

Andreas Bracher

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

91 papers	8,152 citations	41 h-index	90 g-index
111 ext. papers	9,501 ext. citations	14 avg, IF	6.21 L-index

#	Paper	IF	Citations
91	The chaperone Clusterin in neurodegeneration-friend or foe?. <i>BioEssays</i> , 2022 , e2100287	4.1	1
90	The Hsc70 disaggregation machinery removes monomer units directly from β -synuclein fibril ends. <i>Nature Communications</i> , 2021 , 12, 5999	17.4	2
89	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	9.4	1
88	Makrozyklische FKBP51-Liganden enthalten einen transienten Bindungsmodus mit erhöhter Selektivität. <i>Angewandte Chemie</i> , 2021 , 133, 13366-13372	3.6	
87	Macrocyclic FKBP51 Ligands Define a Transient Binding Mode with Enhanced Selectivity. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 13257-13263	16.4	3
86	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	3.4	37
85	The extracellular chaperone Clusterin enhances Tau aggregate seeding in a cellular model. <i>Nature Communications</i> , 2021 , 12, 4863	17.4	8
84	Protein Folding Chaperonins 2021 , 116-120		
83	Structure and conformational cycle of a bacteriophage-encoded chaperonin. <i>PLoS ONE</i> , 2020 , 15, e0230090	3.9	6
82	A Novel Decalin-Based Bicyclic Scaffold for FKBP51-Selective Ligands. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 231-240	8.3	4
81	Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. <i>Cell</i> , 2020 , 183, 457-473.e20	56.2	9
80	Rubisco condensate formation by CcmM in β -carboxysome biogenesis. <i>Nature</i> , 2019 , 566, 131-135	50.4	102
79	Chaperone Function of Hsp1 in the Biogenesis of Eukaryotic Elongation Factor 2. <i>Molecular Cell</i> , 2019 , 74, 88-100.e9	17.6	7
78	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	1.1	5
77	GroEL Ring Separation and Exchange in the Chaperonin Reaction. <i>Cell</i> , 2018 , 172, 605-617.e11	56.2	33
76	Chemogenomic Profiling of Human and Microbial FKBP51-Binding Proteins. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 3660-3673	8.3	20
75	Biogenesis and Metabolic Maintenance of Rubisco. <i>Annual Review of Plant Biology</i> , 2017 , 68, 29-60	30.7	126

74	Mechanism of Enzyme Repair by the AAA Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017 , 67, 744-756. e66	1.66	30
73	Plant RuBisCo assembly in with five chloroplast chaperones including BSD2. <i>Science</i> , 2017 , 358, 1272-1278. e393	1.3	112
72	Crystal structure of the Thermoplasma acidophilum protein Ta1207. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017 , 73, 328-335	1.1	
71	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, 2410-22	8.3	23
70	Structure of human heat-shock transcription factor 1 in complex with DNA. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 140-6	17.6	62
69	The GroEL-GroES Chaperonin Machine: A Nano-Cage for Protein Folding. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 62-76	10.3	205
68	Structure and mechanism of the Rubisco-assembly chaperone Raf1. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 720-8	17.6	45
67	Structure-Affinity Relationship Analysis of Selective FKBP51 Ligands. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 7796-806	8.3	22
66	Selective inhibitors of the FK506-binding protein 51 by induced fit. <i>Nature Chemical Biology</i> , 2015 , 11, 33-7	11.7	128
65	Degradation of potent Rubisco inhibitor by selective sugar phosphatase. <i>Nature Plants</i> , 2015 , 1, 14002	11.5	30
64	Rationales Design und asymmetrische Synthese potenter neuritotropher Liganden für FK506-bindende Proteine (FKBPs). <i>Angewandte Chemie</i> , 2015 , 127, 352-355	3.6	6
63	The nucleotide exchange factors of Hsp70 molecular chaperones. <i>Frontiers in Molecular Biosciences</i> , 2015 , 2, 10	5.6	129
62	Structural Analysis of the Rubisco-Assembly Chaperone RbcX-II from Chlamydomonas reinhardtii. <i>PLoS ONE</i> , 2015 , 10, e0135448	3.7	11
61	Rational design and asymmetric synthesis of potent and neurotrophic ligands for FK506-binding proteins (FKBPs). <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 345-8	16.4	23
60	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	5.5	42
59	GroEL/ES chaperonin modulates the mechanism and accelerates the rate of TIM-barrel domain folding. <i>Cell</i> , 2014 , 157, 922-934	56.2	92
58	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, 5254-7	6.2	23
57	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, 2984-9	11.5	97

