Gustavo F Palacios

List of Publications by Citations

Source: https://exaly.com/author-pdf/29796/gustavo-f-palacios-publications-by-citations.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

108 271 13,532 57 h-index g-index citations papers 16,368 5.63 10.5 293 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
271	A metagenomic survey of microbes in honey bee colony collapse disorder. <i>Science</i> , 2007 , 318, 283-7	33.3	1250
270	Therapeutic efficacy of the small molecule GS-5734 against Ebola virus in rhesus monkeys. <i>Nature</i> , 2016 , 531, 381-5	50.4	923
269	A new arenavirus in a cluster of fatal transplant-associated diseases. <i>New England Journal of Medicine</i> , 2008 , 358, 991-8	59.2	546
268	Genetic detection and characterization of Lujo virus, a new hemorrhagic fever-associated arenavirus from southern Africa. <i>PLoS Pathogens</i> , 2009 , 5, e1000455	7.6	352
267	Proposal for a revised taxonomy of the family Filoviridae: classification, names of taxa and viruses, and virus abbreviations. <i>Archives of Virology</i> , 2010 , 155, 2083-103	2.6	343
266	Molecular Evidence of Sexual Transmission of Ebola Virus. <i>New England Journal of Medicine</i> , 2015 , 373, 2448-54	59.2	302
265	Discovery of an ebolavirus-like filovirus in europe. <i>PLoS Pathogens</i> , 2011 , 7, e1002304	7.6	271
264	MassTag polymerase-chain-reaction detection of respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like illness in New York State during 2004-2005. <i>Journal of Infectious Diseases</i> , 2006 , 194, 1398-402	7	257
263	Panmicrobial oligonucleotide array for diagnosis of infectious diseases. <i>Emerging Infectious Diseases</i> , 2007 , 13, 73-81	10.2	249
262	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
261	Astrovirus encephalitis in boy with X-linked agammaglobulinemia. <i>Emerging Infectious Diseases</i> , 2010 , 16, 918-25	10.2	236
260	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
259	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015 , 161, 1516-26	56.2	210
258	Streptococcus pneumoniae coinfection is correlated with the severity of H1N1 pandemic influenza. <i>PLoS ONE</i> , 2009 , 4, e8540	3.7	208
257	Heart and skeletal muscle inflammation of farmed salmon is associated with infection with a novel reovirus. <i>PLoS ONE</i> , 2010 , 5, e11487	3.7	173
256	Reorganization and expansion of the nidoviral family Arteriviridae. <i>Archives of Virology</i> , 2016 , 161, 755-6	5 8 .6	167
255	Novel borna virus in psittacine birds with proventricular dilatation disease. <i>Emerging Infectious Diseases</i> , 2008 , 14, 1883-6	10.2	164

(2008-2005)

254	Enteroviruses as agents of emerging infectious diseases. <i>Journal of NeuroVirology</i> , 2005 , 11, 424-33	3.9	155
253	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965	2.6	148
252	Diagnostic system for rapid and sensitive differential detection of pathogens. <i>Emerging Infectious Diseases</i> , 2005 , 11, 310-3	10.2	136
251	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019 , 164, 1967-1980	2.6	133
250	Negevirus: a proposed new taxon of insect-specific viruses with wide geographic distribution. <i>Journal of Virology</i> , 2013 , 87, 2475-88	6.6	123
249	Eilat virus, a unique alphavirus with host range restricted to insects by RNA replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14622-7	11.5	122
248	The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. <i>Cell</i> , 2018 , 173, 1098-1110.e18	56.2	121
247	Possible sexual transmission of Ebola virus - Liberia, 2015. <i>Morbidity and Mortality Weekly Report</i> , 2015 , 64, 479-81	31.7	121
246	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294	2.6	111
245	Human metapneumovirus infection in wild mountain gorillas, Rwanda. <i>Emerging Infectious Diseases</i> , 2011 , 17, 711-3	10.2	111
244	Israeli acute paralysis virus: epidemiology, pathogenesis and implications for honey bee health. <i>PLoS Pathogens</i> , 2014 , 10, e1004261	7.6	109
243	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2295-2310	2.6	108
242	Genome-scale phylogeny of the alphavirus genus suggests a marine origin. <i>Journal of Virology</i> , 2012 , 86, 2729-38	6.6	102
241	Novel flaviviruses detected in different species of mosquitoes in Spain. <i>Vector-Borne and Zoonotic Diseases</i> , 2012 , 12, 223-9	2.4	100
240	High prevalence of human enterovirus a infections in natural circulation of human enteroviruses. Journal of Clinical Microbiology, 2006 , 44, 4095-100	9.7	93
239	NS1 protein secretion during the acute phase of West Nile virus infection. <i>Journal of Virology</i> , 2005 , 79, 13924-33	6.6	90
238	Detection of respiratory viruses and subtype identification of influenza A viruses by GreeneChipResp oligonucleotide microarray. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 2359-64	9.7	87
237	Global distribution of novel rhinovirus genotype. Emerging Infectious Diseases, 2008, 14, 944-7	10.2	85

