

Peter Bayer

List of Publications by Year in descending order

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218381

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docs citations

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times ranked

4194
citing authors

#	ARTICLE	IF	CITATIONS
1	Binding Methylarginines and Methyllysines as Free Amino Acids: A Comparative Study of Multiple Host Classes**. ChemBioChem, 2022, 23, .	1.3	4
2	Water-Based Synthesis of Ultrasmall Nanoparticles of Platinum Group Metal Oxides (1.8 nm). Inorganic Chemistry, 2022, 61, 5133-5147.	1.9	6
3	Targeting the Surface of the Protein 14â€³â€³ by Ultrasmall (1.5â€³...nm) Gold Nanoparticles Carrying the Specific Peptide CRaf. ChemBioChem, 2021, 22, 1456-1463.	1.3	10
4	Peptide-Conjugated Ultrasmall Gold Nanoparticles (2 nm) for Selective Protein Targeting. ACS Applied Bio Materials, 2021, 4, 945-965.	2.3	17
5	Specific inhibition of the Survivinâ€“CRM1 interaction by peptide-modified molecular tweezers. Nature Communications, 2021, 12, 1505.	5.8	18
6	Metalâ€“Ligand Interface and Internal Structure of Ultrasmall Silver Nanoparticles (2 nm). Journal of Physical Chemistry B, 2021, 125, 5645-5659.	1.2	10
7	New Tools to Probe the Protein Surface: Ultrasmall Gold Nanoparticles Carry Amino Acid Binders. Journal of Physical Chemistry B, 2021, 125, 115-127.	1.2	12
8	Functional Disruption of the Cancerâ€“Relevant Interaction between Survivin and Histone H3 with a Guanidiniocarbonyl Pyrrole Ligand. Angewandte Chemie - International Edition, 2020, 59, 5567-5571.	7.2	19
9	NMR Spectroscopy of supramolecular chemistry on protein surfaces. Beilstein Journal of Organic Chemistry, 2020, 16, 2505-2522.	1.3	3
10	The other side of the corona: nanoparticles inhibit the protease taspase1 in a size-dependent manner. Nanoscale, 2020, 12, 19093-19103.	2.8	7
11	Funktionelle Inhibition der krebsrelevanten Interaktion von Survivin und Histon H3 mit einem Guanidiniumcarbonylpyrrolâ€“Liganden. Angewandte Chemie, 2020, 132, 5614-5619.	1.6	3
12	Autoâ€“inhibition of Mif2/CENPâ€“ ensures centromereâ€“dependent kinetochore assembly in budding yeast. EMBO Journal, 2020, 39, e102938.	3.5	21
13	Targeting of parvulin interactors by diazirine mediated cross-linking discloses a cellular role of human Par14/17 in actin polymerization. Biological Chemistry, 2020, 401, 955-968.	1.2	1
14	Multivalent Ligands with Tailorâ€“Made Anion Binding Motif as Stabilizers of Proteinâ€“Protein Interactions. ChemBioChem, 2019, 20, 2921-2926.	1.3	13
15	Structural Analysis of the 42 kDa Parvulin of Trypanosoma brucei. Biomolecules, 2019, 9, 93.	1.8	0
16	Click Chemistry on the Surface of Ultrasmall Gold Nanoparticles (2 nm) for Covalent Ligand Attachment Followed by NMR Spectroscopy. Langmuir, 2019, 35, 7191-7204.	1.6	38
17	Structure of the PUB Domain from Ubiquitin Regulatory X Domain Protein 1 (UBXD1) and Its Interaction with the p97 AAA+ ATPase. Biomolecules, 2019, 9, 876.	1.8	5
18	Solution NMR Spectroscopy with Isotope-Labeled Cysteine (¹³C and ¹⁵N) Reveals the Surface Structure of <sc></sc>-Cysteine-Coated Ultrasmall Gold Nanoparticles (1.8) Tj ETQq0 0 0 rgBT /Overlook 10 Tf 50		

