

Joseph Hughes

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

5,960
citations

126907

33
h-index

91884

69
g-index

110
all docs

110
docs citations

110
times ranked

11251
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	6.0	21
2	Exploring the Natural Origins of SARS-CoV-2 in the Light of Recombination. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	93
3	In silico prediction of HIV-1-host molecular interactions and their directionality. <i>PLoS Computational Biology</i> , 2022, 18, e1009720.	3.2	0
4	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
5	Quantifying and Cataloguing Unknown Sequences within Human Microbiomes. <i>MSystems</i> , 2022, 7, e0146821.	3.8	2
6	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. <i>Virus Evolution</i> , 2022, 8, veac023.	4.9	19
7	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	13.3	352
8	The Transmission Route and Selection Pressure in HCV Subtype 3a and 3b Chinese Infections: Evolutionary Kinetics and Selective Force Analysis. <i>Viruses</i> , 2022, 14, 1514.	3.3	3
9	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
10	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
11	A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. <i>PLoS Biology</i> , 2021, 19, e3001091.	5.6	163
12	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	28.9	541
13	Rapid feedback on hospital onset SARS-CoV-2 infections combining epidemiological and sequencing data. <i>ELife</i> , 2021, 10, .	6.0	26
14	Genetic epidemiology of SARS-CoV-2 transmission in renal dialysis units – A high risk community-hospital interface. <i>Journal of Infection</i> , 2021, 83, 96-103.	3.3	12
15	The animal origin of SARS-CoV-2. <i>Science</i> , 2021, 373, 968-970.	12.6	72
16	SARS-CoV-2 lineage B.1.1.7 is associated with greater disease severity among hospitalised women but not men: multicentre cohort study. <i>BMJ Open Respiratory Research</i> , 2021, 8, e001029.	3.0	22
17	A prenylated dsRNA sensor protects against severe COVID-19. <i>Science</i> , 2021, 374, eabj3624.	12.6	124
18	The Alpha variant was not associated with excess nosocomial SARS-CoV-2 infection in a multi-centre UK hospital study. <i>Journal of Infection</i> , 2021, 83, 693-700.	3.3	11

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19	Reorganizing the family Parvoviridae: a revised taxonomy independent of the canonical approach based on host association. <i>Archives of Virology</i> , 2020, 165, 2133-2146.	2.1	154
20	Synonymous Dinucleotide Usage: A Codon-Aware Metric for Quantifying Dinucleotide Representation in Viruses. <i>Viruses</i> , 2020, 12, 462.	3.3	12
21	TRIM69 Inhibits Vesicular Stomatitis Indiana Virus. <i>Journal of Virology</i> , 2019, 93, .	3.4	35
22	Metaviromics Reveals Unknown Viral Diversity in the Biting Midge <i>Culicoides impunctatus</i> . <i>Viruses</i> , 2019, 11, 865.	3.3	11
23	DisCVR: Rapid viral diagnosis from high-throughput sequencing data. <i>Virus Evolution</i> , 2019, 5, vez033.	4.9	5
24	Human Cytomegalovirus Genomes Sequenced Directly From Clinical Material: Variation, Multiple-Strain Infection, Recombination, and Gene Loss. <i>Journal of Infectious Diseases</i> , 2019, 220, 781-791.	4.0	84
25	Inferring epidemiological links from deep sequencing data: a statistical learning approach for human, animal and plant diseases. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180258.	4.0	14
26	Interpreting Viral Deep Sequencing Data with GLUE. <i>Viruses</i> , 2019, 11, 323.	3.3	29
27	Absence of adaptive evolution is the main barrier against influenza emergence in horses in Asia despite frequent virus interspecies transmission from wild birds. <i>PLoS Pathogens</i> , 2019, 15, e1007531.	4.7	12
28	M Segment-Based Minigenomes and Virus-Like Particle Assays as an Approach To Assess the Potential of Tick-Borne <i>Phlebovirus</i> Genome Reassortment. <i>Journal of Virology</i> , 2019, 93, .	3.4	23
29	Highly Diverse Hepatitis C Strains Detected in Sub-Saharan Africa Have Unknown Susceptibility to Direct-Acting Antiviral Treatments. <i>Hepatology</i> , 2019, 69, 1426-1441.	7.3	36
30	ICTV Virus Taxonomy Profile: Parvoviridae. <i>Journal of General Virology</i> , 2019, 100, 367-368.	2.9	312
31	ViCTree: an automated framework for taxonomic classification from protein sequences. <i>Bioinformatics</i> , 2018, 34, 2195-2200.	4.1	6
32	Ranavirus genotypes in the Netherlands and their potential association with virulence in water frogs (<i>Pelophylax</i> spp.). <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	6.5	11
33	Reply to: "Reply to: "Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries" Journal of Hepatology, 2018, 68, 864-866.	3.7	2
34	GLUE: a flexible software system for virus sequence data. <i>BMC Bioinformatics</i> , 2018, 19, 532.	2.6	84
35	Quasispecies Changes with Distinctive Point Mutations in the Hepatitis C Virus Internal Ribosome Entry Site (IRES) Derived from PBMCs and Plasma. <i>Advances in Virology</i> , 2018, 2018, 1-9.	1.1	5
36	Development of reverse genetics systems and investigation of host response antagonism and reassortment potential for Cache Valley and Kairi viruses, two emerging orthobunyaviruses of the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006884.	3.0	12

