

# Elodie Ghedin

## List of Publications by Year in descending order

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181  
papers

17,438  
citations

19636

61  
h-index

15716

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.	6.0	1,496
2	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	6.0	1,273
3	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	13.7	945
4	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713
5	Widespread Lateral Gene Transfer from Intracellular Bacteria to Multicellular Eukaryotes. <i>Science</i> , 2007, 317, 1753-1756.	6.0	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.	2.5	655
7	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	6.0	571
8	The <i>Wolbachia</i> Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. <i>PLoS Biology</i> , 2005, 3, e121.	2.6	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.	5.9	436
10	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005, 437, 1162-1166.	13.7	419
11	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016, 161, 2351-2360.	0.9	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.	2.6	340
13	The Evolutionary Genetics and Emergence of Avian Influenza Viruses in Wild Birds. <i>PLoS Pathogens</i> , 2008, 4, e1000076.	2.1	334
14	The human mycobiome in health and disease. <i>Genome Medicine</i> , 2013, 5, 63.	3.6	292
15	Viral genome sequencing by random priming methods. <i>BMC Genomics</i> , 2008, 9, 5.	1.2	282
16	Multiple Reassortment Events in the Evolutionary History of H1N1 Influenza A Virus Since 1918. <i>PLoS Pathogens</i> , 2008, 4, e1000012.	2.1	243
17	Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses. <i>Emerging Infectious Diseases</i> , 2007, 13, 713-718.	2.0	191
18	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184

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19	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016, 48, 195-200.	9.4	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.	2.5	175
21	Stochastic Processes Are Key Determinants of Short-Term Evolution in Influenza A Virus. <i>PLoS Pathogens</i> , 2006, 2, e125.	2.1	173
22	Taxonomy of the order Mononegavirales: update 2017. <i>Archives of Virology</i> , 2017, 162, 2493-2504.	0.9	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.	3.3	157
24	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	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.	3.3	146
26	Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , 2018, 6, 12.	4.9	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.	1.5	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.	0.5	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.	2.5	120
31	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	13.7	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.	1.9	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.	2.5	113
34	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	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.	5.9	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, .	1.5	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. <i>PLoS Pathogens</i> , 2008, 4, e1000133.	2.1	97
38	Stage-specific proteomic expression patterns of the human filarial parasite <i>Brugia malayi</i> and its endosymbiont <i>Wolbachia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9649-9654.	3.3	97
39	The Microbiome and the Lung. <i>Annals of the American Thoracic Society</i> , 2014, 11, S227-S232.	1.5	97
40	Mimivirus relatives in the Sargasso sea. <i>Virology Journal</i> , 2005, 2, 62.	1.4	96
41	Mixed Infection and the Genesis of Influenza Virus Diversity. <i>Journal of Virology</i> , 2009, 83, 8832-8841.	1.5	95
42	A gene family of cathepsin L-like proteases of filarial nematodes are associated with larval molting and cuticle and eggshell remodeling. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 227-242.	0.5	94
43	Biologic, Antigenic, and Full-Length Genomic Characterization of a Bovine-Like Coronavirus Isolated from a Giraffe. <i>Journal of Virology</i> , 2007, 81, 4981-4990.	1.5	94
44	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
45	Evolutionary History and Attenuation of Myxoma Virus on Two Continents. <i>PLoS Pathogens</i> , 2012, 8, e1002950.	2.1	91
46	Identification of mammalian-adapting mutations in the polymerase complex of an avian H5N1 influenza virus. <i>Nature Communications</i> , 2015, 6, 7491.	5.8	91
47	Bovine-Like Coronaviruses Isolated from Four Species of Captive Wild Ruminants Are Homologous to Bovine Coronaviruses, Based on Complete Genomic Sequences. <i>Journal of Virology</i> , 2008, 82, 12422-12431.	1.5	88
48	Members of a Large Retroposon Family Are Determinants of Post-Transcriptional Gene Expression in <i>Leishmania</i> . <i>PLoS Pathogens</i> , 2007, 3, e136.	2.1	87
49	Helminth Genomics: The Implications for Human Health. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e538.	1.3	86
50	A Deep Sequencing Approach to Comparatively Analyze the Transcriptome of Lifecycle Stages of the Filarial Worm, <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1409.	1.3	86
51	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , 2012, 15, 24-33.	3.0	86
52	Mining Predicted Essential Genes of <i>Brugia malayi</i> for Nematode Drug Targets. <i>PLoS ONE</i> , 2007, 2, e1189.	1.1	85
53	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , 2016, 4, 3.	4.9	83
54	Development of high-yield influenza A virus vaccine viruses. <i>Nature Communications</i> , 2015, 6, 8148.	5.8	81

