

# Teresa Carlomagno

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3562443/publications.pdf>

Version: 2024-02-01

49  
papers

1,661  
citations

331259

21  
h-index

315357

38  
g-index

56  
all docs

56  
docs citations

56  
times ranked

2142  
citing authors

#	ARTICLE	IF	CITATIONS
1	The structure of the box C/D enzyme reveals regulation of RNA methylation. <i>Nature</i> , 2013, 502, 519-523.	13.7	154
2	The INPHARMA Method: Protein-Mediated Interligand NOEs for Pharmacophore Mapping. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 4172-4175.	7.2	151
3	Molecular mechanism of SHP2 activation by PD-1 stimulation. <i>Science Advances</i> , 2020, 6, eaay4458.	4.7	149
4	Binding of the Human Prp31 Nop Domain to a Composite RNA-Protein Platform in U4 snRNP. <i>Science</i> , 2007, 316, 115-120.	6.0	125
5	Six Subgroups and Extensive Recent Duplications Characterize the Evolution of the Eukaryotic Tubulin Protein Family. <i>Genome Biology and Evolution</i> , 2014, 6, 2274-2288.	1.1	110
6	RNA structure determination by solid-state NMR spectroscopy. <i>Nature Communications</i> , 2015, 6, 7024.	5.8	76
7	Protein-RNA Interfaces Probed by <sup>1</sup> H-Detected MAS Solid-State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 2345-2349.	7.2	53
8	Structure of the K-turn U4 RNA: a combined NMR and SANS study. <i>Nucleic Acids Research</i> , 2010, 38, 6274-6285.	6.5	49
9	The INPHARMA technique for pharmacophore mapping: A theoretical guide to the method. <i>Journal of Magnetic Resonance</i> , 2009, 200, 64-73.	1.2	48
10	Crystallography-Independent Determination of Ligand Binding Modes. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7736-7740.	7.2	43
11	Present and future of NMR for RNA-protein complexes: A perspective of integrated structural biology. <i>Journal of Magnetic Resonance</i> , 2014, 241, 126-136.	1.2	43
12	Intermolecular Protein-RNA Interactions Revealed by 2D <sup>31</sup> P- <sup>15</sup> N Magic Angle Spinning Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2010, 132, 3842-3846.	6.6	40
13	M3: an integrative framework for structure determination of molecular machines. <i>Nature Methods</i> , 2017, 14, 897-902.	9.0	39
14	NMR in natural products: understanding conformation, configuration and receptor interactions. <i>Natural Product Reports</i> , 2012, 29, 536.	5.2	33
15	Chemical Analysis of a Miller-Type Complex Prebiotic Broth. <i>Origins of Life and Evolution of Biospheres</i> , 2016, 46, 149-169.	0.8	31
16	A Suite of Solid-State NMR Experiments for RNA Intranucleotide Resonance Assignment in a 21 kDa Protein-RNA Complex. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 9996-10001.	7.2	30
17	Rapid access to RNA resonances by proton-detected solid-state NMR at >100 kHz MAS. <i>Chemical Communications</i> , 2018, 54, 8972-8975.	2.2	29
18	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 653148.	1.6	29

