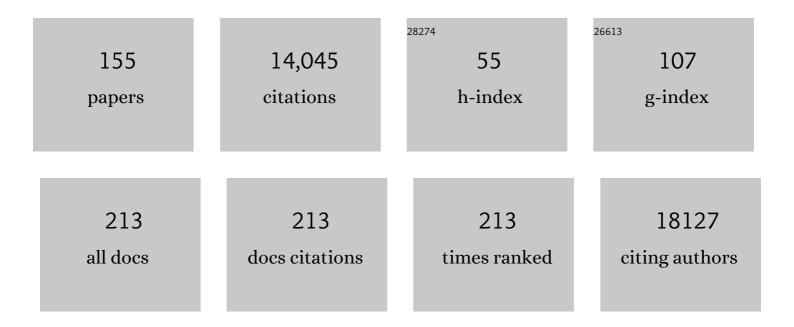
Joseph L Derisi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Actionable Diagnosis of Neuroleptospirosis by Next-Generation Sequencing. New England Journal of Medicine, 2014, 370, 2408-2417.	27.0	760
2	Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis. New England Journal of Medicine, 2019, 380, 2327-2340.	27.0	644
3	Drug target validation and identification of secondary drug target effects using DNA microarrays. Nature Medicine, 1998, 4, 1293-1301.	30.7	635
4	Amplification-free detection of SARS-CoV-2 with CRISPR-Cas13a and mobile phone microscopy. Cell, 2021, 184, 323-333.e9.	28.9	613
5	Chemical genetics of Plasmodium falciparum. Nature, 2010, 465, 311-315.	27.8	515
6	New Components of a System for Phosphate Accumulation and Polyphosphate Metabolism in <i>Saccharomyces cerevisiae</i> Revealed by Genomic Expression Analysis. Molecular Biology of the Cell, 2000, 11, 4309-4321.	2.1	470
7	Zika virus cell tropism in the developing human brain and inhibition by azithromycin. Proceedings of the United States of America, 2016, 113, 14408-14413.	7.1	432
8	A cloud-compatible bioinformatics pipeline for ultrarapid pathogen identification from next-generation sequencing of clinical samples. Genome Research, 2014, 24, 1180-1192.	5.5	421
9	Clonally expanded B cells in multiple sclerosis bind EBV EBNA1 and GlialCAM. Nature, 2022, 603, 321-327.	27.8	343
10	Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids. Nature Medicine, 2021, 27, 115-124.	30.7	329
11	Panâ€Viral Screening of Respiratory Tract Infections in Adults With and Without Asthma Reveals Unexpected Human Coronavirus and Human Rhinovirus Diversity. Journal of Infectious Diseases, 2007, 196, 817-825.	4.0	268
12	PRICE: Software for the Targeted Assembly of Components of (Meta) Genomic Sequence Data. G3: Genes, Genomes, Genetics, 2013, 3, 865-880.	1.8	250
13	Integrating host response and unbiased microbe detection for lower respiratory tract infection diagnosis in critically ill adults. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12353-E12362.	7.1	249
14	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. PLoS Pathogens, 2016, 12, e1005763.	4.7	244
15	Tetracyclines Specifically Target the Apicoplast of the Malaria Parasite Plasmodium falciparum. Antimicrobial Agents and Chemotherapy, 2006, 50, 3124-3131.	3.2	242
16	Recovery of divergent avian bornaviruses from cases of proventricular dilatation disease: Identification of a candidate etiologic agent. Virology Journal, 2008, 5, 88.	3.4	235
17	Chronic Meningitis Investigated via Metagenomic Next-Generation Sequencing. JAMA Neurology, 2018, 75, 947.	9.0	214
18	Shotgun DNA microarrays and stage-specific gene expression in Plasmodium falciparum malaria. Molecular Microbiology, 2000, 35, 6-14.	2.5	207

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19	(+)-SJ733, a clinical candidate for malaria that acts through ATP4 to induce rapid host-mediated clearance of <i>Plasmodium</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5455-62.	7.1	199
20	Metagenomic Sequencing Detects Respiratory Pathogens in Hematopoietic Cellular Transplant Patients. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 524-528.	5.6	187
21	Identification, Characterization, and <i>In Vitro</i> Culture of Highly Divergent Arenaviruses from Boa Constrictors and Annulated Tree Boas: Candidate Etiological Agents for Snake Inclusion Body Disease. MBio, 2012, 3, e00180-12.	4.1	170
