Yan W Asmann

List of Publications by Year
in descending order

98	4,198	126708	133063
papers	citations	33 h-index	59 g-index

103	103	103	9261
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Human whole genome genotype and transcriptome data for Alzheimerâ€™s and other neurodegenerative diseases. Scientific Data, 2016, 3, 160089.	2.4	361
2	Integrated Genomic Characterization Reveals Novel, Therapeutically Relevant Drug Targets in FGFR and EGFR Pathways in Sporadic Intrahepatic Cholangiocarcinoma. PLoS Genetics, 2014, 10, e1004135.	1.5	292
3	MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. BMC Bioinformatics, 2014, 15, 224.	1.2	284
4	APOE4 exacerbates synapse loss and neurodegeneration in Alzheimerâ€™s disease patient iPSC-derived cerebral organoids. Nature Communications, 2020, 11, 5540.	5.8	172
5	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, 701-708.	0.8	171
6	Alzheimerâ€™s Risk Factors Age, APOE Genotype, and Sex Drive Distinct Molecular Pathways. Neuron, 2020, 106, 727-742.e6.	3.8	152
7	3' tag digital gene expression profiling of human brain and universal reference RNA using Illumina Genome Analyzer. BMC Genomics, 2009, 10, 531.	1.2	151
8	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
9	Recurrent PAX3-MAML3 fusion in biphenotypic sinonasal sarcoma. Nature Genetics, 2014, 46, 666-668.	9.4	133
10	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. Genome Biology, 2019, 20, 97.	3.8	122
11	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. Alzheimer's and Dementia, 2018, 14, 352-366.	0.4	116
12	MYC dysregulation in the progression of multiple myeloma. Leukemia, 2020, 34, 322-326.	3.3	108
13	Integrated mate-pair and RNA sequencing identifies novel, targetable gene fusions in peripheral T-cell lymphoma. Blood, 2016, 128, 1234-1245.	0.6	105
14	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.	3.9	90
15	APOE4 exacerbates Î±-synuclein pathology and related toxicity independent of amyloid. Science Translational Medicine, 2020, 12, .	5.8	90
16	Detection of Redundant Fusion Transcripts as Biomarkers or Disease-Specific Therapeutic Targets in Breast Cancer. Cancer Research, 2012, 72, 1921-1928.	0.4	83
17	In-depth clinico-pathological examination of RNA foci in a large cohort of C9ORF72 expansion carriers. Acta Neuropathologica, 2017, 134, 255-269.	3.9	76
18	TYROBP genetic variants in early-onset Alzheimer's disease. Neurobiology of Aging, 2016, 48, 222.e9-222.e15.	1.5	69

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19	Late-onset Alzheimer disease risk variants mark brain regulatory loci. Neurology: Genetics, 2015, 1, e15.	0.9	64
20	BAP1 dependent expression of long non-coding RNA NEAT-1 contributes to sensitivity to gemcitabine in cholangiocarcinoma. Molecular Cancer, 2017, 16, 22.	7.9	64
21	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
22	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	3.9	49
23	Gene Expression, Single Nucleotide Variant and Fusion Transcript Discovery in Archival Material from Breast Tumors. PLoS ONE, 2013, 8, e81925.	1.1	49
24	Differences in genomic abnormalities among African individuals with monoclonal gammopathies using calculated ancestry. Blood Cancer Journal, 2018, 8, 96.	2.8	47
25	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. Acta Neuropathologica, 2018, 136, 709-727.	3.9	47
26	TP53mutations, tetraploidy and homologous recombination repair defects in early stage high-grade serous ovarian cancer. Nucleic Acids Research, 2015, 43, 6945-6958.	6.5	46
27	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.	1.1	45
28	Loss of TMEM106B leads to myelination deficits: implications for frontotemporal dementia treatment strategies. Brain, 2020, 143, 1905-1919.	3.7	44
29	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimerâ€™s disease. Nature Communications, 2021, 12, 2311.	5.8	44
30	PatternCNV: a versatile tool for detecting copy number changes from exome sequencing data. Bioinformatics, 2014, 30, 2678-2680.	1.8	43
31	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.	3.3	43
32	Vascular ApoE4 Impairs Behavior by Modulating Gliovascular Function. Neuron, 2021, 109, 438-447.e6.	3.8	42
33	Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. Acta Neuropathologica Communications, 2019, 7, 150.	2.4	40
34	Cadherin complexes recruit mRNAs and RISC to regulate epithelial cell signaling. Journal of Cell Biology, 2017, 216, 3073-3085.	2.3	39
35	Transcriptome Profiling Using Next-Generation Sequencing. Gastroenterology, 2008, 135, 1466-1468.	0.6	38
36	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.	2.8	37

