Andres Ramos

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6843396/publications.pdf

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38	2,688	236925	330143
papers	citations	25 h-index	37 g-index

39	39	39	4045
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The RNA-binding protein KSRP promotes the biogenesis of a subset of microRNAs. Nature, 2009, 459, 1010-1014.	27.8	588
2	RNA recognition by a Staufen double-stranded RNA-binding domain. EMBO Journal, 2000, 19, 997-1009.	7.8	331
3	Two-Dimensional NMR Lineshape Analysis. Scientific Reports, 2016, 6, 24826.	3.3	161
4	The double-stranded RNA-binding motif, a versatile macromolecular docking platform. FEBS Journal, 2005, 272, 2109-2117.	4.7	113
5	KHâ€“RNA interactions: back in the groove. Current Opinion in Structural Biology, 2015, 30, 63-70.	5.7	112
6	G-quartet-dependent recognition between the FMRP RGG box and RNA. Rna, 2003, 9, 1198-1207.	3.5	111
7	KH domains with impaired nucleic acid binding as a tool for functional analysis. Nucleic Acids Research, 2012, 40, 6873-6886.	14.5	106
8	H19 long noncoding RNA controls the mRNA decay promoting function of KSRP. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5023-8.	7.1	104
9	The Structure of the N-Terminal Domain of the Fragile X Mental Retardation Protein: A Platform for Protein-Protein Interaction. Structure, 2006, 14, 21-31.	3.3	102
10	The Structure of the C-Terminal KH Domains of KSRP Reveals a Noncanonical Motif Important for mRNA Degradation. Structure, 2007, 15, 485-498.	3.3	97
11	Selective inhibition of microRNA accessibility by RBM38 is required for p53 activity. Nature Communications, 2011, 2, 513.	12.8	91
12	A cryptic RNA-binding domain mediates Syncrip recognition and exosomal partitioning of miRNA targets. Nature Communications, 2018, 9, 831.	12.8	86
13	Cyclic AMP signalling controls key components of malaria parasite host cell invasion machinery. PLoS Biology, 2019, 17, e3000264.	5.6	64
14	Molecular basis of FIR-mediated c-myc transcriptional control. Nature Structural and Molecular Biology, 2010, 17, 1058-1064.	8.2	56
15	The sequence selectivity of KSRP explains its flexibility in the recognition of the RNA targets. Nucleic Acids Research, 2008, 36, 5290-5296.	14.5	53
16	Structure of the Rna15 RRMâ€“RNA complex reveals the molecular basis of GU specificity in transcriptional 3â€²-end processing factors. Nucleic Acids Research, 2010, 38, 3119-3132.	14.5	51
17	KSRP, many functions for a single protein. Frontiers in Bioscience - Landmark, 2011, 16, 1787.	3.0	49
18	Mechanism of Î²-actin mRNA Recognition by ZBP1. Cell Reports, 2017, 18, 1187-1199.	6.4	43

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19	Noncanonical G recognition mediates KSRP regulation of let-7 biogenesis. Nature Structural and Molecular Biology, 2012, 19, 1282-1286.	8.2	39
20	KSRP Controls Pleiotropic Cellular Functions. Seminars in Cell and Developmental Biology, 2014, 34, 2-8.	5.0	36
21	Lin28a uses distinct mechanisms of binding to RNA and affects miRNA levels positively and negatively. Rna, 2017, 23, 317-332.	3.5	36
22	Small molecule inhibitor of Igf2bp1 represses Kras and a pro-oncogenic phenotype in cancer cells. RNA Biology, 2022, 19, 26-43.	3.1	35
23	Orientation of the central domains of KSRP and its implications for the interaction with the RNA targets. Nucleic Acids Research, 2010, 38, 5193-5205.	14.5	31
24	An RRMâ€“ZnF RNA recognition module targets RBM10 to exonic sequences to promote exon exclusion. Nucleic Acids Research, 2017, 45, 6761-6774.	14.5	31
25	Scaffold-Independent Analysis of RNAâˆ’Protein Interactions:â€‰ The Nova-1 KH3âˆ’RNA Complex. Journal of the American Chemical Society, 2007, 129, 10205-10210.	13.7	30
26	Structural basis for Fullerene geometry in a human endogenous retrovirus capsid. Nature Communications, 2019, 10, 5822.	12.8	20
27	The role of a clinically important mutation in the fold and RNA-binding properties of KH motifs. Rna, 2003, 9, 293-298.	3.5	17
28	IMP1 KH1 and KH2 domains create a structural platform with unique RNA recognition and re-modelling properties. Nucleic Acids Research, 2019, 47, 4334-4348.	14.5	16
29	The TH1 cell lineage-determining transcription factor T-bet suppresses TH2 gene expression by redistributing GATA3 away from TH2 genes. Nucleic Acids Research, 2022, 50, 4557-4573.	14.5	16
30	The devil is in the domain: understanding protein recognition of multiple RNA targets. Biochemical Society Transactions, 2017, 45, 1305-1311.	3.4	13
31	Proteinâ€“RNA specificity by high-throughput principal component analysis of NMR spectra. Nucleic Acids Research, 2015, 43, e41-e41.	14.5	12
32	The structure of the RbBP5 Î²-propeller domain reveals a surface with potential nucleic acid binding sites. Nucleic Acids Research, 2018, 46, 3802-3812.	14.5	11
33	Joining the dots â€“ proteinâ€•RNA interactions mediating local mRNA translation in neurons. FEBS Letters, 2018, 592, 2932-2947.	2.8	7
34	Secondary structure and stability of the selenocysteine insertion sequences (SECIS) for human thioredoxin reductase and glutathione peroxidase. Nucleic Acids Research, 2004, 32, 1746-1755.	14.5	6
35	A method for the unbiased and efficient segmental labelling of RNA-binding proteins for structure and biophysics. Scientific Reports, 2017, 7, 14083.	3.3	5
36	Biolayer Interferometry: Proteinâ€“RNA Interactions. Methods in Molecular Biology, 2021, 2263, 351-368.	0.9	5

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37	Modular protein-RNA interactions regulating mRNA metabolism: a role for NMR. European Biophysics Journal, 2011, 40, 1317-1325.	2.2	4
38	The distinct RNA-interaction modes of a small ZnF domain underlay TUT4(7) diverse action in miRNA regulation. RNA Biology, 2021, , 1-12.	3.1	0