

Yan W Asmann

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.

96
papers

2,592
citations

28
h-index

49
g-index

103
ext. papers

3,553
ext. citations

7.6
avg, IF

4.37
L-index

#	Paper	IF	Citations
96	Epidemiologic and Clinical Analysis of Tumor Mutational Burden (TMB) in Acute Myeloid Leukemia (AML): Exome Sequencing Study of the Mayo Clinic AML Epidemiology Cohort (MCAEC). <i>Blood</i> , 2021 , 138, 3437-3437	2.2	
95	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. <i>Blood</i> , 2021 , 138, 4101-4101	2.2	
94	Single Cell Transcriptome Profile of Myeloma and Immune Cell Characteristics in Patients with Durable Response Post CART. <i>Blood</i> , 2021 , 138, 3838-3838	2.2	1
93	Inflation of tumor mutation burden by tumor-only sequencing in under-represented groups. <i>Npj Precision Oncology</i> , 2021 , 5, 22	9.8	2
92	Loss of Tmem106b leads to cerebellum Purkinje cell death and motor deficits. <i>Brain Pathology</i> , 2021 , 31, e12945	6	2
91	Human Cerebrospinal Fluid Modulates Pathways Promoting Glioblastoma Malignancy. <i>Frontiers in Oncology</i> , 2021 , 11, 624145	5.3	4
90	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. <i>PLoS ONE</i> , 2021 , 16, e0249305	3.7	0
89	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimer's disease. <i>Nature Communications</i> , 2021 , 12, 2311	17.4	10
88	ABCA7 Regulates Brain Fatty Acid Metabolism During LPS-Induced Acute Inflammation. <i>Frontiers in Neuroscience</i> , 2021 , 15, 647974	5.1	3
87	Targeting of inflammatory pathways with R2CHOP in high-risk DLBCL. <i>Leukemia</i> , 2021 , 35, 522-533	10.7	9
86	Alpha 1-antichymotrypsin contributes to stem cell characteristics and enhances tumorigenicity of glioblastoma. <i>Neuro-Oncology</i> , 2021 , 23, 599-610	1	8
85	Vascular ApoE4 Impairs Behavior by Modulating Gliovascular Function. <i>Neuron</i> , 2021 , 109, 438-447.e6	13.9	8
84	The Prognostic Role of Structural Variants Identified by NGS and FISH in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021 ,	12.9	5
83	Apolipoprotein E regulates lipid metabolism and β -synuclein pathology in human iPSC-derived cerebral organoids. <i>Acta Neuropathologica</i> , 2021 , 142, 807-825	14.3	2
82	-Jacksonville (V236E) variant reduces self-aggregation and risk of dementia. <i>Science Translational Medicine</i> , 2021 , 13, eabc9375	17.5	6
81	Loss of TMEM106B leads to myelination deficits: implications for frontotemporal dementia treatment strategies. <i>Brain</i> , 2020 , 143, 1905-1919	11.2	14
80	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. <i>Blood Cancer Journal</i> , 2020 , 10, 39	7	1

