

Maria R Conte

List of Publications by Year in descending order

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57
papers

1,771
citations

257450

24
h-index

289244

40
g-index

60
all docs

60
docs citations

60
times ranked

2186
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of dimerization and nucleic acid binding of human DBHS proteins NONO and PSCP1. <i>Nucleic Acids Research</i> , 2022, 50, 522-535.	14.5	10
2	Allosteric Regulation of the Soluble Epoxide Hydrolase by Nitro Fatty Acids: a Combined Experimental and Computational Approach. <i>Journal of Molecular Biology</i> , 2022, 434, 167600.	4.2	3
3	Structural dynamics in the La-module of La-related proteins. <i>RNA Biology</i> , 2021, 18, 194-206.	3.1	10
4	The La-related proteins: structures and interactions of a versatile superfamily of RNA-binding proteins. <i>RNA Biology</i> , 2021, 18, 178-193.	3.1	21
5	LARP6C orchestrates posttranscriptional reprogramming of gene expression during hydration to promote pollen tube guidance. <i>Plant Cell</i> , 2021, 33, 2637-2661.	6.6	15
6	A thiol redox sensor in soluble epoxide hydrolase enables oxidative activation by intra-protein disulfide bond formation. <i>Redox Biology</i> , 2021, 46, 102107.	9.0	3
7	Maternal Larp6 controls oocyte development, chorion formation and elevation. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	11
8	Mining the PDB for Tractable Cases Where X-ray Crystallography Combined with Fragment Screens Can Be Used to Systematically Design Protein-Protein Inhibitors: Two Test Cases Illustrated by IL1 β -IL1R and p38 γ -TAB1 Complexes. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 7559-7568.	6.4	18
9	Isothermal Titration Calorimetry Enables Rapid Characterization of Enzyme Kinetics and Inhibition for the Human Soluble Epoxide Hydrolase. <i>Analytical Chemistry</i> , 2019, 91, 14865-14872.	6.5	9
10	Resonance assignment of human LARP4A La module. <i>Biomolecular NMR Assignments</i> , 2019, 13, 169-172.	0.8	4
11	15-deoxy- $\Delta^{12,14}$ -Prostaglandin J2 inhibits human soluble epoxide hydrolase by a dual orthosteric and allosteric mechanism. <i>Communications Biology</i> , 2019, 2, 188.	4.4	16
12	<i>PDXK</i> mutations cause polyneuropathy responsive to pyridoxal 5-phosphate supplementation. <i>Annals of Neurology</i> , 2019, 86, 225-240.	5.3	54
13	LARP4A recognizes polyA RNA via a novel binding mechanism mediated by disordered regions and involving the PAM2w motif, revealing interplay between PABP, LARP4A and mRNA. <i>Nucleic Acids Research</i> , 2019, 47, 4272-4291.	14.5	23
14	Expression, purification, and characterisation of human soluble Epoxide Hydrolase (hsEH) and of its functional C-terminal domain. <i>Protein Expression and Purification</i> , 2019, 153, 105-113.	1.3	9
15	TAB1-Induced Autoactivation of p38 γ Mitogen-Activated Protein Kinase Is Crucially Dependent on Threonine 185. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	19
16	The <sc>La</sc> and related <sc>RNA</sc>-binding proteins (LARPs): structures, functions, and evolving perspectives. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1430.	6.4	99
17	Analysis of the interaction of Plexin-B1 and Plexin-B2 with Rnd family proteins. <i>PLoS ONE</i> , 2017, 12, e0185899.	2.5	11
18	The RNA-binding protein LARP4 regulates cancer cell migration and invasion. <i>Cytoskeleton</i> , 2016, 73, 680-690.	2.0	37

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19	Disulfide-activated protein kinase G $\hat{\pm}$ regulates cardiac diastolic relaxation and fine-tunes the Frank-Starling response. <i>Nature Communications</i> , 2016, 7, 13187.	12.8	46
20	A crystallographic study of human NONO (p54 ^{nrb}): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 761-769.	2.3	11
21	¹ H, ¹⁵ N and ¹³ C chemical shift assignments of the La motif and RRM1 from human LARP6. <i>Biomolecular NMR Assignments</i> , 2015, 9, 337-340.	0.8	1
22	Synergic interplay of the La motif, RRM1 and the interdomain linker of LARP6 in the recognition of collagen mRNA expands the RNA binding repertoire of the La module. <i>Nucleic Acids Research</i> , 2015, 43, 645-660.	14.5	68
23	Solution Structure of the SGTA Dimerisation Domain and Investigation of Its Interactions with the Ubiquitin-Like Domains of BAG6 and UBL4A. <i>PLoS ONE</i> , 2014, 9, e113281.	2.5	18
24	Mechanism and consequence of the autoactivation of p38 $\hat{\pm}$ mitogen-activated protein kinase promoted by TAB1. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1182-1190.	8.2	95
25	The association of a La module with the PABP-interacting motif PAM2 is a recurrent evolutionary process that led to the neofunctionalization of La-related proteins. <i>Rna</i> , 2013, 19, 36-50.	3.5	42
26	Analysis of the interaction with the hepatitis C virus mRNA reveals an alternative mode of RNA recognition by the human La protein. <i>Nucleic Acids Research</i> , 2012, 40, 1381-1394.	14.5	47
27	RNA Chaperone Activity of Human La Protein Is Mediated by Variant RNA Recognition Motif. <i>Journal of Biological Chemistry</i> , 2012, 287, 5472-5482.	3.4	42
28	A more detailed picture of the interactions between virtual screening-derived hits and the DNA G-quadruplex: NMR, molecular modelling and ITC studies. <i>Biochimie</i> , 2011, 93, 1280-1287.	2.6	25
29	Resonance assignment of nsp7 $\hat{\pm}$ from arterivirus. <i>Biomolecular NMR Assignments</i> , 2011, 5, 23-25.	0.8	1
30	La-Related Protein 4 Binds Poly(A), Interacts with the Poly(A)-Binding Protein MLE Domain via a Variant PAM2w Motif, and Can Promote mRNA Stability. <i>Molecular and Cellular Biology</i> , 2011, 31, 542-556.	2.3	89
31	Structure and Genetic Analysis of the Arterivirus Nonstructural Protein 7 $\hat{\pm}$. <i>Journal of Virology</i> , 2011, 85, 7449-7453.	3.4	12
32	Heterodimerization of the human RNase P/MRP subunits Rpp20 and Rpp25 is a prerequisite for interaction with the P3 arm of RNase MRP RNA. <i>Nucleic Acids Research</i> , 2010, 38, 4052-4066.	14.5	31
33	Letter to the Editor: Resonance assignment of SlyD from <i>E. coli</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 235-237.	0.8	3
34	The interaction of the <i>Escherichia coli</i> protein SlyD with nickel ions illuminates the mechanism of regulation of its peptidylprolyl isomerase activity. <i>FEBS Journal</i> , 2009, 276, 4529-4544.	4.7	46
35	Getting to the end of RNA: Structural analysis of protein recognition of 5' and 3' termini. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 653-666.	1.9	21
36	NMR assignment of the N-terminal region of human La free and in complex with RNA. <i>Biomolecular NMR Assignments</i> , 2008, 2, 107-109.	0.8	10

