Remi Charrel

List of Publications by Year in descending order

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339 papers

15,302 citations

15503 65 h-index 27402 106 g-index

351 all docs

351 docs citations

351 times ranked

14992 citing authors

#	Article	IF	Citations
1	Phlebotomine sandflies and the spreading of leishmaniases and other diseases of public health concern. Medical and Veterinary Entomology, 2013, 27, 123-147.	1.5	550
2	Chikungunya Outbreaks â€" The Globalization of Vectorborne Diseases. New England Journal of Medicine, 2007, 356, 769-771.	27.0	394
3	Emerging arboviruses: Why today?. One Health, 2017, 4, 1-13.	3.4	326
4	Novel Chikungunya Virus Variant in Travelers Returning from Indian Ocean Islands. Emerging Infectious Diseases, 2006, 12, 1493-1499.	4.3	295
5	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	2.1	285
6	Tick-borne virus diseases of human interest in Europe. Clinical Microbiology and Infection, 2004, 10, 1040-1055.	6.0	264
7	Chikungunya virus adapts to tiger mosquito via evolutionary convergence: a sign of things to come?. Virology Journal, 2008, 5, 33.	3.4	262
8	Sequences of flavivirus-related RNA viruses persist in DNA form integrated in the genome of Aedes spp. mosquitoes. Journal of General Virology, 2004, 85, 1971-1980.	2.9	250
9	Emergence of Toscana Virus in Europe. Emerging Infectious Diseases, 2005, 11, 1657-1663.	4.3	250
10	Chikungunya Infection. Medicine (United States), 2007, 86, 123-137.	1.0	250
11	First cases of autochthonous dengue fever and chikungunya fever in France: from bad dream to reality!. Clinical Microbiology and Infection, 2010, 16, 1702-1704.	6.0	239
12	Genetic characterization of tick-borne flaviviruses: New insights into evolution, pathogenetic		
	determinants and taxonomy. Virology, 2007, 361, 80-92.	2.4	229
13	Complete Coding Sequence of Zika Virus from a French Polynesia Outbreak in 2013. Genome Announcements, 2014, 2, .	0.8	210
13 14	Complete Coding Sequence of Zika Virus from a French Polynesia Outbreak in 2013. Genome		
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14	Complete Coding Sequence of Zika Virus from a French Polynesia Outbreak in 2013. Genome Announcements, 2014, 2, . On Chikungunya Acute Infection and Chloroquine Treatment. Vector-Borne and Zoonotic Diseases, 2008, 8, 837-840. Concurrent Chikungunya and Dengue Virus Infections during Simultaneous Outbreaks, Gabon, 2007.	0.8	210
14 15	Complete Coding Sequence of Zika Virus from a French Polynesia Outbreak in 2013. Genome Announcements, 2014, 2, . On Chikungunya Acute Infection and Chloroquine Treatment. Vector-Borne and Zoonotic Diseases, 2008, 8, 837-840. Concurrent Chikungunya and Dengue Virus Infections during Simultaneous Outbreaks, Gabon, 2007. Emerging Infectious Diseases, 2009, 15, 591-593.	0.8 1.5 4.3	210 202 194