236	Genetic determinants of virulence in pathogenic lineage 2 West Nile virus strains. <i>Emerging Infectious Diseases</i> , 2008 , 14, 222-30	10.2	78
235	Genetic analysis of Israel acute paralysis virus: distinct clusters are circulating in the United States. <i>Journal of Virology</i> , 2008 , 82, 6209-17	6.6	77
234	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941	2.6	76
233	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016 , 20, 357-367	23.4	76
232	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. <i>Journal of Clinical Virology</i> , 2008 , 43, 219-22	14.5	74
231	Neglected filoviruses. FEMS Microbiology Reviews, 2016, 40, 494-519	15.1	70
230	Identification and pathological characterization of persistent asymptomatic Ebola virus infection in rhesus monkeys. <i>Nature Microbiology</i> , 2017 , 2, 17113	26.6	70
229	Nomenclature- and database-compatible names for the two Ebola virus variants that emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014 , 6, 4760-99	6.2	70
228	Molecular identification of adenoviruses in clinical samples by analyzing a partial hexon genomic region. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 6176-82	9.7	68
227	Air travel is associated with intracontinental spread of dengue virus serotypes 1-3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2769	4.8	67
226	Evolution and Spread of Ebola Virus in Liberia, 2014-2015. Cell Host and Microbe, 2015, 18, 659-69	23.4	66
225	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1135-43	10.2	65
224	Molecular epidemiology of echovirus 30: temporal circulation and prevalence of single lineages. Journal of Virology, 2002 , 76, 4940-9	6.6	63
223	High Infection Rates for Adult Macaques after Intravaginal or Intrarectal Inoculation with Zika Virus. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1274-1281	10.2	60
222	Exposure to toxic metals triggers unique responses from the rat gut microbiota. <i>Scientific Reports</i> , 2018 , 8, 6578	4.9	60
221	Implication of a retrovirus-like glycoprotein peptide in the immunopathogenesis of Ebola and Marburg viruses. <i>FASEB Journal</i> , 2006 , 20, 2519-30	0.9	60
220	Characterization of the Uukuniemi virus group (Phlebovirus: Bunyaviridae): evidence for seven distinct species. <i>Journal of Virology</i> , 2013 , 87, 3187-95	6.6	59
219	Asymptomatic circulation of HEV71 in Norway. <i>Virus Research</i> , 2007 , 123, 19-29	6.4	59

218	Diversity and distribution of hantaviruses in South America. Journal of Virology, 2012, 86, 13756-66	6.6	57
217	Greene SCPrimer: a rapid comprehensive tool for designing degenerate primers from multiple sequence alignments. <i>Nucleic Acids Research</i> , 2006 , 34, 6605-11	20.1	57
216	MassTag polymerase chain reaction for differential diagnosis of viral hemorrhagic fever. <i>Emerging Infectious Diseases</i> , 2006 , 12, 692-5	10.2	56
215	No assembly required: Full-length MHC class I allele discovery by PacBio circular consensus sequencing. <i>Human Immunology</i> , 2015 , 76, 891-6	2.3	55
214	Pre-mRNA splicing-modulatory pharmacophores: the total synthesis of herboxidiene, a pladienolide-herboxidiene hybrid analog and related derivatives. <i>ACS Chemical Biology</i> , 2014 , 9, 643-8	4.9	55
213	Granada virus: a natural phlebovirus reassortant of the sandfly fever Naples serocomplex with low seroprevalence in humans. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010 , 83, 760-5	3.2	55
212	Evaluation of the potential impact of Ebola virus genomic drift on the efficacy of sequence-based candidate therapeutics. <i>MBio</i> , 2015 , 6,	7.8	54
211	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016 , 2, e16	5 0 03 <i>3</i> 78	53
210	Emergence of Ebola Virus Escape Variants in Infected Nonhuman Primates Treated with the MB-003 Antibody Cocktail. <i>Cell Reports</i> , 2015 , 12, 2111-20	10.6	52
209	Virus nomenclature below the species level: a standardized nomenclature for filovirus strains and variants rescued from cDNA. <i>Archives of Virology</i> , 2014 , 159, 1229-37	2.6	52
208	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-12	4 4 .6	50
207	Cell entry by a novel European filovirus requires host endosomal cysteine proteases and Niemann-Pick C1. <i>Virology</i> , 2014 , 468-470, 637-646	3.6	50
206	Sudemycin E influences alternative splicing and changes chromatin modifications. <i>Nucleic Acids Research</i> , 2014 , 42, 4947-61	20.1	50
205	Induction of sterilizing immunity against West Nile Virus (WNV), by immunization with WNV-like particles produced in insect cells. <i>Journal of Infectious Diseases</i> , 2004 , 190, 2104-8	7	50
204	Complete genome sequences for 59 burkholderia isolates, both pathogenic and near neighbor. <i>Genome Announcements</i> , 2015 , 3,		48
203	Optimization of antitumor modulators of pre-mRNA splicing. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 10033-44	8.3	48
202	First report of naturally infected Aedes aegypti with chikungunya virus genotype ECSA in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005630	4.8	46
201	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019 , 178, 1057-1071.e11	56.2	45

200	Lipid signalling enforces functional specialization of T cells in tumours. <i>Nature</i> , 2021 , 591, 306-311	50.4	45
199	Filovirus RefSeq entries: evaluation and selection of filovirus type variants, type sequences, and names. <i>Viruses</i> , 2014 , 6, 3663-82	6.2	44
198	High diversity and ancient common ancestry of lymphocytic choriomeningitis virus. <i>Emerging Infectious Diseases</i> , 2010 , 16, 1093-100	10.2	44
197	Emergence of G9 P[6] human rotaviruses in Argentina: phylogenetic relationships among G9 strains. <i>Journal of Clinical Microbiology</i> , 2001 , 39, 4020-5	9.7	44
196	Characterization of the Candiru antigenic complex (Bunyaviridae: Phlebovirus), a highly diverse and reassorting group of viruses affecting humans in tropical America. <i>Journal of Virology</i> , 2011 , 85, 3811-2	o ^{6.6}	43
195	First report of sylvatic DENV-2-associated dengue hemorrhagic fever in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1251	4.8	42
194	Are all melanomas the same? Spitzoid melanoma is a distinct subtype of melanoma. <i>Cancer</i> , 2006 , 106, 907-13	6.4	42
193	Complete genome sequences for 35 biothreat assay-relevant bacillus species. <i>Genome Announcements</i> , 2015 , 3,		39
192	Genomic variability of monkeypox virus among humans, Democratic Republic of the Congo. <i>Emerging Infectious Diseases</i> , 2014 , 20, 232-9	10.2	39
191	Genetic diversity of Toscana virus. <i>Emerging Infectious Diseases</i> , 2009 , 15, 574-7	10.2	39
190	Complete Genome Sequences of Five Zika Virus Isolates. <i>Genome Announcements</i> , 2016 , 4,		39
189	Persistence of Ebola virus after the end of widespread transmission in Liberia: an outbreak report. Lancet Infectious Diseases, The, 2018 , 18, 1015-1024	25.5	38
188	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). Viruses, 2016, 8,	6.2	38
187	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016 , 7,	7.8	37
186	Rapid molecular strategy for filovirus detection and characterization. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 224-6	9.7	37
185	Nested PCR for rapid detection of mumps virus in cerebrospinal fluid from patients with neurological diseases. <i>Journal of Clinical Microbiology</i> , 2000 , 38, 274-8	9.7	37
184	Ebola virus genome plasticity as a marker of its passaging history: a comparison of in vitro passaging to non-human primate infection. <i>PLoS ONE</i> , 2012 , 7, e50316	3.7	37
183	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. <i>Lancet Infectious Diseases. The</i> 2019 19, 648-657	25.5	36

