

Patrick May

List of Publications by Citations

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Version: 2024-04-25

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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	Mercator: a fast and simple web server for genome scale functional annotation of plant sequence data. <i>Plant, Cell and Environment</i> , 2014 , 37, 1250-8	8.4	373
140	Identification of nutrient-responsive Arabidopsis and rapeseed microRNAs by comprehensive real-time polymerase chain reaction profiling and small RNA sequencing. <i>Plant Physiology</i> , 2009 , 150, 1541-55	6.6	352
139	De novo mutations in synaptic transmission genes including DNM1 cause epileptic encephalopathies. <i>American Journal of Human Genetics</i> , 2014 , 95, 360-70	11	299
138	Integrated multi-omics of the human gut microbiome in a case study of familial type 1 diabetes. <i>Nature Microbiology</i> , 2016 , 2, 16180	26.6	166
137	Stars and symbiosis: microRNA- and microRNA*-mediated transcript cleavage involved in arbuscular mycorrhizal symbiosis. <i>Plant Physiology</i> , 2011 , 156, 1990-2010	6.6	164
136	De novo loss- or gain-of-function mutations in KCNA2 cause epileptic encephalopathy. <i>Nature Genetics</i> , 2015 , 47, 393-399	36.3	162
135	De novo variants in neurodevelopmental disorders with epilepsy. <i>Nature Genetics</i> , 2018 , 50, 1048-1053	36.3	139
134	Mutations in STX1B, encoding a presynaptic protein, cause fever-associated epilepsy syndromes. <i>Nature Genetics</i> , 2014 , 46, 1327-32	36.3	138
133	Metabolomics- and proteomics-assisted genome annotation and analysis of the draft metabolic network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008 , 179, 157-66	4	128
132	Expression pattern suggests a role of MiR399 in the regulation of the cellular response to local Pi increase during arbuscular mycorrhizal symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2010 , 23, 915-26	3.6	121
131	ZIB Structure Prediction Pipeline: Composing a Complex Biological Workflow Through Web Services. <i>Lecture Notes in Computer Science</i> , 2006 , 1148-1158	0.9	121
130	Birth mode is associated with earliest strain-conferred gut microbiome functions and immunostimulatory potential. <i>Nature Communications</i> , 2018 , 9, 5091	17.4	112
129	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. <i>American Journal of Human Genetics</i> , 2019 , 105, 267-282	11	104
128	Genomic sequence diversity and population structure of <i>Saccharomyces cerevisiae</i> assessed by RAD-seq. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 2163-71	3.2	96
127	A novel Fanconi anaemia subtype associated with a dominant-negative mutation in RAD51. <i>Nature Communications</i> , 2015 , 6, 8829	17.4	93
126	The effects of carbon dioxide and temperature on microRNA expression in Arabidopsis development. <i>Nature Communications</i> , 2013 , 4, 2145	17.4	92
125	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. <i>BMC Genomics</i> , 2014 , 15, 1154	4.5	87

124	CHD2 variants are a risk factor for photosensitivity in epilepsy. <i>Brain</i> , 2015 , 138, 1198-207	11.2	81
123	Targeted proteomics for <i>Chlamydomonas reinhardtii</i> combined with rapid subcellular protein fractionation, metabolomics and metabolic flux analyses. <i>Molecular BioSystems</i> , 2010 , 6, 1018-31		81
122	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <i>Genome Biology</i> , 2016 , 17, 260	18.3	81
121	Evaluation of the Molecular Pathogenesis of Adrenocortical Tumors by Whole-Genome Sequencing. <i>Journal of the Endocrine Society</i> , 2021 , 5, A68-A68	0.4	78
120	ChlamyCyc: an integrative systems biology database and web-portal for <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2009 , 10, 209	4.5	72
119	Condensing the omics fog of microbial communities. <i>Trends in Microbiology</i> , 2013 , 21, 325-33	12.4	62
118	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. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015 , 100, E119-28	5.6	61
117	Targeted sequencing of 351 candidate genes for epileptic encephalopathy in a large cohort of patients. <i>Molecular Genetics & Genomic Medicine</i> , 2016 , 4, 568-80	2.3	60
116	Metformin reverses TRAP1 mutation-associated alterations in mitochondrial function in Parkinson's disease. <i>Brain</i> , 2017 , 140, 2444-2459	11.2	59
115	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015 , 1, 15007	8.2	59
114	Recessive mutations in SLC13A5 result in a loss of citrate transport and cause neonatal epilepsy, developmental delay and teeth hypoplasia. <i>Brain</i> , 2015 , 138, 3238-50	11.2	57
113	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014 , 5, 5603	17.4	56
112	An integrative approach towards completing genome-scale metabolic networks. <i>Molecular BioSystems</i> , 2009 , 5, 1889-903		56
111	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. <i>Neurobiology of Aging</i> , 2017 , 57, 247.e9-247.e13	5.6	54
110	Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. <i>BMC Biology</i> , 2020 , 18, 62	7.3	50
109	Frequency of Loss of Function Variants in LRRK2 in Parkinson Disease. <i>JAMA Neurology</i> , 2018 , 75, 1416-1422	17.2	50
108	Loss of SYNJ1 dual phosphatase activity leads to early onset refractory seizures and progressive neurological decline. <i>Brain</i> , 2016 , 139, 2420-30	11.2	49
107	Rare coding variants in genes encoding GABA receptors in genetic generalised epilepsies: an exome-based case-control study. <i>Lancet Neurology</i> , 2018 , 17, 699-708	24.1	44