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19	A Real-Time RT-PCR Method for the Universal Detection and Identification of Flaviviruses. Vector-Borne and Zoonotic Diseases, 2007, 7, 467-478.	1.5	174
20	Prolonged Infectivity of SARS-CoV-2 in Fomites. Emerging Infectious Diseases, 2020, 26, 2256-2257.	4.3	172
21	Past, present, and future of arenavirus taxonomy. Archives of Virology, 2015, 160, 1851-1874.	2.1	158
22	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	2.1	157
23	Sandfly-borne phleboviruses of Eurasia and Africa: Epidemiology, genetic diversity, geographic range, control measures. Antiviral Research, 2013, 100, 54-74.	4.1	153
24	Laboratory readiness and response for novel coronavirus (2019-nCoV) in expert laboratories in 30 EU/EEA countries, January 2020. Eurosurveillance, 2020, 25, .	7.0	153
25	West Nile virus in Europe: emergence, epidemiology, diagnosis, treatment, and prevention. Clinical Microbiology and Infection, 2013, 19, 699-704.	6.0	148
26	Vector-free transmission and persistence of Japanese encephalitis virus in pigs. Nature Communications, 2016, 7, 10832.	12.8	146
27	The N-Terminal Domain of the Arenavirus L Protein Is an RNA Endonuclease Essential in mRNA Transcription. PLoS Pathogens, 2010, 6, e1001038.	4.7	145
28	New Insights into Flavivirus Evolution, Taxonomy and Biogeographic History, Extended by Analysis of Canonical and Alternative Coding Sequences. PLoS ONE, 2015, 10, e0117849.	2.5	139
29	Zoonotic aspects of arenavirus infections. Veterinary Microbiology, 2010, 140, 213-220.	1.9	127
30	Heat Inactivation of Different Types of SARS-CoV-2 Samples: What Protocols for Biosafety, Molecular Detection and Serological Diagnostics?. Viruses, 2020, 12, 735.	3.3	127
31	Complete Coding Sequence of the Alkhurma Virus, a Tick-Borne Flavivirus Causing Severe Hemorrhagic Fever in Humans in Saudi Arabia. Biochemical and Biophysical Research Communications, 2001, 287, 455-461.	2.1	125
32	RNA and DNA Bacteriophages as Molecular Diagnosis Controls in Clinical Virology: A Comprehensive Study of More than 45,000 Routine PCR Tests. PLoS ONE, 2011, 6, e16142.	2.5	121
33	Extracorporeal membrane oxygenation for severe influenzaÂA (H1N1) acute respiratory distress syndrome: a prospective observational comparative study. Intensive Care Medicine, 2010, 36, 1899-1905.	8.2	120
34	How Did Zika Virus Emerge in the Pacific Islands and Latin America?. MBio, 2016, 7, .	4.1	119
35	Evidence for recombination in natural populations of dengue virus type 1 based on the analysis of complete genome sequences. Journal of General Virology, 2001, 82, 1283-1290.	2.9	119
36	Development and validation of real-time one-step reverse transcription-PCR for the detection and typing of dengue viruses. Journal of Clinical Virology, 2009, 45, 61-66.	3.1	117

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37	Cowpox Virus Transmission from Pet Rats to Humans, France. Emerging Infectious Diseases, 2009, 15, 781-784.	4.3	115
38	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	2.1	115
39	Phylogeny of the genus Arenavirus. Current Opinion in Microbiology, 2008, 11, 362-368.	5.1	108
40	Zika virus in asymptomatic blood donors in Martinique. Blood, 2017, 129, 263-266.	1.4	108
41	Respiratory Viruses and Bacteria among Pilgrims during the 2013 Hajj. Emerging Infectious Diseases, 2014, 20, 1821-1827.	4.3	107
42	Background review for diagnostic test development for Zika virus infection. Bulletin of the World Health Organization, 2016, 94, 574-584D.	3.3	104
43	Prevalence of outer membrane porin alteration in beta-lactam-antibiotic-resistant Enterobacter aerogenes. Antimicrobial Agents and Chemotherapy, 1996, 40, 2854-2858.	3.2	103
44	Mass gathering and globalization of respiratory pathogens during the 2013 Hajj. Clinical Microbiology and Infection, 2015, 21, 571.e1-571.e8.	6.0	103
45	Massilia Virus, A Novel <i>Phlebovirus (Bunyaviridae)</i> Isolated from Sandflies in the Mediterranean. Vector-Borne and Zoonotic Diseases, 2009, 9, 519-530.	1.5	94
46	Hepatitis GB Virus C in Patients on Hemodialysis. New England Journal of Medicine, 1996, 334, 1549-1549.	27.0	93
47			
47	The Hexamer Structure of the Rift Valley Fever Virus Nucleoprotein Suggests a Mechanism for its Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030.	4.7	93
48	The Hexamer Structure of the Rift Valley Fever Virus Nucleoprotein Suggests a Mechanism for its Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical and Biophysical Research Communications, 2002, 296, 1118-1124.	4.7 2.1	93
	Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical		
48	Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical and Biophysical Research Communications, 2002, 296, 1118-1124. Circulation of Respiratory Viruses Among Pilgrims During the 2012 Hajj Pilgrimage. Clinical Infectious	2.1	91
48	Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical and Biophysical Research Communications, 2002, 296, 1118-1124. Circulation of Respiratory Viruses Among Pilgrims During the 2012 Hajj Pilgrimage. Clinical Infectious Diseases, 2013, 57, 992-1000. Prevalence of gastrointestinal symptoms in patients with influenza, clinical significance, and pathophysiology of human influenza viruses in faecal samples: what do we know?. Virology Journal,	2.1 5.8	91
48 49 50	Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical and Biophysical Research Communications, 2002, 296, 1118-1124. Circulation of Respiratory Viruses Among Pilgrims During the 2012 Hajj Pilgrimage. Clinical Infectious Diseases, 2013, 57, 992-1000. Prevalence of gastrointestinal symptoms in patients with influenza, clinical significance, and pathophysiology of human influenza viruses in faecal samples: what do we know?. Virology Journal, 2015, 12, 215. Alkhurma Hemorrhagic Fever Virus in	2.1 5.8 3.4	91 90 88
48 49 50 51	Assembly into Ribonucleoprotein Complexes. PLoS Pathogens, 2011, 7, e1002030. Phylogeny of New World arenaviruses based on the complete coding sequences of the small genomic segment identified an evolutionary lineage produced by intrasegmental recombination. Biochemical and Biophysical Research Communications, 2002, 296, 1118-1124. Circulation of Respiratory Viruses Among Pilgrims During the 2012 Hajj Pilgrimage. Clinical Infectious Diseases, 2013, 57, 992-1000. Prevalence of gastrointestinal symptoms in patients with influenza, clinical significance, and pathophysiology of human influenza viruses in faecal samples: what do we know?. Virology Journal, 2015, 12, 215. Alkhurma Hemorrhagic Fever Virus in <i>Ornithodoros savignyi </i> /i>Ticks. Emerging Infectious Diseases, 2007, 13, 153-155.	2.1 5.8 3.4 4.3	91 90 88 85