(2016-2006)

182	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. <i>Journal of Clinical Microbiology</i> , 2006 , 44, 1519-29	9.7	36
181	Molecular identification of mumps virus genotypes from clinical samples: standardized method of analysis. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 1869-78	9.7	36
180	Characterization of the Sandfly fever Naples species complex and description of a new Karimabad species complex (genus Phlebovirus, family Bunyaviridae). <i>Journal of General Virology</i> , 2014 , 95, 292-30	o ^{4.9}	34
179	ICTV Virus Taxonomy Profile: Filoviridae. <i>Journal of General Virology</i> , 2019 , 100, 911-912	4.9	34
178	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020 , 11, 4131	17.4	34
177	Persistent Marburg Virus Infection in the Testes of Nonhuman Primate Survivors. <i>Cell Host and Microbe</i> , 2018 , 24, 405-416.e3	23.4	34
176	Genomic and phylogenetic characterization of viruses included in the Manzanilla and Oropouche species complexes of the genus Orthobunyavirus, family Bunyaviridae. <i>Journal of General Virology</i> , 2014 , 95, 1055-1066	4.9	31
175	Molecular surveillance of circulating dengue genotypes through European travelers. <i>Journal of Travel Medicine</i> , 2011 , 18, 183-90	12.9	31
174	Characteristic and quantifiable COVID-19-like abnormalities in CT- and PET/CT-imaged lungs of SARS-CoV-2-infected crab-eating macaques () 2020 ,		31
173	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. <i>EBioMedicine</i> , 2018 , 30, 217-224	8.8	31
172	Genomic and phylogenetic characterization of Merino Walk virus, a novel arenavirus isolated in South Africa. <i>Journal of General Virology</i> , 2010 , 91, 1315-24	4.9	30
171	Molecular identification of enterovirus by analyzing a partial VP1 genomic region with different methods. <i>Journal of Clinical Microbiology</i> , 2002 , 40, 182-92	9.7	30
170	Rapid sequence-based diagnosis of viral infection. <i>Antiviral Research</i> , 2008 , 79, 1-5	10.8	29
169	Genomic and phylogenetic characterization of Brazilian yellow fever virus strains. <i>Journal of Virology</i> , 2012 , 86, 13263-71	6.6	28
168	Isolation of a Novel Fusogenic Orthoreovirus from Eucampsipoda africana Bat Flies in South Africa. <i>Viruses</i> , 2016 , 8, 65	6.2	28
167	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018 , 22, 1159-1168	10.6	27
166	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. <i>BMC Genomics</i> , 2015 , 16, 1033	4.5	27
165	Complete Genome Sequences of Zika Virus Strains Isolated from the Blood of Patients in Thailand in 2014 and the Philippines in 2012. <i>Genome Announcements</i> , 2016 , 4,		26

164	Phylogeographic analysis of hemorrhagic fever with renal syndrome patients using multiplex PCR-based next generation sequencing. <i>Scientific Reports</i> , 2016 , 6, 26017	4.9	25	
163	Aguacate virus, a new antigenic complex of the genus Phlebovirus (family Bunyaviridae). <i>Journal of General Virology</i> , 2011 , 92, 1445-1453	4.9	25	
162	Genetic and epidemiological characterization of Stretch Lagoon orbivirus, a novel orbivirus isolated from Culex and Aedes mosquitoes in northern Australia. <i>Journal of General Virology</i> , 2009 , 90, 1433-14.	3 9 -9	25	
161	Molecular analysis of echovirus 13 isolates and aseptic meningitis, Spain. <i>Emerging Infectious Diseases</i> , 2003 , 9, 934-41	10.2	25	
160	Real-time polymerase chain reaction for detecting SARS coronavirus, Beijing, 2003. <i>Emerging Infectious Diseases</i> , 2004 , 10, 300-3	10.2	25	
159	Recent successes in therapeutics for Ebola virus disease: no time for complacency. <i>Lancet Infectious Diseases, The</i> , 2020 , 20, e231-e237	25.5	24	
158	Burkholderia humptydooensis sp. nov., a New Species Related to Burkholderia thailandensis and the Fifth Member of the Burkholderia pseudomallei Complex. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	23	
157	Multiplex PCR-Based Next-Generation Sequencing and Global Diversity of Seoul Virus in Humans and Rats. <i>Emerging Infectious Diseases</i> , 2018 , 24, 249-257	10.2	23	
156	Microarray-based detection of viruses causing vesicular or vesicular-like lesions in livestock animals. <i>Veterinary Microbiology</i> , 2009 , 133, 145-53	3.3	23	
155	New recognition of Enterovirus infections in bottlenose dolphins (Tursiops truncatus). <i>Veterinary Microbiology</i> , 2009 , 139, 170-5	3.3	23	
154	Sensitivity and specificity of immunoglobulin G titer for the diagnosis of mumps virus in infected patients depending on vaccination status. <i>Apmis</i> , 2006 , 114, 788-94	3.4	23	
153	Comparison of Transcriptomic Platforms for Analysis of Whole Blood from Ebola-Infected Cynomolgus Macaques. <i>Scientific Reports</i> , 2017 , 7, 14756	4.9	22	
152	Ebola Virus Infections in Nonhuman Primates Are Temporally Influenced by Glycoprotein Poly-U Editing Site Populations in the Exposure Material. <i>Viruses</i> , 2015 , 7, 6739-54	6.2	22	
151	Development and evaluation of a panel of filovirus sequence capture probes for pathogen detection by next-generation sequencing. <i>PLoS ONE</i> , 2014 , 9, e107007	3.7	22	
150	Characterization of the Salehabad virus species complex of the genus Phlebovirus (Bunyaviridae). Journal of General Virology, 2013 , 94, 837-842	4.9	22	
149	Characterization of Durham virus, a novel rhabdovirus that encodes both a C and SH protein. <i>Virus Research</i> , 2011 , 155, 112-22	6.4	22	
148	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases, The</i> , 2019 , 19, 1371-1378	25.5	21	
147	Evaluation of Jatropha isabelli natural products and their synthetic analogs as potential antimalarial therapeutic agents. <i>European Journal of Medicinal Chemistry</i> , 2013 , 65, 376-80	6.8	21	

