

Antoine ClÃ©ry

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4574144/publications.pdf>

Version: 2024-02-01

21
papers

1,825
citations

516710

16
h-index

713466

21
g-index

25
all docs

25
docs citations

25
times ranked

3097
citing authors

#	ARTICLE	IF	CITATIONS
1	40S hnRNP particles are a novel class of nuclear biomolecular condensates. <i>Nucleic Acids Research</i> , 2022, 50, 6300-6312.	14.5	8
2	RNAâ€PROTACs: Degradars of RNAâ€Binding Proteins. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 3163-3169.	13.8	95
3	RNAâ€PROTACs: Degradars of RNAâ€Binding Proteins. <i>Angewandte Chemie</i> , 2021, 133, 3200-3206.	2.0	12
4	An <i>in vitro</i> reconstituted U1 snRNP allows the study of the disordered regions of the particle and the interactions with proteins and ligands. <i>Nucleic Acids Research</i> , 2021, 49, e63-e63.	14.5	12
5	Inosine Substitutions in RNA Activate Latent G-Quadruplexes. <i>Journal of the American Chemical Society</i> , 2021, 143, 15120-15130.	13.7	12
6	Structure of SRSF1 RRM1 bound to RNA reveals an unexpected bimodal mode of interaction and explains its involvement in SMN1 exon7 splicing. <i>Nature Communications</i> , 2021, 12, 428.	12.8	37
7	Structural basis of a small molecule targeting RNA for a specific splicing correction. <i>Nature Chemical Biology</i> , 2019, 15, 1191-1198.	8.0	89
8	Specific inhibition of splicing factor activity by decoy RNA oligonucleotides. <i>Nature Communications</i> , 2019, 10, 1590.	12.8	70
9	The Solution Structure of FLIS Bound to RNA Reveals a Bipartite Mode of RNA Recognition with Both Sequence and Shape Specificity. <i>Molecular Cell</i> , 2019, 73, 490-504.e6.	9.7	151
10	Structural Flexibility Enables Alternative Maturation, ARGONAUTE Sorting and Activities of miR168, a Global Gene Silencing Regulator in Plants. <i>Molecular Plant</i> , 2018, 11, 1008-1023.	8.3	43
11	Plastidial NAD-Dependent Malate Dehydrogenase: A Moonlighting Protein Involved in Early Chloroplast Development through Its Interaction with an FtsH12-FtsHi Protease Complex. <i>Plant Cell</i> , 2018, 30, 1745-1769.	6.6	55
12	Control of the polyamine biosynthesis pathway by G2-quadruplexes. <i>ELife</i> , 2018, 7, .	6.0	20
13	switchSENSE: A new technology to study protein-RNA interactions. <i>Methods</i> , 2017, 118-119, 137-145.	3.8	29
14	Structural study of the Fox-1 RRM protein hydration reveals a role for key water molecules in RRM-RNA recognition. <i>Nucleic Acids Research</i> , 2017, 45, 8046-8063.	14.5	28
15	Binding to SMN2 pre-mRNA-protein complex elicits specificity for small molecule splicing modifiers. <i>Nature Communications</i> , 2017, 8, 1476.	12.8	155
16	Tandem hnRNP A1 RNA recognition motifs act in concert to repress the splicing of survival motor neuron exon 7. <i>ELife</i> , 2017, 6, .	6.0	72
17	Synergy between NMR measurements and MD simulations of protein/RNA complexes: application to the RRM, the most common RNA recognition motifs. <i>Nucleic Acids Research</i> , 2016, 44, 6452-6470.	14.5	48
18	One, Two, Three, Four! How Multiple RRMs Read the Genome Sequence. <i>Methods in Enzymology</i> , 2015, 558, 235-278.	1.0	72

#	ARTICLE	IF	CITATIONS
19	SRSF1-Regulated Alternative Splicing in Breast Cancer. <i>Molecular Cell</i> , 2015, 60, 105-117.	9.7	290
20	Single-Stranded Nucleic Acid Recognition: Is There a Code after All?. <i>Structure</i> , 2013, 21, 4-6.	3.3	6
21	RNA recognition motifs: boring? Not quite. <i>Current Opinion in Structural Biology</i> , 2008, 18, 290-298.	5.7	520