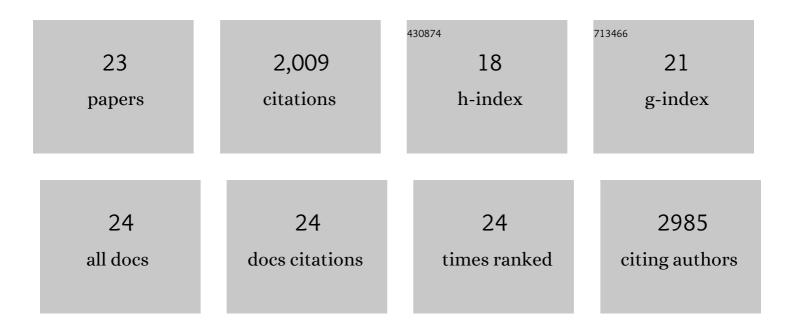
Luciano Brocchieri

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Quantitative frame analysis and the annotation of GC-rich (and other) prokaryotic genomes. An application toAnaeromyxobacter dehalogenans. Bioinformatics, 2015, 31, 3254-3261.	4.1	4
2	Gene identification in Pseudomonas aeruginosa : from bioinformatics to experimental analysis. FASEB Journal, 2012, 26, 978.3.	0.5	0
3	Chaperonin genes on the rise: new divergent classes and intense duplication in human and other vertebrate genomes. BMC Evolutionary Biology, 2010, 10, 64.	3.2	30
4	A Comprehensive Classification and Evolutionary Analysis of Plant Homeobox Genes. Molecular Biology and Evolution, 2009, 26, 2775-2794.	8.9	383
5	hsp70 genes in the human genome: Conservation and differentiation patterns predict a wide array of overlapping and specialized functions. BMC Evolutionary Biology, 2008, 8, 19.	3.2	224
6	Chaperonomics, a new tool to study ageing and associated diseases. Mechanisms of Ageing and Development, 2007, 128, 125-136.	4.6	18
7	Evolution of a Protein-Folding Machine: Genomic and Evolutionary Analyses Reveal Three Lineages of the Archaeal hsp70(dnaK) Gene. Journal of Molecular Evolution, 2006, 63, 74-86.	1.8	21
8	Distinguishing features of δ-proteobacterial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11352-11357.	7.1	27
9	Predicting Coding Potential from Genome Sequence: Application to Betaherpesviruses Infecting Rats and Mice. Journal of Virology, 2005, 79, 7570-7596.	3.4	61
10	Genomic and proteomic comparisons between bacterial and archaeal genomes and related comparisons with the yeast and fly genomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7309-7314.	7.1	22
11	Protein length in eukaryotic and prokaryotic proteomes. Nucleic Acids Research, 2005, 33, 3390-3400.	14.5	342
12	Predicted highly expressed genes in archaeal genomes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7303-7308.	7.1	52
13	Environmental signatures in proteome properties. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8257-8258.	7.1	16
14	The composition, structure and stability of a group II chaperonin are temperature regulated in a hyperthermophilic archaeon. Molecular Microbiology, 2003, 48, 143-156.	2.5	65
15	Allostery and Induced Fit: NMR and Molecular Modeling Study of the trp Repressor-mtr DNA Complex. ACS Symposium Series, 2002, , 340-366.	O.5	2
16	Heterogeneity of Genome and Proteome Content in Bacteria, Archaea, and Eukaryotes. Theoretical Population Biology, 2002, 61, 367-390.	1.1	41
17	Phylogenetic Inferences from Molecular Sequences: Review and Critique. Theoretical Population Biology, 2001, 59, 27-40.	1.1	91
18	Conservation among HSP60 sequences in relation to structure, function, and evolution. Protein Science, 2000, 9, 476-486.	7.6	155

#	Article	IF	CITATIONS
19	Significant Segment Alignment of Pairs of Protein Sequences from Animals, Plants and Fungi. , 1999, , 213-221.		0
20	Heat Shock Protein 70 Family: Multiple Sequence Comparisons, Function, and Evolution. Journal of Molecular Evolution, 1998, 47, 565-577.	1.8	168
21	A symmetric-iterated multiple alignment of protein sequences. Journal of Molecular Biology, 1998, 276, 249-264.	4.2	71
22	Evolutionary Comparisons of RecA-Like Proteins Across All Major Kingdoms of Living Organisms. Journal of Molecular Evolution, 1997, 44, 528-541.	1.8	125
23	Measuring Residue Association in Protein Structures Possible Implications for Protein Folding. Journal of Molecular Biology, 1994, 239, 227-248.	4.2	88