

Paul Kellam

List of Publications by Year in descending order

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173
papers

17,463
citations

13827

67
h-index

16127

124
g-index

187
all docs

187
docs citations

187
times ranked

20510
citing authors

#	ARTICLE	IF	CITATIONS
1	Hospital Outbreak of Middle East Respiratory Syndrome Coronavirus. <i>New England Journal of Medicine</i> , 2013, 369, 407-416.	13.9	1,044
2	Resistance to ddl and sensitivity to AZT induced by a mutation in HIV-1 reverse transcriptase. <i>Science</i> , 1991, 253, 1557-1559.	6.0	779
3	IFITM3 restricts the morbidity and mortality associated with influenza. <i>Nature</i> , 2012, 484, 519-523.	13.7	668
4	Distribution of human herpesvirus-8 latently infected cells in Kaposi's sarcoma, multicentric Castleman's disease, and primary effusion lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 4546-4551.	3.3	641
5	HHV-8 is associated with a plasmablastic variant of Castleman disease that is linked to HHV-8 "positive" plasmablastic lymphoma. <i>Blood</i> , 2000, 95, 1406-1412.	0.6	583
6	Fifth mutation in human immunodeficiency virus type 1 reverse transcriptase contributes to the development of high-level resistance to zidovudine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 1934-1938.	3.3	448
7	Elicitation of Potent Neutralizing Antibody Responses by Designed Protein Nanoparticle Vaccines for SARS-CoV-2. <i>Cell</i> , 2020, 183, 1367-1382.e17.	13.5	420
8	LEDGF/p75 functions downstream from preintegration complex formation to effect gene-specific HIV-1 integration. <i>Genes and Development</i> , 2007, 21, 1767-1778.	2.7	408
9	Ordered Appearance of Zidovudine Resistance Mutations during Treatment of 18 Human Immunodeficiency Virus-Positive Subjects. <i>Journal of Infectious Diseases</i> , 1992, 165, 105-110.	1.9	390
10	Poxvirus genomes: a phylogenetic analysis. <i>Journal of General Virology</i> , 2004, 85, 105-117.	1.3	339
11	Kaposi's Sarcoma-Associated Herpesvirus Latent and Lytic Gene Expression as Revealed by DNA Arrays. <i>Journal of Virology</i> , 2001, 75, 891-902.	1.5	333
12	Human Infection with MERS Coronavirus after Exposure to Infected Camels, Saudi Arabia, 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, 1012-1015.	2.0	305
13	The dynamics of humoral immune responses following SARS-CoV-2 infection and the potential for reinfection. <i>Journal of General Virology</i> , 2020, 101, 791-797.	1.3	300
14	Zidovudine resistance predicted by direct detection of mutations in DNA from HIV-infected lymphocytes. <i>Aids</i> , 1991, 5, 137-144.	1.0	282
15	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet</i> , 2013, 382, 1993-2002.	6.3	282
16	Antibody response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2020, 15, e0244126.	1.1	269
17	Spread, Circulation, and Evolution of the Middle East Respiratory Syndrome Coronavirus. <i>MBio</i> , 2014, 5, .	1.8	235
18	Interferon-induced transmembrane protein-3 genetic variant rs12252-C is associated with severe influenza in Chinese individuals. <i>Nature Communications</i> , 2013, 4, 1418.	5.8	228