79	Alzheimer's Risk Factors Age, APOE Genotype, and Sex Drive Distinct Molecular Pathways. <i>Neuron</i> , 2020 , 106, 727-742.e6	13.9	52
78	APOE4 exacerbates β -synuclein pathology and related toxicity independent of amyloid. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	40
77	HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. <i>Oncolmmunology</i> , 2020 , 9, 1744947	7.2	15
76	Molecular Epidemiology of AML: Association of Somatic Gene Mutations with Epidemiologic Exposures and Outcomes in the Mayo Clinic AML Epidemiology Cohort. <i>Blood</i> , 2020 , 136, 35-36	2.2	
75	Heterogeneity of MYC Abnormalities in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 2-3	2.2	
74	Clonal Somatic Mutations Are a Biomarker for Inferior Prognosis in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2020 , 136, 26-27	2.2	0
73	ApoE (Apolipoprotein E) in Brain Pericytes Regulates Endothelial Function in an Isoform-Dependent Manner by Modulating Basement Membrane Components. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020 , 40, 128-144	9.4	20
72	APOE4 exacerbates synapse loss and neurodegeneration in Alzheimer's disease patient iPSC-derived cerebral organoids. <i>Nature Communications</i> , 2020 , 11, 5540	17.4	59
71	MYC dysregulation in the progression of multiple myeloma. <i>Leukemia</i> , 2020 , 34, 322-326	10.7	56
70	Amplification of 9p24.1 in diffuse large B-cell lymphoma identifies a unique subset of cases that resemble primary mediastinal large B-cell lymphoma. <i>Blood Cancer Journal</i> , 2019 , 9, 73	7	19
69	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. <i>Genome Biology</i> , 2019 , 20, 97	18.3	68
68	Host genetic variation in tumor necrosis factor and nuclear factor- κ B pathways and overall survival in mantle cell lymphoma: A discovery and replication study. <i>American Journal of Hematology</i> , 2019 , 94, E153-E155	7.1	1
67	Genome-wide analyses as part of the international FTLT-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLT. <i>Acta Neuropathologica</i> , 2019 , 137, 879-899	14.3	50
66	Managing genomic variant calling workflows with Swift/T. <i>PLoS ONE</i> , 2019 , 14, e0211608	3.7	6
65	Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 150	7.3	18
64	ABCA7 haplo deficiency disturbs microglial immune responses in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23790-23796	11.5	22
63	Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. <i>Blood</i> , 2019 , 134, 4366-4366	2.2	
62	Genomic Landscape Including Novel Mutational Drivers in Relapsed/Refractory Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2019 , 134, 919-919	2.2	

61	Clustering of Transcriptomic Signatures in Newly Diagnosed Diffuse Large B-Cell Lymphoma Identifies Two High-Risk Subgroups Which Increase in Prevalence at Relapse. <i>Blood</i> , 2019 , 134, 923-923	2.2	
60	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. <i>Blood</i> , 2019 , 134, 4362-4362	2.2	
59	Genomic Analysis of R2CHOP-Treated DLBCL Reveals a High-Risk Population Driven By Inflammatory Pathways. <i>Blood</i> , 2019 , 134, 1480-1480	2.2	
58	NucMap: a database of genome-wide nucleosome positioning map across species. <i>Nucleic Acids Research</i> , 2019 , 47, D163-D169	20.1	15
57	A susceptibility locus for classical Hodgkin lymphoma at 8q24 near MYC/PVT1 predicts patient outcome in two independent cohorts. <i>British Journal of Haematology</i> , 2018 , 180, 286-290	4.5	11
56	Chromoanasythesis is a common mechanism that leads to ERBB2 amplifications in a cohort of early stage HER2 breast cancer samples. <i>BMC Cancer</i> , 2018 , 18, 738	4.8	10
55	TMEM106B haplotypes have distinct gene expression patterns in aged brain. <i>Molecular Neurodegeneration</i> , 2018 , 13, 35	19	15
54	Identification of missing variants by combining multiple analytic pipelines. <i>BMC Bioinformatics</i> , 2018 , 19, 139	3.6	9
53	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2018 , 136, 709-727	14.3	28
52	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. <i>Blood</i> , 2018 , 132, 4458-4458	2.2	
51	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. <i>Alzheimer's and Dementia</i> , 2018 , 14, 352-366	1.2	72
50	point mutations and familial intracranial aneurysms. <i>Neurology</i> , 2018 , 91, e2170-e2181	6.5	13
49	Loss of TNFAIP3 enhances MYD88-driven signaling in non-Hodgkin lymphoma. <i>Blood Cancer Journal</i> , 2018 , 8, 97	7	16
48	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. <i>Blood Cancer Journal</i> , 2018 , 8, 96	7	29
47	Human Pegivirus infection and lymphoma risk and prognosis: a North American study. <i>British Journal of Haematology</i> , 2018 , 182, 644-653	4.5	15
46	BAP1 dependent expression of long non-coding RNA NEAT-1 contributes to sensitivity to gemcitabine in cholangiocarcinoma. <i>Molecular Cancer</i> , 2017 , 16, 22	42.1	59
45	In-depth clinico-pathological examination of RNA foci in a large cohort of C9ORF72 expansion carriers. <i>Acta Neuropathologica</i> , 2017 , 134, 255-269	14.3	57
44	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. <i>Neurology: Genetics</i> , 2017 , 3, e141	3.8	15

