

Elodie Ghedin

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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.

180
papers

13,876
citations

56
h-index

116
g-index

198
ext. papers

15,984
ext. citations

10.1
avg, IF

5.72
L-index

#	Paper	IF	Citations
180	The genome of the African trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005 , 309, 416-22	33.3	1323
179	The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , 2005 , 309, 409-15	33.3	1085
178	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009 , 460, 352-8	50.4	822
177	Comparative genomics of trypanosomatid parasitic protozoa. <i>Science</i> , 2005 , 309, 404-9	33.3	614
176	Widespread lateral gene transfer from intracellular bacteria to multicellular eukaryotes. <i>Science</i> , 2007 , 317, 1753-6	33.3	608
175	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , 2007 , 317, 1756-60	33.3	513
174	Comparison of the respiratory microbiome in healthy nonsmokers and smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 1067-75	10.2	501
173	The <i>Wolbachia</i> genome of <i>Brugia malayi</i> : endosymbiont evolution within a human pathogenic nematode. <i>PLoS Biology</i> , 2005 , 3, e121	9.7	452
172	Large-scale sequencing of human influenza reveals the dynamic nature of viral genome evolution. <i>Nature</i> , 2005 , 437, 1162-6	50.4	354
171	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016 , 161, 2351-60	2.6	324
170	The evolutionary genetics and emergence of avian influenza viruses in wild birds. <i>PLoS Pathogens</i> , 2008 , 4, e1000076	7.6	291
169	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	9.7	291
168	Enrichment of the lung microbiome with oral taxa is associated with lung inflammation of a Th17 phenotype. <i>Nature Microbiology</i> , 2016 , 1, 16031	26.6	268
167	Viral genome sequencing by random priming methods. <i>BMC Genomics</i> , 2008 , 9, 5	4.5	235
166	The human mycobiome in health and disease. <i>Genome Medicine</i> , 2013 , 5, 63	14.4	204
165	Multiple reassortment events in the evolutionary history of H1N1 influenza A virus since 1918. <i>PLoS Pathogens</i> , 2008 , 4, e1000012	7.6	201
164	Genome analysis linking recent European and African influenza (H5N1) viruses. <i>Emerging Infectious Diseases</i> , 2007 , 13, 713-8	10.2	164

163	Stochastic processes are key determinants of short-term evolution in influenza a virus. <i>PLoS Pathogens</i> , 2006 , 2, e125	7.6	152
162	Widespread colonization of the lung by <i>Tropheryma whipplei</i> in HIV infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 187, 1110-7	10.2	140
161	Taxonomy of the order Mononegavirales: update 2017. <i>Archives of Virology</i> , 2017 , 162, 2493-2504	2.6	137
160	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016 , 48, 195-200	36.3	132
159	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, 19359-64	11.5	130
158	Identification and overexpression of the A2 amastigote-specific protein in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 1996 , 78, 79-90	1.9	119
157	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2283-2294	2.6	111
156	Sequence analysis of in vivo defective interfering-like RNA of influenza A H1N1 pandemic virus. <i>Journal of Virology</i> , 2013 , 87, 8064-74	6.6	111
155	The early diversification of influenza A/H1N1pdm. <i>PLOS Currents</i> , 2009 , 1, RRN1126		108
154	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019 , 4, 1727-1736	26.6	100
153	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	11.5	99
152	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, 1335-44	10.2	97
151	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, 932-42	10.2	93
150	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, 168-74	7	91
149	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, 227-42	1.9	88
148	Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , 2018 , 6, 12	16.6	85
147	Mixed infection and the genesis of influenza virus diversity. <i>Journal of Virology</i> , 2009 , 83, 8832-41	6.6	85
146	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	7.6	83

