Giovanni Bussotti

List of Publications by Year
in descending order

33 papers	9,076 citations	361045 20 h-index	395343 33 g-index
41 all docs	41 docs citations	41 times ranked	16708 citing authors

#	Article	IF	Citations
1	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
2	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
3	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
4	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. Journal of Molecular and Cellular Cardiology, 2015, 89, 98-112.	0.9	223
5	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	9.0	155
6	Multiple sequence alignment modeling: methods and applications. Briefings in Bioinformatics, 2016, 17, 1009-1023.	3.2	153
7	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	1.2	127
8	Haplotype selection as an adaptive mechanism in the protozoan pathogen Leishmania donovani. Nature Ecology and Evolution, 2017, 1, 1961-1969.	3.4	95
9	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. Nature Protocols, 2011, 6, 1669-1682.	5.5	87
10	*Leishmania* Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. MBio, 2018, 9, .	1.8	82
11	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	5.8	73
12	Targeting Macrophage Histone H3 Modification as a Leishmania Strategy to Dampen the NF-ĸB/NLRP3-Mediated Inflammatory Response. Cell Reports, 2020, 30, 1870-1882.e4.	2.9	58
13	T-Coffee: Tree-Based Consistency Objective Function for Alignment Evaluation. Methods in Molecular Biology, 2014, 1079, 117-129.	0.4	56
14	Intron retention-dependent gene regulation in Cryptococcus neoformans. Scientific Reports, 2016, 6, 32252.	1.6	48
15	Non-coding RNA Expression, Function, and Variation during Drosophila Embryogenesis. Current Biology, 2018, 28, 3547-3561.e9.	1.8	44
16	Transposon‐driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. EMBO Reports, 2017, 18, 1231-1247.	2.0	34
17	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
18	Colonization and genetic diversification processes of Leishmania infantum in the Americas. Communications Biology, 2021, 4, 139.	2.0	32

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19	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in *Drosophila* embryogenesis. Genes and Development, 2010, 24, 129-134.	2.7	30
20	BlastRâ€"fast and accurate database searches for non-coding RNAs. Nucleic Acids Research, 2011, 39, 6886-6895.	6.5	28
21	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. Nucleic Acids Research, 2012, 40, e52-e52.	6.5	23
22	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. International Journal of Molecular Sciences, 2013, 14, 15423-15458.	1.8	22
23	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. Bioinformatics, 2013, 29, 1112-1119.	1.8	20
24	The transcriptional response of pathogenic Leptospira to peroxide reveals new defenses against infection-related oxidative stress. PLoS Pathogens, 2020, 16, e1008904.	2.1	18
25	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. PLoS Pathogens, 2021, 17, e1009875.	2.1	18
26	Genome instability drives epistatic adaptation in the human pathogen *Leishmania*. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
27	Trans-Atlantic Spillover: Deconstructing the Ecological Adaptation of Leishmania infantum in the Americas. Genes, 2020, 11, 4.	1.0	10
28	Nuclear and mitochondrial genome sequencing of North-African Leishmania infantum isolates from cured and relapsed visceral leishmaniasis patients reveals variations correlating with geography and phenotype. Microbial Genomics, 2020, 6, .	1.0	9
29	Experimental evolution links post-transcriptional regulation to Leishmania fitness gain. PLoS Pathogens, 2022, 18, e1010375.	2.1	9
30	The MoVIN server for the analysis of protein interaction networks. BMC Bioinformatics, 2008, 9, S11.	1.2	7
31	The oxidative stress response of pathogenic Leptospira is controlled by two peroxide stress regulators which putatively cooperate in controlling virulence. PLoS Pathogens, 2021, 17, e1009087.	2.1	6
32	GIP: an open-source computational pipeline for mapping genomic instability from protists to cancer cells. Nucleic Acids Research, 2022, 50, e36-e36.	6.5	5
33	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. Nucleic Acids Research, 2014, 42, W356-W360.	6.5	3