Bruno Charpentier

List of Publications by Year
in descending order

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43	1,651	361413	289244
papers	citations	20 h-index	40 g-index

45	45	45	1482
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The interaction between RPAP3 and TRBP reveals a possible involvement of the HSP90/R2TP chaperone complex in the regulation of miRNA activity. Nucleic Acids Research, 2022, 50, 2172-2189.	14.5	4
2	Phylogenetic and Molecular Analyses Identify SNORD116 Targets Involved in the Praderâ€“Willi Syndrome. Molecular Biology and Evolution, 2022, 39, .	8.9	13
3	The box C/D snoRNP assembly factor Bcd1 interacts with the histone chaperone Rtt106 and controls its transcription dependent activity. Nature Communications, 2021, 12, 1859.	12.8	3
4	Emerging Data on the Diversity of Molecular Mechanisms Involving C/D snoRNAs. Non-coding RNA, 2021, 7, 30.	2.6	9
5	NOPCHAP1 is a PAQosome cofactor that helps loading NOP58 on RUVBL1/2 during box C/D snoRNP biogenesis. Nucleic Acids Research, 2021, 49, 1094-1113.	14.5	14
6	Bcd1p controls RNA loading of the core protein Nop58 during C/D box snoRNP biogenesis. Rna, 2019, 25, 496-506.	3.5	16
7	The yeast C/D box snoRNA U14 adopts a â€œweakâ€•K-turn like conformation recognized by the Snu13 core protein in solution. Biochimie, 2019, 164, 70-82.	2.6	16
8	NMR assignment and solution structure of the external DII domain of the yeast Rvb2 protein. Biomolecular NMR Assignments, 2018, 12, 243-247.	0.8	1
9	Contribution of protein Gar1 to the RNA-guided and RNA-independent rRNA:Î¨-synthase activities of the archaeal Cbf5 protein. Scientific Reports, 2018, 8, 13815.	3.3	7
10	The RPAP3-Cterminal domain identifies R2TP-like quaternary chaperones. Nature Communications, 2018, 9, 2093.	12.8	59
11	Deep Structural Analysis of RPAP3 and PIH1D1, Two Components of the HSP90 Co-chaperone R2TP Complex. Structure, 2018, 26, 1196-1209.e8.	3.3	36
12	Implication of the box C/D snoRNP assembly factor Rsa1p in U3 snoRNP assembly. Nucleic Acids Research, 2017, 45, 7455-7473.	14.5	17
13	MicroRNA-29b Contributes to Collagens Imbalance in Human Osteoarthritic and Dedifferentiated Articular Chondrocytes. BioMed Research International, 2017, 2017, 1-12.	1.9	17
14	Functional and Structural Insights of the Zinc-Finger HIT protein family members Involved in Box C/D snoRNP Biogenesis. Journal of Molecular Biology, 2016, 428, 2488-2506.	4.2	20
15	Structural Features of the Box C/D snoRNP Pre-assembly Process Are Conserved through Species. Structure, 2016, 24, 1693-1706.	3.3	15
16	NUFIP and the HSP90/R2TP chaperone bind the SMN complex and facilitate assembly of U4-specific proteins. Nucleic Acids Research, 2015, 43, 8973-8989.	14.5	49
17	Combining native MS approaches to decipher archaeal box H/ACA ribonucleoprotein particle structure and activity. Proteomics, 2015, 15, 2851-2861.	2.2	9
18	Contribution of two conserved histidines to the dual activity of archaeal RNA guide-dependent and -independent pseudouridine synthase Cbf5. Rna, 2015, 21, 1233-1239.	3.5	3

