

# Beate Bersch

## List of Publications by Year in descending order

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50  
papers

1,444  
citations

331259

21  
h-index

329751

37  
g-index

51  
all docs

51  
docs citations

51  
times ranked

1817  
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct inhibition by nitric oxide of the transcriptional ferric uptake regulation protein via nitrosylation of the iron. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16619-16624.	3.3	162
2	Oxonol VI as an optical indicator for membrane potentials in lipid vesicles. Biochimica Et Biophysica Acta - Biomembranes, 1987, 903, 480-494.	1.4	159
3	Structural Changes of Escherichia coli Ferric Uptake Regulator during Metal-dependent Dimerization and Activation Explored by NMR and X-ray Crystallography. Journal of Biological Chemistry, 2006, 281, 21286-21295.	1.6	96
4	Structural Basis of Membrane Protein Chaperoning through the Mitochondrial Intermembrane Space. Cell, 2018, 175, 1365-1379.e25.	13.5	87
5	Proton-Detected Solid-State NMR Spectroscopy of a Zinc Diffusion Facilitator Protein in Native Nanodiscs. Angewandte Chemie - International Edition, 2017, 56, 2508-2512.	7.2	70
6	Structural biology of C1: dissection of a complex molecular machinery. Immunological Reviews, 2001, 180, 136-145.	2.8	69
7	Solution Structure of the Epidermal Growth Factor (EGF)-like Module of Human Complement Protease C1r, an Atypical Member of the EGF Family. Biochemistry, 1998, 37, 1204-1214.	1.2	50
8	New Insights into Histidine Triad Proteins: Solution Structure of a Streptococcus pneumoniae PhtD Domain and Zinc Transfer to AdcAll. PLoS ONE, 2013, 8, e81168.	1.1	48
9	How Detergent Impacts Membrane Proteins: Atomic-Level Views of Mitochondrial Carriers in Dodecylphosphocholine. Journal of Physical Chemistry Letters, 2018, 9, 933-938.	2.1	41
10	Reversible Redox- and Zinc-Dependent Dimerization of the Escherichia coli Fur Protein. Biochemistry, 2007, 46, 1329-1342.	1.2	40
11	Optimized set of two-dimensional experiments for fast sequential assignment, secondary structure determination, and backbone fold validation of <sup>13</sup> C/ <sup>15</sup> N-labelled proteins. Journal of Biomolecular NMR, 2003, 27, 57-67.	1.6	37
12	The mitochondrial carrier pathway transports non-canonical substrates with an odd number of transmembrane segments. BMC Biology, 2020, 18, 2.	1.7	34
13	Molecular Structure and Metal-binding Properties of the Periplasmic CopK Protein Expressed in Cupriavidus metallidurans CH34 During Copper Challenge. Journal of Molecular Biology, 2008, 380, 386-403.	2.0	30
14	Assessment of prediction methods for protein structures determined by NMR in CASP14: Impact of AlphaFold2. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	1.5	30
15	Structural and Metal Binding Characterization of the C-Terminal Metallochaperone Domain of Membrane Fusion Protein SilB from Cupriavidus metallidurans CH34. Biochemistry, 2011, 50, 2194-2204.	1.2	28
16	CopK from Cupriavidus metallidurans CH34 Binds Cu(I) in a Tetrathioether Site: Characterization by X-ray Absorption and NMR Spectroscopy. Journal of the American Chemical Society, 2010, 132, 3770-3777.	6.6	26
17	CopH from Cupriavidus metallidurans CH34. A Novel Periplasmic Copper-Binding Protein. Biochemistry, 2006, 45, 5557-5566.	1.2	25
18	Direct Structure Determination Using Residual Dipolar Couplings: Reaction-Site Conformation of Methionine Sulfoxide Reductase in Solution. Journal of the American Chemical Society, 2002, 124, 13709-13715.	6.6	24