106	New insights into <i>Chlamydomonas reinhardtii</i> hydrogen production processes by combined microarray/RNA-seq transcriptomics. <i>Plant Biotechnology Journal</i> , 2013 , 11, 717-33	11.6	42
105	Docking without docking: ISEARCH--prediction of interactions using known interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 839-44	4.2	42
104	Connectivity independent protein-structure alignment: a hierarchical approach. <i>BMC Bioinformatics</i> , 2006 , 7, 510	3.6	42
103	A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. <i>American Journal of Human Genetics</i> , 2019 , 104, 1060-1072 ¹	11.2	39
102	Small RNA profiling of low biomass samples: identification and removal of contaminants. <i>BMC Biology</i> , 2018 , 16, 52	7.3	38
101	Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019 , 142, 3473-3481	11.2	38
100	Confronting the catalytic dark matter encoded by sequenced genomes. <i>Nucleic Acids Research</i> , 2017 , 45, 11495-11514	20.1	38
99	Recessive loss-of-function mutations in AP4S1 cause mild fever-sensitive seizures, developmental delay and spastic paraplegia through loss of AP-4 complex assembly. <i>Human Molecular Genetics</i> , 2015 , 24, 2218-27	5.6	37
98	Biallelic Variants in OTUD6B Cause an Intellectual Disability Syndrome Associated with Seizures and Dysmorphic Features. <i>American Journal of Human Genetics</i> , 2017 , 100, 676-688	11	36
97	Mutations in Disrupt Endoplasmic Reticulum-Mitochondria Contact Sites Interfering with Calcium Homeostasis and Mitochondrial Dynamics in Parkinson's Disease. <i>Antioxidants and Redox Signaling</i> , 2019 , 31, 1213-1234	8.4	33
96	The RNA Complement of Outer Membrane Vesicles From Serovar Typhimurium Under Distinct Culture Conditions. <i>Frontiers in Microbiology</i> , 2018 , 9, 2015	5.7	31
95	Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. <i>Nature Genetics</i> , 2021 , 53, 294-303	36.3	31
94	Sequence-structure relationships in RNA loops: establishing the basis for loop homology modeling. <i>Nucleic Acids Research</i> , 2010 , 38, 970-80	20.1	30
93	Distribution pattern of small RNA and degradome reads provides information on miRNA gene structure and regulation. <i>Plant Signaling and Behavior</i> , 2011 , 6, 1609-11	2.5	30
92	Identification and classification of ncRNA molecules using graph properties. <i>Nucleic Acids Research</i> , 2009 , 37, e66	20.1	29
91	Predicting functional effects of missense variants in voltage-gated sodium and calcium channels. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	27
90	Biallelic VARS variants cause developmental encephalopathy with microcephaly that is recapitulated in vars knockout zebrafish. <i>Nature Communications</i> , 2019 , 10, 708	17.4	27
89	A rare loss-of-function variant of ADAM17 is associated with late-onset familial Alzheimer disease. <i>Molecular Psychiatry</i> , 2020 , 25, 629-639	15.1	27