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37	APOE3 -Jacksonville (V236E) variant reduces self-aggregation and risk of dementia. Science Translational Medicine, 2021, 13, eabc9375.	5.8	37
38	Loss of TNFAIP3 enhances MYD88L265P-driven signaling in non-Hodgkin lymphoma. Blood Cancer Journal, 2018, 8, 97.	2.8	36
39	RVboost: RNA-seq variants prioritization using a boosting method. Bioinformatics, 2014, 30, 3414-3416.	1.8	34
40	Jak1â€“STAT3 Signals Are Essential Effectors of the USP6/TRE17 Oncogene in Tumorigenesis. Cancer Research, 2016, 76, 5337-5347.	0.4	32
41	TMEM106B haplotypes have distinct gene expression patterns in aged brain. Molecular Neurodegeneration, 2018, 13, 35.	4.4	30
42	Targeting of inflammatory pathways with R2CHOP in high-risk DLBCL. Leukemia, 2021, 35, 522-533.	3.3	28
43	NucMap: a database of genome-wide nucleosome positioning map across species. Nucleic Acids Research, 2019, 47, D163-D169.	6.5	27
44	HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. OncoImmunology, 2020, 9, 1744947.	2.1	26
45	Expression of Polarity Genes in Human Cancer. Cancer Informatics, 2015, 14s3, CIN.S18964.	0.9	25
46	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. Neurology: Genetics, 2017, 3, e141.	0.9	25
47	Apolipoprotein E regulates lipid metabolism and Î±-synuclein pathology in human iPSC-derived cerebral organoids. Acta Neuropathologica, 2021, 142, 807-825.	3.9	25
48	Alpha 1-antichymotrypsin contributes to stem cell characteristics and enhances tumorigenicity of glioblastoma. Neuro-Oncology, 2021, 23, 599-610.	0.6	23
49	PCNT point mutations and familial intracranial aneurysms. Neurology, 2018, 91, e2170-e2181.	1.5	22
50	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.	2.2	21
51	Human Pegivirus infection and lymphoma risk and prognosis: a North American study. British Journal of Haematology, 2018, 182, 644-653.	1.2	20
52	Inflation of tumor mutation burden by tumor-only sequencing in under-represented groups. Npj Precision Oncology, 2021, 5, 22.	2.3	17
53	Impaired innate, humoral, and cellular immunity despite a take in smallpox vaccine recipients. Vaccine, 2016, 34, 3283-3290.	1.7	16
54	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15

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55	The Prognostic Role of MYC Structural Variants Identified by NGS and FISH in Multiple Myeloma. Clinical Cancer Research, 2021, 27, 5430-5439.	3.2	14
56	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. Scientific Reports, 2016, 6, 25521.	1.6	13
57	A susceptibility locus for classical Hodgkin lymphoma at 8q24 near <scp>MYC</scp><scp>PVT</scp>1 predicts patient outcome in two independent cohorts. British Journal of Haematology, 2018, 180, 286-290.	1.2	13
58	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.	1.1	13
59	Abnormal expression of homeobox genes and transthyretin in C9ORF72 expansion carriers. Neurology: Genetics, 2017, 3, e161.	0.9	12
60	ABCA7 Regulates Brain Fatty Acid Metabolism During LPS-Induced Acute Inflammation. Frontiers in Neuroscience, 2021, 15, 647974.	1.4	12
61	Whole Exome Sequencing of a Patient with Metastatic Hidradenocarcinoma and Review of the Literature. Rare Tumors, 2015, 7, 29-33.	0.3	11
62	Frequent occurrence of large duplications at reciprocal genomic rearrangement breakpoints in multiple myeloma and other tumors. Nucleic Acids Research, 2016, 44, 8189-8198.	6.5	11
63	Human Cerebrospinal Fluid Modulates Pathways Promoting Glioblastoma Malignancy. Frontiers in Oncology, 2021, 11, 624145.	1.3	11
64	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	1.2	10
65	Comprehensive Genomic Profiling of a Rare Thyroid Follicular Dendritic Cell Sarcoma. Rare Tumors, 2017, 9, 50-53.	0.3	8
66	Loss of Tmem106b leads to cerebellum Purkinje cell death and motor deficits. Brain Pathology, 2021, 31, e12945.	2.1	8
67	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.	1.6	7
68	Managing genomic variant calling workflows with Swift/T. PLoS ONE, 2019, 14, e0211608.	1.1	7
69	Lower Exome Sequencing Coverage of Ancestrally African Patients in The Cancer Genome Atlas. Journal of the National Cancer Institute, 2022, 114, 1192-1199.	3.0	6
70	Shared brain transcriptomic signature in TDP-43 type A FTLD patients with or without GRN mutations. Brain, 2022, 145, 2472-2485.	3.7	6
71	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. PLoS ONE, 2021, 16, e0249305.	1.1	5
72	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. Blood Cancer Journal, 2020, 10, 39.	2.8	4