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19	Backbone and side-chain chemical shift assignments of full-length, apo, human Pin1, a phosphoprotein regulator with interdomain allostery. <i>Biomolecular NMR Assignments</i> , 2019, 13, 85-89.	0.4	6
20	Structure and function of the human parvulins Pin1 and Par14/17. <i>Biological Chemistry</i> , 2018, 399, 101-125.	1.2	29
21	Cell entry of a host-targeting protein of oomycetes requires gp96. <i>Nature Communications</i> , 2018, 9, 2347.	5.8	28
22	The RxLR Motif of the Host Targeting Effector AVR3a of <i>Phytophthora infestans</i> Is Cleaved before Secretion. <i>Plant Cell</i> , 2017, 29, 1184-1195.	3.1	123
23	NmPin from the marine thaumarchaeote <i>Nitrosopumilus maritimus</i> is an active membrane associated prolyl isomerase. <i>BMC Biology</i> , 2016, 14, 53.	1.7	8
24	Structural Characterization of the Loop at the Alpha-Subunit C-Terminus of the Mixed Lineage Leukemia Protein Activating Protease Taspase1. <i>PLoS ONE</i> , 2016, 11, e0151431.	1.1	8
25	Determinants of tyrosylprotein sulfation coding and substrate specificity of tyrosylprotein sulfotransferases in metazoans. <i>Chemico-Biological Interactions</i> , 2016, 259, 17-22.	1.7	7
26	Molecular tweezers target a protein-protein interface and thereby modulate complex formation. <i>Chemical Communications</i> , 2016, 52, 14141-14144.	2.2	16
27	Structural Model of the Bilirubin Translocase Transmembrane Domain Supported by NMR and FRET Data. <i>PLoS ONE</i> , 2015, 10, e0135455.	1.1	8
28	The N-terminal Region of the Ubiquitin Regulatory X (UBX) Domain-containing Protein 1 (UBXD1) Modulates Interdomain Communication within the Valosin-containing Protein p97. <i>Journal of Biological Chemistry</i> , 2015, 290, 29414-29427.	1.6	26
29	Heterodimers of Tyrosylprotein Sulfotransferases Suggest Existence of a Higher Organization Level of Transferases in the Membrane of the trans-Golgi Apparatus. <i>Journal of Molecular Biology</i> , 2015, 427, 1404-1412.	2.0	16
30	Human DNA-binding peptidyl-prolyl cis/trans isomerase Par14 is cell cycle dependently expressed and associates with chromatin in vivo. <i>BMC Biochemistry</i> , 2015, 16, 4.	4.4	9
31	Peptidyl Succinimidyl Peptides as Taspase 1 Inhibitors. <i>ChemBioChem</i> , 2014, 15, 2233-2237.	1.3	14
32	Transient Domain Interactions Enhance the Affinity of the Mitotic Regulator Pin1 toward Phosphorylated Peptide Ligands. <i>Structure</i> , 2013, 21, 1769-1777.	1.6	24
33	Identification and characterization of peptides that bind the PPlase domain of Parvulin17. <i>Journal of Peptide Science</i> , 2013, 19, 362-369.	0.8	13
34	Design of a Modular Protein-Based MRI Contrast Agent for Targeted Application. <i>PLoS ONE</i> , 2013, 8, e65346.	1.1	13
35	Host-targeting protein 1 (SpHtp1) from the oomycete <i>Saprolegnia parasitica</i> translocates specifically into fish cells in a tyrosine-O-sulphate-dependent manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2096-2101.	3.3	79
36	Structure of the corrinoid:coenzyme M methyltransferase MtaA from <i>Methanosarcina mazei</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1549-1557.	2.5	7

