

R Colina

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

77
papers

1,774
citations

17
h-index

40
g-index

77
ext. papers

2,009
ext. citations

6.6
avg, IF

4.18
L-index

#	Paper	IF	Citations
77	eIF2alpha phosphorylation bidirectionally regulates the switch from short- to long-term synaptic plasticity and memory. <i>Cell</i> , 2007 , 129, 195-206	56.2	359
76	Translational control of the innate immune response through IRF-7. <i>Nature</i> , 2008 , 452, 323-8	50.4	249
75	Leishmania repression of host translation through mTOR cleavage is required for parasite survival and infection. <i>Cell Host and Microbe</i> , 2011 , 9, 331-41	23.4	129
74	Molecular evolution of hepatitis A virus: a new classification based on the complete VP1 protein. <i>Journal of Virology</i> , 2002 , 76, 9516-25	6.6	122
73	Evidence of intratypic recombination in natural populations of hepatitis C virus. <i>Journal of General Virology</i> , 2004 , 85, 31-37	4.9	113
72	Translational control of the activation of transcription factor NF- κ B and production of type I interferon by phosphorylation of the translation factor eIF4E. <i>Nature Immunology</i> , 2012 , 13, 543-550	19.1	86
71	Genetic variability of hepatitis A virus in South America reveals heterogeneity and co-circulation during epidemic outbreaks. <i>Journal of General Virology</i> , 2001 , 82, 2647-2652	4.9	45
70	Evidence of structural genomic region recombination in Hepatitis C virus. <i>Virology Journal</i> , 2006 , 3, 53	6.1	37
69	Assessment of gastroenteric viruses from wastewater directly discharged into Uruguay River, Uruguay. <i>Food and Environmental Virology</i> , 2014 , 6, 116-24	4	36
68	Evidence of recombination in Hepatitis C Virus populations infecting a hemophiliac patient. <i>Virology Journal</i> , 2009 , 6, 203	6.1	32
67	Human enteric viruses in a wastewater treatment plant: evaluation of activated sludge combined with UV disinfection process reveals different removal performances for viruses with different features. <i>Letters in Applied Microbiology</i> , 2018 , 66, 215-221	2.9	22
66	Bayesian coalescent inference reveals high evolutionary rates and expansion of Norovirus populations. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 927-32	4.5	22
65	Molecular diversity of bovine viral diarrhea virus in Uruguay. <i>Archives of Virology</i> , 2016 , 161, 529-35	2.6	20
64	Bovine coronavirus in Uruguay: genetic diversity, risk factors and transboundary introductions from neighboring countries. <i>Archives of Virology</i> , 2019 , 164, 2715-2724	2.6	18
63	Tracking enteric viruses in green vegetables from central Argentina: potential association with viral contamination of irrigation waters. <i>Science of the Total Environment</i> , 2018 , 637-638, 665-671	10.2	18
62	Borrelia infection in Ixodes parvicinus ticks (Acari: Ixodidae) from northwestern Argentina. <i>Acta Tropica</i> , 2014 , 139, 1-4	3.2	18
61	Evidence of increasing diversification of hepatitis C viruses. <i>Journal of General Virology</i> , 1999 , 80 (Pt 6), 1377-1382	4.9	18