88	Clinical spectrum of -related epileptic disorders. <i>Neurology</i> , 2019 , 92, e1238-e1249	6.5	25
87	Rare GABRA3 variants are associated with epileptic seizures, encephalopathy and dysmorphic features. <i>Brain</i> , 2017 , 140, 2879-2894	11.2	24
86	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020 , 140, 919-949	14.3	24
85	Spectrum of GABAA receptor variants in epilepsy. <i>Current Opinion in Neurology</i> , 2019 , 32, 183-190	7.1	24
84	Insufficient evidence for pathogenicity of SNCA His50Gln (H50Q) in Parkinson's disease. <i>Neurobiology of Aging</i> , 2018 , 64, 159.e5-159.e8	5.6	23
83	Comprehensive characterization of amino acid positions in protein structures reveals molecular effect of missense variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28201-28211	11.5	22
82	Simple ClinVar: an interactive web server to explore and retrieve gene and disease variants aggregated in ClinVar database. <i>Nucleic Acids Research</i> , 2019 , 47, W99-W105	20.1	21
81	Give It AGO: The Search for miRNA-Argonaute Sorting Signals in Arabidopsis thaliana Indicates a Relevance of Sequence Positions Other than the 5S Position Alone. <i>Frontiers in Plant Science</i> , 2012 , 3, 272	6.2	20
80	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020 , 11, 5281	17.4	19
79	Comparative analysis of miRNAs and their targets across four plant species. <i>BMC Research Notes</i> , 2011 , 4, 483	2.3	18
78	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. <i>Frontiers in Microbiology</i> , 2021 , 12, 635781	5.7	18
77	Metabolic networks are NP-hard to reconstruct. <i>Journal of Theoretical Biology</i> , 2008 , 254, 807-16	2.3	17
76	Natural variation of chronological aging in the species reveals diet-dependent mechanisms of life span control. <i>Npj Aging and Mechanisms of Disease</i> , 2018 , 4, 3	5.5	16
75	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021 , 6, 123-135	26.6	16
74	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. <i>Cancer Research</i> , 2019 , 79, 2466-2479	10.1	14
73	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17 458 subjects. <i>Brain</i> , 2020 , 143, 2106-2118	11.2	14
72	Identification of pathogenic variant enriched regions across genes and gene families. <i>Genome Research</i> , 2020 , 30, 62-71	9.7	14
71	Gene family information facilitates variant interpretation and identification of disease-associated genes in neurodevelopmental disorders. <i>Genome Medicine</i> , 2020 , 12, 28	14.4	13

70	High-throughput tetrad analysis. <i>Nature Methods</i> , 2013 , 10, 671-5	21.6	13
69	PTGL--a web-based database application for protein topologies. <i>Bioinformatics</i> , 2004 , 20, 3277-9	7.2	13
68	Single-cell sequencing of human midbrain reveals glial activation and a Parkinson-specific neuronal state.. <i>Brain</i> , 2021 ,	11.2	13
67	Bi-allelic GAD1 variants cause a neonatal onset syndromic developmental and epileptic encephalopathy. <i>Brain</i> , 2020 , 143, 1447-1461	11.2	12
66	Exome-wide analysis of mutational burden in patients with typical and atypical Rolandic epilepsy. <i>European Journal of Human Genetics</i> , 2018 , 26, 258-264	5.3	12
65	Non-Coding RNAs in the Brain-Heart Axis: The Case of Parkinson's Disease. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	12
64	Major changes of cell function and toxicant sensitivity in cultured cells undergoing mild, quasi-natural genetic drift. <i>Archives of Toxicology</i> , 2018 , 92, 3487-3503	5.8	12
63	Enrichment of damaging missense variants in genes related with axonal guidance signalling in sporadic Meniere's disease. <i>Journal of Medical Genetics</i> , 2020 , 57, 82-88	5.8	11
62	Missing heritability in Parkinson's disease: the emerging role of non-coding genetic variation. <i>Journal of Neural Transmission</i> , 2020 , 127, 729-748	4.3	11
61	Proteomic Analysis of Dhh1 Complexes Reveals a Role for Hsp40 Chaperone Ydj1 in Yeast P-Body Assembly. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 2497-511	3.2	11
60	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. <i>Microbiome</i> , 2021 , 9, 49	16.6	11
59	Recessive mutations in SLC35A3 cause early onset epileptic encephalopathy with skeletal defects. <i>American Journal of Medical Genetics, Part A</i> , 2017 , 173, 1119-1123	2.5	10
58	Extraction and Analysis of RNA Isolated from Pure Bacteria-Derived Outer Membrane Vesicles. <i>Methods in Molecular Biology</i> , 2018 , 1737, 213-230	1.4	10
57	PTGL: a database for secondary structure-based protein topologies. <i>Nucleic Acids Research</i> , 2010 , 38, D326-30	20.1	10
56	Evaluation of Presumably Disease Causing SCN1A Variants in a Cohort of Common Epilepsy Syndromes. <i>PLoS ONE</i> , 2016 , 11, e0150426	3.7	10
55	A patient-based model of RNA mis-splicing uncovers treatment targets in Parkinson's disease. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	10
54	Burden of rare variants in synaptic genes in patients with severe tinnitus: An exome based extreme phenotype study. <i>EBioMedicine</i> , 2021 , 66, 103309	8.8	10
53	Rare variants in 2 German families with Alzheimer disease. <i>Neurology: Genetics</i> , 2018 , 4, e224	3.8	9

