

Elodie Ghedin

List of Publications by Year in descending order

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181
papers

17,438
citations

19657
61
h-index

15732
125
g-index

198
all docs

198
docs citations

198
times ranked

20226
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	12.6	1,496
2	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	12.6	1,273
3	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
4	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
5	Widespread Lateral Gene Transfer from Intracellular Bacteria to Multicellular Eukaryotes. <i>Science</i> , 2007, 317, 1753-1756.	12.6	693
6	Comparison of the Respiratory Microbiome in Healthy Nonsmokers and Smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1067-1075.	5.6	655
7	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	12.6	571
8	The Wolbachia Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. <i>PLoS Biology</i> , 2005, 3, e121.	5.6	529
9	Enrichment of the lung microbiome with oral taxa is associated with lung inflammation of a Th17 phenotype. <i>Nature Microbiology</i> , 2016, 1, 16031.	13.3	436
10	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.	27.8	419
11	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016, 161, 2351-2360.	2.1	407
12	Whole-Genome Analysis of Human Influenza A Virus Reveals Multiple Persistent Lineages and Reassortment among Recent H3N2 Viruses. <i>PLoS Biology</i> , 2005, 3, e300.	5.6	340
13	The Evolutionary Genetics and Emergence of Avian Influenza Viruses in Wild Birds. <i>PLoS Pathogens</i> , 2008, 4, e1000076.	4.7	334
14	The human mycobiome in health and disease. <i>Genome Medicine</i> , 2013, 5, 63.	8.2	292
15	Viral genome sequencing by random priming methods. <i>BMC Genomics</i> , 2008, 9, 5.	2.8	282
16	Multiple Reassortment Events in the Evolutionary History of H1N1 Influenza A Virus Since 1918. <i>PLoS Pathogens</i> , 2008, 4, e1000012.	4.7	243
17	Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses. <i>Emerging Infectious Diseases</i> , 2007, 13, 713-718.	4.3	191
18	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184

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19	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016, 48, 195-200.	21.4	182
20	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1110-1117.	5.6	175
21	Stochastic Processes Are Key Determinants of Short-Term Evolution in Influenza A Virus. <i>PLoS Pathogens</i> , 2006, 2, e125.	4.7	173
22	Taxonomy of the order Mononegavirales: update 2017. <i>Archives of Virology</i> , 2017, 162, 2493-2504.	2.1	173
23	A rapid and label-free platform for virus capture and identification from clinical samples. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 895-901.	7.1	157
24	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	2.1	153
25	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	7.1	146
26	Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , 2018, 6, 12.	11.1	146
27	Sequence Analysis of <i>In Vivo</i> Defective Interfering-Like RNA of Influenza A H1N1 Pandemic Virus. <i>Journal of Virology</i> , 2013, 87, 8064-8074.	3.4	144
28	Identification and overexpression of the A2 amastigote-specific protein in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 1996, 78, 79-90.	1.1	130
29	The early diversification of influenza A/H1N1pdm. <i>PLOS Currents</i> , 2009, 1, RRN1126.	1.4	121
30	Multicenter Comparison of Lung and Oral Microbiomes of HIV-infected and HIV-uninfected Individuals. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 1335-1344.	5.6	120
31	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	27.8	117
32	Deep Sequencing Reveals Mixed Infection with 2009 Pandemic Influenza A (H1N1) Virus Strains and the Emergence of Oseltamivir Resistance. <i>Journal of Infectious Diseases</i> , 2011, 203, 168-174.	4.0	113
33	Topographic Diversity of the Respiratory Tract Mycobiome and Alteration in HIV and Lung Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 932-942.	5.6	113
34	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	13.3	107
35	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. <i>Nature Microbiology</i> , 2021, 6, 1245-1258.	13.3	101
36	Transmission Bottleneck Size Estimation from Pathogen Deep-Sequencing Data, with an Application to Human Influenza A Virus. <i>Journal of Virology</i> , 2017, 91, .	3.4	100

