Gustavo F Palacios

List of Publications by Year
in descending order

280 papers	18,420 citations	17429 63 h-index	17090 122 g-index
295 all docs	295 docs citations	295 times ranked	20186 citing authors

#	Article	IF	Citations
1	A Metagenomic Survey of Microbes in Honey Bee Colony Collapse Disorder. Science, 2007, 318, 283-287.	6.0	1,481
2	Therapeutic efficacy of the small molecule GS-5734 against Ebola virus in rhesus monkeys. Nature, 2016, 531, 381-385.	13.7	1,245
3	A New Arenavirus in a Cluster of Fatal Transplant-Associated Diseases. New England Journal of Medicine, 2008, 358, 991-998.	13.9	650
4	Genetic Detection and Characterization of Lujo Virus, a New Hemorrhagic Feverâ€“Associated Arenavirus from Southern Africa. PLoS Pathogens, 2009, 5, e1000455.	2.1	423
5	Proposal for a revised taxonomy of the family Filoviridae: classification, names of taxa and viruses, and virus abbreviations. Archives of Virology, 2010, 155, 2083-2103.	0.9	407
6	Molecular Evidence of Sexual Transmission of Ebola Virus. New England Journal of Medicine, 2015, 373, 2448-2454.	13.9	380
7	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	13.7	346
8	Discovery of an Ebolavirus-Like Filovirus in Europe. PLoS Pathogens, 2011, 7, e1002304.	2.1	340
9	MassTag Polymeraseâ€Chainâ€Reaction Detection of Respiratory Pathogens, Including a New Rhinovirus Genotype, That Caused Influenzaâ€Like Illness in New York State during 2004â€“2005. Journal of Infectious Diseases, 2006, 194, 1398-1402.	1.9	303
10	Panmicrobial Oligonucleotide Array for Diagnosis of Infectious Diseases. Emerging Infectious Diseases, 2007, 13, 73-81.	2.0	298
11	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	13.7	298
12	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	0.9	285
13	Astrovirus Encephalitis in Boy with X-linked Agammaglobulinemia. Emerging Infectious Diseases, 2010, 16, 918-925.	2.0	283
14	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	13.5	275
15	Reorganization and expansion of the nidoviral family Arteriviridae. Archives of Virology, 2016, 161, 755-768.	0.9	254
16	Streptococcus pneumoniae Coinfection Is Correlated with the Severity of H1N1 Pandemic Influenza. PLoS ONE, 2009, 4, e8540.	1.1	239
17	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	0.9	224
18	The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. Cell, 2018, 173, 1098-1110.e18.	13.5	220

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19	Genomic Variability of Monkeypox Virus among Humans, Democratic Republic of the Congo. Emerging Infectious Diseases, 2014, 20, 232-9.	2.0	219
20	Novel Borna Virus in Psittacine Birds with Proventricular Dilatation Disease. Emerging Infectious Diseases, 2008, 14, 1883-1886.	2.0	201
21	Heart and Skeletal Muscle Inflammation of Farmed Salmon Is Associated with Infection with a Novel Reovirus. PLoS ONE, 2010, 5, e11487.	1.1	198
22	Lipid signalling enforces functional specialization of Treg cells in tumours. Nature, 2021, 591, 306-311.	13.7	187
23	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	0.9	184
24	Enteroviruses as agents of emerging infectious diseases. Journal of NeuroVirology, 2005, 11, 424-433.	1.0	178
25	Israeli Acute Paralysis Virus: Epidemiology, Pathogenesis and Implications for Honey Bee Health. PLoS Pathogens, 2014, 10, e1004261.	2.1	173
26	Negevirus: a Proposed New Taxon of Insect-Specific Viruses with Wide Geographic Distribution. Journal of Virology, 2013, 87, 2475-2488.	1.5	166
27	Eilat virus, a unique alphavirus with host range restricted to insects by RNA replication. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14622-14627.	3.3	161
