Juan Cristina

List of Publications by Year
in descending order

60 papers	**1,859** citations	279701 **23** h-index	265120 **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. Virus Research, 2022, 311, 198688.	1.1	1
2	An evolutionary insight into Severe Acute Respiratory Syndrome Coronavirus 2 Omicron variant of concern.. Virus Research, 2022, 314, 198753.	1.1	9
3	An overview of dinucleotide and codon usage in all viruses. Archives of Virology, 2022, 167, 1443-1448.	0.9	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. Frontiers in Microbiology, 2021, 12, 646300.	1.5	25
6	In the era of rapid mRNA-based vaccines: Why is there no effective hepatitis C virus vaccine yet?. World Journal of Hepatology, 2021, 13, 1234-1268.	0.8	6
7	An evolutionary insight into emerging Ebolavirus strains isolated in Africa. Journal of Medical Virology, 2020, 92, 988-995.	2.5	2
8	Evidence of increasing diversification of emergingÂSevere Acute Respiratory Syndrome Coronavirus 2 strains. Journal of Medical Virology, 2020, 92, 2165-2172.	2.5	23
9	A comprehensive analysis of genome composition and codon usage patterns of emerging coronaviruses. Virus Research, 2020, 283, 197976.	1.1	47
10	The 1918 influenza pandemic in Montevideo: The southernmost capital city in the Americas. Influenza and Other Respiratory Viruses, 2019, 13, 219-225.	1.5	4
11	Molecular Biology of RNA Viruses Isolated in Antarctica. Springer Polar Sciences, 2019, , 197-217.	0.0	1
12	An Evolutionary Insight into Zika Virus Strains Isolated in the Latin American Region. Viruses, 2018, 10, 698.	1.5	9
13	Genome-wide analysis of codon usage bias in Bovine Coronavirus. Virology Journal, 2017, 14, 115.	1.4	21
14	Evidence of increasing diversification of Zika virus strains isolated in the American continent. Journal of Medical Virology, 2017, 89, 2059-2063.	2.5	4
15	Molecular Evolution of Hepatitis C Virus: From Epidemiology to Antiviral Therapy (Current Research) Tj ETQq1 1 0.784314 rgBT /Overl 0		
16	Emergence and Spreading Potential of Zika Virus. Frontiers in Microbiology, 2016, 7, 1667.	1.5	33
17	Bayesian coalescent inference reveals high evolutionary rates and diversification of Zika virus populations. Journal of Medical Virology, 2016, 88, 1672-1676.	2.5	9
18	A detailed comparative analysis of codon usage bias in Zika virus. Virus Research, 2016, 223, 147-152.	1.1	35

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19	An evolutionary insight into Newcastle disease viruses isolated in Antarctica. Archives of Virology, 2015, 160, 1893-1900.	0.9	11
20	Hepatitis C virus genetic variability and evolution. World Journal of Hepatology, 2015, 7, 831.	0.8	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.	1.1	2
22	Genome-wide analysis of codon usage bias in Ebolavirus. Virus Research, 2015, 196, 87-93.	1.1	76
23	Human endogenous retrovirus np9 gene is over expressed in chronic lymphocytic leukemia patients. Leukemia Research Reports, 2014, 3, 70-72.	0.2	26
24	A detailed molecular analysis of complete Bovine Leukemia Virus genomes isolated from B-cell lymphosarcomas. Veterinary Research, 2013, 44, 19.	1.1	34
25	A detailed comparative analysis on the overall codon usage patterns in West Nile virus. Infection, Genetics and Evolution, 2013, 14, 396-400.	1.0	70
26	Bayesian coalescent analysis of pandemic H1N1 influenza A virus circulating in the South American region. Virus Research, 2012, 170, 91-101.	1.1	2
27	Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. Virology Journal, 2012, 9, 263.	1.4	42
28	A detailed comparative analysis on the overall codon usage patterns in Hepatitis A virus. Virus Research, 2011, 157, 19-24.	1.1	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.	0.9	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.	0.9	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.	0.4	2
32	Evolution of Dengue Virus Type 3 Genotype III in Venezuela: Diversification, Rates and Population Dynamics. Virology Journal, 2010, 7, 329.	1.4	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.	1.1	21
34	Evidence of diversification of dengue virus type 3 genotype III in the South American region. Archives of Virology, 2009, 154, 699-707.	0.9	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.	1.0	4
36	Bayesian coalescent inference reveals high evolutionary rates and expansion of Norovirus populations. Infection, Genetics and Evolution, 2009, 9, 927-932.	1.0	24