52	A protein prioritization approach tailored for the FA/BRCA pathway. <i>PLoS ONE</i> , 2013 , 8, e62017	3.7	8
51	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows.. <i>Nature Communications</i> , 2021 , 12, 7305	17.4	8
50	Integration of proteomic and metabolomic profiling as well as metabolic modeling for the functional analysis of metabolic networks. <i>Methods in Molecular Biology</i> , 2011 , 694, 341-63	1.4	8
49	Semantic Similarity Analysis Reveals Robust Gene-Disease Relationships in Developmental and Epileptic Encephalopathies. <i>American Journal of Human Genetics</i> , 2020 , 107, 683-697	11	8
48	Critical Assessment of Metaproteome Investigation (CAMPI): A Multi-Lab Comparison of Established Workflows		8
47	Identification, Recovery, and Refinement of Hitherto Undescribed Population-Level Genomes from the Human Gastrointestinal Tract. <i>Frontiers in Microbiology</i> , 2016 , 7, 884	5.7	8
46	Genotype-phenotype correlations in SCN8A-related disorders reveal prognostic and therapeutic implications. <i>Brain</i> , 2021 ,	11.2	8
45	Genetic Architecture of Parkinson's Disease in the Indian Population: Harnessing Genetic Diversity to Address Critical Gaps in Parkinson's Disease Research. <i>Frontiers in Neurology</i> , 2020 , 11, 524	4.1	7
44	JAIL: a structure-based interface library for macromolecules. <i>Nucleic Acids Research</i> , 2009 , 37, D338-41	20.1	7
43	Persistence of birth mode-dependent effects on gut microbiome composition, immune system stimulation and antimicrobial resistance during the first year of life. <i>ISME Communications</i> , 2021 , 1,		7
42	Mantis: flexible and consensus-driven genome annotation. <i>GigaScience</i> , 2021 , 10,	7.6	7
41	Gene family information facilitates variant interpretation and identification of disease-associated genes		6
40	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 965-982	11	6
39	Understanding the role of genetic variability in LRRK2 in Indian population. <i>Movement Disorders</i> , 2019 , 34, 496-505	7	6
38	Guideline-based and bioinformatic reassessment of lesion-associated gene and variant pathogenicity in focal human epilepsies. <i>Epilepsia</i> , 2018 , 59, 2145-2152	6.4	6
37	Variant Score Ranker-a web application for intuitive missense variant prioritization. <i>Bioinformatics</i> , 2019 , 35, 4478-4479	7.2	5
36	The new protein topology graph library web server. <i>Bioinformatics</i> , 2016 , 32, 474-6	7.2	4
35	Intestinal-Cell Kinase and Juvenile Myoclonic Epilepsy. <i>New England Journal of Medicine</i> , 2019 , 380, e24	59.2	4