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19	Solution Structure of the Sulfite Reductase Flavodoxin-like Domain from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2005, 44, 9086-9095.	1.2	23
20	Structure and functions of the interaction domains of C1r and C1s: keystones of the architecture of the C1 complex. <i>Immunopharmacology</i> , 1999, 42, 3-13.	2.0	22
21	Characterization of substance P-membrane interaction by transferred nuclear Overhauser effect. <i>Biopolymers</i> , 2000, 54, 297-306.	1.2	22
22	Study of the New Stability Properties Induced by Amino Acid Replacement of Tyrosine 64 in Cytochrome c553 from <i>Desulfovibrio vulgaris</i> Hildenborough Using Electrospray Ionization Mass Spectrometry. <i>Biochemical and Biophysical Research Communications</i> , 1996, 218, 97-103.	1.0	21
23	Biophysical characterization of the MerP-like amino-terminal extension of the mercuric reductase from <i>Ralstonia metallidurans</i> CH34. <i>Journal of Biological Inorganic Chemistry</i> , 2004, 9, 49-58.	1.1	21
24	Chemical synthesis and characterization of the epidermal growth factor $\alpha$ -like module of human complement protease C1r. <i>Chemical Biology and Drug Design</i> , 1997, 49, 221-231.	1.2	21
25	Structural basis of client specificity in mitochondrial membrane-protein chaperones. <i>Science Advances</i> , 2020, 6, .	4.7	21
26	Reactivity, Secondary Structure, and Molecular Topology of the <i>Escherichia coli</i> Sulfite Reductase Flavodoxin-like Domain. <i>Biochemistry</i> , 2002, 41, 3770-3780.	1.2	19
27	<sup>1</sup> H nuclear magnetic resonance determination of the membrane-bound conformation of senktide, a highly selective neurokinin B agonist. <i>Journal of Biomolecular NMR</i> , 1993, 3, 443-61.	1.6	18
28	Side Chain Orientation from Methyl <sup>1</sup> H $\rightarrow$ <sup>1</sup> H Residual Dipolar Couplings Measured in Highly Deuterated Proteins. <i>Journal of the American Chemical Society</i> , 2002, 124, 14616-14625.	6.6	18
29	How do Chaperones Bind (Partly) Unfolded Client Proteins?. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 762005.	1.6	17
30	Effects of the Tyr64 Substitution on the Stability of Cytochrome c553, a low Oxidoreduction-Potential Cytochrome from <i>Desulfovibrio vulgaris</i> Hildenborough. <i>FEBS Journal</i> , 1994, 226, 423-432.	0.2	16
31	Second Double-Stranded RNA Binding Domain of Dicer-like Ribonuclease 1: Structural and Biochemical Characterization. <i>Biochemistry</i> , 2012, 51, 10159-10166.	1.2	16
32	Structural and Functional Studies on C1r and C1s: New Insights into the Mechanisms Involved in C1 Activity and Assembly. <i>Immunobiology</i> , 1998, 199, 303-316.	0.8	15
33	Solution Structure of the C-terminal Domain of A20, the Missing Brick for the Characterization of the Interface between Vaccinia Virus DNA Polymerase and its Processivity Factor. <i>Journal of Molecular Biology</i> , 2021, 433, 167009.	2.0	14
34	Impact of selective excitation on carbon longitudinal relaxation: Towards fast solid-state NMR techniques. <i>Journal of Magnetic Resonance</i> , 2009, 200, 153-160.	1.2	13
35	Functional reconstitution of cell-free synthesized purified Kv channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 2373-2380.	1.4	13
36	Ectothiorhodospira halophila Ferrocyclochromec551: Solution Structure and Comparison with Bacterial Cytochromesc. <i>Journal of Molecular Biology</i> , 1996, 264, 567-584.	2.0	9

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37	Site-directed mutagenesis reveals a conservation of the copper-binding site and the crucial role of His24 in CopH from <i>Cupriavidus metallidurans</i> CH34. <i>Journal of Inorganic Biochemistry</i> , 2009, 103, 1721-1728.	1.5	9
38	Biostructural analysis of the metal-sensor domain of CnrX from <i>Cupriavidus metallidurans</i> CH34. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 141-148.	0.7	8
39	Dynamics and interactions of AAC3 in DPC are not functionally relevant. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 745-747.	3.6	8
40	<sup>1</sup> H and <sup>13</sup> C NMR Assignments and Structural Aspects of a Ferrocycytochrome c-551 from the Purple Phototrophic Bacterium <i>Ectothiorhodospira halophila</i> . <i>FEBS Journal</i> , 1995, 227, 249-260.	0.2	7
41	Composition and phase behaviour of polar lipids isolated from <i>Spirulina maxima</i> cells grown in a perdeuterated medium. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1996, 1284, 196-202.	1.4	7
42	<sup>1</sup> H-NMR study of the structural influence of Y64 substitution in <i>Desulfovibrio vulgaris</i> Hildenborough cytochrome c553. <i>FEBS Journal</i> , 1998, 251, 787-794.	0.2	7
43	A Recombinant Chimeric Epidermal Growth Factor-like Module with High Binding Affinity for Integrins. <i>Journal of Biological Chemistry</i> , 2003, 278, 19834-19843.	1.6	6
44	Structural and Functional Investigation of the Ag <sup>+</sup> /Cu <sup>+</sup> Binding Domains of the Periplasmic Adaptor Protein SilB from <i>Cupriavidus metallidurans</i> CH34. <i>Biochemistry</i> , 2016, 55, 2883-2897.	1.2	6
45	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N assignment of the flavodoxin-like domain of the <i>Escherichia coli</i> sulfite reductase. <i>Journal of Biomolecular NMR</i> , 2001, 21, 71-72.	1.6	5
46	New conformational properties induced by the replacement of Tyr-64 in <i>Desulfovibrio vulgaris</i> Hildenborough ferricytochrome c553 using isotopic exchanges monitored by mass spectrometry. <i>FEBS Letters</i> , 1996, 395, 53-57.	1.3	4
47	Backbone H(N), N, C $\alpha$ , C $\prime$ and C $\beta$ assignment of the 25 kDa peptide methionine sulfoxide reductase from <i>Erwinia chrysanthemi</i> . <i>Journal of Biomolecular NMR</i> , 2001, 20, 97-98.	1.6	2
48	Structural and Metal-Binding Characterization of the C-terminal Metallochaperone Domain of the Membrane Fusion Protein SilB from <i>Cupriavidus Metallidurans</i> CH34. <i>Biophysical Journal</i> , 2010, 98, 247a-248a.	0.2	0
49	Applications of Structural Biology and Bioinformatics in the Investigation of Oxidative Stress-Related Processes. , 2014, , 505-534.		0
50	Protein Structure and Dynamics by NMR in Solution. , 2000, , 91-116.		0