Peter Simmonds

List of Publications by Year in descending order

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546 papers	51,863 citations	944 115 h-index	2500 196 g-index
589 all docs	589 docs citations	589 times ranked	32081 citing authors

#	Article	IF	Citations
1	Classification of hepatitis C virus into six major genotypes and a series of subtypes by phylogenetic analysis of the NS-5 region. Journal of General Virology, 1993, 74, 2391-2399.	1.3	1,340
2	Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. Hepatology, 2005, 42, 962-973.	3.6	1,303
3	Expanded classification of hepatitis C virus into 7 genotypes and 67 subtypes: Updated criteria and genotype assignment web resource. Hepatology, 2014, 59, 318-327.	3.6	1,141
4	Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. Nature Immunology, 2020, 21, 1336-1345.	7.0	1,066
5	A proposed system for the nomenclature of hepatitis C viral genotypes. Hepatology, 1994, 19, 1321-1324.	3.6	962
6	Genetic diversity and evolution of hepatitis C virus â€“ 15â€…years on. Journal of General Virology, 2004, 85, 3173-3188.	1.3	772
7	Human immunodeficiency virus-infected individuals contain provirus in small numbers of peripheral mononuclear cells and at low copy numbers. Journal of Virology, 1990, 64, 864-872.	1.5	625
8	Prevalence of Kaposi's sarcoma associated herpesvirus infection measured by antibodies to recombinant capsid protein and latent immunofluorescence antigen. Lancet, The, 1996, 348, 1133-1138.	6.3	608
9	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	13.6	590
10	Epidemiology and Clinical Presentations of the Four Human Coronaviruses 229E, HKU1, NL63, and OC43 Detected over 3 Years Using a Novel Multiplex Real-Time PCR Method. Journal of Clinical Microbiology, 2010, 48, 2940-2947.	1.8	585
11	Consensus proposals for classification of the family Hepeviridae. Journal of General Virology, 2014, 95, 2223-2232.	1.3	570
12	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). Archives of Virology, 2018, 163, 2601-2631.	0.9	567
13	ICTV Virus Taxonomy Profile: Flaviviridae. Journal of General Virology, 2017, 98, 2-3.	1.3	537
14	Variability of hepatitis C virus. Hepatology, 1995, 21, 570-583.	3.6	531
15	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). Archives of Virology, 2017, 162, 2505-2538.	0.9	506
16	Selection for specific sequences in the external envelope protein of human immunodeficiency virus type 1 upon primary infection. Journal of Virology, 1993, 67, 3345-3356.	1.5	503
17	Hepatitis C virus genotypes: An investigation of type-specific differences in geographic origin and disease. Hepatology, 1994, 19, 13-18.	3.6	481
18	Sequence variability in the 5' non-coding region of hepatitis C virus: identification of a new virus type and restrictions on sequence diversity. Journal of General Virology, 1993, 74, 661-668.	1.3	444

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19	Analysis of a new hepatitis C virus type and its phylogenetic relationship to existing variants. Journal of General Virology, 1992, 73, 1131-1141.	1.3	427
20	Classification, nomenclature, and database development for hepatitis C virus (HCV) and related viruses: proposals for standardization. Archives of Virology, 1998, 143, 2493-2503.	0.9	427
21	Survey of major genotypes and subtypes of hepatitis C virus using RFLP of sequences amplified from the 5' non-coding region. Journal of General Virology, 1995, 76, 1197-1204.	1.3	420
22	Detection of a novel DNA virus (TT virus) in blood donors and blood products. Lancet, The, 1998, 352, 191-195.	6.3	399
23	ICTV Virus Taxonomy Profile: Picornaviridae. Journal of General Virology, 2017, 98, 2421-2422.	1.3	374
24	New DNA Viruses Identified in Patients with Acute Viral Infection Syndrome. Journal of Virology, 2005, 79, 8230-8236.	1.5	350