60	Detection of Common, Emerging and Uncommon VP4, and VP7 Human Group A Rotavirus Genotypes from Urban Sewage Samples in Uruguay. <i>Food and Environmental Virology</i> , 2015 , 7, 342-53	4	17
59	Comparison of hepatitis C viral loads in patients with or without coinfection with different genotypes. <i>Vaccine Journal</i> , 2004 , 11, 433-5		17
58	Deficiency in either 4E-BP1 or 4E-BP2 augments innate antiviral immune responses. <i>PLoS ONE</i> , 2014 , 9, e114854	3.7	17
57	Norovirus molecular detection in Uruguayan sewage samples reveals a high genetic diversity and GII.4 variant replacement along time. <i>Journal of Applied Microbiology</i> , 2016 , 120, 1427-35	4.7	17
56	Genome-wide analysis of codon usage bias in Bovine Coronavirus. <i>Virology Journal</i> , 2017 , 14, 115	6.1	16
55	Molecular epidemiology of group A rotavirus among children admitted to hospital in Salto, Uruguay, 2011-2012: first detection of the emerging genotype G12. <i>Journal of Medical Virology</i> , 2015 , 87, 754-63	19.7	16
54	Environmental assessment reveals the presence of MLB-1 human astrovirus in Uruguay. <i>Journal of Applied Microbiology</i> , 2015 , 119, 859-67	4.7	16
53	Phylogenetic analyses of Norovirus strains detected in Uruguay reveal the circulation of the novel GII.P7/GII.6 recombinant variant. <i>Infection, Genetics and Evolution</i> , 2014 , 28, 328-32	4.5	16
52	Evidence of increasing diversification of emerging Severe Acute Respiratory Syndrome Coronavirus 2 strains. <i>Journal of Medical Virology</i> , 2020 , 92, 2165-2172	19.7	15
51	Detection and Molecular Characterization of Aichivirus 1 in Wastewater Samples from Uruguay. <i>Food and Environmental Virology</i> , 2016 , 8, 13-7	4	13
50	The First Case of Bovine Astrovirus-Associated Encephalitis in the Southern Hemisphere (Uruguay), Uncovers Evidence of Viral Introduction to the Americas From Europe. <i>Frontiers in Microbiology</i> , 2019 , 10, 1240	5.7	12
49	Sewage surveillance reveals the presence of canine GVII norovirus and canine astrovirus in Uruguay. <i>Archives of Virology</i> , 2015 , 160, 2839-43	2.6	12
48	Diversification of hepatitis C viruses in South America reveals a novel genetic lineage. <i>Archives of Virology</i> , 2001 , 146, 1623-9	2.6	12
47	Epidemiology and genetic diversity of classic human astrovirus among hospitalized children with acute gastroenteritis in Uruguay. <i>Journal of Medical Virology</i> , 2017 , 89, 1775-1781	19.7	11
46	Evidence of diversification of dengue virus type 3 genotype III in the South American region. <i>Archives of Virology</i> , 2009 , 154, 699-707	2.6	11
45	Prevalence and viability of group A rotavirus in dairy farm water sources. <i>Journal of Applied Microbiology</i> , 2018 , 124, 922-929	4.7	10
44	Phylogenetic Studies of the Three RNA Silencing Suppressor Genes of South American CTV Isolates Reveal the Circulation of a Novel Genetic Lineage. <i>Viruses</i> , 2015 , 7, 4152-68	6.2	10
43	Environmental Assessment of Classical Human Astrovirus in Uruguay. <i>Food and Environmental Virology</i> , 2015 , 7, 142	4	10

42	Causes of neonatal calf diarrhea and mortality in pasture-based dairy herds in Uruguay: a farm-matched case-control study. <i>Brazilian Journal of Microbiology</i> , 2021 , 52, 977-988	2.2	10
41	Microbial Source Tracking Analysis Using Viral Indicators in Santa Lucía and Uruguay Rivers, Uruguay. <i>Food and Environmental Virology</i> , 2019 , 11, 259-267	4	8
40	Phylodynamics of Merkel-cell polyomavirus and human polyomavirus 6: A long-term history with humans. <i>Molecular Phylogenetics and Evolution</i> , 2018 , 126, 210-220	4.1	8
39	Evolution of naturally occurring 5' non-coding region variants of Hepatitis C virus in human populations of the South American region. <i>Virology Journal</i> , 2007 , 4, 79	6.1	8
38	Effect of the administration of spp. strains on neonatal diarrhoea, immune parameters and pathogen abundance in pre-weaned calves. <i>Beneficial Microbes</i> , 2020 , 11, 477-488	4.9	8
37	Bovine Astrovirus Surveillance in Uruguay Reveals High Detection Rate of a Novel Species. <i>Viruses</i> , 2019 , 12,	6.2	8
36	<i>Borrelia burgdorferi</i> sensu lato infecting Ixodes auritulus ticks in Uruguay. <i>Experimental and Applied Acarology</i> , 2020 , 80, 109-125	2.1	8
35	Application of a simple and affordable protocol for isolating plant total nucleic acids for RNA and DNA virus detection. <i>Journal of Virological Methods</i> , 2016 , 237, 14-17	2.6	7
34	Modeling gene sequences over time in 2009 H1N1 influenza A virus populations. <i>Virology Journal</i> , 2009 , 6, 215	6.1	7
33	Phylogenetic Analyses of Rotavirus A from Cattle in Uruguay Reveal the Circulation of Common and Uncommon Genotypes and Suggest Interspecies Transmission. <i>Pathogens</i> , 2020 , 9,	4.5	7
32	Wastewater contamination in Antarctic melt-water streams evidenced by virological and organic molecular markers. <i>Science of the Total Environment</i> , 2017 , 609, 225-231	10.2	6
31	The Evolutionary History and Spatiotemporal Dynamics of the NC Lineage of Citrus Tristeza Virus. <i>Viruses</i> , 2017 , 9,	6.2	6
30	Modeling gene sequence changes over time in type 3 dengue viruses from Ecuador. <i>Virus Research</i> , 2009 , 141, 105-9	6.4	6
29	Analysis of genetic heterogeneity of hepatitis C viruses in Central America reveals a novel genetic lineage. Brief report. <i>Archives of Virology</i> , 2002 , 147, 2239-46	2.6	6
28	Human Bocavirus: Detection, Quantification and Molecular Characterization in Sewage and Surface Waters in Uruguay. <i>Food and Environmental Virology</i> , 2018 , 10, 193-200	4	5
27	Evaluation of Bacterial Contamination as an Indicator of Viral Contamination in a Sedimentary Aquifer in Uruguay. <i>Food and Environmental Virology</i> , 2018 , 10, 305-315	4	5
26	Phylogenetic prediction of cis-acting elements: a cre-like sequence in Norovirus genome?. <i>BMC Research Notes</i> , 2009 , 2, 176	2.3	5
25	Causes of abortion in dairy cows in Uruguay. <i>Pesquisa Veterinaria Brasileira</i> , 2020 , 40, 325-332	0.4	5

