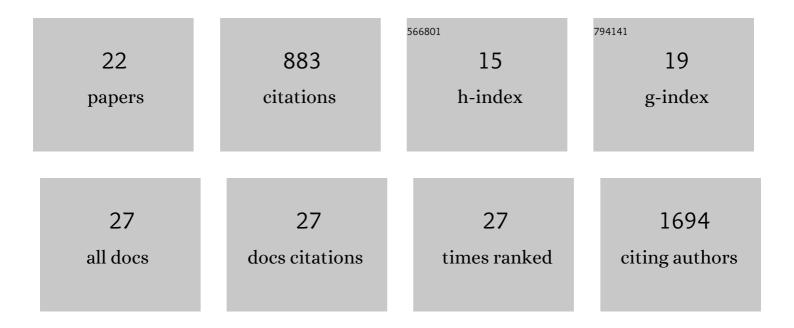
## **Giancarlo Russo**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7519373/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Targeted Combinatorial Alternative Splicing Generates Brain Region-Specific Repertoires of Neurexins. Neuron, 2014, 84, 386-398.	3.8	165
2	Strictly co-isogenic C57BL/6J- <i>Prnp</i> â^'/â^' mice: A rigorous resource for prion science. Journal of Experimental Medicine, 2016, 213, 313-327.	4.2	98
3	Post-mortem whole-exome analysis in a large sudden infant death syndrome cohort with a focus on cardiovascular and metabolic genetic diseases. European Journal of Human Genetics, 2017, 25, 404-409.	1.4	98
4	SIRPα polymorphisms, but not the prion protein, control phagocytosis of apoptotic cells. Journal of Experimental Medicine, 2013, 210, 2539-2552.	4.2	67
5	Stable core virome despite variable microbiome after fecal transfer. Gut Microbes, 2017, 8, 214-220.	4.3	60
6	Long-term changes of bacterial and viral compositions in the intestine of a recovered <i>Clostridium difficile</i> patient after fecal microbiota transplantation. Journal of Physical Education and Sports Management, 2016, 2, a000448.	0.5	50
7	RNase H As Gene Modifier, Driver of Evolution and Antiviral Defense. Frontiers in Microbiology, 2017, 8, 1745.	1.5	49
8	Genome-wide transcriptomics identifies an early preclinical signature of prion infection. PLoS Pathogens, 2020, 16, e1008653.	2.1	40
9	Lack of the pH-sensing Receptor TDAG8 [GPR65] in Macrophages Plays a Detrimental Role in Murine Models of Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2019, 13, 245-258.	0.6	39
10	Exome analysis in 34 sudden unexplained death (SUD) victims mainly identified variants in channelopathy-associated genes. International Journal of Legal Medicine, 2018, 132, 1057-1065.	1.2	38
11	Germâ€free and microbiotaâ€associated mice yield small intestinal epithelial organoids with equivalent and robust transcriptome/proteome expression phenotypes. Cellular Microbiology, 2020, 22, e13191.	1.1	26
12	Cell Cycle Constraints and Environmental Control of Local DNA Hypomethylation in α-Proteobacteria. PLoS Genetics, 2016, 12, e1006499.	1.5	25
13	Transcription and microbial profiling of body fluids using a massively parallel sequencing approach. Forensic Science International: Genetics, 2019, 43, 102149.	1.6	23
14	Degradation of human mRNA transcripts over time as an indicator of the time since deposition (TsD) in biological crime scene traces. Forensic Science International: Genetics, 2021, 53, 102524.	1.6	23
15	Periodontal bacterial supernatants modify differentiation, migration and inflammatory cytokine expression in human periodontal ligament stem cells. PLoS ONE, 2019, 14, e0219181.	1.1	17
16	Assessing time dependent changes in microbial composition of biological crime scene traces using microbial RNA markers. Forensic Science International: Genetics, 2021, 53, 102537.	1.6	17
17	Highly sensitive, non-invasive detection of colorectal cancer mutations using single molecule, third generation sequencing. Applied & Translational Genomics, 2015, 7, 32-39.	2.1	16
18	Re-evaluation of single nucleotide variants and identification of structural variants in a cohort of 45 sudden unexplained death cases. International Journal of Legal Medicine, 2021, 135, 1341-1349.	1.2	8

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#	Article	IF	CITATIONS
19	De novo genome sequencing and comparative stage-specific transcriptomic analysis of Dirofilaria repens. International Journal for Parasitology, 2019, 49, 911-919.	1.3	3
20	Strictly co-isogenic C57BL/6J-Prnpâ^'/â^'mice: A rigorous resource for prion science. Journal of Cell Biology, 2016, 212, 2126OIA42.	2.3	0
21	Genome-wide transcriptomics identifies an early preclinical signature of prion infection. , 2020, 16, e1008653.		0
22	Genome-wide transcriptomics identifies an early preclinical signature of prion infection. , 2020, 16, e1008653.		0