

James R White

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

10,594
citations

94433

37
h-index

168389

53
g-index

60
all docs

60
docs citations

60
times ranked

17931
citing authors

#	ARTICLE	IF	CITATIONS
1	Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. <i>New England Journal of Medicine</i> , 2018, 378, 1976-1986.	27.0	1,495
2	Direct detection of early-stage cancers using circulating tumor DNA. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	808
3	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	14.5	799
4	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	27.8	764
5	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. <i>Cancer Discovery</i> , 2017, 7, 264-276.	9.4	706
6	Medical Management of Kidney Stones: AUA Guideline. <i>Journal of Urology</i> , 2014, 192, 316-324.	0.4	692
7	Microbiota organization is a distinct feature of proximal colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18321-18326.	7.1	572
8	Clinical implications of genomic alterations in the tumour and circulation of pancreatic cancer patients. <i>Nature Communications</i> , 2015, 6, 7686.	12.8	393
9	Establishing guidelines to harmonize tumor mutational burden (TMB): in silico assessment of variation in TMB quantification across diagnostic platforms: phase I of the Friends of Cancer Research TMB Harmonization Project. , 2020, 8, e000147.		329
10	Metabolism Links Bacterial Biofilms and Colon Carcinogenesis. <i>Cell Metabolism</i> , 2015, 21, 891-897.	16.2	288
11	CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. <i>BMC Bioinformatics</i> , 2011, 12, 356.	2.6	246
12	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Nonâ€“Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1214-1225.	0.9	226
13	Baseline survey of the anatomical microbial ecology of an important food plant: <i>Solanum lycopersicum</i> (tomato). <i>BMC Microbiology</i> , 2013, 13, 114.	3.3	221
14	Proof of Concept of Microbiome-Metabolome Analysis and Delayed Gluten Exposure on Celiac Disease Autoimmunity in Genetically At-Risk Infants. <i>PLoS ONE</i> , 2012, 7, e33387.	2.5	219
15	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <i>Microbiome</i> , 2015, 3, 50.	11.1	175
16	Detection and characterization of lung cancer using cell-free DNA fragmentomes. <i>Nature Communications</i> , 2021, 12, 5060.	12.8	161
17	Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1423-32.	7.1	146
18	Human colon mucosal biofilms from healthy or colon cancer hosts are carcinogenic. <i>Journal of Clinical Investigation</i> , 2019, 129, 1699-1712.	8.2	145

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19	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <i>BMC Microbiology</i> , 2016, 16, 275.	3.3	143
20	Multimodal genomic features predict outcome of immune checkpoint blockade in non-small-cell lung cancer. <i>Nature Cancer</i> , 2020, 1, 99-111.	13.2	141
21	Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. <i>ISME Journal</i> , 2013, 7, 1354-1366.	9.8	135
22	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. <i>Oncotarget</i> , 2018, 9, 28561-28571.	1.8	129
23	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	121
24	Anticoagulation and Antiplatelet Therapy in Urological Practice: ICUD/AUA Review Paper. <i>Journal of Urology</i> , 2014, 192, 1026-1034.	0.4	118
25	Urinary Microbiome and Cytokine Levels in Women With Interstitial Cystitis. <i>Obstetrics and Gynecology</i> , 2017, 129, 500-506.	2.4	118
26	Noninvasive Detection of Microsatellite Instability and High Tumor Mutation Burden in Cancer Patients Treated with PD-1 Blockade. <i>Clinical Cancer Research</i> , 2019, 25, 7024-7034.	7.0	104
27	Pyrosequencing of Bacterial Symbionts within <i>Axinella corrugata</i> Sponges: Diversity and Seasonal Variability. <i>PLoS ONE</i> , 2012, 7, e38204.	2.5	85
28	A machine learning approach for somatic mutation discovery. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	80
29	Genomic characterization of malignant progression in neoplastic pancreatic cysts. <i>Nature Communications</i> , 2020, 11, 4085.	12.8	77
30	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. <i>PLoS ONE</i> , 2011, 6, e26624.	2.5	75
31	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. <i>Cell Reports</i> , 2018, 25, 2617-2633.	6.4	74
32	Characterization of tumor mutation burden, PD-L1 and DNA repair genes to assess relationship to immune checkpoint inhibitors response in metastatic renal cell carcinoma. , 2020, 8, e000319.		67
33	Bacterial community diversity and variation in spray water sources and the tomato fruit surface. <i>BMC Microbiology</i> , 2011, 11, 81.	3.3	65
34	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota $\hat{\pm}$ -Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	5.8	65
35	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. <i>BMC Bioinformatics</i> , 2010, 11, 152.	2.6	63
36	Durvalumab with platinum-pemetrexed for unresectable pleural mesothelioma: survival, genomic and immunologic analyses from the phase 2 PrE0505 trial. <i>Nature Medicine</i> , 2021, 27, 1910-1920.	30.7	62

