconstruct. *Journal of Theoretical Biology*, **2008**, 254, 807-16	2.3	17
14	Docking without docking: ISEARCH--prediction of interactions using known interfaces. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 839-44	4.2	42
13	Accelerated microRNA-Precursor Detection Using the Smith-Waterman Algorithm on FPGAs **2007**, 19-32		1
12	Connectivity independent protein-structure alignment: a hierarchical approach. *BMC Bioinformatics*, **2006**, 7, 510	3.6	42
11	ZIB Structure Prediction Pipeline: Composing a Complex Biological Workflow Through Web Services. *Lecture Notes in Computer Science*, **2006**, 1148-1158	0.9	121
10	PTGL--a web-based database application for protein topologies. *Bioinformatics*, **2004**, 20, 3277-9	7.2	13
9	De novo Variants in Neurodevelopmental Disorders with Epilepsy		3
8	Gene family information facilitates variant interpretation and identification of disease-associated genes		6
7	Mantis: flexible and consensus-driven genome annotation		4
6	Isolation of nucleic acids from low biomass samples: detection and removal of sRNA contaminants		1
5	Predicting Functional Effects of Missense Variants in Voltage-Gated Sodium and Calcium Channels		1
4	Burden analysis of missense variants in 1,330 disease-associated genes on 3D provides insights into the mutation effects		2
3	Genotype-phenotype correlations in SCN8A-related disorders reveal prognostic and therapeutic implications		2
2	Critical Assessment of Metaproteome Investigation (CAMPI): A Multi-Lab Comparison of Established Workflows		8
1	binny: an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets		1