24	Hand-foot-and-mouth disease in uruguay: Coxsackievirus A6 identified as causative of an outbreak in a rural childcare center. <i>Journal of Medical Virology</i> , 2020 , 92, 167-173	19.7	5
23	Detection, Quantification, and Microbial Risk Assessment of Group A Rotavirus in Rivers from Uruguay. <i>Food and Environmental Virology</i> , 2020 , 12, 89-98	4	5
22	First Report of the Citrus tristeza virus Trifoliolate Resistance-Breaking (RB) Genotype in Newhall Sweet Orange in South America. <i>Plant Disease</i> , 2017 , 101, 1063	1.5	4
21	Epidemic history of major genotypes of hepatitis C virus in Uruguay. <i>Infection, Genetics and Evolution</i> , 2015 , 32, 231-8	4.5	4
20	Proposal of a pathway for enteric virus groups detection as indicators of faecal contamination to enhance the evaluation of microbiological quality in freshwater in Argentina. <i>Science of the Total Environment</i> , 2021 , 760, 143400	10.2	4
19	Environmental Surveillance through Next-Generation Sequencing to Unveil the Diversity of Human Enteroviruses beyond the Reported Clinical Cases. <i>Viruses</i> , 2021 , 13,	6.2	4
18	Complete Genome Sequence of a Novel Recombinant , a Resistance-Breaking Isolate from Uruguay. <i>Genome Announcements</i> , 2018 , 6,		4
17	Evaluation of low-cost viral concentration methods in wastewaters: Implications for SARS-CoV-2 pandemic surveillances. <i>Journal of Virological Methods</i> , 2021 , 297, 114249	2.6	4
16	Biological and molecular characterization of Uruguayan citrus tristeza virus field isolates. <i>Journal of Plant Pathology</i> , 2019 , 101, 97-105	1	3
15	Modeling the Transport of Human Rotavirus and Norovirus in Standardized and in Natural Soil Matrix-Water Systems. <i>Food and Environmental Virology</i> , 2020 , 12, 58-67	4	3
14	Detection, risk factors and molecular diversity of norovirus GIII in cattle in Uruguay. <i>Infection, Genetics and Evolution</i> , 2020 , 86, 104613	4.5	2
13	An Environmental Surveillance in Uruguay Reveals the Presence of Highly Divergent Types of Human Enterovirus Species C and a High Frequency of Species A and B Types. <i>Food and Environmental Virology</i> , 2018 , 10, 343-352	4	2
12	Isotopic biomarker discovery and application in translational medicine. <i>Drug Discovery Today</i> , 2010 , 15, 127-36	8.8	2
11	Analysis of genetic variability of Indian isolates of Hepatitis C virus. <i>Archives of Virology</i> , 2004 , 149, 1185-98	2.2	2
10	Diseases associated with bovine viral diarrhea virus subtypes 1a and 2b in beef and dairy cattle in Uruguay. <i>Brazilian Journal of Microbiology</i> , 2020 , 51, 357-368	2.2	2
9	An extensive field study reveals the circulation of new genetic variants of subtype 1a of bovine viral diarrhea virus in Uruguay. <i>Archives of Virology</i> , 2020 , 165, 145-156	2.6	2
8	Hepatitis C virus phylogeny: a useful clinical tool. <i>Acta Virologica</i> , 2002 , 46, 179-82	2.2	2
7	Diversity of Uruguayan citrus tristeza virus populations segregated after single aphid transmission. <i>Tropical Plant Pathology</i> , 2019 , 44, 352-362	2.5	1

6	GII.4 human norovirus and G8P[1] bovine-like rotavirus in oysters (<i>Crassostrea gigas</i>) from Argentina.. <i>International Journal of Food Microbiology</i> , 2022 , 365, 109553	5.8	1
5	Description of a human Bocavirus recombinant strain in the Americas. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019 , 114, e190219	2.6	1
4	Human Enterovirus Diversity by Next-Generation Sequencing Analysis in Urban Sewage Samples From Buenos Aires Metropolitan Area, Argentina: A Retrospective Study. <i>Food and Environmental Virology</i> , 2021 , 13, 259-269	4	1
3	Evolutionary history and spatiotemporal dynamic of GIII norovirus: From emergence to classification in four genotypes. <i>Transboundary and Emerging Diseases</i> , 2021 ,	4.2	1
2	Viral Enteritis in Cattle: To Well Known Viruses and Beyond. <i>Microbiology Research</i> , 2021 , 12, 663-682	1	0
1	First evidence of enterovirus A71 and echovirus 30 in Uruguay and genetic relationship with strains circulating in the South American region. <i>PLoS ONE</i> , 2021 , 16, e0255846	3.7	