145	Mimivirus relatives in the Sargasso sea. <i>Virology Journal</i> , 2005 , 2, 62	6.1	83
144	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004 , 134, 183-91	1.9	83
143	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, 9649-54	11.5	82
142	Members of a large retroposon family are determinants of post-transcriptional gene expression in <i>Leishmania</i> . <i>PLoS Pathogens</i> , 2007 , 3, 1291-307	7.6	81
141	Helminth genomics: The implications for human health. <i>PLoS Neglected Tropical Diseases</i> , 2009 , 3, e538	4.8	79
140	Mining predicted essential genes of <i>Brugia malayi</i> for nematode drug targets. <i>PLoS ONE</i> , 2007 , 2, e11893	3.7	79
139	Biologic, antigenic, and full-length genomic characterization of a bovine-like coronavirus isolated from a giraffe. <i>Journal of Virology</i> , 2007 , 81, 4981-90	6.6	77
138	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	10	76
137	First sequenced genome of a parasitic nematode. <i>Trends in Parasitology</i> , 2004 , 20, 151-3	6.4	74
136	Evolutionary history and attenuation of myxoma virus on two continents. <i>PLoS Pathogens</i> , 2012 , 8, e1002950	7.5	71
135	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2016 , 2, 16216	26.6	69
134	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	4.8	69
133	Transmission Bottleneck Size Estimation from Pathogen Deep-Sequencing Data, with an Application to Human Influenza A Virus. <i>Journal of Virology</i> , 2017 , 91,	6.6	68
132	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, e27194	4.8	67
131	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, 12422-31	6.6	66
130	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	3.7	65
129	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , 2016 , 4, 3	16.6	62
128	The microbiome and the lung. <i>Annals of the American Thoracic Society</i> , 2014 , 11 Suppl 4, S227-32	4.7	60

127	Identification of mammalian-adapting mutations in the polymerase complex of an avian H5N1 influenza virus. <i>Nature Communications</i> , 2015 , 6, 7491	17.4	58
126	Development of high-yield influenza A virus vaccine viruses. <i>Nature Communications</i> , 2015 , 6, 8148	17.4	57
125	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, 1504-11	7	56
124	Secretory and endocytic pathways converge in a dynamic endosomal system in a primitive protozoan. <i>Traffic</i> , 2001 , 2, 175-88	5.7	56
123	Myxoma virus and the Leporipoxviruses: an evolutionary paradigm. <i>Viruses</i> , 2015 , 7, 1020-61	6.2	52
122	Mesoniviruses are mosquito-specific viruses with extensive geographic distribution and host range. <i>Virology Journal</i> , 2014 , 11, 97	6.1	52
121	Role of viral regulatory and accessory proteins in HIV-1 replication. <i>Frontiers in Bioscience - Landmark</i> , 2004 , 9, 2388-413	2.8	51
120	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019 , 164, 1233-1244.6		50
119	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	3.6	49
118	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003 , 31, 4856-63.1		48
117	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, 828-34	6.6	46
116	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, 424-35	3.6	45
115	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, 16366-72	5.4	45
114	Cyclic avian mass mortality in the northeastern United States is associated with a novel orthomyxovirus. <i>Journal of Virology</i> , 2015 , 89, 1389-403	6.6	44
113	Intrahost dynamics of antiviral resistance in influenza A virus reflect complex patterns of segment linkage, reassortment, and natural selection. <i>MBio</i> , 2015 , 6,	7.8	43
112	Identification of non-autonomous non-LTR retrotransposons in the genome of <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2002 , 124, 73-8	1.9	40
111	<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	4.8	39
110	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	4.9	38

