

# Juan Cristina

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

1,859  
citations

279798

23  
h-index

265206

42  
g-index

61  
all docs

61  
docs citations

61  
times ranked

2205  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic analysis of SARS-CoV-2 viruses circulating in the South American region: Genetic relations and vaccine strain match. <i>Virus Research</i> , 2022, 311, 198688.	2.2	1
2	An evolutionary insight into Severe Acute Respiratory Syndrome Coronavirus 2 Omicron variant of concern.. <i>Virus Research</i> , 2022, 314, 198753.	2.2	9
3	An overview of dinucleotide and codon usage in all viruses. <i>Archives of Virology</i> , 2022, 167, 1443-1448.	2.1	4
4	Molecular evolution and codon usage bias of Zika virus. , 2021, , 409-418.		0
5	Nucleotide Composition and Codon Usage Across Viruses and Their Respective Hosts. <i>Frontiers in Microbiology</i> , 2021, 12, 646300.	3.5	25
6	In the era of rapid mRNA-based vaccines: Why is there no effective hepatitis C virus vaccine yet?. <i>World Journal of Hepatology</i> , 2021, 13, 1234-1268.	2.0	6
7	An evolutionary insight into emerging Ebolavirus strains isolated in Africa. <i>Journal of Medical Virology</i> , 2020, 92, 988-995.	5.0	2
8	Evidence of increasing diversification of emerging Severe Acute Respiratory Syndrome Coronavirus 2 strains. <i>Journal of Medical Virology</i> , 2020, 92, 2165-2172.	5.0	23
9	A comprehensive analysis of genome composition and codon usage patterns of emerging coronaviruses. <i>Virus Research</i> , 2020, 283, 197976.	2.2	47
10	The 1918 influenza pandemic in Montevideo: The southernmost capital city in the Americas. <i>Influenza and Other Respiratory Viruses</i> , 2019, 13, 219-225.	3.4	4
11	Molecular Biology of RNA Viruses Isolated in Antarctica. <i>Springer Polar Sciences</i> , 2019, , 197-217.	0.1	1
12	An Evolutionary Insight into Zika Virus Strains Isolated in the Latin American Region. <i>Viruses</i> , 2018, 10, 698.	3.3	9
13	Genome-wide analysis of codon usage bias in Bovine Coronavirus. <i>Virology Journal</i> , 2017, 14, 115.	3.4	21
14	Evidence of increasing diversification of Zika virus strains isolated in the American continent. <i>Journal of Medical Virology</i> , 2017, 89, 2059-2063.	5.0	4
15	Molecular Evolution of Hepatitis C Virus: From Epidemiology to Antiviral Therapy (Current Research) Tj ETQq1 1 0.784314 rgBT /Overl		
16	Emergence and Spreading Potential of Zika Virus. <i>Frontiers in Microbiology</i> , 2016, 7, 1667.	3.5	33
17	Bayesian coalescent inference reveals high evolutionary rates and diversification of Zika virus populations. <i>Journal of Medical Virology</i> , 2016, 88, 1672-1676.	5.0	9
18	A detailed comparative analysis of codon usage bias in Zika virus. <i>Virus Research</i> , 2016, 223, 147-152.	2.2	35

#	ARTICLE	IF	CITATIONS
19	An evolutionary insight into Newcastle disease viruses isolated in Antarctica. Archives of Virology, 2015, 160, 1893-1900.	2.1	11
20	Hepatitis C virus genetic variability and evolution. World Journal of Hepatology, 2015, 7, 831.	2.0	85
21	Phylogenetic analysis of the neuraminidase gene of pandemic H1N1 influenza A virus circulating in the South American region. Virus Research, 2015, 197, 1-7.	2.2	2
22	Genome-wide analysis of codon usage bias in Ebolavirus. Virus Research, 2015, 196, 87-93.	2.2	76
23	Human endogenous retrovirus np9 gene is over expressed in chronic lymphocytic leukemia patients. Leukemia Research Reports, 2014, 3, 70-72.	0.4	26
24	A detailed molecular analysis of complete Bovine Leukemia Virus genomes isolated from B-cell lymphosarcomas. Veterinary Research, 2013, 44, 19.	3.0	34
25	A detailed comparative analysis on the overall codon usage patterns in West Nile virus. Infection, Genetics and Evolution, 2013, 14, 396-400.	2.3	70
26	Bayesian coalescent analysis of pandemic H1N1 influenza A virus circulating in the South American region. Virus Research, 2012, 170, 91-101.	2.2	2
27	Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. Virology Journal, 2012, 9, 263.	3.4	42
28	A detailed comparative analysis on the overall codon usage patterns in Hepatitis A virus. Virus Research, 2011, 157, 19-24.	2.2	34
29	Phylogenetic analysis of pandemic 2009 influenza A virus circulating in the South American region: genetic relationships and vaccine strain match. Archives of Virology, 2011, 156, 87-94.	2.1	8
30	Phylogenetic analysis of bovine leukemia viruses isolated in South America reveals diversification in seven distinct genotypes. Archives of Virology, 2010, 155, 481-489.	2.1	54
31	Establishing a quality assurance plan for nucleic acid-based diagnostic laboratories: from planning to implementation. Accreditation and Quality Assurance, 2010, 15, 89-97.	0.8	2
32	Evolution of Dengue Virus Type 3 Genotype III in Venezuela: Diversification, Rates and Population Dynamics. Virology Journal, 2010, 7, 329.	3.4	19
33	Genetic History of Hepatitis C Virus in Venezuela: High Diversity and Long Time of Evolution of HCV Genotype 2. PLoS ONE, 2010, 5, e14315.	2.5	21
34	Evidence of diversification of dengue virus type 3 genotype III in the South American region. Archives of Virology, 2009, 154, 699-707.	2.1	11
35	Human influenza A viruses isolated in South America: Genetic relations, adamantane resistance and vaccine strain match. Infection, Genetics and Evolution, 2009, 9, 229-234.	2.3	4
36	Bayesian coalescent inference reveals high evolutionary rates and expansion of Norovirus populations. Infection, Genetics and Evolution, 2009, 9, 927-932.	2.3	24

