

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 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
2	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
3	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
4	Mechanism and consequence of the autoactivation of p38 β mitogen-activated protein kinase promoted by TAB1. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1182-1190.	8.2	95
5	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
6	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. <i>Structure</i> , 2004, 12, 1631-1643.	3.3	87
7	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
8	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
9	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
10	Retroviral Matrix Proteins: A Structural Perspective. <i>Virology</i> , 1998, 246, 191-198.	2.4	58
11	<i>PDXK</i> mutations cause polyneuropathy responsive to pyridoxal 5-phosphate supplementation. <i>Annals of Neurology</i> , 2019, 86, 225-240.	5.3	54
12	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
13	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
14	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
15	Disulfide-activated protein kinase G β regulates cardiac diastolic relaxation and fine-tunes the Frank-Starling response. <i>Nature Communications</i> , 2016, 7, 13187.	12.8	46
16	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
17	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
18	Hydration of the RNA duplex r(CGCAAUUUGCG) ₂ determined by NMR. <i>Nucleic Acids Research</i> , 1996, 24, 3693-3699.	14.5	38

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19	The RNA-binding protein LARP4 regulates cancer cell migration and invasion. <i>Cytoskeleton</i> , 2016, 73, 680-690.	2.0	37
20	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
21	Solid phase synthesis of 5-hydroxymethyluracil containing DNA. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1992, 2, 79-82.	2.2	29
22	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
23	Interaction of Minor-Groove-Binding Diamidine Ligands with an Asymmetric DNA Duplex. <i>NMR and Molecular Modelling Studies</i> . <i>FEBS Journal</i> , 1995, 229, 433-444.	0.2	25
24	Chemical shift mapping of RNA interactions with the polypyrimidine tract binding protein. <i>Nucleic Acids Research</i> , 2002, 30, 456-462.	14.5	25
25	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
26	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
27	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
28	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
29	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
30	TAB1-Induced Autoactivation of p38 Mitogen-Activated Protein Kinase Is Crucially Dependent on Threonine 185. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	19
31	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
32	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
33	Sterestructures of new bioactive sesterterpenes isolated from the Caribbean sponge <i>Cacospongia</i> cf. <i>linteiformis</i> . <i>Tetrahedron</i> , 1995, 51, 10751-10758.	1.9	16
34	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
35	15-deoxy- γ -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
36	A terminal affair: 3'-end recognition by the human La protein. <i>Trends in Biochemical Sciences</i> , 2006, 31, 303-305.	7.5	15

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37	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
38	Structure and Genetic Analysis of the Arterivirus Nonstructural Protein 7 \hat{I} . <i>Journal of Virology</i> , 2011, 85, 7449-7453.	3.4	12
39	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
40	Maternal Larp6 controls oocyte development, chorion formation and elevation. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	11
41	Analysis of the interaction of Plexin-B1 and Plexin-B2 with Rnd family proteins. <i>PLoS ONE</i> , 2017, 12, e0185899.	2.5	11
42	Structure and absolute stereochemistry of cyclolinteinone a novel monocarbocyclic sesterterpene from <i>Cacospongia cf. linteiformis</i> . <i>Tetrahedron</i> , 1994, 50, 13469-13476.	1.9	10
43	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
44	Structural dynamics in the La-module of La-related proteins. <i>RNA Biology</i> , 2021, 18, 194-206.	3.1	10
45	Structural basis of dimerization and nucleic acid binding of human DBHS proteins NONO and PSPC1. <i>Nucleic Acids Research</i> , 2022, 50, 522-535.	14.5	10
46	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
47	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
48	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
49	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
50	Resonance assignment of human LARP4A La module. <i>Biomolecular NMR Assignments</i> , 2019, 13, 169-172.	0.8	4
51	Letter to the Editor: Resonance assignment of SlyD from <i>E.Âcoli</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 235-237.	0.8	3
52	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
53	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
54	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1999, 14, 383-384.	2.8	2

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55	Resonance assignment of nsp7 [±] from arterivirus. <i>Biomolecular NMR Assignments</i> , 2011, 5, 23-25.	0.8	1
56	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
57	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