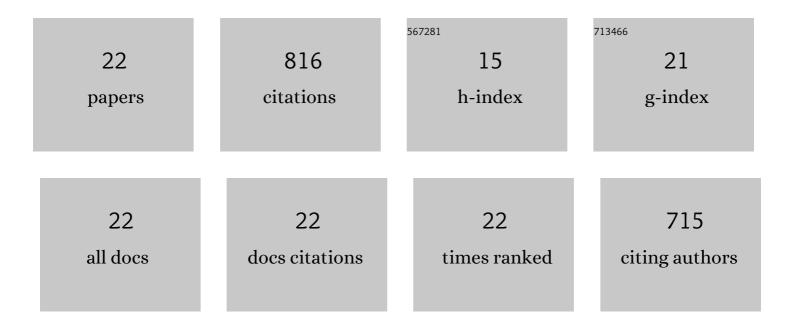
Héctor Musto

List of Publications by Year in descending order

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ΗÃ@στορ Μμετο

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

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