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19	Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: A global consortium study. <i>Science</i> , 2021, 374, 472-478.	6.0	228
20	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021, 16, e0245532.	1.1	228
21	Recombinant virus assay: a rapid, phenotypic assay for assessment of drug susceptibility of human immunodeficiency virus type 1 isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 1994, 38, 23-30.	1.4	218
22	HHV-8 is associated with a plasmablastic variant of Castleman disease that is linked to HHV-8-positive plasmablastic lymphoma. <i>Blood</i> , 2000, 95, 1406-12.	0.6	215
23	Quantitative detection of HIV-1 drug resistance mutations by automated DNA sequencing. <i>Nature</i> , 1993, 365, 671-673.	13.7	205
24	Genome Diversity of Epstein-Barr Virus from Multiple Tumor Types and Normal Infection. <i>Journal of Virology</i> , 2015, 89, 5222-5237.	1.5	204
25	Zidovudine sensitivity of human immunodeficiency viruses from high-risk, symptom-free individuals during therapy. <i>Lancet, The</i> , 1990, 336, 585-590.	6.3	193
26	Specific Capture and Whole-Genome Sequencing of Viruses from Clinical Samples. <i>PLoS ONE</i> , 2011, 6, e27805.	1.1	193
27	Bim-mediated deletion of antigen-specific CD8+ T cells in patients unable to control HBV infection. <i>Journal of Clinical Investigation</i> , 2008, 118, 1835-1845.	3.9	187
28	Kaposi's sarcoma-associated herpesvirus-infected primary effusion lymphoma has a plasma cell gene expression profile. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10399-10404.	3.3	181
29	IVA: accurate <i>de novo</i> assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015, 31, 2374-2376.	1.8	179
30	Analysis of the B cell receptor repertoire in six immune-mediated diseases. <i>Nature</i> , 2019, 574, 122-126.	13.7	178
31	Convergent combination therapy can select viable multidrug-resistant HIV-1 in vitro. <i>Nature</i> , 1993, 365, 451-453.	13.7	172
32	Viral population analysis and minority-variant detection using short read next-generation sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120205.	1.8	168
33	Respiratory Tract Samples, Viral Load, and Genome Fraction Yield in Patients With Middle East Respiratory Syndrome. <i>Journal of Infectious Diseases</i> , 2014, 210, 1590-1594.	1.9	156
34	The CD225 Domain of IFITM3 Is Required for both IFITM Protein Association and Inhibition of Influenza A Virus and Dengue Virus Replication. <i>Journal of Virology</i> , 2013, 87, 7837-7852.	1.5	154
35	Resistance of Transmitted Founder HIV-1 to IFITM-Mediated Restriction. <i>Cell Host and Microbe</i> , 2016, 20, 429-442.	5.1	154
36	KSHV-encoded miRNAs target MAF to induce endothelial cell reprogramming. <i>Genes and Development</i> , 2010, 24, 195-205.	2.7	148

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37	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015, 89, 9920-9931.	1.5	148
38	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	2.8	146
39	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111.	0.9	141
40	Retroviral recombination can lead to linkage of reverse transcriptase mutations that confer increased zidovudine resistance. <i>Journal of Virology</i> , 1995, 69, 669-674.	1.5	141
41	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	2.0	131
42	The RING-CH Ligase K5 Antagonizes Restriction of KSHV and HIV-1 Particle Release by Mediating Ubiquitin-Dependent Endosomal Degradation of Tetherin. <i>PLoS Pathogens</i> , 2010, 6, e1000843.	2.1	129
43	Network properties derived from deep sequencing of human B-cell receptor repertoires delineate B-cell populations. <i>Genome Research</i> , 2013, 23, 1874-1884.	2.4	128
44	Consensus clustering and functional interpretation of gene-expression data. <i>Genome Biology</i> , 2004, 5, R94.	13.9	122
45	Universal Amplification, Next-Generation Sequencing, and Assembly of HIV-1 Genomes. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3838-3844.	1.8	119
46	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018, 217, 1728-1739.	1.9	116
47	IFITM proteins are cellular inhibitors of viral entry. <i>Current Opinion in Virology</i> , 2014, 4, 71-77.	2.6	112
48	Amphotericin B Increases Influenza A Virus Infection by Preventing IFITM3-Mediated Restriction. <i>Cell Reports</i> , 2013, 5, 895-908.	2.9	108
49	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
50	Zidovudine treatment results in the selection of human immunodeficiency virus type 1 variants whose genotypes confer increasing levels of drug resistance. <i>Journal of General Virology</i> , 1994, 75, 341-351.	1.3	103
51	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18.	1.5	101
52	X Box Binding Protein XBP-1s Transactivates the Kaposi's Sarcoma-Associated Herpesvirus (KSHV) ORF50 Promoter, Linking Plasma Cell Differentiation to KSHV Reactivation from Latency. <i>Journal of Virology</i> , 2007, 81, 13578-13586.	1.5	98
53	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. <i>Science Immunology</i> , 2019, 4, .	5.6	98
54	Generation and characterization of influenza A viruses with altered polymerase fidelity. <i>Nature Communications</i> , 2014, 5, 4794.	5.8	94

