Yan W Asmann

List of Publications by Citations

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	Integrated genomic characterization reveals novel, therapeutically relevant drug targets in FGFR and EGFR pathways in sporadic intrahepatic cholangiocarcinoma. *PLoS Genetics*, **2014**, 10, e1004135	6	239
95	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. *BMC Bioinformatics*, **2014**, 15, 224	3.6	191
94	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. *Scientific Data*, **2016**, 3, 160089	8.2	179
93	Genomic analysis reveals that immune function genes are strongly linked to clinical outcome in the North Central Cancer Treatment Group n9831 Adjuvant Trastuzumab Trial. *Journal of Clinical Oncology*, **2015**, 33, 701-8	2.2	142
92	3' tag digital gene expression profiling of human brain and universal reference RNA using Illumina Genome Analyzer. *BMC Genomics*, **2009**, 10, 531	4.5	132
91	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. *Nature Genetics*, **2014**, 46, 1233-8	36.3	108
90	Recurrent PAX3-MAML3 fusion in biphenotypic sinonasal sarcoma. *Nature Genetics*, **2014**, 46, 666-8	36.3	96
89	Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. *Blood*, **2016**, 128, 1234-45	2.2	77
88	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. *Alzheimer's and Dementia*, **2018**, 14, 352-366	1.2	72
87	Detection of redundant fusion transcripts as biomarkers or disease-specific therapeutic targets in breast cancer. *Cancer Research*, **2012**, 72, 1921-8	10.1	71
86	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. *Genome Biology*, **2019**, 20, 97	18.3	68
85	BAP1 dependent expression of long non-coding RNA NEAT-1 contributes to sensitivity to gemcitabine in cholangiocarcinoma. *Molecular Cancer*, **2017**, 16, 22	42.1	59
84	APOE4 exacerbates synapse loss and neurodegeneration in Alzheimer's disease patient iPSC-derived cerebral organoids. *Nature Communications*, **2020**, 11, 5540	17.4	59
83	In-depth clinico-pathological examination of RNA foci in a large cohort of C9ORF72 expansion carriers. *Acta Neuropathologica*, **2017**, 134, 255-269	14.3	57
82	MYC dysregulation in the progression of multiple myeloma. *Leukemia*, **2020**, 34, 322-326	10.7	56
81	Alzheimer's Risk Factors Age, APOE Genotype, and Sex Drive Distinct Molecular Pathways. *Neuron*, **2020**, 106, 727-742.e6	13.9	52
80	Late-onset Alzheimer disease risk variants mark brain regulatory loci. *Neurology: Genetics*, **2015**, 1, e15	3.8	51

79	TYROBP genetic variants in early-onset Alzheimer's disease. *Neurobiology of Aging*, **2016**, 48, 222.e9-222.e15	5.1	51
78	Genome-wide analyses as part of the international FTLD-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLD. *Acta Neuropathologica*, **2019**, 137, 879-899	14.3	50
77	Gene expression, single nucleotide variant and fusion transcript discovery in archival material from breast tumors. *PLoS ONE*, **2013**, 8, e81925	3.7	42
76	APOE4 exacerbates -synuclein pathology and related toxicity independent of amyloid. *Science Translational Medicine*, **2020**, 12,	17.5	40
75	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. *Human Molecular Genetics*, **2016**, 25, 1663-76	5.6	39
74	TP53 mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. *Nucleic Acids Research*, **2015**, 43, 6945-58	20.1	37
73	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. *Bioinformatics*, **2014**, 30, 2678-80	7.2	35
72	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. *Acta Neuropathologica*, **2016**, 132, 197-211	14.3	35
71	Transcriptome profiling using next-generation sequencing. *Gastroenterology*, **2008**, 135, 1466-8	13.3	34
70	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. *Blood Cancer Journal*, **2018**, 8, 96	7	29
69	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. *Acta Neuropathologica*, **2018**, 136, 709-727	14.3	28
68	Cadherin complexes recruit mRNAs and RISC to regulate epithelial cell signaling. *Journal of Cell Biology*, **2017**, 216, 3073-3085	7.3	25
67	Jak1-STAT3 Signals Are Essential Effectors of the USP6/TRE17 Oncogene in Tumorigenesis. *Cancer Research*, **2016**, 76, 5337-47	10.1	23
66	ABCA7 haplodeficiency disturbs microglial immune responses in the mouse brain. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 23790-23796	11.5	22
65	RVboost: RNA-seq variants prioritization using a boosting method. *Bioinformatics*, **2014**, 30, 3414-6	7.2	21
64	ApoE (Apolipoprotein E) in Brain Pericytes Regulates Endothelial Function in an Isoform-Dependent Manner by Modulating Basement Membrane Components. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2020**, 40, 128-144	9.4	20
63	Amplification of 9p24.1 in diffuse large B-cell lymphoma identifies a unique subset of cases that resemble primary mediastinal large B-cell lymphoma. *Blood Cancer Journal*, **2019**, 9, 73	7	19
62	Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. *Acta Neuropathologica Communications*, **2019**, 7, 150	7.3	18

