

# Joseph N Paulson

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,481  
citations

430874

18  
h-index

377865

34  
g-index

49  
all docs

49  
docs citations

49  
times ranked

8902  
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential abundance analysis for microbial marker-gene surveys. <i>Nature Methods</i> , 2013, 10, 1200-1202.	19.0	1,921
2	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	27.8	724
3	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	3.2	691
4	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. <i>Science</i> , 2019, 366, 606-612.	12.6	621
5	Polatuzumab Vedotin in Relapsed or Refractory Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2020, 38, 155-165.	1.6	488
6	Dynamic metabolic exchange governs a marine algal-bacterial interaction. <i>ELife</i> , 2016, 5, .	6.0	213
7	Exploring regulation in tissues with eQTL networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7841-E7850.	7.1	82
8	Smooth quantile normalization. <i>Biostatistics</i> , 2018, 19, 185-198.	1.5	78
9	Multisystem Analysis of <i>Mycobacterium tuberculosis</i> Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. <i>MBio</i> , 2018, 9, .	4.1	57
10	Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic <i>Escherichia coli</i> and subsequent ciprofloxacin treatment. <i>BMC Genomics</i> , 2016, 17, 440.	2.8	55
11	Disentangling the genetic basis of rhizosphere microbiome assembly in tomato. <i>Nature Communications</i> , 2022, 13, .	12.8	53
12	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017, 18, 723.	2.8	51
13	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017, 18, 437.	2.6	45
14	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. <i>Microbiome</i> , 2016, 4, 38.	11.1	43
15	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. <i>Science of the Total Environment</i> , 2018, 639, 1126-1137.	8.0	43
16	<i>Paenibacillus</i> infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	39
17	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. <i>Microbiome</i> , 2017, 5, 22.	11.1	33
18	Metaviz: interactive statistical and visual analysis of metagenomic data. <i>Nucleic Acids Research</i> , 2018, 46, 2777-2787.	14.5	29

#	ARTICLE	IF	CITATIONS
19	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018, 5, 80-89.	4.1	19
20	<i>MicrobiomeExplorer</i> : an R package for the analysis and visualization of microbial communities. <i>Bioinformatics</i> , 2021, 37, 1317-1318.	4.1	19
21	Estimating gene regulatory networks with pandaR. <i>Bioinformatics</i> , 2017, 33, 2232-2234.	4.1	15
22	Normal childhood brain growth and a universal sex and anthropomorphic relationship to cerebrospinal fluid. <i>Journal of Neurosurgery: Pediatrics</i> , 2021, 28, 458-468.	1.3	15
23	Reply to: "A fair comparison". <i>Nature Methods</i> , 2014, 11, 359-360.	19.0	14
24	Risk profiling of patients with relapsed/refractory diffuse large B-cell lymphoma by measuring circulating tumor DNA. <i>Blood Advances</i> , 2022, 6, 1651-1660.	5.2	14
25	Complete Genome Sequences of the Human Pathogen <i>Paenibacillus thiaminolyticus</i> Mbale and Type Strain P. <i>thiaminolyticus</i> NRRL B-4156. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	10
26	Immune activation during <i>Paenibacillus</i> brain infection in African infants with frequent cytomegalovirus co-infection. <i>IScience</i> , 2021, 24, 102351.	4.1	10
27	Methylome Analysis in Chickens Immunized with Infectious Laryngotracheitis Vaccine. <i>PLoS ONE</i> , 2015, 10, e0100476.	2.5	10
28	Nasal Microbiota and Infectious Complications After Elective Surgical Procedures. <i>JAMA Network Open</i> , 2021, 4, e218386.	5.9	6
29	Vaginal microbiome topic modeling of laboring Ugandan women with and without fever. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 75.	6.4	5
30	<i>metagenomeFeatures</i> : an R package for working with 16S rRNA reference databases and marker-gene survey feature data. <i>Bioinformatics</i> , 2019, 35, 3870-3872.	4.1	4
31	Patient-reported outcomes provide prognostic information for survival in patients with diffuse large B-cell lymphoma: Analysis of 1239 patients from the GOYA study. <i>Cancer Medicine</i> , 2022, 11, 3312-3322.	2.8	4
32	Prognostic mutational subtyping in de novo diffuse large B-cell lymphoma. <i>BMC Cancer</i> , 2022, 22, 231.	2.6	4
33	<i>mirTarRnaSeq</i> : An R/Bioconductor Statistical Package for miRNA-mRNA Target Identification and Interaction Analysis. <i>BMC Genomics</i> , 2022, 23, .	2.8	3
34	Cytomegalovirus Infections in Ugandan Infants: Newborn-Mother Pairs, Neonates with Sepsis, and Infants with Hydrocephalus. <i>International Journal of Infectious Diseases</i> , 2022, , .	3.3	2
35	TRAIL Score: A Simple Model to Predict Immunochemotherapy Tolerability in Patients With Diffuse Large B-Cell Lymphoma. <i>JCO Clinical Cancer Informatics</i> , 2022, 6, e2100121.	2.1	1