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55	Genomic Diversity of Epstein-Barr Virus Genomes Isolated from Primary Nasopharyngeal Carcinoma Biopsy Samples. <i>Journal of Virology</i> , 2014, 88, 10662-10672.	1.5	93
56	Identification of New Herpesvirus Gene Homologs in the Human Genome. <i>Genome Research</i> , 2002, 12, 1739-1748.	2.4	86
57	Chicken Interferon-Inducible Transmembrane Protein 3 Restricts Influenza Viruses and Lyssaviruses <i>In Vitro</i> . <i>Journal of Virology</i> , 2013, 87, 12957-12966.	1.5	84
58	Accumulation of Human-Adapting Mutations during Circulation of A(H1N1)pdm09 Influenza Virus in Humans in the United Kingdom. <i>Journal of Virology</i> , 2014, 88, 13269-13283.	1.5	84
59	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 13050-13056.	1.5	81
60	Phylogenetic Studies of Transmission Dynamics in Generalized HIV Epidemics. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 67, 181-195.	0.9	80
61	Community Case Clusters of Middle East Respiratory Syndrome Coronavirus in Hafr Al-Batin, Kingdom of Saudi Arabia: A Descriptive Genomic study. <i>International Journal of Infectious Diseases</i> , 2014, 23, 63-68.	1.5	80
62	Evolution of an Eurasian Avian-like Influenza Virus in Naïve and Vaccinated Pigs. <i>PLoS Pathogens</i> , 2012, 8, e1002730.	2.1	79
63	Deep Sequencing of Norovirus Genomes Defines Evolutionary Patterns in an Urban Tropical Setting. <i>Journal of Virology</i> , 2014, 88, 11056-11069.	1.5	78
64	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	2.1	78
65	Metagenomics and the molecular identification of novel viruses. <i>Veterinary Journal</i> , 2011, 190, 191-198.	0.6	76
66	Sequence Variation of Epstein-Barr Virus: Viral Types, Geography, Codon Usage, and Diseases. <i>Journal of Virology</i> , 2018, 92, .	1.5	75
67	Local Evolutionary Patterns of Human Respiratory Syncytial Virus Derived from Whole-Genome Sequencing. <i>Journal of Virology</i> , 2015, 89, 3444-3454.	1.5	74
68	A Membrane Topology Model for Human Interferon Inducible Transmembrane Protein 1. <i>PLoS ONE</i> , 2014, 9, e104341.	1.1	72
69	Full Genome Virus Detection in Fecal Samples Using Sensitive Nucleic Acid Preparation, Deep Sequencing, and a Novel Iterative Sequence Classification Algorithm. <i>PLoS ONE</i> , 2014, 9, e93269.	1.1	71
70	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2007, 36, D414-D418.	6.5	68
71	Natural Variation of Epstein-Barr Virus Genes, Proteins, and Primary MicroRNA. <i>Journal of Virology</i> , 2017, 91, .	1.5	68
72	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	2.2	64

