

Andrew Davison

List of Publications by Citations

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141
papers

11,159
citations

52
h-index

105
g-index

149
ext. papers

12,880
ext. citations

6.7
avg, IF

5.94
L-index

#	Paper	IF	Citations
141	The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1. <i>Journal of General Virology</i> , 1988 , 69 (Pt 7), 1531-74	4.9	1289
140	The order Herpesvirales. <i>Archives of Virology</i> , 2009 , 154, 171-7	2.6	655
139	The DNA sequence of equine herpesvirus-1. <i>Virology</i> , 1992 , 189, 304-16	3.6	482
138	Genetic content of wild-type human cytomegalovirus. <i>Journal of General Virology</i> , 2004 , 85, 1301-1312	4.9	439
137	Genetic content and evolution of adenoviruses. <i>Journal of General Virology</i> , 2003 , 84, 2895-2908	4.9	403
136	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). <i>Archives of Virology</i> , 2017 , 162, 2505-2538	3.6	398
135	Consensus statement: Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017 , 15, 161-168	22.2	375
134	Topics in herpesvirus genomics and evolution. <i>Virus Research</i> , 2006 , 117, 90-104	6.4	369
133	The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome. <i>Journal of General Virology</i> , 2003 , 84, 17-28	4.9	326
132	Herpesvirus systematics. <i>Veterinary Microbiology</i> , 2010 , 143, 52-69	3.3	227
131	Downregulation of natural killer cell-activating ligand CD155 by human cytomegalovirus UL141. <i>Nature Immunology</i> , 2005 , 6, 181-8	19.1	207
130	Channel catfish virus: a new type of herpesvirus. <i>Virology</i> , 1992 , 186, 9-14	3.6	206
129	A novel class of herpesvirus with bivalve hosts. <i>Journal of General Virology</i> , 2005 , 86, 41-53	4.9	201
128	Modulation of natural killer cells by human cytomegalovirus. <i>Journal of Clinical Virology</i> , 2008 , 41, 206-12	4.5	196
127	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). <i>Archives of Virology</i> , 2016 , 161, 2921-49	2.6	195
126	Genome sequences of three koi herpesvirus isolates representing the expanding distribution of an emerging disease threatening koi and common carp worldwide. <i>Journal of Virology</i> , 2007 , 81, 5058-65	6.6	195
125	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018 , 163, 2601-2631	3.6	187

124	The DNA sequence of equine herpesvirus 2. <i>Journal of Molecular Biology</i> , 1995 , 249, 520-8	6.5	173
123	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). <i>Archives of Virology</i> , 2019 , 164, 2417-2429	2.6	171
122	Reconstruction of the complete human cytomegalovirus genome in a BAC reveals RL13 to be a potent inhibitor of replication. <i>Journal of Clinical Investigation</i> , 2010 , 120, 3191-208	15.9	168
121	High-resolution human cytomegalovirus transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19755-60	11.5	161
120	Koi herpesvirus represents a third cyprinid herpesvirus (CyHV-3) in the family Herpesviridae. <i>Journal of General Virology</i> , 2005 , 86, 1659-1667	4.9	152
119	Evolution and diversity in human herpes simplex virus genomes. <i>Journal of Virology</i> , 2014 , 88, 1209-27	6.6	141
118	Sequential mutations associated with adaptation of human cytomegalovirus to growth in cell culture. <i>Journal of General Virology</i> , 2010 , 91, 1535-46	4.9	140
117	Analysis of the genome of equine herpesvirus type 1: arrangement of cleavage sites for restriction endonucleases EcoRI, BglII and BamHI. <i>Journal of General Virology</i> , 1981 , 57, 307-23	4.9	123
116	Identification of a spliced gene from Kaposi's sarcoma-associated herpesvirus encoding a protein with similarities to latent membrane proteins 1 and 2A of Epstein-Barr virus. <i>Journal of Virology</i> , 1999 , 73, 6953-63	6.6	121
115	Two novel spliced genes in human cytomegalovirus. <i>Journal of General Virology</i> , 2003 , 84, 1117-1122	4.9	116
114	Kaposi's sarcoma-associated herpesvirus immune modulation: an overview. <i>Journal of General Virology</i> , 2006 , 87, 1781-1804	4.9	105
113	Phylogenetic relationships in the family Alloherpesviridae. <i>Diseases of Aquatic Organisms</i> , 2009 , 84, 179-94	4.7	97
112	Two novel human cytomegalovirus NK cell evasion functions target MICA for lysosomal degradation. <i>PLoS Pathogens</i> , 2014 , 10, e1004058	7.6	96
111	The DNA sequence of adenovirus type 40. <i>Journal of Molecular Biology</i> , 1993 , 234, 1308-16	6.5	91
110	Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. <i>Journal of General Virology</i> , 2010 , 91, 605-15	4.9	91
109	Variability and evolution of Kaposi's sarcoma-associated herpesvirus in Europe and Africa. International Collaborative Group. <i>Aids</i> , 1999 , 13, 1165-76	3.5	89
108	Comparative genomics of carp herpesviruses. <i>Journal of Virology</i> , 2013 , 87, 2908-22	6.6	86
107	High-throughput sequence analysis of variants of human cytomegalovirus strains Towne and AD169. <i>Journal of General Virology</i> , 2009 , 90, 2375-2380	4.9	86