43	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. <i>Rare Tumors</i> , 2017 , 9, 6834	1.1	5
42	Cadherin complexes recruit mRNAs and RISC to regulate epithelial cell signaling. <i>Journal of Cell Biology</i> , 2017 , 216, 3073-3085	7.3	25
41	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. <i>Lupus Science and Medicine</i> , 2017 , 4, e000187	4.6	10
40	Abnormal expression of homeobox genes and transthyretin in expansion carriers. <i>Neurology: Genetics</i> , 2017 , 3, e161	3.8	9
39	Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. <i>Blood</i> , 2016 , 128, 1234-45	2.2	77
38	Jak1-STAT3 Signals Are Essential Effectors of the USP6/TRE17 Oncogene in Tumorigenesis. <i>Cancer Research</i> , 2016 , 76, 5337-47	10.1	23
37	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. <i>Scientific Reports</i> , 2016 , 6, 25521	4.9	11
36	Impaired innate, humoral, and cellular immunity despite a take in smallpox vaccine recipients. <i>Vaccine</i> , 2016 , 34, 3283-90	4.1	9
35	Frequent occurrence of large duplications at reciprocal genomic rearrangement breakpoints in multiple myeloma and other tumors. <i>Nucleic Acids Research</i> , 2016 , 44, 8189-98	20.1	8
34	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , 2016 , 25, 1663-76	5.6	39
33	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. <i>Scientific Data</i> , 2016 , 3, 160089	8.2	179
32	Validation of Gene Expression Signatures to Identify Low-risk Clear-cell Renal Cell Carcinoma Patients at Higher Risk for Disease-related Death. <i>European Urology Focus</i> , 2016 , 2, 608-615	5.1	4
31	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. <i>Acta Neuropathologica</i> , 2016 , 132, 197-211	14.3	35
30	TYROBP genetic variants in early-onset Alzheimer's disease. <i>Neurobiology of Aging</i> , 2016 , 48, 222.e9-222.e15	5.1	51
29	Whole exome sequencing of a patient with metastatic hidradenocarcinoma and review of the literature. <i>Rare Tumors</i> , 2015 , 7, 5719	1.1	4
28	TP53 mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. <i>Nucleic Acids Research</i> , 2015 , 43, 6945-58	20.1	37
27	Late-onset Alzheimer disease risk variants mark brain regulatory loci. <i>Neurology: Genetics</i> , 2015 , 1, e15	3.8	51
26	The relationship between quantitative human epidermal growth factor receptor 2 gene expression by the 21-gene reverse transcriptase polymerase chain reaction assay and adjuvant trastuzumab benefit in Alliance N9831. <i>Breast Cancer Research</i> , 2015 , 17, 133	8.3	17