25	Proposed reference sequences for hepatitis E virus subtypes. Journal of General Virology, 2016, 97, 537-542.	1.3	339
26	Analysis of sequence diversity in hypervariable regions of the external glycoprotein of human immunodeficiency virus type 1. Journal of Virology, 1990, 64, 5840-5850.	1.5	330
27	Human Bocaviruses Are Highly Diverse, Dispersed, Recombination Prone, and Prevalent in Enteric Infections. Journal of Infectious Diseases, 2010, 201, 1633-1643.	1.9	320
28	Detection of Zoonotic Pathogens and Characterization of Novel Viruses Carried by Commensal Rattus norvegicus in New York City. MBio, 2014, 5, e01933-14.	1.8	310
29	Early and nonreversible decrease of CD161++/MAIT cells in HIV infection. Blood, 2013, 121, 951-961.	0.6	307
30	Extrahepatic Immunologic Manifestations in Chronic Hepatitis C and Hepatitis C Virus Serotypes. Annals of Internal Medicine, 1995, 122, 169.	2.0	295
31	Detection of three types of hepatitis C virus in blood donors: investigation of type-specific differences in serologic reactivity and rate of alanine aminotransferase abnormalities. Transfusion, 1993, 33, 7-13.	0.8	292
32	The Fecal Virome of Pigs on a High-Density Farm. Journal of Virology, 2011, 85, 11697-11708.	1.5	289
33	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	0.9	285
34	A Newly Identified Bocavirus Species in Human Stool. Journal of Infectious Diseases, 2009, 199, 196-200.	1.9	283
35	SARS-CoV-2 within-host diversity and transmission. Science, 2021, 372, .	6.0	278
36	Identification of Genotypes of Hepatitis C Virus by Sequence Comparisons in the Core, E1 and NS-5 Regions. Journal of General Virology, 1994, 75, 1053-1061.	1.3	264

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37	Proposed revision to the taxonomy of the genus Pestivirus, family Flaviviridae. Journal of General Virology, 2017, 98, 2106-2112.	1.3	264
38	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	0.9	263
39	Convergent and divergent sequence evolution in the surface envelope glycoprotein of human immunodeficiency virus type 1 within a single infected patient.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 4835-4839.	3.3	262
40	The origin of hepatitis C virus genotypes.. Journal of General Virology, 1997, 78, 321-328.	1.3	259
41	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). Archives of Virology, 2019, 164, 2417-2429.	0.9	257
42	Mapping of serotype-specific, immunodominant epitopes in the NS-4 region of hepatitis C virus (HCV): use of type-specific peptides to serologically differentiate infections with HCV types 1, 2, and 3. Journal of Clinical Microbiology, 1993, 31, 1493-1503.	1.8	255
43	The GB viruses: a review and proposed classification of GBV-A, GBV-C (HGV), and GBV-D in genus Pegivirus within the family Flaviviridae. Journal of General Virology, 2011, 92, 233-246.	1.3	251
44	Characterization of a canine homolog of hepatitis C virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11608-11613.	3.3	250
45	Influence of HAART on HIV-Related CNS Disease and Neuroinflammation. Journal of Neuropathology and Experimental Neurology, 2005, 64, 529-536.	0.9	249
46	Investigation of the pattern of hepatitis C virus sequence diversity in different geographical regions: implications for virus classification. Journal of General Virology, 1995, 76, 2493-2507.	1.3	249
47	Concurrent evolution of human immunodeficiency virus type 1 in patients infected from the same source: rate of sequence change and low frequency of inactivating mutations. Journal of Virology, 1990, 64, 6221-6233.	1.5	238
48	Infection with hepatitis G virus among recipients of plasma products. Lancet, The, 1996, 348, 1352-1355.	6.3	236
49	Hepatitis C quantification and sequencing in blood products, haemophiliacs, and drug users. Lancet, The, 1990, 336, 1469-1472.	6.3	235
