Luciano Brocchieri

List of Publications by Year
in descending order

23	2,009	430874 18	713466 21
papers	citations	h-index	g-index

24	24	24	2985
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Comprehensive Classification and Evolutionary Analysis of Plant Homeobox Genes. Molecular Biology and Evolution, 2009, 26, 2775-2794.	8.9	383
2	Protein length in eukaryotic and prokaryotic proteomes. Nucleic Acids Research, 2005, 33, 3390-3400.	14.5	342
3	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
4	Heat Shock Protein 70 Family: Multiple Sequence Comparisons, Function, and Evolution. Journal of Molecular Evolution, 1998, 47, 565-577.	1.8	168
5	Conservation among HSP60 sequences in relation to structure, function, and evolution. Protein Science, 2000, 9, 476-486.	7.6	155
6	Evolutionary Comparisons of RecA-Like Proteins Across All Major Kingdoms of Living Organisms. Journal of Molecular Evolution, 1997, 44, 528-541.	1.8	125
7	Phylogenetic Inferences from Molecular Sequences: Review and Critique. Theoretical Population Biology, 2001, 59, 27-40.	1.1	91
8	Measuring Residue Association in Protein Structures Possible Implications for Protein Folding. Journal of Molecular Biology, 1994, 239, 227-248.	4.2	88
9	A symmetric-iterated multiple alignment of protein sequences. Journal of Molecular Biology, 1998, 276, 249-264.	4.2	71
10	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
11	Predicting Coding Potential from Genome Sequence: Application to Betaherpesviruses Infecting Rats and Mice. Journal of Virology, 2005, 79, 7570-7596.	3.4	61
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	Heterogeneity of Genome and Proteome Content in Bacteria, Archaea, and Eukaryotes. Theoretical Population Biology, 2002, 61, 367-390.	1.1	41
14	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
15	Distinguishing features of Î˜-proteobacterial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11352-11357.	7.1	27
16	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
17	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
18	Chaperonomics, a new tool to study ageing and associated diseases. Mechanisms of Ageing and Development, 2007, 128, 125-136.	4.6	18

#	Article	IF	Citations
19	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
20	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
21	Allostery and Induced Fit: NMR and Molecular Modeling Study of the trp Repressor-mtr DNA Complex. ACS Symposium Series, 2002, , 340-366.	0.5	2
22	Gene identification in Pseudomonas aeruginosa : from bioinformatics to experimental analysis. FASEB Journal, 2012, 26, 978.3.	0.5	0
23	Significant Segment Alignment of Pairs of Protein Sequences from Animals, Plants and Fungi. , 1999, , 213-221.		0