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37	The Envelope Gene of Transmitted HIV-1 Resists a Late Interferon Gamma-Induced Block. <i>Journal of Virology</i> , 2017, 91, .	3.4	26
38	Vaccine immune pressure influences viral population complexity of avian influenza virus during infection. <i>Veterinary Microbiology</i> , 2017, 203, 88-94.	1.9	10
39	Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries. <i>Journal of Hepatology</i> , 2017, 67, 1348-1350.	3.7	31
40	Complete Genome Sequence of Frog virus 3 , Isolated from a Strawberry Poison Frog (<i>Oophaga</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6	0.8	5
41	Fundamental properties of the mammalian innate immune system revealed by multispecies comparison of type I interferon responses. <i>PLoS Biology</i> , 2017, 15, e2004086.	5.6	272
42	Tracking TCR β Sequence Clonotype Expansions during Antiviral Therapy Using High-Throughput Sequencing of the Hypervariable Region. <i>Frontiers in Immunology</i> , 2016, 7, 131.	4.8	4
43	Late Ebola virus relapse causing meningoencephalitis: a case report. <i>Lancet, The</i> , 2016, 388, 498-503.	13.7	291
44	Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. <i>Journal of Virology</i> , 2016, 90, 6401-6411.	3.4	14
45	Phylogenetic analysis of porcine circovirus type 2 reveals global waves of emerging genotypes and the circulation of recombinant forms. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 269-280.	2.7	135
46	Phylogenetic analysis of porcine circovirus type 2: Methodological approach and datasets. <i>Data in Brief</i> , 2016, 8, 549-552.	1.0	5
47	Full Genome Sequence and sfRNA Interferon Antagonist Activity of Zika Virus from Recife, Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005048.	3.0	193
48	Investigation of Amphibian Mortality Events in Wildlife Reveals an On-Going Ranavirus Epidemic in the North of the Netherlands. <i>PLoS ONE</i> , 2016, 11, e0157473.	2.5	28
49	Bioinformatics tools for analysing viral genomic data. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 271-285.	1.2	16
50	Evolutionary trajectories of two distinct avian influenza epidemics: Parallelisms and divergences. <i>Infection, Genetics and Evolution</i> , 2015, 34, 457-466.	2.3	16
51	Reply. <i>Hepatology</i> , 2015, 61, 1438-1438.	7.3	0
52	Rapid evolution of the env gene leader sequence in cats naturally infected with feline immunodeficiency virus. <i>Journal of General Virology</i> , 2015, 96, 893-903.	2.9	10
53	Next-generation sequencing sheds light on the natural history of hepatitis C infection in patients who fail treatment. <i>Hepatology</i> , 2015, 61, 88-97.	7.3	36
54	Genetic analysis of members of the species Oropouche virus and identification of a novel M segment sequence. <i>Journal of General Virology</i> , 2015, 96, 1636-1650.	2.9	36