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37	Modeling gene sequence changes over time in type 3 dengue viruses from Ecuador. <i>Virus Research</i> , 2009, 141, 105-109.	2.2	6
38	Modeling gene sequences over time in 2009 H1N1 Influenza A Virus populations. <i>Virology Journal</i> , 2009, 6, 215.	3.4	7
39	Evidence of recombination in Hepatitis C Virus populations infecting a hemophiliac patient. <i>Virology Journal</i> , 2009, 6, 203.	3.4	33
40	Analysis of the full-length genome of hepatitis A virus isolated in South America: heterogeneity and evolutionary constraints. <i>Archives of Virology</i> , 2008, 153, 1473-1478.	2.1	12
41	Topology of evolving, mutagenized viral populations: quasispecies expansion, compression, and operation of negative selection. <i>BMC Evolutionary Biology</i> , 2008, 8, 207.	3.2	31
42	Phylogenetic analysis of the NS5 gene of dengue viruses isolated in Ecuador. <i>Virus Research</i> , 2008, 132, 197-200.	2.2	17
43	Bayesian coalescent inference of hepatitis A virus populations: evolutionary rates and patterns. <i>Journal of General Virology</i> , 2007, 88, 3039-3042.	2.9	34
44	Hepatitis C virus: quasispecies dynamics, virus persistence and antiviral therapy. <i>Expert Opinion on Therapeutic Patents</i> , 2007, 17, 499-510.	5.0	0
45	Influenza B viruses isolated in Uruguay during the 2002-2005 seasons: Genetic relations and vaccine strain match. <i>Virus Research</i> , 2007, 123, 100-104.	2.2	1
46	Genetic variability and molecular evolution of Hepatitis A virus. <i>Virus Research</i> , 2007, 127, 151-157.	2.2	103
47	Hepatitis C virus genetic variability in patients undergoing antiviral therapy. <i>Virus Research</i> , 2007, 127, 185-194.	2.2	22
48	Hepatitis viruses in the XXI century. <i>Virus Research</i> , 2007, 127, 129-130.	2.2	2
49	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.	3.4	8
50	Evidence of recombination in quasispecies populations of a Hepatitis C Virus patient undergoing anti-viral therapy. <i>Virology Journal</i> , 2006, 3, 87.	3.4	26
51	Evidence of structural genomic region recombination in Hepatitis C virus. <i>Virology Journal</i> , 2006, 3, 53.	3.4	38
52	Analysis of sequential hepatitis A virus strains reveals coexistence of distinct viral subpopulations. <i>Journal of General Virology</i> , 2006, 87, 115-118.	2.9	21
53	Genetic diversity and evolution of hepatitis C virus in the Latin American region. <i>Journal of Clinical Virology</i> , 2005, 34, S1-S7.	3.1	152
54	Evidence of intratypic recombination in natural populations of hepatitis C virus. <i>Journal of General Virology</i> , 2004, 85, 31-37.	2.9	119

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55	Comparison of Hepatitis C Viral Loads in Patients with or without Coinfection with Different Genotypes. <i>Vaccine Journal</i> , 2004, 11, 433-435.	2.6	22
56	Evidence of recombination in natural populations of hepatitis A virus. <i>Virology</i> , 2003, 311, 51-59.	2.4	53
57	Genetic variability of hepatitis A virus. <i>Journal of General Virology</i> , 2003, 84, 3191-3201.	2.9	141
58	Molecular Evolution of Hepatitis A Virus: a New Classification Based on the Complete VP1 Protein. <i>Journal of Virology</i> , 2002, 76, 9516-9525.	3.4	146
59	Genetic analysis of hepatitis a virus outbreak in france confirms the co-circulation of subgenotypes Ia, Ib and reveals a new genetic lineage. <i>Journal of Medical Virology</i> , 2001, 65, 233-240.	5.0	56
60	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.	2.9	51