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73	Effects of discontinuation of zidovudine treatment on zidovudine sensitivity of human immunodeficiency virus type 1 isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 1993, 37, 1525-1530.	1.4	62
74	Capturing needles in haystacks: a comparison of B-cell receptor sequencing methods. <i>BMC Immunology</i> , 2014, 15, 29.	0.9	62
75	Genomewide Function Conservation and Phylogeny in the Herpesviridae. <i>Genome Research</i> , 2001, 11, 43-54.	2.4	61
76	Epstein-Barr virus nuclear protein EBNA3C directly induces expression of AID and somatic mutations in B cells. <i>Journal of Experimental Medicine</i> , 2016, 213, 921-928.	4.2	60
77	Defining the Range of Pathogens Susceptible to Ifitm3 Restriction Using a Knockout Mouse Model. <i>PLoS ONE</i> , 2013, 8, e80723.	1.1	60
78	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183.	2.1	59
79	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. <i>BMC Bioinformatics</i> , 2012, 13, 47.	1.2	58
80	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.	2.1	57
81	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018, 4, vey035.	2.2	56
82	Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. <i>Virus Evolution</i> , 2016, 2, vew027.	2.2	52
83	Infectious causes of cancer and their detection. <i>Journal of Biology</i> , 2009, 8, 67.	2.7	50
84	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	5.8	50
85	Gammaherpesvirus Lytic Gene Expression as Characterized by DNA Array. <i>Journal of Virology</i> , 2002, 76, 6244-6256.	1.5	49
86	X-Box Binding Protein 1 Contributes to Induction of the Kaposi's Sarcoma-Associated Herpesvirus Lytic Cycle under Hypoxic Conditions. <i>Journal of Virology</i> , 2009, 83, 7202-7209.	1.5	49
87	Activation of the B Cell Antigen Receptor Triggers Reactivation of Latent Kaposi's Sarcoma-Associated Herpesvirus in B Cells. <i>Journal of Virology</i> , 2013, 87, 8004-8016.	1.5	49
88	Interferon-Induced Protein 44 and Interferon-Induced Protein 44-Like Restrict Replication of Respiratory Syncytial Virus. <i>Journal of Virology</i> , 2020, 94, .	1.5	49
89	Infectogenomics: Insights from the Host Genome into Infectious Diseases. <i>Cell</i> , 2006, 124, 695-697.	13.5	48
90	Interferon-Induced Transmembrane Protein 1 Restricts Replication of Viruses That Enter Cells via the Plasma Membrane. <i>Journal of Virology</i> , 2019, 93, .	1.5	48

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91	Post-genomic virology: the impact of bioinformatics, microarrays and proteomics on investigating host and pathogen interactions. <i>Reviews in Medical Virology</i> , 2001, 11, 313-329.	3.9	47
92	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015, 12, 726-735.	0.9	47
93	Eye on the B-ALL: B-cell receptor repertoires reveal persistence of numerous B-lymphoblastic leukemia subclones from diagnosis to relapse. <i>Leukemia</i> , 2016, 30, 2312-2321.	3.3	47
94	Mouse Models of Influenza Infection with Circulating Strains to Test Seasonal Vaccine Efficacy. <i>Frontiers in Immunology</i> , 2018, 9, 126.	2.2	46
95	Different Patterns of Epstein-Barr Virus Latency in Endemic Burkitt Lymphoma (BL) Lead to Distinct Variants within the BL-Associated Gene Expression Signature. <i>Journal of Virology</i> , 2013, 87, 2882-2894.	1.5	45
96	The antiviral restriction factor IFN-induced transmembrane protein 3 prevents cytokine-driven CMV pathogenesis. <i>Journal of Clinical Investigation</i> , 2017, 127, 1463-1474.	3.9	43
97	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012, 93, 2326-2336.	1.3	42
98	Alphavirus Restriction by <i>IFITM</i> Proteins. <i>Traffic</i> , 2016, 17, 997-1013.	1.3	42
99	Emergence of a novel subclade of influenza A(H3N2) virus in London, December 2016 to January 2017. <i>Eurosurveillance</i> , 2017, 22, .	3.9	42
100	Determining the Mutation Bias of Favipiravir in Influenza Virus Using Next-Generation Sequencing. <i>Journal of Virology</i> , 2019, 93, .	1.5	42
101	The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120382.	1.8	40
102	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
103	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017, 15, e2001855.	2.6	38
104	VIDA: a virus database system for the organization of animal virus genome open reading frames. <i>Nucleic Acids Research</i> , 2001, 29, 133-136.	6.5	34
105	Evolution of Equine Influenza Virus in Vaccinated Horses. <i>Journal of Virology</i> , 2013, 87, 4768-4771.	1.5	34
106	Endoplasmic Reticulum Degradation-Enhancing α -Mannosidase-like Protein 1 Targets Misfolded HLA-B27 Dimers for Endoplasmic Reticulum-Associated Degradation. <i>Arthritis and Rheumatology</i> , 2014, 66, 2976-2988.	2.9	33
107	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140241.	1.8	33
108	Assessment of automated genotyping protocols as tools for surveillance of HIV-1 genetic diversity. <i>Aids</i> , 2006, 20, 1521-1529.	1.0	32