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55	First sequenced genome of a parasitic nematode. <i>Trends in Parasitology</i> , 2004, 20, 151-153.	1.5	80
56	Genomic and Protein Structural Maps of Adaptive Evolution of Human Influenza A Virus to Increased Virulence in the Mouse. <i>PLoS ONE</i> , 2011, 6, e21740.	1.1	79
57	Myxoma Virus and the Leporipoxviruses: An Evolutionary Paradigm. <i>Viruses</i> , 2015, 7, 1020-1061.	1.5	79
58	Deliberate Attenuation of Chikungunya Virus by Adaptation to Heparan Sulfate-Dependent Infectivity: A Model for Rational Arboviral Vaccine Design. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2719.	1.3	78
59	Presence of Oseltamivir-Resistant Pandemic A/H1N1 Minor Variants Before Drug Therapy With Subsequent Selection and Transmission. <i>Journal of Infectious Diseases</i> , 2012, 206, 1504-1511.	1.9	70
60	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 1233-1244.	0.9	70
61	Cyclic Avian Mass Mortality in the Northeastern United States Is Associated with a Novel Orthomyxovirus. <i>Journal of Virology</i> , 2015, 89, 1389-1403.	1.5	68
62	Mesoniviruses are mosquito-specific viruses with extensive geographic distribution and host range. <i>Virology Journal</i> , 2014, 11, 97.	1.4	65
63	Role of viral regulatory and accessory proteins in HIV-1 replication. <i>Frontiers in Bioscience - Landmark</i> , 2004, 9, 2388.	3.0	61
64	Secretory and Endocytic Pathways Converge in a Dynamic Endosomal System in a Primitive Protozoan. <i>Traffic</i> , 2001, 2, 175-188.	1.3	60
65	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003, 31, 4856-4863.	6.5	59
66	Quasispecies of bovine enteric and respiratory coronaviruses based on complete genome sequences and genetic changes after tissue culture adaptation. <i>Virology</i> , 2007, 363, 1-10.	1.1	58
67	Intrahost Dynamics of Antiviral Resistance in Influenza A Virus Reflect Complex Patterns of Segment Linkage, Reassortment, and Natural Selection. <i>MBio</i> , 2015, 6, .	1.8	58
68	The lung mycobiome in the next-generation sequencing era. <i>Virulence</i> , 2017, 8, 334-341.	1.8	57
69	Phylogeography of the Spring and Fall Waves of the H1N1/09 Pandemic Influenza Virus in the United States. <i>Journal of Virology</i> , 2011, 85, 828-834.	1.5	54
70	Molecular characterization of a new species in the genus Alphacoronavirus associated with mink epizootic catarrhal gastroenteritis. <i>Journal of General Virology</i> , 2011, 92, 1369-1379.	1.3	53
71	Dissection of the Functional Domains of the <i>Leishmania</i> Surface Membrane 3'-Nucleotidase/Nuclease, a Unique Member of the Class I Nuclease Family. <i>Journal of Biological Chemistry</i> , 2000, 275, 16366-16372.	1.6	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. <i>Virology</i> , 2007, 358, 424-435.	1.1	50

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73	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1110-1115.	15.2	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.	1.3	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, .	1.8	45
76	The genome of <i>Brugia malayi</i> "All worms are not created equal. <i>Parasitology International</i> , 2009, 58, 6-11.	0.6	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.	1.5	43
78	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. <i>Microbiome</i> , 2016, 4, 38.	4.9	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.	1.3	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.	0.5	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.	4.9	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.	1.3	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.	1.3	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.	3.3	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.	1.3	38
86	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	5.8	38
87	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020, 11, .	1.8	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.	1.6	35
89	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , 2009, 10, 267.	1.2	35
90	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , 2013, 1, 354-356.	5.2	35