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37	Molecular Epidemiology of A/H3N2 and A/H1N1 Influenza Virus during a Single Epidemic Season in the United States. PLoS Pathogens, 2008, 4, e1000133.	4.7	97
38	Stage-specific proteomic expression patterns of the human filarial parasite <i>Brugia malayi</i> and its endosymbiont <i>Wolbachia</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9649-9654.	7.1	97
39	The Microbiome and the Lung. Annals of the American Thoracic Society, 2014, 11, S227-S232.	3.2	97
40	Mimivirus relatives in the Sargasso sea. Virology Journal, 2005, 2, 62.	3.4	96
41	Mixed Infection and the Genesis of Influenza Virus Diversity. Journal of Virology, 2009, 83, 8832-8841.	3.4	95
42	A gene family of cathepsin L-like proteases of filarial nematodes are associated with larval molting and cuticle and eggshell remodeling. Molecular and Biochemical Parasitology, 2004, 136, 227-242.	1.1	94
43	Biologic, Antigenic, and Full-Length Genomic Characterization of a Bovine-Like Coronavirus Isolated from a Giraffe. Journal of Virology, 2007, 81, 4981-4990.	3.4	94
44	Gene synteny and evolution of genome architecture in trypanosomatids. Molecular and Biochemical Parasitology, 2004, 134, 183-191.	1.1	92
45	Evolutionary History and Attenuation of Myxoma Virus on Two Continents. PLoS Pathogens, 2012, 8, e1002950.	4.7	91
46	Identification of mammalian-adapting mutations in the polymerase complex of an avian H5N1 influenza virus. Nature Communications, 2015, 6, 7491.	12.8	91
47	Bovine-Like Coronaviruses Isolated from Four Species of Captive Wild Ruminants Are Homologous to Bovine Coronaviruses, Based on Complete Genomic Sequences. Journal of Virology, 2008, 82, 12422-12431.	3.4	88
48	Members of a Large Retroposon Family Are Determinants of Post-Transcriptional Gene Expression in Leishmania. PLoS Pathogens, 2007, 3, e136.	4.7	87
49	Helminth Genomics: The Implications for Human Health. PLoS Neglected Tropical Diseases, 2009, 3, e538.	3.0	86
50	A Deep Sequencing Approach to Comparatively Analyze the Transcriptome of Lifecycle Stages of the Filarial Worm, <i>Brugia malayi</i> . PLoS Neglected Tropical Diseases, 2011, 5, e1409.	3.0	86
51	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. Ecology Letters, 2012, 15, 24-33.	6.4	86
52	Mining Predicted Essential Genes of <i>Brugia malayi</i> for Nematode Drug Targets. PLoS ONE, 2007, 2, e1189.	2.5	85
53	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. Microbiome, 2016, 4, 3.	11.1	83
54	Development of high-yield influenza A virus vaccine viruses. Nature Communications, 2015, 6, 8148.	12.8	81

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55	First sequenced genome of a parasitic nematode. Trends in Parasitology, 2004, 20, 151-153.	3.3	80
56	Genomic and Protein Structural Maps of Adaptive Evolution of Human Influenza A Virus to Increased Virulence in the Mouse. PLoS ONE, 2011, 6, e21740.	2.5	79
57	Myxoma Virus and the Leporipoxviruses: An Evolutionary Paradigm. Viruses, 2015, 7, 1020-1061.	3.3	79
58	Deliberate Attenuation of Chikungunya Virus by Adaptation to Heparan Sulfate-Dependent Infectivity: A Model for Rational Arboviral Vaccine Design. PLoS Neglected Tropical Diseases, 2014, 8, e2719.	3.0	78
59	Presence of Oseltamivir-Resistant Pandemic A/H1N1 Minor Variants Before Drug Therapy With Subsequent Selection and Transmission. Journal of Infectious Diseases, 2012, 206, 1504-1511.	4.0	70
60	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	2.1	70
61	Cyclic Avian Mass Mortality in the Northeastern United States Is Associated with a Novel Orthomyxovirus. Journal of Virology, 2015, 89, 1389-1403.	3.4	68
62	Mesoniviruses are mosquito-specific viruses with extensive geographic distribution and host range. Virology Journal, 2014, 11, 97.	3.4	65
63	Role of viral regulatory and accessory proteins in HIV-1 replication. Frontiers in Bioscience - Landmark, 2004, 9, 2388.	3.0	61
64	Secretory and Endocytic Pathways Converge in a Dynamic Endosomal System in a Primitive Protozoan. Traffic, 2001, 2, 175-188.	2.7	60
65	The sequence and analysis of Trypanosoma brucei chromosome II. Nucleic Acids Research, 2003, 31, 4856-4863.	14.5	59
66	Quasispecies of bovine enteric and respiratory coronaviruses based on complete genome sequences and genetic changes after tissue culture adaptation. Virology, 2007, 363, 1-10.	2.4	58
67	Intrahost Dynamics of Antiviral Resistance in Influenza A Virus Reflect Complex Patterns of Segment Linkage, Reassortment, and Natural Selection. MBio, 2015, 6, .	4.1	58
68	The lung mycobiome in the next-generation sequencing era. Virulence, 2017, 8, 334-341.	4.4	57
69	Phylogeography of the Spring and Fall Waves of the H1N1/09 Pandemic Influenza Virus in the United States. Journal of Virology, 2011, 85, 828-834.	3.4	54
70	Molecular characterization of a new species in the genus Alphacoronavirus associated with mink epizootic catarrhal gastroenteritis. Journal of General Virology, 2011, 92, 1369-1379.	2.9	53
71	Dissection of the Functional Domains of the Leishmania Surface Membrane 3'-Nucleotidase/Nuclease, a Unique Member of the Class I Nuclease Family. Journal of Biological Chemistry, 2000, 275, 16366-16372.	3.4	50
72	Complete genomic sequences, a key residue in the spike protein and deletions in nonstructural protein 3b of US strains of the virulent and attenuated coronaviruses, transmissible gastroenteritis virus and porcine respiratory coronavirus. Virology, 2007, 358, 424-435.	2.4	50

