

# Giancarlo Russo

## List of Publications by Citations

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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.

24  
papers

627  
citations

13  
h-index

25  
g-index

27  
ext. papers

840  
ext. citations

6.3  
avg, IF

3.87  
L-index

#	Paper	IF	Citations
24	Targeted combinatorial alternative splicing generates brain region-specific repertoires of neurexins. <i>Neuron</i> , <b>2014</b> , 84, 386-98	13.9	118
23	Strictly co-isogenic C57BL/6J-Prnp <sup>0/0</sup> mice: A rigorous resource for prion science. <i>Journal of Cell Biology</i> , <b>2016</b> , 212, 2126OIA42	7.3	78
22	Post-mortem whole-exome analysis in a large sudden infant death syndrome cohort with a focus on cardiovascular and metabolic genetic diseases. <i>European Journal of Human Genetics</i> , <b>2017</b> , 25, 404-409	5.3	66
21	Strictly co-isogenic C57BL/6J-Prnp <sup>0/0</sup> mice: A rigorous resource for prion science. <i>Journal of Experimental Medicine</i> , <b>2016</b> , 213, 313-27	16.6	58
20	SIRP $\alpha$ polymorphisms, but not the prion protein, control phagocytosis of apoptotic cells. <i>Journal of Experimental Medicine</i> , <b>2013</b> , 210, 2539-52	16.6	54
19	Stable core virome despite variable microbiome after fecal transfer. <i>Gut Microbes</i> , <b>2017</b> , 8, 214-220	8.8	44
18	Long-term changes of bacterial and viral compositions in the intestine of a recovered <i>Clostridium difficile</i> patient after fecal microbiota transplantation. <i>Journal of Physical Education and Sports Management</i> , <b>2016</b> , 2, a000448	2.8	37
17	Exome analysis in 34 sudden unexplained death (SUD) victims mainly identified variants in channelopathy-associated genes. <i>International Journal of Legal Medicine</i> , <b>2018</b> , 132, 1057-1065	3.1	30
16	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1745	5.7	26
15	Lack of the pH-sensing Receptor TDAG8 [GPR65] in Macrophages Plays a Detrimental Role in Murine Models of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , <b>2019</b> , 13, 245-258	1.5	19
14	Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in $\beta$ -Proteobacteria. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006499	6	17
13	Germ-free and microbiota-associated mice yield small intestinal epithelial organoids with equivalent and robust transcriptome/proteome expression phenotypes. <i>Cellular Microbiology</i> , <b>2020</b> , 22, e13191	3.9	15
12	Genome-wide transcriptomics identifies an early preclinical signature of prion infection. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008653	7.6	14
11	Highly sensitive, non-invasive detection of colorectal cancer mutations using single molecule, third generation sequencing. <i>Applied &amp; Translational Genomics</i> , <b>2015</b> , 7, 32-9		12
10	Transcription and microbial profiling of body fluids using a massively parallel sequencing approach. <i>Forensic Science International: Genetics</i> , <b>2019</b> , 43, 102149	4.3	11
9	Periodontal bacterial supernatants modify differentiation, migration and inflammatory cytokine expression in human periodontal ligament stem cells. <i>PLoS ONE</i> , <b>2019</b> , 14, e0219181	3.7	9
8	Chromosome-scale de novo diploid assembly of the apple cultivar 'Gala Galaxy'		4

7	Re-evaluation of single nucleotide variants and identification of structural variants in a cohort of 45 sudden unexplained death cases. <i>International Journal of Legal Medicine</i> , <b>2021</b> , 135, 1341-1349	3-1	4
6	Degradation of human mRNA transcripts over time as an indicator of the time since deposition (TsD) in biological crime scene traces. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 53, 102524	4-3	3
5	De novo genome sequencing and comparative stage-specific transcriptomic analysis of <i>Dirofilaria repens</i> . <i>International Journal for Parasitology</i> , <b>2019</b> , 49, 911-919	4-3	2
4	Genome-wide transcriptomics identifies an early preclinical signature of prion infection		2
3	Assessing time dependent changes in microbial composition of biological crime scene traces using microbial RNA markers. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 53, 102537	4-3	2
2	Genome-wide transcriptomics identifies an early preclinical signature of prion infection <b>2020</b> , 16, e1008653		
1	Genome-wide transcriptomics identifies an early preclinical signature of prion infection <b>2020</b> , 16, e1008653		