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55	Cocirculation of 2 Genotypes of Toscana Virus, Southeastern France. Emerging Infectious Diseases, 2007, 13, 465-468.	4.3	81
56	Measles among healthcare workers: a potential for nosocomial outbreaks. Eurosurveillance, 2011, 16, .	7.0	81
57	The nasopharyngeal microbiota in patients with viral respiratory tract infections is enriched in bacterial pathogens. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 1725-1733.	2.9	78
58	Molecular epidemiology of Enterobacter aerogenes acquisition: one-year prospective study in two intensive care units. Journal of Clinical Microbiology, 1996, 34, 1474-1480.	3.9	78
59	Lack of nasal carriage of novel corona virus (HCoV-EMC) in French Hajj pilgrims returning from the Hajj 2012, despite a high rate of respiratory symptoms. Clinical Microbiology and Infection, 2013, 19, E315-E317.	6.0	77
60	Genomics and evolution of Aedes-borne flaviviruses. Journal of General Virology, 2010, 91, 87-94.	2.9	74
61	Lack of MERS Coronavirus but Prevalence of Influenza Virus in French Pilgrims after 2013 Hajj. Emerging Infectious Diseases, 2014, 20, 726-728.	4.3	72
62	Phlebotomine sand fly–borne pathogens in the Mediterranean Basin: Human leishmaniasis and phlebovirus infections. PLoS Neglected Tropical Diseases, 2017, 11, e0005660.	3.0	72
63	The Whitewater Arroyo Virus: Natural Evidence for Genetic Recombination among Tacaribe Serocomplex Viruses (Family Arenaviridae). Virology, 2001, 283, 161-166.	2.4	71
64	Punique virus, a novel phlebovirus, related to sandfly fever Naples virus, isolated from sandflies collected in Tunisia. Journal of General Virology, 2010, 91, 1275-1283.	2.9	70
65	Toscana Virus RNA in <i>Sergentomyia minuta</i> Flies. Emerging Infectious Diseases, 2006, 12, 1299-1300.	4.3	70
66	Evaluation of the first commercial chikungunya virus indirect immunofluorescence test. Journal of Virological Methods, 2008, 149, 175-179.	2.1	69
67	Variations in DNA concentrations significantly affect the reproducibility of RAPD fingerprint patterns. Research in Microbiology, 1995, 146, 561-568.	2.1	66
68	ICTV Virus Taxonomy Profile: Arenaviridae. Journal of General Virology, 2019, 100, 1200-1201.	2.9	66
69	First Detection of Leishmania major DNA in Sergentomyia (Spelaeomyia) darlingi from Cutaneous Leishmaniasis Foci in Mali. PLoS ONE, 2012, 7, e28266.	2.5	66
70	Revolutionizing Clinical Microbiology Laboratory Organization in Hospitals with In Situ Point-of-Care. PLoS ONE, 2011, 6, e22403.	2.5	65
71	Sandfly Fever Sicilian Virus, Algeria. Emerging Infectious Diseases, 2008, 14, 795-797.	4.3	64
72	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	2.1	62

