

Andrew Davison

List of Publications by Year in descending order

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140
papers

15,119
citations

25034

57
h-index

19749

117
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149
all docs

149
docs citations

149
times ranked

11102
citing authors

#	ARTICLE	IF	CITATIONS
1	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, .	7.1	24
2	Genome Sequences of Five Arenaviruses from Pygmy Mice (<i>Mus minutoides</i>) in Sierra Leone. <i>Microbiology Resource Announcements</i> , 2022, 11, e0009522.	0.6	3
3	LoReTTA, a user-friendly tool for assembling viral genomes from PacBio sequence data. <i>Virus Evolution</i> , 2021, 7, veab042.	4.9	4
4	Monoclonal antibodies targeting nonstructural viral antigens can activate ADCC against human cytomegalovirus. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	17
5	Detection of Genotype-Specific Antibody Responses to Glycoproteins B and H in Primary and Non-Primary Human Cytomegalovirus Infections by Peptide-Based ELISA. <i>Viruses</i> , 2021, 13, 399.	3.3	4
6	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.	4.1	2
7	Human Cytomegalovirus Genome Diversity in Longitudinally Collected Breast Milk Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 664247.	3.9	8
8	Genomes of Anguillid Herpesvirus 1 Strains Reveal Evolutionary Disparities and Low Genetic Diversity in the Genus <i>Cyprinivirus</i> . <i>Microorganisms</i> , 2021, 9, 998.	3.6	10
9	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.	2.1	219
10	Variation in human herpesvirus 6B telomeric integration, excision, and transmission between tissues and individuals. <i>ELife</i> , 2021, 10, .	6.0	6
11	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.	3.4	2
12	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.	4.8	4
13	GRACy: A tool for analysing human cytomegalovirus sequence data. <i>Virus Evolution</i> , 2021, 7, veaa099.	4.9	4
14	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	2.1	51
15	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , 2020, 11, 5951.	12.8	18
16	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.	7.1	42
17	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.	3.9	12
18	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	2.1	202

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19	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.	3.9	17
20	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever. <i>PLoS Pathogens</i> , 2020, 16, e1008405.	4.7	4
21	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. <i>PLoS Pathogens</i> , 2020, 16, e1008390.	4.7	31
22	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin. <i>PLoS Pathogens</i> , 2020, 16, e1009166.	4.7	11
23	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
24	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
25	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
26	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. , 2020, 16, e1008390.		0
27	Title is missing!. , 2020, 16, e1008405.		0
28	Title is missing!. , 2020, 16, e1008405.		0
29	Title is missing!. , 2020, 16, e1008405.		0
30	Title is missing!. , 2020, 16, e1008405.		0
31	Title is missing!. , 2020, 16, e1009166.		0
32	Title is missing!. , 2020, 16, e1009166.		0
33	Title is missing!. , 2020, 16, e1009166.		0
34	Title is missing!. , 2020, 16, e1009166.		0
35	Title is missing!. , 2020, 16, e1009166.		0
36	Analysis of Paramyxovirus Transcription and Replication by High-Throughput Sequencing. <i>Journal of Virology</i> , 2019, 93, .	3.4	35

