

Ditlev E Brodersen

List of Publications by Year in descending order

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68

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126907

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73

docs citations

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times ranked

7492

citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Remodelling of the Carbon-Phosphorus Enzymatic Machinery by a Dual ATP-Binding Cassette Module. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
2	Structural variations between small alarmone hydrolase dimers support different modes of regulation of the stringent response. <i>Journal of Biological Chemistry</i> , 2022, 298, 102142.	3.4	4
3	Structural Basis for Toxin Inhibition in the VapXD Toxin-Antitoxin System. <i>Structure</i> , 2021, 29, 139-150.e3.	3.3	12
4	Phylogeny Reveals Novel HipA-Homologous Kinase Families and Toxin-Antitoxin Gene Organizations. <i>MBio</i> , 2021, 12, e0105821.	4.1	12
5	Two P or Not Two P: Understanding Regulation by the Bacterial Second Messengers (p)ppGpp. <i>Annual Review of Microbiology</i> , 2021, 75, 383-406.	7.3	32
6	Evolving complex insulation. <i>Nature Chemical Biology</i> , 2021, 17, 1216-1217.	8.0	0
7	Structural basis for inhibition of an archaeal CRISPR-Cas type I-D large subunit by an anti-CRISPR protein. <i>Nature Communications</i> , 2020, 11, 5993.	12.8	17
8	Structure and Function of the Bacterial Protein Toxin Phenomycin. <i>Structure</i> , 2020, 28, 528-539.e9.	3.3	2
9	The E. coli HicB Antitoxin Contains a Structurally Stable Helix-Turn-Helix DNA Binding Domain. <i>Structure</i> , 2019, 27, 1675-1685.e3.	3.3	23
10	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	4.1	25
11	(p)ppGpp Regulates a Bacterial Nucleosidase by an Allosteric Two-Domain Switch. <i>Molecular Cell</i> , 2019, 74, 1239-1249.e4.	9.7	39
12	The Prodigal Compound: Return of Ribosyl 1,5-Bisphosphate as an Important Player in Metabolism. <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	6.6	2
13	The RES domain toxins of RES-Xre toxin-antitoxin modules induce cell stasis by degrading NAD ⁺ . <i>Molecular Microbiology</i> , 2019, 111, 221-236.	2.5	46
14	Evolution of the bacterial nucleosidase PpnN and its relation to the stringent response. <i>Microbial Cell</i> , 2019, 6, 450-453.	3.2	8
15	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	13.3	118
16	Toxins, Targets, and Triggers: An Overview of Toxin-Antitoxin Biology. <i>Molecular Cell</i> , 2018, 70, 768-784.	9.7	521
17	Structural basis for (p)ppGpp synthesis by the <i>Staphylococcus aureus</i> small alarmone synthetase RelP. <i>Journal of Biological Chemistry</i> , 2018, 293, 3254-3264.	3.4	46
18	The Abc of Phosphonate Breakdown: A Mechanism for Bacterial Survival. <i>BioEssays</i> , 2018, 40, e1800091.	2.5	28

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19	Higher-Order Structure in Bacterial VapBC Toxin-Antitoxin Complexes. Sub-Cellular Biochemistry, 2017, 83, 381-412.	2.4	15
20	Structural conservation of the PIN domain active site across all domains of life. Protein Science, 2017, 26, 1474-1492.	7.6	33
21	Structural analysis of the active site architecture of the VapC toxin from <i>Shigella flexneri</i> . Proteins: Structure, Function and Bioinformatics, 2016, 84, 892-899.	2.6	11
22	Toxin inhibition in <i>C. crescentus</i> VapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. Nucleic Acids Research, 2016, 45, gkw1266.	14.5	13
23	RRM domain of human RBM7: purification, crystallization and structure determination. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 397-402.	0.8	6
24	The transcriptional regulator GalR self-assembles to form highly regular tubular structures. Scientific Reports, 2016, 6, 27672.	3.3	2
25	Computational discovery of specificity-conferring sites in non-ribosomal peptide synthetases. Bioinformatics, 2016, 32, 325-329.	4.1	26
26	Identification of the non-ribosomal peptide synthetase responsible for biosynthesis of the potential anti-cancer drug sansalvamide in <i>Fusarium solani</i> . Current Genetics, 2016, 62, 799-807.	1.7	22
27	An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in <i>Fusarium</i> . Fungal Genetics and Biology, 2015, 75, 20-29.	2.1	123
28	Cut to the chase—Regulating translation through RNA cleavage. Biochimie, 2015, 114, 10-17.	2.6	12
29	Structural insights into the bacterial carbon—phosphorus lyase machinery. Nature, 2015, 525, 68-72.	27.8	63
30	Structural basis for RNA-genome recognition during bacteriophage ϕ 22 replication. Nucleic Acids Research, 2015, 43, 10893-10906.	14.5	22
31	Structural analysis of the yeast exosome Rps6p—Rps47p complex by small-angle X-ray scattering. Biochemical and Biophysical Research Communications, 2014, 450, 634-640.	2.1	5
32	VapC20 of <i>Mycobacterium tuberculosis</i> cleaves the Sarcin—Ricin loop of 23S rRNA. Nature Communications, 2013, 4, 2796.	12.8	112
33	Mutational analysis of the yeast RNA helicase Sub2p reveals conserved domains required for growth, mRNA export, and genomic stability. Rna, 2013, 19, 1363-1371.	3.5	21
34	Protein expression, crystallization and preliminary X-ray crystallographic analysis of the isolated <i>Shigella flexneri</i> VapC toxin. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 762-765.	0.7	6
35	<i>Mimer</i> : an automated spreadsheet-based crystallization screening system. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 815-820.	0.7	13
36	<i>Saccharomyces cerevisiae</i> Ng13p is an active 3'→5' exonuclease with a specificity towards poly-A RNA reminiscent of cellular deadenylases. Nucleic Acids Research, 2012, 40, 837-846.	14.5	11

