

# Andrew Davison

## 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.

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	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> , <b>2022</b> , 119,	11.5	4
140	Genome Sequences of Five Arenaviruses from Pygmy Mice ( <i>Mus minutoides</i> ) in Sierra Leone.. <i>Microbiology Resource Announcements</i> , <b>2022</b> , e0009522	1.3	0
139	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> , <b>2021</b> , 210, 291-304	4	1
138	GRACy: A tool for analysing human cytomegalovirus sequence data. <i>Virus Evolution</i> , <b>2021</b> , 7, veaa099	3.7	1
137	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> , <b>2021</b> , 188, 105024	10.8	1
136	Human Cytomegalovirus Genome Diversity in Longitudinally Collected Breast Milk Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2021</b> , 11, 664247	5.9	1
135	Genomes of Anguillid Herpesvirus 1 Strains Reveal Evolutionary Disparities and Low Genetic Diversity in the Genus. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	2
134	LoReTTA, a user-friendly tool for assembling viral genomes from PacBio sequence data. <i>Virus Evolution</i> , <b>2021</b> , 7, veab042	3.7	3
133	Monoclonal antibodies targeting nonstructural viral antigens can activate ADCC against human cytomegalovirus. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,	15.9	3
132	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> , <b>2021</b> , 166, 2633-2648	2.6	52
131	Variation in human herpesvirus 6B telomeric integration, excision, and transmission between tissues and individuals. <i>ELife</i> , <b>2021</b> , 10,	8.9	2
130	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> , <b>2021</b> , 95, e0069821	6.6	1
129	Whole-Genome Approach to Assessing Human Cytomegalovirus Dynamics in Transplant Patients Undergoing Antiviral Therapy. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 267	5.9	5
128	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008405	7.6	1
127	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1009166	7.6	7
126	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , <b>2020</b> , 165, 519-525	2.6	27
125	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. <i>Nature Communications</i> , <b>2020</b> , 11, 5951	17.4	5

124	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> , <b>2020</b> , 117, 18771-18779	11.5	22
123	Human Cytomegalovirus Long Non-coding RNA1.2 Suppresses Extracellular Release of the Pro-inflammatory Cytokine IL-6 by Blocking NF- $\kappa$ B Activation. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2020</b> , 10, 361	5.9	5
122	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008390	7.6	14
121	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication <b>2020</b> , 16, e1008390		
120	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication <b>2020</b> , 16, e1008390		
119	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication <b>2020</b> , 16, e1008390		
118	Human cytomegalovirus long noncoding RNA4.9 regulates viral DNA replication <b>2020</b> , 16, e1008390		
117	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever <b>2020</b> , 16, e1008405		
116	Alcelaphine herpesvirus 1 genes A7 and A8 regulate viral spread and are essential for malignant catarrhal fever <b>2020</b> , 16, e1008405		
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113	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin <b>2020</b> , 16, e1009166		
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110	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin <b>2020</b> , 16, e1009166		
109	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin <b>2020</b> , 16, e1009166		
108	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , <b>2019</b> , 164, 943-946	2.6	66
107	Michael Adams: new life member of the International Committee on Taxonomy of Viruses (ICTV). <i>Archives of Virology</i> , <b>2019</b> , 164, 2221	2.6	1

106	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> , <b>2019</b> , 164, 2417-2429	2.6	171
105	Human Cytomegalovirus Genomes Sequenced Directly From Clinical Material: Variation, Multiple-Strain Infection, Recombination, and Gene Loss. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 781-791	7.1	43
104	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> , <b>2019</b> , 220, 792-801	7	23
103	Complete Genome Sequence of an Ictalurid Herpesvirus 1 Strain Isolated from Blue Catfish ( <i>Ictalurus furcatus</i> ). <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	4
102	Analysis of Paramyxovirus Transcription and Replication by High-Throughput Sequencing. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	15
101	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. <i>ELife</i> , <b>2019</b> , 8,	8.9	32
100	The switch between acute and persistent paramyxovirus infection caused by single amino acid substitutions in the RNA polymerase P subunit. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007561	7.6	15
99	ViCTree: an automated framework for taxonomic classification from protein sequences. <i>Bioinformatics</i> , <b>2018</b> , 34, 2195-2200	7.2	5
98	Biocontrol of invasive carp: Risks abound. <i>Science</i> , <b>2018</b> , 359, 877	33.3	17
97	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> , <b>2018</b> , 115, 4998-5003	11.5	36
96	Genetic diversity of equine herpesvirus 1 isolated from neurological, abortigenic and respiratory disease outbreaks. <i>Transboundary and Emerging Diseases</i> , <b>2018</b> , 65, 817-832	4.2	23
95	Genomic and biologic comparisons of cyprinid herpesvirus 3 strains. <i>Veterinary Research</i> , <b>2018</b> , 49, 40	3.8	18
94	High-Definition Analysis of Host Protein Stability during Human Cytomegalovirus Infection Reveals Antiviral Factors and Viral Evasion Mechanisms. <i>Cell Host and Microbe</i> , <b>2018</b> , 24, 447-460.e11	23.4	47
93	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> , <b>2018</b> , 163, 2601-2631	23.6	187
92	Conserved Fever Pathways across Vertebrates: A Herpesvirus Expressed Decoy TNF- $\alpha$ Receptor Delays Behavioral Fever in Fish. <i>Cell Host and Microbe</i> , <b>2017</b> , 21, 244-253	23.4	38
91	Genomic analysis of chimeric human cytomegalovirus vaccine candidates derived from strains Towne and Toledo. <i>Virus Genes</i> , <b>2017</b> , 53, 650-655	2.3	7
90	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , <b>2017</b> , 162, 1441-1446	2.6	53
89	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> , <b>2017</b> , 162, 2505-2538	23.6	398

