

# Elodie Ghedin

## 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.

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	Defining the risk of SARS-CoV-2 variants on immune protection.. <i>Nature</i> , <b>2022</b> ,	50.4	7
179	Sex disparities in influenza: A multiscale network analysis.. <i>IScience</i> , <b>2022</b> , 25, 104192	6.1	
178	Evaluation of determinants of the serological response to the quadrivalent split-inactivated influenza vaccine.. <i>Molecular Systems Biology</i> , <b>2022</b> , 18, e10724	12.2	0
177	Structurally conserved domains between flavivirus and alphavirus fusion glycoproteins contribute to replication and infectious virion production. <i>Journal of Virology</i> , <b>2021</b> , JVI0177421	6.6	0
176	Microbial signatures in the lower airways of mechanically ventilated COVID19 patients associated with poor clinical outcome <b>2021</b> ,		6
175	Detection of SARS-CoV2 variants by Mesa Accula. <i>Journal of Clinical Virology</i> , <b>2021</b> , 141, 104901	14.5	
174	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1245-1258	26.6	24
173	Functional lower airways genomic profiling of the microbiome to capture active microbial metabolism. <i>European Respiratory Journal</i> , <b>2021</b> , 58,	13.6	10
172	New Proteomic Signatures to Distinguish Between Zika and Dengue Infections. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100052	7.6	2
171	Nearly Complete Genome Sequence of <i>Brugia malayi</i> Strain FR3. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	7
170	Initial Mapping of the New York City Wastewater Virome. <i>MSystems</i> , <b>2020</b> , 5,	7.6	11
169	Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. <i>Microbiome</i> , <b>2020</b> , 8, 39	16.6	18
168	Prediction pipeline for discovery of regulatory motifs associated with <i>Brugia malayi</i> molting. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008275	4.8	13
167	Quantifying between-Host Transmission in Influenza Virus Infections. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2020</b> , 10,	5.4	6
166	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , <b>2020</b> , 11, 1964	17.4	20
165	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. <i>ELife</i> , <b>2020</b> , 9,	8.9	6
164	Mapping the evolutionary landscape of Zika virus infection in immunocompromised mice. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa092	3.7	2

163	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> , <b>2020</b> , 117, 895-901	11.5	99
162	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> , <b>2020</b> , 117, 26926-26935	11.5	15
161	Age-Dependent Glycomic Response to the 2009 Pandemic H1N1 Influenza Virus and Its Association with Disease Severity. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 4486-4495	5.6	4
160	iGenomics: Comprehensive DNA sequence analysis on your Smartphone. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	9
159	A Meta-Analysis of Transcriptomics Reveals a Stage-Specific Transcriptional Response Shared Across Different Hosts. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3243-3260	3.2	1
158	CRISPR-mediated Transfection of <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008627	4.8	11
157	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , <b>2020</b> , 11,	7.8	15
156	CRISPR-mediated Transfection of <i>Brugia malayi</i> <b>2020</b> , 14, e0008627		
155	CRISPR-mediated Transfection of <i>Brugia malayi</i> <b>2020</b> , 14, e0008627		
154	CRISPR-mediated Transfection of <i>Brugia malayi</i> <b>2020</b> , 14, e0008627		
153	CRISPR-mediated Transfection of <i>Brugia malayi</i> <b>2020</b> , 14, e0008627		
152	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> , <b>2019</b> , 15, e1008085	7.6	8
151	Age-Related Pathology Associated with H1N1 A/California/07/2009 Influenza Virus Infection. <i>American Journal of Pathology</i> , <b>2019</b> , 189, 2389-2399	5.8	11
150	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , <b>2019</b> , 164, 1233-1244	4.6	50
149	Reply to <b>Reconciling disparate estimates of viral genetic diversity during human influenza infections</b> <i>Nature Genetics</i> , <b>2019</b> , 51, 1301-1303	36.3	1
148	Development and Characterization of a Reverse-Genetics System for Influenza D Virus. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	8
147	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1727-1736	26.6	100
146	Microbial Composition of the Human Nasopharynx Varies According to Influenza Virus Type and Vaccination Status. <i>MBio</i> , <b>2019</b> , 10,	7.8	18