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73	Sandfly fever due to Toscana virus: an emerging infection in southern France. European Journal of Internal Medicine, 2004, 15, 316-317.	2.2	57
74	Phylogeny and evolution of old world arenaviruses. Virology, 2006, 350, 251-257.	2.4	56
75	Low Diversity of Alkhurma Hemorrhagic Fever Virus, Saudi Arabia, 1994–1999. Emerging Infectious Diseases, 2005, 11, 683-688.	4.3	55
76	Arenaviruses. Current Topics in Microbiology and Immunology, 2007, 315, 253-288.	1.1	55
77	Antiviral Treatment of Chikungunya Virus Infection. Infectious Disorders - Drug Targets, 2009, 9, 101-104.	0.8	55
78	Concurrent Dengue and Malaria. Emerging Infectious Diseases, 2005, 11, 1153-1154.	4.3	54
79	Mopeia Virus–related Arenavirus in Natal Multimammate Mice <i>>,</i>) Morogoro, Tanzania. Emerging Infectious Diseases, 2009, 15, 2008-2012.	4.3	54
80	A Sero-epidemiological Study of Arboviral Fevers in Djibouti, Horn of Africa. PLoS Neglected Tropical Diseases, 2014, 8, e3299.	3.0	54
81	Diagnosis of West Nile Virus Human Infections: Overview and Proposal of Diagnostic Protocols Considering the Results of External Quality Assessment Studies. Viruses, 2013, 5, 2329-2348.	3.3	53
82	Emerging viral respiratory tract infectionsâ€"environmental risk factors and transmission. Lancet Infectious Diseases, The, 2014, 14, 1113-1122.	9.1	53
83	Prospective and retrospective evaluation of the Cepheid Xpert \hat{A}^{\otimes} Flu/RSV XC assay for rapid detection of influenza A, influenza B, and respiratory syncytial virus. Diagnostic Microbiology and Infectious Disease, 2015, 81, 256-258.	1.8	53
84	Serratia marcescens nosocomial outbreak due to contamination of hexetidine solution. Journal of Hospital Infection, 1996, 33, 217-224.	2.9	52
85	Likely Correlation between Sources of Information and Acceptability of A/H1N1 Swine-Origin Influenza Virus Vaccine in Marseille, France. PLoS ONE, 2010, 5, e11292.	2.5	52
86	Geographic Distribution and Genetic Diversity of Whitewater Arroyo Virus in the Southwestern United States. Emerging Infectious Diseases, 2001, 7, 403-407.	4.3	51
87	New insights into the evolutionary relationships between arenaviruses provided by comparative analysis of small and large segment sequences. Virology, 2003, 317, 191-196.	2.4	51
88	Prospective detection of chikungunya virus in blood donors, Caribbean 2014. Blood, 2014, 123, 3679-3681.	1.4	51
89	Isolation, Genetic Characterization, and Seroprevalence of Adana Virus, a Novel Phlebovirus Belonging to the Salehabad Virus Complex, in Turkey. Journal of Virology, 2015, 89, 4080-4091.	3.4	51
90	Neurologic Disorders and Hepatitis E, France, 2010. Emerging Infectious Diseases, 2011, 17, 1510-2.	4.3	50