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73	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1110-1115.	30.7	47
74	Prediction pipeline for discovery of regulatory motifs associated with <i>Brugia malayi</i> molting. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008275.	3.0	46
75	Stage-Specific Transcriptome and Proteome Analyses of the Filarial Parasite <i>Onchocerca volvulus</i> and Its <i>Wolbachia</i> Endosymbiont. <i>MBio</i> , 2016, 7, .	4.1	45
76	The genome of <i>Brugia malayi</i> "All worms are not created equal. <i>Parasitology International</i> , 2009, 58, 6-11.	1.3	43
77	Extensive Geographical Mixing of 2009 Human H1N1 Influenza A Virus in a Single University Community. <i>Journal of Virology</i> , 2011, 85, 6923-6929.	3.4	43
78	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. <i>Microbiome</i> , 2016, 4, 38.	11.1	43
79	Defining <i>Brugia malayi</i> and <i>Wolbachia</i> symbiosis by stage-specific dual RNA-seq. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005357.	3.0	43
80	Identification of non-autonomous non-LTR retrotransposons in the genome of <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 124, 73-78.	1.1	41
81	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. <i>Microbiome</i> , 2020, 8, 39.	11.1	41
82	<i>Brugia malayi</i> Gene Expression in Response to the Targeting of the <i>Wolbachia</i> Endosymbiont by Tetracycline Treatment. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e525.	3.0	40
83	Arboretum and Puerto Almendras viruses: two novel rhabdoviruses isolated from mosquitoes in Peru. <i>Journal of General Virology</i> , 2014, 95, 787-792.	2.9	39
84	Glycomic analysis of host response reveals high mannose as a key mediator of influenza severity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26926-26935.	7.1	39
85	A Potential Role for the Interaction of <i>Wolbachia</i> Surface Proteins with the <i>Brugia malayi</i> Glycolytic Enzymes and Cytoskeleton in Maintenance of Endosymbiosis. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2151.	3.0	38
86	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	12.8	38
87	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020, 11, .	4.1	38
88	Molecular Dissection of the Functional Domains of a Unique, Tartrate-resistant, Surface Membrane Acid Phosphatase in the Primitive Human Pathogen <i>Leishmania donovani</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 17994-18001.	3.4	35
89	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , 2009, 10, 267.	2.8	35
90	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , 2013, 1, 354-356.	10.7	35

