

Bettina Bäjtcher

List of Publications by Year in descending order

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85
papers

4,831
citations

81900

39
h-index

98798

67
g-index

109
all docs

109
docs citations

109
times ranked

5535
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	12.6	440
2	Structure-Based Assembly of Protein Complexes in Yeast. <i>Science</i> , 2004, 303, 2026-2029.	12.6	367
3	Hrr25-dependent phosphorylation state regulates organization of the pre-40S subunit. <i>Nature</i> , 2006, 441, 651-655.	27.8	191
4	Proofreading of pre-40S ribosome maturation by a translation initiation factor and 60S subunits. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 744-753.	8.2	173
5	A Conformational Change in the Adeno-Associated Virus Type 2 Capsid Leads to the Exposure of Hidden VP1 N Termini. <i>Journal of Virology</i> , 2005, 79, 5296-5303.	3.4	153
6	Mechanochemical Removal of Ribosome Biogenesis Factors from Nascent 60S Ribosomal Subunits. <i>Cell</i> , 2009, 138, 911-922.	28.9	141
7	The Assembly-Activating Protein Promotes Capsid Assembly of Different Adeno-Associated Virus Serotypes. <i>Journal of Virology</i> , 2011, 85, 12686-12697.	3.4	136
8	Cathelicidins Have Direct Antiviral Activity against Respiratory Syncytial Virus In Vitro and Protective Function In Vivo in Mice and Humans. <i>Journal of Immunology</i> , 2016, 196, 2699-2710.	0.8	129
9	The gross structure of the respiratory complex I: a Lego System. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004, 1608, 1-9.	1.0	127
10	Electron cryo-microscopy and image reconstruction of adeno-associated virus type 2 empty capsids. <i>EMBO Reports</i> , 2001, 2, 997-1002.	4.5	126
11	Geminate Structures of African Cassava Mosaic Virus. <i>Journal of Virology</i> , 2004, 78, 6758-6765.	3.4	107
12	Structure of the pre-60S ribosomal subunit with nuclear export factor Arx1 bound at the exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1234-1241.	8.2	103
13	Purification of Nuclear Poly(A)-binding Protein Nab2 Reveals Association with the Yeast Transcriptome and a Messenger Ribonucleoprotein Core Structure. <i>Journal of Biological Chemistry</i> , 2009, 284, 34911-34917.	3.4	99
14	Direct indication for the existence of a double stalk in CF O F 1 1 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1998, 281, 757-762.	4.2	98
15	Cryo-electron microscopy of hepatitis B virions reveals variability in envelope capsid interactions. <i>EMBO Journal</i> , 2007, 26, 4160-4167.	7.8	95
16	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002, 3, 628-635.	4.5	89
17	Architecture of the mycobacterial type VII secretion system. <i>Nature</i> , 2019, 576, 321-325.	27.8	89
18	A Novel, Enzymatically Active Conformation of the Escherichia coli NADH:Ubiquinone Oxidoreductase (Complex I). <i>Journal of Biological Chemistry</i> , 2002, 277, 17970-17977.	3.4	88

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19	Molecular basis for the functional interaction of dynein light chain with the nuclear-pore complex. <i>Nature Cell Biology</i> , 2007, 9, 788-796.	10.3	84
20	Insights into Transcription Initiation and Termination from the Electron Microscopy Structure of Yeast RNA Polymerase III. <i>Molecular Cell</i> , 2007, 25, 813-823.	9.7	74
21	Three-dimensional Map of a Plant V-ATPase Based on Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2002, 277, 13115-13121.	3.4	70
22	A Different Conformation for EGC Stator Subcomplex in Solution and in the Assembled Yeast V-ATPase: Possible Implications for Regulatory Disassembly. <i>Structure</i> , 2008, 16, 1789-1798.	3.3	69
23	Hepatitis B virus core protein phosphorylation: Identification of the SRPK1 target sites and impact of their occupancy on RNA binding and capsid structure. <i>PLoS Pathogens</i> , 2018, 14, e1007488.	4.7	67
24	Homologous bd oxidases share the same architecture but differ in mechanism. <i>Nature Communications</i> , 2019, 10, 5138.	12.8	65
25	Conformational flexibility of RNA polymerase III during transcriptional elongation. <i>EMBO Journal</i> , 2010, 29, 3762-3772.	7.8	64
26	The structure of photosystem I from the thermophilic cyanobacterium <i>Synechococcus</i> sp. determined by electron microscopy of two-dimensional crystals. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1992, 1100, 125-136.	1.0	59
27	Direct visualisation of conformational changes in EF0F1 by electron microscopy 1 Edited by W. Baumeister. <i>Journal of Molecular Biology</i> , 2000, 296, 449-457.	4.2	58
28	Packaging of up to 240 subunits of a 17 kDa nuclease into the interior of recombinant hepatitis B virus capsids. <i>FEBS Letters</i> , 2000, 481, 169-176.	2.8	55
29	Structure of the Mechanosensitive Channel MscS Embedded in the Membrane Bilayer. <i>Journal of Molecular Biology</i> , 2019, 431, 3081-3090.	4.2	52
30	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , 2017, 6, .	6.0	51
31	Building the Stator of the Yeast Vacuolar-ATPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 40670-40676.	3.4	49
32	Think Beyond the Core: Impact of the Hydrophilic Corona on Drug Solubilization Using Polymer Micelles. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 24531-24543.	8.0	49
33	Hepatitis B Virus Capsid-like Particles Can Display the Complete, Dimeric Outer Surface Protein C and Stimulate Production of Protective Antibody Responses against <i>Borrelia burgdorferi</i> Infection. <i>Journal of Biological Chemistry</i> , 2006, 281, 17474-17481.	3.4	48
34	The structure of ATP synthase from chloroplasts. Conformational changes of CF1 studied by electron microscopy. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1992, 1098, 131-143.	1.0	46
35	The structure of the H ⁺ -ATP synthase from chloroplasts and its subcomplexes as revealed by electron microscopy. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1458, 404-416.	1.0	46
36	The <i>Leishmania tarentolae</i> exosome: Purification and structural analysis by electron microscopy. <i>Molecular and Biochemical Parasitology</i> , 2008, 159, 24-29.	1.1	46

