

# Giovanni Bussotti

## List of Publications by Citations

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**Version:** 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35  
papers

6,870  
citations

19  
h-index

41  
g-index

41  
ext. papers

8,328  
ext. citations

12.4  
avg, IF

4.65  
L-index

#	Paper	IF	Citations
35	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , <b>2012</b> , 22, 1775-89	9.7	3408
34	Long noncoding RNAs with enhancer-like function in human cells. <i>Cell</i> , <b>2010</b> , 143, 46-58	56.2	1422
33	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , <b>2014</b> , 515, 355-64	50.4	1026
32	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2015</b> , 89, 98-112	5.8	173
31	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , <b>2015</b> , 12, 339-42	21.6	119
30	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 1009-1023	13.4	85
29	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , <b>2011</b> , 6, 1669-82	18.8	80
28	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , <b>2011</b> , 12, 552	4.5	72
27	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , <b>2017</b> , 1, 1961-1969	12.3	65
26	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , <b>2015</b> , 6, 5903	17.4	56
25	Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. <i>MBio</i> , <b>2018</b> , 9,	7.8	46
24	T-Coffee: Tree-based consistency objective function for alignment evaluation. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1079, 117-29	1.4	41
23	Intron retention-dependent gene regulation in <i>Cryptococcus neoformans</i> . <i>Scientific Reports</i> , <b>2016</b> , 6, 32252	4.9	33
22	Targeting Macrophage Histone H3 Modification as a <i>Leishmania</i> Strategy to Dampen the NF- $\kappa$ B/NLRP3-Mediated Inflammatory Response. <i>Cell Reports</i> , <b>2020</b> , 30, 1870-1882.e4	10.6	27
21	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , <b>2017</b> , 18, 1231-1247	6.5	26
20	BlastR—fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 6886-6891	2.5	26
19	Non-coding RNA Expression, Function, and Variation during <i>Drosophila</i> Embryogenesis. <i>Current Biology</i> , <b>2018</b> , 28, 3547-3561.e9	6.3	26

18	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , <b>2016</b> , 26, 705-16	9.7	23
17	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in <i>Drosophila</i> embryogenesis. <i>Genes and Development</i> , <b>2010</b> , 24, 129-34	12.6	22
16	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. <i>Bioinformatics</i> , <b>2013</b> , 29, 1112-9	7.2	18
15	Detecting and comparing non-coding RNAs in the high-throughput era. <i>International Journal of Molecular Sciences</i> , <b>2013</b> , 14, 15423-58	6.3	16
14	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, e52	20.1	14
13	The transcriptional response of pathogenic <i>Leptospira</i> to peroxide reveals new defenses against infection-related oxidative stress. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008904	7.6	9
12	Trans-Atlantic Spill Over: Deconstructing the Ecological Adaptation of in the Americas. <i>Genes</i> , <b>2019</b> , 11,	4.2	7
11	The MoVIN server for the analysis of protein interaction networks. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S11	3.6	5
10	Short- and long-range cis interactions between integrated HPV genomes and cellular chromatin dysregulate host gene expression in early cervical carcinogenesis. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009875	7.6	5
9	Colonization and genetic diversification processes of <i>Leishmania infantum</i> in the Americas. <i>Communications Biology</i> , <b>2021</b> , 4, 139	6.7	4
8	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W356-60	20.1	3
7	Genome instability drives epistatic adaptation in the human pathogen .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	3
6	The oxidative stress response of pathogenic <i>Leptospira</i> is controlled by two peroxide stress regulators which putatively cooperate in controlling virulence		2
5	Nuclear and mitochondrial genome sequencing of North-African isolates from cured and relapsed visceral leishmaniasis patients reveals variations correlating with geography and phenotype. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	2
4	Genome instability drives epistatic adaptation in the human pathogen <i>Leishmania</i>		2
3	The oxidative stress response of pathogenic <i>Leptospira</i> is controlled by two peroxide stress regulators which putatively cooperate in controlling virulence. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009087	7.6	1
2	Post-transcriptional regulation of <i>Leishmania</i> fitness gain		1
1	Experimental evolution links post-transcriptional regulation to <i>Leishmania</i> fitness gain.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010375	7.6	1

