

Paul Kellam

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

180
papers

13,526
citations

61
h-index

114
g-index

187
ext. papers

15,650
ext. citations

10
avg, IF

6.24
L-index

#	Paper	IF	Citations
180	Hospital outbreak of Middle East respiratory syndrome coronavirus. <i>New England Journal of Medicine</i> , 2013 , 369, 407-16	59.2	884
179	Resistance to ddl and sensitivity to AZT induced by a mutation in HIV-1 reverse transcriptase. <i>Science</i> , 1991 , 253, 1557-9	33.3	672
178	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, 4546-51	11.5	584
177	IFITM3 restricts the morbidity and mortality associated with influenza. <i>Nature</i> , 2012 , 484, 519-23	50.4	537
176	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	2.2	497
175	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, 1934-8	11.5	369
174	LEDGF/p75 functions downstream from preintegration complex formation to effect gene-specific HIV-1 integration. <i>Genes and Development</i> , 2007 , 21, 1767-78	12.6	353
173	Ordered appearance of zidovudine resistance mutations during treatment of 18 human immunodeficiency virus-positive subjects. <i>Journal of Infectious Diseases</i> , 1992 , 165, 105-10	7	340
172	Kaposi's sarcoma-associated herpesvirus latent and lytic gene expression as revealed by DNA arrays. <i>Journal of Virology</i> , 2001 , 75, 891-902	6.6	304
171	Poxvirus genomes: a phylogenetic analysis. <i>Journal of General Virology</i> , 2004 , 85, 105-117	4.9	281
170	Human infection with MERS coronavirus after exposure to infected camels, Saudi Arabia, 2013. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1012-5	10.2	260
169	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet, The</i> , 2013 , 382, 1993-2002	40	234
168	Zidovudine resistance predicted by direct detection of mutations in DNA from HIV-infected lymphocytes. <i>Aids</i> , 1991 , 5, 137-44	3.5	218
167	Elicitation of Potent Neutralizing Antibody Responses by Designed Protein Nanoparticle Vaccines for SARS-CoV-2. <i>Cell</i> , 2020 , 183, 1367-1382.e17	56.2	217
166	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	4.9	211
165	Spread, circulation, and evolution of the Middle East respiratory syndrome coronavirus. <i>MBio</i> , 2014 , 5,	7.8	207
164	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	5.9	180

163	Quantitative detection of HIV-1 drug resistance mutations by automated DNA sequencing. <i>Nature</i> , 1993 , 365, 671-3	50.4	179
162	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	2.2	177
161	Interferon-induced transmembrane protein-3 genetic variant rs12252-C is associated with severe influenza in Chinese individuals. <i>Nature Communications</i> , 2013 , 4, 1418	17.4	174
160	Zidovudine sensitivity of human immunodeficiency viruses from high-risk, symptom-free individuals during therapy. <i>Lancet, The</i> , 1990 , 336, 585-90	40	173
159	Bim-mediated deletion of antigen-specific CD8 T cells in patients unable to control HBV infection. <i>Journal of Clinical Investigation</i> , 2008 , 118, 1835-45	15.9	166
158	Kaposi 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, 10399-404	11.5	164
157	Specific capture and whole-genome sequencing of viruses from clinical samples. <i>PLoS ONE</i> , 2011 , 6, e27805	9.7	159
156	Genome diversity of Epstein-Barr virus from multiple tumor types and normal infection. <i>Journal of Virology</i> , 2015 , 89, 5222-37	6.6	150
155	Convergent combination therapy can select viable multidrug-resistant HIV-1 in vitro. <i>Nature</i> , 1993 , 365, 451-3	50.4	148
154	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	5.8	140
153	Respiratory tract samples, viral load, and genome fraction yield in patients with Middle East respiratory syndrome. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1590-4	7	131
152	Antibody response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2020 , 15, e0244136	3.6	130
151	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010 , 7, 111	3.6	128
150	KSHV-encoded miRNAs target MAF to induce endothelial cell reprogramming. <i>Genes and Development</i> , 2010 , 24, 195-205	12.6	124
149	IVA: accurate de novo assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015 , 31, 2374-6	7.2	123
148	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, 7837-52	6.6	120
147	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B	10.2	117
146	Resistance of Transmitted Founder HIV-1 to IFITM-Mediated Restriction. <i>Cell Host and Microbe</i> , 2016 , 20, 429-442	23.4	115