28	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	0.9	157
29	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	0.9	153
30	Diagnostic System for Rapid and Sensitive Differential Detection of Pathogens. Emerging Infectious Diseases, 2005, 11, 310-313.	2.0	148
31	Human Metapneumovirus Infection in Wild Mountain Gorillas, Rwanda. Emerging Infectious Diseases, 2011, 17, 711-713.	2.0	135
32	Possible sexual transmission of Ebola virus - Liberia, 2015. Morbidity and Mortality Weekly Report, 2015, 64, 479-81.	9.0	132
33	Genome-Scale Phylogeny of the Alphavirus Genus Suggests a Marine Origin. Journal of Virology, 2012, 86, 2729-2738.	1.5	128
34	A Multicomponent Animal Virus Isolated from Mosquitoes. Cell Host and Microbe, 2016, 20, 357-367.	5.1	123
35	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	0.9	115
36	Monkeypox outbreak in Madrid (Spain): Clinical and virological aspects. Journal of Infection, 2022, 85, 412-417.	1.7	109

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37	Novel Flaviviruses Detected in Different Species of Mosquitoes in Spain. Vector-Borne and Zoonotic Diseases, 2012, 12, 223-229.	0.6	108
38	Neglected filoviruses. FEMS Microbiology Reviews, 2016, 40, 494-519.	3.9	106
39	Identification and pathological characterization of persistent asymptomatic Ebola virus infection in rhesus monkeys. Nature Microbiology, 2017, 2, 17113.	5.9	104
40	NS1 Protein Secretion during the Acute Phase of West Nile Virus Infection. Journal of Virology, 2005, 79, 13924-13933.	1.5	101
41	High Prevalence of Human Enterovirus A Infections in Natural Circulation of Human Enteroviruses. Journal of Clinical Microbiology, 2006, 44, 4095-4100.	1.8	101
42	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. Nature Communications, 2020, 11, 4131.	5.8	101
43	Virus nomenclature below the species level: a standardized nomenclature for natural variants of viruses assigned to the family Filoviridae. Archives of Virology, 2013, 158, 301-311.	0.9	99
44	Detection of Respiratory Viruses and Subtype Identification of Influenza A Viruses by GreeneChipResp Oligonucleotide Microarray. Journal of Clinical Microbiology, 2007, 45, 2359-2364.	1.8	97
45	Global Distribution of Novel Rhinovirus Genotype. Emerging Infectious Diseases, 2008, 14, 944-947.	2.0	97
46	Exposure to toxic metals triggers unique responses from the rat gut microbiota. Scientific Reports, 2018, 8, 6578.	1.6	95
47	Genetic Determinants of Virulence in Pathogenic Lineage 2 West Nile Virus Strains. Emerging Infectious Diseases, 2008, 14, 222-230.	2.0	91
48	Air Travel Is Associated with Intracontinental Spread of Dengue Virus Serotypes 1â€“3 in Brazil. PLoS Neglected Tropical Diseases, 2014, 8, e2769.	1.3	91
49	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. MBio, 2014, 5, e01360-14.	1.8	89
50	Genetic Analysis of Israel Acute Paralysis Virus: Distinct Clusters Are Circulating in the United States. Journal of Virology, 2008, 82, 6209-6217.	1.5	88
51	Evolution and Spread of Ebola Virus in Liberia, 2014â€“2015. Cell Host and Microbe, 2015, 18, 659-669.	5.1	87
52	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. Viruses, 2014, 6, 4760-4799.	1.5	83
53	Multiplex MassTag-PCR for respiratory pathogens in pediatric nasopharyngeal washes negative by conventional diagnostic testing shows a high prevalence of viruses belonging to a newly recognized rhinovirus clade. Journal of Clinical Virology, 2008, 43, 219-222.	1.6	82
54	Complete Genome Sequences for 59 Burkholderia Isolates, Both Pathogenic and Near Neighbor. Genome Announcements, 2015, 3, .	0.8	82