(2008-2010)

146	First report of sudden death due to myocarditis caused by adenovirus serotype 3. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 642-5	9.7	21
145	Genomic and phylogenetic characterization of Leanyer virus, a novel orthobunyavirus isolated in northern Australia. <i>Journal of General Virology</i> , 2011 , 92, 1676-1687	4.9	21
144	Persistence and Intra-Host Genetic Evolution of Zika Virus Infection in Symptomatic Adults: A Special View in the Male Reproductive System. <i>Viruses</i> , 2018 , 10,	6.2	21
143	Recombinant Lassa Virus Expressing Green Fluorescent Protein as a Tool for High-Throughput Drug Screens and Neutralizing Antibody Assays. <i>Viruses</i> , 2018 , 10,	6.2	21
142	Complete Coding Genome Sequence for Mogiana Tick Virus, a Jingmenvirus Isolated from Ticks in Brazil. <i>Genome Announcements</i> , 2017 , 5,		20
141	Thirty-Two Complete Genome Assemblies of Nine Yersinia Species, Including Y. pestis, Y. pseudotuberculosis, and Y. enterocolitica. <i>Genome Announcements</i> , 2015 , 3,		20
140	Marburg Virus Infection in Egyptian Rousette Bats, South Africa, 2013-2014. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1134-1137	10.2	20
139	Whole-genome assemblies of 56 burkholderia species. <i>Genome Announcements</i> , 2014 , 2,		20
138	Isolation of a novel orthobunyavirus from bat flies (Eucampsipoda africana). <i>Journal of General Virology</i> , 2017 , 98, 935-945	4.9	20
137	In vivo CRISPR screening reveals nutrient signaling processes underpinning CD8 T cell fate decisions. <i>Cell</i> , 2021 , 184, 1245-1261.e21	56.2	20
136	Delayed Time-to-Treatment of an Antisense Morpholino Oligomer Is Effective against Lethal Marburg Virus Infection in Cynomolgus Macaques. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004456	5 ^{4.8}	20
135	Circulation of mumps virus genotypes in Spain from 1996 to 2007. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 1245-54	9.7	19
134	Error baseline rates of five sample preparation methods used to characterize RNA virus populations. <i>PLoS ONE</i> , 2017 , 12, e0171333	3.7	19
133	Spontaneous Mutation at Amino Acid 544 of the Ebola Virus Glycoprotein Potentiates Virus Entry and Selection in Tissue Culture. <i>Journal of Virology</i> , 2017 , 91,	6.6	18
132	Characterization of the Punta Toro species complex (genus Phlebovirus, family Bunyaviridae). <i>Journal of General Virology</i> , 2015 , 96, 2079-2085	4.9	18
131	Reidentification of Ebola Virus E718 and ME as Ebola Virus/H.sapiens-tc/COD/1976/Yambuku-Ecran. <i>Genome Announcements</i> , 2014 , 2,		18
130	Evaluation of two molecular methods for the detection of Yellow fever virus genome. <i>Journal of Virological Methods</i> , 2011 , 174, 29-34	2.6	18
129	Comprehensive viral oligonucleotide probe design using conserved protein regions. <i>Nucleic Acids Research</i> , 2008 , 36, e3	20.1	18

128	Cluster analysis of the origins of the new influenza A(H1N1) virus. Eurosurveillance, 2009, 14,	19.8	18
127	2018 Ebola virus disease outbreak in quateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. <i>Lancet Infectious Diseases, The</i> , 2019 , 19, 641-647	25.5	17
126	Genomic characterisation of human monkeypox virus in Nigeria. <i>Lancet Infectious Diseases, The</i> , 2018 , 18, 246	25.5	17
125	A conserved transcriptional response to intranasal Ebola virus exposure in nonhuman primates prior to onset of fever. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	17
124	Genomic and antigenic characterization of Jos virus. <i>Journal of General Virology</i> , 2012 , 93, 293-298	4.9	17
123	"Super-Spreaders" and Person-to-Person Transmission of Andes Virus in Argentina. <i>New England Journal of Medicine</i> , 2020 , 383, 2230-2241	59.2	17
122	Prospective Cohort Study of Next-Generation Sequencing as a Diagnostic Modality for Unexplained Encephalitis in Children. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2020 , 9, 326-333	4.8	17
121	Draft Genome Assembly of Acinetobacter baumannii ATCC 19606. <i>Genome Announcements</i> , 2014 , 2,		16
12 0	Rapid molecular strategy for orbivirus detection and characterization. <i>Journal of Clinical Microbiology</i> , 2011 , 49, 2314-7	9.7	16
119	High diversity of rabies viruses associated with insectivorous bats in Argentina: presence of several independent enzootics. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1635	4.8	16
118	A small stem-loop structure of the Ebola virus trailer is essential for replication and interacts with heat-shock protein A8. <i>Nucleic Acids Research</i> , 2016 , 44, 9831-9846	20.1	15
117	An attenuated Machupo virus with a disrupted L-segment intergenic region protects guinea pigs against lethal Guanarito virus infection. <i>Scientific Reports</i> , 2017 , 7, 4679	4.9	15
116	Ebola virus persistence as a new focus in clinical research. Current Opinion in Virology, 2017, 23, 43-48	7·5	14
115	Genome Sequence of Weissella ceti NC36, an Emerging Pathogen of Farmed Rainbow Trout in the United States. <i>Genome Announcements</i> , 2013 , 1,		14
114	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016 , 214, S102-S109	7	14
113	Asymptomatic Infection of Marburg Virus Reservoir Bats Is Explained by a Strategy of Immunoprotective Disease Tolerance. <i>Current Biology</i> , 2021 , 31, 257-270.e5	6.3	14
112	Genome sequencing of 18 francisella strains to aid in assay development and testing. <i>Genome Announcements</i> , 2015 , 3,		13
111	Genetic Characterization of Enterovirus A71 Circulating in Africa. <i>Emerging Infectious Diseases</i> , 2018 , 24, 754-757	10.2	13

