

Giovanni Bussotti

List of Publications by Year in Descending Order

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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	Experimental evolution links post-transcriptional regulation to Leishmania fitness gain.. <i>PLoS Pathogens</i> , 2022 , 18, e1010375	7.6	1
34	The oxidative stress response of pathogenic Leptospira is controlled by two peroxide stress regulators which putatively cooperate in controlling virulence. <i>PLoS Pathogens</i> , 2021 , 17, e1009087	7.6	1
33	Colonization and genetic diversification processes of Leishmania infantum in the Americas. <i>Communications Biology</i> , 2021 , 4, 139	6.7	4
32	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> , 2021 , 17, e1009875	7.6	5
31	Genome instability drives epistatic adaptation in the human pathogen .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
30	Targeting Macrophage Histone H3 Modification as a Leishmania Strategy to Dampen the NF- κ B/NLRP3-Mediated Inflammatory Response. <i>Cell Reports</i> , 2020 , 30, 1870-1882.e4	10.6	27
29	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> , 2020 , 6,	4.4	2
28	The transcriptional response of pathogenic Leptospira to peroxide reveals new defenses against infection-related oxidative stress. <i>PLoS Pathogens</i> , 2020 , 16, e1008904	7.6	9
27	Trans-Atlantic Spill Over: Deconstructing the Ecological Adaptation of in the Americas. <i>Genes</i> , 2019 , 11,	4.2	7
26	Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. <i>MBio</i> , 2018 , 9,	7.8	46
25	Non-coding RNA Expression, Function, and Variation during Drosophila Embryogenesis. <i>Current Biology</i> , 2018 , 28, 3547-3561.e9	6.3	26
24	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017 , 18, 1231-1247	6.5	26
23	Haplotype selection as an adaptive mechanism in the protozoan pathogen Leishmania donovani. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1961-1969	12.3	65
22	Intron retention-dependent gene regulation in Cryptococcus neoformans. <i>Scientific Reports</i> , 2016 , 6, 32252	4.9	33
21	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1009-1023	13.4	85
20	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016 , 26, 705-16	9.7	23
19	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <i>Nature Methods</i> , 2015 , 12, 339-42	21.6	119

18	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. <i>Journal of Molecular and Cellular Cardiology</i> , 2015 , 89, 98-112	5.8	173
17	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903	17.4	56
16	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
15	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. <i>Nucleic Acids Research</i> , 2014 , 42, W356-60	20.1	3
14	T-Coffee: Tree-based consistency objective function for alignment evaluation. <i>Methods in Molecular Biology</i> , 2014 , 1079, 117-29	1.4	41
13	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. <i>Bioinformatics</i> , 2013 , 29, 1112-9	7.2	18
12	Detecting and comparing non-coding RNAs in the high-throughput era. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 15423-58	6.3	16
11	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
10	Use of CHIP-Seq data for the design of a multiple promoter-alignment method. <i>Nucleic Acids Research</i> , 2012 , 40, e52	20.1	14
9	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , 2011 , 6, 1669-82	18.8	80
8	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011 , 12, 552	4.5	72
7	BlastR--fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , 2011 , 39, 6886-2051	20.1	26
6	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in Drosophila embryogenesis. <i>Genes and Development</i> , 2010 , 24, 129-34	12.6	22
5	Long noncoding RNAs with enhancer-like function in human cells. <i>Cell</i> , 2010 , 143, 46-58	56.2	1422
4	The MoVIN server for the analysis of protein interaction networks. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 2, S11	3.6	5
3	The oxidative stress response of pathogenic <i>Leptospira</i> is controlled by two peroxide stress regulators which putatively cooperate in controlling virulence		2
2	Post-transcriptional regulation of <i>Leishmania</i> fitness gain		1
1	Genome instability drives epistatic adaptation in the human pathogen <i>Leishmania</i>		2

