

Christine M Dunham

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

3,146
citations

331538

21
h-index

265120

42
g-index

50
all docs

50
docs citations

50
times ranked

2794
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the 70S Ribosome Complexed with mRNA and tRNA. <i>Science</i> , 2006, 313, 1935-1942.	6.0	1,186
2	The Structure of the Ribosome with Elongation Factor G Trapped in the Posttranslocational State. <i>Science</i> , 2009, 326, 694-699.	6.0	465
3	Crystal Structures of the Ribosome in Complex with Release Factors RF1 and RF2 Bound to a Cognate Stop Codon. <i>Cell</i> , 2005, 123, 1255-1266.	13.5	239
4	The Structural Basis for mRNA Recognition and Cleavage by the Ribosome-Dependent Endonuclease RelE. <i>Cell</i> , 2009, 139, 1084-1095.	13.5	194
5	Crystal structure of the ribosome recycling factor bound to the ribosome. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 733-737.	3.6	99
6	Growth-regulating Mycobacterium tuberculosis VapC-mt4 toxin is an isoacceptor-specific tRNase. <i>Nature Communications</i> , 2015, 6, 7480.	5.8	79
7	Structure of the Proteus vulgaris HigB-(HigA) ₂ -HigB Toxin-Antitoxin Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 1060-1070.	1.6	78
8	Doc Toxin Is a Kinase That Inactivates Elongation Factor Tu. <i>Journal of Biological Chemistry</i> , 2014, 289, 7788-7798.	1.6	72
9	Structural insights into +1 frameshifting promoted by expanded or modification-deficient anticodon stem loops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12740-12745.	3.3	57
10	Structures of tRNAs with an expanded anticodon loop in the decoding center of the 30S ribosomal subunit. <i>Rna</i> , 2007, 13, 817-823.	1.6	52
11	Uniformity of Peptide Release Is Maintained by Methylation of Release Factors. <i>Cell Reports</i> , 2016, 17, 11-18.	2.9	49
12	Molecular recognition and modification of the 30S ribosome by the aminoglycoside-resistance methyltransferase NpmA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6275-6280.	3.3	45
13	Mechanisms of Toxin Inhibition and Transcriptional Repression by Escherichia coli DinJ-YafQ. <i>Journal of Biological Chemistry</i> , 2014, 289, 20559-20569.	1.6	42
14	Mechanism of tRNA-mediated +1 ribosomal frameshifting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11226-11231.	3.3	37
15	Mechanism of endonuclease cleavage by the HigB toxin. <i>Nucleic Acids Research</i> , 2016, 44, 7944-7953.	6.5	35
16	Functionally critical residues in the aminoglycoside resistance-associated methyltransferase RmtC play distinct roles in 30S substrate recognition. <i>Journal of Biological Chemistry</i> , 2019, 294, 17642-17653.	1.6	32
17	Molecular basis of ribosome recognition and mRNA hydrolysis by the <i>E. coli</i> YafQ toxin. <i>Nucleic Acids Research</i> , 2015, 43, 8002-8012.	6.5	31
18	Reorganization of an intersubunit bridge induced by disparate 16S ribosomal ambiguity mutations mimics an EF-Tu-bound state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9716-9721.	3.3	30

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19	Defining the mRNA recognition signature of a bacterial toxin protein. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13862-13867.	3.3	30
20	Alternative Mode of E-Site tRNA Binding in the Presence of a Downstream mRNA Stem Loop at the Entrance Channel. Structure, 2018, 26, 437-445.e3.	1.6	30
21	Structural insights into mRNA reading frame regulation by tRNA modification and slippery codon-anticodon pairing. ELife, 2020, 9, .	2.8	28
22	Structural insights into translational recoding by frameshift suppressor tRNA ^{SufJ} . Rna, 2014, 20, 1944-1954.	1.6	26
23	Importance of a tRNA anticodon loop modification and a conserved, noncanonical anticodon stem pairing in tRNACGG ^{Pro} for decoding. Journal of Biological Chemistry, 2019, 294, 5281-5291.	1.6	25
24	Mechanisms of mRNA frame maintenance and its subversion during translation of the genetic code. Biochimie, 2015, 114, 90-96.	1.3	21
25	trans-Translation inhibitors bind to a novel site on the ribosome and clear Neisseria gonorrhoeae in vivo. Nature Communications, 2021, 12, 1799.	5.8	20
26	The structure and function of Mycobacterium tuberculosis MazF-mt6 toxin provide insights into conserved features of MazF endonucleases. Journal of Biological Chemistry, 2017, 292, 7718-7726.	1.6	19
27	Structural basis of transcriptional regulation by the HigA antitoxin. Molecular Microbiology, 2019, 111, 1449-1462.	1.2	19
28	Structural Insights into Oxygen-Dependent Signal Transduction within Globin Coupled Sensors. Inorganic Chemistry, 2018, 57, 14386-14395.	1.9	17
29	Monomeric YoeB toxin retains RNase activity but adopts an obligate dimeric form for thermal stability. Nucleic Acids Research, 2019, 47, 10400-10413.	6.5	15
30	mRNA bound to the 30S subunit is a HigB toxin substrate. Rna, 2016, 22, 1261-1270.	1.6	12
31	Ribosomal ambiguity (ram) mutations promote the open (off) to closed (on) transition and thereby increase miscoding. Nucleic Acids Research, 2019, 47, 1557-1563.	6.5	10
32	50S subunit recognition and modification by the Mycobacterium tuberculosis ribosomal RNA methyltransferase TlyA. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120352119.	3.3	10
33	Importance of the E. coli DinJ antitoxin carboxy terminus for toxin suppression and regulated proteolysis. Molecular Microbiology, 2017, 104, 65-77.	1.2	9
34	Disruption of evolutionarily correlated tRNA elements impairs accurate decoding. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16333-16338.	3.3	9
35	Doc toxin is a kinase that inactivates elongation factor Tu. Journal of Biological Chemistry, 2014, 289, 19276.	1.6	5
36	Oxidation alters the architecture of the phenylalanyl-tRNA synthetase editing domain to confer hyperaccuracy. Nucleic Acids Research, 2021, 49, 11800-11809.	6.5	4

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37	Digging the tunnel for chemical space. <i>Nature Chemical Biology</i> , 2017, 13, 1061-1062.	3.9	3
38	Bacterial Warfare again Targets the Ribosome. <i>Structure</i> , 2014, 22, 661-662.	1.6	2
39	Myeloma Patient-Derived MCL1 Point Mutations Can Influence MCL1-Inhibitor Function. <i>Blood</i> , 2018, 132, 951-951.	0.6	2
40	Editorial: Ribosome survey and summary collection 2020. <i>Nucleic Acids Research</i> , 2020, 48, 1011-1012.	6.5	1
41	Seeing gene expression in cells: the future of structural biology. <i>Faculty Reviews</i> , 2021, 10, 79.	1.7	1
42	ESKAPE velocity: total synthesis platforms promise to increase the pace and diversity of antibiotic development. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 3-4.	3.6	1
43	Importance of the m ¹ G37 modification and 32â€“38 pairing in tRNA ^{Pro} (CCG) on decoding and tRNA stability. <i>FASEB Journal</i> , 2019, 33, 630.6.	0.2	0
44	Dissecting the gene regulation of <i>Proteus vulgaris</i> Rts1 HigBâ€“HigA toxinâ€“antitoxin system. <i>FASEB Journal</i> , 2019, 33, 458.20.	0.2	0
45	RNAâ€“mediated Mechanisms of Translation Control. <i>FASEB Journal</i> , 2019, 33, 100.1.	0.2	0