

Scot Federman

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

5,326
citations

331259

21
h-index

433756

31
g-index

35
all docs

35
docs citations

35
times ranked

9465
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. <i>New England Journal of Medicine</i> , 2019, 380, 2327-2340.	13.9	644
2	Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 99.	3.6	456
3	Transmission, infectivity, and neutralization of a spike L452R SARS-CoV-2 variant. <i>Cell</i> , 2021, 184, 3426-3437.e8.	13.5	424
4	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. <i>Genome Research</i> , 2014, 24, 1180-1192.	2.4	421
5	Laboratory validation of a clinical metagenomic sequencing assay for pathogen detection in cerebrospinal fluid. <i>Genome Research</i> , 2019, 29, 831-842.	2.4	349
6	A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012-14): a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 671-682.	4.6	348
7	Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids. <i>Nature Medicine</i> , 2021, 27, 115-124.	15.2	329
8	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. <i>Scientific Reports</i> , 2017, 7, 18022.	1.6	264
9	Diagnosis of Neuroinvasive Astrovirus Infection in an Immunocompromised Adult With Encephalitis by Unbiased Next-Generation Sequencing. <i>Clinical Infectious Diseases</i> , 2015, 60, 919-923.	2.9	262
10	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
11	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	6.0	217
12	An ensemble strategy that significantly improves de novo assembly of microbial genomes from metagenomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e46-e46.	6.5	213
13	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	5.8	132
14	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
15	Clinical metagenomic identification of <i>Balamuthia mandrillaris</i> encephalitis and assembly of the draft genome: the continuing case for reference genome sequencing. <i>Genome Medicine</i> , 2015, 7, 113.	3.6	102
16	A diagnostic host response biosignature for COVID-19 from RNA profiling of nasal swabs and blood. <i>Science Advances</i> , 2021, 7, .	4.7	79
17	Longitudinal Transcriptome Analysis Reveals a Sustained Differential Gene Expression Signature in Patients Treated for Acute Lyme Disease. <i>MBio</i> , 2016, 7, e00100-16.	1.8	76
18	Clinical features, diagnostics, and outcomes of patients presenting with acute respiratory illness: A retrospective cohort study of patients with and without COVID-19. <i>EClinicalMedicine</i> , 2020, 27, 100518.	3.2	59

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19	Identification of high-risk human papillomavirus and Rb/E2F pathway genomic alterations in mutually exclusive subsets of colorectal neuroendocrine carcinoma. <i>Modern Pathology</i> , 2019, 32, 290-305.	2.9	45
20	Utility of Metagenomic Next-Generation Sequencing for Characterization of HIV and Human Pegivirus Diversity. <i>PLoS ONE</i> , 2015, 10, e0141723.	1.1	37
21	Polyoma virus-associated carcinomas of the urologic tract: a clinicopathologic and molecular study. <i>Modern Pathology</i> , 2018, 31, 1429-1441.	2.9	25
22	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. <i>Clinical Infectious Diseases</i> , 2017, 64, 476-481.	2.9	21
23	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	17
24	Timely intervention and control of a novel coronavirus (COVID-19) outbreak at a large skilled nursing facility—San Francisco, California, 2020. <i>Infection Control and Hospital Epidemiology</i> , 2021, 42, 1173-1180.	1.0	17
25	Detection of cryptogenic malignancies from metagenomic whole genome sequencing of body fluids. <i>Genome Medicine</i> , 2021, 13, 98.	3.6	16
26	Detection of Neoplasms by Metagenomic Next-Generation Sequencing of Cerebrospinal Fluid. <i>JAMA Neurology</i> , 2021, 78, 1355.	4.5	14
27	Associations of Early COVID-19 Cases in San Francisco With Domestic and International Travel. <i>Clinical Infectious Diseases</i> , 2020, 71, 2976-2980.	2.9	8
28	Metagenomic sequencing of stool samples in Bangladeshi infants: virome association with poliovirus shedding after oral poliovirus vaccination. <i>Scientific Reports</i> , 2020, 10, 15392.	1.6	6
29	A Child With Intermittent Headaches and Eosinophilic Meningitis. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2018, 7, 355-357.	0.6	4
30	Introduction, Transmission Dynamics, and Fate of Early Severe Acute Respiratory Syndrome Coronavirus 2 Lineages in Santa Clara County, California. <i>Journal of Infectious Diseases</i> , 2021, 224, 207-217.	1.9	2