145	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015 , 89, 9920-31	6.6	113
144	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	7.6	113
143	Retroviral recombination can lead to linkage of reverse transcriptase mutations that confer increased zidovudine resistance. <i>Journal of Virology</i> , 1995 , 69, 669-74	6.6	107
142	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217	8.9	106
141	Consensus clustering and functional interpretation of gene-expression data. <i>Genome Biology</i> , 2004 , 5, R94	18.3	101
140	Universal amplification, next-generation sequencing, and assembly of HIV-1 genomes. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 3838-44	9.7	96
139	Network properties derived from deep sequencing of human B-cell receptor repertoires delineate B-cell populations. <i>Genome Research</i> , 2013 , 23, 1874-84	9.7	90
138	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016	3.7	89
137	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, 13578-86	6.6	89
136	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1728-1739	7	87
135	Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , 2012 , 86, 11-8	6.6	87
134	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 (Pt 2), 341-51	4.9	83
133	IFITM proteins-cellular inhibitors of viral entry. <i>Current Opinion in Virology</i> , 2014 , 4, 71-7	7.5	81
132	Amphotericin B increases influenza A virus infection by preventing IFITM3-mediated restriction. <i>Cell Reports</i> , 2013 , 5, 895-908	10.6	78
131	Genomic diversity of Epstein-Barr virus genomes isolated from primary nasopharyngeal carcinoma biopsy samples. <i>Journal of Virology</i> , 2014 , 88, 10662-72	6.6	75
130	Identification of new herpesvirus gene homologs in the human genome. <i>Genome Research</i> , 2002 , 12, 1739-48	9.7	74
129	Generation and characterization of influenza A viruses with altered polymerase fidelity. <i>Nature Communications</i> , 2014 , 5, 4794	17.4	72
128	Phylogenetic surveillance of viral genetic diversity and the evolving molecular epidemiology of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2007 , 81, 13050-6	6.6	72

127	Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: A global consortium study. <i>Science</i> , 2021 , 374, 472-478	33.3	72
126	Evolution of an Eurasian avian-like influenza virus in naïve and vaccinated pigs. <i>PLoS Pathogens</i> , 2012 , 8, e1002730	7.6	69
125	Phylogenetic studies of transmission dynamics in generalized HIV epidemics: an essential tool where the burden is greatest?. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014 , 67, 181-95 ^{3.1}	3.1	68
124	Metagenomics and the molecular identification of novel viruses. <i>Veterinary Journal</i> , 2011 , 190, 191-198	2.5	66
123	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, 63-8	10.5	65
122	Analysis of the B cell receptor repertoire in six immune-mediated diseases. <i>Nature</i> , 2019 , 574, 122-126	50.4	65
121	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2008 , 36, D414-8	20.1	64
120	Chicken interferon-inducible transmembrane protein 3 restricts influenza viruses and lyssaviruses in vitro. <i>Journal of Virology</i> , 2013 , 87, 12957-66	6.6	62
119	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, 13269-83	6.6	58
118	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	3.7	58
117	Deep sequencing of norovirus genomes defines evolutionary patterns in an urban tropical setting. <i>Journal of Virology</i> , 2014 , 88, 11056-69	6.6	57
116	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749	7.6	55
115	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	3.6	55
114	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. <i>Science Immunology</i> , 2019 , 4,	28	54
113	Local evolutionary patterns of human respiratory syncytial virus derived from whole-genome sequencing. <i>Journal of Virology</i> , 2015 , 89, 3444-54	6.6	53
112	Genomewide function conservation and phylogeny in the Herpesviridae. <i>Genome Research</i> , 2001 , 11, 43-54	9.7	51
111	Effects of discontinuation of zidovudine treatment on zidovudine sensitivity of human immunodeficiency virus type 1 isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 1993 , 37, 1525-30	5.9	50
110	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	7.6	48

109	Gammaherpesvirus lytic gene expression as characterized by DNA array. <i>Journal of Virology</i> , 2002 , 76, 6244-56	6.6	48
108	Defining the range of pathogens susceptible to Ifitm3 restriction using a knockout mouse model. <i>PLoS ONE</i> , 2013 , 8, e80723	3.7	48
107	A membrane topology model for human interferon inducible transmembrane protein 1. <i>PLoS ONE</i> , 2014 , 9, e104341	3.7	48
106	Sequence Variation of Epstein-Barr Virus: Viral Types, Geography, Codon Usage, and Diseases. <i>Journal of Virology</i> , 2018 , 92,	6.6	47
105	Natural Variation of Epstein-Barr Virus Genes, Proteins, and Primary MicroRNA. <i>Journal of Virology</i> , 2017 , 91,	6.6	46
104	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, 921-8	16.6	46
103	Infectogenomics: insights from the host genome into infectious diseases. <i>Cell</i> , 2006 , 124, 695-7	56.2	43
102	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021 , 16, e0245532	3.7	43
101	X-box binding protein 1 contributes to induction of the Kaposi sarcoma-associated herpesvirus lytic cycle under hypoxic conditions. <i>Journal of Virology</i> , 2009 , 83, 7202-9	6.6	42
100	Activation of the B cell antigen receptor triggers reactivation of latent Kaposi sarcoma-associated herpesvirus in B cells. <i>Journal of Virology</i> , 2013 , 87, 8004-16	6.6	41
99	Capturing needles in haystacks: a comparison of B-cell receptor sequencing methods. <i>BMC Immunology</i> , 2014 , 15, 29	3.7	39
98	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, 2882-94	6.6	38
97	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018 , 4, vey007	3.7	38
96	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015 , 12, 726-35	3.1	37
95	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012 , 93, 2326-2336	4.9	36
94	Infectious causes of cancer and their detection. <i>Journal of Biology</i> , 2009 , 8, 67		36
93	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	5.8	35
92	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	3.7	35