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55	Molecular Identification of Adenoviruses in Clinical Samples by Analyzing a Partial Hexon Genomic Region. Journal of Clinical Microbiology, 2005, 43, 6176-6182.	1.8	79
56	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. Emerging Infectious Diseases, 2015, 21, 1135-1143.	2.0	79
57	ICTV Virus Taxonomy Profile: Filoviridae. Journal of General Virology, 2019, 100, 911-912.	1.3	78
58	High Infection Rates for Adult Macaques after Intravaginal or Intrarectal Inoculation with Zika Virus. Emerging Infectious Diseases, 2017, 23, 1274-1281.	2.0	74
59	Molecular Epidemiology of Echovirus 30: Temporal Circulation and Prevalence of Single Lineages. Journal of Virology, 2002, 76, 4940-4949.	1.5	71
60	Characterization of the Uukuniemi Virus Group (Phlebovirus: Bunyaviridae): Evidence for Seven Distinct Species. Journal of Virology, 2013, 87, 3187-3195.	1.5	70
61	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	0.9	70
62	Greene SCPrimer: a rapid comprehensive tool for designing degenerate primers from multiple sequence alignments. Nucleic Acids Research, 2006, 34, 6605-6611.	6.5	69
63	No assembly required: Full-length MHC class I allele discovery by PacBio circular consensus sequencing. Human Immunology, 2015, 76, 891-896.	1.2	68
64	Emergence of Ebola Virus Escape Variants in Infected Nonhuman Primates Treated with the MB-003 Antibody Cocktail. Cell Reports, 2015, 12, 2111-2120.	2.9	68
65	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. Cell, 2019, 178, 1057-1071.e11.	13.5	68
66	InÂvivo CRISPR screening reveals nutrient signaling processes underpinning CD8+ TÂcell fate decisions. Cell, 2021, 184, 1245-1261.e21.	13.5	68
67	Asymptomatic circulation of HEV71 in Norway. Virus Research, 2007, 123, 19-29.	1.1	67
68	Granada Virus: a Natural Phlebovirus Reassortant of the Sandfly Fever Naples Serocomplex with Low Seroprevalence in Humans. American Journal of Tropical Medicine and Hygiene, 2010, 83, 760-765.	0.6	67
69	Diversity and Distribution of Hantaviruses in South America. Journal of Virology, 2012, 86, 13756-13766.	1.5	67
70	MassTag Polymerase Chain Reaction for Differential Diagnosis of Viral Hemorrhagic Fevers. Emerging Infectious Diseases, 2006, 12, 692-695.	2.0	65
71	Implication of a retrovirusâ€like glycoprotein peptide in the immunopathogenesis of Ebola and Marburg viruses. FASEB Journal, 2006, 20, 2519-2530.	0.2	64
72	Pre-mRNA Splicing-Modulatory Pharmacophores: The Total Synthesis of Herboxidiene, a Pladienolideâ€“Herboxidiene Hybrid Analog and Related Derivatives. ACS Chemical Biology, 2014, 9, 643-648.	1.6	62

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73	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. MBio, 2015, 6, .	1.8	62
74	Reduced evolutionary rate in reemerged Ebola virus transmission chains. Science Advances, 2016, 2, e1600378.	4.7	62
75	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. Lancet Infectious Diseases, The, 2019, 19, 648-657.	4.6	62
76	Metabolic control of TFH cells and humoral immunity by phosphatidylethanolamine. Nature, 2021, 595, 724-729.	13.7	62
77	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	0.9	62
78	High Diversity and Ancient Common Ancestry of Lymphocytic Choriomeningitis Virus. Emerging Infectious Diseases, 2010, 16, 1093-1100.	2.0	59
79	Virus nomenclature below the species level: a standardized nomenclature for filovirus strains and variants rescued from cDNA. Archives of Virology, 2014, 159, 1229-37.	0.9	59
80	Genomic characterisation of human monkeypox virus in Nigeria. Lancet Infectious Diseases, The, 2018, 18, 246.	4.6	59