50	Epidemiological Profile and Clinical Associations of Human Bocavirus and Other Human Parvoviruses. Journal of Infectious Diseases, 2006, 194, 1283-1290.	1.9	234
51	Frequency and Dynamics of Recombination within Different Species of Human Enteroviruses. Journal of Virology, 2006, 80, 483-493.	1.5	233
52	SSE: a nucleotide and amino acid sequence analysis platform. BMC Research Notes, 2012, 5, 50.	0.6	233
53	High Variety of Known and New RNA and DNA Viruses of Diverse Origins in Untreated Sewage. Journal of Virology, 2012, 86, 12161-12175.	1.5	231
54	Variation of the hepatitis C virus 5' non-coding region: implications for secondary structure, virus detection and typing. Journal of General Virology, 1995, 76, 1749-1761.	1.3	229

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55	Discontinuous sequence change of human immunodeficiency virus (HIV) type 1 env sequences in plasma viral and lymphocyte-associated proviral populations in vivo: implications for models of HIV pathogenesis. Journal of Virology, 1991, 65, 6266-6276.	1.5	227
56	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	0.9	224
57	Update: proposed reference sequences for subtypes of hepatitis E virus (species Orthohepevirus A). Journal of General Virology, 2020, 101, 692-698.	1.3	221
58	Serology-Enabled Discovery of Genetically Diverse Hepaciviruses in a New Host. Journal of Virology, 2012, 86, 6171-6178.	1.5	219
59	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	0.9	219
60	Application of Six Hepatitis C Virus Genotyping Systems to Sera from Chronic Hepatitis C Patients in the United States. Journal of Infectious Diseases, 1995, 171, 281-289.	1.9	214
61	Recombination in the Genesis and Evolution of Hepatitis B Virus Genotypes. Journal of Virology, 2005, 79, 15467-15476.	1.5	214
62	A proposed system for the nomenclature of hepatitis C viral genotypes. Hepatology, 1994, 19, 1321-4.	3.6	213
63	2000 Fleming Lecture. The origin and evolution of hepatitis viruses in humans. Journal of General Virology, 2001, 82, 693-712.	1.3	207
64	Epidemiology and Clinical Associations of Human Parechovirus Respiratory Infections. Journal of Clinical Microbiology, 2008, 46, 3446-3453.	1.8	206
65	Rampant Câ†'U Hypermutation in the Genomes of SARS-CoV-2 and Other Coronaviruses: Causes and Consequences for Their Short- and Long-Term Evolutionary Trajectories. MSphere, 2020, 5, .	1.3	204
66	Viral heterogeneity of the hepatitis C virus. Journal of Hepatology, 1999, 31, 54-60.	1.8	202
67	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	0.9	202
68	Norovirus Regulation of the Innate Immune Response and Apoptosis Occurs via the Product of the Alternative Open Reading Frame 4. PLoS Pathogens, 2011, 7, e1002413.	2.1	200
69	Proposals for the classification of human rhinovirus species C into genotypically assigned types. Journal of General Virology, 2010, 91, 2409-2419.	1.3	199
70	Virus 'quasispecies': making a mountain out of a molehill?. Journal of General Virology, 1997, 78, 1511-1519.	1.3	194
71	Proposals for the classification of human rhinovirus species A, B and C into genotypically assigned types. Journal of General Virology, 2013, 94, 1791-1806.	1.3	190
72	HLA HAPLOTYPE A1 B8 DR3 AS A RISK FACTOR FOR HIV-RELATED DISEASE. Lancet, The, 1988, 331, 1185-1188.	6.3	189

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73	Cerebral Infarction in Adult AIDS Patients. Stroke, 2000, 31, 2117-2126.	1.0	189
74	Identification of Rodent Homologs of Hepatitis C Virus and Pegiviruses. MBio, 2013, 4, e00216-13.	1.8	187
75	HIV encephalitis, proviral load and dementia in drug users and homosexuals with AIDS. Effect of neocortical involvement. Brain, 1998, 121, 2043-2052.	3.7	185
76	Detection of genome-scale ordered RNA structure (GORS) in genomes of positive-stranded RNA viruses: Implications for virus evolution and host persistence. Rna, 2004, 10, 1337-1351.	1.6	184