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37	Modeling gene sequence changes over time in type 3 dengue viruses from Ecuador. Virus Research, 2009, 141, 105-109.	1.1	6
38	Modeling gene sequences over time in 2009 H1N1 Influenza A Virus populations. Virology Journal, 2009, 6, 215.	1.4	7
39	Evidence of recombination in Hepatitis C Virus populations infecting a hemophiliac patient. Virology Journal, 2009, 6, 203.	1.4	33
40	Analysis of the full-length genome of hepatitis A virus isolated in South America: heterogeneity and evolutionary constraints. Archives of Virology, 2008, 153, 1473-1478.	0.9	12
41	Topology of evolving, mutagenized viral populations: quasispecies expansion, compression, and operation of negative selection. BMC Evolutionary Biology, 2008, 8, 207.	3.2	31
42	Phylogenetic analysis of the NS5 gene of dengue viruses isolated in Ecuador. Virus Research, 2008, 132, 197-200.	1.1	17
43	Bayesian coalescent inference of hepatitis A virus populations: evolutionary rates and patterns. Journal of General Virology, 2007, 88, 3039-3042.	1.3	34
44	Hepatitis C virus: quasispecies dynamics, virus persistance and antiviral therapy. Expert Opinion on Therapeutic Patents, 2007, 17, 499-510.	2.4	0
45	Influenza B viruses isolated in Uruguay during the 2002–2005 seasons: Genetic relations and vaccine strain match. Virus Research, 2007, 123, 100-104.	1.1	1
46	Genetic variability and molecular evolution of Hepatitis A virus. Virus Research, 2007, 127, 151-157.	1.1	103
47	Hepatitis C virus genetic variability in patients undergoing antiviral therapy. Virus Research, 2007, 127, 185-194.	1.1	22
48	Hepatitis viruses in the XXI century. Virus Research, 2007, 127, 129-130.	1.1	2
49	Evolution of naturally occurring 5'non-coding region variants of Hepatitis C virus in human populations of the South American region. Virology Journal, 2007, 4, 79.	1.4	8
50	Evidence of recombination in quasispecies populations of a Hepatitis C Virus patient undergoing anti-viral therapy. Virology Journal, 2006, 3, 87.	1.4	26
51	Evidence of structural genomic region recombination in Hepatitis C virus. Virology Journal, 2006, 3, 53.	1.4	38
52	Analysis of sequential hepatitis A virus strains reveals coexistence of distinct viral subpopulations. Journal of General Virology, 2006, 87, 115-118.	1.3	21
53	Genetic diversity and evolution of hepatitis C virus in the Latin American region. Journal of Clinical Virology, 2005, 34, S1-S7.	1.6	152
54	Evidence of intratypic recombination in natural populations of hepatitis C virus. Journal of General Virology, 2004, 85, 31-37.	1.3	119

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55	Comparison of Hepatitis C Viral Loads in Patients with or without Coinfection with Different Genotypes. Vaccine Journal, 2004, 11, 433-435.	2.6	22
56	Evidence of recombination in natural populations of hepatitis A virus. Virology, 2003, 311, 51-59.	1.1	53
57	Genetic variability of hepatitis A virus. Journal of General Virology, 2003, 84, 3191-3201.	1.3	141
58	Molecular Evolution of Hepatitis A Virus: a New Classification Based on the Complete VP1 Protein. Journal of Virology, 2002, 76, 9516-9525.	1.5	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. Journal of Medical Virology, 2001, 65, 233-240.	2.5	56
60	Genetic variability of hepatitis A virus in South America reveals heterogeneity and co-circulation during epidemic outbreaks. Journal of General Virology, 2001, 82, 2647-2652.	1.3	51