Akinyemi I Ojesina

List of Publications by Year
in descending order

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	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
2	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
3	Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma. Genome Research, 2012, 22, 292-298.	2.4	1,587
4	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
5	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
6	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
7	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
8	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
9	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	3.3	317
10	PathSeq: software to identify or discover microbes by deep sequencing of human tissue. Nature Biotechnology, 2011, 29, 393-396.	9.4	289
11	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. Nature Genetics, 2013, 45, 1483-1486.	9.4	275
12	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	2.9	245
13	Sequence-Based Discovery of *Bradyrhizobium enterica* in Cord Colitis Syndrome. New England Journal of Medicine, 2013, 369, 517-528.	13.9	148
14	GATK PathSeq: a customizable computational tool for the discovery and identification of microbial sequences in libraries from eukaryotic hosts. Bioinformatics, 2018, 34, 4287-4289.	1.8	70
15	The tumor virus landscape of AIDS-related lymphomas. Blood, 2015, 125, e14-e22.	0.6	67
16	Racial disparities in individual breast cancer outcomes by hormone-receptor subtype, area-level socio-economic status and healthcare resources. Breast Cancer Research and Treatment, 2016, 157, 575-586.	1.1	63
17	Notch Signaling Activation Is Associated with Patient Mortality and Increased FGF1-Mediated Invasion in Squamous Cell Carcinoma of the Oral Cavity. Molecular Cancer Research, 2016, 14, 883-891.	1.5	41
18	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade–specific epigenome and transcriptome landscapes. Nature Genetics, 2020, 52, 800-810.	9.4	40

#	Article	IF	Citations
19	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
20	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. International Journal of Cancer, 2015, 137, 776-783.	2.3	39
21	Clinicopathologic and molecular markers in cervical carcinoma: a prospective cohort study. American Journal of Obstetrics and Gynecology, 2017, 217, 432.e1-432.e17.	0.7	38
22	Pathway-Structured Predictive Model for Cancer Survival Prediction: A Two-Stage Approach. Genetics, 2017, 205, 89-100.	1.2	31
23	The Complexity of Circulating HIV Type 1 Strains in Oyo State, Nigeria. AIDS Research and Human Retroviruses, 2007, 23, 1020-1025.	0.5	26
24	Metagenomic Characterization of Microbial Communities In Situ Within the Deeper Layers of the Ileum in Crohn's Disease. Cellular and Molecular Gastroenterology and Hepatology, 2016, 2, 563-566.e5.	2.3	23
25	Gain of function in somatic TP53 mutations is associated with immune-rich breast tumors and changes in tumor-associated macrophages. Molecular Genetics & Genomic Medicine, 2019, 7, e1001.	0.6	17
26	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
27	A 10-gene prognostic signature points to LIMCH1 and HLA-DQB1 as important players in aggressive cervical cancer disease. British Journal of Cancer, 2021, 124, 1690-1698.	2.9	15
28	Genomic Characterization and Therapeutic Targeting of HPV Undetected Cervical Carcinomas. Cancers, 2021, 13, 4551.	1.7	13
29	Genomic alterations associated with mutational signatures, DNA damage repair and chromatin remodeling pathways in cervical carcinoma. Npj Genomic Medicine, 2021, 6, 82.	1.7	9
30	Correspondence. Journal of Pediatric Surgery, 2004, 39, 1446-1447.	0.8	7
31	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
32	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
33	Immunophenotype-associated gene signature in ductal breast tumors varies by receptor subtype, but the expression of individual signature genes remains consistent. Cancer Medicine, 2021, 10, 5712-5720.	1.3	5
34	HIV-1 Subtype and Reverse Transcriptase Genotype: Role for Geographical Location and Founder Effects. PLoS Medicine, 2006, 3, e540.	3.9	4
35	HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports, 2020, 10, 14340.	1.6	3
36	Dissection of PIK3CA Aberration for Cervical Adenocarcinoma Outcomes. Cancers, 2021, 13, 3218.	1.7	2

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37	Race/ethnicity, sex and insurance disparities in colorectal cancer screening among individuals with and without cardiovascular disease. Preventive Medicine Reports, 2021, 21, 101263.	0.8	1
38	A two-stage approach for combining gene expression and mutation with clinical data improves survival prediction in myelodysplastic syndromes and ovarian cancer. Journal of Bioinformatics and Genomics, 2016, 1, .	0.0	1
39	Pathogen discovery in AIDS-related lymphoma by high-throughput sequencing. Infectious Agents and Cancer, 2012, 7, .	1.2	0
40	Launching into the deep: the musings of a budding physician-scientist. Archives of Ibadan Medicine, 2005, 6, .	0.0	0
41	Abstract 949: PathSeq: A comprehensive computational tool for pathogen discovery by deep sequencing of human cancer tissues. , 2011, , .		0
42	Abstract 1501: Pan-cancer PathSeq analysis on TCGA data for pathogen discovery.. , 2013, , .		0
43	Abstract 4604: Landscape of human and viral genomic alterations in cervical carcinomas.. , 2013, , .		0
44	Abstract 4692: Relationships between somatic genomic alterations, tumor stage and progression-free survival in cervical cancer. , 2014, , .		0
45	Abstract LB-120: HER2 as a potential predictive marker and target for therapy in cervical cancer. , 2015, , .		0
46	Abstract 3301: Breast cancer subtypes have distinct microbial and immune cytolytic transcriptomic signatures. , 2016, , .		0
47	Abstract 2453: Chromatin remodeling genes are frequently somatically altered in cervical carcinomas. , 2017, , .		0
48	Genome-wide variants and polygenic risk scores for cognitive impairment following blood or marrow transplantation. Bone Marrow Transplantation, 2022, , .	1.3	0
49	Partnership status and retention in care among cisgender heterosexual newly diagnosed people with HIV: a cohort study. AIDS Care - Psychological and Socio-Medical Aspects of AIDS/HIV, 2022, , 1-9.	0.6	0