

# 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	50S subunit recognition and modification by the <i>Mycobacterium tuberculosis</i> ribosomal RNA methyltransferase TlyA. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120352119.	3.3	10
2	ESKAPE velocity: total synthesis platforms promise to increase the pace and diversity of antibiotic development. Nature Structural and Molecular Biology, 2022, 29, 3-4.	3.6	1
3	trans-Translation inhibitors bind to a novel site on the ribosome and clear <i>Neisseria gonorrhoeae</i> in vivo. Nature Communications, 2021, 12, 1799.	5.8	20
4	Oxidation alters the architecture of the phenylalanyl-tRNA synthetase editing domain to confer hyperaccuracy. Nucleic Acids Research, 2021, 49, 11800-11809.	6.5	4
5	Seeing gene expression in cells: the future of structural biology. Faculty Reviews, 2021, 10, 79.	1.7	1
6	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
7	Editorial: Ribosome survey and summary collection 2020. Nucleic Acids Research, 2020, 48, 1011-1012.	6.5	1
8	Structural insights into mRNA reading frame regulation by tRNA modification and slippery codon-anticodon pairing. ELife, 2020, 9, .	2.8	28
9	Functionally critical residues in the aminoglycoside resistance-associated methyltransferase RmtC play distinct roles in 30S substrate recognition. Journal of Biological Chemistry, 2019, 294, 17642-17653.	1.6	32
10	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
11	Structural basis of transcriptional regulation by the HigA antitoxin. Molecular Microbiology, 2019, 111, 1449-1462.	1.2	19
12	Importance of a tRNA anticodon loop modification and a conserved, noncanonical anticodon stem pairing in tRNACGGPro for decoding. Journal of Biological Chemistry, 2019, 294, 5281-5291.	1.6	25
13	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
14	Importance of the m <sup>1</sup> G37 modification and 32-38 pairing in tRNA <sup>Pro</sup> (CCG) on decoding and tRNA stability. FASEB Journal, 2019, 33, 630.6.	0.2	0
15	Dissecting the gene regulation of <i>Proteus vulgaris</i> Rts1 HigB-HigA toxin-antitoxin system. FASEB Journal, 2019, 33, 458.20.	0.2	0
16	RNA-mediated Mechanisms of Translation Control. FASEB Journal, 2019, 33, 100.1.	0.2	0
17	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
18	Mechanism of tRNA-mediated +1 ribosomal frameshifting. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11226-11231.	3.3	37

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19	Structural Insights into Oxygen-Dependent Signal Transduction within Globin Coupled Sensors. <i>Inorganic Chemistry</i> , 2018, 57, 14386-14395.	1.9	17
20	Myeloma Patient-Derived MCL1 Point Mutations Can Influence MCL1-Inhibitor Function. <i>Blood</i> , 2018, 132, 951-951.	0.6	2
21	Importance of the <i>E. coli</i> DinJ antitoxin carboxy terminus for toxin suppression and regulated proteolysis. <i>Molecular Microbiology</i> , 2017, 104, 65-77.	1.2	9
22	The structure and function of Mycobacterium tuberculosis MazF-mt6 toxin provide insights into conserved features of MazF endonucleases. <i>Journal of Biological Chemistry</i> , 2017, 292, 7718-7726.	1.6	19
23	Digging the tunnel for chemical space. <i>Nature Chemical Biology</i> , 2017, 13, 1061-1062.	3.9	3
24	Mechanism of endonuclease cleavage by the HigB toxin. <i>Nucleic Acids Research</i> , 2016, 44, 7944-7953.	6.5	35
25	Uniformity of Peptide Release Is Maintained by Methylation of Release Factors. <i>Cell Reports</i> , 2016, 17, 11-18.	2.9	49
26	mRNA bound to the 30S subunit is a HigB toxin substrate. <i>Rna</i> , 2016, 22, 1261-1270.	1.6	12
27	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
28	Growth-regulating Mycobacterium tuberculosis VapC-mt4 toxin is an isoacceptor-specific tRNase. <i>Nature Communications</i> , 2015, 6, 7480.	5.8	79
29	Mechanisms of mRNA frame maintenance and its subversion during translation of the genetic code. <i>Biochimie</i> , 2015, 114, 90-96.	1.3	21
30	Defining the mRNA recognition signature of a bacterial toxin protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13862-13867.	3.3	30
31	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
32	Structural insights into translational recoding by frameshift suppressor tRNA <sup>SufJ</sup> . <i>Rna</i> , 2014, 20, 1944-1954.	1.6	26
33	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
34	Doc toxin is a kinase that inactivates elongation factor Tu.. <i>Journal of Biological Chemistry</i> , 2014, 289, 19276.	1.6	5
35	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
36	Doc Toxin Is a Kinase That Inactivates Elongation Factor Tu. <i>Journal of Biological Chemistry</i> , 2014, 289, 7788-7798.	1.6	72

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37	Bacterial Warfare again Targets the Ribosome. <i>Structure</i> , 2014, 22, 661-662.	1.6	2
38	Structure of the <i>Proteus vulgaris</i> HigB-(HigA) <sub>2</sub> -HigB Toxin-Antitoxin Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 1060-1070.	1.6	78
39	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
40	The Structural Basis for mRNA Recognition and Cleavage by the Ribosome-Dependent Endonuclease RelE. <i>Cell</i> , 2009, 139, 1084-1095.	13.5	194
41	The Structure of the Ribosome with Elongation Factor G Trapped in the Posttranslocational State. <i>Science</i> , 2009, 326, 694-699.	6.0	465
42	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
43	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
44	Structure of the 70S Ribosome Complexed with mRNA and tRNA. <i>Science</i> , 2006, 313, 1935-1942.	6.0	1,186
45	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