81	First report of naturally infected Aedes aegypti with chikungunya virus genotype ECSA in the Americas. PLoS Neglected Tropical Diseases, 2017, 11, e0005630.	1.3	59
82	Optimization of Antitumor Modulators of Pre-mRNA Splicing. Journal of Medicinal Chemistry, 2013, 56, 10033-10044.	2.9	57
83	Sudemycin E influences alternative splicing and changes chromatin modifications. Nucleic Acids Research, 2014, 42, 4947-4961.	6.5	57
84	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). Viruses, 2016, 8, 164.	1.5	57
85	ICTV Virus Taxonomy Profile: Nairoviridae. Journal of General Virology, 2020, 101, 798-799.	1.3	56
86	Cell entry by a novel European filovirus requires host endosomal cysteine proteases and Niemannâ€“Pick C1. Virology, 2014, 468-470, 637-646.	1.1	55
87	Persistent Marburg Virus Infection in the Testes of Nonhuman Primate Survivors. Cell Host and Microbe, 2018, 24, 405-416.e3.	5.1	55
88	Virus nomenclature below the species level: a standardized nomenclature for laboratory animal-adapted strains and variants of viruses assigned to the family Filoviridae. Archives of Virology, 2013, 158, 1425-1432.	0.9	54
89	Characterization of the Candiru Antigenic Complex (Bunyaviridae: Phlebovirus), a Highly Diverse and Reassorting Group of Viruses Affecting Humans in Tropical America. Journal of Virology, 2011, 85, 3811-3820.	1.5	53
90	Complete Genome Sequences for 35 Biothreat Assay-Relevant Bacillus Species. Genome Announcements, 2015, 3, .	0.8	52

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91	â€œSuper-Spreadersâ€•and Person-to-Person Transmission of Andes Virus in Argentina. New England Journal of Medicine, 2020, 383, 2230-2241.	13.9	52
92	Emergence of G9 P[6] Human Rotaviruses in Argentina: Phylogenetic Relationships among G9 Strains. Journal of Clinical Microbiology, 2001, 39, 4020-4025.	1.8	51
93	Induction of Sterilizing Immunity against West Nile Virus (WNV), by Immunization with WNVâ€Like Particles Produced in Insect Cells. Journal of Infectious Diseases, 2004, 190, 2104-2108.	1.9	51
94	First Report of Sylvatic DENV-2-Associated Dengue Hemorrhagic Fever in West Africa. PLoS Neglected Tropical Diseases, 2011, 5, e1251.	1.3	51
95	Asymptomatic Infection of Marburg Virus Reservoir Bats Is Explained by a Strategy of Immunoprotective Disease Tolerance. Current Biology, 2021, 31, 257-270.e5.	1.8	51
96	Nested PCR for Rapid Detection of Mumps Virus in Cerebrospinal Fluid from Patients with Neurological Diseases. Journal of Clinical Microbiology, 2000, 38, 274-278.	1.8	51
97	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. Viruses, 2014, 6, 3663-3682.	1.5	49
98	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. MBio, 2016, 7, .	1.8	49
99	Persistence of Ebola virus after the end of widespread transmission in Liberia: an outbreak report. Lancet Infectious Diseases, The, 2018, 18, 1015-1024.	4.6	48
100	Are all melanomas the same?. Cancer, 2006, 106, 907-913.	2.0	47
101	Genetic Diversity of Toscana Virus. Emerging Infectious Diseases, 2009, 15, 574-577.	2.0	46
102	Use of a Short Fragment of the C-Terminal E Gene for Detection and Characterization of Two New Lineages of Dengue Virus 1 in India. Journal of Clinical Microbiology, 2006, 44, 1519-1529.	1.8	45
103	Rapid Molecular Strategy for Filovirus Detection and Characterization. Journal of Clinical Microbiology, 2007, 45, 224-226.	1.8	45
104	Burkholderia humptydooensis sp. nov., a New Species Related to Burkholderia thailandensis and the Fifth Member of the Burkholderia pseudomallei Complex. Applied and Environmental Microbiology, 2017, 83, .	1.4	45
105	Ebola Virus Genome Plasticity as a Marker of Its Passaging History: A Comparison of In Vitro Passaging to Non-Human Primate Infection. PLoS ONE, 2012, 7, e50316.	1.1	44
