

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	Automated next-generation profiling of genomic alterations in human cancers. <i>Nature Communications</i> , 2022, 13, .	12.8	8
2	Natural Language Processing Approaches for Retrieval of Clinically Relevant Genomic Information in Cancer. <i>Studies in Health Technology and Informatics</i> , 2022, , .	0.3	0
3	Human Colon Cancerâ€™Derived <i>Clostridioides difficile</i> Strains Drive Colonic Tumorigenesis in Mice. <i>Cancer Discovery</i> , 2022, 12, 1873-1885.	9.4	38
4	Abstract 1617: Sex-specific genomic determinants of response to immunotherapy. , 2021, , .		0
5	Detection and characterization of lung cancer using cell-free DNA fragmentomes. <i>Nature Communications</i> , 2021, 12, 5060.	12.8	161
6	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
7	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota Î±-Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	5.8	65
8	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
9	A Central Role for Lipocalin-2 in the Adaptation to Short-Bowel Syndrome Through Down-Regulation of IL22 in Mice. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 309-326.	4.5	2
10	Integrative Tumor and Immune Cell Multi-omic Analyses Predict Response to Immune Checkpoint Blockade in Melanoma. <i>Cell Reports Medicine</i> , 2020, 1, 100139.	6.5	45
11	Genomic characterization of malignant progression in neoplastic pancreatic cysts. <i>Nature Communications</i> , 2020, 11, 4085.	12.8	77
12	Microbiome within Primary Tumor Tissue from Renal Cell Carcinoma May Be Associated with PD-L1 Expression of the Venous Tumor Thrombus. <i>Advances in Urology</i> , 2020, 2020, 1-6.	1.3	15
13	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
14	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
15	â€™Hey CIRI, Whatâ€™s My Prognosis?â€™ <i>Cell</i> , 2019, 178, 518-520.	28.9	6
16	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	27.8	764
17	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz062.	0.9	12
18	Microbiome diversity in carriers of fluoroquinolone resistant <i>Escherichia coli</i> . <i>Investigative and Clinical Urology</i> , 2019, 60, 75.	2.0	3

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19	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
20	Dynamics of Tumor and Immune Responses during Immune Checkpoint Blockade in Non-“Small Cell Lung Cancer. <i>Cancer Research</i> , 2019, 79, 1214-1225.	0.9	226
21	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
22	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
23	PD03-01-“RNASEQ MICROBIAL ANALYSIS IDENTIFY VARIABILITY BETWEEN RENAL CELL CARCINOMA PRIMARY TUMOR AND INTRAVASCULAR TUMOR EXTENSION. <i>Journal of Urology</i> , 2019, 201, .	0.4	0
24	Neoadjuvant PD-1 Blockade in Resectable Lung Cancer. <i>New England Journal of Medicine</i> , 2018, 378, 1976-1986.	27.0	1,495
25	Ipilimumab plus nivolumab and DNA-repair defects in AR-V7-expressing metastatic prostate cancer. <i>Oncotarget</i> , 2018, 9, 28561-28571.	1.8	129
26	Integrated Genomic, Epigenomic, and Expression Analyses of Ovarian Cancer Cell Lines. <i>Cell Reports</i> , 2018, 25, 2617-2633.	6.4	74
27	Commensal bacteria contribute to insulin resistance in aging by activating innate B1a cells. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	121
28	Microbiomes Associated With Foods From Plant and Animal Sources. <i>Frontiers in Microbiology</i> , 2018, 9, 2540.	3.5	35
29	A machine learning approach for somatic mutation discovery. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	80
30	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
31	Abstract 3668: ctDNA and TCR dynamics predict response to immune checkpoint blockade in non-small cell lung cancer. , 2018, , .		0
32	Urinary Microbiome and Cytokine Levels in Women With Interstitial Cystitis. <i>Obstetrics and Gynecology</i> , 2017, 129, 500-506.	2.4	118
33	Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-“Small Cell Lung Cancer. <i>Cancer Discovery</i> , 2017, 7, 264-276.	9.4	706
34	Direct detection of early-stage cancers using circulating tumor DNA. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	808
35	High-Resolution Microbiome Profiling for Detection and Tracking of <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1587.	3.5	31
36	Early Recovery of <i>Salmonella</i> from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. <i>Frontiers in Microbiology</i> , 2016, 7, 2103.	3.5	38

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37	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
38	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <i>Microbiome</i> , 2015, 3, 50.	11.1	175
39	Clinical implications of genomic alterations in the tumour and circulation of pancreatic cancer patients. <i>Nature Communications</i> , 2015, 6, 7686.	12.8	393
40	Metabolism Links Bacterial Biofilms and Colon Carcinogenesis. <i>Cell Metabolism</i> , 2015, 21, 891-897.	16.2	288
41	Cilantro microbiome before and after nonselective pre-enrichment for <i>Salmonella</i> using 16S rRNA and metagenomic sequencing. <i>BMC Microbiology</i> , 2015, 15, 160.	3.3	53
42	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
43	Anticoagulation and Antiplatelet Therapy in Urological Practice: ICUD/AUA Review Paper. <i>Journal of Urology</i> , 2014, 192, 1026-1034.	0.4	118
44	Medical Management of Kidney Stones: AUA Guideline. <i>Journal of Urology</i> , 2014, 192, 316-324.	0.4	692
45	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
46	Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial <i>Wolbachia</i> endosymbiont to its host filarial nematode <i>Brugia malayi</i> . <i>BMC Genomics</i> , 2013, 14, 639.	2.8	37
47	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
48	Characterization of microflora in Latin-style cheeses by next-generation sequencing technology. <i>BMC Microbiology</i> , 2012, 12, 254.	3.3	54
49	Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. <i>BMC Research Notes</i> , 2012, 5, 378.	1.4	37
50	Pyrosequencing of Bacterial Symbionts within <i>Axinella corrugata</i> Sponges: Diversity and Seasonal Variability. <i>PLoS ONE</i> , 2012, 7, e38204.	2.5	85
51	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
52	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
53	Bacterial community diversity and variation in spray water sources and the tomato fruit surface. <i>BMC Microbiology</i> , 2011, 11, 81.	3.3	65
54	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

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55	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624.	2.5	75
56	Alignment and clustering of phylogenetic markers - implications for microbial diversity studies. BMC Bioinformatics, 2010, 11, 152.	2.6	63
57	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. Journal of Computational Biology, 2010, 17, 503-516.	1.6	29
58	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
59	Improving Phrap-Based Assembly of the Rat Using "Reliable" Overlaps. PLoS ONE, 2008, 3, e1836.	2.5	4