109	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,	7.8	37
108	The lung mycobiome in the next-generation sequencing era. <i>Virulence</i> , 2017 , 8, 334-341	4.7	37
107	The genome of <i>Brugia malayi</i> - all worms are not created equal. <i>Parasitology International</i> , 2009 , 58, 6-112.1		36
106	Extensive geographical mixing of 2009 human H1N1 influenza A virus in a single university community. <i>Journal of Virology</i> , 2011 , 85, 6923-9	6.6	35
105	Arboretum and Puerto Almendras viruses: two novel rhabdoviruses isolated from mosquitoes in Peru. <i>Journal of General Virology</i> , 2014 , 95, 787-792	4.9	34
104	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , 2013 , 1, 354-6	35.1	33
103	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. <i>Microbiome</i> , 2016 , 4, 38	16.6	32
102	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , 2009 , 10, 267	4.5	31
101	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	4.8	30
100	Role of transposable elements in trypanosomatids. <i>Microbes and Infection</i> , 2008 , 10, 575-81	9.3	30
99	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, 158-70	1.9	29
98	The ingi and RIME non-LTR retrotransposons are not randomly distributed in the genome of <i>Trypanosoma brucei</i> . <i>Molecular Biology and Evolution</i> , 2004 , 21, 520-8	8.3	29
97	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, 17994-8001	5.4	29
96	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	4.8	28
95	Inducible expression of suicide genes in <i>Leishmania donovani</i> amastigotes. <i>Journal of Biological Chemistry</i> , 1998 , 273, 22997-3003	5.4	27
94	Mammalian adaptation in the PB2 gene of avian H5N1 influenza virus. <i>Journal of Virology</i> , 2013 , 87, 10884-8		26
93	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	26.6	24
92	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	4.9	23

91	Genome scale evolution of myxoma virus reveals host-pathogen adaptation and rapid geographic spread. <i>Journal of Virology</i> , 2013 , 87, 12900-15	6.6	23
90	In vivo transfection of developmentally competent <i>Brugia malayi</i> infective larvae. <i>International Journal for Parasitology</i> , 2011 , 41, 355-62	4.3	23
89	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, 411-20	8.3	23
88	A large-scale immuno-epidemiological simulation of influenza A epidemics. <i>BMC Public Health</i> , 2014 , 14, 1019	4.1	21
87	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	18.3	21
86	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 3492-3501	9.7	20
85	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020 , 11, 1964	17.4	20
84	Niakha virus: a novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. <i>Virology</i> , 2013 , 444, 80-9	3.6	20
83	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,	6.6	20
82	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , 2010 , 38, D754-64	20.1	20
81	Differential HHV-6A gene expression in T cells and primary human astrocytes based on multi-virus array analysis. <i>Glia</i> , 2006 , 53, 789-98	9	20
80	Glucose and Glycogen Metabolism in <i>Brugia malayi</i> Is Associated with <i>Wolbachia</i> Symbiont Fitness. <i>PLoS ONE</i> , 2016 , 11, e0153812	3.7	19
79	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. <i>Microbiome</i> , 2020 , 8, 39	16.6	18
78	Microbial Composition of the Human Nasopharynx Varies According to Influenza Virus Type and Vaccination Status. <i>MBio</i> , 2019 , 10,	7.8	18
77	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, 12080-9	6.6	18
76	Viral evolution: beyond drift and shift. <i>Current Opinion in Microbiology</i> , 2015 , 26, 109-15	7.9	17
75	Filarial and <i>Wolbachia</i> genomics. <i>Parasite Immunology</i> , 2012 , 34, 121-9	2.2	17
74	Sequences necessary for trans-splicing in transiently transfected <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , 2007 , 156, 62-73	1.9	15

73	Mechanisms of HTLV-1 transformation. <i>Frontiers in Bioscience - Landmark</i> , 2004 , 9, 2347-72	2.8	15
72	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	3.6	15
71	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	11.5	15
70	Network inference from multimodal data: A review of approaches from infectious disease transmission. <i>Journal of Biomedical Informatics</i> , 2016 , 64, 44-54	10.2	15
69	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020 , 11,	7.8	15
68	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	2.2	15
67	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. <i>Microbiome</i> , 2018 , 6, 180	16.6	15
66	Getting the flu: 5 key facts about influenza virus evolution. <i>PLoS Pathogens</i> , 2017 , 13, e1006450	7.6	14
65	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, 267-77	4	14
64	A2rel: a constitutively expressed <i>Leishmania</i> gene linked to an amastigote-stage-specific gene. <i>Molecular and Biochemical Parasitology</i> , 1998 , 93, 23-9	1.9	14
63	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	7.6	14
62	Prediction pipeline for discovery of regulatory motifs associated with <i>Brugia malayi</i> molting. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008275	4.8	13
61	Interaction of a <i>Wolbachia</i> WSP-like protein with a nuclear-encoded protein of <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2011 , 41, 1053-61	4.3	13
60	Unseasonal transmission of H3N2 influenza A virus during the swine-origin H1N1 pandemic. <i>Journal of Virology</i> , 2010 , 84, 5715-8	6.6	13
59	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , 2017 , 66, 463-473	8.4	12
58	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, 159-64	3.2	12
57	Age-Related Pathology Associated with H1N1 A/California/07/2009 Influenza Virus Infection. <i>American Journal of Pathology</i> , 2019 , 189, 2389-2399	5.8	11
56	Initial Mapping of the New York City Wastewater Virome. <i>MSystems</i> , 2020 , 5,	7.6	11