106	Molecular Identification of Mumps Virus Genotypes from Clinical Samples: Standardized Method of Analysis. Journal of Clinical Microbiology, 2005, 43, 1869-1878.	1.8	43
107	Genomic and phylogenetic characterization of viruses included in the Manzanilla and Oropouche species complexes of the genus Orthobunyavirus, family Bunyaviridae. Journal of General Virology, 2014, 95, 1055-1066.	1.3	43
108	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. BMC Genomics, 2015, 16, 1033.	1.2	42

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109	Ebola Virus Persistence in Ocular Tissues and Fluids (EVICT) Study: Reverse Transcription-Polymerase Chain Reaction and Cataract Surgery Outcomes of Ebola Survivors in Sierra Leone. EBioMedicine, 2018, 30, 217-224.	2.7	42
110	Recent successes in therapeutics for Ebola virus disease: no time for complacency. Lancet Infectious Diseases, The, 2020, 20, e231-e237.	4.6	42
111	Genomic and Phylogenetic Characterization of Brazilian Yellow Fever Virus Strains. Journal of Virology, 2012, 86, 13263-13271.	1.5	41
112	Characterization of the Sandfly fever Naples species complex and description of a new Karimabad species complex (genus Phlebovirus, family Bunyaviridae). Journal of General Virology, 2014, 95, 292-300.	1.3	41
113	Isolation of a Novel Fusogenic Orthoreovirus from Eucampsipoda africana Bat Flies in South Africa. Viruses, 2016, 8, 65.	1.5	41
114	Complete Genome Sequences of Five Zika Virus Isolates. Genome Announcements, 2016, 4, .	0.8	40
115	Molecular Identification of Enterovirus by Analyzing a Partial VP1 Genomic Region with Different Methods. Journal of Clinical Microbiology, 2002, 40, 182-192.	1.8	39
116	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. Cell Reports, 2018, 22, 1159-1168.	2.9	37
117	Rapid sequence-based diagnosis of viral infection. Antiviral Research, 2008, 79, 1-5.	1.9	36
118	Molecular Surveillance of Circulating Dengue Genotypes Through European Travelers. Journal of Travel Medicine, 2011, 18, 183-190.	1.4	36
119	Recombinant Lassa Virus Expressing Green Fluorescent Protein as a Tool for High-Throughput Drug Screens and Neutralizing Antibody Assays. Viruses, 2018, 10, 655.	1.5	35
120	Marburg Virus Infection in Egyptian Rousette Bats, South Africa, 2013â€“20141. Emerging Infectious Diseases, 2018, 24, 1134-1137.	2.0	35
121	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. Nature Medicine, 2021, 27, 710-716.	15.2	35
122	Multiplex PCRâˆ’Based Next-Generation Sequencing and Global Diversity of Seoul Virus in Humans and Rats. Emerging Infectious Diseases, 2018, 24, 249-257.	2.0	33
123	Sensitivity and specificity of immunoglobulin G titer for the diagnosis of mumps virus in infected patients depending on vaccination status. Apmis, 2006, 114, 788-794.	0.9	32
124	Genomic and phylogenetic characterization of Merino Walk virus, a novel arenavirus isolated in South Africa. Journal of General Virology, 2010, 91, 1315-1324.	1.3	32
125	Comparison of Transcriptomic Platforms for Analysis of Whole Blood from Ebola-Infected Cynomolgus Macaques. Scientific Reports, 2017, 7, 14756.	1.6	32
126	Prospective Cohort Study of Next-Generation Sequencing as a Diagnostic Modality for Unexplained Encephalitis in Children. Journal of the Pediatric Infectious Diseases Society, 2020, 9, 326-333.	0.6	32

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127	Thirty-Two Complete Genome Assemblies of Nine Yersinia Species, Including Y. pestis, Y. pseudotuberculosis, and Y. enterocolitica. Genome Announcements, 2015, 3, .	0.8	31