110	Discovery of an orthoreovirus in the aborted fetus of a Steller sea lion (Eumetopias jubatus). <i>Journal of General Virology</i> , 2011 , 92, 2558-2565	4.9	13
109	ICTV Virus Taxonomy Profile:. Journal of General Virology, 2020, 101, 798-799	4.9	13
108	Sequence-Independent, Single-Primer Amplification Next-Generation Sequencing of Hantaan Virus Cell Culture-Based Isolates. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017 , 96, 389-394	3.2	12
107	Viral genomics in Ebola virus research. <i>Nature Reviews Microbiology</i> , 2020 , 18, 365-378	22.2	12
106	Pathosphere.org: pathogen detection and characterization through a web-based, open source informatics platform. <i>BMC Bioinformatics</i> , 2015 , 16, 416	3.6	12
105	Alterations in the host transcriptome in vitro following Rift Valley fever virus infection. <i>Scientific Reports</i> , 2017 , 7, 14385	4.9	12
104	Novel ALK fusion in anaplastic large cell lymphoma involving EEF1G, a subunit of the eukaryotic elongation factor-1 complex. <i>Leukemia</i> , 2017 , 31, 743-747	10.7	12
103	Enterovirus 75 and aseptic meningitis, Spain, 2005. Emerging Infectious Diseases, 2006, 12, 1609-11	10.2	12
102	Metabolic control of T cells and humoral immunity by phosphatidylethanolamine. <i>Nature</i> , 2021 , 595, 724-729	50.4	12
101	First Evidence of Antibodies Against Lloviu Virus in Schreiber's Bent-Winged Insectivorous Bats Demonstrate a Wide Circulation of the Virus in Spain. <i>Viruses</i> , 2019 , 11,	6.2	11
100	Characterization of Farmington virus, a novel virus from birds that is distantly related to members of the family Rhabdoviridae. <i>Virology Journal</i> , 2013 , 10, 219	6.1	11
99	Comparison of targeted next-generation sequencing for whole-genome sequencing of Hantaan orthohantavirus in Apodemus agrarius lung tissues. <i>Scientific Reports</i> , 2019 , 9, 16631	4.9	11
98	Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. <i>Clinical Infectious Diseases</i> , 2020 , 70, 464-473	11.6	11
97	Essentials of filoviral load quantification. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, e134-e138	25.5	10
96	Pharmacodynamic assays to facilitate preclinical and clinical development of pre-mRNA splicing modulatory drug candidates. <i>Pharmacology Research and Perspectives</i> , 2015 , 3, e00158	3.1	10
95	Full Genomic Characterization of a Saffold Virus Isolated in Peru. <i>Pathogens</i> , 2015 , 4, 816-25	4.5	10
94	Host Dependent Evolutionary Patterns and the Origin of 2009 H1N1 Pandemic Influenza: Alexander Solovyov*, Benjamin Greenbaum*, Gustavo Palacios, W. Ian Lipkin and Raul Rabadan (* Joint First Authors). <i>PLOS Currents</i> , 2010 , 2, RRN1147		10
93	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566	2.6	10

92	T-705 induces lethal mutagenesis in Ebola and Marburg populations in macaques. <i>Antiviral Research</i> , 2019 , 170, 104529	10.8	9
91	Ribavirin Had Demonstrable Effects on the Crimean-Congo Hemorrhagic Fever Virus (CCHFV) Population and Load in a Patient With CCHF Infection. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1952-19	936	9
90	Complete coding sequences of eastern equine encephalitis virus and venezuelan equine encephalitis virus strains isolated from human cases. <i>Genome Announcements</i> , 2015 , 3,		9
89	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. <i>BMC Genomics</i> , 2014 , 15, 846	4.5	9
88	Lymphocytic choriomeningitis virus-associated meningitis, southern Spain. <i>Emerging Infectious Diseases</i> , 2012 , 18, 855-8	10.2	9
87	Informing the Historical Record of Experimental Nonhuman Primate Infections with Ebola Virus: Genomic Characterization of USAMRIID Ebola Virus/H.sapiens-tc/COD/1995/Kikwit-9510621 Challenge Stock "R4368" and Its Replacement "R4415". <i>PLoS ONE</i> , 2016 , 11, e0150919	3.7	9
86	Two stable variants of Burkholderia pseudomallei strain MSHR5848 express broadly divergent in vitro phenotypes associated with their virulence differences. <i>PLoS ONE</i> , 2017 , 12, e0171363	3.7	9
85	Divergent Simian Arteriviruses Cause Simian Hemorrhagic Fever of Differing Severities in Macaques. <i>MBio</i> , 2016 , 7, e02009-15	7.8	9
84	Transcriptomics Reveal Antiviral Gene Induction in the Egyptian Rousette Bat Is Antagonized In Vitro by Marburg Virus Infection. <i>Viruses</i> , 2018 , 10,	6.2	9
83	Qualitative Profiling of the Humoral Immune Response Elicited by rVSV- G -EBOV-GP Using a Systems Serology Assay, Domain Programmable Arrays. <i>Cell Reports</i> , 2018 , 24, 1050-1059.e5	10.6	8
82	Gene duplication and phylogeography of North American members of the Hart Park serogroup of avian rhabdoviruses. <i>Virology</i> , 2014 , 448, 284-92	3.6	8
81	Viral diversity and clonal evolution from unphased genomic data. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S17	4.5	8
80	Complete Genome Assembly of Enterococcus faecalis 29212, a Laboratory Reference Strain. <i>Genome Announcements</i> , 2014 , 2,		8
79	Genome Sequences of Simian Hemorrhagic Fever Virus Variant NIH LVR42-0/M6941 Isolates (Arteriviridae: Arterivirus). <i>Genome Announcements</i> , 2014 , 2,		8
78	Whole-genome sequences of 24 Brucella strains. <i>Genome Announcements</i> , 2014 , 2,		8
77	More toxin tests needed. Science, 2008, 319, 725-6	33.3	8
76	A spontaneous mutation in kdsD, a biosynthesis gene for 3 Deoxy-D-manno-Octulosonic Acid, occurred in a ciprofloxacin resistant strain of Francisella tularensis and caused a high level of attenuation in murine models of tularemia. <i>PLoS ONE</i> , 2017 , 12, e0174106	3.7	8
75	Shedding of Marburg Virus in Naturally Infected Egyptian Rousette Bats, South Africa, 2017. Emerging Infectious Diseases, 2020 , 26, 3051-3055	10.2	8