91	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , 2018 , 4, vey035	3.7	35
90	Post-genomic virology: the impact of bioinformatics, microarrays and proteomics on investigating host and pathogen interactions. <i>Reviews in Medical Virology</i> , 2001 , 11, 313-29	11.7	34
89	Emergence of a novel subclade of influenza A(H3N2) virus in London, December 2016 to January 2017. <i>Eurosurveillance</i> , 2017 , 22,	19.8	31
88	Interferon-Induced Transmembrane Protein 1 Restricts Replication of Viruses That Enter Cells via the Plasma Membrane. <i>Journal of Virology</i> , 2019 , 93,	6.6	31
87	Determining the Mutation Bias of Favipiravir in Influenza Virus Using Next-Generation Sequencing. <i>Journal of Virology</i> , 2019 , 93,	6.6	31
86	VIDA: a virus database system for the organization of animal virus genome open reading frames. <i>Nucleic Acids Research</i> , 2001 , 29, 133-6	20.1	30
85	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	10.7	30
84	Alphavirus Restriction by IFITM Proteins. <i>Traffic</i> , 2016 , 17, 997-1013	5.7	29
83	Evolution of equine influenza virus in vaccinated horses. <i>Journal of Virology</i> , 2013 , 87, 4768-71	6.6	28
82	The antiviral restriction factor IFN-induced transmembrane protein 3 prevents cytokine-driven CMV pathogenesis. <i>Journal of Clinical Investigation</i> , 2017 , 127, 1463-1474	15.9	28
81	Assessment of automated genotyping protocols as tools for surveillance of HIV-1 genetic diversity. <i>Aids</i> , 2006 , 20, 1521-9	3.5	27
80	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26
79	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV,the</i> , 2020 , 7, e173-e183	7.8	26
78	Microarray-based determination of the lytic cascade of human herpesvirus 6B. <i>Journal of General Virology</i> , 2009 , 90, 2581-2591	4.9	26
77	Endoplasmic reticulum degradation-enhancing β mannosidase-like protein 1 targets misfolded HLA-B27 dimers for endoplasmic reticulum-associated degradation. <i>Arthritis and Rheumatology</i> , 2014 , 66, 2976-88	9.5	25
76	Genome-wide innate immune responses in HIV-1-infected macrophages are preserved despite attenuation of the NF-kappa B activation pathway. <i>Journal of Immunology</i> , 2009 , 182, 319-28	5.3	25
75	Interferon-Induced Protein 44 and Interferon-Induced Protein 44-Like Restrict Replication of Respiratory Syncytial Virus. <i>Journal of Virology</i> , 2020 , 94,	6.6	24
74	Mouse Models of Influenza Infection with Circulating Strains to Test Seasonal Vaccine Efficacy. <i>Frontiers in Immunology</i> , 2018 , 9, 126	8.4	24

73	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370,	5.8	23
72	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	6.4	21
71	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	9.7	21
70	Attacking pathogens through their hosts. <i>Genome Biology</i> , 2006 , 7, 201	18.3	19
69	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017 , 216, 1063-1069	7	18
68	Transmission patterns and evolution of respiratory syncytial virus in a community outbreak identified by genomic analysis. <i>Virus Evolution</i> , 2017 , 3, vex006	3.7	17
67	Bat IFITM3 restriction depends on S-palmitoylation and a polymorphic site within the CD225 domain. <i>Life Science Alliance</i> , 2020 , 3,	5.8	17
66	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	4.9	16
65	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	3.7	16
64	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , 2016 , 2, vew005	3.7	16
63	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	16.6	15
62	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	5.8	15
61	Structure and mechanism of monoclonal antibody binding to the junctional epitope of Plasmodium falciparum circumsporozoite protein. <i>PLoS Pathogens</i> , 2020 , 16, e1008373	7.6	15
60	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	3.6	15
59	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,	6.6	15
58	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, 10909-13	6.6	15
57	Autologous antibody capture to enrich immunogenic viruses for viral discovery. <i>PLoS ONE</i> , 2013 , 8, e78454	3.7	15
56	Permissive and restricted virus infection of murine embryonic stem cells. <i>Journal of General Virology</i> , 2012 , 93, 2118-2130	4.9	15

