

Andreas Bracher

List of Publications by Year in descending order

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89
papers

10,501
citations

61984

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53230

85
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111
all docs

111
docs citations

111
times ranked

12754
citing authors

#	ARTICLE	IF	CITATIONS
1	The chaperone Clusterin in neurodegeneration—friend or foe?. <i>BioEssays</i> , 2022, 44, e2100287.	2.5	18
2	High-resolution structure and biophysical characterization of the nucleocapsid phosphoprotein dimerization domain from the Covid-19 severe acute respiratory syndrome coronavirus 2. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 54-62.	2.1	100
3	Makrozyklische FKBP51-Liganden enthallen einen transienten Bindungsmodus mit erhohter Selektivitat. <i>Angewandte Chemie</i> , 2021, 133, 13366-13372.	2.0	0
4	Macrocyclic FKBP51 Ligands Define a Transient Binding Mode with Enhanced Selectivity. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 13257-13263.	13.8	13
5	The extracellular chaperone Clusterin enhances Tau aggregate seeding in a cellular model. <i>Nature Communications</i> , 2021, 12, 4863.	12.8	35
6	Protein Folding Chaperonins. , 2021, , 116-120.		0
7	The Hsc70 disaggregation machinery removes monomer units directly from α -synuclein fibril ends. <i>Nature Communications</i> , 2021, 12, 5999.	12.8	37
8	Picomolar FKBP inhibitors enabled by a single water-displacing methyl group in bicyclic [4.3.1] aza-amides. <i>Chemical Science</i> , 2021, 12, 14758-14765.	7.4	19
9	A Novel Decalin-Based Bicyclic Scaffold for FKBP51-Selective Ligands. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 231-240.	6.4	9
10	Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. <i>Cell</i> , 2020, 183, 457-473.e20.	28.9	30
11	Structure and conformational cycle of a bacteriophage-encoded chaperonin. <i>PLoS ONE</i> , 2020, 15, e0230090.	2.5	8
12	Rubisco condensate formation by CcmM in α -carboxysome biogenesis. <i>Nature</i> , 2019, 566, 131-135.	27.8	185
13	Chaperone Function of Hgh1 in the Biogenesis of Eukaryotic Elongation Factor 2. <i>Molecular Cell</i> , 2019, 74, 88-100.e9.	9.7	18
14	Crystal structure of phosphoribulokinase from <i>Synechococcus</i> sp. strain PCC 6301. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 278-289.	0.8	15
15	GroEL Ring Separation and Exchange in the Chaperonin Reaction. <i>Cell</i> , 2018, 172, 605-617.e11.	28.9	43
16	Chemogenomic Profiling of Human and Microbial FK506-Binding Proteins. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 3660-3673.	6.4	42
17	Biogenesis and Metabolic Maintenance of Rubisco. <i>Annual Review of Plant Biology</i> , 2017, 68, 29-60.	18.7	176
18	Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6.	9.7	47

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19	Plant RuBisCo assembly in <i>E. coli</i> with five chloroplast chaperones including BSD2. <i>Science</i> , 2017, 358, 1272-1278.	12.6	172
20	Crystal structure of the <i>Thermoplasma acidophilum</i> protein Ta1207. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 328-335.	0.8	0
21	Rapid, Structure-Based Exploration of Pipecolic Acid Amides as Novel Selective Antagonists of the FK506-Binding Protein 51. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 2410-2422.	6.4	31
22	Structure of human heat-shock transcription factor 1 in complex with DNA. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 140-146.	8.2	87
23	The GroEL-GroES Chaperonin Machine: A Nano-Cage for Protein Folding. <i>Trends in Biochemical Sciences</i> , 2016, 41, 62-76.	7.5	325
24	Degradation of potent Rubisco inhibitor by selective sugar phosphatase. <i>Nature Plants</i> , 2015, 1, 14002.	9.3	38
25	The nucleotide exchange factors of Hsp70 molecular chaperones. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 10.	3.5	172
26	Structural Analysis of the Rubisco-Assembly Chaperone RbcX-II from <i>Chlamydomonas reinhardtii</i> . <i>PLoS ONE</i> , 2015, 10, e0135448.	2.5	13
27	Rational Design and Asymmetric Synthesis of Potent and Neurotrophic Ligands for FK506-Binding Proteins (FKBPs). <i>Angewandte Chemie - International Edition</i> , 2015, 54, 345-348.	13.8	27
28	Structure and mechanism of the Rubisco-assembly chaperone Raf1. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 720-728.	8.2	61
29	Structure-Affinity Relationship Analysis of Selective FKBP51 Ligands. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 7796-7806.	6.4	32
30	Selective inhibitors of the FK506-binding protein 51 by induced fit. <i>Nature Chemical Biology</i> , 2015, 11, 33-37.	8.0	188
31	GrpE, Hsp110/Grp170, HspBP1/Sil1 and BAG Domain Proteins: Nucleotide Exchange Factors for Hsp70 Molecular Chaperones. <i>Sub-Cellular Biochemistry</i> , 2015, 78, 1-33.	2.4	59
32	Crystal structure of the proteasomal deubiquitylation module Rpn8-Rpn11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2984-2989.	7.1	120
33	Maintaining photosynthetic CO ₂ fixation via protein remodelling: the Rubisco activases. <i>Photosynthesis Research</i> , 2014, 119, 191-201.	2.9	40
34	GroEL/ES Chaperonin Modulates the Mechanism and Accelerates the Rate of TIM-Barrel Domain Folding. <i>Cell</i> , 2014, 157, 922-934.	28.9	116
35	Stereoselective Construction of the 5-Hydroxy Diazabicyclo[4.3.1]decane-2-one Scaffold, a Privileged Motif for FK506-Binding Proteins. <i>Organic Letters</i> , 2014, 16, 5254-5257.	4.6	26
36	Crystal Structures of the Free and Ligand-Bound FK1-FK2 Domain Segment of FKBP52 Reveal a Flexible Inter-Domain Hinge. <i>Journal of Molecular Biology</i> , 2013, 425, 4134-4144.	4.2	41