56	Maintaining photosynthetic CO ₂ fixation via protein remodelling: the Rubisco activases. <i>Photosynthesis Research</i> , 2014 , 119, 191-201	3.7	36
55	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, 4134-44	6.5	31
54	Increasing the efficiency of ligands for FK506-binding protein 51 by conformational control. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 3922-35	8.3	47
53	Molecular chaperone functions in protein folding and proteostasis. <i>Annual Review of Biochemistry</i> , 2013 , 82, 323-55	29.1	937
52	Structure and function of Hip, an attenuator of the Hsp70 chaperone cycle. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 929-35	17.6	55
51	Large FK506-binding proteins shape the pharmacology of rapamycin. <i>Molecular and Cellular Biology</i> , 2013 , 33, 1357-67	4.8	84
50	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. <i>Structure</i> , 2012 , 20, 814-25	5.2	216
49	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, 21208-15	11.5	40
48	Evaluation of synthetic FK506 analogues as ligands for the FK506-binding proteins 51 and 52. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 4114-22	8.3	52
47	Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. <i>Science</i> , 2012 , 337, 1348-52	33.3	323
46	Exploration of pipicolate sulfonamides as binders of the FK506-binding proteins 51 and 52. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 4123-31	8.3	41
45	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, 149-54	11.5	118
44	Structure of green-type Rubisco activase from tobacco. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1366-70	17.6	89
43	Molecular chaperones in protein folding and proteostasis. <i>Nature</i> , 2011 , 475, 324-32	50.4	2147
42	Structural characterization of the PPIase domain of FKBP51, a cochaperone of human Hsp90. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 549-59		47
41	Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. <i>Nature</i> , 2011 , 479, 194-9	50.4	117
40	Firefly luciferase mutants as sensors of proteome stress. <i>Nature Methods</i> , 2011 , 8, 879-84	21.6	125
39	Crystal structure of a chaperone-bound assembly intermediate of form I Rubisco. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 875-80	17.6	50

38	Coupled chaperone action in folding and assembly of hexadecameric Rubisco. <i>Nature</i> , 2010 , 463, 197-203	10.4	143
37	Interaction of the Hsp110 molecular chaperones from <i>S. cerevisiae</i> with substrate protein. <i>Journal of Molecular Biology</i> , 2010 , 401, 696-707	6.5	32
36	Structural basis for the cooperation of Hsp70 and Hsp110 chaperones in protein folding. <i>Cell</i> , 2008 , 133, 1068-79	56.2	195
35	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	6.5	1
34	Structure and function of RbcX, an assembly chaperone for hexadecameric Rubisco. <i>Cell</i> , 2007 , 129, 1189-200	3.2	107
33	Nucleotide Exchange Factors for Hsp70 Molecular Chaperones 2007 , 1-12		3
32	Fes1p acts as a nucleotide exchange factor for the ribosome-associated molecular chaperone Ssb1p. <i>Biological Chemistry</i> , 2006 , 387, 1593-600	4.5	28
31	Crystal structure of an archaeal actin homolog. <i>Journal of Molecular Biology</i> , 2006 , 358, 145-56	6.5	39
30	Structural basis for subunit assembly in UDP-glucose pyrophosphorylase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2006 , 364, 551-60	6.5	33
29	Molecular chaperones of the Hsp110 family act as nucleotide exchange factors of Hsp70s. <i>EMBO Journal</i> , 2006 , 25, 2519-28	13	270
28	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	6.5	24
27	Regulation of Hsp70 function by HspBP1: structural analysis reveals an alternate mechanism for Hsp70 nucleotide exchange. <i>Molecular Cell</i> , 2005 , 17, 367-79	17.6	172
26	Structure of a halophilic nucleoside diphosphate kinase from <i>Halobacterium salinarum</i> . <i>FEBS Letters</i> , 2005 , 579, 6595-600	3.8	33
25	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, 9320-9	5.4	41
24	Towards a complete structure of Hsp90. <i>Structure</i> , 2005 , 13, 501-2	5.2	1
23	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	2.7	8
22	The matrix protein VP40 from Ebola virus octamerizes into pore-like structures with specific RNA binding properties. <i>Structure</i> , 2003 , 11, 423-33	5.2	117
21	Biosynthesis of pteridines. Reaction mechanism of GTP cyclohydrolase I. <i>Journal of Molecular Biology</i> , 2003 , 326, 503-16	6.5	62