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91	Contribution of a shelter-based survey for screening respiratory diseases in the homeless. European Journal of Public Health, 2009, 19, 157-160.	0.3	47
92	Yellow fever in the diagnostics laboratory. Emerging Microbes and Infections, 2018, 7, 1-15.	6.5	47
93	Delayed Laboratory Response to COVID-19 Caused by Molecular Diagnostic Contamination. Emerging Infectious Diseases, 2020, 26, 1944-1946.	4.3	47
94	Prevalence of Toscana Virus Antibodies in Volunteer Blood Donors and Patients with Central Nervous System Infections in Southeastern France. Vector-Borne and Zoonotic Diseases, 2007, 7, 275-277.	1.5	44
95	Epidemiology of Chikungunya Virus Outbreaks in Guadeloupe and Martinique, 2014: An Observational Study in Volunteer Blood Donors. PLoS Neglected Tropical Diseases, 2017, 11, e0005254.	3.0	44
96	Sandfly-Borne Phlebovirus Isolations from Turkey: New Insight into the Sandfly fever Sicilian and Sandfly fever Naples Species. PLoS Neglected Tropical Diseases, 2016, 10, e0004519.	3.0	44
97	Arenaviruses and hantaviruses: From epidemiology and genomics to antivirals. Antiviral Research, 2011, 90, 102-114.	4.1	43
98	Mouse-to-Human Transmission of Variant Lymphocytic Choriomeningitis Virus. Emerging Infectious Diseases, 2007, 13, 472-475.	4.3	42
99	Globalization of Chikungunya: 10 years to invade the world. Clinical Microbiology and Infection, 2014, 20, 662-663.	6.0	42
100	Flavivirus RNA in Phlebotomine Sandflies. Vector-Borne and Zoonotic Diseases, 2010, 10, 195-197.	1.5	41
101	Patterns of Kingella kingae Disease Outbreaks. Pediatric Infectious Disease Journal, 2016, 35, 340-346.	2.0	41
102	Association of TT Virus Primary Infection with Rhinitis in a Newborn. Clinical Infectious Diseases, 2003, 36, 128-129.	5.8	39
103	Toscana Virus Isolated from Sandflies, Tunisia. Emerging Infectious Diseases, 2013, 19, 322-324.	4.3	38
104	A nosocomial outbreak due to Enterobacter cloacae strains with the E. hormaechei genotype in patients treated with fluoroquinolones. Journal of Clinical Microbiology, 1997, 35, 1008-1010.	3.9	38
105	Sheep-to-Human Transmission of Orf Virus during Eid al-Adha Religious Practices, France. Emerging Infectious Diseases, 2013, 19, 102-105.	4.3	37
106	Meta-Analysis of Human IgG anti-HEV Seroprevalence in Industrialized Countries and a Review of Literature. Viruses, 2019, 11, 84.	3.3	37
107	Seroprevalence of Sandflyâ∈Borne Phleboviruses Belonging to Three Serocomplexes (Sandfly fever) Tj ETQq1 1 Test. PLoS Neglected Tropical Diseases, 2016, 10, e0005063.	0.784314 3.0	rgBT /Overloc 37
108	Prospective Investigation of a Large Outbreak of Meningitis Due to Echovirus 30 During Summer 2000 in Marseilles, France. Medicine (United States), 2004, 83, 245-253.	1.0	36

