

# Emmanuel Giudice

## List of Publications by Year in descending order

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28  
papers

1,474  
citations

516710

16  
h-index

501196

28  
g-index

32  
all docs

32  
docs citations

32  
times ranked

1740  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the ribosomal <i>trans</i> -translation rescue system: lessons from recent structural studies. <i>FEBS Journal</i> , 2023, 290, 1461-1472.	4.7	1
2	Trans-Translation Is an Appealing Target for the Development of New Antimicrobial Compounds. <i>Microorganisms</i> , 2022, 10, 3.	3.6	7
3	Substrate recognition and cryo-EM structure of the ribosome-bound TAC toxin of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2022, 13, 2641.	12.8	5
4	Structures of tmRNA and SmpB as they transit through the ribosome. <i>Nature Communications</i> , 2021, 12, 4909.	12.8	16
5	Capsicumicine, a New Bioinspired Peptide from Red Peppers Prevents Staphylococcal Biofilm In Vitro and In Vivo via a Matrix Anti-Assembly Mechanism of Action. <i>Microbiology Spectrum</i> , 2021, 9, e0047121.	3.0	2
6	Red pepper peptide coatings control <i>Staphylococcus epidermidis</i> adhesion and biofilm formation. <i>International Journal of Pharmaceutics</i> , 2020, 574, 118872.	5.2	12
7	The structure of an elongation factor G-ribosome complex captured in the absence of inhibitors. <i>Nucleic Acids Research</i> , 2018, 46, 3211-3217.	14.5	14
8	Dystrophin's central domain forms a complex filament that becomes disorganized by in-frame deletions. <i>Journal of Biological Chemistry</i> , 2018, 293, 6637-6646.	3.4	19
9	A Genetic Tool to Quantify <i>trans</i> -Translation Activity in Vivo. <i>Journal of Molecular Biology</i> , 2017, 429, 3617-3625.	4.2	11
10	Becker muscular dystrophy severity is linked to the structure of dystrophin. <i>Human Molecular Genetics</i> , 2015, 24, 1267-1279.	2.9	71
11	Mechanism of eIF6 release from the nascent 60S ribosomal subunit. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 914-919.	8.2	168
12	Trans-translation exposed: understanding the structures and functions of tmRNA-SmpB. <i>Frontiers in Microbiology</i> , 2014, 5, 113.	3.5	39
13	Visualizing Compaction of Polysomes in Bacteria. <i>Journal of Molecular Biology</i> , 2014, 426, 377-388.	4.2	12
14	Molecular Clues about the Dystrophin-Neuronal Nitric Oxide Synthase Interaction: A Theoretical Approach. <i>Biochemistry</i> , 2013, 52, 7777-7784.	2.5	10
15	The task force that rescues stalled ribosomes in bacteria. <i>Trends in Biochemical Sciences</i> , 2013, 38, 403-411.	7.5	46
16	Structural organization of the polysomes adjacent to mammalian processing bodies (P-bodies). <i>RNA Biology</i> , 2013, 10, 314-320.	3.1	14
17	Computational Study of the Human Dystrophin Repeats: Interaction Properties and Molecular Dynamics. <i>PLoS ONE</i> , 2011, 6, e23819.	2.5	26
18	Importance of viral genomic composition in modulating glycoprotein content on the surface of influenza virus particles. <i>Virology</i> , 2011, 414, 51-62.	2.4	36

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19	tmRNAâ€™SmpB: a journey to the centre of the bacterial ribosome. EMBO Journal, 2010, 29, 3810-3818.	7.8	51
20	Biochemical and Biophysical Characterization of the Mg <sup>2+</sup> -induced 90-kDa Heat Shock Protein Oligomers. Journal of Biological Chemistry, 2010, 285, 15100-15110.	3.4	26
21	Apoâ€™Hsp90 coexists in two open conformational states in solution. Biology of the Cell, 2008, 100, 413-425.	2.0	62
22	Molecular Dynamics Simulations of the 136 Unique Tetranucleotide Sequences of DNA Oligonucleotides. II: Sequence Context Effects on the Dynamical Structures of the 10 Unique Dinucleotide Steps. Biophysical Journal, 2005, 89, 3721-3740.	0.5	216
23	Molecular Dynamics Simulations of the 136 Unique Tetranucleotide Sequences of DNA Oligonucleotides. I. Research Design and Results on d(CpG) Steps. Biophysical Journal, 2004, 87, 3799-3813.	0.5	245
24	Nucleic Acid Base Pair Dynamics:â€™ The Impact of Sequence and Structure Using Free-Energy Calculations. Journal of the American Chemical Society, 2003, 125, 4998-4999.	13.7	46
25	Base pair opening within B-DNA: free energy pathways for GC and AT pairs from umbrella sampling simulations. Nucleic Acids Research, 2003, 31, 1434-1443.	14.5	153
26	Simulations of Nucleic Acids and Their Complexes. Accounts of Chemical Research, 2002, 35, 350-357.	15.6	116
27	Analysis of peptide rotational diffusion by homonuclear NMR. Biopolymers, 2002, 63, 335-342.	2.4	2
28	Energetic and Conformational Aspects of A:T Base-Pair Opening within the DNA Double Helix. ChemPhysChem, 2001, 2, 673-677.	2.1	42