(2013-2018)

A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. <i>Scientific Reports</i> , 2018 , 8, 9584	4.9	8
Severe acute respiratory syndrome coronavirus persistence in Vero cells. <i>Chinese Medical Journal</i> , 2005 , 118, 451-9	2.9	8
Person-to-Person Transmission of Andes Virus in Hantavirus Pulmonary Syndrome, Argentina, 2014. <i>Emerging Infectious Diseases</i> , 2020 , 26, 756-759	10.2	7
A novel sheet-like virus particle array is a hallmark of Zika virus infection. <i>Emerging Microbes and Infections</i> , 2018 , 7, 69	18.9	7
Cynomolgus macaque (Macaca fascicularis) immunoglobulin heavy chain locus description. <i>Immunogenetics</i> , 2016 , 68, 417-428	3.2	7
Growth-Adaptive Mutations in the Ebola Virus Makona Glycoprotein Alter Different Steps in the Virus Entry Pathway. <i>Journal of Virology</i> , 2018 , 92,	6.6	7
Epitope mapping of Ebola virus dominant and subdominant glycoprotein epitopes facilitates construction of an epitope-based DNA vaccine able to focus the antibody response in mice. <i>Human Vaccines and Immunotherapeutics</i> , 2017 , 13, 2883-2893	4.4	7
Whole-Genome Yersinia sp. Assemblies from 10 Diverse Strains. <i>Genome Announcements</i> , 2014 , 2,		7
Diagnostics and discovery in viral hemorrhagic fevers. <i>Annals of the New York Academy of Sciences</i> , 2009 , 1171 Suppl 1, E6-11	6.5	7
Phosphoproteomic analysis reveals Smad protein family activation following Rift Valley fever virus infection. <i>PLoS ONE</i> , 2018 , 13, e0191983	3.7	7
Oropouche orthobunyavirus: Genetic characterization of full-length genomes and development of molecular methods to discriminate natural reassortments. <i>Infection, Genetics and Evolution</i> , 2019 , 68, 16-22	4.5	7
Functionality of Two Origins of Replication in Strains With a Single Chromosome. <i>Frontiers in Microbiology</i> , 2018 , 9, 2932	5.7	7
Modeling mosquito-borne and sexual transmission of Zika virus in an enzootic host, the African green monkey. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008107	4.8	6
Complete Genome Coding Sequences of Artashat, Burana, Caspiy, Chim, Geran, Tamdy, and Uzun-Agach Viruses (: :). <i>Genome Announcements</i> , 2017 , 5,		6
Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. <i>Frontiers in Microbiology</i> , 2019 , 10, 856	5.7	6
Identification and characterization of Highlands J virus from a Mississippi sandhill crane using unbiased next-generation sequencing. <i>Journal of Virological Methods</i> , 2014 , 206, 42-5	2.6	6
Full-Genome Assembly of Reference Strain Providencia stuartii ATCC 33672. <i>Genome Announcements</i> , 2014 , 2,		6
Alteration of de novo glucose production contributes to fasting hypoglycaemia in Fyn deficient mice. <i>PLoS ONE</i> , 2013 , 8, e81866	3.7	6
	Severe acute respiratory syndrome coronavirus persistence in Vero cells. Chinese Medical Journal, 2005, 118, 451-9 Person-to-Person Transmission of Andes Virus in Hantavirus Pulmonary Syndrome, Argentina, 2014. Emerging Infectious Diseases, 2020, 26, 756-759 A novel sheet-like virus particle array is a hallmark of Zika virus infection. Emerging Microbes and Infections, 2018, 7, 69 Cynomolgus macaque (Macaca fascicularis) immunoglobulin heavy chain locus description. Immunogenetics, 2016, 68, 417-428 Growth-Adaptive Mutations in the Ebola Virus Makona Glycoprotein Alter Different Steps in the Virus Entry Pathway. Journal of Virology, 2018, 92. Epitope mapping of Ebola virus dominant and subdominant glycoprotein epitopes facilitates construction of an epitope-based DNA vaccine able to focus the antibody response in mice. Human Vaccines and Immunotherapeutics, 2017, 13, 2883-2893 Whole-Genome Yersinia sp. Assemblies from 10 Diverse Strains. Genome Announcements, 2014, 2, Diagnostics and discovery in viral hemorrhagic fevers. Annals of the New York Academy of Sciences, 2009, 1171 Suppl 1, E6-11 Phosphoproteomic analysis reveals Smad protein family activation following Rift Valley fever virus infection. PLoS ONE, 2018, 13, e0191983 Oropouche orthobunyavirus: Genetic characterization of full-length genomes and development of molecular methods to discriminate natural reassortments. Infection, Genetics and Evolution, 2019, 68, 16-22 Functionality of Two Origins of Replication in Strains With a Single Chromosome. Frontiers in Microbiology, 2018, 9, 2932 Modeling mosquito-borne and sexual transmission of Zika virus in an enzootic host, the African green monkey. PLoS Neglected Tropical Diseases, 2020, 14, e0008107 Complete Genome Coding Sequences of Artashat, Burana, Caspiy, Chim, Geran, Tamdy, and Uzun-Agach Viruses (:). Genome Announcements, 2017, 5. Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. Frontiers in Microbiology, 2019, 10, 856 Identification and	Severe acute respiratory syndrome coronavirus persistence in Vero cells. Chinese Medical Journal, 2005, 118, 451-9 Person-to-Person Transmission of Andes Virus in Hantavirus Pulmonary Syndrome, Argentina, 2014. Emerging Infectious Diseases, 2020, 26, 756-759 A novel sheet-like virus particle array is a hallmark of Zika virus infection. Emerging Microbes and Infections, 2018, 7, 69 Cynomolgus macaque (Macaca fascicularis) immunoglobulin heavy chain locus description. Immunogenetics, 2016, 68, 417-428 Growth-Adaptive Mutations in the Ebola Virus Makona Glycoprotein Alter Different Steps in the Virus Entry Pathway. Journal of Virology, 2018, 92, Epitope mapping of Ebola virus dominant and subdominant glycoprotein epitopes facilitates construction of an epitope-based DNA vaccine able to focus the antibody response in mice. Human Vaccines and Immunotherapeutics, 2017, 13, 2883-2893 Whole-Genome Yersinia sp. Assemblies from 10 Diverse Strains. Genome Announcements, 2014, 2, Diagnostics and discovery in viral hemorrhagic fevers. Annals of the New York Academy of Sciences, 2009, 1171 Suppl 1, E6-11 Phosphoproteomic analysis reveals Smad protein family activation following Rift Valley fever virus infection. PLoS ONE, 2018, 13, e0191983 Oropouche orthobunyavirus: Genetic characterization of full-length genomes and development of molecular methods to discriminate natural reassortments. Infection, Genetics and Evolution, 2019, 68, 16-22 Functionality of Two Origins of Replication in Strains With a Single Chromosome. Frontiers in Microbiology, 2018, 9, 2932 Modeling mosquito-borne and sexual transmission of Zika virus in an enzootic host, the African green monkey. PLoS Neglected Tropical Diseases, 2020, 14, e0008107 Compete Genome Coding Sequences of Artashat, Burana, Caspiy, Chim, Geran, Tamdy, and Uzun-Agach Viruses (:). Genome Announcements, 2017, 5, Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. Frontiers in Microbiology, 2019, 10, 856 Identification and c