88	Characterization of Human Cytomegalovirus Genome Diversity in Immunocompromised Hosts by Whole-Genome Sequencing Directly From Clinical Specimens. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 215, 1673-1683	7	58
87	Consensus statement: Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 161-168	22.2	375
86	Inherited Chromosomally Integrated Human Herpesvirus 6 Genomes Are Ancient, Intact, and Potentially Able To Reactivate from Telomeres. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	29
85	Proteomic and Functional Analyses of the Virion Transmembrane Proteome of Cyprinid Herpesvirus 3. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	17
84	Identification of an essential virulence gene of cyprinid herpesvirus 3. <i>Antiviral Research</i> , <b>2017</b> , 145, 60-69	6.8	12
83	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , <b>2017</b> , 6,	8.9	46
82	Author response: Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation <b>2017</b> ,		2
81	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). <i>Archives of Virology</i> , <b>2016</b> , 161, 2921-49	2.6	195
80	Eric Carstens: new life member of the International Committee on Taxonomy of Viruses (ICTV). <i>Archives of Virology</i> , <b>2016</b> , 161, 3601	2.6	1
79	Genome Sequence of the Parainfluenza Virus 5 Strain That Persistently Infects AGS Cells. <i>Genome Announcements</i> , <b>2016</b> , 4,		4
78	Genetic Stability of Bacterial Artificial Chromosome-Derived Human Cytomegalovirus during Culture In Vitro. <i>Journal of Virology</i> , <b>2016</b> , 90, 3929-43	6.6	43
77	Bioinformatics tools for analysing viral genomic data. <i>OIE Revue Scientifique Et Technique</i> , <b>2016</b> , 35, 271-85	8.5	7
76	Genome Sequence of Canine Herpesvirus. <i>PLoS ONE</i> , <b>2016</b> , 11, e0156015	3.7	10
75	Genomic duplication and translocation of reactivation transactivator and bZIP-homolog genes is a conserved event in alcelaphine herpesvirus 1. <i>Scientific Reports</i> , <b>2016</b> , 6, 38607	4.9	3
74	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> , <b>2016</b> , 6, 22730	4.9	18
73	Genome Sequences of Two Pseudorabies Virus Strains Isolated in Greece. <i>Genome Announcements</i> , <b>2016</b> , 4,		7
72	Rational development of an attenuated recombinant cyprinid herpesvirus 3 vaccine using prokaryotic mutagenesis and in vivo bioluminescent imaging. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004690	7.6	35
71	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> , <b>2015</b> , 11, e1004811	7.6	55