61	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. *Breast Cancer Research*, **2015**, 17, 133	8.3	17
60	Loss of TNFAIP3 enhances MYD88-driven signaling in non-Hodgkin lymphoma. *Blood Cancer Journal* , **2018**, 8, 97	7	16
59	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. *Neurology: Genetics*, **2017**, 3, e141	3.8	15
58	HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. *OncoImmunology*, **2020**, 9, 1744947	7.2	15
57	TMEM106B haplotypes have distinct gene expression patterns in aged brain. *Molecular Neurodegeneration*, **2018**, 13, 35	19	15
56	Expression of polarity genes in human cancer. *Cancer Informatics*, **2015**, 14, 15-28	2.4	15
55	NucMap: a database of genome-wide nucleosome positioning map across species. *Nucleic Acids Research*, **2019**, 47, D163-D169	20.1	15
54	Human Pegivirus infection and lymphoma risk and prognosis: a North American study. *British Journal of Haematology*, **2018**, 182, 644-653	4.5	15
53	Loss of TMEM106B leads to myelination deficits: implications for frontotemporal dementia treatment strategies. *Brain*, **2020**, 143, 1905-1919	11.2	14
52	point mutations and familial intracranial aneurysms. *Neurology*, **2018**, 91, e2170-e2181	6.5	13
51	A susceptibility locus for classical Hodgkin lymphoma at 8q24 near MYC/PVT1 predicts patient outcome in two independent cohorts. *British Journal of Haematology*, **2018**, 180, 286-290	4.5	11
50	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. *Scientific Reports*, **2016**, 6, 25521	4.9	11
49	Chromoanasynthesis is a common mechanism that leads to ERBB2 amplifications in a cohort of early stage HER2 breast cancer samples. *BMC Cancer*, **2018**, 18, 738	4.8	10
48	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. *Lupus Science and Medicine*, **2017**, 4, e000187	4.6	10
47	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimer's disease. *Nature Communications*, **2021**, 12, 2311	17.4	10
46	Impaired innate, humoral, and cellular immunity despite a take in smallpox vaccine recipients. *Vaccine*, **2016**, 34, 3283-90	4.1	9
45	Identification of missing variants by combining multiple analytic pipelines. *BMC Bioinformatics*, **2018**, 19, 139	3.6	9
44	Abnormal expression of homeobox genes and transthyretin in expansion carriers. *Neurology: Genetics*, **2017**, 3, e161	3.8	9

43	Targeting of inflammatory pathways with R2CHOP in high-risk DLBCL. *Leukemia*, **2021**, 35, 522-533	10.7	9
42	Frequent occurrence of large duplications at reciprocal genomic rearrangement breakpoints in multiple myeloma and other tumors. *Nucleic Acids Research*, **2016**, 44, 8189-98	20.1	8
41	Alpha 1-antichymotrypsin contributes to stem cell characteristics and enhances tumorigenicity of glioblastoma. *Neuro-Oncology*, **2021**, 23, 599-610	1	8
40	Vascular ApoE4 Impairs Behavior by Modulating Gliovascular Function. *Neuron*, **2021**, 109, 438-447.e6	13.9	8
39	Managing genomic variant calling workflows with Swift/T. *PLoS ONE*, **2019**, 14, e0211608	3.7	6
38	-Jacksonville (V236E) variant reduces self-aggregation and risk of dementia. *Science Translational Medicine*, **2021**, 13, eabc9375	17.5	6
37	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. *Rare Tumors*, **2017**, 9, 6834	1.1	5
36	The Prognostic Role of Structural Variants Identified by NGS and FISH in Multiple Myeloma. *Clinical Cancer Research*, **2021**,	12.9	5
35	Whole exome sequencing of a patient with metastatic hidradenocarcinoma and review of the literature. *Rare Tumors*, **2015**, 7, 5719	1.1	4
34	Human Cerebrospinal Fluid Modulates Pathways Promoting Glioblastoma Malignancy. *Frontiers in Oncology*, **2021**, 11, 624145	5.3	4
33	Validation of Gene Expression Signatures to Identify Low-risk Clear-cell Renal Cell Carcinoma Patients at Higher Risk for Disease-related Death. *European Urology Focus*, **2016**, 2, 608-615	5.1	4
32	ABCA7 Regulates Brain Fatty Acid Metabolism During LPS-Induced Acute Inflammation. *Frontiers in Neuroscience*, **2021**, 15, 647974	5.1	3
31	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Record-Linked Genome-Wide Association Study: A Case Series. *Journal of Investigative Medicine High Impact Case Reports*, **2013**, 1, 2324709613508932	1.2	2
30	Leveraging selective hippocampal vulnerability among Alzheimer disease subtypes reveals a novel tau binding partner SERPINA5		2
29	Inflation of tumor mutation burden by tumor-only sequencing in under-represented groups. *Npj Precision Oncology*, **2021**, 5, 22	9.8	2
28	Loss of Tmem106b leads to cerebellum Purkinje cell death and motor deficits. *Brain Pathology*, **2021**, 31, e12945	6	2
27	Apolipoprotein E regulates lipid metabolism and synuclein pathology in human iPSC-derived cerebral organoids. *Acta Neuropathologica*, **2021**, 142, 807-825	14.3	2
26	Host genetic variation in tumor necrosis factor and nuclear factor- B pathways and overall survival in mantle cell lymphoma: A discovery and replication study. *American Journal of Hematology*, **2019**, 94, E153-E155	7.1	1

