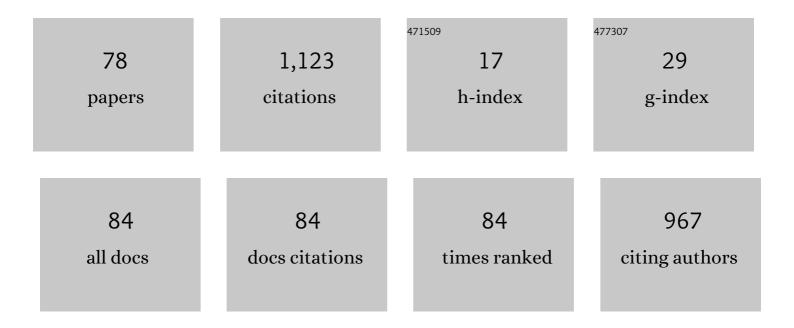
List of Publications by Year in descending order

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MARCO VIOSÃO

#	Article	IF	CITATIONS
1	Poincaré plot indexes of heart rate variability capture dynamic adaptations after haemodialysis in chronic renal failure patients. Clinical Physiology and Functional Imaging, 2003, 23, 72-80.	1.2	113
2	Limitations of current diagnostic procedures for the diagnosis of Taenia solium cysticercosis in rural pigs. Veterinary Parasitology, 1998, 79, 299-313.	1.8	80
3	Origin and Evolution of RNA-Dependent RNA Polymerase. Frontiers in Genetics, 2017, 8, 125.	2.3	61
4	The genome project of Taenia solium. Parasitology International, 2006, 55, S127-S130.	1.3	49
5	Origin and evolution of the Peptidyl Transferase Center from protoâ€ŧRNAs. FEBS Open Bio, 2014, 4, 175-178.	2.3	49
6	Randomised trial of albendazole and pyrantel in symptomless trichuriasis in children. Lancet, The, 1998, 352, 1103-1108.	13.7	41
7	Scaling properties and symmetrical patterns in the epidemiology of rotavirus infection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2003, 358, 1625-1641.	4.0	30
8	Human tumor growth is inhibited by a vaccinia virus carrying the E2 gene of bovine papillomavirus. , 2000, 88, 1650-1662.		28
9	A Mathematical Analysis for the Cardiovascular Control Adaptations in Chronic Renal Failure. Artificial Organs, 2004, 28, 398-409.	1.9	27
10	Inhibitory Role of Antibodies in the Development ofTaenia soliumandTaenia crassicepsToward Reproductive and Pathogenic Stages. Journal of Parasitology, 2001, 87, 582-586.	0.7	26
11	tRNA Core Hypothesis for the Transition from the RNA World to the Ribonucleoprotein World. Life, 2016, 6, 15.	2.4	26
12	An Extended RNA Code and its Relationship to the Standard Genetic Code: An Algebraic and Geometrical Approach. Bulletin of Mathematical Biology, 2007, 69, 215-243.	1.9	24
13	Nonlinear dynamics of heart rate variability in response to orthostatism and hemodialysis in chronic renal failure patients: Recurrence analysis approach. Medical Engineering and Physics, 2013, 35, 178-187.	1.7	24
14	Vaccination against Taenia solium cysticercosis in underfed rustic pigs of México: roles of age, genetic background and antibody response. Veterinary Parasitology, 2000, 90, 209-219.	1.8	23
15	A unified model of the standard genetic code. Royal Society Open Science, 2017, 4, 160908.	2.4	23
16	On the Evolution of the Standard Genetic Code: Vestiges of Critical Scale Invariance from the RNA World in Current Prokaryote Genomes. PLoS ONE, 2009, 4, e4340.	2.5	23
17	Evolution of transfer RNA and the origin of the translation system. Frontiers in Genetics, 2014, 5, 303.	2.3	20
18	How to eliminate taeniasis/cysticercosis: porcine vaccination and human chemotherapy (Part 2). Theoretical Biology and Medical Modelling, 2019, 16, 4.	2.1	18