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91	Role of transposable elements in trypanosomatids. <i>Microbes and Infection</i> , 2008, 10, 575-581.	1.0	34
92	Microbial Composition of the Human Nasopharynx Varies According to Influenza Virus Type and Vaccination Status. <i>MBio</i> , 2019, 10, .	1.8	34
93	Functional lower airways genomic profiling of the microbiome to capture active microbial metabolism. <i>European Respiratory Journal</i> , 2021, 58, 2003434.	3.1	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.	1.5	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.	0.5	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.	1.1	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.	3.5	30
98	Mammalian Adaptation in the PB2 Gene of Avian H5N1 Influenza Virus. <i>Journal of Virology</i> , 2013, 87, 10884-10888.	1.5	30
99	A large-scale immuno-epidemiological simulation of influenza A epidemics. <i>BMC Public Health</i> , 2014, 14, 1019.	1.2	30
100	Inducible Expression of Suicide Genes in <i>Leishmania donovani</i> Amastigotes. <i>Journal of Biological Chemistry</i> , 1998, 273, 22997-23003.	1.6	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.	1.8	29
102	In vivo transfection of developmentally competent <i>Brugia malayi</i> infective larvae. <i>International Journal for Parasitology</i> , 2011, 41, 355-362.	1.3	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.	1.3	28
104	Niakha virus: A novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. <i>Virology</i> , 2013, 444, 80-89.	1.1	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, .	1.5	26
106	CRISPR-mediated Transfection of <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008627.	1.3	26
107	Initial Mapping of the New York City Wastewater Virome. <i>MSystems</i> , 2020, 5, .	1.7	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.	3.5	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.	6.5	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.	2.5	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.	13.9	24
112	Filarial and <i>Wolbachia</i> genomics. <i>Parasite Immunology</i> , 2012, 34, 121-129.	0.7	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.	4.9	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.	0.6	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.	2.1	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.	1.5	21
117	Viral evolution: beyond drift and shift. <i>Current Opinion in Microbiology</i> , 2015, 26, 109-115.	2.3	21
118	Getting the flu: 5 key facts about influenza virus evolution. <i>PLoS Pathogens</i> , 2017, 13, e1006450.	2.1	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.	2.1	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.	1.9	19
121	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , 2020, 9, .	3.3	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, .	3.3	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.	1.4	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.	2.5	17
126	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , 2016, 66, syw096.	2.7	17



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127	Interaction of a Wolbachia WSP-like protein with a nuclear-encoded protein of <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2011, 41, 1053-1061.	1.3	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. <i>Molecular and Biochemical Parasitology</i> , 1998, 93, 23-29.	0.5	15
129	Use of a multi-virus array for the study of human viral and retroviral pathogens: gene expression studies and ChIP-chip analysis. <i>Retrovirology</i> , 2004, 1, 10.	0.9	15
130	Sequences necessary for trans-splicing in transiently transfected <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 62-73.	0.5	15
131	Unseasonal Transmission of H3N2 Influenza A Virus During the Swine-Origin H1N1 Pandemic. <i>Journal of Virology</i> , 2010, 84, 5715-5718.	1.5	15
132	Development and Characterization of a Reverse-Genetics System for Influenza D Virus. <i>Journal of Virology</i> , 2019, 93, .	1.5	15
133	Whole Genome Analysis of Sierra Nevada Virus, a Novel Mononegavirus in the Family Nyamiviridae. <i>American Journal of Tropical Medicine and Hygiene</i> , 2014, 91, 159-164.	0.6	14
134	Lessons from the genomes and transcriptomes of filarial nematodes. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 23-29.	0.5	14
135	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. <i>ELife</i> , 2020, 9, .	2.8	14
136	Functional analysis of putative operons in <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2010, 40, 63-71.	1.3	13
137	Nearly Complete Genome Sequence of <i>Brugia malayi</i> Strain FR3. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	13
138	Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. <i>Journal of General Virology</i> , 2017, 98, 2258-2266.	1.3	13
139	<i>Tropheryma whipplei</i> colonization in HIV-infected individuals is not associated with lung function or inflammation. <i>PLoS ONE</i> , 2018, 13, e0205065.	1.1	12
140	Age-Dependent Glycomic Response to the 2009 Pandemic H1N1 Influenza Virus and Its Association with Disease Severity. <i>Journal of Proteome Research</i> , 2020, 19, 4486-4495.	1.8	12
141	A virus with big ambitions. <i>Trends in Microbiology</i> , 2005, 13, 56-57.	3.5	11
142	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. <i>Npj Systems Biology and Applications</i> , 2017, 3, 35.	1.4	11
143	The role of 'omics' in the quest to eliminate human filariasis. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005464.	1.3	11
144	Evaluation of determinants of the serological response to the quadrivalent split-inactivated influenza vaccine. <i>Molecular Systems Biology</i> , 2022, 18, e10724.	3.2	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.	1.5	10
147	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	1.5	10
148	New Proteomic Signatures to Distinguish Between Zika and Dengue Infections. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100052.	2.5	10
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