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37	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.	2.1	102
38	Michael Adams: new life member of the International Committee on Taxonomy of Viruses (ICTV). Archives of Virology, 2019, 164, 2221-2221.	2.1	1
39	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.	2.1	257
40	Human Cytomegalovirus Genomes Sequenced Directly From Clinical Material: Variation, Multiple-Strain Infection, Recombination, and Gene Loss. Journal of Infectious Diseases, 2019, 220, 781-791.	4.0	84
41	Multiple-Strain Infections of Human Cytomegalovirus With High Genomic Diversity Are Common in Breast Milk From Human Immunodeficiency Virus-Infected Women in Zambia. Journal of Infectious Diseases, 2019, 220, 792-801.	4.0	37
42	Complete Genome Sequence of an Ictalurid Herpesvirus 1 Strain Isolated from Blue Catfish (Ictalurus Tj ETQq0 0 0 rgBT /Overlock 10 TF	0.8	9
43	The switch between acute and persistent paramyxovirus infection caused by single amino acid substitutions in the RNA polymerase P subunit. PLoS Pathogens, 2019, 15, e1007561.	4.7	23
44	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. ELife, 2019, 8, .	6.0	84
45	ViCTree: an automated framework for taxonomic classification from protein sequences. Bioinformatics, 2018, 34, 2195-2200.	4.1	6
46	Biocontrol of invasive carp: Risks abound. Science, 2018, 359, 877-877.	12.6	23
47	Suppression of costimulation by human cytomegalovirus promotes evasion of cellular immune defenses. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4998-5003.	7.1	61
48	Genetic diversity of equine herpesvirus 1 isolated from neurological, abortigenic and respiratory disease outbreaks. Transboundary and Emerging Diseases, 2018, 65, 817-832.	3.0	40
49	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.	2.1	567
50	Genomic and biologic comparisons of cyprinid herpesvirus 3 strains. Veterinary Research, 2018, 49, 40.	3.0	26
51	High-Definition Analysis of Host Protein Stability during Human Cytomegalovirus Infection Reveals Antiviral Factors and Viral Evasion Mechanisms. Cell Host and Microbe, 2018, 24, 447-460.e11.	11.0	93
52	Conserved Fever Pathways across Vertebrates: A Herpesvirus Expressed Decoy TNF-Î± Receptor Delays Behavioral Fever in Fish. Cell Host and Microbe, 2017, 21, 244-253.	11.0	57
53	Genomic analysis of chimeric human cytomegalovirus vaccine candidates derived from strains Towne and Toledo. Virus Genes, 2017, 53, 650-655.	1.6	10
54	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. Archives of Virology, 2017, 162, 1441-1446.	2.1	72

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55	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.	2.1	506
56	Characterization of Human Cytomegalovirus Genome Diversity in Immunocompromised Hosts by Whole-Genome Sequencing Directly From Clinical Specimens. Journal of Infectious Diseases, 2017, 215, 1673-1683.	4.0	88
57	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	28.6	590
58	Inherited Chromosomally Integrated Human Herpesvirus 6 Genomes Are Ancient, Intact, and Potentially Able To Reactivate from Telomeres. Journal of Virology, 2017, 91, .	3.4	36
59	Proteomic and Functional Analyses of the Virion Transmembrane Proteome of Cyprinid Herpesvirus 3. Journal of Virology, 2017, 91, .	3.4	24
60	Identification of an essential virulence gene of cyprinid herpesvirus 3. Antiviral Research, 2017, 145, 60-69.	4.1	18
61	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. ELife, 2017, 6, .	6.0	67
62	Genome Sequence of Canine Herpesvirus. PLoS ONE, 2016, 11, e0156015.	2.5	14
63	Genomic duplication and translocation of reactivation transactivator and bZIP-homolog genes is a conserved event in alcelaphine herpesvirus 1. Scientific Reports, 2016, 6, 38607.	3.3	3
64	HHV-8-unrelated primary effusion-like lymphoma associated with clonal loss of inherited chromosomally-integrated human herpesvirus-6A from the telomere of chromosome 19q. Scientific Reports, 2016, 6, 22730.	3.3	21
65	Genome Sequences of Two Pseudorabies Virus Strains Isolated in Greece. Genome Announcements, 2016, 4, .	0.8	8
66	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	2.1	263
67	Eric Carstens: new life member of the International Committee on Taxonomy of Viruses (ICTV). Archives of Virology, 2016, 161, 3601-3601.	2.1	1
68	Genome Sequence of the Parainfluenza Virus 5 Strain That Persistently Infects AGS Cells. Genome Announcements, 2016, 4, .	0.8	4
69	Genetic Stability of Bacterial Artificial Chromosome-Derived Human Cytomegalovirus during Culture <i>In Vitro</i> . Journal of Virology, 2016, 90, 3929-3943.	3.4	62
70	Bioinformatics tools for analysing viral genomic data. OIE Revue Scientifique Et Technique, 2016, 35, 271-285.	1.2	16
71	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). Archives of Virology, 2015, 160, 1837-1850.	2.1	126
72	Cyprinid Herpesvirus 3. Advances in Virus Research, 2015, 93, 161-256.	2.1	52