106	Human cytomegalovirus: taking the strain. <i>Medical Microbiology and Immunology</i> , 2015 , 204, 273-84	4	76
105	Equine herpesviruses 2 and 5 are gamma-herpesviruses. <i>Virology</i> , 1993 , 195, 492-9	3.6	71
104	Homology between the human cytomegalovirus RL11 gene family and human adenovirus E3 genes. <i>Journal of General Virology</i> , 2003 , 84, 657-663	4.9	69
103	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019 , 164, 943-946	2.6	66
102	The human herpesvirus-8 ORF 57 gene and its properties. <i>Journal of General Virology</i> , 1999 , 80 (Pt 12), 3207-3215	4.9	65
101	Identification of structural proteins of channel catfish virus by mass spectrometry. <i>Virology</i> , 1995 , 206, 1035-43	3.6	64
100	Human cytomegalovirus UL40 signal peptide regulates cell surface expression of the NK cell ligands HLA-E and gpUL18. <i>Journal of Immunology</i> , 2012 , 188, 2794-804	5.3	61
99	Impact of sequence variation in the UL128 locus on production of human cytomegalovirus in fibroblast and epithelial cells. <i>Journal of Virology</i> , 2013 , 87, 10489-500	6.6	60
98	Transcription mapping of human herpesvirus 8 genes encoding viral interferon regulatory factors. <i>Journal of General Virology</i> , 2003 , 84, 1471-1483	4.9	59
97	Structural features of ribonucleotide reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986 , 1, 376-84	4.2	59
96	Characterization of Human Cytomegalovirus Genome Diversity in Immunocompromised Hosts by Whole-Genome Sequencing Directly From Clinical Specimens. <i>Journal of Infectious Diseases</i> , 2017 , 215, 1673-1683	7	58
95	New genes from old: redeployment of dUTPase by herpesviruses. <i>Journal of Virology</i> , 2005 , 79, 12880-926.6		58
94	Plasma membrane profiling defines an expanded class of cell surface proteins selectively targeted for degradation by HCMV US2 in cooperation with UL141. <i>PLoS Pathogens</i> , 2015 , 11, e1004811	7.6	55
93	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017 , 162, 1441-1446	2.6	53
92	The capsid architecture of channel catfish virus, an evolutionarily distant herpesvirus, is largely conserved in the absence of discernible sequence homology with herpes simplex virus. <i>Virology</i> , 1996 , 215, 134-41	3.6	53
91	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021 , 166, 2633-2648	2.6	52
90	Evolution of sexually transmitted and sexually transmissible human herpesviruses. <i>Annals of the New York Academy of Sciences</i> , 2011 , 1230, E37-49	6.5	51
89	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. <i>Journal of General Virology</i> , 2001 , 82, 2393-2404	4.9	50