77	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	0.9	184
78	Distribution of Hepatitis C Virus Genotypes Determined by Line Probe Assay in Patients with Chronic Hepatitis C Seen at Tertiary Referral Centers in the United States. Annals of Internal Medicine, 1996, 124, 868.	2.0	183
79	Complete nucleotide sequence of a type 4 hepatitis C virus variant, the predominant genotype in the Middle East.. Journal of General Virology, 1997, 78, 1341-1347.	1.3	182
80	Human parechoviruses: Biology, epidemiology and clinical significance. Journal of Clinical Virology, 2009, 45, 1-9.	1.6	182
81	Identification of Shared Populations of Human Immunodeficiency Virus Type 1 Infecting Microglia and Tissue Macrophages outside the Central Nervous System. Journal of Virology, 2001, 75, 11686-11699.	1.5	181
82	A highly prevalent and genetically diversified Picornaviridae genus in South Asian children. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20482-20487.	3.3	179
83	Severity of liver disease in liver transplantation recipients with hepatitis C virus infection: Relationship to genotype and level of viremia. Hepatology, 1996, 24, 1041-1046.	3.6	178
84	Biological Analysis of Human Immunodeficiency Virus Type 1 R5 Envelopes Amplified from Brain and Lymph Node Tissues of AIDS Patients with Neuropathology Reveals Two Distinct Tropism Phenotypes and Identifies Envelopes in the Brain That Confer an Enhanced Tropism and Fusigenicity for Macrophages. Journal of Virology, 2004, 78, 6915-6926.	1.5	177
85	Recombination and Selection in the Evolution of Picornaviruses and Other Mammalian Positive-Stranded RNA Viruses. Journal of Virology, 2006, 80, 11124-11140.	1.5	172
86	Comparison of plasma virus loads among individuals infected with hepatitis C virus (HCV) genotypes 1, 2, and 3 by quantiplex HCV RNA assay versions 1 and 2, Roche Monitor assay, and an in-house limiting dilution method. Journal of Clinical Microbiology, 1997, 35, 187-192.	1.8	168
87	Recommendations for enterovirus diagnostics and characterisation within and beyond Europe. Journal of Clinical Virology, 2018, 101, 11-17.	1.6	161
88	Infrequent Vertical Transmission of Hepatitis C Virus. Journal of Infectious Diseases, 1993, 167, 572-576.	1.9	160
89	The influence of CpG and UpA dinucleotide frequencies on RNA virus replication and characterization of the innate cellular pathways underlying virus attenuation and enhanced replication. Nucleic Acids Research, 2014, 42, 4527-4545.	6.5	160
90	Human Immunodeficiency Virus and the Brain: Investigation of Virus Load and Neuropathologic Changes in Pre-AIDS Subjects. Journal of Infectious Diseases, 1993, 168, 818-824.	1.9	159

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91	Comparison of Tissue Distribution, Persistence, and Molecular Epidemiology of Parvovirus B19 and Novel Human Parvoviruses PARV4 and Human Bocavirus. Journal of Infectious Diseases, 2007, 195, 1345-1352.	1.9	158
92	Specific Association of Human Parechovirus Type 3 with Sepsis and Fever in Young Infants, as Identified by Direct Typing of Cerebrospinal Fluid Samples. Journal of Infectious Diseases, 2009, 199, 1753-1760.	1.9	158
93	Molecular epidemiology of an outbreak of infection with hepatitis C virus in recipients of anti-D immunoglobulin. Lancet, The, 1995, 345, 1211-1213.	6.3	157
94	Detection of parvovirus B19 in donated blood: a model system for screening by polymerase chain reaction. Journal of Clinical Microbiology, 1993, 31, 323-328.	1.8	156
95	HIV-1 tropism and co-receptor use. Nature, 1997, 385, 495-496.	13.7	151
96	The Origin of Hepatitis C Virus. Current Topics in Microbiology and Immunology, 2013, 369, 1-15.	0.7	149