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73	Genome Sequences of Equid Herpesviruses 2 and 5. <i>Genome Announcements</i> , 2015, 3, .	0.8	15
74	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.	4.7	43
75	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.	4.7	73
76	Human cytomegalovirus: taking the strain. <i>Medical Microbiology and Immunology</i> , 2015, 204, 273-284.	4.8	119
77	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, 3826-3836.	3.4	40
78	Two Novel Human Cytomegalovirus NK Cell Evasion Functions Target MICA for Lysosomal Degradation. <i>PLoS Pathogens</i> , 2014, 10, e1004058.	4.7	123
79	Evolution and Diversity in Human Herpes Simplex Virus Genomes. <i>Journal of Virology</i> , 2014, 88, 1209-1227.	3.4	187
80	HCMV pUL135 Remodels the Actin Cytoskeleton to Impair Immune Recognition of Infected Cells. <i>Cell Host and Microbe</i> , 2014, 16, 201-214.	11.0	67
81	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.	3.3	48
82	Comparative Genomics of Carp Herpesviruses. <i>Journal of Virology</i> , 2013, 87, 2908-2922.	3.4	117
83	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, 10489-10500.	3.4	77
84	Complete Genome Sequences of Elephant Endotheliotropic Herpesviruses 1A and 1B Determined Directly from Fatal Cases. <i>Journal of Virology</i> , 2013, 87, 6700-6712.	3.4	52
85	Bacterial Artificial Chromosome Clones of Viruses Comprising the Towne Cytomegalovirus Vaccine. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-8.	3.0	25
86	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, 2794-2804.	0.8	77
87	Anguillid Herpesvirus 1 Transcriptome. <i>Journal of Virology</i> , 2012, 86, 10150-10161.	3.4	14
88	Evolution of sexually transmitted and sexually transmissible human herpesviruses. <i>Annals of the New York Academy of Sciences</i> , 2011, 1230, E37-49.	3.8	63
89	High-resolution human cytomegalovirus transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19755-19760.	7.1	209
90	Herpesvirus systematics. <i>Veterinary Microbiology</i> , 2010, 143, 52-69.	1.9	279

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91	Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. <i>Journal of General Virology</i> , 2010, 91, 605-615.	2.9	108
92	Sequential mutations associated with adaptation of human cytomegalovirus to growth in cell culture. <i>Journal of General Virology</i> , 2010, 91, 1535-1546.	2.9	164
93	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, 3191-3208.	8.2	222
94	Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. <i>Virology</i> , 2009, 395, 21-32.	2.4	26
95	The order Herpesvirales. <i>Archives of Virology</i> , 2009, 154, 171-177.	2.1	790
96	High-throughput sequence analysis of variants of human cytomegalovirus strains Towne and AD169. <i>Journal of General Virology</i> , 2009, 90, 2375-2380.	2.9	101
97	Phylogenetic relationships in the family Alloherpesviridae. <i>Diseases of Aquatic Organisms</i> , 2009, 84, 179-194.	1.0	119
98	Genotypic analysis of two hypervariable human cytomegalovirus genes. <i>Journal of Medical Virology</i> , 2008, 80, 1615-1623.	5.0	54
99	Modulation of natural killer cells by human cytomegalovirus. <i>Journal of Clinical Virology</i> , 2008, 41, 206-212.	3.1	236
100	Molecular Evolution of the Herpesvirales. , 2008, , 447-475.		12
101	Comparative analysis of the genomes. , 2007, , 10-26.		23
102	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, 5058-5065.	3.4	222
103	Topics in herpesvirus genomics and evolution. <i>Virus Research</i> , 2006, 117, 90-104.	2.2	458
104	Kaposi's sarcoma-associated herpesvirus immune modulation: an overview. <i>Journal of General Virology</i> , 2006, 87, 1781-1804.	2.9	119
105	Genome sequences of two frog herpesviruses. <i>Journal of General Virology</i> , 2006, 87, 3509-3514.	2.9	48
106	Downregulation of natural killer cell-activating ligand CD155 by human cytomegalovirus UL141. <i>Nature Immunology</i> , 2005, 6, 181-188.	14.5	231
107	New Genes from Old: Redeployment of dUTPase by Herpesviruses. <i>Journal of Virology</i> , 2005, 79, 12880-12892.	3.4	66
108	Koi herpesvirus represents a third cyprinid herpesvirus (CyHV-3) in the family Herpesviridae. <i>Journal of General Virology</i> , 2005, 86, 1659-1667.	2.9	179