25	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. *Blood Cancer Journal*, **2020**, 10, 39	7	1
24	Association of Gene-Environment Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. *Blood*, **2011**, 118, 2295-2295	2.2	1
23	Single Cell Transcriptome Profile of Myeloma and Immune Cell Characteristics in Patients with Durable Response Post CART. *Blood*, **2021**, 138, 3838-3838	2.2	1
22	Whole-Exome Analysis Of DLBCL Tumors Reveals a Unique Genetic Signature Associated With Aggressive Disease. *Blood*, **2013**, 122, 499-499	2.2	1
21	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. *Blood*, **2013**, 122, 76-76	2.2	1
20	Clonal Somatic Mutations Are a Biomarker for Inferior Prognosis in Diffuse Large B-Cell Lymphoma. *Blood*, **2020**, 136, 26-27	2.2	0
19	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. *PLoS ONE*, **2021**, 16, e0249305	3.7	0
18	Molecular Epidemiology of AML: Association of Somatic Gene Mutations with Epidemiologic Exposures and Outcomes in the Mayo Clinic AML Epidemiology Cohort. *Blood*, **2020**, 136, 35-36	2.2	
17	Heterogeneity of MYC Abnormalities in Multiple Myeloma. *Blood*, **2020**, 136, 2-3	2.2	
16	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). *Blood*, **2021**, 138, 3437-3437	2.2	
15	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. *Blood*, **2021**, 138, 4101-4101	2.2	
14	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. *Blood*, **2018**, 132, 4458-4458	2.2	
13	Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. *Blood*, **2019**, 134, 4366-4366	2.2	
12	Genomic Landscape Including Novel Mutational Drivers in Relapsed/Refractory Diffuse Large B Cell Lymphoma. *Blood*, **2019**, 134, 919-919	2.2	
11	Clustering of Transcriptomic Signatures in Newly Diagnosed Diffuse Large B-Cell Lymphoma Identifies Two High-Risk Subgroups Which Increase in Prevalence at Relapse. *Blood*, **2019**, 134, 923-923	2.2	
10	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. *Blood*, **2019**, 134, 4362-4362	2.2	
9	Genomic Analysis of R2CHOP-Treated DLBCL Reveals a High-Risk Population Driven By Inflammatory Pathways. *Blood*, **2019**, 134, 1480-1480	2.2	
8	Study of the Subclonal Mutations in Primary Diffuse Large B-Cell Lymphoma. *Blood*, **2015**, 126, 131-131	2.2	

7	Assessment of Multiple Myeloma IGHV Intraclonal Variation by Massively Parallel Pyrosequencing. *Blood*, **2011**, 118, 1814-1814	2.2
6	Association of Gene-Gene Interactions with Venous Thromboembolism (VTE): A Merged/Imputed Genome-Wide Scan/Candidate-Gene Case-Control Study. *Blood*, **2011**, 118, 1242-1242	2.2
5	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. *Blood*, **2011**, 118, 709-709	2.2
4	Germline Genetic Variation and Risk of Follicular Lymphoma Transformation in the Modern Treatment Era. *Blood*, **2012**, 120, 149-149	2.2
3	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. *Blood*, **2012**, 120, 3637-3637	2.2
2	CXCR5 Polymorphisms in Non-Hodgkin Lymphoma (NHL) Risk and Prognosis.. *Blood*, **2012**, 120, 2702-2702	2.2
1	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. *Blood*, **2013**, 122, 1784-1784	2.2