55	Regulation of the Epstein-Barr virus Zp promoter in B lymphocytes during reactivation from latency. <i>Journal of General Virology</i> , 2010 , 91, 622-9	4.9	14
54	X-box binding protein 1 induces the expression of the lytic cycle transactivator of Kaposi sarcoma-associated herpesvirus but not Epstein-Barr virus in co-infected primary effusion lymphoma. <i>Journal of General Virology</i> , 2011 , 92, 421-31	4.9	14
53	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 ^{8.4}	8.4	14
52	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	1.6	13
51	A framework for modelling virus gene expression data. <i>Intelligent Data Analysis</i> , 2002 , 6, 267-279	1.1	13
50	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	3.7	13
49	Genome-Wide Sequence Analysis of Kaposi Sarcoma-Associated Herpesvirus Shows Diversification Driven by Recombination. <i>Journal of Infectious Diseases</i> , 2018 , 218, 1700-1710	7	13
48	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	4.9	12
47	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , 2019 , 9, 10076	4.9	12
46	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	3.7	12
45	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , 2014 , 2,		12
44	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018 , 15, 7	3.6	11
43	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 ^{5.6}	5.6	10
42	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015 , 12, 55	3.6	10
41	Distinct genetic architectures and environmental factors associate with host response to the γ -herpesvirus infections. <i>Nature Communications</i> , 2020 , 11, 3849	17.4	9
40	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intrahost HIV Infection. <i>Genetics</i> , 2016 , 202, 1449-72	4	8
39	Rabbit endogenous retrovirus-H encodes a functional protease. <i>Journal of General Virology</i> , 2003 , 84, 215-225	4.9	8
38	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. <i>Archives of Virology</i> , 2019 , 164, 509-522	2.6	8

37	Virus bioinformatics: databases and recent applications. <i>Applied Bioinformatics</i> , 2002 , 1, 37-42		8
36	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	2.9	7
35	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	5.8	7
34	Accurate characterization of the IFITM locus using MiSeq and PacBio sequencing shows genetic variation in Galliformes. <i>BMC Genomics</i> , 2017 , 18, 419	4.5	6
33	Dynamic variation of CD5 surface expression levels within individual chronic lymphocytic leukemia clones. <i>Experimental Hematology</i> , 2017 , 46, 31-37.e10	3.1	6
32	Similarity clustering of proteins using substantive knowledge and reconstruction of evolutionary gene histories in herpesvirus. <i>Theoretical Chemistry Accounts</i> , 2010 , 125, 569-581	1.9	5
31	Robust Selection of Predictive Genes via a Simple Classifier. <i>Applied Bioinformatics</i> , 2006 , 5, 1-11		5
30	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
29	Antibody response to SARS-CoV-2 infection in humans: a systematic review		5
28	Development of Lentiviral Vectors Pseudotyped With Influenza B Hemagglutinins: Application in Vaccine Immunogenicity, mAb Potency, and Sero-Surveillance Studies. <i>Frontiers in Immunology</i> , 2021 , 12, 661379	8.4	5
27	Comparative analysis of the chicken IFITM locus by targeted genome sequencing reveals evolution of the locus and positive selection in IFITM1 and IFITM3. <i>BMC Genomics</i> , 2019 , 20, 272	4.5	4
26	Modeling the association of space, time, and host species with variation of the HA, NA, and NS genes of H5N1 highly pathogenic avian influenza viruses isolated from birds in Romania in 2005-2007. <i>Avian Diseases</i> , 2013 , 57, 612-21	1.6	4
25	Viral Bioinformatics: Computational Views of Host and Pathogen. <i>Novartis Foundation Symposium</i> , 2008 , 234-249		4
24	Optimisation of memory B cell expansion/differentiation for interrogation of rare peripheral memory B cell subset responses. <i>Wellcome Open Research</i> , 2017 , 2, 97	4.8	4
23	High-throughput pipeline for the de novo viral genome assembly and the identification of minority variants from Next-Generation Sequencing of residual diagnostic samples		4
22	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4
21	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
20	Optimisation of ex vivo memory B cell expansion/differentiation for interrogation of rare peripheral memory B cell subset responses. <i>Wellcome Open Research</i> , 2017 , 2, 97	4.8	3

19	Aggregating Homologous Protein Families in Evolutionary Reconstructions of Herpesviruses 2006 ,		2
18	Protecting fetal development. <i>Science</i> , 2019 , 365, 118-119	33.3	2
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