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91	Role of transposable elements in trypanosomatids. <i>Microbes and Infection</i> , 2008, 10, 575-581.	1.9	34
92	Microbial Composition of the Human Nasopharynx Varies According to Influenza Virus Type and Vaccination Status. <i>MBio</i> , 2019, 10, .	4.1	34
93	Functional lower airways genomic profiling of the microbiome to capture active microbial metabolism. <i>European Respiratory Journal</i> , 2021, 58, 2003434.	6.7	34
94	Genome Scale Evolution of Myxoma Virus Reveals Host-Pathogen Adaptation and Rapid Geographic Spread. <i>Journal of Virology</i> , 2013, 87, 12900-12915.	3.4	32
95	Evolution of non-LTR retrotransposons in the trypanosomatid genomes: <i>Leishmania major</i> has lost the active elements. <i>Molecular and Biochemical Parasitology</i> , 2006, 145, 158-170.	1.1	31
96	Glucose and Glycogen Metabolism in <i>Brugia malayi</i> Is Associated with <i>Wolbachia</i> Symbiont Fitness. <i>PLoS ONE</i> , 2016, 11, e0153812.	2.5	31
97	The <i>ingi</i> and <i>RIME</i> non-LTR Retrotransposons Are Not Randomly Distributed in the Genome of <i>Trypanosoma brucei</i> . <i>Molecular Biology and Evolution</i> , 2003, 21, 520-528.	8.9	30
98	Mammalian Adaptation in the PB2 Gene of Avian H5N1 Influenza Virus. <i>Journal of Virology</i> , 2013, 87, 10884-10888.	3.4	30
99	A large-scale immuno-epidemiological simulation of influenza A epidemics. <i>BMC Public Health</i> , 2014, 14, 1019.	2.9	30
100	Inducible Expression of Suicide Genes in <i>Leishmania donovani</i> Amastigotes. <i>Journal of Biological Chemistry</i> , 1998, 273, 22997-23003.	3.4	29
101	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3492-3501.	3.9	29
102	In vivo transfection of developmentally competent <i>Brugia malayi</i> infective larvae. <i>International Journal for Parasitology</i> , 2011, 41, 355-362.	3.1	28
103	Kolente virus, a rhabdovirus species isolated from ticks and bats in the Republic of Guinea. <i>Journal of General Virology</i> , 2013, 94, 2609-2615.	2.9	28
104	Niakha virus: A novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. <i>Virology</i> , 2013, 444, 80-89.	2.4	26
105	Evolution and Cryo-electron Microscopy Capsid Structure of a North American Bat Adenovirus and Its Relationship to Other Mastadenoviruses. <i>Journal of Virology</i> , 2017, 91, .	3.4	26
106	CRISPR-mediated Transfection of <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008627.	3.0	26
107	Initial Mapping of the New York City Wastewater Virome. <i>MSystems</i> , 2020, 5, .	3.8	26
108	The <i>Trypanosoma cruzi</i> L1Tc and NARTc Non-LTR Retrotransposons Show Relative Site Specificity for Insertion. <i>Molecular Biology and Evolution</i> , 2006, 23, 411-420.	8.9	25

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109	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010, 38, D754-D764.	14.5	25
110	Differential HHV-6A gene expression in T cells and primary human astrocytes based on multi-virus array analysis. <i>Glia</i> , 2006, 53, 789-798.	4.9	24
111	The role of RNA folding free energy in the evolution of the polymerase genes of the influenza A virus. <i>Genome Biology</i> , 2009, 10, R18.	9.6	24
112	Filarial and <i>Wolbachia</i> genomics. <i>Parasite Immunology</i> , 2012, 34, 121-129.	1.5	23
113	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. <i>Microbiome</i> , 2018, 6, 180.	11.1	23
114	Comparison of the nasopharynx microbiome between influenza and non-influenza cases of severe acute respiratory infections: A pilot study. <i>Health Science Reports</i> , 2018, 1, e47.	1.5	22
115	Genomic and phenotypic characterization of myxoma virus from Great Britain reveals multiple evolutionary pathways distinct from those in Australia. <i>PLoS Pathogens</i> , 2017, 13, e1006252.	4.7	22
116	Comparative Analysis of the Complete Genome Sequence of the California MSW Strain of Myxoma Virus Reveals Potential Host Adaptations. <i>Journal of Virology</i> , 2013, 87, 12080-12089.	3.4	21
117	Viral evolution: beyond drift and shift. <i>Current Opinion in Microbiology</i> , 2015, 26, 109-115.	5.1	21
118	Getting the flu: 5 key facts about influenza virus evolution. <i>PLoS Pathogens</i> , 2017, 13, e1006450.	4.7	20
119	Pyruvate produced by <i>Brugia</i> spp. via glycolysis is essential for maintaining the mutualistic association between the parasite and its endosymbiont, <i>Wolbachia</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008085.	4.7	20
120	Age-Related Pathology Associated with H1N1 A/California/07/2009 Influenza Virus Infection. <i>American Journal of Pathology</i> , 2019, 189, 2389-2399.	3.8	19
121	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , 2020, 9, .	6.4	19
122	Accurate virus identification with interpretable Raman signatures by machine learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	19
123	Mechanisms of HTLV-1 transformation. <i>Frontiers in Bioscience - Landmark</i> , 2004, 9, 2347.	3.0	17
124	Potential involvement of <i>Brugia malayi</i> cysteine proteases in the maintenance of the endosymbiotic relationship with <i>Wolbachia</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014, 4, 267-277.	3.4	17
125	Network inference from multimodal data: A review of approaches from infectious disease transmission. <i>Journal of Biomedical Informatics</i> , 2016, 64, 44-54.	4.3	17
126	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , 2016, 66, syw096.	5.6	17