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109	Coordinated Implementation of Chikungunya Virus Reverse Transcription–PCR. Emerging Infectious Diseases, 2009, 15, 469-471.	4.3	36
110	An Outbreak of Kingella kingae Infections Associated with Hand, Foot and Mouth Disease/Herpangina Virus Outbreak in Marseille, France, 2013. Pediatric Infectious Disease Journal, 2015, 34, 246-250.	2.0	34
111	Seasonality of mosquitoes and chikungunya in Italy. Lancet Infectious Diseases, The, 2008, 8, 5-6.	9.1	33
112	Epidemiologic Relationship between Toscana Virus Infection and Leishmania infantum Due to Common Exposure to Phlebotomus perniciosus Sandfly Vector. PLoS Neglected Tropical Diseases, 2011, 5, e1328.	3.0	33
113	First detection of Leishmania infantum DNA in Phlebotomus longicuspis Nitzulescu, 1930 from visceral leishmaniasis endemic focus in Algeria. Parasitology Research, 2012, 111, 419-422.	1.6	33
114	Co-Circulation of Toscana Virus and Punique Virus in Northern Tunisia: A Microneutralisation-Based Seroprevalence Study. PLoS Neglected Tropical Diseases, 2013, 7, e2429.	3.0	33
115	Widespread circulation of a new echovirus 30 variant causing aseptic meningitis and non-specific viral illness, South-East France, 2013. Journal of Clinical Virology, 2014, 61, 118-124.	3.1	33
116	Sarcoptes scabiei mites in humans are distributed into three genetically distinct clades. Clinical Microbiology and Infection, 2015, 21, 1107-1114.	6.0	33
117	Virus isolation, genetic characterization and seroprevalence of Toscana virus in Algeria. Clinical Microbiology and Infection, 2015, 21, 1040.e1-1040.e9.	6.0	33
118	Of phlebotomines (sandflies) and viruses: a comprehensive perspective on a complex situation. Current Opinion in Insect Science, 2017, 22, 117-124.	4.4	33
119	Lineage-Specific Real-Time RT-PCR for Yellow Fever Virus Outbreak Surveillance, Brazil. Emerging Infectious Diseases, 2017, 23, 1867-1871.	4.3	33
120	An update on Toscana virus distribution, genetics, medical and diagnostic aspects. Clinical Microbiology and Infection, 2020, 26, 1017-1023.	6.0	33
121	Phylogenetic analysis of GB viruses A and C: evidence for cospeciation between virus isolates and their primate hosts. Journal of General Virology, 1999, 80, 2329-2335.	2.9	33
122	Alkhurma haemorrhagic fever—a viral haemorrhagic disease unique to the Arabian Peninsula. International Journal of Antimicrobial Agents, 2010, 36, S53-S57.	2.5	31
123	Ecuador Paraiso Escondido Virus, a New Flavivirus Isolated from New World Sand Flies in Ecuador, Is the First Representative of a Novel Clade in the Genus Flavivirus. Journal of Virology, 2015, 89, 11773-11785.	3.4	31
124	Hepatitis E in High-Income Countries: What Do We Know? And What Are the Knowledge Gaps?. Viruses, 2018, 10, 285.	3.3	31
125	Neutralization-based seroprevalence of Toscana virus and sandfly fever Sicilian virus in dogs and cats from Portugal. Journal of General Virology, 2016, 97, 2816-2823.	2.9	31
126	Dengue Virus Type 3 Infection in Traveler Returning from West Africa. Emerging Infectious Diseases, 2009, 15, 1871-1872.	4.3	30