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37	The Crystal Structure of the Intact E.Âcoli RelBE Toxin-Antitoxin Complex Provides the Structural Basis for Conditional Cooperativity. <i>Structure</i> , 2012, 20, 1641-1648.	3.3	88
38	Crystal Structure of the VapBC Toxinâ€Antitoxin Complex from <i>Shigella flexneri</i> Reveals a Hetero-Octameric DNA-Binding Assembly. <i>Journal of Molecular Biology</i> , 2011, 414, 713-722.	4.2	75
39	Human 2â€²-phosphodiesterase localizes to the mitochondrial matrix with a putative function in mitochondrial RNA turnover. <i>Nucleic Acids Research</i> , 2011, 39, 3754-3770.	14.5	39
40	The activity and selectivity of fission yeast Pop2p are affected by a high affinity for Zn ²⁺ and Mn ²⁺ in the active site. <i>Rna</i> , 2009, 15, 850-861.	3.5	35
41	Origins and activities of the eukaryotic exosome. <i>Journal of Cell Science</i> , 2009, 122, 1487-1494.	2.0	146
42	Cyanobacteria contain a structural homologue of the Hfq protein with altered RNAâ€binding properties. <i>FEBS Journal</i> , 2009, 276, 3904-3915.	4.7	47
43	The Structural Basis for mRNA Recognition and Cleavage by the Ribosome-Dependent Endonuclease RelE. <i>Cell</i> , 2009, 139, 1084-1095.	28.9	194
44	Take the â€œAâ€tailâ€ quality control of ribosomal and transfer RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 532-537.	1.9	15
45	Exonucleolysis is required for nuclear mRNA quality control in yeast THO mutants. <i>Rna</i> , 2008, 14, 2305-2313.	3.5	48
46	An Hfq-like protein in archaea: Crystal structure and functional characterization of the Sm protein from <i>Methanococcus jannaschii</i> . <i>Rna</i> , 2007, 13, 2213-2223.	3.5	65
47	The 1.4-Å crystal structure of the <i>S. pombe</i> Pop2p deadenylase subunit unveils the configuration of an active enzyme. <i>Nucleic Acids Research</i> , 2007, 35, 3153-3164.	14.5	49
48	Structure of the nuclear exosome component Rrp6p reveals an interplay between the active site and the HRDC domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11898-11903.	7.1	81
49	The social life of ribosomal proteins. <i>FEBS Journal</i> , 2005, 272, 2098-2108.	4.7	105
50	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.	28.9	239
51	Phasing the 30S ribosomal subunit structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2044-2050.	2.5	12
52	Shape can be seductive. <i>Nature Structural Biology</i> , 2003, 10, 78-80.	9.7	11
53	Role of 16S rRNA Helix 44 in Ribosomal Resistance to Hygromycin B. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 1496-1502.	3.2	49
54	Crystal structure of the 30 s ribosomal subunit from <i>Thermus thermophilus</i> : structure of the proteins and their interactions with 16 s RNA. <i>Journal of Molecular Biology</i> , 2002, 316, 725-768.	4.2	345

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55	Crystal structure of the 30 S ribosomal subunit from <i>Thermus thermophilus</i> : purification, crystallization and structure determination. <i>Journal of Molecular Biology</i> , 2001, 310, 827-843.	4.2	128
56	Recognition of Cognate Transfer RNA by the 30S Ribosomal Subunit. <i>Science</i> , 2001, 292, 897-902.	12.6	1,085
57	Crystal Structure of an Initiation Factor Bound to the 30S Ribosomal Subunit. <i>Science</i> , 2001, 291, 498-501.	12.6	348
58	Atomic Structures of the 30S Subunit and Its Complexes with Ligands and Antibiotics. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2001, 66, 17-32.	1.1	14
59	Applications of single-wavelength anomalous dispersion at high and atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 431-441.	2.5	41
60	Structure of the 30S ribosomal subunit. <i>Nature</i> , 2000, 407, 327-339.	27.8	1,891
61	Functional insights from the structure of the 30S ribosomal subunit and its interactions with antibiotics. <i>Nature</i> , 2000, 407, 340-348.	27.8	1,477
62	The Structural Basis for the Action of the Antibiotics Tetracycline, Pactamycin, and Hygromycin B on the 30S Ribosomal Subunit. <i>Cell</i> , 2000, 103, 1143-1154.	28.9	816
63	Structural Investigations of Calcium and Zinc Binding in Proteins. <i>Science Progress</i> , 1999, 82, 295-312.	1.9	1
64	XAct: a program for construction, automated setup and bookkeeping of crystallization experiments. <i>Journal of Applied Crystallography</i> , 1999, 32, 1012-1016.	4.5	3
65	Zinc-Binding Site of an S100 Protein Revealed. Two Crystal Structures of Ca ²⁺ -Bound Human Psoriasin (S100A7) in the Zn ²⁺ -Loaded and Zn ²⁺ -Free States. <i>Biochemistry</i> , 1999, 38, 1695-1704.	2.5	140
66	EF-hands at atomic resolution: the structure of human psoriasin (S100A7) solved by MAD phasing. <i>Structure</i> , 1998, 6, 477-489.	3.3	106
67	Structural Research on the Methylamine Dehydrogenase Redox Chain of <i>Paracoccus Denitrificans</i> . , 1998, , 129-146.		3
68	Enzymatic and Electron Transfer Activities in Crystalline Protein Complexes. <i>Journal of Biological Chemistry</i> , 1996, 271, 9177-9180.	3.4	53