97	RNA virus attenuation by codon pair deoptimisation is an artefact of increases in CpG/UpA dinucleotide frequencies. ELife, 2014, 3, e04531.	2.8	148
98	Accelerated Tau deposition in the brains of individuals infected with human immunodeficiency virus-1 before and after the advent of highly active anti-retroviral therapy. Acta Neuropathologica, 2006, 111, 529-538.	3.9	146
99	Use of NS-4 peptides to identify type-specific antibody to hepatitis C virus genotypes 1, 2, 3, 4, 5 and 6. Journal of General Virology, 1995, 76, 1737-1748.	1.3	145
100	The hepatitis C virus epidemic among injecting drug users. Infection, Genetics and Evolution, 2005, 5, 131-139.	1.0	143
101	Frequent Reinfection And Reactivation Of Hepatitis C Virus Genotypes In Multitransfused Hemophiliacs. Journal of Infectious Diseases, 1994, 170, 1018-1022.	1.9	141
102	Structural Constraints on RNA Virus Evolution. Journal of Virology, 1999, 73, 5787-5794.	1.5	140
103	Proposed update to the taxonomy of the genera Hepacivirus and Pegivirus within the Flaviviridae family. Journal of General Virology, 2016, 97, 2894-2907.	1.3	139
104	A proposed system for the nomenclature of hepatitis C viral genotypes. Hepatology, 1994, 19, 1321-1324.	3.6	136
105	Evolutionary analysis of variants of hepatitis C virus found in South-East Asia: comparison with classifications based upon sequence similarity. Journal of General Virology, 1996, 77, 3013-3024.	1.3	136
106	Screening Respiratory Samples for Detection of Human Rhinoviruses (HRVs) and Enteroviruses: Comprehensive VP4-VP2 Typing Reveals High Incidence and Genetic Diversity of HRV Species C. Journal of Clinical Microbiology, 2009, 47, 3958-3967.	1.8	135
107	Hepatitis C virus genotypes: an investigation of type-specific differences in geographic origin and disease. Hepatology, 1994, 19, 13-8.	3.6	135
108	Frequent infection of peripheral blood CD8-positive T-lymphocytes with HIV-1. Lancet, The, 1996, 348, 649-654.	6.3	133

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109	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. Nature Genetics, 2017, 49, 666-673.	9.4	129
110	Parechoviruses in children: understanding a new infection. Current Opinion in Infectious Diseases, 2010, 23, 224-230.	1.3	128
111	Global Distribution of Transfusion-Transmitted Virus. New England Journal of Medicine, 1998, 339, 776-777.	13.9	127
112	Hepatitis C Serotype and Response to Interferon Therapy. New England Journal of Medicine, 1994, 330, 143-143.	13.9	126
113	Spread of Hepatitis C Virus among European Injection Drug Users Infected with HIV: A Phylogenetic Analysis. Journal of Infectious Diseases, 2004, 189, 292-302.	1.9	126
114	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). Archives of Virology, 2015, 160, 1837-1850.	0.9	126
115	A Highly Divergent Picornavirus in a Marine Mammal. Journal of Virology, 2008, 82, 311-320.	1.5	125
116	Nomenclature and Numbering of the Hepatitis C Virus. Methods in Molecular Biology, 2009, 510, 33-53.	0.4	124
117	Genetic Variability and the Classification of Hepatitis E Virus. Journal of Virology, 2013, 87, 4161-4169.	1.5	122
118	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	0.9	122
119	Prisoners of war â€" host adaptation and its constraints on virus evolution. Nature Reviews Microbiology, 2019, 17, 321-328.	13.6	117
120	No evidence for an association between infections with WU and KI polyomaviruses and respiratory disease. Journal of Clinical Virology, 2007, 40, 307-311.	1.6	115
121	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	0.9	115
122	Survey of type 6 group variants of hepatitis C virus in Southeast Asia by using a core-based genotyping assay. Journal of Clinical Microbiology, 1996, 34, 417-423.	1.8	113
123	Thermodynamic and phylogenetic prediction of RNA secondary structures in the coding region of hepatitis C virus. Rna, 2002, 8, 824-841.	1.6	112
