

# Caroline Mas

## List of Publications by Year in descending order

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papers

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docs citations

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times ranked

1424  
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#	ARTICLE	IF	CITATIONS
1	Structural insights into ring-building motif domains involved in bacterial sporulation. <i>Journal of Structural Biology</i> , 2022, 214, 107813.	2.8	6
2	Structural and biochemical characterisation of the <i>Providencia stuartii</i> arginine decarboxylase shows distinct polymerisation and regulation. <i>Communications Biology</i> , 2022, 5, 317.	4.4	1
3	Structural Dynamics of the C-terminal X Domain of Nipah and Hendra Viruses Controls the Attachment to the C-terminal Tail of the Nucleocapsid Protein. <i>Journal of Molecular Biology</i> , 2022, 434, 167551.	4.2	3
4	Structural and functional analysis of the <i>Francisella lysine</i> decarboxylase as a key actor in oxidative stress resistance. <i>Scientific Reports</i> , 2021, 11, 972.	3.3	9
5	Reproducibility and accuracy of microscale thermophoresis in the NanoTemper Monolith: a multi laboratory benchmark study. <i>European Biophysics Journal</i> , 2021, 50, 411-427.	2.2	13
6	A plant-like mechanism coupling m6A reading to polyadenylation safeguards transcriptome integrity and developmental gene partitioning in <i>Toxoplasma</i> . <i>ELife</i> , 2021, 10, .	6.0	19
7	Structural Description of the Nipah Virus Phosphoprotein and Its Interaction with STAT1. <i>Biophysical Journal</i> , 2020, 118, 2470-2488.	0.5	28
8	The structure of the nucleoprotein of Influenza D shows that all Orthomyxoviridae nucleoproteins have a similar NPCORE, with or without a NPTAIL for nuclear transport. <i>Scientific Reports</i> , 2019, 9, 600.	3.3	17
9	Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. <i>Nature Communications</i> , 2019, 10, 1528.	12.8	101
10	Structural characterization of the sporulation protein GerM from <i>Bacillus subtilis</i> . <i>Journal of Structural Biology</i> , 2018, 204, 481-490.	2.8	8
11	microRNA-122 amplifies hepatitis C virus translation by shaping the structure of the internal ribosomal entry site. <i>Nature Communications</i> , 2018, 9, 2613.	12.8	90
12	A molecular code for endosomal recycling of phosphorylated cargos by the SNX27-retromer complex. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 921-932.	8.2	131
13	Recombinant production of functional full-length and truncated human TRAM/TICAM-2 adaptor protein involved in Toll-like receptor and interferon signaling. <i>Protein Expression and Purification</i> , 2015, 106, 31-40.	1.3	3
14	Structural Basis for Different Phosphoinositide Specificities of the PX Domains of Sorting Nexins Regulating G-protein Signaling. <i>Journal of Biological Chemistry</i> , 2014, 289, 28554-28568.	3.4	43
15	A unique PDZ domain and arrestin-like fold interaction reveals mechanistic details of endocytic recycling by SNX27-retromer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3604-13.	7.1	151
16	Backbone resonance assignments of the monomeric DUF59 domain of human Fam96a. <i>Biomolecular NMR Assignments</i> , 2013, 7, 117-120.	0.8	8
17	NMR assignment and secondary structure of the C-terminal DNA binding domain of <i>Arabidopsis thaliana</i> VERNALIZATION1. <i>Biomolecular NMR Assignments</i> , 2012, 6, 5-8.	0.8	7
18	Structural and functional characterization of an atypical activation domain in erythroid KrÄppel-like factor (EKLF). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10484-10489.	7.1	45

#	ARTICLE	IF	CITATIONS
19	GATA-1 associates with and inhibits p53. <i>Blood</i> , 2009, 114, 165-173.	1.4	44
20	NMR Structure of the Complex between the Tfb1 Subunit of TFIID and the Activation Domain of VP16: Structural Similarities between VP16 and p53. <i>Journal of the American Chemical Society</i> , 2008, 130, 10596-10604.	13.7	48
21	p53 and TFIID share a common binding site on the Tfb1/p62 subunit of TFIID. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 106-111.	7.1	45