

Paul Kellam

List of Publications by Year in Descending Order

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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	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
179	Identification of missed viruses by metagenomic sequencing of clinical respiratory samples from Kenya.. <i>Scientific Reports</i> , 2022 , 12, 202	4.9	1
178	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , 2022 , 8, veac022	3.7	
177	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
176	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
175	Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: A global consortium study. <i>Science</i> , 2021 , 374, 472-478	33.3	72
174	T cell response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2021 , 16, e0245532	3.7	43
173	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
172	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
171	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
170	Recombination Analysis of Near Full-Length HIV-1 Sequences and the Identification of a Potential New Circulating Recombinant Form from Rakai, Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020 , 36, 467-474	1.6	1
169	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	7.8	26
168	Antibody response to SARS-CoV-2 infection in humans: A systematic review. <i>PLoS ONE</i> , 2020 , 15, e0244126	3.7	130
167	Antibody response to SARS-CoV-2 infection in humans: A systematic review 2020 , 15, e0244126		1
166	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
165	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
164	Distinct genetic architectures and environmental factors associate with host response to the β -herpesvirus infections. <i>Nature Communications</i> , 2020 , 11, 3849	17.4	9

163	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
162	Antibody response to SARS-CoV-2 infection in humans: A systematic review 2020 , 15, e0244126		
161	Antibody response to SARS-CoV-2 infection in humans: A systematic review 2020 , 15, e0244126		
160	Antibody response to SARS-CoV-2 infection in humans: A systematic review 2020 , 15, e0244126		
159	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	10
158	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
157	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
156	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
155	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
154	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. <i>Science Immunology</i> , 2019 , 4,	28	54
153	Protecting fetal development. <i>Science</i> , 2019 , 365, 118-119	33.3	2
152	Analysis of the B cell receptor repertoire in six immune-mediated diseases. <i>Nature</i> , 2019 , 574, 122-126	50.4	65
151	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
150	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
149	Determining the Mutation Bias of Favipiravir in Influenza Virus Using Next-Generation Sequencing. <i>Journal of Virology</i> , 2019 , 93,	6.6	31
148	Human Coronavirus NL63 Molecular Epidemiology and Evolutionary Patterns in Rural Coastal Kenya. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1728-1739	7	87
147	Mouse Models of Influenza Infection with Circulating Strains to Test Seasonal Vaccine Efficacy. <i>Frontiers in Immunology</i> , 2018 , 9, 126	8.4	24
146	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

145	Sequence Variation of Epstein-Barr Virus: Viral Types, Geography, Codon Usage, and Diseases. <i>Journal of Virology</i> , 2018 , 92,	6.6	47
144	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
143	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
142	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
141	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
140	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
139	Natural Variation of Epstein-Barr Virus Genes, Proteins, and Primary MicroRNA. <i>Journal of Virology</i> , 2017 , 91,	6.6	46
138	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
137	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
136	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017 , 216, 1063-1069	7	18
135	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749	7.6	55
134	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
133	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
132	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
131	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
130	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
129	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
128	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

127	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
126	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
125	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
124	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
123	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , 2016 , 202, 1449-72	4	8
122	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217	8.9	106
121	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
120	Complete Genome Characterization of Two Wild-Type Measles Viruses from Vietnamese Infants during the 2014 Outbreak. <i>Genome Announcements</i> , 2016 , 4,		2
119	Genome Sequences of a Novel Vietnamese Bat Bunyavirus. <i>Genome Announcements</i> , 2016 , 4,		2
118	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
117	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
116	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , 2016 , 2, vew005	3.7	16
115	Resistance of Transmitted Founder HIV-1 to IFITM-Mediated Restriction. <i>Cell Host and Microbe</i> , 2016 , 20, 429-442	23.4	115
114	Alphavirus Restriction by IFITM Proteins. <i>Traffic</i> , 2016 , 17, 997-1013	5.7	29
113	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
112	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
111	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
110	IVA: accurate de novo assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015 , 31, 2374-6	7.2	123

