## Chase A Weidmann

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3803909/publications.pdf

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686830 996533 1,403 15 13 15 citations h-index g-index papers 21 21 21 2050 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	mRNA structure determines specificity of a polyQ-driven phase separation. Science, 2018, 360, 922-927.	6.0	421
2	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. Molecular Cell, 2020, 80, 1078-1091.e6.	4.5	255
3	Human Pumilio Proteins Recruit Multiple Deadenylases to Efficiently Repress Messenger RNAs. Journal of Biological Chemistry, 2012, 287, 36370-36383.	1.6	165
4	Guidelines for SHAPE Reagent Choice and Detection Strategy for RNA Structure Probing Studies. Biochemistry, 2019, 58, 2655-2664.	1.2	91
5	The RNA binding domain of Pumilio antagonizes poly-adenosine binding protein and accelerates deadenylation. Rna, 2014, 20, 1298-1319.	1.6	71
6	<i>Drosophila</i> Pumilio Protein Contains Multiple Autonomous Repression Domains That Regulate mRNAs Independently of Nanos and Brain Tumor. Molecular and Cellular Biology, 2012, 32, 527-540.	1.1	70
7	Drosophila Nanos acts as a molecular clamp that modulates the RNA-binding and repression activities of Pumilio. ELife, 2016, 5, .	2.8	66
8	Combinatorial control of messenger RNAs by Pumilio, Nanos and Brain Tumor Proteins. RNA Biology, 2017, 14, 1445-1456.	1.5	51
9	Analysis of RNA–protein networks with RNP-MaP defines functional hubs on RNA. Nature Biotechnology, 2021, 39, 347-356.	9.4	50
10	Targeting the Oncogenic Long Non-coding RNA SLNCR1 by Blocking Its Sequence-Specific Binding to the Androgen Receptor. Cell Reports, 2020, 30, 541-554.e5.	2.9	47
11	Discovery of a large-scale, cell-state-responsive allosteric switch in the 7SK RNA using DANCE-MaP. Molecular Cell, 2022, 82, 1708-1723.e10.	4.5	40
12	Direct Duplex Detection: An Emerging Tool in the RNA Structure Analysis Toolbox. Trends in Biochemical Sciences, 2016, 41, 734-736.	3.7	25
13	Integrated analysis of RNA-binding protein complexes using in vitro selection and high-throughput sequencing and sequence specificity landscapes (SEQRS). Methods, 2017, 118-119, 171-181.	1.9	24
14	Distinct MUNC lncRNA structural domains regulate transcription of different promyogenic factors. Cell Reports, 2022, 38, 110361.	2.9	13
15	SHAPE Probing Reveals Human rRNAs Are Largely Unfolded in Solution. Biochemistry, 2019, 58, 3377-3385.	1.2	11