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37	Human PAPS Synthase Isoforms Are Dynamically Regulated Enzymes with Access to Nucleus and Cytoplasm. <i>PLoS ONE</i> , 2012, 7, e29559.	1.1	31
38	Crystallographic Proof for an Extended Hydrogen-Bonding Network in Small Prolyl Isomerases. <i>Journal of the American Chemical Society</i> , 2011, 133, 20096-20099.	6.6	30
39	A potential transcriptional regulator is out-of-frame translated from the metallothionein 2A messenger RNA. <i>Analytical Biochemistry</i> , 2011, 409, 159-161.	1.1	9
40	Single-Domain Parvulins Constitute a Specific Marker for Recently Proposed Deep-Branching Archaeal Subgroups. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S7683.	0.6	4
41	Structure and Dynamics of the First Archaeal Parvulin Reveal a New Functionally Important Loop in Parvulin-type Prolyl Isomerases. <i>Journal of Biological Chemistry</i> , 2011, 286, 6554-6565.	1.6	23
42	The solution structure of pGolemi, a high affinity Mena EVH1 binding miniature protein, suggests explanations for paralog-specific binding to Ena/VASP homology (EVH) 1 domains. <i>Biological Chemistry</i> , 2009, 390, 417-426.	1.2	2
43	Small Family with Key Contacts: Par14 and Par17 Parvulin Proteins, Relatives of Pin1, Now Emerge in Biomedical Research. <i>Perspectives in Medicinal Chemistry</i> , 2008, 2, PMC.S496.	4.6	22
44	The DNA binding parvulin Par17 is targeted to the mitochondrial matrix by a recently evolved prepeptide uniquely present in Hominidae. <i>BMC Biology</i> , 2007, 5, 37.	1.7	29
45	15N magnetic relaxation study of backbone dynamics of the ribosome-associated cold shock response protein Yfia of <i>Escherichia coli</i> . <i>Acta Biochimica Polonica</i> , 2007, 54, 769-775.	0.3	7
46	Human TPST1 Transmembrane Domain Triggers Enzyme Dimerisation and Localisation to the Golgi Compartment. <i>Journal of Molecular Biology</i> , 2006, 361, 436-449.	2.0	24
47	Isotopic labeling of recombinant proteins expressed in the protozoan host <i>Leishmania tarentolae</i> . <i>Protein Expression and Purification</i> , 2006, 48, 167-172.	0.6	15
48	Characterization of novel elongated Parvulin isoforms that are ubiquitously expressed in human tissues and originate from alternative transcription initiation. <i>BMC Molecular Biology</i> , 2006, 7, 9.	3.0	35
49	GTP-Ras Disrupts the Intramolecular Complex of C1 and RA Domains of Nore1. <i>Structure</i> , 2006, 14, 881-888.	1.6	60
50	Specification of SUMO1- and SUMO2-interacting Motifs*. <i>Journal of Biological Chemistry</i> , 2006, 281, 16117-16127.	1.6	491
51	Identification of hPin1 inhibitors that induce apoptosis in a mammalian Ras transformed cell line. <i>Chemical Communications</i> , 2005, , 516.	2.2	25
52	The Crystal Structure of Human PAPS Synthetase 1 Reveals Asymmetry in Substrate Binding. <i>Journal of Molecular Biology</i> , 2005, 347, 623-635.	2.0	45
53	Structure and function of the phenazine biosynthetic protein PhzF from <i>Pseudomonas fluorescens</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16431-16436.	3.3	92
54	Expression, purification and crystallization of human 3â€²-phosphoadenosine-5â€²-phosphosulfate synthetase 1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 350-352.	2.5	8