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109	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.	2.9	30
110	A novel class of herpesvirus with bivalve hosts. <i>Journal of General Virology</i> , 2005, 86, 41-53.	2.9	260
111	Genetic content of wild-type human cytomegalovirus. <i>Journal of General Virology</i> , 2004, 85, 1301-1312.	2.9	500
112	Characterization and manipulation of the human adenovirus 4 genome. <i>Journal of General Virology</i> , 2004, 85, 3361-3366.	2.9	14
113	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.	2.9	34
114	Genetic content and evolution of adenoviruses. <i>Journal of General Virology</i> , 2003, 84, 2895-2908.	2.9	500
115	The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome FN1. <i>Journal of General Virology</i> , 2003, 84, 17-28.	2.9	361
116	Transcription mapping of human herpesvirus 8 genes encoding viral interferon regulatory factors. <i>Journal of General Virology</i> , 2003, 84, 1471-1483.	2.9	70
117	Two novel spliced genes in human cytomegalovirus. <i>Journal of General Virology</i> , 2003, 84, 1117-1122.	2.9	126
118	Homology between the human cytomegalovirus RL11 gene family and human adenovirus E3 genes. <i>Journal of General Virology</i> , 2003, 84, 657-663.	2.9	79
119	Fundamental and accessory systems in herpesviruses. <i>Antiviral Research</i> , 2002, 56, 1-11.	4.1	51
120	Comments on the phylogenetics and evolution of herpesviruses and other large DNA viruses. <i>Virus Research</i> , 2001, 82, 127-132.	2.2	16
121	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. <i>Journal of General Virology</i> , 2001, 82, 2393-2404.	2.9	58
122	Variability and evolution of Kaposi's sarcoma-associated herpesvirus in Europe and Africa. <i>Aids</i> , 1999, 13, 1165-1176.	2.2	107
123	The human herpesvirus-8 ORF 57 gene and its properties. <i>Journal of General Virology</i> , 1999, 80, 3207-3215.	2.9	71
124	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, 6953-6963.	3.4	137
125	The Genome of Salmonid Herpesvirus 1. <i>Journal of Virology</i> , 1998, 72, 1974-1982.	3.4	47
126	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, 134-141.	2.4	63

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127	Identification of Structural Proteins of Channel Catfish Virus by Mass Spectrometry. <i>Virology</i> , 1995, 206, 1035-1043.	2.4	73
128	The DNA Sequence of Equine Herpesvirus 2. <i>Journal of Molecular Biology</i> , 1995, 249, 520-528.	4.2	225
129	Herpesvirus Genes. <i>Reviews in Medical Virology</i> , 1993, 3, 237-244.	8.3	25
130	Equine Herpesviruses 2 and 5 Are β -Herpesviruses. <i>Virology</i> , 1993, 195, 492-499.	2.4	85
131	The DNA Sequence of Adenovirus Type 40. <i>Journal of Molecular Biology</i> , 1993, 234, 1308-1316.	4.2	113
132	Channel catfish virus: A new type of herpesvirus. <i>Virology</i> , 1992, 186, 9-14.	2.4	254
133	The DNA sequence of equine herpesvirus-1. <i>Virology</i> , 1992, 189, 304-316.	2.4	617
134	Experience in shotgun sequencing a 134 kilobase pair DNA molecule. <i>DNA Sequence</i> , 1991, 1, 389-394.	0.7	24
135	Varicella-zoster virus. <i>Journal of General Virology</i> , 1991, 72, 475-486.	2.9	65
136	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, 1531-1574.	2.9	1,843
137	Structural features of ribonucleotide reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1986, 1, 376-384.	2.6	83
138	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, 307-323.	2.9	145
139	Overview of classification. , 0, , 3-9.		20
140	Comparative betaherpes viral genome and virion structure. , 0, , 177-203.		11