56	Nonparametric methods for the analysis of single-color pathogen microarrays. <i>BMC Bioinformatics</i> , 2010 , 11, 354	3.6	6
55	Isolation of Complete Equine Encephalitis Virus Genome from Human Swab Specimen, Peru. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1578-1580	10.2	5
54	Draft Genome Assemblies of Proteus mirabilis ATCC 7002 and Proteus vulgaris ATCC 49132. <i>Genome Announcements</i> , 2014 , 2,		5
53	Genome Sequence of Moraxella macacae 0408225, a Novel Bacterial Species Isolated from a Cynomolgus Macaque with Epistaxis. <i>Genome Announcements</i> , 2013 , 1,		5
52	Evolution of Antibiotic Resistance in Surrogates of (LVS and): Effects on Biofilm Formation and Fitness. <i>Frontiers in Microbiology</i> , 2020 , 11, 593542	5.7	5
51	Rousette Bat Dendritic Cells Overcome Marburg Virus-Mediated Antiviral Responses by Upregulation of Interferon-Related Genes While Downregulating Proinflammatory Disease Mediators. <i>MSphere</i> , 2019 , 4,	5	5
50	Twenty Whole-Genome Bacillus sp. Assemblies. <i>Genome Announcements</i> , 2014 , 2,		4
49	Draft Genome Assembly of Klebsiella pneumoniae Type Strain ATCC 13883. <i>Genome Announcements</i> , 2014 , 2,		4
48	Complete Genome Sequence of Type Strain Pasteurella multocida subsp. multocida ATCC 43137. <i>Genome Announcements</i> , 2014 , 2,		4
47	Complete Genome Assembly of a Quality Control Reference Isolate, Moraxella catarrhalis Strain ATCC 25240. <i>Genome Announcements</i> , 2014 , 2,		4
46	Development of real-time PCR assays for the detection of Moraxella macacae associated with bloody nose syndrome in rhesus (Macaca mulatta) and cynomolgus (Macaca fascicularis) macaques. <i>Journal of Medical Primatology</i> , 2015 , 44, 364-72	0.7	4
45	Whole-genome sequences of nine francisella isolates. <i>Genome Announcements</i> , 2014 , 2,		4
44	Molecular characterization of severe and mild cases of influenza A (H1N1) 2009 strain from Argentina. <i>Medicina</i> , 2010 , 70, 518-23	1	4
43	Standard finishing categories for high-throughput sequencing of viral genomes. <i>OIE Revue Scientifique Et Technique</i> , 2016 , 35, 43-52	2.5	4
42	Beatrice Hill Virus Represents a Novel Species in the Genus Tibrovirus (Mononegavirales: Rhabdoviridae). <i>Genome Announcements</i> , 2017 , 5,		3
41	Whole-Genome Sequences of Variants of Sterne and Their Toxin Gene Deletion Mutants. <i>Genome Announcements</i> , 2017 , 5,		3
40	Complete Genome Assembly of Reference Strain Ochrobactrum anthropi ATCC 49687. <i>Genome Announcements</i> , 2014 , 2,		3
39	Identifying hosts of families of viruses: a machine learning approach. PLoS ONE, 2011, 6, e27631	3.7	3

(2020-2022)