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109	Bat IFITM3 restriction depends on S-palmitoylation and a polymorphic site within the CD225 domain. <i>Life Science Alliance</i> , 2020, 3, e201900542.	1.3	32
110	Role of HIV-specific CD8+ T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , 2017, 214, 3239-3261.	4.2	31
111	Attacking pathogens through their hosts. <i>Genome Biology</i> , 2006, 7, 201.	13.9	30
112	Structure and mechanism of monoclonal antibody binding to the junctional epitope of Plasmodium falciparum circumsporozoite protein. <i>PLoS Pathogens</i> , 2020, 16, e1008373.	2.1	30
113	Microarray-based determination of the lytic cascade of human herpesvirus 6B. <i>Journal of General Virology</i> , 2009, 90, 2581-2591.	1.3	28
114	Genome-Wide Innate Immune Responses in HIV-1-Infected Macrophages Are Preserved Despite Attenuation of the NF- κ B Activation Pathway. <i>Journal of Immunology</i> , 2009, 182, 319-328.	0.4	28
115	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , 2016, 2, vew005.	2.2	26
116	Transmission patterns and evolution of respiratory syncytial virus in a community outbreak identified by genomic analysis. <i>Virus Evolution</i> , 2017, 3, vex006.	2.2	26
117	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. <i>Journal of Infectious Diseases</i> , 2018, 218, 1700-1710.	1.9	25
118	Essential role of inverted repeat in Epstein-Barr virus IR-1 in B cell transformation; geographical variation of the viral genome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180299.	1.8	25
119	A high HIV-1 strain variability in London, UK, revealed by full-genome analysis: Results from the ICONIC project. <i>PLoS ONE</i> , 2018, 13, e0192081.	1.1	25
120	Heterogeneity of the Epstein-Barr Virus (EBV) Major Internal Repeat Reveals Evolutionary Mechanisms of EBV and a Functional Defect in the Prototype EBV Strain B95-8. <i>Journal of Virology</i> , 2017, 91, .	1.5	24
121	Distinct genetic architectures and environmental factors associate with host response to the β 2-herpesvirus infections. <i>Nature Communications</i> , 2020, 11, 3849.	5.8	24
122	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. <i>Virus Research</i> , 2017, 239, 10-16.	1.1	23
123	Combined Influence of B-Cell Receptor Rearrangement and Somatic Hypermutation on B-Cell Class-Switch Fate in Health and in Chronic Lymphocytic Leukemia. <i>Frontiers in Immunology</i> , 2018, 9, 1784.	2.2	22
124	Bat and pig IFN-induced transmembrane protein 3 restrict cell entry by influenza virus and lyssaviruses. <i>Journal of General Virology</i> , 2015, 96, 991-1005.	1.3	21
125	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	1.9	20
126	Assessment of a 44 Gene Classifier for the Evaluation of Chronic Fatigue Syndrome from Peripheral Blood Mononuclear Cell Gene Expression. <i>PLoS ONE</i> , 2011, 6, e16872.	1.1	19