145	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , <b>2018</b> , 163, 2283-2294	2.6	111
144	Measuring associations between the microbiota and repeated measures of continuous clinical variables using a lasso-penalized generalized linear mixed model. <i>BioData Mining</i> , <b>2018</b> , 11, 12	4.3	3
143	Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , <b>2018</b> , 6, 12	16.6	85
142	Using Clinical Research Networks to Assess Severity of an Emerging Influenza Pandemic. <i>Clinical Infectious Diseases</i> , <b>2018</b> , 67, 341-349	11.6	6
141	Comparison of the nasopharynx microbiome between influenza and non-influenza cases of severe acute respiratory infections: A pilot study. <i>Health Science Reports</i> , <b>2018</b> , 1, e47	2.2	15
140	<i>Tropheryma whippelii</i> colonization in HIV-infected individuals is not associated with lung function or inflammation. <i>PLoS ONE</i> , <b>2018</b> , 13, e0205065	3.7	3
139	Profiling the airway in the macaque model of tuberculosis reveals variable microbial dysbiosis and alteration of community structure. <i>Microbiome</i> , <b>2018</b> , 6, 180	16.6	15
138	Lessons from the genomes and transcriptomes of filarial nematodes. <i>Molecular and Biochemical Parasitology</i> , <b>2017</b> , 215, 23-29	1.9	7
137	Taxonomy of the order Mononegavirales: update 2017. <i>Archives of Virology</i> , <b>2017</b> , 162, 2493-2504	2.6	137
136	Transmission Bottleneck Size Estimation from Pathogen Deep-Sequencing Data, with an Application to Human Influenza A Virus. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	68
135	Host response: Pregnancy impairs flu defences. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17077	26.6	2
134	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. <i>Journal of Clinical Microbiology</i> , <b>2017</b> , 55, 3492-3501	9.7	20
133	Getting the flu: 5 key facts about influenza virus evolution. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006450	7.6	14
132	Defining <i>Brugia malayi</i> and <i>Wolbachia</i> symbiosis by stage-specific dual RNA-seq. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005357	4.8	30
131	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , <b>2017</b> , 66, 463-473	8.4	12
130	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. <i>Npj Systems Biology and Applications</i> , <b>2017</b> , 3, 35	5	7
129	Evolution and Cryo-electron Microscopy Capsid Structure of a North American Bat Adenovirus and Its Relationship to Other Mastadenoviruses. <i>Journal of Virology</i> , <b>2017</b> , 91,	6.6	20
128	The lung mycobiome in the next-generation sequencing era. <i>Virulence</i> , <b>2017</b> , 8, 334-341	4.7	37

