

Teresa Carlomagno

List of Publications by Year in descending order

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49
papers

1,661
citations

331538

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56
all docs

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docs citations

56
times ranked

2142
citing authors

#	ARTICLE	IF	CITATIONS
1	Phosphotyrosine couples peptide binding and SHP2 activation via a dynamic allosteric network. Computational and Structural Biotechnology Journal, 2021, 19, 2398-2415.	1.9	28
2	High-resolution structure of eukaryotic Fibrillarlin interacting with Nop56 amino-terminal domain. Rna, 2021, 27, 496-512.	1.6	2
3	1H, 13C, and 15N backbone chemical-shift assignments of SARS-CoV-2 non-structural protein 1 (leader) Tj ETQq1 1.0784314 rgBT /C 0.4 13	1.0784314	13
4	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. Frontiers in Molecular Biosciences, 2021, 8, 653148.	1.6	29
5	Recruitment of phospholipase C β 1 to the non-structural membrane protein pK15 of Kaposi Sarcoma-associated herpesvirus promotes its Src-dependent phosphorylation. PLoS Pathogens, 2021, 17, e1009635.	2.1	2
6	Identification of RNA Base Pairs and Complete Assignment of Nucleobase Resonances by Proton-Detected Solid-State NMR Spectroscopy at 100 μ s kHz MAS. Angewandte Chemie - International Edition, 2021, 60, 23903-23910.	7.2	8
7	Eukaryotic Box C/D methylation machinery has two non-symmetric protein assembly sites. Scientific Reports, 2021, 11, 17561.	1.6	1
8	Observing Protein Degradation by the PAN-20S Proteasome by Time-Resolved Neutron Scattering. Biophysical Journal, 2020, 119, 375-388.	0.2	8
9	Structural and functional roles of 2 β -O-ribose methylations and their enzymatic machinery across multiple classes of RNAs. Current Opinion in Structural Biology, 2020, 65, 42-50.	2.6	13
10	Specificity and regulation of phosphotyrosine signaling through SH2 domains. Journal of Structural Biology: X, 2020, 4, 100026.	0.7	18
11	Structure of a Protein-RNA Complex by Solid-State NMR Spectroscopy. Angewandte Chemie, 2020, 132, 6933-6940.	1.6	5
12	Molecular mechanism of SHP2 activation by PD-1 stimulation. Science Advances, 2020, 6, eaay4458.	4.7	149
13	Structure of a Protein-RNA Complex by Solid-State NMR Spectroscopy. Angewandte Chemie - International Edition, 2020, 59, 6866-6873.	7.2	22
14	1H, 13C, 15N chemical shift assignments of SHP2 SH2 domains in complex with PD-1 immune-tyrosine motifs. Biomolecular NMR Assignments, 2020, 14, 179-188.	0.4	3
15	Small-Angle Neutron Scattering of RNA-Protein Complexes. Methods in Molecular Biology, 2020, 2113, 165-188.	0.4	10
16	The guide sRNA sequence determines the activity level of box C/D RNPs. ELife, 2020, 9, .	2.8	10
17	Histone chaperone exploits intrinsic disorder to switch acetylation specificity. Nature Communications, 2019, 10, 3435.	5.8	21
18	Solid-State NMR Spectroscopy of RNA. Methods in Enzymology, 2019, 615, 333-371.	0.4	18

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19	Isotope labeling for studying RNA by solid-state NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2018, 71, 151-164.	1.6	22
20	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
21	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
22	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
23	M3: an integrative framework for structure determination of molecular machines. <i>Nature Methods</i> , 2017, 14, 897-902.	9.0	39
24	Optimization of protein samples for NMR using thermal shift assays. <i>Journal of Biomolecular NMR</i> , 2016, 64, 281-289.	1.6	17
25	Archaea box C/D enzymes methylate two distinct substrate rRNA sequences with different efficiency. <i>Rna</i> , 2016, 22, 764-772.	1.6	11
26	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
27	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
28	RNA structure determination by solid-state NMR spectroscopy. <i>Nature Communications</i> , 2015, 6, 7024.	5.8	76
29	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
30	Identification of new hit scaffolds by INPHARMA-guided virtual screening. <i>MedChemComm</i> , 2015, 6, 1501-1507.	3.5	1
31	The structure of the SOLE element of <i>oskar</i> mRNA. <i>Rna</i> , 2015, 21, 1444-1453.	1.6	20
32	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
33	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
34	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
35	The structure of the box C/D enzyme reveals regulation of RNA methylation. <i>Nature</i> , 2013, 502, 519-523.	13.7	154
36	Structural Principles of RNA Catalysis in a Lariat-Forming Ribozyme. <i>Journal of the American Chemical Society</i> , 2013, 135, 4403-4411.	6.6	16

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37	Proteinâ€“RNA Interfaces Probed by ¹ Hâ€“Detected MAS Solidâ€“State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 2345-2349.	7.2	53
38	Accounting for Conformational Variability in Proteinâ€“Ligand Docking with NMR-Guided Rescoring. <i>Journal of the American Chemical Society</i> , 2013, 135, 5819-5827.	6.6	22
39	A Suite of Solidâ€“State NMR Experiments for RNA Intranucleotide Resonance Assignment in a 21â€“kDa Proteinâ€“RNA Complex. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 9996-10001.	7.2	30
40	NMR in natural products: understanding conformation, configuration and receptor interactions. <i>Natural Product Reports</i> , 2012, 29, 536.	5.2	33
41	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
42	Intermolecular Proteinâ€“RNA Interactions Revealed by 2D 31Pâ€“15N Magic Angle Spinning Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2010, 132, 3842-3846.	6.6	40
43	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
44	NMR assignments of HIV-2 TAR RNA. <i>Biomolecular NMR Assignments</i> , 2008, 2, 167-169.	0.4	3
45	Specific Methyl Group Protonation for the Measurement of Pharmacophoreâ€“Specific Interligand NOE Interactions. <i>Chemistry - A European Journal</i> , 2008, 14, 7517-7520.	1.7	17
46	Crystallographyâ€“Independent Determination of Ligand Binding Modes. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 7736-7740.	7.2	43
47	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
48	The INPHARMA Method: Protein-Mediated Interligand NOEs for Pharmacophore Mapping. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 4172-4175.	7.2	151
49	Identifizierung von RNAâ€“Basenpaaren und vollstÃ¤ndige Zuordnung von Nukleobasenâ€“Resonanzen durch Protonenâ€“detektierte FestkÃ¶rperâ€“NMRâ€“Spektroskopie bei MAS Geschwindigkeiten von 100â€“kHz. <i>Angewandte Chemie</i> , 0, , .	1.6	0