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55	Uneven Genetic Robustness of HIV-1 Integrase. <i>Journal of Virology</i> , 2015, 89, 552-567.	3.4	20
56	Origins and Evolutionary Dynamics of H3N2 Canine Influenza Virus. <i>Journal of Virology</i> , 2015, 89, 5406-5418.	3.4	65
57	Characterization of a second open reading frame in genome segment 10 of bluetongue virus. <i>Journal of General Virology</i> , 2015, 96, 3280-3293.	2.9	93
58	Widespread Reassortment Shapes the Evolution and Epidemiology of Bluetongue Virus following European Invasion. <i>PLoS Pathogens</i> , 2015, 11, e1005056.	4.7	117
59	Complete Genome Sequence of a Common Midwife Toad Virus-Like Ranavirus Associated with Mass Mortalities in Wild Amphibians in the Netherlands. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
60	Feline immunodeficiency virus (FIV) envrecombinants are common in natural infections. <i>Retrovirology</i> , 2014, 11, 80.	2.0	11
61	Host and Viral Determinants of Mx2 Antiretroviral Activity. <i>Journal of Virology</i> , 2014, 88, 7738-7752.	3.4	144
62	Emergence of a Highly Pathogenic Avian Influenza Virus from a Low-Pathogenic Progenitor. <i>Journal of Virology</i> , 2014, 88, 4375-4388.	3.4	124
63	Genetic Imprint of Vaccination on Simian/Human Immunodeficiency Virus Type 1 Transmitted Viral Genomes in Rhesus Macaques. <i>PLoS ONE</i> , 2013, 8, e70814.	2.5	1
64	Transmission of Equine Influenza Virus during an Outbreak Is Characterized by Frequent Mixed Infections and Loose Transmission Bottlenecks. <i>PLoS Pathogens</i> , 2012, 8, e1003081.	4.7	57
65	Evolution of an Eurasian Avian-like Influenza Virus in Naïve and Vaccinated Pigs. <i>PLoS Pathogens</i> , 2012, 8, e1002730.	4.7	79
66	Genomic resources for the brown planthopper, <i>Nilaparvata lugens</i> : Transcriptome pyrosequencing and microarray design. <i>Insect Science</i> , 2012, 19, 1-12.	3.0	23
67	TreeRipper web application: towards a fully automated optical tree recognition software. <i>BMC Bioinformatics</i> , 2011, 12, 178.	2.6	9
68	Hacking the JPEG/PDF tree format. <i>Nature Precedings</i> , 2011, , .	0.1	0
69	On the origin of <i>Halipeurus heraldicus</i> on Round Island petrels: Cophylogenetic relationships between petrels and their chewing lice. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1111-1120.	2.7	5
70	TreeRipper: towards a fully automated optical tree recognition software. <i>Nature Precedings</i> , 2010, , .	0.1	0
71	Evolutionary history of the UCP gene family: gene duplication and selection. <i>BMC Evolutionary Biology</i> , 2008, 8, 306.	3.2	44
72	Multiple Cophylogenetic Analyses Reveal Frequent Cospeciation between Pelecaniform Birds and Pectinopygus Lice. <i>Systematic Biology</i> , 2007, 56, 232-251.	5.6	87

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73	Comparative tests of ectoparasite species richness in seabirds. <i>BMC Evolutionary Biology</i> , 2007, 7, 227.	3.2	37
74	Avian UCP: The Killjoy in the Evolution of the Mitochondrial Uncoupling Proteins. <i>Journal of Molecular Evolution</i> , 2007, 65, 392-402.	1.8	47
75	Gene expression in the gut of keratin-feeding clothes moths (<i>Tineola</i>) and keratin beetles (<i>Trox</i>) revealed by subtracted cDNA libraries. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 584-592.	2.7	29
76	The spatial scale of genetic differentiation in a model organism: the wild yeast <i>Saccharomyces paradoxus</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1941-1946.	4.0	81
77	Dense Taxonomic EST Sampling and Its Applications for Molecular Systematics of the Coleoptera (Beetles). <i>Molecular Biology and Evolution</i> , 2006, 23, 268-278.	8.9	86
78	ECOMORPHOLOGICAL ADAPTATION OF ACORN WEEVILS TO THEIR OVIPOSITION SITE. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 1971.	2.3	1
79	ECOMORPHOLOGICAL ADAPTATION OF ACORN WEEVILS TO THEIR OVIPOSITION SITE. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 1971-1983.	2.3	51
80	The phylogeny of acorn weevils (genus <i>Curculio</i>) from mitochondrial and nuclear DNA sequences: the problem of incomplete data. <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 601-615.	2.7	82
81	The Evolutionary Dynamics and Epidemiological History of Hepatitis C Virus Genotype 6, Including Unique Strains from the Li Community of Hainan Island, China. <i>Virus Evolution</i> , 0, , .	4.9	1
82	Hacking the JPEG/PDF tree format. <i>Nature Precedings</i> , 0, , .	0.1	0