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127	Interaction of a Wolbachia WSP-like protein with a nuclear-encoded protein of <i>Brugia malayi</i> . International Journal for Parasitology, 2011, 41, 1053-1061.	3.1	16
128	A2rel: a constitutively expressed <i>Leishmania</i> gene linked to an amastigote-stage-specific gene1Note: The sequence is also available on GenBank®, accession number AF016403.1. Molecular and Biochemical Parasitology, 1998, 93, 23-29.	1.1	15
129	Use of a multi-virus array for the study of human viral and retroviral pathogens: gene expression studies and ChIP-chip analysis. Retrovirology, 2004, 1, 10.	2.0	15
130	Sequences necessary for trans-splicing in transiently transfected <i>Brugia malayi</i> . Molecular and Biochemical Parasitology, 2007, 156, 62-73.	1.1	15
131	Unseasonal Transmission of H3N2 Influenza A Virus During the Swine-Origin H1N1 Pandemic. Journal of Virology, 2010, 84, 5715-5718.	3.4	15
132	Development and Characterization of a Reverse-Genetics System for Influenza D Virus. Journal of Virology, 2019, 93, .	3.4	15
133	Whole Genome Analysis of Sierra Nevada Virus, a Novel Mononegavirus in the Family Nyamiviridae. American Journal of Tropical Medicine and Hygiene, 2014, 91, 159-164.	1.4	14
134	Lessons from the genomes and transcriptomes of filarial nematodes. Molecular and Biochemical Parasitology, 2017, 215, 23-29.	1.1	14
135	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. ELife, 2020, 9, .	6.0	14
136	Functional analysis of putative operons in <i>Brugia malayi</i> . International Journal for Parasitology, 2010, 40, 63-71.	3.1	13
137	Nearly Complete Genome Sequence of <i>Brugia malayi</i> Strain FR3. Microbiology Resource Announcements, 2020, 9, .	0.6	13
138	Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. Journal of General Virology, 2017, 98, 2258-2266.	2.9	13
139	<i>Tropheryma whipplei</i> colonization in HIV-infected individuals is not associated with lung function or inflammation. PLoS ONE, 2018, 13, e0205065.	2.5	12
140	Age-Dependent Glycomic Response to the 2009 Pandemic H1N1 Influenza Virus and Its Association with Disease Severity. Journal of Proteome Research, 2020, 19, 4486-4495.	3.7	12
141	A virus with big ambitions. Trends in Microbiology, 2005, 13, 56-57.	7.7	11
142	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. Npj Systems Biology and Applications, 2017, 3, 35.	3.0	11
143	The role of 'omics' in the quest to eliminate human filariasis. PLoS Neglected Tropical Diseases, 2017, 11, e0005464.	3.0	11
144	Evaluation of determinants of the serological response to the quadrivalent split-inactivated influenza vaccine. Molecular Systems Biology, 2022, 18, e10724.	7.2	11

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145	Genes encoding putative biogenic amine receptors in the parasitic nematode <i>Brugia malayi</i> . <i>Invertebrate Neuroscience</i> , 2007, 7, 227-244.	1.8	10
146	Emerging and Resistant Infections. <i>Annals of the American Thoracic Society</i> , 2014, 11, S193-S200.	3.2	10
147	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	3.4	10
148	New Proteomic Signatures to Distinguish Between Zika and Dengue Infections. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100052.	3.8	10
149	Quantifying between-Host Transmission in Influenza Virus Infections. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a038422.	6.2	9
150	Mapping the evolutionary landscape of Zika virus infection in immunocompromised mice. <i>Virus Evolution</i> , 2020, 6, veaa092.	4.9	9
151	Genetic diversity of the 2013-14 human isolates of influenza H7N9 in China. <i>BMC Infectious Diseases</i> , 2015, 15, 109.	2.9	8
152	Measuring associations between the microbiota and repeated measures of continuous clinical variables using a lasso-penalized generalized linear mixed model. <i>BioData Mining</i> , 2018, 11, 12.	4.0	8
153	LdARF1 in Trafficking and Structural Maintenance of the trans-Golgi Cisternal Network in the Protozoan Pathogen <i>Leishmania donovani</i> . <i>Traffic</i> , 2004, 5, 868-883.	2.7	7
154	Sex disparities in influenza: A multiscale network analysis. <i>IScience</i> , 2022, 25, 104192.	4.1	7
155	Using Clinical Research Networks to Assess Severity of an Emerging Influenza Pandemic. <i>Clinical Infectious Diseases</i> , 2018, 67, 341-349.	5.8	6
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