55	Functional analysis of putative operons in <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2010 , 40, 63-71	4.3	11
54	A virus with big ambitions. <i>Trends in Microbiology</i> , 2005 , 13, 56-7	12.4	11
53	Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. <i>Journal of General Virology</i> , 2017 , 98, 2258-2266	4.9	11
52	CRISPR-mediated Transfection of <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008627	4.8	11
51	Genes encoding putative biogenic amine receptors in the parasitic nematode <i>Brugia malayi</i> . <i>Invertebrate Neuroscience</i> , 2007 , 7, 227-44	1.2	10
50	Functional lower airways genomic profiling of the microbiome to capture active microbial metabolism. <i>European Respiratory Journal</i> , 2021 , 58,	13.6	10
49	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , 2020 , 9,	7.6	9
48	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	7.6	8
47	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015 , 89, 9689-92	6.6	8
46	Development and Characterization of a Reverse-Genetics System for Influenza D Virus. <i>Journal of Virology</i> , 2019 , 93,	6.6	8
45	The role of <i>Toxins</i> in the quest to eliminate human filariasis. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005464	4.8	8
44	Lessons from the genomes and transcriptomes of filarial nematodes. <i>Molecular and Biochemical Parasitology</i> , 2017 , 215, 23-29	1.9	7
43	Genetic diversity of the 2013-14 human isolates of influenza H7N9 in China. <i>BMC Infectious Diseases</i> , 2015 , 15, 109	4	7
42	Nearly Complete Genome Sequence of <i>Brugia malayi</i> Strain FR3. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	7
41	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	5	7
40	Defining the risk of SARS-CoV-2 variants on immune protection.. <i>Nature</i> , 2022 ,	50.4	7
39	Quantifying between-Host Transmission in Influenza Virus Infections. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020 , 10,	5.4	6
38	Using Clinical Research Networks to Assess Severity of an Emerging Influenza Pandemic. <i>Clinical Infectious Diseases</i> , 2018 , 67, 341-349	11.6	6

37	Emerging and resistant infections. <i>Annals of the American Thoracic Society</i> , 2014 , 11 Suppl 4, S193-200	4.7	6
36	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, 868-83	5.7	6
35	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. <i>ELife</i> , 2020 , 9,	8.9	6
34	Microbial signatures in the lower airways of mechanically ventilated COVID19 patients associated with poor clinical outcome 2021 ,		6
33	Transmission Bottleneck Size Estimation from Pathogen Deep-Sequencing Data, with an Application to Human Influenza A Virus		5
32	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage		5
31	Functional analysis of microRNA activity in <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , 2015 , 45, 579-83	4.3	4
30	Panning for molecular gold in whipworm genomes. <i>Nature Genetics</i> , 2014 , 46, 661-3	36.3	4
29	Large-scale sequencing and the natural history of model human RNA viruses. <i>Future Virology</i> , 2012 , 7, 563-573	2.4	4
28	Analysis of transcriptional regulation of tetracycline responsive genes in <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , 2011 , 180, 106-11	1.9	4
27	Detection of HHV-6B in post-mortem central nervous system tissue of a post-bone marrow transplant recipient: a multi-virus array analysis. <i>Journal of Clinical Virology</i> , 2006 , 37 Suppl 1, S57-62	14.5	4
26	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	5.6	4
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