128	Phylogeographic analysis of hemorrhagic fever with renal syndrome patients using multiplex PCR-based next generation sequencing. Scientific Reports, 2016, 6, 26017.	1.6	31
129	First Report of Sudden Death Due to Myocarditis Caused by Adenovirus Serotype 3. Journal of Clinical Microbiology, 2010, 48, 642-645.	1.8	30
130	Characterization of the Salehabad virus species complex of the genus Phlebovirus (Bunyaviridae). Journal of General Virology, 2013, 94, 837-842.	1.3	30
131	Complete Genome Sequences of Zika Virus Strains Isolated from the Blood of Patients in Thailand in 2014 and the Philippines in 2012. Genome Announcements, 2016, 4, .	0.8	30
132	Complete Coding Genome Sequence for Mogiana Tick Virus, a Jingmenvirus Isolated from Ticks in Brazil. Genome Announcements, 2017, 5, .	0.8	30
133	Persistence and Intra-Host Genetic Evolution of Zika Virus Infection in Symptomatic Adults: A Special View in the Male Reproductive System. Viruses, 2018, 10, 615.	1.5	30
134	Lassa virus circulating in Liberia: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 1371-1378.	4.6	30
135	Viral genomics in Ebola virus research. Nature Reviews Microbiology, 2020, 18, 365-378.	13.6	30
136	Molecular Analysis of Echovirus 13 Isolates and Aseptic Meningitis, Spain. Emerging Infectious Diseases, 2003, 9, 934-941.	2.0	29
137	Real-Time Polymerase Chain Reaction for Detecting SARS Coronavirus, Beijing, 2003. Emerging Infectious Diseases, 2004, 10, 311-316.	2.0	29
138	Ebola Virus Infections in Nonhuman Primates Are Temporally Influenced by Glycoprotein Poly-U Editing Site Populations in the Exposure Material. Viruses, 2015, 7, 6739-6754.	1.5	29
139	Isolation of a novel orthobunyavirus from bat flies (Eucampsipoda africana). Journal of General Virology, 2017, 98, 935-945.	1.3	29
140	Development and Evaluation of a Panel of Filovirus Sequence Capture Probes for Pathogen Detection by Next-Generation Sequencing. PLoS ONE, 2014, 9, e107007.	1.1	28
141	Genetic and epidemiological characterization of Stretch Lagoon orbivirus, a novel orbivirus isolated from Culex and Aedes mosquitoes in northern Australia. Journal of General Virology, 2009, 90, 1433-1439.	1.3	27
142	Aguacate virus, a new antigenic complex of the genus Phlebovirus (family Bunyaviridae). Journal of General Virology, 2011, 92, 1445-1453.	1.3	27
143	Whole-Genome Assemblies of 56 Burkholderia Species. Genome Announcements, 2014, 2, .	0.8	27
144	2018 Ebola virus disease outbreak in Ã‰quateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 641-647.	4.6	27

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145	Evaluation of two molecular methods for the detection of Yellow fever virus genome. Journal of Virological Methods, 2011, 174, 29-34.	1.0	26
146	Microarray-based detection of viruses causing vesicular or vesicular-like lesions in livestock animals. Veterinary Microbiology, 2009, 133, 145-153.	0.8	25
147	New recognition of Enterovirus infections in bottlenose dolphins (Tursiops truncatus). Veterinary Microbiology, 2009, 139, 170-175.	0.8	25
148	Circulation of Mumps Virus Genotypes in Spain from 1996 to 2007. Journal of Clinical Microbiology, 2010, 48, 1245-1254.	1.8	25
149	A conserved transcriptional response to intranasal Ebola virus exposure in nonhuman primates prior to onset of fever. Science Translational Medicine, 2018, 10, .	5.8	25
150	Characterization of Durham virus, a novel rhabdovirus that encodes both a C and SH protein. Virus Research, 2011, 155, 112-122.	1.1	24
151	Evaluation of Jatropha isabelli natural products and their synthetic analogs as potential antimalarial therapeutic agents. European Journal of Medicinal Chemistry, 2013, 65, 376-380.	2.6	24