22	IDseq—An open source cloud-based pipeline and analysis service for metagenomic pathogen detection and monitoring. GigaScience, 2020, 9, .	6.4	170
23	Kelch-like Protein 11 Antibodies in Seminoma-Associated Paraneoplastic Encephalitis. New England Journal of Medicine, 2019, 381, 47-54.	27.0	169
24	FLASH: a next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. Nucleic Acids Research, 2019, 47, e83-e83.	14.5	168
25	Past, present, and future of arenavirus taxonomy. Archives of Virology, 2015, 160, 1851-1874.	2.1	158
26	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	2.1	157
27	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. Science Translational Medicine, 2021, 13, eabh2624.	12.4	155
28	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	2.5	153
29	Virus Identification in Unknown Tropical Febrile Illness Cases Using Deep Sequencing. PLoS Neglected Tropical Diseases, 2012, 6, e1485.	3.0	148
30	Illuminating uveitis: metagenomic deep sequencing identifies common and rare pathogens. Genome Medicine, 2016, 8, 90.	8.2	148
31	Performance Characteristics of a Rapid Severe Acute Respiratory Syndrome Coronavirus 2 Antigen Detection Assay at a Public Plaza Testing Site in San Francisco. Journal of Infectious Diseases, 2021, 223, 1139-1144.	4.0	131
32	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. Cell Reports Medicine, 2021, 2, 100288.	6.5	121
33	A pathogenic and clonally expanded B cell transcriptome in active multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22932-22943.	7.1	119
34	Human Enterovirus 109: a Novel Interspecies Recombinant Enterovirus Isolated from a Case of Acute Pediatric Respiratory Illness in Nicaragua. Journal of Virology, 2010, 84, 9047-9058.	3.4	118
35	Upper airway gene expression reveals suppressed immune responses to SARS-CoV-2 compared with other respiratory viruses. Nature Communications, 2020, 11, 5854.	12.8	118
36	Diagnosing <scp><i>Balamuthia mandrillaris</i></scp> <scp>E</scp> ncephalitis <scp>W</scp> ith <scp>M</scp> etagenomic <scp>D</scp> eep <scp> S</scp> equencing. Annals of Neurology, 2015, 78, 722-730.	5.3	117

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37	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	2.1	115
38	Genome-wide regulatory dynamics of translation in the Plasmodium falciparum asexual blood stages. ELife, 2014, 3, .	6.0	115
39	Pulmonary Metagenomic Sequencing Suggests Missed Infections in Immunocompromised Children. Clinical Infectious Diseases, 2019, 68, 1847-1855.	5.8	112
40	A novel cause of chronic viral meningoencephalitis: <scp>C</scp> ache Valley virus. Annals of Neurology, 2017, 82, 105-114.	5.3	111
41	A potent antimalarial benzoxaborole targets a Plasmodium falciparum cleavage and polyadenylation specificity factor homologue. Nature Communications, 2017, 8, 14574.	12.8	110
42	Expanded Clinical Phenotype, Oncological Associations, and Immunopathologic Insights of Paraneoplastic Kelch-like Protein-11 Encephalitis. JAMA Neurology, 2020, 77, 1420.	9.0	109
43	The Macronuclear Genome of Stentor coeruleus Reveals Tiny Introns in a Giant Cell. Current Biology, 2017, 27, 569-575.	3.9	105
44	Pan-viral serology implicates enteroviruses in acute flaccid myelitis. Nature Medicine, 2019, 25, 1748-1752.	30.7	93
45	Field Performance and Public Health Response Using the BinaxNOWTM Rapid Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antigen Detection Assay During Community-Based Testing. Clinical Infectious Diseases, 2021, 73, e3098-e3101.	5.8	87
