

Chen Davidovich

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,407
citations

471371

17
h-index

526166

27
g-index

34
all docs

34
docs citations

34
times ranked

3155
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA Duplex Map in Living Cells Reveals Higher-Order Transcriptome Structure. <i>Cell</i> , 2016, 165, 1267-1279.	13.5	520
2	Promiscuous RNA binding by Polycomb repressive complex 2. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1250-1257.	3.6	404
3	The recruitment of chromatin modifiers by long noncoding RNAs: lessons from PRC2. <i>Rna</i> , 2015, 21, 2007-2022.	1.6	248
4	Toward a Consensus on the Binding Specificity and Promiscuity of PRC2 for RNA. <i>Molecular Cell</i> , 2015, 57, 552-558.	4.5	190
5	Targeting of Polycomb Repressive Complex 2 to RNA by Short Repeats of Consecutive Guanines. <i>Molecular Cell</i> , 2017, 65, 1056-1067.e5.	4.5	185
6	Induced-fit tightens pleuromutilins binding to ribosomes and remote interactions enable their selectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4291-4296.	3.3	181
7	RNA exploits an exposed regulatory site to inhibit the enzymatic activity of PRC2. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 237-247.	3.6	88
8	The evolving ribosome: from non-coded peptide bond formation to sophisticated translation machinery. <i>Research in Microbiology</i> , 2009, 160, 487-492.	1.0	71
9	The structure of ribosome-lankacidin complex reveals ribosomal sites for synergistic antibiotics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1983-1988.	3.3	63
10	Ancient machinery embedded in the contemporary ribosome. <i>Biochemical Society Transactions</i> , 2010, 38, 422-427.	1.6	55
11	Structural basis for cross-resistance to ribosomal PTC antibiotics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20665-20670.	3.3	54
12	A dimeric state for PRC2. <i>Nucleic Acids Research</i> , 2014, 42, 9236-9248.	6.5	43
13	The Proto-Ribosome: An Ancient Nano-machine for Peptide Bond Formation. <i>Israel Journal of Chemistry</i> , 2010, 50, 29-35.	1.0	38
14	Origin of life: protoribosome forms peptide bonds and links RNA and protein dominated worlds. <i>Nucleic Acids Research</i> , 2022, 50, 1815-1828.	6.5	38
15	Structural basis of specific H2A K13/K15 ubiquitination by RNF168. <i>Nature Communications</i> , 2019, 10, 1751.	5.8	37
16	Ribosome's mode of function: myths, facts and recent results. <i>Journal of Peptide Science</i> , 2009, 15, 122-130.	0.8	34
17	The Heat Shock Protein YbeY Is Required for Optimal Activity of the 30S Ribosomal Subunit. <i>Journal of Bacteriology</i> , 2010, 192, 4592-4596.	1.0	30
18	Identification of the prebiotic translation apparatus within the contemporary ribosome. <i>Nature Precedings</i> , 0, , .	0.1	19

#	ARTICLE	IF	CITATIONS
19	PAL11 facilitates DNA and nucleosome binding by PRC2 and triggers an allosteric activation of catalysis. <i>Nature Communications</i> , 2021, 12, 4592.	5.8	18
20	Structural basis of rotavirus RNA chaperone displacement and RNA annealing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
21	The Ribosomal Protein uL22 Modulates the Shape of the Protein Exit Tunnel. <i>Structure</i> , 2017, 25, 1233-1241.e3.	1.6	17
22	Not just a writer: PRC2 as a chromatin reader. <i>Biochemical Society Transactions</i> , 2021, 49, 1159-1170.	1.6	17
23	DNA binding by polycomb-group proteins: searching for the link to CpG islands. <i>Nucleic Acids Research</i> , 2022, 50, 4813-4839.	6.5	15
24	Ribosomal Antibiotics: Contemporary Challenges. <i>Antibiotics</i> , 2016, 5, 24.	1.5	8
25	Allosteric regulation of histone lysine methyltransferases: from context-specific regulation to selective drugs. <i>Biochemical Society Transactions</i> , 2021, 49, 591-607.	1.6	4
26	Targeting PRC2: RNA offers new opportunities. <i>Oncotarget</i> , 2017, 8, 107346-107347.	0.8	3
27	An added layer of repression for human genes. <i>Nature</i> , 2022, 604, 41-42.	13.7	1
28	crisscrosslinkeR: identification and visualization of proteinâ€“RNA and proteinâ€“protein interactions from crosslinking mass spectrometry. <i>Bioinformatics</i> , 2021, 36, 5530-5532.	1.8	0