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37	Reconstitution of Nup157 and Nup145N into the Nup84 Complex*[boxes]. <i>Journal of Biological Chemistry</i> , 2005, 280, 18442-18451.	3.4	45
38	Elucidation of the Stator Organization in the V-ATPase of <i>Neurospora crassa</i> . <i>Journal of Molecular Biology</i> , 2005, 349, 659-669.	4.2	43
39	Structural Basis of Poxvirus Transcription: Vaccinia RNA Polymerase Complexes. <i>Cell</i> , 2019, 179, 1537-1550.e19.	28.9	41
40	High Plasticity of the Hepatitis B Virus Capsid Revealed by Conformational Stress. <i>Journal of Molecular Biology</i> , 2006, 356, 812-822.	4.2	40
41	A Unique Resting Position of the ATP-synthase from Chloroplasts. <i>Journal of Biological Chemistry</i> , 2003, 278, 18544-18549.	3.4	39
42	Structure of Mutant Hepatitis B Core Protein Capsids with Premature Secretion Phenotype. <i>Journal of Molecular Biology</i> , 2018, 430, 4941-4954.	4.2	39
43	The Mitosis and Neurodevelopment Proteins NDE1 and NDEL1 Form Dimers, Tetramers, and Polymers with a Folded Back Structure in Solution. <i>Journal of Biological Chemistry</i> , 2012, 287, 32381-32393.	3.4	38
44	Crystal structure of Schmallenberg orthobunyavirus nucleoprotein-RNA complex reveals a novel RNA sequestration mechanism. <i>Rna</i> , 2013, 19, 1129-1136.	3.5	37
45	Precise mapping of subunits in multiprotein complexes by a versatile electron microscopy label. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 775-778.	8.2	36
46	Structural organization of the V-ATPase and its implications for regulatory assembly and disassembly. <i>Biochemical Society Transactions</i> , 2008, 36, 1027-1031.	3.4	35
47	Two structurally distinct domains of the nucleoporin Nup170 cooperate to tether a subset of nucleoporins to nuclear pores. <i>Journal of Cell Biology</i> , 2009, 185, 387-395.	5.2	35
48	Insights into the structure of the CCR4-NOT complex by electron microscopy. <i>FEBS Letters</i> , 2011, 585, 2182-2186.	2.8	35
49	Near-Atomic Resolution Structure of a Plant Geminivirus Determined by Electron Cryomicroscopy. <i>Structure</i> , 2017, 25, 1303-1309.e3.	3.3	35
50	Peripheral Stator of the Yeast V-ATPase: Stoichiometry and Specificity of Interaction between the EG Complex and Subunits C and H. <i>Biochemistry</i> , 2005, 44, 15906-15914.	2.5	34
51	K ⁺ -Translocating KdpFABC P-Type ATPase from <i>Escherichia coli</i> Acts as a Functional and Structural Dimer. <i>Biochemistry</i> , 2008, 47, 3564-3575.	2.5	32
52	Mechanosensitive channel gating by delipidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	32
53	The MscS-like channel YnaI has a gating mechanism based on flexible pore helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28754-28762.	7.1	30
54	Inverse Thermogelation of Aqueous Triblock Copolymer Solutions into Macroporous Shear-Thinning 3D Printable Inks. <i>ACS Applied Materials & Interfaces</i> , 2020, 12, 12445-12456.	8.0	28