88	Genotypic analysis of two hypervariable human cytomegalovirus genes. <i>Journal of Medical Virology</i> , 2008 , 80, 1615-23	19.7	48
87	High-Definition Analysis of Host Protein Stability during Human Cytomegalovirus Infection Reveals Antiviral Factors and Viral Evasion Mechanisms. <i>Cell Host and Microbe</i> , 2018 , 24, 447-460.e11	23.4	47
86	HCMV pUL135 remodels the actin cytoskeleton to impair immune recognition of infected cells. <i>Cell Host and Microbe</i> , 2014 , 16, 201-214	23.4	46
85	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017 , 6,	8.9	46
84	Fundamental and accessory systems in herpesviruses. <i>Antiviral Research</i> , 2002 , 56, 1-11	10.8	45
83	Varicella-zoster virus. The Fourteenth Fleming lecture. <i>Journal of General Virology</i> , 1991 , 72 (Pt 3), 475-869		45
82	Human Cytomegalovirus Genomes Sequenced Directly From Clinical Material: Variation, Multiple-Strain Infection, Recombination, and Gene Loss. <i>Journal of Infectious Diseases</i> , 2019 , 220, 781-791	7.1	43
81	Genetic Stability of Bacterial Artificial Chromosome-Derived Human Cytomegalovirus during Culture In Vitro. <i>Journal of Virology</i> , 2016 , 90, 3929-43	6.6	43
80	Cyprinid Herpesvirus 3: An Archetype of Fish Alloherpesviruses. <i>Advances in Virus Research</i> , 2015 , 93, 161-256	10.7	43
79	Complete genome sequences of elephant endotheliotropic herpesviruses 1A and 1B determined directly from fatal cases. <i>Journal of Virology</i> , 2013 , 87, 6700-12	6.6	43
78	Genome sequences of two frog herpesviruses. <i>Journal of General Virology</i> , 2006 , 87, 3509-3514	4.9	43
77	First fatality associated with elephant endotheliotropic herpesvirus 5 in an Asian elephant: pathological findings and complete viral genome sequence. <i>Scientific Reports</i> , 2014 , 4, 6299	4.9	41
76	Conserved Fever Pathways across Vertebrates: A Herpesvirus Expressed Decoy TNF- α Receptor Delays Behavioral Fever in Fish. <i>Cell Host and Microbe</i> , 2017 , 21, 244-253	23.4	38
75	The genome of salmonid herpesvirus 1. <i>Journal of Virology</i> , 1998 , 72, 1974-82	6.6	37
74	Suppression of costimulation by human cytomegalovirus promotes evasion of cellular immune defenses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4998-5003	11.5	36
73	Rational development of an attenuated recombinant cyprinid herpesvirus 3 vaccine using prokaryotic mutagenesis and in vivo bioluminescent imaging. <i>PLoS Pathogens</i> , 2015 , 11, e1004690	7.6	35
72	Analysis of the first complete genome sequence of an Old World monkey adenovirus reveals a lineage distinct from the six human adenovirus species. <i>Journal of General Virology</i> , 2004 , 85, 2799-2807	4.9	32
71	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. <i>ELife</i> , 2019 , 8,	8.9	32