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37	Increasing the Efficiency of Ligands for FK506-Binding Protein 51 by Conformational Control. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 3922-3935.	6.4	53
38	Molecular Chaperone Functions in Protein Folding and Proteostasis. <i>Annual Review of Biochemistry</i> , 2013, 82, 323-355.	11.1	1,218
39	Structure and function of Hip, an attenuator of the Hsp70 chaperone cycle. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 929-935.	8.2	60
40	Large FK506-Binding Proteins Shape the Pharmacology of Rapamycin. <i>Molecular and Cellular Biology</i> , 2013, 33, 1357-1367.	2.3	106
41	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 149-154.	7.1	136
42	Folding of large multidomain proteins by partial encapsulation in the chaperonin TRiC/CCT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21208-21215.	7.1	52
43	Evaluation of Synthetic FK506 Analogues as Ligands for the FK506-Binding Proteins 51 and 52. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 4114-4122.	6.4	59
44	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352.	12.6	357
45	Exploration of Pipecolate Sulfonamides as Binders of the FK506-Binding Proteins 51 and 52. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 4123-4131.	6.4	46
46	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	3.3	261
47	Structure of green-type Rubisco activase from tobacco. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1366-1370.	8.2	97
48	Molecular chaperones in protein folding and proteostasis. <i>Nature</i> , 2011, 475, 324-332.	27.8	2,762
49	Structural characterization of the PPIase domain of FKBP51, a cochaperone of human Hsp90. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 549-559.	2.5	57
50	Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. <i>Nature</i> , 2011, 479, 194-199.	27.8	141
51	Firefly luciferase mutants as sensors of proteome stress. <i>Nature Methods</i> , 2011, 8, 879-884.	19.0	190
52	Crystal structure of a chaperone-bound assembly intermediate of form I Rubisco. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 875-880.	8.2	56
53	Coupled chaperone action in folding and assembly of hexadecameric Rubisco. <i>Nature</i> , 2010, 463, 197-202.	27.8	165
54	Interaction of the Hsp110 Molecular Chaperones from <i>S. cerevisiae</i> with Substrate Protein. <i>Journal of Molecular Biology</i> , 2010, 401, 696-707.	4.2	38