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127	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019, 9, 10076.	1.6	19
128	Regulation of the Epstein-Barr virus Zp promoter in B lymphocytes during reactivation from latency. <i>Journal of General Virology</i> , 2010, 91, 622-629.	1.3	18
129	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
130	Nosocomial transmission of influenza: A retrospective cross-sectional study using next generation sequencing at a hospital in England (2012-2014). <i>Influenza and Other Respiratory Viruses</i> , 2019, 13, 556-563.	1.5	18
131	Permissive and restricted virus infection of murine embryonic stem cells. <i>Journal of General Virology</i> , 2012, 93, 2118-2130.	1.3	18
132	A framework for modelling virus gene expression data. <i>Intelligent Data Analysis</i> , 2002, 6, 267-279.	0.4	17
133	Restriction of V3 region sequence divergence in the HIV-1 envelope gene during antiretroviral treatment in a cohort of recent seroconverters. <i>Retrovirology</i> , 2013, 10, 8.	0.9	17
134	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
135	X-box binding protein 1 induces the expression of the lytic cycle transactivator of Kaposi's sarcoma-associated herpesvirus but not Epstein-Barr virus in co-infected primary effusion lymphoma. <i>Journal of General Virology</i> , 2011, 92, 421-431.	1.3	16
136	Autologous Antibody Capture to Enrich Immunogenic Viruses for Viral Discovery. <i>PLoS ONE</i> , 2013, 8, e78454.	1.1	16
137	Phylogenetic Analysis of Murine Leukemia Virus Sequences from Longitudinally Sampled Chronic Fatigue Syndrome Patients Suggests PCR Contamination Rather than Viral Evolution. <i>Journal of Virology</i> , 2011, 85, 10909-10913.	1.5	15
138	Segmentation and shielding of the most vulnerable members of the population as elements of an exit strategy from COVID-19 lockdown. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200275.	1.8	15
139	Host Genetic Variants and Gene Expression Patterns Associated with Epstein-Barr Virus Copy Number in Lymphoblastoid Cell Lines. <i>PLoS ONE</i> , 2014, 9, e108384.	1.1	14
140	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018, 15, 7.	0.9	13
141	Discovery of a polyomavirus in European badgers (<i>Meles meles</i>) and the evolution of host range in the family Polyomaviridae. <i>Journal of General Virology</i> , 2015, 96, 1411-1422.	1.3	12
142	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015, 12, 55.	0.9	11
143	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. <i>Genetics</i> , 2016, 202, 1449-1472.	1.2	11
144	Whole-genome association study of antibody response to Epstein-Barr virus in an African population: a pilot. <i>Global Health, Epidemiology and Genomics</i> , 2017, 2, e18.	0.2	11

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145	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. <i>Archives of Virology</i> , 2019, 164, 509-522.	0.9	11
146	Dynamic variation of CD5 surface expression levels within individual chronic lymphocytic leukemia clones. <i>Experimental Hematology</i> , 2017, 46, 31-37.e10.	0.2	10
147	Virus bioinformatics: databases and recent applications. <i>Applied Bioinformatics</i> , 2002, 1, 37-42.	1.7	10
148	Accurate characterization of the IFITM locus using MiSeq and PacBio sequencing shows genetic variation in Galliformes. <i>BMC Genomics</i> , 2017, 18, 419.	1.2	9
149	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	2.2	9
150	Rabbit endogenous retrovirus-H encodes a functional protease FN1. <i>Journal of General Virology</i> , 2003, 84, 215-225.	1.3	8
151	Similarity clustering of proteins using substantive knowledge and reconstruction of evolutionary gene histories in herpesvirus. <i>Theoretical Chemistry Accounts</i> , 2010, 125, 569-581.	0.5	8
152	Viral Bioinformatics: Computational Views of Host and Pathogen. <i>Novartis Foundation Symposium</i> , 2008, , 234-249.	1.2	6
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