70	Human cytomegalovirus: taking the strain. <i>Medical Microbiology and Immunology</i> , <b>2015</b> , 204, 273-84	4	76
69	Cyprinid Herpesvirus 3: An Archetype of Fish Alloherpesviruses. <i>Advances in Virus Research</i> , <b>2015</b> , 93, 161-256	10.7	43
68	Genome sequences of equid herpesviruses 2 and 5. <i>Genome Announcements</i> , <b>2015</b> , 3,		11
67	Evolution and diversity in human herpes simplex virus genomes. <i>Journal of Virology</i> , <b>2014</b> , 88, 1209-27	6.6	141
66	HCMV pUL135 remodels the actin cytoskeleton to impair immune recognition of infected cells. <i>Cell Host and Microbe</i> , <b>2014</b> , 16, 201-214	23.4	46
65	First fatality associated with elephant endotheliotropic herpesvirus 5 in an Asian elephant: pathological findings and complete viral genome sequence. <i>Scientific Reports</i> , <b>2014</b> , 4, 6299	4.9	41
64	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> , <b>2014</b> , 88, 3826-36	6.6	31
63	Two novel human cytomegalovirus NK cell evasion functions target MICA for lysosomal degradation. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1004058	7.6	96
62	Comparative genomics of carp herpesviruses. <i>Journal of Virology</i> , <b>2013</b> , 87, 2908-22	6.6	86
61	Impact of sequence variation in the UL128 locus on production of human cytomegalovirus in fibroblast and epithelial cells. <i>Journal of Virology</i> , <b>2013</b> , 87, 10489-500	6.6	60
60	Complete genome sequences of elephant endotheliotropic herpesviruses 1A and 1B determined directly from fatal cases. <i>Journal of Virology</i> , <b>2013</b> , 87, 6700-12	6.6	43
59	Bacterial artificial chromosome clones of viruses comprising the townes cytomegalovirus vaccine. <i>Journal of Biomedicine and Biotechnology</i> , <b>2012</b> , 2012, 428498		24
58	Human cytomegalovirus UL40 signal peptide regulates cell surface expression of the NK cell ligands HLA-E and gpUL18. <i>Journal of Immunology</i> , <b>2012</b> , 188, 2794-804	5.3	61
57	Anguillid herpesvirus 1 transcriptome. <i>Journal of Virology</i> , <b>2012</b> , 86, 10150-61	6.6	12
56	Evolution of sexually transmitted and sexually transmissible human herpesviruses. <i>Annals of the New York Academy of Sciences</i> , <b>2011</b> , 1230, E37-49	6.5	51
55	High-resolution human cytomegalovirus transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 19755-60	11.5	161
54	Herpesvirus systematics. <i>Veterinary Microbiology</i> , <b>2010</b> , 143, 52-69	3.3	227
53	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> , <b>2010</b> , 120, 3191-208	15.9	168

52	Sequences of complete human cytomegalovirus genomes from infected cell cultures and clinical specimens. <i>Journal of General Virology</i> , <b>2010</b> , 91, 605-15	4.9	91
51	Sequential mutations associated with adaptation of human cytomegalovirus to growth in cell culture. <i>Journal of General Virology</i> , <b>2010</b> , 91, 1535-46	4.9	140
50	Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. <i>Virology</i> , <b>2009</b> , 395, 21-32	3.6	23
49	The order Herpesvirales. <i>Archives of Virology</i> , <b>2009</b> , 154, 171-7	2.6	655
48	Phylogenetic relationships in the family Alloherpesviridae. <i>Diseases of Aquatic Organisms</i> , <b>2009</b> , 84, 179-94	4.7	97
47	High-throughput sequence analysis of variants of human cytomegalovirus strains Towne and AD169. <i>Journal of General Virology</i> , <b>2009</b> , 90, 2375-2380	4.9	86
46	Modulation of natural killer cells by human cytomegalovirus. <i>Journal of Clinical Virology</i> , <b>2008</b> , 41, 206-12	4.5	196
45	Molecular Evolution of the Herpesvirales <b>2008</b> , 447-475		12
44	Genotypic analysis of two hypervariable human cytomegalovirus genes. <i>Journal of Medical Virology</i> , <b>2008</b> , 80, 1615-23	19.7	48
43	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> , <b>2007</b> , 81, 5058-65	6.6	195
42	Kaposi's sarcoma-associated herpesvirus immune modulation: an overview. <i>Journal of General Virology</i> , <b>2006</b> , 87, 1781-1804	4.9	105
41	Genome sequences of two frog herpesviruses. <i>Journal of General Virology</i> , <b>2006</b> , 87, 3509-3514	4.9	43
40	Topics in herpesvirus genomics and evolution. <i>Virus Research</i> , <b>2006</b> , 117, 90-104	6.4	369
39	A novel class of herpesvirus with bivalve hosts. <i>Journal of General Virology</i> , <b>2005</b> , 86, 41-53	4.9	201
38	Downregulation of natural killer cell-activating ligand CD155 by human cytomegalovirus UL141. <i>Nature Immunology</i> , <b>2005</b> , 6, 181-8	19.1	207
37	New genes from old: redeployment of dUTPase by herpesviruses. <i>Journal of Virology</i> , <b>2005</b> , 79, 12880-92	6.6	58
36	Koi herpesvirus represents a third cyprinid herpesvirus (CyHV-3) in the family Herpesviridae. <i>Journal of General Virology</i> , <b>2005</b> , 86, 1659-1667	4.9	152
35	Complete genome sequence of simian adenovirus 1: an Old World monkey adenovirus with two fiber genes. <i>Journal of General Virology</i> , <b>2005</b> , 86, 1681-1686	4.9	28