109	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
108	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
107	Disease progression despite protective HLA expression in an HIV-infected transmission pair. <i>Retrovirology</i> , 2015 , 12, 55	3.6	10
106	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
105	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
104	IFITM proteins-cellular inhibitors of viral entry. <i>Current Opinion in Virology</i> , 2014 , 4, 71-7	7.5	81
103	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
102	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
101	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
100	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
99	Generation and characterization of influenza A viruses with altered polymerase fidelity. <i>Nature Communications</i> , 2014 , 5, 4794	17.4	72
98	Capturing needles in haystacks: a comparison of B-cell receptor sequencing methods. <i>BMC Immunology</i> , 2014 , 15, 29	3.7	39
97	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
96	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
95	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
94	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
93	Complete Genome Sequence of the WHO International Standard for HIV-1 RNA Determined by Deep Sequencing. <i>Genome Announcements</i> , 2014 , 2,		12
92	Spread, circulation, and evolution of the Middle East respiratory syndrome coronavirus. <i>MBio</i> , 2014 , 5,	7.8	207

91	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}		68
90	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
89	A membrane topology model for human interferon inducible transmembrane protein 1. <i>PLoS ONE</i> , 2014 , 9, e104341	3.7	48
88	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
87	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	4.0	234
86	Hospital outbreak of Middle East respiratory syndrome coronavirus. <i>New England Journal of Medicine</i> , 2013 , 369, 407-16	59.2	884
85	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
84	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
83	Amphotericin B increases influenza A virus infection by preventing IFITM3-mediated restriction. <i>Cell Reports</i> , 2013 , 5, 895-908	10.6	78
82	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
81	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
80	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
79	Evolution of equine influenza virus in vaccinated horses. <i>Journal of Virology</i> , 2013 , 87, 4768-71	6.6	28
78	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B	10.2	117
77	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, 8004-16	6.6	41
76	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
75	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
74	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

73	Autologous antibody capture to enrich immunogenic viruses for viral discovery. <i>PLoS ONE</i> , 2013 , 8, e78454	3.4	15
72	Defining the range of pathogens susceptible to Ifitm3 restriction using a knockout mouse model. <i>PLoS ONE</i> , 2013 , 8, e80723	3.7	48
71	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012 , 93, 2326-2336	4.9	36
70	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
69	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
68	Evolution of an Eurasian avian-like influenza virus in naïve and vaccinated pigs. <i>PLoS Pathogens</i> , 2012 , 8, e1002730	7.6	69
67	Universal amplification, next-generation sequencing, and assembly of HIV-1 genomes. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 3838-44	9.7	96
66	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
65	IFITM3 restricts the morbidity and mortality associated with influenza. <i>Nature</i> , 2012 , 484, 519-23	50.4	537
64	Permissive and restricted virus infection of murine embryonic stem cells. <i>Journal of General Virology</i> , 2012 , 93, 2118-2130	4.9	15
63	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
62	Metagenomics and the molecular identification of novel viruses. <i>Veterinary Journal</i> , 2011 , 190, 191-198	2.5	66
61	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
60	Specific capture and whole-genome sequencing of viruses from clinical samples. <i>PLoS ONE</i> , 2011 , 6, e27805	3.7	159
59	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, 421-31	4.9	14
58	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
57	KSHV-encoded miRNAs target MAF to induce endothelial cell reprogramming. <i>Genes and Development</i> , 2010 , 24, 195-205	12.6	124
56	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