127	The role of <i>Toxoplasma</i> in the quest to eliminate human filariasis. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005464	4.8	8
126	Genomic and phenotypic characterization of myxoma virus from Great Britain reveals multiple evolutionary pathways distinct from those in Australia. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006252	7.6	14
125	Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. <i>Journal of General Virology</i> , <b>2017</b> , 98, 2258-2266	4.9	11
124	ICTV Virus Taxonomy Profile: Nyamiviridae. <i>Journal of General Virology</i> , <b>2017</b> , 98, 2914-2915	4.9	2
123	Stage-Specific Transcriptome and Proteome Analyses of the Filarial Parasite <i>Onchocerca volvulus</i> and Its <i>Wolbachia</i> Endosymbiont. <i>MBio</i> , <b>2016</b> , 7,	7.8	37
122	Enrichment of the lung microbiome with oral taxa is associated with lung inflammation of a Th17 phenotype. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16031	26.6	268
121	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , <b>2016</b> , 4, 3	16.6	62
120	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , <b>2016</b> , 48, 195-200	36.3	132
119	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16216	26.6	69
118	Glucose and Glycogen Metabolism in <i>Brugia malayi</i> Is Associated with <i>Wolbachia</i> Symbiont Fitness. <i>PLoS ONE</i> , <b>2016</b> , 11, e0153812	3.7	19
117	Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection. <i>Microbiome</i> , <b>2016</b> , 4, 38	16.6	32
116	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , <b>2016</b> , 161, 2351-60	2.6	324
115	Network inference from multimodal data: A review of approaches from infectious disease transmission. <i>Journal of Biomedical Informatics</i> , <b>2016</b> , 64, 44-54	10.2	15
114	Topographic diversity of the respiratory tract mycobiome and alteration in HIV and lung disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2015</b> , 191, 932-42	10.2	93
113	Identification of mammalian-adapting mutations in the polymerase complex of an avian H5N1 influenza virus. <i>Nature Communications</i> , <b>2015</b> , 6, 7491	17.4	58
112	Myxoma virus and the Leporipoxviruses: an evolutionary paradigm. <i>Viruses</i> , <b>2015</b> , 7, 1020-61	6.2	52
111	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , <b>2015</b> , 89, 9689-92	6.6	8
110	Viral evolution: beyond drift and shift. <i>Current Opinion in Microbiology</i> , <b>2015</b> , 26, 109-15	7.9	17

109	Genetic diversity of the 2013-14 human isolates of influenza H7N9 in China. <i>BMC Infectious Diseases</i> , <b>2015</b> , 15, 109	4	7
108	Multicenter Comparison of Lung and Oral Microbiomes of HIV-infected and HIV-uninfected Individuals. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2015</b> , 192, 1335-44	10.2	97
107	Development of high-yield influenza A virus vaccine viruses. <i>Nature Communications</i> , <b>2015</b> , 6, 8148	17.4	57
106	Cyclic avian mass mortality in the northeastern United States is associated with a novel orthomyxovirus. <i>Journal of Virology</i> , <b>2015</b> , 89, 1389-403	6.6	44
105	Functional analysis of microRNA activity in <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , <b>2015</b> , 45, 579-83	4.3	4
104	Intrahost dynamics of antiviral resistance in influenza A virus reflect complex patterns of segment linkage, reassortment, and natural selection. <i>MBio</i> , <b>2015</b> , 6,	7.8	43
103	Identification and analysis of ingi-related retroposons in the trypanosomatid genomes. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1201, 109-22	1.4	3
102	The microbiome and the lung. <i>Annals of the American Thoracic Society</i> , <b>2014</b> , 11 Suppl 4, S227-32	4.7	60
101	Whole genome analysis of sierra nevada virus, a novel mononegavirus in the family nyamiviridae. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2014</b> , 91, 159-64	3.2	12
100	Arboretum and Puerto Almendras viruses: two novel rhabdoviruses isolated from mosquitoes in Peru. <i>Journal of General Virology</i> , <b>2014</b> , 95, 787-792	4.9	34
99	Mesoniviruses are mosquito-specific viruses with extensive geographic distribution and host range. <i>Virology Journal</i> , <b>2014</b> , 11, 97	6.1	52
98	Panning for molecular gold in whipworm genomes. <i>Nature Genetics</i> , <b>2014</b> , 46, 661-3	36.3	4
97	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> , <b>2014</b> , 8, e2719	4.8	67
96	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> , <b>2014</b> , 4, 267-77	4	14
95	Emerging and resistant infections. <i>Annals of the American Thoracic Society</i> , <b>2014</b> , 11 Suppl 4, S193-200	4.7	6
94	A large-scale immuno-epidemiological simulation of influenza A epidemics. <i>BMC Public Health</i> , <b>2014</b> , 14, 1019	4.1	21
93	Niakha virus: a novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. <i>Virology</i> , <b>2013</b> , 444, 80-9	3.6	20
92	Kolente virus, a rhabdovirus species isolated from ticks and bats in the Republic of Guinea. <i>Journal of General Virology</i> , <b>2013</b> , 94, 2609-2615	4.9	23

