

HÃ©ctor Musto

List of Publications by Year in descending order

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22
papers

816
citations

567281

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713466

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all docs

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22
times ranked

715
citing authors

#	ARTICLE	IF	CITATIONS
1	Codon usage in <i>Chlamydia trachomatis</i> is the result of strand-specific mutational biases and a complex pattern of selective forces. <i>Nucleic Acids Research</i> , 2000, 28, 2084-2090.	14.5	164
2	Genome-wide analysis of codon usage bias in Ebolavirus. <i>Virus Research</i> , 2015, 196, 87-93.	2.2	76
3	A detailed comparative analysis on the overall codon usage patterns in West Nile virus. <i>Infection, Genetics and Evolution</i> , 2013, 14, 396-400.	2.3	70
4	The influence of translational selection on codon usage in fishes from the family Cyprinidae. <i>Gene</i> , 2003, 317, 141-147.	2.2	69
5	Synonymous Codon Choices in the Extremely GC-Poor Genome of <i>Plasmodium falciparum</i> : Compositional Constraints and Translational Selection. <i>Journal of Molecular Evolution</i> , 1999, 49, 27-35.	1.8	61
6	Translational Selection on Codon Usage in <i>Xenopus laevis</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1703-1707.	8.9	56
7	Codon Usage Bias: An Endless Tale. <i>Journal of Molecular Evolution</i> , 2021, 89, 589-593.	1.8	44
8	Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. <i>Virology Journal</i> , 2012, 9, 263.	3.4	42
9	Compositional properties of nuclear genes from <i>Plasmodium falciparum</i> . <i>Gene</i> , 1995, 152, 127-132.	2.2	39
10	A detailed comparative analysis of codon usage bias in Zika virus. <i>Virus Research</i> , 2016, 223, 147-152.	2.2	35
11	Translational selection is operative for synonymous codon usage in <i>Clostridium perfringens</i> and <i>Clostridium acetobutylicum</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 855-863.	1.8	27
12	Nucleotide Composition and Codon Usage Across Viruses and Their Respective Hosts. <i>Frontiers in Microbiology</i> , 2021, 12, 646300.	3.5	25
13	Compositional Correlations in the Chicken Genome. <i>Journal of Molecular Evolution</i> , 1999, 49, 325-329.	1.8	24
14	Genome-wide analysis of codon usage bias in Bovine Coronavirus. <i>Virology Journal</i> , 2017, 14, 115.	3.4	21
15	Host influence in the genomic composition of flaviviruses: A multivariate approach. <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 572-578.	2.1	18
16	Trends of Amino Acid Usage in the Proteins from the Human Genome. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 25, 55-59.	3.5	15
17	CpG islands are the second main factor shaping codon usage in human genes. <i>Biochemical and Biophysical Research Communications</i> , 2006, 343, 1257-1261.	2.1	9
18	General Trends in Selectively Driven Codon Usage Biases in the Domain Archaea. <i>Journal of Molecular Evolution</i> , 2014, 79, 105-110.	1.8	6

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19	Codon usage in the flatworm <i>Schistosoma mansoni</i> is shaped by the mutational bias towards A+T and translational selection, which increases GC-ending codons in highly expressed genes. <i>Molecular and Biochemical Parasitology</i> , 2022, 247, 111445.	1.1	6
20	Dinucleotide biases in the platyhelminth <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology</i> , 1994, 24, 277-283.	3.1	5
21	An overview of dinucleotide and codon usage in all viruses. <i>Archives of Virology</i> , 2022, 167, 1443-1448.	2.1	4
22	In Memoriam of Giorgio Bernardi and Noboru Sueoka: A Personal View. <i>Journal of Molecular Evolution</i> , 0, , .	1.8	0