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37	Characterization of microflora in Latin-style cheeses by next-generation sequencing technology. BMC Microbiology, 2012, 12, 254.	3.3	54
38	Cilantro microbiome before and after nonselective pre-enrichment for Salmonella using 16S rRNA and metagenomic sequencing. BMC Microbiology, 2015, 15, 160.	3.3	53
39	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. Cell Reports Medicine, 2020, 1, 100139.	6.5	45
40	Early Recovery of Salmonella from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. Frontiers in Microbiology, 2016, 7, 2103.	3.5	38
41	Human Colon Cancerâ€œDerived <i>Clostridioides difficile</i> Strains Drive Colonic Tumorigenesis in Mice. Cancer Discovery, 2022, 12, 1873-1885.	9.4	38
42	Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. BMC Research Notes, 2012, 5, 378.	1.4	37
43	Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial Wolbachia endosymbiont to its host filarial nematode Brugia malayi. BMC Genomics, 2013, 14, 639.	2.8	37
44	Microbiomes Associated With Foods From Plant and Animal Sources. Frontiers in Microbiology, 2018, 9, 2540.	3.5	35
45	Extensive Genome Rearrangements and Multiple Horizontal Gene Transfers in a Population of <i>Pyrococcus</i> Isolates from Vulcano Island, Italy. Applied and Environmental Microbiology, 2008, 74, 6447-6451.	3.1	33
46	High-Resolution Microbiome Profiling for Detection and Tracking of Salmonella enterica. Frontiers in Microbiology, 2017, 8, 1587.	3.5	31
47	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Journal of Computational Biology, 2010, 17, 503-516.	1.6	29
48	Microbiome within Primary Tumor Tissue from Renal Cell Carcinoma May Be Associated with PD-L1 Expression of the Venous Tumor Thrombus. Advances in Urology, 2020, 2020, 1-6.	1.3	15
49	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. Open Forum Infectious Diseases, 2019, 6, ofz062.	0.9	12
50	Automated next-generation profiling of genomic alterations in human cancers. Nature Communications, 2022, 13, .	12.8	8
51	â€œHey CIRI, Whatâ€™s My Prognosis?â€ Cell, 2019, 178, 518-520.	28.9	6
52	Improving Phrap-Based Assembly of the Rat Using â€œReliableâ€ Overlaps. PLoS ONE, 2008, 3, e1836.	2.5	4
53	Microbiome diversity in carriers of fluoroquinolone resistant <i>Escherichia coli</i> . Investigative and Clinical Urology, 2019, 60, 75.	2.0	3
54	A Central Role for Lipocalin-2 in the Adaptation to Short-Bowel Syndrome Through Down-Regulation of IL22 in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2020, 10, 309-326.	4.5	2

#	ARTICLE	IF	CITATIONS
55	Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , .		0
56	Abstract 570: High-resolution microbiome profiling of 16SrRNA sequencing data, Microbiome Arrays, and expression arrays identifies differential bacterial communities in head and neck cancer patients treated with surgery, chemo-radiation, and PD-1 checkpoint blockade therapy. , 2018, , .		0
57	Abstract 3668: ctDNA and TCR dynamics predict response to immune checkpoint blockade in non-small cell lung cancer. , 2018, , .		0
58	PD03-01â€fRNASEQ MICROBIAL ANALYSIS IDENTIFY VARIABILITY BETWEEN RENAL CELL CARCINOMA PRIMARY TUMOR AND INTRAVASCULAR TUMOR EXTENSION. Journal of Urology, 2019, 201, .	0.4	0
59	Natural Language Processing Approaches for Retrieval of Clinically Relevant Genomic Information in Cancer. Studies in Health Technology and Informatics, 2022, , .	0.3	0