46	Ball Python Nidovirus: a Candidate Etiologic Agent for Severe Respiratory Disease in <i>Python regius</i> . MBio, 2014, 5, e01484-14.	4.1	82
47	Unbiased Metagenomic Sequencing for Pediatric Meningitis in Bangladesh Reveals Neuroinvasive Chikungunya Virus Outbreak and Other Unrealized Pathogens. MBio, 2019, 10, .	4.1	79
48	Widespread Recombination, Reassortment, and Transmission of Unbalanced Compound Viral Genotypes in Natural Arenavirus Infections. PLoS Pathogens, 2015, 11, e1004900.	4.7	72
49	A Chemical Rescue Screen Identifies a Plasmodium falciparum Apicoplast Inhibitor Targeting MEP Isoprenoid Precursor Biosynthesis. Antimicrobial Agents and Chemotherapy, 2015, 59, 356-364.	3.2	72
50	Determination of ubiquitin fitness landscapes under different chemical stresses in a classroom setting. ELife, 2016, 5, .	6.0	71
51	ReScan, a Multiplex Diagnostic Pipeline, Pans Human Sera for SARS-CoV-2 Antigens. Cell Reports Medicine, 2020, 1, 100123.	6.5	70
52	Multiple sclerosis therapies differentially affect SARS-CoV-2 vaccine–induced antibody and T cell immunity and function. JCl Insight, 2022, 7, .	5.0	69
53	Destructin-1 is a collagen-degrading endopeptidase secreted by <i>Pseudogymnoascus destructans</i> , the causative agent of white-nose syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7478-7483.	7.1	68
54	Topical silver diamine fluoride for dental caries arrest in preschool children: A randomized controlled trial and microbiological analysis of caries associated microbes and resistance gene expression. Journal of Dentistry, 2018, 68, 72-78.	4.1	67

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55	Clinical, genomic, and metagenomic characterization of oral tongue squamous cell carcinoma in patients who do not smoke. Head and Neck, 2015, 37, 1642-1649.	2.0	66
56	Metagenomic next-generation sequencing of samples from pediatric febrile illness in Tororo, Uganda. PLoS ONE, 2019, 14, e0218318.	2.5	66
57	Identification of a Polymorphism in the N Gene of SARS-CoV-2 That Adversely Impacts Detection by Reverse Transcription-PCR. Journal of Clinical Microbiology, 2020, 59, .	3.9	66
58	Asexual Populations of the Human Malaria Parasite, Plasmodium falciparum, Use a Two-Step Genomic Strategy to Acquire Accurate, Beneficial DNA Amplifications. PLoS Pathogens, 2013, 9, e1003375.	4.7	65
59	A Draft Genome of the Honey Bee Trypanosomatid Parasite Crithidia mellificae. PLoS ONE, 2014, 9, e95057.	2.5	60
60	Clinical features, diagnostics, and outcomes of patients presenting with acute respiratory illness: A retrospective cohort study of patients with and without COVID-19. EClinicalMedicine, 2020, 27, 100518.	7.1	59
61	Antimalarial Benzoxaboroles Target Plasmodium falciparum Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 4886-4895.	3.2	58
62	The Kinase Regulator Mob1 Acts as a Patterning Protein for Stentor Morphogenesis. PLoS Biology, 2014, 12, e1001861.	5.6	55
63	Metagenomic DNA Sequencing for the Diagnosis of Intraocular Infections. Ophthalmology, 2017, 124, 1247-1248.	5.2	54
64	Neutralizing Autoantibodies to Type I Interferons in COVID-19 Convalescent Donor Plasma. Journal of Clinical Immunology, 2021, 41, 1169-1171.	3.8	53
65	Comparison of SARS-CoV-2 Reverse Transcriptase Polymerase Chain Reaction and BinaxNOW Rapid Antigen Tests at a Community Site During an Omicron Surge. Annals of Internal Medicine, 2022, 175, 682-690.	3.9	49
66	How duplicated transcription regulators can diversify to govern the expression of nonoverlapping sets of genes. Genes and Development, 2014, 28, 1272-1277.	5.9	48