70	Stability of the parainfluenza virus 5 genome revealed by deep sequencing of strains isolated from different hosts and following passage in cell culture. <i>Journal of Virology</i> , 2014 , 88, 3826-36	6.6	31
69	Inherited Chromosomally Integrated Human Herpesvirus 6 Genomes Are Ancient, Intact, and Potentially Able To Reactivate from Telomeres. <i>Journal of Virology</i> , 2017 , 91,	6.6	29
68	Complete genome sequence of simian adenovirus 1: an Old World monkey adenovirus with two fiber genes. <i>Journal of General Virology</i> , 2005 , 86, 1681-1686	4.9	28
67	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020 , 165, 519-525	2.6	27
66	Bacterial artificial chromosome clones of viruses comprising the townes cytomegalovirus vaccine. <i>Journal of Biomedicine and Biotechnology</i> , 2012 , 2012, 428498		24
65	Multiple-Strain Infections of Human Cytomegalovirus With High Genomic Diversity Are Common in Breast Milk From Human Immunodeficiency Virus-Infected Women in Zambia. <i>Journal of Infectious Diseases</i> , 2019 , 220, 792-801	7	23
64	Genetic diversity of equine herpesvirus 1 isolated from neurological, abortigenic and respiratory disease outbreaks. <i>Transboundary and Emerging Diseases</i> , 2018 , 65, 817-832	4.2	23
63	Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. <i>Virology</i> , 2009 , 395, 21-32	3.6	23
62	Experience in shotgun sequencing a 134 kilobase pair DNA molecule. <i>DNA Sequence</i> , 1991 , 1, 389-94		22
61	Herpesvirus Genes. <i>Reviews in Medical Virology</i> , 1993 , 3, 237-244	11.7	22
60	Human cytomegalovirus protein pUL36: A dual cell death pathway inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18771-18779	11.5	22
59	Genomic and biologic comparisons of cyprinid herpesvirus 3 strains. <i>Veterinary Research</i> , 2018 , 49, 40	3.8	18
58	HHV-8-unrelated primary effusion-like lymphoma associated with clonal loss of inherited chromosomally-integrated human herpesvirus-6A from the telomere of chromosome 19q. <i>Scientific Reports</i> , 2016 , 6, 22730	4.9	18
57	Biocontrol of invasive carp: Risks abound. <i>Science</i> , 2018 , 359, 877	33.3	17
56	Proteomic and Functional Analyses of the Virion Transmembrane Proteome of Cyprinid Herpesvirus 3. <i>Journal of Virology</i> , 2017 , 91,	6.6	17
55	Comparative analysis of the genomes10-26		17
54	Overview of classification3-9		16
53	Comments on the phylogenetics and evolution of herpesviruses and other large DNA viruses. <i>Virus Research</i> , 2002 , 82, 127-32	6.4	16

52	Analysis of Paramyxovirus Transcription and Replication by High-Throughput Sequencing. <i>Journal of Virology</i> , 2019 , 93,	6.6	15
51	The switch between acute and persistent paramyxovirus infection caused by single amino acid substitutions in the RNA polymerase P subunit. <i>PLoS Pathogens</i> , 2019 , 15, e1007561	7.6	15
50	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. <i>PLoS Pathogens</i> , 2020 , 16, e1008390	7.6	14
49	Characterization and manipulation of the human adenovirus 4 genome. <i>Journal of General Virology</i> , 2004 , 85, 3361-3366	4.9	13
48	Identification of an essential virulence gene of cyprinid herpesvirus 3. <i>Antiviral Research</i> , 2017 , 145, 60-69	6.8	12
47	Anguillid herpesvirus 1 transcriptome. <i>Journal of Virology</i> , 2012 , 86, 10150-61	6.6	12
46	Molecular Evolution of the Herpesvirales 2008 , 447-475		12
45	Genome sequences of equid herpesviruses 2 and 5. <i>Genome Announcements</i> , 2015 , 3,		11
44	Comparative betaherpes viral genome and virion structure		11
43	Genome Sequence of Canine Herpesvirus. <i>PLoS ONE</i> , 2016 , 11, e0156015	3.7	10
42	Genomic analysis of chimeric human cytomegalovirus vaccine candidates derived from strains Towne and Toledo. <i>Virus Genes</i> , 2017 , 53, 650-655	2.3	7
41	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin. <i>PLoS Pathogens</i> , 2020 , 16, e1009166	7.6	7
40	Bioinformatics tools for analysing viral genomic data. <i>OIE Revue Scientifique Et Technique</i> , 2016 , 35, 271-285		7
39	Genome Sequences of Two Pseudorabies Virus Strains Isolated in Greece. <i>Genome Announcements</i> , 2016 , 4,		7
38	Whole-Genome Approach to Assessing Human Cytomegalovirus Dynamics in Transplant Patients Undergoing Antiviral Therapy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 267	5.9	5
37	ViCTree: an automated framework for taxonomic classification from protein sequences. <i>Bioinformatics</i> , 2018 , 34, 2195-2200	7.2	5
36	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020 , 11, 5951	17.4	5
35	Human Cytomegalovirus Long Non-coding RNA1.2 Suppresses Extracellular Release of the Pro-inflammatory Cytokine IL-6 by Blocking NF- κ B Activation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 361	5.9	5