34	MISCAST: Missense variant to protein StruCTure Analysis web SuiTe. <i>Nucleic Acids Research</i> , 2020 , 48, W132-W139	20.1	4
33	Excess of singleton loss-of-function variants in Parkinson's disease contributes to genetic risk. <i>Journal of Medical Genetics</i> , 2020 , 57, 617-623	5.8	4
32	Assessment of genetic variant burden in epilepsy-associated brain lesions. <i>European Journal of Human Genetics</i> , 2019 , 27, 1738-1744	5.3	4
31	Modeling RNA loops using sequence homology and geometric constraints. <i>Bioinformatics</i> , 2010 , 26, 1671-2	4.2	4
30	Breast and prostate cancer risk: The interplay of polygenic risk, rare pathogenic germline variants, and family history.. <i>Genetics in Medicine</i> , 2021 ,	8.1	4
29	Mantis: flexible and consensus-driven genome annotation		4
28	POMO--Plotting Omics analysis results for Multiple Organisms. <i>BMC Genomics</i> , 2013 , 14, 918	4.5	3
27	Algebraic connectivity may explain the evolution of gene regulatory networks. <i>Journal of Theoretical Biology</i> , 2010 , 267, 7-14	2.3	3
26	Mendelian Randomisation Study of Smoking, Alcohol, and Coffee Drinking in Relation to Parkinson's Disease. <i>Journal of Parkinson's Disease</i> , 2021 ,	5.3	3
25	Genome Sequencing of SARS-CoV-2 Allows Monitoring of Variants of Concern through Wastewater. <i>Water (Switzerland)</i> , 2021 , 13, 3018	3	3
24	De novo Variants in Neurodevelopmental Disorders with Epilepsy		3
23	Rare gene deletions in genetic generalized and Rolandic epilepsies. <i>PLoS ONE</i> , 2018 , 13, e0202022	3.7	3
22	Machine learning-based identification and characterization of 15 novel pathogenic SUOX missense mutations. <i>Molecular Genetics and Metabolism</i> , 2021 , 134, 188-194	3.7	3
21	BSA4Yeast: Web-based quantitative trait locus linkage analysis and bulk segregant analysis of yeast sequencing data. <i>GigaScience</i> , 2019 , 8,	7.6	2
20	Reply: No evidence for rare TRAP1 mutations influencing the risk of idiopathic Parkinson's disease. <i>Brain</i> , 2018 , 141, e17	11.2	2
19	Dairy Intake and Parkinson's Disease: A Mendelian Randomization Study.. <i>Movement Disorders</i> , 2022 ,	7	2
18	Genome-wide linkage analysis of families with primary hyperhidrosis. <i>PLoS ONE</i> , 2020 , 15, e0244565	3.7	2
17	Burden analysis of missense variants in 1,330 disease-associated genes on 3D provides insights into the mutation effects		2

16	Genotype-phenotype correlations in SCN8A-related disorders reveal prognostic and therapeutic implications	2	
15	Variant-DB: A Tool for Efficiently Exploring Millions of Human Genetic Variants and Their Annotations. <i>Lecture Notes in Computer Science</i> , 2017 , 22-28	0.9	1
14	Accelerated microRNA-Precursor Detection Using the Smith-Waterman Algorithm on FPGAs 2007 , 19-32		1
13	Isolation of nucleic acids from low biomass samples: detection and removal of sRNA contaminants		1
12	Predicting Functional Effects of Missense Variants in Voltage-Gated Sodium and Calcium Channels		1
11	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. <i>Epilepsia</i> , 2021 , 62, 1518-1527	6.4	1
10	Challenges, Strategies, and Perspectives for Reference-Independent Longitudinal Multi-Omic Microbiome Studies. <i>Frontiers in Genetics</i> , 2021 , 12, 666244	4.5	1
9	binny: an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets		1
8	Replication of a Novel Parkinson's Locus in a European Ancestry Population. <i>Movement Disorders</i> , 2021 , 36, 1689-1695	7	0
7	Unification of functional annotation descriptions using text mining. <i>Biological Chemistry</i> , 2021 , 402, 983-990	4.5	0
6	Distinct gene-set burden patterns underlie common generalized and focal epilepsies. <i>EBioMedicine</i> , 2021 , 72, 103588	8.8	0
5	Systematic characterization of human gut microbiome-secreted molecules by integrated multi-omics. <i>ISME Communications</i> , 2021 , 1, 82		0
4	[P21108]: IDENTIFICATION OF A RARE GENE VARIANT THAT IS ASSOCIATED WITH FAMILIAL ALZHEIMER DISEASE AND REGULATES APP EXPRESSION 2017 , 13, P648-P648		
3	Hierarchical representation of supersecondary structures using a graph-theoretical approach. <i>Methods in Molecular Biology</i> , 2013 , 932, 7-33	1.4	
2	Evaluation of Cell Line Suitability for Disease Specific Perturbation Experiments. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2015 , 297-307	0.2	
1	Mapping the Gene Expression Diversity Across Hematological and Lymphoid Malignancies. <i>Blood</i> , 2015 , 126, 4805-4805	2.2	