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19	RNA size is a critical factor for U-containing substrate selectivity and permanent pseudouridylated product release during the RNA:Î¨-synthase reaction catalyzed by box H/ACA sRNP enzyme at high temperature. Biochimie, 2015, 113, 134-142.	2.6	2
20	Structure/Function Analysis of Proteinâ€“Protein Interactions Developed by the Yeast Pih1 Platform Protein and Its Partners in Box C/D snoRNP Assembly. Journal of Molecular Biology, 2015, 427, 2816-2839.	4.2	22
21	1H, 15N and 13C resonance assignments of the yeast Pih1 and Tah1 C-terminal domains complex. Biomolecular NMR Assignments, 2015, 9, 71-73.	0.8	3
22	1H, 15N and 13C resonance assignments of the two TPR domains from the human RPAP3 protein. Biomolecular NMR Assignments, 2015, 9, 99-102.	0.8	7
23	Protein Hit1, a novel box C/D snoRNP assembly factor, controls cellular concentration of the scaffolding protein Rsa1 by direct interaction. Nucleic Acids Research, 2014, 42, 10731-10747.	14.5	37
24	Characterization of the interaction between protein Snu13p/15.5K and the Rsa1p/NUFIP factor and demonstration of its functional importance for snoRNP assembly. Nucleic Acids Research, 2014, 42, 2015-2036.	14.5	34
25	Proteomic and 3D structure analyses highlight the C/D box snoRNP assembly mechanism and its control. Journal of Cell Biology, 2014, 207, 463-480.	5.2	57
26	High-Resolution Structural Analysis Shows How Tah1 Tethers Hsp90 to the R2TP Complex. Structure, 2013, 21, 1834-1847.	3.3	42
27	Comparative Study of Two Box H/ACA Ribonucleoprotein Pseudouridine-Synthases: Relation between Conformational Dynamics of the Guide RNA, Enzyme Assembly and Activity. PLoS ONE, 2013, 8, e70313.	2.5	11
28	The sRNA RyhB Regulates the Synthesis of the Escherichia coli Methionine Sulfoxide Reductase MsrB but Not MsrA. PLoS ONE, 2013, 8, e63647.	2.5	29
29	Combined in silico and experimental identification of the Pyrococcus abyssi H/ACA sRNAs and their target sites in ribosomal RNAs. Nucleic Acids Research, 2008, 36, 2459-2475.	14.5	44
30	The Hsp90 chaperone controls the biogenesis of L7Ae RNPs through conserved machinery. Journal of Cell Biology, 2008, 180, 579-595.	5.2	196
31	A Dedicated Computational Approach for the Identification of Archaeal H/ACA sRNAs. Methods in Enzymology, 2007, 425, 355-387.	1.0	13
32	Reconstitution of Archaeal H/ACA sRNPs and Test of their Activity. Methods in Enzymology, 2007, 425, 389-405.	1.0	10
33	Identification of determinants in the protein partners aCBF5 and aNOP10 necessary for the tRNA:Â55-synthase and RNA-guided RNA:Â-synthase activities. Nucleic Acids Research, 2007, 35, 5610-5624.	14.5	35
34	Crystal structure determination and site-directed mutagenesis of the Pyrococcus abyssi aCBF5-aNOP10 complex reveal crucial roles of the C-terminal domains of both proteins in H/ACA sRNP activity. Nucleic Acids Research, 2006, 34, 826-839.	14.5	72
35	Reconstitution of archaeal H/ACA small ribonucleoprotein complexes active in pseudouridylation. Nucleic Acids Research, 2005, 33, 3133-3144.	14.5	115
36	Characterization of the molecular mechanisms involved in the differential production of erythrose-4-phosphate dehydrogenase, 3-phosphoglycerate kinase and class II fructose-1,6-bisphosphate aldolase inEscherichia coli. Molecular Microbiology, 2005, 57, 1265-1287.	2.5	22

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37	Purification, crystallization and preliminary X-ray diffraction data of L7Ae sRNP core protein fromPyrococcus abyssii. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 122-124.	2.5	12
38	The strong efficiency of the Escherichia coli gapA P1 promoter depends on a complex combination of functional determinants. Biochemical Journal, 2004, 383, 371-382.	3.7	38
39	A structural, phylogenetic, and functional study of 15.5-kD/Snu13 protein binding on U3 small nucleolar RNA. Rna, 2003, 9, 821-838.	3.5	59
40	RNomics in Archaea reveals a further link between splicing of archaeal introns and rRNA processing. Nucleic Acids Research, 2002, 30, 921-930.	14.5	124
41	Both pH and Carbon Flux Influence the Level of Rubredoxin in Clostridium butyricum. Current Microbiology, 2001, 43, 434-439.	2.2	0
42	A Common Core RNP Structure Shared between the Small Nucleoar Box C/D RNPs and the Spliceosomal U4 snRNP. Cell, 2000, 103, 457-466.	28.9	318
43	A dynamic in Vivo view of the HIV-IRev-RRE interaction. Journal of Molecular Biology, 1997, 266, 950-962.	4.2	39