25	Expression of polarity genes in human cancer. <i>Cancer Informatics</i> , 2015 , 14, 15-28	2.4	15
24	Genomic analysis reveals that immune function genes are strongly linked to clinical outcome in the North Central Cancer Treatment Group n9831 Adjuvant Trastuzumab Trial. <i>Journal of Clinical Oncology</i> , 2015 , 33, 701-8	2.2	142
23	Study of the Subclonal Mutations in Primary Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2015 , 126, 131-131	2.2	
22	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014 , 46, 1233-8	36.3	108
21	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. <i>BMC Bioinformatics</i> , 2014 , 15, 224	3.6	191
20	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. <i>Bioinformatics</i> , 2014 , 30, 2678-80	7.2	35
19	Recurrent PAX3-MAML3 fusion in biphenotypic sinonasal sarcoma. <i>Nature Genetics</i> , 2014 , 46, 666-8	36.3	96
18	Integrated genomic characterization reveals novel, therapeutically relevant drug targets in FGFR and EGFR pathways in sporadic intrahepatic cholangiocarcinoma. <i>PLoS Genetics</i> , 2014 , 10, e1004135	6	239
17	RVboost: RNA-seq variants prioritization using a boosting method. <i>Bioinformatics</i> , 2014 , 30, 3414-6	7.2	21
16	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Record-Linked Genome-Wide Association Study: A Case Series. <i>Journal of Investigative Medicine High Impact Case Reports</i> , 2013 , 1, 2324709613508932	1.2	2
15	Gene expression, single nucleotide variant and fusion transcript discovery in archival material from breast tumors. <i>PLoS ONE</i> , 2013 , 8, e81925	3.7	42
14	Whole-Exome Analysis Of DLBCL Tumors Reveals a Unique Genetic Signature Associated With Aggressive Disease. <i>Blood</i> , 2013 , 122, 499-499	2.2	1
13	A Genome-Wide Association Study (GWAS) Of Event-Free Survival In Diffuse Large B-Cell Lymphoma (DLBCL) Treated With Rituximab and Anthracycline-Based Chemotherapy: A Lysa and Iowa/Mayo Clinic SPORE Multistage Study. <i>Blood</i> , 2013 , 122, 76-76	2.2	1
12	Comparison Of Single Nucleotide Mutations (SNVs) and Copy Number Variants (CNVs) Detection In Formalin Fixed Paraffin Embedded (FFPE) and Paired Frozen Tumor Tissues Using Target Capture and Sequencing Approach. <i>Blood</i> , 2013 , 122, 1784-1784	2.2	
11	Detection of redundant fusion transcripts as biomarkers or disease-specific therapeutic targets in breast cancer. <i>Cancer Research</i> , 2012 , 72, 1921-8	10.1	71
10	Germline Genetic Variation and Risk of Follicular Lymphoma Transformation in the Modern Treatment Era. <i>Blood</i> , 2012 , 120, 149-149	2.2	
9	Prognostic Value of Six Germline Single Nucleotide Polymorphisms At the REL, HLA-DRA, GATA3 and PVT1 Loci Identified in a Classical Hodgkin Lymphoma Genome-Wide Association Study: A Meta-Analysis of 601 Patients for Progression-Free Survival From Two Independent Studies. <i>Blood</i> , 2012 , 120, 3637-3637	2.2	
8	CXCR5 Polymorphisms in Non-Hodgkin Lymphoma (NHL) Risk and Prognosis.. <i>Blood</i> , 2012 , 120, 2702-2702		

7	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. <i>Blood</i> , 2011 , 118, 2295-2295	2.2	1
6	Assessment of Multiple Myeloma IGHV Intraclonal Variation by Massively Parallel Pyrosequencing. <i>Blood</i> , 2011 , 118, 1814-1814	2.2	
5	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. <i>Blood</i> , 2011 , 118, 1242-1242	2.2	
4	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. <i>Blood</i> , 2011 , 118, 709-709	2.2	
3	3' tag digital gene expression profiling of human brain and universal reference RNA using Illumina Genome Analyzer. <i>BMC Genomics</i> , 2009 , 10, 531	4.5	132
2	Transcriptome profiling using next-generation sequencing. <i>Gastroenterology</i> , 2008 , 135, 1466-8	13.3	34
1	Leveraging selective hippocampal vulnerability among Alzheimer's disease subtypes reveals a novel tau binding partner SERPINA5		2