#	ARTICLE	IF	CITATIONS
19	The histone chaperone sNASP binds a conserved peptide motif within the globular core of histone H3 through its TPR repeats. <i>Nucleic Acids Research</i> , 2016, 44, 3105-3117.	6.5	28
20	Phosphotyrosine couples peptide binding and SHP2 activation via a dynamic allosteric network. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2398-2415.	1.9	28
21	Accounting for Conformational Variability in Protein-Ligand Docking with NMR-Guided Rescoring. <i>Journal of the American Chemical Society</i> , 2013, 135, 5819-5827.	6.6	22
22	Isotope labeling for studying RNA by solid-state NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2018, 71, 151-164.	1.6	22
23	Structure of a Protein-RNA Complex by Solid-State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 6866-6873.	7.2	22
24	Histone chaperone exploits intrinsic disorder to switch acetylation specificity. <i>Nature Communications</i> , 2019, 10, 3435.	5.8	21
25	The structure of the SOLE element of <i>oskar</i> mRNA. <i>Rna</i> , 2015, 21, 1444-1453.	1.6	20
26	Solid-State NMR Spectroscopy of RNA. <i>Methods in Enzymology</i> , 2019, 615, 333-371.	0.4	18
27	Specificity and regulation of phosphotyrosine signaling through SH2 domains. <i>Journal of Structural Biology: X</i> , 2020, 4, 100026.	0.7	18
28	Specific Methyl Group Protonation for the Measurement of Pharmacophore-Specific Interligand NOE Interactions. <i>Chemistry - A European Journal</i> , 2008, 14, 7517-7520.	1.7	17
29	Optimization of protein samples for NMR using thermal shift assays. <i>Journal of Biomolecular NMR</i> , 2016, 64, 281-289.	1.6	17
30	Structural Principles of RNA Catalysis in a 2 <sup>â€²</sup> â€²5 <sup>â€²</sup> Lariat-Forming Ribozyme. <i>Journal of the American Chemical Society</i> , 2013, 135, 4403-4411.	6.6	16
31	Structural characterization of the Asf1-Rtt109 interaction and its role in histone acetylation. <i>Nucleic Acids Research</i> , 2018, 46, 2279-2289.	6.5	16
32	Structural and functional roles of 2 <sup>â€²</sup> -O-ribose methylations and their enzymatic machinery across multiple classes of RNAs. <i>Current Opinion in Structural Biology</i> , 2020, 65, 42-50.	2.6	13
33	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N backbone chemical-shift assignments of SARS-CoV-2 non-structural protein 1 (leader) Tj ETQq1 1_0,784314.rgBT /Ove	0.4	13
34	Archaea box C/D enzymes methylate two distinct substrate rRNA sequences with different efficiency. <i>Rna</i> , 2016, 22, 764-772.	1.6	11
35	A Distinct, Sequence-Induced Conformation Is Required for Recognition of the Constitutive Decay Element RNA by Roquin. <i>Structure</i> , 2015, 23, 1437-1447.	1.6	10
36	Small-Angle Neutron Scattering of RNA-Protein Complexes. <i>Methods in Molecular Biology</i> , 2020, 2113, 165-188.	0.4	10

#	ARTICLE	IF	CITATIONS
37	The guide sRNA sequence determines the activity level of box C/D RNPs. <i>ELife</i> , 2020, 9, .	2.8	10
38	On-the-Fly Integration of Data from a Spin-Diffusion-Based NMR Experiment into Protein-Ligand Docking. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1962-1972.	2.5	8
39	Observing Protein Degradation by the PAN-20S Proteasome by Time-Resolved Neutron Scattering. <i>Biophysical Journal</i> , 2020, 119, 375-388.	0.2	8
40	Identification of RNA Base Pairs and Complete Assignment of Nucleobase Resonances by Proton-Detected Solid-State NMR Spectroscopy at 100 MHz MAS. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 23903-23910.	7.2	8
41	Structure of a Protein-RNA Complex by Solid-State NMR Spectroscopy. <i>Angewandte Chemie</i> , 2020, 132, 6933-6940.	1.6	5
42	NMR assignments of HIV-2 TAR RNA. <i>Biomolecular NMR Assignments</i> , 2008, 2, 167-169.	0.4	3
43	<sup>1</sup> H, <sup>13</sup> C, <sup>15</sup> N chemical shift assignments of SHP2 SH2 domains in complex with PD-1 immune-tyrosine motifs. <i>Biomolecular NMR Assignments</i> , 2020, 14, 179-188.	0.4	3
44	High-resolution structure of eukaryotic Fibrillarin interacting with Nop56 amino-terminal domain. <i>Rna</i> , 2021, 27, 496-512.	1.6	2
45	Recruitment of phospholipase C <sup>β</sup> 1 to the non-structural membrane protein pK15 of Kaposi Sarcoma-associated herpesvirus promotes its Src-dependent phosphorylation. <i>PLoS Pathogens</i> , 2021, 17, e1009635.	2.1	2
46	Identification of new hit scaffolds by INPHARMA-guided virtual screening. <i>MedChemComm</i> , 2015, 6, 1501-1507.	3.5	1
47	Structure-Based Design of Scaffolds Targeting PDE10A by INPHARMA-NMR. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 1488-1498.	2.5	1
48	Eukaryotic Box C/D methylation machinery has two non-symmetric protein assembly sites. <i>Scientific Reports</i> , 2021, 11, 17561.	1.6	1
49	Identifizierung von RNA-Basenpaaren und vollständige Zuordnung von Nucleobasen-Resonanzen durch Protonen-detektierte Festkörperl-NMR-Spektroskopie bei MAS Geschwindigkeiten von 100 MHz. <i>Angewandte Chemie</i> , 0, , .	1.6	0