34	Complete Genome Sequence of an Ictalurid Herpesvirus 1 Strain Isolated from Blue Catfish (<i>Ictalurus furcatus</i>). <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	4
33	Genome Sequence of the Parainfluenza Virus 5 Strain That Persistently Infects AGS Cells. <i>Genome Announcements</i> , 2016 , 4,		4
32	Human cytomegalovirus protein RL1 degrades the antiviral factor SLFN11 via recruitment of the CRL4 E3 ubiquitin ligase complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
31	Human Cytomegalovirus Genomes Sequenced Directly from Clinical Material: Variation, Multiple-Strain Infection, Recombination and Mutation		3
30	Genomic duplication and translocation of reactivation transactivator and bZIP-homolog genes is a conserved event in alcelaphine herpesvirus 1. <i>Scientific Reports</i> , 2016 , 6, 38607	4.9	3
29	LoReTTA, a user-friendly tool for assembling viral genomes from PacBio sequence data. <i>Virus Evolution</i> , 2021 , 7, veab042	3.7	3
28	Monoclonal antibodies targeting nonstructural viral antigens can activate ADCC against human cytomegalovirus. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	3
27	Author response: Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation 2017 ,		2
26	Genomes of Anguillid Herpesvirus 1 Strains Reveal Evolutionary Disparities and Low Genetic Diversity in the Genus. <i>Microorganisms</i> , 2021 , 9,	4.9	2
25	Variation in human herpesvirus 6B telomeric integration, excision, and transmission between tissues and individuals. <i>ELife</i> , 2021 , 10,	8.9	2
24	Michael Adams: new life member of the International Committee on Taxonomy of Viruses (ICTV). <i>Archives of Virology</i> , 2019 , 164, 2221	2.6	1
23	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever. <i>PLoS Pathogens</i> , 2020 , 16, e1008405	7.6	1
22	Eric Carstens: new life member of the International Committee on Taxonomy of Viruses (ICTV). <i>Archives of Virology</i> , 2016 , 161, 3601	2.6	1
21	Human cytomegalovirus multiple-strain infections and viral population diversity in haematopoietic stem cell transplant recipients analysed by high-throughput sequencing. <i>Medical Microbiology and Immunology</i> , 2021 , 210, 291-304	4	1
20	Multiple-Strain Infections of Human Cytomegalovirus with High Genomic Diversity are Common In Breast Milk from HIV-Positive Women in Zambia		1
19	GRACy: A tool for analysing human cytomegalovirus sequence data. <i>Virus Evolution</i> , 2021 , 7, veaa099	3.7	1
18	Post-HSCT graft failure due to refractory human cytomegalovirus successfully treated with haploidentical donor-derived immunoglobulins and stem cell graft infusion: A case report. <i>Antiviral Research</i> , 2021 , 188, 105024	10.8	1
17	Human Cytomegalovirus Genome Diversity in Longitudinally Collected Breast Milk Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 664247	5.9	1

16	Human cytomegalovirus protein RL1 degrades the antiviral factor SLFN11 via recruitment of the CRL4 E3 ubiquitin ligase complex		1
15	Human Cytomegalovirus RNA2.7 Is Required for Upregulating Multiple Cellular Genes To Promote Cell Motility and Viral Spread Late in Lytic Infection. <i>Journal of Virology</i> , 2021 , 95, e0069821	6.6	1
14	Genome Sequences of Five Arenaviruses from Pygmy Mice (<i>Mus minutoides</i>) in Sierra Leone.. <i>Microbiology Resource Announcements</i> , 2022 , e0009522	1.3	0
13	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication 2020 , 16, e1008390		
12	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication 2020 , 16, e1008390		
11	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication 2020 , 16, e1008390		
10	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication 2020 , 16, e1008390		
9	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever 2020 , 16, e1008405		
8	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever 2020 , 16, e1008405		
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5	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin 2020 , 16, e1009166		
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