91	The human mycobiome in health and disease. <i>Genome Medicine</i> , <b>2013</b> , 5, 63	14.4	204
90	Genome scale evolution of myxoma virus reveals host-pathogen adaptation and rapid geographic spread. <i>Journal of Virology</i> , <b>2013</b> , 87, 12900-15	6.6	23
89	Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. <i>Lancet Respiratory Medicine</i> , <b>2013</b> , 1, 354-6	35.1	33
88	Comparison of the respiratory microbiome in healthy nonsmokers and smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2013</b> , 187, 1067-75	10.2	501
87	Widespread colonization of the lung by <i>Tropheryma whipplei</i> in HIV infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2013</b> , 187, 1110-7	10.2	140
86	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> , <b>2013</b> , 7, e2151	4.8	28
85	Mammalian adaptation in the PB2 gene of avian H5N1 influenza virus. <i>Journal of Virology</i> , <b>2013</b> , 87, 10884-8	6.6	26
84	Sequence analysis of in vivo defective interfering-like RNA of influenza A H1N1 pandemic virus. <i>Journal of Virology</i> , <b>2013</b> , 87, 8064-74	6.6	111
83	Comparative analysis of the complete genome sequence of the California MSW strain of myxoma virus reveals potential host adaptations. <i>Journal of Virology</i> , <b>2013</b> , 87, 12080-9	6.6	18
82	Filarial and <i>Wolbachia</i> genomics. <i>Parasite Immunology</i> , <b>2012</b> , 34, 121-9	2.2	17
81	Large-scale sequencing and the natural history of model human RNA viruses. <i>Future Virology</i> , <b>2012</b> , 7, 563-573	2.4	4
80	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , <b>2012</b> , 15, 24-33	10	76
79	Evolutionary history and attenuation of myxoma virus on two continents. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002950	7.5	71
78	Presence of oseltamivir-resistant pandemic A/H1N1 minor variants before drug therapy with subsequent selection and transmission. <i>Journal of Infectious Diseases</i> , <b>2012</b> , 206, 1504-11	7	56
77	Genomic and protein structural maps of adaptive evolution of human influenza A virus to increased virulence in the mouse. <i>PLoS ONE</i> , <b>2011</b> , 6, e21740	3.7	65
76	Analysis of transcriptional regulation of tetracycline responsive genes in <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , <b>2011</b> , 180, 106-11	1.9	4
75	In vivo transfection of developmentally competent <i>Brugia malayi</i> infective larvae. <i>International Journal for Parasitology</i> , <b>2011</b> , 41, 355-62	4.3	23
74	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> , <b>2011</b> , 41, 1053-61	4.3	13

73	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> , <b>2011</b> , 203, 168-74	7	91
72	Phylogeography of the spring and fall waves of the H1N1/09 pandemic influenza virus in the United States. <i>Journal of Virology</i> , <b>2011</b> , 85, 828-34	6.6	46
71	Molecular characterization of a new species in the genus Alphacoronavirus associated with mink epizootic catarrhal gastroenteritis. <i>Journal of General Virology</i> , <b>2011</b> , 92, 1369-1379	4.9	38
70	Extensive geographical mixing of 2009 human H1N1 influenza A virus in a single university community. <i>Journal of Virology</i> , <b>2011</b> , 85, 6923-9	6.6	35
69	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> , <b>2011</b> , 108, 9649-54	11.5	82
68	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> , <b>2011</b> , 108, 19359-64	11.5	130
67	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> , <b>2011</b> , 5, e1409	4.8	69
66	The Human Lung Microbiome <b>2011</b> , 117-143		
65	GeMInA, Genomic Metadata for Infectious Agents, a geospatial surveillance pathogen database. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D754-64	20.1	20
64	Unseasonal transmission of H3N2 influenza A virus during the swine-origin H1N1 pandemic. <i>Journal of Virology</i> , <b>2010</b> , 84, 5715-8	6.6	13
63	Functional analysis of putative operons in <i>Brugia malayi</i> . <i>International Journal for Parasitology</i> , <b>2010</b> , 40, 63-71	4.3	11
62	Mixed infection and the genesis of influenza virus diversity. <i>Journal of Virology</i> , <b>2009</b> , 83, 8832-41	6.6	85
61	Helminth genomics: The implications for human health. <i>PLoS Neglected Tropical Diseases</i> , <b>2009</b> , 3, e538	4.8	79
60	<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> , <b>2009</b> , 3, e525	4.8	39
59	A multi-reservoir model of influenza evolution. <i>Journal of Critical Care</i> , <b>2009</b> , 24, e33-e34	4	
58	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , <b>2009</b> , 10, 267	4.5	31
57	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , <b>2009</b> , 460, 352-8	50.4	822
56	The genome of <i>Brugia malayi</i> - all worms are not created equal. <i>Parasitology International</i> , <b>2009</b> , 58, 6-11	12.1	36