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127	The viral etiology of an influenzaâ€like illness during the 2009 pandemic. Journal of Medical Virology, 2012, 84, 1071-1079.	5.0	30
128	The European Virus Archive goes global: A growing resource for research. Antiviral Research, 2018, 158, 127-134.	4.1	30
129	Molecular and Serological Evidence for the Presence of Novel Phleboviruses in Sandflies from Northern Algeria~!2009-11-23~!2009-12-31~!2010-04-22~!. The Open Virology Journal, 2010, 4, 15-21.	1.8	30
130	Phlebotomus sergenti a common vector of Leishmania tropica and Toscana virus in Morocco. Journal of Vector Borne Diseases, 2014, 51, 86-90.	0.4	30
131	Prevalence of antibody against West Nile virus in volunteer blood donors living in southeastern France. Transfusion, 2001, 41, 1320-1321.	1.6	29
132	Phlebotomus sergenti in a Cutaneous Leishmaniasis Focus in Azilal Province (High Atlas, Morocco): Molecular Detection and Genotyping of Leishmania tropica, and Feeding Behavior. PLoS Neglected Tropical Diseases, 2015, 9, e0003687.	3.0	29
133	External Quality Assessment for Zika Virus Molecular Diagnostic Testing, Brazil. Emerging Infectious Diseases, 2018, 24, 888-892.	4.3	29
134	A Retrospective Overview of Enterovirus Infection Diagnosis and Molecular Epidemiology in the Public Hospitals of Marseille, France (1985–2005). PLoS ONE, 2011, 6, e18022.	2.5	29
135	Point of Care Strategy for Rapid Diagnosis of Novel A/H1N1 Influenza Virus. PLoS ONE, 2010, 5, e9215.	2.5	28
136	Ngoye virus: a novel evolutionary lineage within the genus Flavivirus. Journal of General Virology, 2006, 87, 3273-3277.	2.9	27
137	Influenza C virus high seroprevalence rates observed in 3 different population groups. Journal of Infection, 2014, 69, 182-189.	3.3	27
138	Identification of essential outstanding questions for an adequate European laboratory response to Ebolavirus Zaire West Africa 2014. Journal of Clinical Virology, 2015, 62, 124-134.	3.1	27
139	Molecular investigation of tick-borne pathogens in ixodid ticks infesting domestic animals (cattle and) Tj ETQq $1\ 1$	0,784314 2.7	rgBT /Over
140	Host-Associated Metagenomics: A Guide to Generating Infectious RNA Viromes. PLoS ONE, 2015, 10, e0139810.	2.5	27
141	The VIZIER project: Preparedness against pathogenic RNA viruses. Antiviral Research, 2008, 78, 37-46.	4.1	26
142	Effect of Chemical Stabilizers on the Thermostability and Infectivity of a Representative Panel of Freeze Dried Viruses. PLoS ONE, 2015, 10, e0118963.	2.5	26
143	Clinical and virological factors associated with gastrointestinal symptoms in patients with acute respiratory infection: a two-year prospective study in general practice medicine. BMC Infectious Diseases, 2017, 17, 729.	2.9	26
144	Microcephaly Caused by Lymphocytic Choriomeningitis Virus. Emerging Infectious Diseases, 2017, 23, 1548-1550.	4.3	26

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145	Evaluation of four PCR systems amplifying different genomic regions for molecular diagnosis of GB virus C infections. Journal of Virological Methods, 1997, 64, 131-135.	2.1	25
146	Novel Virus Influenza A (H1N1sw) in South-Eastern France, April-August 2009. PLoS ONE, 2010, 5, e9214.	2.5	25
147	Isolation of Toscana Virus from the Cerebrospinal Fluid of a Man with Meningitis in Marseille, France, 2010. Vector-Borne and Zoonotic Diseases, 2013, 13, 685-688.	1.5	25
148	Variable Sensitivity in Molecular Detection of Zika Virus in European Expert Laboratories: External Quality Assessment, November 2016. Journal of Clinical Microbiology, 2017, 55, 3219-3226.	3.9	25
149	Biosafety and Biosecurity in European Containment Level 3 Laboratories: Focus on French Recent Progress and Essential Requirements. Frontiers in Public Health, 2017, 5, 121.	2.7	25
150	Epidemiology and Clinical Symptoms Related to Seasonal Coronavirus Identified in Patients with Acute Respiratory Infections Consulting in Primary Care over Six Influenza Seasons (2014–2020) in France. Viruses, 2020, 12, 630.	3.3	25
151	Epidemiological investigation of Pseudomonas aeruginosa nosocomial bacteraemia isolates by PCR-based DNA fingerprinting analysis. Journal of Medical Microbiology, 1996, 45, 359-365.	1.8	24
152	Analytical validation of a lymphocytic choriomeningitis virus real-time RT-PCR assay. Journal of Virological Methods, 2011, 177, 118-122.	2.1	24
153	Long PCR Product Sequencing (LoPPS): a shotgun-based approach to sequence long PCR products. Nature Protocols, 2007, 2, 340-346.	12.0	23
154	Travelâ€Related Influenza A/H1N1 Infection at a Rock Festival in Hungary: One Virus May Hide Another One. Journal of Travel Medicine, 2010, 17, 197-198.	3.0	23
155	Impact of diagnostic procedures on patient management and hospitalization cost during the 2000 and 2005 enterovirus epidemics in Marseilles, France. Clinical Microbiology and Infection, 2010, 16, 651-656.	6.0	22
156	Comparative detection of enterovirus RNA in cerebrospinal fluid: GeneXpert system vs. real-time RT-PCR assay. Clinical Microbiology and Infection, 2011, 17, 1890-1894.	6.0	22
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