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37	Structural Analysis Reveals Conformational Plasticity in the Recognition of RNA 3' Ends by the Human La Protein. <i>Structure</i> , 2008, 16, 852-862.	3.3	71
38	Structure of the Eukaryotic Initiation Factor (eIF) 5 Reveals a Fold Common to Several Translation Factors. <i>Biochemistry</i> , 2006, 45, 4550-4558.	2.5	53
39	Resonance assignment for the N-terminal region of the eukaryotic initiation factor 5 (eIF5). <i>Journal of Biomolecular NMR</i> , 2006, 36, 42-42.	2.8	0
40	A terminal affair: 3'-end recognition by the human La protein. <i>Trends in Biochemical Sciences</i> , 2006, 31, 303-305.	7.5	15
41	Structural analysis of cooperative RNA binding by the La motif and central RRM domain of human La protein. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 323-329.	8.2	128
42	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. <i>Structure</i> , 2004, 12, 1631-1643.	3.3	87
43	Letter to the Editor: Resonance Assignment and Secondary Structure of the La Motif. <i>Journal of Biomolecular NMR</i> , 2004, 29, 449-450.	2.8	5
44	Resonance assignment and secondary structure of an N-terminal fragment of the human La protein. <i>Journal of Biomolecular NMR</i> , 2003, 27, 93-94.	2.8	16
45	Structure of the C-Terminal Domain of Human La Protein Reveals a Novel RNA Recognition Motif Coupled to a Helical Nuclear Retention Element. <i>Structure</i> , 2003, 11, 833-843.	3.3	96
46	Chemical shift mapping of RNA interactions with the polypyrimidine tract binding protein. <i>Nucleic Acids Research</i> , 2002, 30, 456-462.	14.5	25
47	Resonance assignment and secondary structure determination of a C-terminal fragment of the lupus autoantigen (La) protein containing a putative RNA recognition motif (RRM). <i>Journal of Biomolecular NMR</i> , 2002, 22, 387-388.	2.8	5
48	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1999, 14, 383-384.	2.8	2
49	Retroviral Matrix Proteins: A Structural Perspective. <i>Virology</i> , 1998, 246, 191-198.	2.4	58
50	The three-dimensional solution structure of the matrix protein from the type D retrovirus, the Mason-Pfizer monkey virus, and implications for the morphology of retroviral assembly. <i>EMBO Journal</i> , 1997, 16, 5819-5826.	7.8	62
51	Determination of sugar conformations by NMR in larger DNA duplexes using both dipolar and scalar data: Application to d(CATGTGACGTCACATG) ₂ . <i>Journal of Biomolecular NMR</i> , 1996, 7, 190-206.	2.8	23
52	Hydration of the RNA duplex r(CGAAUUUGCG) ₂ determined by NMR. <i>Nucleic Acids Research</i> , 1996, 24, 3693-3699.	14.5	38
53	Interaction of Minor-Groove-Binding Diamidine Ligands with an Asymmetric DNA Duplex. <i>NMR and Molecular Modelling Studies. FEBS Journal</i> , 1995, 229, 433-444.	0.2	25
54	Sterestructures of new bioactive sesterterpenes isolated from the Caribbean sponge <i>Cacospongia cf. linteiformis</i> . <i>Tetrahedron</i> , 1995, 51, 10751-10758.	1.9	16

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55	Lintenolides, new pentacyclic bioactive sesterterpenes from the caribbean sponge <i>Cacospongia</i> cf. <i>linteiformis</i> . <i>Tetrahedron</i> , 1994, 50, 849-856.	1.9	26
56	Structure and absolute stereochemistry of cyclolinteinone a novel monocarbocyclic sesterterpene from <i>Cacospongia</i> cf. <i>linteiformis</i> . <i>Tetrahedron</i> , 1994, 50, 13469-13476.	1.9	10
57	Solid phase synthesis of 5-hydroxymethyluracil containing DNA. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1992, 2, 79-82.	2.2	29