67	Tracheal aspirate RNA sequencing identifies distinct immunological features of COVID-19 ARDS. Nature Communications, 2021, 12, 5152.	12.8	47
68	Multi-modality analysis supports APOBEC as a major source of mutations in head and neck squamous cell carcinoma. Oral Oncology, 2017, 74, 8-14.	1.5	46
69	Plasmid-free CRISPR/Cas9 genome editing in Plasmodium falciparum confirms mutations conferring resistance to the dihydroisoquinolone clinical candidate SJ733. PLoS ONE, 2017, 12, e0178163.	2.5	44
70	Miniaturization and optimization of 384-well compatible RNA sequencing library preparation. PLoS ONE, 2019, 14, e0206194.	2.5	43
71	Identification of novel, clinically correlated autoantigens in the monogenic autoimmune syndrome APS1 by proteome-wide PhIP-Seq. ELife, 2020, 9, .	6.0	43
72	Krüppel Mediates the Selective Rebalancing of Ion Channel Expression. Neuron, 2014, 82, 537-544.	8.1	42

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73	Functional Assessment of 2,177 U.S. and International Drugs Identifies the Quinoline Nitroxoline as a Potent Amoebicidal Agent against the Pathogen <i>Balamuthia mandrillaris</i> . MBio, 2018, 9, .	4.1	41
74	High-resolution epitope mapping of anti-Hu and anti-Yo autoimmunity by programmable phage display. Brain Communications, 2020, 2, fcaa059.	3.3	41
75	Viral Load Among Vaccinated and Unvaccinated, Asymptomatic and Symptomatic Persons Infected With the SARS-CoV-2 Delta Variant. Open Forum Infectious Diseases, 2022, 9, ofac135.	0.9	40
76	Estimation of Secondary Household Attack Rates for Emergent Spike L452R Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants Detected by Genomic Surveillance at a Community-Based Testing Site in San Francisco. Clinical Infectious Diseases, 2022, 74, 32-39.	5.8	39
77	Differential Disease Susceptibilities in Experimentally Reptarenavirus-Infected Boa Constrictors and Ball Pythons. Journal of Virology, 2017, 91, .	3.4	38
78	An exploration of ambigrammatic sequences in narnaviruses. Scientific Reports, 2019, 9, 17982.	3.3	36
79	Metagenomic comparison of tracheal aspirate and mini-bronchial alveolar lavage for assessment of respiratory microbiota. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2019, 316, L578-L584.	2.9	36
80	SARS-CoV-2 Variant Exposures Elicit Antibody Responses With Differential Cross-Neutralization of Established and Emerging Strains Including Delta and Omicron. Journal of Infectious Diseases, 2022, 225, 1909-1914.	4.0	35
81	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	11.9	35
82	Anti–SARS-CoV-2 and Autoantibody Profiles in the Cerebrospinal Fluid of 3 Teenaged Patients With COVID-19 and Subacute Neuropsychiatric Symptoms. JAMA Neurology, 2021, 78, 1503.	9.0	34
83	Novel Picornavirus Associated with Avian Keratin Disorder in Alaskan Birds. MBio, 2016, 7, .	4.1	31
84	Fatal Powassan Encephalitis (Deer Tick Virus, Lineage II) in a Patient With Fever and Orchitis Receiving Rituximab. JAMA Neurology, 2018, 75, 746.	9.0	31
85	Complete Genome Sequence of a Novel Coronavirus (SARS-CoV-2) Isolate from Bangladesh. Microbiology Resource Announcements, 2020, 9, .	0.6	31
86	Identification of Plasmodium falciparum specific translation inhibitors from the MMV Malaria Box using a high throughput in vitro translation screen. Malaria Journal, 2016, 15, 173.	2.3	28
87	Neurologic Complications of Common Variable Immunodeficiency. Journal of Clinical Immunology, 2016, 36, 793-800.	3.8	28