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55	Phosphorylation of the N-terminal Domain Regulates Subcellular Localization and DNA Binding Properties of the Peptidyl-prolyl cis/trans Isomerase hPar14. <i>Journal of Molecular Biology</i> , 2003, 330, 955-966.	2.0	26
56	Structural Analysis of the Mitotic Regulator hPin1 in Solution. <i>Journal of Biological Chemistry</i> , 2003, 278, 26183-26193.	1.6	115
57	Shear stress mediates tyrosylprotein sulfotransferase isoform shift in human endothelial cells. <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 541-546.	1.0	15
58	Solution structure of the ribosome-associated cold shock response protein Yfia of <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2002, 299, 710-714.	1.0	21
59	The N-terminal Basic Domain of Human Parvulin hPar14 is Responsible for the Entry to the Nucleus and High-affinity DNA-binding. <i>Journal of Molecular Biology</i> , 2002, 321, 235-247.	2.0	32
60	Structural attributes in the conjugation of Ubiquitin SUMO and RUB to protein substrates. <i>Frontiers in Bioscience - Landmark</i> , 2002, 7, a148-162.	3.0	0
61	¹ H, ¹³ C and ¹⁵ N resonance assignments of the ribosome-associated cold shock response protein Yfia of <i>Escherichia coli</i> . <i>Journal of Biomolecular NMR</i> , 2002, 23, 335-336.	1.6	7
62	Structural attributes in the conjugation of Ubiquitin, SUMO and RUB to protein substrates. <i>Frontiers in Bioscience - Landmark</i> , 2002, 7, a148.	3.0	11
63	Increased Backbone Flexibility in Threonine45-Phosphorylated Hirudin upon pH Change. <i>Biochemistry</i> , 2001, 40, 7957-7963.	1.2	11
64	Structure prediction of protein complexes by an NMR-based protein docking algorithm. <i>Journal of Biomolecular NMR</i> , 2001, 20, 15-21.	1.6	16
65	[¹⁴ N] Nuclear magnetic resonance methods to study RNA-protein complexes. <i>Methods in Enzymology</i> , 2000, 317, 198-220.	0.4	3
66	Solution Structures of Human Parathyroid Hormone Fragments hPTH(1-34) and hPTH(1-39) and Bovine Parathyroid Hormone Fragment bPTH(1-37). <i>Biochemical and Biophysical Research Communications</i> , 2000, 267, 213-220.	1.0	70
67	NMR solution structure of h Par14 reveals similarity to the peptidyl prolyl cis/trans isomerase domain of the mitotic regulator h Pin1 but indicates a different functionality of the protein 1 Edited by A. Fersht. <i>Journal of Molecular Biology</i> , 2000, 301, 1003-1017.	2.0	60
68	Refinement of the structure of protein-RNA complexes by residual dipolar coupling analysis. <i>Journal of Biomolecular NMR</i> , 1999, 14, 149-155.	1.6	69
69	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain from <i>Drosophila</i> Staufen protein. <i>Biopolymers</i> , 1999, 52, 181-196.	1.2	22
70	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain from <i>Drosophila</i> Staufen protein. , 1999, 52, 181.		1
71	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain from <i>Drosophila</i> Staufen protein. , 1999, 52, 181.		1
72	Structure Determination of the Ras-Binding Domain of the Ral-Specific Guanine Nucleotide Exchange Factor Rlf. <i>Biochemistry</i> , 1998, 37, 13453-13462.	1.2	40

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73	Equine infectious anemia virus transactivator is a homeodomain-type protein 1 Edited by J. Karn. Journal of Molecular Biology, 1998, 277, 749-755.	2.0	8
74	Structure determination of the small ubiquitin-related modifier SUMO-1. Journal of Molecular Biology, 1998, 280, 275-286.	2.0	356
75	Structure-Activity Relation of NH2-terminal Human Parathyroid Hormone Fragments. Journal of Biological Chemistry, 1998, 273, 4308-4316.	1.6	25
76	The Cdc42/Rac Interactive Binding Region Motif of the Wiskott Aldrich Syndrome Protein (WASP) Is Necessary but Not Sufficient for Tight Binding to Cdc42 and Structure Formation. Journal of Biological Chemistry, 1998, 273, 18067-18076.	1.6	128
77	The Interaction of HIV-1 Tat(32-72) with its Target RNA: A Fluorescence and Nuclear Magnetic Resonance Study. Biochemical and Biophysical Research Communications, 1997, 241, 31-36.	1.0	20
78	Spectroscopic investigations of HIV-1 trans-activator and related peptides in aqueous solutions. Biophysical Chemistry, 1997, 63, 87-96.	1.5	8
79	Secondary structure of an armadillo single repeat from the APC protein. FEBS Letters, 1996, 383, 31-36.	1.3	12
80	Sequence-Specific Resonance Assignments of the 1H-NMR Spectra and Structural Characterization in Solution of the HIV-1 Transframe Protein p6*. FEBS Journal, 1996, 237, 383-392.	0.2	29
81	The Structure of Lentiviral Tat Proteins in Solution. , 1996, , 287-303.		0
82	Structure of Amyloid A4-(1-40)-Peptide of Alzheimer's Disease. FEBS Journal, 1995, 233, 293-298.	0.2	273
83	Nonenzymatic hydrolysis of adenosinetriphosphate (ATP) at high temperatures and high pressures. Biophysical Chemistry, 1995, 54, 175-180.	1.5	28
84	Structure of Human Parathyroid Hormone 1 α 37 in Solution. Journal of Biological Chemistry, 1995, 270, 15194-15202.	1.6	66
85	Structural studies of HIV-1 tat protein. Journal of Molecular Biology, 1995, 247, 529-535.	2.0	120
86	Structural studies of HIV-1 Tat protein. Journal of Molecular Biology, 1995, 247, 529-535.	2.0	170
87	Equine infectious anemia virus Tat is a predominantly helical protein. FEBS Journal, 1993, 218, 973-976.	0.2	24