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55	Target highlights in <sc>CASP14</sc>: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	2.6	27
56	Assembly of the Eukaryotic PLP-Synthase Complex from Plasmodium and Activation of the Pdx1 Enzyme. <i>Structure</i> , 2012, 20, 172-184.	3.3	26
57	Structure of <i>Escherichia coli</i> cytochrome bd-II type oxidase with bound aurachin D. <i>Nature Communications</i> , 2021, 12, 6498.	12.8	25
58	Modular architecture of eukaryotic RNase P and RNase MRP revealed by electron microscopy. <i>Nucleic Acids Research</i> , 2012, 40, 3275-3288.	14.5	23
59	Capabilities of the Falcon III detector for single-particle structure determination. <i>Ultramicroscopy</i> , 2019, 203, 145-154.	1.9	21
60	Geometrical and Structural Dynamics of Imatinib within Biorelevant Colloids. <i>Molecular Pharmaceutics</i> , 2018, 15, 4470-4480.	4.6	20
61	Electron cryomicroscopy of two-dimensional crystals of the H ⁺ -ATPase from chloroplasts. <i>FEBS Letters</i> , 1995, 373, 262-264.	2.8	19
62	Conformational Changes in Adeno-Associated Virus Type 1 Induced by Genome Packaging. <i>Journal of Molecular Biology</i> , 2011, 409, 427-438.	4.2	19
63	The Structure of YnaI Implies Structural and Mechanistic Conservation in the MscS Family of Mechanosensitive Channels. <i>Structure</i> , 2015, 23, 1705-1714.	3.3	19
64	Molybdate-Uptake Genes and Molybdopterin-Biosynthesis Genes on a Bacterial Plasmid. Characterization of MoeA as a Filament-Forming Protein with Adenosinetriphosphatase Activity. <i>FEBS Journal</i> , 1997, 250, 524-531.	0.2	17
65	Nucleotide-induced conformational changes in the <i>Escherichia coli</i> NADH:ubiquinone oxidoreductase (complex I). <i>Biochemical Society Transactions</i> , 2008, 36, 971-975.	3.4	17
66	Slowly folding surface extension in the prototypic avian hepatitis B virus capsid governs stability. <i>ELife</i> , 2020, 9, .	6.0	13
67	Analyzing RNA polymerase III by electron cryomicroscopy. <i>RNA Biology</i> , 2011, 8, 760-765.	3.1	12
68	Structural basis of the complete poxvirus transcription initiation process. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 779-788.	8.2	12
69	Conformational Plasticity of Hepatitis B Core Protein Spikes Promotes Peptide Binding Independent of the Secretion Phenotype. <i>Microorganisms</i> , 2021, 9, 956.	3.6	10
70	The Structure of the ATP-Synthase from Chloroplasts. , 1990, , 247-276.		10
71	Biophysical Characterization and Activity of Lymphostatin, a Multifunctional Virulence Factor of Attaching and Effacing <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 5803-5816.	3.4	9
72	Calcium phosphate-based biomaterials trigger human macrophages to release extracellular traps. <i>Biomaterials</i> , 2022, 285, 121521.	11.4	9

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73	Electron cryo-microscopy of graphite in amorphous ice. <i>Ultramicroscopy</i> , 1995, 58, 417-424.	1.9	8
74	Systematic Bioinformatics and Experimental Validation of Yeast Complexes Reduces the Rate of Attrition during Structural Investigations. <i>Structure</i> , 2010, 18, 1075-1082.	3.3	8
75	Controlling Supramolecular Structures of Drugs by Light. <i>Molecular Pharmaceutics</i> , 2020, 17, 4704-4708.	4.6	7
76	Dealing with Particles in Different Conformational States by Electron Microscopy and Image Processing. <i>Journal of Structural Biology</i> , 2001, 133, 214-220.	2.8	6
77	Solution structure of the KdpFABC P-type ATPase from <i>Escherichia coli</i> by electron microscopic single particle analysis. <i>Journal of Structural Biology</i> , 2009, 166, 295-302.	2.8	6
78	Regulatory assembly of the vacuolar proton pump V o V 1 -ATPase in yeast cells by FLIM-FRET. , 2010, , .		6
79	Concentration and composition dependent aggregation of Pluronic- and Poly-(2-oxazolin)-Efavirenz formulations in biorelevant media. <i>Journal of Colloid and Interface Science</i> , 2022, 606, 1179-1192.	9.4	6
80	ATP synthase. <i>EMBO Reports</i> , 2000, 1, 223-224.	4.5	5
81	Binding of a Pocket Factor to Hepatitis B Virus Capsids Changes the Rotamer Conformation of Phenylalanine 97. <i>Viruses</i> , 2021, 13, 2115.	3.3	4
82	Single-particle applications at intermediate resolution. <i>Advances in Protein Chemistry and Structural Biology</i> , 2010, 81, 61-88.	2.3	3
83	More Than Just Closed and Open: Unraveling a Mechanosensor. <i>Trends in Biochemical Sciences</i> , 2021, 46, 623-625.	7.5	3
84	The Structure of ATPsynthases in Photosynthesis and Respiration. <i>Advances in Photosynthesis and Respiration</i> , 2014, , 111-132.	1.0	1
85	Hepatitis B Core Protein Capsids. <i>Sub-Cellular Biochemistry</i> , 2021, 96, 451-470.	2.4	1