88	Deep profiling of protease substrate specificity enabled by dual random and scanned human proteome substrate phage libraries. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25464-25475.	7.1	28
89	Northern Spotted Owl (Strix occidentalis caurina) Genome: Divergence with the Barred Owl (Strix) Tj ETQq1 1 2522-2545.	0.784314 rg 2.5	gBT /Overlock 27
90	Metagenomic deep sequencing of aqueous fluid detects intraocular lymphomas. British Journal of Ophthalmology, 2018, 102, 6-8.	3.9	27

#	Article	IF	CITATIONS
91	Assessing biosynthetic potential of agricultural groundwater through metagenomic sequencing: A diverse anammox community dominates nitrate-rich groundwater. PLoS ONE, 2017, 12, e0174930.	2.5	26
92	Structural Characterization of the Glycoprotein GP2 Core Domain from the CAS Virus, a Novel Arenavirus-Like Species. Journal of Molecular Biology, 2014, 426, 1452-1468.	4.2	25
93	The Plasmodium falciparum cytoplasmic translation apparatus: a promising therapeutic target not yet exploited by clinically approved anti-malarials. Malaria Journal, 2018, 17, 465.	2.3	25
94	Discovering disease-causing pathogens in resource-scarce Southeast Asia using a global metagenomic pathogen monitoring system. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115285119.	7.1	25
95	Metagenomic prediction of antimicrobial resistance in critically ill patients with lower respiratory tract infections. Genome Medicine, 2022, 14, .	8.2	25
96	A Herpesviral induction of RAE-1 NKG2D ligand expression occurs through release of HDAC mediated repression. ELife, 2016, 5, .	6.0	24
97	Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics. Lancet Microbe, The, 2022, 3, e284-e293.	7.3	24
98	Investigating Transfusion-related Sepsis Using Culture-Independent Metagenomic Sequencing. Clinical Infectious Diseases, 2020, 71, 1179-1185.	5.8	21
99	Identification of anisomycin, prodigiosin and obatoclax as compounds with broad-spectrum anti-parasitic activity. PLoS Neglected Tropical Diseases, 2020, 14, e0008150.	3.0	20
100	Persistence of Ambigrammatic Narnaviruses Requires Translation of the Reverse Open Reading Frame. Journal of Virology, 2021, 95, e0010921.	3.4	20
101	Multiplexed Metagenomic Deep Sequencing To Analyze the Composition of High-Priority Pathogen Reagents. MSystems, 2016, 1, .	3.8	19
102	Interaction between FMDV Lpro and transcription factor ADNP is required for optimal viral replication. Virology, 2017, 505, 12-22.	2.4	19
103	Plasmodium falciparum Resistance to a Lead Benzoxaborole Due to Blocked Compound Activation and Altered Ubiquitination or Sumoylation. MBio, 2020, 11, .	4.1	19
104	Genomic and serologic characterization of enterovirus A71 brainstem encephalitis. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	19
105	Avian keratin disorder of Alaska black-capped chickadees is associated with Poecivirus infection. Virology Journal, 2018, 15, 100.	3.4	18
106	Genome Sequence of a Divergent Avian Metapneumovirus from a Monk Parakeet (<i>Myiopsitta) Tj ETQq0 0 0 ا</i>	gBT /Overl	ock 10 Tf 50
107	METAGENOMIC NEXT-GENERATION SEQUENCING REVEALS MIAMIENSIS AVIDUS (CILIOPHORA:) Tj ETQq1 1 0.78 BAY, CALIFORNIA, USA. Journal of Wildlife Diseases, 2019, 55, 375.	34314 rgB ⁻ 0.8	[/Overlock] 18

#	Article	IF	CITATIONS
109	The pulmonary metatranscriptome prior to pediatric HCT identifies post-HCT lung injury. Blood, 2021, 137, 1679-1689.	1.4	18
110	Use of unbiased metagenomic and transcriptomic analyses to investigate the association between feline calicivirus and feline chronic gingivostomatitis in domestic cats. American Journal of Veterinary Research, 2021, 82, 381-394.	0.6	18