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19	Analysis of bilateral inverse symmetry in whole bacterial chromosomes. Biochemical and Biophysical Research Communications, 2002, 299, 126-134.	2.1	17
20	Three-base periodicity patterns and self-similarity in whole bacterial chromosomes. Biochemical and Biophysical Research Communications, 2004, 325, 467-478.	2.1	17
21	The Ancient History of Peptidyl Transferase Center Formation as Told by Conservation and Information Analyses. Life, 2020, 10, 134.	2.4	17
22	Transfer RNA: The molecular demiurge in the origin of biological systems. Progress in Biophysics and Molecular Biology, 2020, 153, 28-34.	2.9	17
23	Multiple Origins of Extracellular DNA Traps. Frontiers in Immunology, 2021, 12, 621311.	4.8	17
24	The Spike Protein of SARS-CoV-2 Is Adapting Because of Selective Pressures. Vaccines, 2022, 10, 864.	4.4	17
25	Alternative interpretation of unusual scatchard plots: contribution of interactions and heterogeneity. Mathematical Biosciences, 1982, 58, 159-170.	1.9	16
26	Genetic Hotels for the Standard Genetic Code: Evolutionary Analysis Based upon Novel Three-Dimensional Algebraic Models. Bulletin of Mathematical Biology, 2011, 73, 1443-1476.	1.9	16
27	A proposal of the proteome before the last universal common ancestor (LUCA). International Journal of Astrobiology, 2016, 15, 27-31.	1.6	16
28	Origin of the 16S Ribosomal Molecule from Ancestor tRNAs. Sci, 2019, 1, 8.	3.0	16
29	Mathematical model of the life cycle of taenia-cysticercosis: transmission dynamics and chemotherapy (Part 1). Theoretical Biology and Medical Modelling, 2018, 15, 18.	2.1	14
30	Epidemiological model of diarrhoeal diseases and its application in prevention and control. Vaccine, 1994, 12, 109-116.	3.8	13
31	Peptidyl Transferase Center and the Emergence of the Translation System. Life, 2017, 7, 21.	2.4	13
32	Neutral evolution test of the spike protein of SARS-CoV-2 and its implications in the binding to ACE2. Scientific Reports, 2021, 11, 18847.	3.3	13
33	Symmetrical and Thermodynamic Properties of Phenotypic Graphs of Amino Acids Encoded by the Primeval RNY Code. Origins of Life and Evolution of Biospheres, 2015, 45, 77-83.	1.9	12
34	Preserved autonomic heart rate modulation in chronic renal failure patients in response to hemodialysis and orthostatism. Clinical and Experimental Nephrology, 2015, 19, 309-318.	1.6	12
35	On the Uniqueness of the Standard Genetic Code. Life, 2017, 7, 7.	2.4	12
36	Three-Dimensional Algebraic Models of the tRNA Code and 12 Graphs for Representing the Amino Acids. Life, 2014, 4, 341-373.	2.4	11

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37	Effects of Orthostatism and Hemodialysis on Mean Heart Period and Fractal Heart Rate Properties of Chronic Renal Failure Patients. Artificial Organs, 2017, 41, 1026-1034.	1.9	11
38	Identity Elements of tRNA as Derived from Information Analysis. Origins of Life and Evolution of Biospheres, 2018, 48, 73-81.	1.9	11
39	Origin of the 16S Ribosomal Molecule from Ancestor tRNAs. Journal of Molecular Evolution, 2021, 89, 249-256.	1.8	9
40	Is it possible that cells have had more than one origin?. BioSystems, 2021, 202, 104371.	2.0	9
41	Structural evolution of Glycyl-tRNA synthetases alpha subunit and its implication in the initial organization of the decoding system. Progress in Biophysics and Molecular Biology, 2019, 142, 43-50.	2.9	8
42	The Theory of Chemical Symbiosis: A Margulian View for the Emergence of Biological Systems (Origin) Tj ETQq(	0 0 0 rgBT /	Overlock 10 1
43	Ligand binding systems at equilibrium: Specificity, heterogeneity, cross-reactivity, and site-site interactions. Analytical Biochemistry, 1985, 144, 494-503.	2.4	7
44	Statistical properties of DNA sequences revisited: the role of inverse bilateral symmetry in bacterial chromosomes. Physica A: Statistical Mechanics and Its Applications, 2005, 351, 477-498.	2.6	7
45	HIV–1 dynamics at different time scales under antiretroviral therapy. Journal of Theoretical Biology, 2006, 238, 220-229.	1.7	7
46	Periodic Distribution of a Putative Nucleosome Positioning Motif in Human, Nonhuman Primates, and Archaea: Mutual Information Analysis. International Journal of Genomics, 2013, 2013, 1-13.	1.6	7
47	The evolution of proteome: From the primeval to the very dawn of LUCA. BioSystems, 2019, 181, 1-10.	2.0	7
48	Information theory unveils the evolution of tRNA identity elements in the three domains of life. Theory in Biosciences, 2020, 139, 77-85.	1.4	7
49	On the solution of mathematical models of herd immunity in human helminth infections. Journal of Mathematical Biology, 1989, 27, 707-715.	1.9	6
50	From RNA to DNA: Insights about the transition of informational molecule in the biological systems based on the structural proximity between the polymerases. BioSystems, 2021, 206, 104442.	2.0	6
51	Phenotypic Graphs and Evolution Unfold the Standard Genetic Code as the Optimal. Origins of Life and Evolution of Biospheres, 2018, 48, 83-91.	1.9	5
52	A neutral evolution test derived from a theoretical amino acid substitution model. Journal of Theoretical Biology, 2019, 467, 31-38.	1.7	5
53	Statistical analysis of the distribution of amino acids in Borrelia burgdorferi genome under different genetic codes. Physica A: Statistical Mechanics and Its Applications, 2004, 342, 288-293.	2.6	4
54	Human repetitive sequence densities are mostly negatively correlated with R/Y-based nucleosome-positioning motifs and positively correlated with W/S-based motifs. Genomics, 2013, 101, 125-133.	2.9	4