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55	Structural Basis for the Cooperation of Hsp70 and Hsp110 Chaperones in Protein Folding. <i>Cell</i> , 2008, 133, 1068-1079.	28.9	235
56	Structure and Function of RbcX, an Assembly Chaperone for Hexadecameric Rubisco. <i>Cell</i> , 2007, 129, 1189-1200.	28.9	137
57	L25 functions as a conserved ribosomal docking site shared by nascent chain-associated complex and signal-recognition particle. <i>EMBO Reports</i> , 2007, 8, 1086-1086.	4.5	7
58	Nucleotide Exchange Factors for Hsp70 Molecular Chaperones. , 2007, , 1-12.		5
59	Crystal Structure of an Archaeal Actin Homolog. <i>Journal of Molecular Biology</i> , 2006, 358, 145-156.	4.2	49
60	Structural Basis for Subunit Assembly in UDP-glucose Pyrophosphorylase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2006, 364, 551-560.	4.2	49
61	Hsp90 structure: when two ends meet. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 478-480.	8.2	17
62	Molecular chaperones of the Hsp110 family act as nucleotide exchange factors of Hsp70s. <i>EMBO Journal</i> , 2006, 25, 2519-2528.	7.8	310
63	L25 functions as a conserved ribosomal docking site shared by nascent chain-associated complex and signal-recognition particle. <i>EMBO Reports</i> , 2006, 7, 78-84.	4.5	24
64	Fes1p acts as a nucleotide exchange factor for the ribosome-associated molecular chaperone Ssb1p. <i>Biological Chemistry</i> , 2006, 387, 1593-1600.	2.5	30
65	Pathogenic Mutations Located in the Hydrophobic Core of the Prion Protein Interfere with Folding and Attachment of the Glycosylphosphatidylinositol Anchor. <i>Journal of Biological Chemistry</i> , 2005, 280, 9320-9329.	3.4	41
66	Towards a Complete Structure of Hsp90. <i>Structure</i> , 2005, 13, 501-502.	3.3	1
67	Regulation of Hsp70 Function by HspBP1. <i>Molecular Cell</i> , 2005, 17, 367-379.	9.7	185
68	Structure of a halophilic nucleoside diphosphate kinase from <i>Halobacterium salinarum</i> . <i>FEBS Letters</i> , 2005, 579, 6595-6600.	2.8	34
69	Crystal structure of the Habc domain of neuronal syntaxin from the squid <i>Loligo pealei</i> reveals conformational plasticity at its C-terminus. <i>BMC Structural Biology</i> , 2004, 4, 6.	2.3	9
70	The Matrix Protein VP40 from Ebola Virus Octamerizes into Pore-like Structures with Specific RNA Binding Properties. <i>Structure</i> , 2003, 11, 423-433.	3.3	137
71	Biosynthesis of Pteridines. Reaction Mechanism of GTP Cyclohydrolase I. <i>Journal of Molecular Biology</i> , 2003, 326, 503-516.	4.2	70
72	X-ray Structure of a Neuronal Complexin-SNARE Complex from Squid. <i>Journal of Biological Chemistry</i> , 2002, 277, 26517-26523.	3.4	111

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73	Reaction mechanism of GTP cyclohydrolase I: single turnover experiments using a kinetically competent reaction intermediate. <i>Journal of Molecular Biology</i> , 2002, 316, 829-837.	4.2	29
74	Crystal structure of the GABA A receptor-associated protein, GABARAP. <i>EMBO Reports</i> , 2002, 3, 183-189.	4.5	65
75	Structural basis for the Golgi membrane recruitment of Sly1p by Sed5p. <i>EMBO Journal</i> , 2002, 21, 6114-6124.	7.8	159
76	Studies on the Reaction Mechanism of GTP Cyclohydrolase I. , 2002, , 169-173.		0
77	Crystal structures of neuronal squid Sec1 implicate inter-domain hinge movement in the release of t-SNAREs11 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 7-13.	4.2	42
78	Biosynthesis of Pteridines. Stopped-Flow Kinetic Analysis of GTP Cyclohydrolase I. <i>Biochemistry</i> , 2001, 40, 7896-7902.	2.5	29
79	Ring Opening Is Not Rate-limiting in the GTP Cyclohydrolase I Reaction. <i>Journal of Biological Chemistry</i> , 2001, 276, 2622-2626.	3.4	18
80	Biosynthesis of Riboflavin. <i>Journal of Biological Chemistry</i> , 2001, 276, 44157-44162.	3.4	23
81	Biosynthesis of Riboflavin. <i>Journal of Biological Chemistry</i> , 2001, 276, 22273-22277.	3.4	43
82	Crystallization and preliminary X-ray analysis of squid neuronal Sec1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 501-503.	2.5	5
83	Zinc plays a key role in human and bacterial GTP cyclohydrolase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13567-13572.	7.1	131
84	The X-ray crystal structure of neuronal Sec1 from squid sheds new light on the role of this protein in exocytosis. <i>Structure</i> , 2000, 8, 685-694.	3.3	45
85	Histidine 179 Mutants of GTP Cyclohydrolase I Catalyze the Formation of 2-Amino-5-formylamino-6-ribofuranosylamino-4(3H)-pyrimidinone Triphosphate. <i>Journal of Biological Chemistry</i> , 1999, 274, 16727-16735.	3.4	46
86	Complementation of the fol2 Deletion in <i>Saccharomyces cerevisiae</i> by Human and <i>Escherichia coli</i> Genes Encoding GTP Cyclohydrolase I. <i>Biochemical and Biophysical Research Communications</i> , 1999, 255, 521-527.	2.1	10
87	Biosynthesis of Pteridines. <i>Journal of Biological Chemistry</i> , 1998, 273, 28132-28141.	3.4	62
88	Structure and mechanism of GTP cyclohydrolase I of <i>Escherichia coli</i> . <i>Biochemical Society Transactions</i> , 1996, 24, 37S-37S.	3.4	9
89	Active site topology and reaction mechanism of GTP cyclohydrolase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 12120-12125.	7.1	122