

# Ditlev E Brodersen

## List of Publications by Year in descending order

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68  
papers

9,206  
citations

126858

33  
h-index

98753

67  
g-index

73  
all docs

73  
docs citations

73  
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, .	0.2	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.	1.6	4
3	Structural Basis for Toxin Inhibition in the VapXD Toxin-Antitoxin System. <i>Structure</i> , 2021, 29, 139-150.e3.	1.6	12
4	Phylogeny Reveals Novel HipA-Homologous Kinase Families and Toxin-Antitoxin Gene Organizations. <i>MBio</i> , 2021, 12, e0105821.	1.8	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.	2.9	32
6	Evolving complex insulation. <i>Nature Chemical Biology</i> , 2021, 17, 1216-1217.	3.9	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.	5.8	17
8	Structure and Function of the Bacterial Protein Toxin Phenomycin. <i>Structure</i> , 2020, 28, 528-539.e9.	1.6	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.	1.6	23
10	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	1.8	25
11	(p)ppGpp Regulates a Bacterial Nucleosidase by an Allosteric Two-Domain Switch. <i>Molecular Cell</i> , 2019, 74, 1239-1249.e4.	4.5	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, .	2.9	2
13	The RES domain toxins of RES-Xre toxin-antitoxin modules induce cell stasis by degrading NAD <sup>+</sup> . <i>Molecular Microbiology</i> , 2019, 111, 221-236.	1.2	46
14	Evolution of the bacterial nucleosidase PpnN and its relation to the stringent response. <i>Microbial Cell</i> , 2019, 6, 450-453.	1.4	8
15	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	5.9	118
16	Toxins, Targets, and Triggers: An Overview of Toxin-Antitoxin Biology. <i>Molecular Cell</i> , 2018, 70, 768-784.	4.5	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.	1.6	46
18	The Abc of Phosphonate Breakdown: A Mechanism for Bacterial Survival. <i>BioEssays</i> , 2018, 40, e1800091.	1.2	28

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19	Higher-Order Structure in Bacterial VapBC Toxin-Antitoxin Complexes. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 381-412.	1.0	15
20	Structural conservation of the PIN domain active site across all domains of life. <i>Protein Science</i> , 2017, 26, 1474-1492.	3.1	33
21	Structural analysis of the active site architecture of the VapC toxin from <i>Shigella flexneri</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 892-899.	1.5	11
22	Toxin inhibition in <i>C. crescentus</i> VapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. <i>Nucleic Acids Research</i> , 2016, 45, gkw1266.	6.5	13
23	RRM domain of human RBM7: purification, crystallization and structure determination. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 397-402.	0.4	6
24	The transcriptional regulator GalR self-assembles to form highly regular tubular structures. <i>Scientific Reports</i> , 2016, 6, 27672.	1.6	2
25	Computational discovery of specificity-conferring sites in non-ribosomal peptide synthetases. <i>Bioinformatics</i> , 2016, 32, 325-329.	1.8	26
26	Identification of the non-ribosomal peptide synthetase responsible for biosynthesis of the potential anti-cancer drug sansalvamide in <i>Fusarium solani</i> . <i>Current Genetics</i> , 2016, 62, 799-807.	0.8	22
27	An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in <i>Fusarium</i> . <i>Fungal Genetics and Biology</i> , 2015, 75, 20-29.	0.9	123
28	Cut to the chase—Regulating translation through RNA cleavage. <i>Biochimie</i> , 2015, 114, 10-17.	1.3	12
29	Structural insights into the bacterial carbon-phosphorus lyase machinery. <i>Nature</i> , 2015, 525, 68-72.	13.7	63
30	Structural basis for RNA-genome recognition during bacteriophage Q $\beta$ replication. <i>Nucleic Acids Research</i> , 2015, 43, 10893-10906.	6.5	22
31	Structural analysis of the yeast exosome Rps47p complex by small-angle X-ray scattering. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 634-640.	1.0	5
32	VapC20 of <i>Mycobacterium tuberculosis</i> cleaves the Sarcin-Ricin loop of 23S rRNA. <i>Nature Communications</i> , 2013, 4, 2796.	5.8	112
33	Mutational analysis of the yeast RNA helicase Sub2p reveals conserved domains required for growth, mRNA export, and genomic stability. <i>Rna</i> , 2013, 19, 1363-1371.	1.6	21
34	Protein expression, crystallization and preliminary X-ray crystallographic analysis of the isolated <i>Shigella flexneri</i> VapC toxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 762-765.	0.7	6
35	Mimer: an automated spreadsheet-based crystallization screening system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 815-820.	0.7	13
36	<i>Saccharomyces cerevisiae</i> Ng13p is an active 5' to 3' exonuclease with a specificity towards poly-A RNA reminiscent of cellular deadenylases. <i>Nucleic Acids Research</i> , 2012, 40, 837-846.	6.5	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.	1.6	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.	2.0	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.	6.5	39
40	The activity and selectivity of fission yeast Pop2p are affected by a high affinity for Zn<sup>2+</sup> and Mn<sup>2+</sup> in the active site. <i>Rna</i> , 2009, 15, 850-861.	1.6	35
41	Origins and activities of the eukaryotic exosome. <i>Journal of Cell Science</i> , 2009, 122, 1487-1494.	1.2	146
42	Cyanobacteria contain a structural homologue of the Hfq protein with altered RNAâ€binding properties. <i>FEBS Journal</i> , 2009, 276, 3904-3915.	2.2	47
43	The Structural Basis for mRNA Recognition and Cleavage by the Ribosome-Dependent Endonuclease RelE. <i>Cell</i> , 2009, 139, 1084-1095.	13.5	194
44	Take the â€œAâ€tail â€ quality control of ribosomal and transfer RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 532-537.	0.9	15
45	Exonucleolysis is required for nuclear mRNA quality control in yeast THO mutants. <i>Rna</i> , 2008, 14, 2305-2313.	1.6	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.	1.6	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.	6.5	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.	3.3	81
49	The social life of ribosomal proteins. <i>FEBS Journal</i> , 2005, 272, 2098-2108.	2.2	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.	13.5	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.	1.4	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.	2.0	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.	2.0	128
56	Recognition of Cognate Transfer RNA by the 30S Ribosomal Subunit. <i>Science</i> , 2001, 292, 897-902.	6.0	1,085
57	Crystal Structure of an Initiation Factor Bound to the 30S Ribosomal Subunit. <i>Science</i> , 2001, 291, 498-501.	6.0	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.	2.0	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.	13.7	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.	13.7	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.	13.5	816
63	Structural Investigations of Calcium and Zinc Binding in Proteins. <i>Science Progress</i> , 1999, 82, 295-312.	1.0	1
64	XAct: a program for construction, automated setup and bookkeeping of crystallization experiments. <i>Journal of Applied Crystallography</i> , 1999, 32, 1012-1016.	1.9	3
65	Zinc-Binding Site of an S100 Protein Revealed. Two Crystal Structures of Ca <sup>2+</sup> -Bound Human Psoriasin (S100A7) in the Zn <sup>2+</sup> -Loaded and Zn <sup>2+</sup> -Free States. <i>Biochemistry</i> , 1999, 38, 1695-1704.	1.2	140
66	EF-hands at atomic resolution: the structure of human psoriasin (S100A7) solved by MAD phasing. <i>Structure</i> , 1998, 6, 477-489.	1.6	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.	1.6	53