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55	A Proposal of the Ur-proteome. Origins of Life and Evolution of Biospheres, 2018, 48, 245-258.	1.9	4
56	Multivariate Entropy Characterizes the Gene Expression and Protein-Protein Networks in Four Types of Cancer. Entropy, 2018, 20, 154.	2.2	4
57	Novel gene signatures for stage classification of the squamous cell carcinoma of the lung. Scientific Reports, 2021, 11, 4835.	3.3	4
58	Structural Computational Analysis of the Natural History of Class I aminoacyl-tRNA Synthetases Suggests their Role in Establishing the Genetic Code. Journal of Molecular Evolution, 2021, 89, 611-617.	1.8	4
59	Symmetrical Properties of Graph Representations of Genetic Codes: From Genotype to Phenotype. Symmetry, 2018, 10, 388.	2.2	3
60	On the Importance of Asymmetry in the Phenotypic Expression of the Genetic Code upon the Molecular Evolution of Proteins. Symmetry, 2020, 12, 997.	2.2	3
61	Probability Distributions of Thermodynamic Affinities for Heterogeneous Receptor Populations. Journal of Theoretical Biology, 1998, 190, 85-92.	1.7	2
62	Inhibitory Role of Antibodies in the Development of Taenia solium and Taenia crassiceps toward Reproductive and Pathogenic Stages. Journal of Parasitology, 2001, 87, 582.	0.7	2
63	Positive cooperativity induces multimodal site and thermodynamic affinity distributions in multivalent proteins. Analytical Biochemistry, 2003, 313, 226-233.	2.4	2
64	A lattice-based model of rotavirus epidemics. Physica A: Statistical Mechanics and Its Applications, 2006, 359, 525-537.	2.6	2
65	Mutual information analysis reveals bigeminy patterns in Andersen–Tawil syndrome and in subjects with a history of sudden cardiac death. Physica A: Statistical Mechanics and Its Applications, 2012, 391, 693-707.	2.6	2
66	Flow of Information during an Evolutionary Process: The Case of Influenza A Viruses. Entropy, 2013, 15, 3065-3087.	2.2	2
67	Genomic signatures in viral sequences by in-frame and out-frame mutual information. Journal of Theoretical Biology, 2016, 403, 1-9.	1.7	2
68	Rhythms found in human DNA. Physics World, 2004, 17, 26-26.	0.0	1
69	Origin of the 16S Ribosomal Molecule from Ancestor tRNAs. Sci, 2019, 1, 46.	3.0	1
70	Origin of the 16S Ribosomal Molecule from Ancestor tRNAs. Sci, 2020, 2, 69.	3.0	1
71	Treatment of trichuris infection with albendazole. Lancet, The, 1999, 353, 238.	13.7	0

72 Evolution of tRNAs Was Driven by Entropic Forces. , 2016, , 1-7.

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#	Article	IF	CITATIONS
73	Anticipation of ventricular tachyarrhythmias by a novel mathematical method: Further insights towards an early warning system in implantable cardioverter defibrillators. PLoS ONE, 2020, 15, e0235101.	2.5	0
74	PROBABILITY DISTRIBUTIONS OF GC CONTENT REFLECT THE EVOLUTION OF PRIMATE SPECIES. , 2014, , .		0
75	Title is missing!. , 2020, 15, e0235101.		Ο
76	Title is missing!. , 2020, 15, e0235101.		0
77	Title is missing!. , 2020, 15, e0235101.		Ο
78	Title is missing!. , 2020, 15, e0235101.		0