55	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010 , 7, 111	3.6	128
54	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
53	Microarray-based determination of the lytic cascade of human herpesvirus 6B. <i>Journal of General Virology</i> , 2009 , 90, 2581-2591	4.9	26
52	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, 7202-9	6.6	42
51	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
50	Infectious causes of cancer and their detection. <i>Journal of Biology</i> , 2009 , 8, 67		36
49	Viral Bioinformatics: Computational Views of Host and Pathogen. <i>Novartis Foundation Symposium</i> , 2008 , 234-249		4
48	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2008 , 36, D414-8	20.1	64
47	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
46	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
45	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
44	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
43	Attacking pathogens through their hosts. <i>Genome Biology</i> , 2006 , 7, 201	18.3	19
42	Robust Selection of Predictive Genes via a Simple Classifier. <i>Applied Bioinformatics</i> , 2006 , 5, 1-11		5
41	Aggregating Homologous Protein Families in Evolutionary Reconstructions of Herpesviruses 2006 ,		2
40	Infectogenomics: insights from the host genome into infectious diseases. <i>Cell</i> , 2006 , 124, 695-7	56.2	43
39	Assessment of automated genotyping protocols as tools for surveillance of HIV-1 genetic diversity. <i>Aids</i> , 2006 , 20, 1521-9	3.5	27
38	Poxvirus genomes: a phylogenetic analysis. <i>Journal of General Virology</i> , 2004 , 85, 105-117	4.9	281

37	Consensus clustering and functional interpretation of gene-expression data. <i>Genome Biology</i> , 2004 , 5, R94	18.3	101
36	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, 10399-404	11.5	164
35	Rabbit endogenous retrovirus-H encodes a functional protease. <i>Journal of General Virology</i> , 2003 , 84, 215-225	4.9	8
34	Identification of new herpesvirus gene homologs in the human genome. <i>Genome Research</i> , 2002 , 12, 1739-48	9.7	74
33	Gammaherpesvirus lytic gene expression as characterized by DNA array. <i>Journal of Virology</i> , 2002 , 76, 6244-56	6.6	48
32	A framework for modelling virus gene expression data. <i>Intelligent Data Analysis</i> , 2002 , 6, 267-279	1.1	13
31	Virus bioinformatics: databases and recent applications. <i>Applied Bioinformatics</i> , 2002 , 1, 37-42		8
30	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
29	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
28	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
27	Genomewide function conservation and phylogeny in the Herpesviridae. <i>Genome Research</i> , 2001 , 11, 43-54	9.7	51
26	Gene expression following HIV-1 infection. <i>Genome Biology</i> , 2000 , 1, 1	18.3	
25	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
24	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
23	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
22	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
21	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
20	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

19	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
18	Convergent combination therapy can select viable multidrug-resistant HIV-1 in vitro. <i>Nature</i> , 1993 , 365, 451-3	50.4	148
17	Quantitative detection of HIV-1 drug resistance mutations by automated DNA sequencing. <i>Nature</i> , 1993 , 365, 671-3	50.4	179
16	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
15	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
14	Zidovudine resistance predicted by direct detection of mutations in DNA from HIV-infected lymphocytes. <i>Aids</i> , 1991 , 5, 137-44	3.5	218
13	Resistance to ddI and sensitivity to AZT induced by a mutation in HIV-1 reverse transcriptase. <i>Science</i> , 1991 , 253, 1557-9	33.3	672
12	The isolation and characterisation of plant sequences homologous to human hypervariable minisatellites. <i>Exs</i> , 1991 , 58, 330-41		1
11	Zidovudine sensitivity of human immunodeficiency viruses from high-risk, symptom-free individuals during therapy. <i>Lancet, The</i> , 1990 , 336, 585-90	40	173
10	Optimisation of ex vivo memory B cell expansion/differentiation for interrogation of rare peripheral memory B cell subset responses. <i>Wellcome Open Research</i> , 2 , 97	4.8	3
9	A computational method for immune repertoire mining that identifies novel binders from different clonotypes, demonstrated by identifying anti-Pertussis toxoid antibodies		1
8	Antibody response to SARS-CoV-2 infection in humans: a systematic review		5
7	Cellular immune response to SARS-CoV-2 infection in humans: a systematic review		2
6	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
5	Easy and Accurate Reconstruction of Whole HIV Genomes from Short-Read Sequence Data		4
4	Determining the Mutation Bias of Favipiravir in Influenza Using Next-generation Sequencing		2
3	Coalescent inference using serially sampled, high-throughput sequencing data from intra-host HIV infection		1
2	A High HIV-1 Strain Variability in London, UK, Revealed by Full-Genome Analysis: Results from the ICONIC Project		1

1 MERS-CoV spillover at the camel-human interface

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