20	Structural basis for the Golgi membrane recruitment of Sly1p by Sed5p. <i>EMBO Journal</i> , 2002 , 21, 6114-24	3	136
19	X-ray structure of a neuronal complexin-SNARE complex from squid. <i>Journal of Biological Chemistry</i> , 2002 , 277, 26517-23	5-4	93
18	Reaction mechanism of GTP cyclohydrolase I: single turnover experiments using a kinetically competent reaction intermediate. <i>Journal of Molecular Biology</i> , 2002 , 316, 829-37	6-5	26
17	Crystal structure of the GABA(A)-receptor-associated protein, GABARAP. <i>EMBO Reports</i> , 2002 , 3, 183-9	6-5	54
16	Studies on the Reaction Mechanism of GTP Cyclohydrolase I 2002 , 169-173		
15	Ring opening is not rate-limiting in the GTP cyclohydrolase I reaction. <i>Journal of Biological Chemistry</i> , 2001 , 276, 2622-6	5-4	15
14	Biosynthesis of riboflavin. Single turnover kinetic analysis of GTP cyclohydrolase II. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44157-62	5-4	22
13	Biosynthesis of riboflavin: studies on the mechanism of GTP cyclohydrolase II. <i>Journal of Biological Chemistry</i> , 2001 , 276, 22273-7	5-4	39
12	Crystal structures of neuronal squid Sec1 implicate inter-domain hinge movement in the release of t-SNAREs. <i>Journal of Molecular Biology</i> , 2001 , 306, 7-13	6-5	33
11	Biosynthesis of pteridines. Stopped-flow kinetic analysis of GTP cyclohydrolase I. <i>Biochemistry</i> , 2001 , 40, 7896-902	3-2	27
10	Crystallization and preliminary X-ray analysis of squid neuronal Sec1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 501-3		5
9	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, 13567-72	11-5	117
8	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, 685-94	5-2	36
7	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, 16727-35	5-4	42
6	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, 521-7	3-4	9
5	Biosynthesis of pteridines. NMR studies on the reaction mechanisms of GTP cyclohydrolase I, pyruvoyltetrahydropterin synthase, and sepiapterin reductase. <i>Journal of Biological Chemistry</i> , 1998 , 273, 28132-41	5-4	52
4	Structure and mechanism of GTP cyclohydrolase I of <i>Escherichia coli</i> . <i>Biochemical Society Transactions</i> , 1996 , 24, 37S	5-1	7
3	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, 12120-5	11-5	110

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| 2 | Dual Role of a Rubisco Activase in Metabolic Repair and Carboxysome Organization | 3 |
| 1 | The Hsc70 Disaggregation Machinery Removes Monomer Units Directly from β -Synuclein Fibril Ends | 3 |