38	Ebola virus persistence and disease recrudescence in the brains of antibody-treated nonhuman primate survivors <i>Science Translational Medicine</i> , 2022 , 14, eabi5229	17.5	3
37	Innovative Technologies for Advancement of WHO Risk Group 4 Pathogens Research 2019 , 437-469		3
36	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. <i>Nature Medicine</i> , 2021 , 27, 710-716	50.5	3
35	Phylodynamic Analysis of Ebola Virus Disease Transmission in Sierra Leone. Viruses, 2019 , 11,	6.2	2
34	Molecular characterization of plasmid pMoma1of Moraxella macacae, a newly described bacterial pathogen of macaques. <i>Folia Microbiologica</i> , 2015 , 60, 235-9	2.8	2
33	Complete Coding Sequence of Western Equine Encephalitis Virus Strain Fleming, Isolated from a Human Case. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
32	Draft Genomes for Eight Burkholderia mallei Isolates from Turkey. <i>Genome Announcements</i> , 2016 , 4,		2
31	Target-independent high-throughput sequencing methods provide evidence that already known human viral pathogens play a main role in respiratory infections with unexplained etiology. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1054-1065	18.9	2
30	Reverse genetics systems as tools to overcome the genetic diversity of Lassa virus. <i>Current Opinion in Virology</i> , 2019 , 37, 91-96	7.5	2
29	Draft Genome Assemblies of Enterobacter aerogenes CDC 6003-71, Enterobacter cloacae CDC 442-68, and Pantoea agglomerans UA 0804-01. <i>Genome Announcements</i> , 2014 , 2,		2
28	Comparative Genomics Analyses Support the Reclassification of Bisgaard Taxon 40 as gen. nov., With sp. nov. as Type Species: Novel Insights Into the Phylogeny and Virulence Factors of a e Family Member Associated With Mortality Events in Seabirds. <i>Frontiers in Microbiology</i> , 2021 , 12, 667356	5.7	2
27	Operationalizing genomic epidemiology during the Nord-Kivu Ebola outbreak, Democratic Republic of the Congo		2
26	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
25	A Model for the Production of Regulatory Grade Viral Hemorrhagic Fever Exposure Stocks: From Field Surveillance to Advanced Characterization of SFTSV. <i>Viruses</i> , 2020 , 12,	6.2	2
24	Genomic features of humoral immunity support tolerance model in Egyptian rousette bats. <i>Cell Reports</i> , 2021 , 35, 109140	10.6	2
23	Cross-Border Transmission of Ebola Virus as the Cause of a Resurgent Outbreak in Liberia in April 2016. <i>Clinical Infectious Diseases</i> , 2018 , 67, 1147-1149	11.6	2
22	The growing landscape of metabolomics and lipidomics: applications to medicinal chemistry and drug discovery. <i>Future Medicinal Chemistry</i> , 2019 , 11, 495-498	4.1	1
21	Complete genomic sequences of Venezuelan equine encephalitis virus subtype IIID isolates from mosquitoes. <i>Archives of Virology</i> , 2020 , 165, 1715-1717	2.6	1

20	Draft Genome Assembly of Bordetella bronchiseptica ATCC 10580, a Historical Canine Clinical Isolate. <i>Genome Announcements</i> , 2014 , 2,		1
19	Draft Genome Assembly of Neisseria lactamica Type Strain A7515. <i>Genome Announcements</i> , 2014 , 2,		1
18	Complete Genome Sequence of Salmonella enterica subsp. enterica Serovar Enteritidis Strain SEJ. <i>Genome Announcements</i> , 2014 , 2,		1
17	Microbe hunting in laboratory animal research. ILAR Journal, 2010, 51, 245-54	1.7	1
16	International travelers and genomics uncover a Bidden Zika outbreak		1
15	Development and Characterization of a cDNA-Launch Recombinant Simian Hemorrhagic Fever Virus Expressing Enhanced Green Fluorescent Protein: ORF 2b' Is Not Required for In Vitro Virus Replication. <i>Viruses</i> , 2021 , 13,	6.2	1
14	Molecular analysis of the 2012 Bundibugyo virus disease outbreak. Cell Reports Medicine, 2021, 2, 1003.	51 8	1
13	Posterior Segment Ophthalmic Manifestations in Ebola Survivors, Sierra Leone. <i>Ophthalmology</i> , 2021 , 128, 1371-1373	7.3	1
12	Approach to Cataract Surgery in an Ebola Virus Disease Survivor with Prior Ocular Viral Persistence. <i>Emerging Infectious Diseases</i> , 2020 , 26, 1553-1556	10.2	Ο
11	Delayed viral clearance despite high number of activated T cells during the acute phase in Argentinean patients with hantavirus pulmonary syndrome <i>EBioMedicine</i> , 2022 , 75, 103765	8.8	Ο
10	Novel viruses in hard ticks collected in the Republic of Korea unveiled by metagenomic high-throughput sequencing analysis. <i>Ticks and Tick-borne Diseases</i> , 2021 , 12, 101820	3.6	0
9	Detection, phenotyping and quantification of dengue virus-specific B cells using fluorescent probes. <i>Human Vaccines and Immunotherapeutics</i> , 2017 , 13, 2780-2784	4.4	
8	Reply to "Expanding the conversation on high-throughput virome sequencing standards to include consideration of microbial contamination sources". <i>MBio</i> , 2014 , 5, e02084	7.8	
7	MassTag polymerase chain reaction investigation of neonatal sepsis. <i>Journal of Neonatal-Perinatal Medicine</i> , 2011 , 4, 323-327	1.3	
6	Prior Evidence of Putative NovelRhinovirusSpecies, Australia. <i>Emerging Infectious Diseases</i> , 2008 , 14, 1824-1825	10.2	
5	Emerging Tools for Microbial Diagnosis, Surveillance, and Discovery413-435		
4	Animal-Borne Viruses515-526		
3	Human enteroviruses 2010 , 1528-1538		

Unique Features of Immunity within the Immunoglobulin Heavy Chain Locus of Egyptian Rousette Bats. *Proceedings (mdpi)*, **2020**, 50, 142

0.3

Overlooking the importance of immunoassays - Authors' reply. *Lancet Infectious Diseases, The*, **2016**, 16, 1110

25.5