124	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. Journal of Clinical Microbiology, 2016, 54, 2470-2484.	1.8	112
125	Low level or absent in vivo replication of hepatitis C virus and hepatitis G virus/GB virus C in peripheral blood mononuclear cells.. Journal of General Virology, 1998, 79, 705-714.	1.3	110
126	Long-Term Evolution of the Hypervariable Region of Hepatitis C Virus in a Common-Source-Infected Cohort. Journal of Virology, 1998, 72, 4893-4905.	1.5	108

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127	The Association of Recombination Events in the Founding and Emergence of Subgenogroup Evolutionary Lineages of Human Enterovirus 71. Journal of Virology, 2012, 86, 2676-2685.	1.5	107
128	Bioinformatic and functional analysis of RNA secondary structure elements among different genera of human and animal caliciviruses. Nucleic Acids Research, 2008, 36, 2530-2546.	6.5	106
129	Detection, quantification and sequencing of HIV-1 from the plasma of seropositive individuals and from factor VIII concentrates. Aids, 1991, 5, 675-682.	1.0	105
130	A comprehensive system for consistent numbering of HCV sequences, proteins and epitopes. Hepatology, 2006, 44, 1355-1361.	3.6	105
131	Serological responses to infection with three different types of hepatitis C virus. Lancet, The, 1991, 338, 1391.	6.3	104
132	Discrimination of hepatitis G virus/GBV-C geographical variants by analysis of the 5' non-coding region.. Journal of General Virology, 1997, 78, 1533-1542.	1.3	104
133	Early Acquisition of TT Virus (TTV) in an Area Endemic for TTV Infection. Journal of Infectious Diseases, 1999, 179, 1070-1076.	1.9	103
134	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). Archives of Virology, 2019, 164, 943-946.	0.9	102
135	Detection of Hepatitis B Virus Infection in Wild-Born Chimpanzees (Pan troglodytes verus): Phylogenetic Relationships with Human and Other Primate Genotypes. Journal of Virology, 2000, 74, 4253-4257.	1.5	101
136	Comparison of human parechovirus and enterovirus detection frequencies in cerebrospinal fluid samples collected over a 5â€yyear period in edinburgh: HPeV type 3 identified as the most common picornavirus type. Journal of Medical Virology, 2011, 83, 889-896.	2.5	100
137	In vivo distribution and cytopathology of variants of human immunodeficiency virus type 1 showing restricted sequence variability in the V3 loop. Journal of Virology, 1994, 68, 5991-6005.	1.5	100
138	Investigation of the dynamics of the spread of human immunodeficiency virus to brain and other tissues by evolutionary analysis of sequences from the p17gag and env genes. Journal of Virology, 1997, 71, 1272-1280.	1.5	100
139	Detailed mapping of RNA secondary structures in core and NS5B-encoding region sequences of hepatitis C virus by RNase cleavage and novel bioinformatic prediction methods. Journal of General Virology, 2004, 85, 3037-3047.	1.3	99
140	Antiviral RNA Interference Responses Induced by Semliki Forest Virus Infection of Mosquito Cells: Characterization, Origin, and Frequency-Dependent Functions of Virus-Derived Small Interfering RNAs. Journal of Virology, 2011, 85, 2907-2917.	1.5	99
141	Implications of variations of "conserved" regions of hepatitis C virus genome. Lancet, The, 1995, 346, 425-426.	6.3	98
142	Nonprimate Hepaciviruses in Domestic Horses, United Kingdom. Emerging Infectious Diseases, 2012, 18, 1976-1982.	2.0	98
143	Use of several second generation serological assays to determine the true prevalence of hepatitis C virus infection in haemophiliacs treated with nonâ€virus inactivated factor VIII and IX concentrates. British Journal of Haematology, 1992, 80, 514-518.	1.2	97
144	A Hepatitis C Virus cis -Acting Replication Element Forms a Long-Range RNA-RNA Interaction with Upstream RNA Sequences in NS5B. Journal of Virology, 2008, 82, 9008-9022.	1.5	97