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73	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Recordâ€“Linked Genome-Wide Association Study. Journal of Investigative Medicine High Impact Case Reports, 2013, 1, 232470961350893.	0.3	3
74	Whole-Exome Analysis Of DLBCL Tumors Reveals a Unique Genetic Signature Associated With Aggressive Disease. Blood, 2013, 122, 499-499.	0.6	2
75	Host genetic variation in tumor necrosis factor and nuclear factorâ€ºB pathways and overall survival in mantle cell lymphoma: A discovery and replication study. American Journal of Hematology, 2019, 94, E153-E155.	2.0	1
76	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.	0.6	1
77	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.	0.6	1
78	Single Cell Transcriptome Profile of Myeloma and Immune Cell Characteristics in Patients with Durable Response Post CART. Blood, 2021, 138, 3838-3838.	0.6	1
79	Clonal Somatic Mutations Are a Biomarker for Inferior Prognosis in Diffuse Large B-Cell Lymphoma. Blood, 2020, 136, 26-27.	0.6	1
80	Assessment of Multiple Myeloma IGHV Intraclonal Variation by Massively Parallel Pyrosequencing. Blood, 2011, 118, 1814-1814.	0.6	0
81	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.	0.6	0
82	Identification of Venous Thromboembolism (VTE)-Associated Novel Variants in the ABO Gene Using Targeted Deep Sequencing. Blood, 2011, 118, 709-709.	0.6	0
83	Germline Genetic Variation and Risk of Follicular Lymphoma Transformation in the Modern Treatment Era. Blood, 2012, 120, 149-149.	0.6	0
84	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.	0.6	0
85	CXCR5 Polymorphisms in Non-Hodgkin Lymphoma (NHL) Risk and Prognosis.. Blood, 2012, 120, 2702-2702.	0.6	0
86	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.	0.6	0
87	Study of the Subclonal Mutations in Primary Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 131-131.	0.6	0
88	Genomic Abnormalities Among African Individuals with Monoclonal Gammopathies Using Calculated Ancestry. Blood, 2018, 132, 4458-4458.	0.6	0
89	Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. Blood, 2019, 134, 4366-4366.	0.6	0
90	Genomic Landscape Including Novel Mutational Drivers in Relapsed/Refractory Diffuse Large B Cell Lymphoma. Blood, 2019, 134, 919-919.	0.6	0

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91	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.	0.6	0
92	The CCND1 870G Risk Allele Is Enriched in African Individuals with Plasma Cell Dyscrasias. Blood, 2019, 134, 4362-4362.	0.6	0
93	Genomic Analysis of R2CHOP-Treated DLBCL Reveals a High-Risk Population Driven By Inflammatory Pathways. Blood, 2019, 134, 1480-1480.	0.6	0
94	Clinical Correlates of Autosomal Chromosomal Abnormalities in an Electronic Medical Record-Linked Genome-Wide Association Study: A Case Series. Journal of Investigative Medicine, 2013, 1, .	0.7	0
95	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.	0.6	0
96	False-Negative Centromere 15 Probe Results in Association with African Ancestry in Plasma Cell Dyscrasias. Blood, 2021, 138, 4101-4101.	0.6	0
97	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.	0.6	0
98	Heterogeneity of MYC Abnormalities in Multiple Myeloma. Blood, 2020, 136, 2-3.	0.6	0