111	Rapid deployment of SARS-CoV-2 testing: The CLIAHUB. PLoS Pathogens, 2020, 16, e1008966.	4.7	18
112	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. Systematic Biology, 2016, 66, syw096.	5.6	17
113	Extending chemical perturbations of the ubiquitin fitness landscape in a classroom setting reveals new constraints on sequence tolerance. Biology Open, 2018, 7, .	1.2	17
114	Metagenomic characterization of swine slurry in a North American swine farm operation. Scientific Reports, 2021, 11, 16994.	3.3	17
115	<scp>ZSCAN1</scp> Autoantibodies Are Associated with Pediatric Paraneoplastic <scp>ROHHAD</scp> . Annals of Neurology, 2022, 92, 279-291.	5.3	17
116	Detection of cryptogenic malignancies from metagenomic whole genome sequencing of body fluids. Genome Medicine, 2021, 13, 98.	8.2	16
117	Whole Exome Sequencing of Growing and Non-Growing Cutaneous Neurofibromas from a Single Patient with Neurofibromatosis Type 1. PLoS ONE, 2017, 12, e0170348.	2.5	15
118	Elevated N-Linked Glycosylation of IgG V Regions in Myasthenia Gravis Disease Subtypes. Journal of Immunology, 2021, 207, 2005-2014.	0.8	14
119	Detection of Neoplasms by Metagenomic Next-Generation Sequencing of Cerebrospinal Fluid. JAMA Neurology, 2021, 78, 1355.	9.0	14
120	Exploratory proteomic analysis implicates the alternative complement cascade in primary CNS vasculitis. Neurology, 2019, 93, e433-e444.	1.1	13
121	Full Genome Nobecovirus Sequences From Malagasy Fruit Bats Define a Unique Evolutionary History for This Coronavirus Clade. Frontiers in Public Health, 2022, 10, 786060.	2.7	13
122	Autoantibodies to Perilipin-1 Define a Subset of Acquired Generalized Lipodystrophy. Diabetes, 2023, 72, 59-70.	0.6	13
123	Clinicopathology conference: 41â€yearâ€old woman with chronic relapsing meningitis. Annals of Neurology, 2019, 85, 161-169.	5.3	12
124	Label-free imaging and classification of live P. falciparum enables high performance parasitemia quantification without fixation or staining. PLoS Computational Biology, 2021, 17, e1009257.	3.2	12
125	Isolation of a Complete Circular Virus Genome Sequence from an Alaskan Black-Capped Chickadee () Tj ETQq1	1 0.784314 0.8	4 rgBT /Overlo
126	Exploratory analysis of the potential for advanced diagnostic testing to reduce healthcare expenditures of patients hospitalized with meningitis or encephalitis. PLoS ONE, 2020, 15, e0226895.	2.5	10

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127	Draft Genome Sequences of Ciliovirus and Brinovirus from San Francisco Wastewater. Genome Announcements, 2015, 3, .	0.8	9
128	Altered Plasmodium falciparum Sensitivity to the Antiretroviral Protease Inhibitor Lopinavir Associated with Polymorphisms in <i>pfmdr1</i> . Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	9
129	Longâ€ŧerm MRI changes in a patient with Kelchâ€like protein 11â€associated paraneoplastic neurological syndrome. European Journal of Neurology, 2021, 28, 4261-4266.	3.3	9
130	Genomic Profiling of Evolving Daptomycin Resistance in a Patient with Recurrent Staphylococcus argenteus Sepsis. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	8
131	Targeted next-generation sequencing of TP53 in oral tongue carcinoma from non-smokers. Journal of Otolaryngology - Head and Neck Surgery, 2016, 45, 47.	1.9	7
132	Enhanced Tooth Structure Via Silver Microwires Following Treatment with 38 Percent Silver Diamine Fluoride. Pediatric Dentistry (discontinued), 2020, 42, 226-231.	0.4	7