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145	Reactivation and Mutation of Newly Discovered WU, KI, and Merkel Cell Carcinoma Polyomaviruses in Immunosuppressed Individuals. Journal of Infectious Diseases, 2009, 199, 398-404.	1.9	97
146	Molecular Investigation of Human Immunodeficiency Virus (HIV) Infection in a Patient of an HIV-Infected Surgeon. Journal of Infectious Diseases, 1993, 167, 1411-1414.	1.9	96
147	Redistribution of HIV outside the lymphoid system with onset of AIDS. Lancet, The, 1994, 343, 382-385.	6.3	96
148	Transmission Networks and Population Turnover of Echovirus 30. Journal of Virology, 2009, 83, 2109-2118.	1.5	96
149	Characteristics of Nucleotide Substitution in the Hepatitis C Virus Genome: Constraints on Sequence Change in Coding Regions at Both Ends of the Genome. Journal of Molecular Evolution, 1997, 45, 238-246.	0.8	95
150	Non-Macrophage-Tropic Human Immunodeficiency Virus Type 1 R5 Envelopes Predominate in Blood, Lymph Nodes, and Semen: Implications for Transmission and Pathogenesis. Journal of Virology, 2006, 80, 6324-6332.	1.5	95
151	Evolutionary Dynamics and Temporal/Geographical Correlates of Recombination in the Human Enterovirus Echovirus Types 9, 11, and 30. Journal of Virology, 2010, 84, 9292-9300.	1.5	95
152	Bioinformatic and Physical Characterizations of Genome-Scale Ordered RNA Structure in Mammalian RNA Viruses. Journal of Virology, 2008, 82, 11824-11836.	1.5	93
153	Recommendations for the nomenclature of enteroviruses and rhinoviruses. Archives of Virology, 2020, 165, 793-797.	0.9	93
154	Direct identification of human enterovirus serotypes in cerebrospinal fluid by amplification and sequencing of the VP1 region. Journal of Clinical Virology, 2009, 44, 119-124.	1.6	90
155	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. Systematic Biology, 2020, 69, 110-123.	2.7	89
156	HCV confirmatory testing of blood donors. Lancet, The, 1991, 338, 1024.	6.3	88
157	Influence of risk group and zidovudine therapy on the development of HIV encephalitis and cognitive impairment in AIDS patients. Aids, 1996, 10, 493-499.	1.0	88
158	The Molecular Epidemiology Of Human Immunodeficiency Virus Type 1 In Edinburgh. Journal of Infectious Diseases, 1995, 171, 45-53.	1.9	87
159	Surveying the global virome: Identification and characterization of HCV-related animal hepaciviruses. Antiviral Research, 2015, 115, 83-93.	1.9	86
160	Elevation of CpG frequencies in influenza A genome attenuates pathogenicity but enhances host response to infection. ELife, 2016, 5, e12735.	2.8	86
161	Allelic Variation of HERV-K(HML-2) Endogenous Retroviral Elements in Human Populations. Journal of Molecular Evolution, 2004, 59, 642-656.	0.8	85
162	The Complete Coding Sequence of Hepatitis C Virus Genotype 5a, the Predominant Genotype in South Africa. Biochemical and Biophysical Research Communications, 1997, 236, 44-49.	1.0	84

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163	Evaluating the evidence for virus/host co-evolution. Current Opinion in Virology, 2011, 1, 436-441.	2.6	84
164	Atypical hand, foot, and mouth disease associated with coxsackievirus A6 infection, Edinburgh, United Kingdom, January to February 2014. Eurosurveillance, 2014, 19, 20745.	3.9	83
165	Outbreak of acute hepatitis C following the use of anti-hepatitis C virus--screened intravenous immunoglobulin therapy. Gastroenterology, 1996, 110, 1120-1126.	0.6	82
166	A comparative method for finding and folding RNA secondary structures within protein-coding regions. Nucleic Acids Research, 2004, 32, 4925-4936.	6.5	82
167	Identification of a Pegivirus (GB Virus-Like Virus) That Infects Horses. Journal of Virology, 2013, 87, 7185-7190.	1.5	82
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