

# Akinyemi I Ojesina

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

9,829  
citations

279487

23  
h-index

329751

37  
g-index

50  
all docs

50  
docs citations

50  
times ranked

19751  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide variants and polygenic risk scores for cognitive impairment following blood or marrow transplantation. <i>Bone Marrow Transplantation</i> , 2022, , .	1.3	0
2	Partnership status and retention in care among cisgender heterosexual newly diagnosed people with HIV: a cohort study. <i>AIDS Care - Psychological and Socio-Medical Aspects of AIDS/HIV</i> , 2022, , 1-9.	0.6	0
3	A 10-gene prognostic signature points to LIMCH1 and HLA-DQB1 as important players in aggressive cervical cancer disease. <i>British Journal of Cancer</i> , 2021, 124, 1690-1698.	2.9	15
4	Race/ethnicity, sex and insurance disparities in colorectal cancer screening among individuals with and without cardiovascular disease. <i>Preventive Medicine Reports</i> , 2021, 21, 101263.	0.8	1
5	Immunophenotype-associated gene signature in ductal breast tumors varies by receptor subtype, but the expression of individual signature genes remains consistent. <i>Cancer Medicine</i> , 2021, 10, 5712-5720.	1.3	5
6	Dissection of PIK3CA Aberration for Cervical Adenocarcinoma Outcomes. <i>Cancers</i> , 2021, 13, 3218.	1.7	2
7	Genomic Characterization and Therapeutic Targeting of HPV Undetected Cervical Carcinomas. <i>Cancers</i> , 2021, 13, 4551.	1.7	13
8	Genomic alterations associated with mutational signatures, DNA damage repair and chromatin remodeling pathways in cervical carcinoma. <i>Npj Genomic Medicine</i> , 2021, 6, 82.	1.7	9
9	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. <i>Nature Genetics</i> , 2020, 52, 800-810.	9.4	40
10	HPV-EM: an accurate HPV detection and genotyping EM algorithm. <i>Scientific Reports</i> , 2020, 10, 14340.	1.6	3
11	Gain of function in somatic TP53 mutations is associated with immune-rich breast tumors and changes in tumor-associated macrophages. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e1001.	0.6	17
12	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
13	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
14	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
15	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , 2018, 9, 4182.	5.8	15
16	GATK PathSeq: a customizable computational tool for the discovery and identification of microbial sequences in libraries from eukaryotic hosts. <i>Bioinformatics</i> , 2018, 34, 4287-4289.	1.8	70
17	Pathway-Structured Predictive Model for Cancer Survival Prediction: A Two-Stage Approach. <i>Genetics</i> , 2017, 205, 89-100.	1.2	31
18	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794

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19	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
20	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
21	Clinicopathologic and molecular markers in cervical carcinoma: a prospective cohort study. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 217, 432.e1-432.e17.	0.7	38
22	Abstract 2453: Chromatin remodeling genes are frequently somatically altered in cervical carcinomas. , 2017, , .		0
23	Racial disparities in individual breast cancer outcomes by hormone-receptor subtype, area-level socio-economic status and healthcare resources. <i>Breast Cancer Research and Treatment</i> , 2016, 157, 575-586.	1.1	63
24	Metagenomic Characterization of Microbial Communities In Situ Within the Deeper Layers of the Ileum in Crohn's Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016, 2, 563-566.e5.	2.3	23
25	Notch Signaling Activation Is Associated with Patient Mortality and Increased FGF1-Mediated Invasion in Squamous Cell Carcinoma of the Oral Cavity. <i>Molecular Cancer Research</i> , 2016, 14, 883-891.	1.5	41
26	A two-stage approach for combining gene expression and mutation with clinical data improves survival prediction in myelodysplastic syndromes and ovarian cancer. <i>Journal of Bioinformatics and Genomics</i> , 2016, 1, .	0.0	1
27	Abstract 3301: Breast cancer subtypes have distinct microbial and immune cytolytic transcriptomic signatures. , 2016, , .		0
28	The tumor virus landscape of AIDS-related lymphomas. <i>Blood</i> , 2015, 125, e14-e22.	0.6	67
29	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. <i>International Journal of Cancer</i> , 2015, 137, 776-783.	2.3	39
30	Abstract LB-120: HER2 as a potential predictive marker and target for therapy in cervical cancer. , 2015, , .		0
31	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708
32	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	3.3	317
33	Abstract 4692: Relationships between somatic genomic alterations, tumor stage and progression-free survival in cervical cancer. , 2014, , .		0
34	Sequence-Based Discovery of <i>Bradyrhizobium enterica</i> in Cord Colitis Syndrome. <i>New England Journal of Medicine</i> , 2013, 369, 517-528.	13.9	148
35	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013, 45, 1483-1486.	9.4	275
36	Abstract 1501: Pan-cancer PathSeq analysis on TCGA data for pathogen discovery.. , 2013, , .		0

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37	Abstract 4604: Landscape of human and viral genomic alterations in cervical carcinomas.. , 2013, , .		0
38	Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3879-3884.	3.3	853
39	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. Genome Research, 2012, 22, 292-298.	2.4	1,587
40	Pathogen discovery in AIDS-related lymphoma by high-throughput sequencing. Infectious Agents and Cancer, 2012, 7, .	1.2	0
41	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. Nature Biotechnology, 2011, 29, 393-396.	9.4	289
42	Abstract 949: PathSeq: A comprehensive computational tool for pathogen discovery by deep sequencing of human cancer tissues. , 2011, , .		0
43	Interplay of Reverse Transcriptase Inhibitor Therapy and Gag p6 Diversity in HIV Type 1 Subtype G and CRF02_AG. AIDS Research and Human Retroviruses, 2008, 24, 1167-1174.	0.5	6
44	Characterization of HIV Type 1 Reverse Transcriptase Mutations in Infants Infected by Mothers Who Received Peripartum Nevirapine Prophylaxis in Jos, Nigeria. AIDS Research and Human Retroviruses, 2007, 23, 1587-1592.	0.5	5
45	The Complexity of Circulating HIV Type 1 Strains in Oyo State, Nigeria. AIDS Research and Human Retroviruses, 2007, 23, 1020-1025.	0.5	26
46	HIV-1 Subtype and Reverse Transcriptase Genotype: Role for Geographical Location and Founder Effects. PLoS Medicine, 2006, 3, e540.	3.9	4
47	Subtype-Specific Patterns in HIV Type 1 Reverse Transcriptase and Protease in Oyo State, Nigeria: Implications for Drug Resistance and Host Response. AIDS Research and Human Retroviruses, 2006, 22, 770-779.	0.5	39
48	Launching into the deep: the musings of a budding physician-scientist. Archives of Ibadan Medicine, 2005, 6, .	0.0	0
49	Correspondence. Journal of Pediatric Surgery, 2004, 39, 1446-1447.	0.8	7