133	Pneumonia surveillance with culture-independent metatranscriptomics in HIV-positive adults in Uganda: a cross-sectional study. Lancet Microbe, The, 2022, 3, e357-e365.	7.3	7
134	Prolonged silent carriage, genomic virulence potential and transmission between staff and patients characterize a neonatal intensive care unit (NICU) outbreak of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA). Infection Control and Hospital Epidemiology, 2023, 44, 40-46.	1.8	7
135	Upper airway gene expression shows a more robust adaptive immune response to SARS-CoV-2 in children. Nature Communications, 2022, 13, .	12.8	7
136	Functional genomic analysis of a commercial wine strain of Saccharomyces cerevisiae under differing nitrogen conditions. FEMS Yeast Research, 2001, 1, 111-125.	2.3	6
137	Central Nervous System Virus Infection in African Children with Cerebral Malaria. American Journal of Tropical Medicine and Hygiene, 2020, 103, 200-205.	1.4	6
138	Pulmonary microbiome and gene expression signatures differentiate lung function in pediatric hematopoietic cell transplant candidates. Science Translational Medicine, 2022, 14, eabm8646.	12.4	6
139	Whole-Genome mRNA Gene Expression Differs Between Patients With and Without Delirium. Journal of Geriatric Psychiatry and Neurology, 2018, 31, 203-210.	2.3	5
140	MinorityReport, software for generalized analysis of causal genetic variants. Malaria Journal, 2017, 16, 90.	2.3	4
141	A fixed moderate-dose combination of tiletamine+zolazepam outperforms midazolam in induction of short-term immobilization of ball pythons (Python regius). PLoS ONE, 2018, 13, e0199339.	2.5	4
142	POECIVIRUS IS PRESENT IN INDIVIDUALS WITH BEAK DEFORMITIES IN SEVEN SPECIES OF NORTH AMERICAN BIRDS. Journal of Wildlife Diseases, 2021, 57, 273-281.	0.8	4
143	Genome-Wide Knockout Screen Identifies Human Sialomucin CD164 as an Essential Entry Factor for Lymphocytic Choriomeningitis Virus. MBio, 2022, 13, e0020522.	4.1	4
144	βIV-Spectrin Autoantibodies in 2 Individuals With Neuropathy of Possible Paraneoplastic Origin. Neurology: Neuroimmunology and NeuroInflammation, 2022, 9, .	6.0	4

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145	Ebola virus, but not Marburg virus, replicates efficiently and without required adaptation in snake cells. Virus Evolution, 2018, 4, vey034.	4.9	3
146	Complete Genome Sequence of a Divergent Human Rhinovirus C Isolate from an Infant with Severe Community-Acquired Pneumonia in Colorado, USA. Genome Announcements, 2017, 5, .	0.8	2
147	Functional characterization of 5′ UTR cis-acting sequence elements that modulate translational efficiency in Plasmodium falciparum and humans. Malaria Journal, 2022, 21, 15.	2.3	2
148	Neuroglial stem cell-derived inflammatory pseudotumor (n-SCIPT): clinicopathologic characterization of a novel lesion of the lumbosacral spinal cord and nerve roots following intrathecal allogeneic stem cell intervention. Acta Neuropathologica, 2019, 138, 1103-1106.	7.7	1
149	SARS-CoV-2 transmission dynamics and immune responses in a household of vaccinated persons. Clinical Infectious Diseases, 2022, , .	5.8	1
150	Misinterpretation of Study Data—Reply. JAMA Neurology, 2019, 76, 113.	9.0	0
151	Genome-Wide Ribosome Profiling of the Plasmodium falciparum Intraerythrocytic Developmental Cycle. Methods in Molecular Biology, 2021, 2252, 57-87.	0.9	0
152	Title is missing!. , 2020, 14, e0008150.		0
153	Title is missing!. , 2020, 14, e0008150.		0
154	Title is missing!. , 2020, 14, e0008150.		0
155	Title is missing!. , 2020, 14, e0008150.		Ο