152	Delayed Time-to-Treatment of an Antisense Morpholino Oligomer Is Effective against Lethal Marburg Virus Infection in Cynomolgus Macaques. PLoS Neglected Tropical Diseases, 2016, 10, e0004456.	1.3	24
153	Spontaneous Mutation at Amino Acid 544 of the Ebola Virus Glycoprotein Potentiates Virus Entry and Selection in Tissue Culture. Journal of Virology, 2017, 91, .	1.5	24
154	Transcriptomics Reveal Antiviral Gene Induction in the Egyptian Rousette Bat Is Antagonized In Vitro by Marburg Virus Infection. Viruses, 2018, 10, 607.	1.5	24
155	Cluster analysis of the origins of the new influenza A(H1N1) virus. Eurosurveillance, 2009, 14, .	3.9	24
156	Characterization of the Punta Toro species complex (genus Phlebovirus, family Bunyaviridae). Journal of General Virology, 2015, 96, 2079-2085.	1.3	23
157	Comparison of targeted next-generation sequencing for whole-genome sequencing of Hantaan orthohantavirus in Apodemus agrarius lung tissues. Scientific Reports, 2019, 9, 16631.	1.6	23
158	Shedding of Marburg Virus in Naturally Infected Egyptian Rousette Bats, South Africa, 2017. Emerging Infectious Diseases, 2020, 26, 3051-3055.	2.0	23
159	High Diversity of Rabies Viruses Associated with Insectivorous Bats in Argentina: Presence of Several Independent Enzootics. PLoS Neglected Tropical Diseases, 2012, 6, e1635.	1.3	22
160	Reidentification of Ebola Virus E718 and ME as Ebola Virus/H.sapiens-tc/COD/1976/Yambuku-Ecran. Genome Announcements, 2014, 2, .	0.8	22
161	Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. Clinical Infectious Diseases, 2020, 70, 464-473.	2.9	22
162	Ebola virus persistence and disease recrudescence in the brains of antibody-treated nonhuman primate survivors. Science Translational Medicine, 2022, 14, eabi5229.	5.8	22

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163	Comprehensive viral oligonucleotide probe design using conserved protein regions. Nucleic Acids Research, 2008, 36, e3-e3.	6.5	21
164	Genomic and phylogenetic characterization of Leanyer virus, a novel orthobunyavirus isolated in northern Australia. Journal of General Virology, 2011, 92, 1676-1687.	1.3	21
165	Genomic and antigenic characterization of Jos virus. Journal of General Virology, 2012, 93, 293-298.	1.3	21
166	An attenuated Machupo virus with a disrupted L-segment intergenic region protects guinea pigs against lethal Guanarito virus infection. Scientific Reports, 2017, 7, 4679.	1.6	21
167	Person-to-Person Transmission of Andes Virus in Hantavirus Pulmonary Syndrome, Argentina, 2014. Emerging Infectious Diseases, 2020, 26, 756-759.	2.0	21
168	Error baseline rates of five sample preparation methods used to characterize RNA virus populations. PLoS ONE, 2017, 12, e0171333.	1.1	21
169	Draft Genome Assembly of Acinetobacter baumannii ATCC 19606. Genome Announcements, 2014, 2, .	0.8	20
170	Ribavirin Had Demonstrable Effects on the Crimean-Congo Hemorrhagic Fever Virus (CCHFV) Population and Load in a Patient With CCHF Infection. Journal of Infectious Diseases, 2018, 217, 1952-1956.	1.9	20
171	Rousette Bat Dendritic Cells Overcome Marburg Virus-Mediated Antiviral Responses by Upregulation of Interferon-Related Genes While Downregulating Proinflammatory Disease Mediators. MSphere, 2019, 4, .	1.3	20
172	Rapid Molecular Strategy for Orbivirus Detection and Characterization. Journal of Clinical Microbiology, 2011, 49, 2314-2317.	1.8	19
173	Ebola Virus Epidemiology and Evolution in Nigeria. Journal of Infectious Diseases, 2016, 214, S102-S109.	1.9	19
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