34	Genetic content of wild-type human cytomegalovirus. <i>Journal of General Virology</i> , <b>2004</b> , 85, 1301-1312	4.9	439
33	Characterization and manipulation of the human adenovirus 4 genome. <i>Journal of General Virology</i> , <b>2004</b> , 85, 3361-3366	4.9	13
32	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> , <b>2004</b> , 85, 2799-2807	4.9	32
31	Transcription mapping of human herpesvirus 8 genes encoding viral interferon regulatory factors. <i>Journal of General Virology</i> , <b>2003</b> , 84, 1471-1483	4.9	59
30	Two novel spliced genes in human cytomegalovirus. <i>Journal of General Virology</i> , <b>2003</b> , 84, 1117-1122	4.9	116
29	Genetic content and evolution of adenoviruses. <i>Journal of General Virology</i> , <b>2003</b> , 84, 2895-2908	4.9	403
28	The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome. <i>Journal of General Virology</i> , <b>2003</b> , 84, 17-28	4.9	326
27	Homology between the human cytomegalovirus RL11 gene family and human adenovirus E3 genes. <i>Journal of General Virology</i> , <b>2003</b> , 84, 657-663	4.9	69
26	Fundamental and accessory systems in herpesviruses. <i>Antiviral Research</i> , <b>2002</b> , 56, 1-11	10.8	45
25	Comments on the phylogenetics and evolution of herpesviruses and other large DNA viruses. <i>Virus Research</i> , <b>2002</b> , 82, 127-32	6.4	16
24	Recombination in human herpesvirus-8 strains from Uganda and evolution of the K15 gene. <i>Journal of General Virology</i> , <b>2001</b> , 82, 2393-2404	4.9	50
23	Variability and evolution of Kaposi's sarcoma-associated herpesvirus in Europe and Africa. International Collaborative Group. <i>Aids</i> , <b>1999</b> , 13, 1165-76	3.5	89
22	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> , <b>1999</b> , 73, 6953-63	6.6	121
21	The human herpesvirus-8 ORF 57 gene and its properties. <i>Journal of General Virology</i> , <b>1999</b> , 80 ( Pt 12), 3207-3215	4.9	65
20	The genome of salmonid herpesvirus 1. <i>Journal of Virology</i> , <b>1998</b> , 72, 1974-82	6.6	37
19	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> , <b>1996</b> , 215, 134-41	3.6	53
18	Identification of structural proteins of channel catfish virus by mass spectrometry. <i>Virology</i> , <b>1995</b> , 206, 1035-43	3.6	64
17	The DNA sequence of equine herpesvirus 2. <i>Journal of Molecular Biology</i> , <b>1995</b> , 249, 520-8	6.5	173



16	The DNA sequence of adenovirus type 40. <i>Journal of Molecular Biology</i> , <b>1993</b> , 234, 1308-16	6.5	91
15	Herpesvirus Genes. <i>Reviews in Medical Virology</i> , <b>1993</b> , 3, 237-244	11.7	22
14	Equine herpesviruses 2 and 5 are gamma-herpesviruses. <i>Virology</i> , <b>1993</b> , 195, 492-9	3.6	71
13	Channel catfish virus: a new type of herpesvirus. <i>Virology</i> , <b>1992</b> , 186, 9-14	3.6	206
12	The DNA sequence of equine herpesvirus-1. <i>Virology</i> , <b>1992</b> , 189, 304-16	3.6	482
11	Experience in shotgun sequencing a 134 kilobase pair DNA molecule. <i>DNA Sequence</i> , <b>1991</b> , 1, 389-94		22
10	Varicella-zoster virus. The Fourteenth Fleming lecture. <i>Journal of General Virology</i> , <b>1991</b> , 72 ( Pt 3), 475-869		45
9	The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1. <i>Journal of General Virology</i> , <b>1988</b> , 69 ( Pt 7), 1531-74	4.9	1289
8	Structural features of ribonucleotide reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1986</b> , 1, 376-84	4.2	59
7	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> , <b>1981</b> , 57, 307-23	4.9	123
6	Overview of classification3-9		16
5	Comparative betaherpes viral genome and virion structure177-203		11
4	Multiple-Strain Infections of Human Cytomegalovirus with High Genomic Diversity are Common In Breast Milk from HIV-Positive Women in Zambia		1
3	Human Cytomegalovirus Genomes Sequenced Directly from Clinical Material: Variation, Multiple-Strain Infection, Recombination and Mutation		3
2	Comparative analysis of the genomes10-26		17
1	Human cytomegalovirus protein RL1 degrades the antiviral factor SLFN11 via recruitment of the CRL4 E3 ubiquitin ligase complex		1