55	The role of RNA folding free energy in the evolution of the polymerase genes of the influenza A virus. <i>Genome Biology</i> , <b>2009</b> , 10, R18	18.3	21
54	The early diversification of influenza A/H1N1pdm. <i>PLOS Currents</i> , <b>2009</b> , 1, RRN1126		108
53	Viral genome sequencing by random priming methods. <i>BMC Genomics</i> , <b>2008</b> , 9, 5	4.5	235
52	Multiple reassortment events in the evolutionary history of H1N1 influenza A virus since 1918. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000012	7.6	201
51	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> , <b>2008</b> , 82, 12422-31	6.6	66
50	The evolutionary genetics and emergence of avian influenza viruses in wild birds. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000076	7.6	291
49	Molecular epidemiology of A/H3N2 and A/H1N1 influenza virus during a single epidemic season in the United States. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000133	7.6	83
48	Role of transposable elements in trypanosomatids. <i>Microbes and Infection</i> , <b>2008</b> , 10, 575-81	9.3	30
47	Mining predicted essential genes of <i>Brugia malayi</i> for nematode drug targets. <i>PLoS ONE</i> , <b>2007</b> , 2, e11893	3.7	79
46	Genome analysis linking recent European and African influenza (H5N1) viruses. <i>Emerging Infectious Diseases</i> , <b>2007</b> , 13, 713-8	10.2	164
45	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> , <b>2007</b> , 358, 424-35	3.6	45
44	Quasispecies of bovine enteric and respiratory coronaviruses based on complete genome sequences and genetic changes after tissue culture adaptation. <i>Virology</i> , <b>2007</b> , 363, 1-10	3.6	49
43	Sequences necessary for trans-splicing in transiently transfected <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , <b>2007</b> , 156, 62-73	1.9	15
42	Widespread lateral gene transfer from intracellular bacteria to multicellular eukaryotes. <i>Science</i> , <b>2007</b> , 317, 1753-6	33.3	608
41	Genes encoding putative biogenic amine receptors in the parasitic nematode <i>Brugia malayi</i> . <i>Invertebrate Neuroscience</i> , <b>2007</b> , 7, 227-44	1.2	10
40	Biologic, antigenic, and full-length genomic characterization of a bovine-like coronavirus isolated from a giraffe. <i>Journal of Virology</i> , <b>2007</b> , 81, 4981-90	6.6	77
39	Members of a large retroposon family are determinants of post-transcriptional gene expression in <i>Leishmania</i> . <i>PLoS Pathogens</i> , <b>2007</b> , 3, 1291-307	7.6	81
38	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , <b>2007</b> , 317, 1756-60	33.3	513

37	Gemina: A Web-Based Epidemiology and Genomic Metadata System Designed to Identify Infectious Agents <b>2007</b> , 228-229		1
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3	Cell-to-cell variation in defective virus expression and effects on host responses during influenza virus infection		3
2	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage		5

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