## Peter Bayer

## List of Publications by Year in descending order

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		218381	155451
87	3,388	26	55
papers	citations	h-index	g-index
07	07	07	4104
0/	07	0/	4134
all docs	docs citations	times ranked	citing authors
87 all docs	87 docs citations	87 times ranked	4194 citing authors

#	Article	IF	CITATIONS
1	Specification of SUMO1- and SUMO2-interacting Motifs*. Journal of Biological Chemistry, 2006, 281, 16117-16127.	1.6	491
2	Structure determination of the small ubiquitin-related modifier SUMO-1. Journal of Molecular Biology, 1998, 280, 275-286.	2.0	356
3	Structure of Amyloid A4-(1-40)-Peptide of Alzheimer's Disease. FEBS Journal, 1995, 233, 293-298.	0.2	273
4	Structural studies of HIV-1 Tat protein. Journal of Molecular Biology, 1995, 247, 529-535.	2.0	170
5	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
6	The RxLR Motif of the Host Targeting Effector AVR3a of <i>Phytophthora infestans</i> Is Cleaved before Secretion. Plant Cell, 2017, 29, 1184-1195.	3.1	123
7	Structural studies of HIV-1 tat protein. Journal of Molecular Biology, 1995, 247, 529-535.	2.0	120
8	Structural Analysis of the Mitotic Regulator hPin1 in Solution. Journal of Biological Chemistry, 2003, 278, 26183-26193.	1.6	115
9	Structure and function of the phenazine biosynthetic protein PhzF from Pseudomonas fluorescens. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16431-16436.	3.3	92
10	Host-targeting protein 1 (SpHtp1) from the oomycete <i>Saprolegnia parasitica</i> translocates specifically into fish cells in a tyrosine-O-sulphate–dependent manner. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2096-2101.	3.3	79
11	Solution Structures of Human Parathyroid Hormone Fragments hPTH(1–34) and hPTH(1–39) and Bovine Parathyroid Hormone Fragment bPTH(1–37). Biochemical and Biophysical Research Communications, 2000, 267, 213-220.	1.0	70
12	Refinement of the structure of protein-RNA complexes by residual dipolar coupling analysis. Journal of Biomolecular NMR, 1999, 14, 149-155.	1.6	69
13	Structure of Human Parathyroid Hormone 1–37 in Solution. Journal of Biological Chemistry, 1995, 270, 15194-15202.	1.6	66
14	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 1Edited by A. Fersht. Journal of Molecular Biology, 2000, 301, 1003-1017.	2.0	60
15	GTP-Ras Disrupts the Intramolecular Complex of C1 and RA Domains of Nore1. Structure, 2006, 14, 881-888.	1.6	60
16	The Crystal Structure of Human PAPS Synthetase 1 Reveals Asymmetry in Substrate Binding. Journal of Molecular Biology, 2005, 347, 623-635.	2.0	45
17	Structure Determination of the Ras-Binding Domain of the Ral-Specific Guanine Nucleotide Exchange Factor Rlf,. Biochemistry, 1998, 37, 13453-13462.	1.2	40
18	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

#	Article	IF	CITATIONS
19	Characterization of novel elongated Parvulin isoforms that are ubiquitously expressed in human tissues and originate from alternative transcription initiation. BMC Molecular Biology, 2006, 7, 9.	3.0	35
20	The N-terminal Basic Domain of Human Parvulin hPar14 is Responsible for the Entry to the Nucleus and High-affinity DNA-binding. Journal of Molecular Biology, 2002, 321, 235-247.	2.0	32
21	Human PAPS Synthase Isoforms Are Dynamically Regulated Enzymes with Access to Nucleus and Cytoplasm. PLoS ONE, 2012, 7, e29559.	1.1	31
22	Crystallographic Proof for an Extended Hydrogen-Bonding Network in Small Prolyl Isomerases. Journal of the American Chemical Society, 2011, 133, 20096-20099.	6.6	30
23	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
24	The DNA binding parvulin Par17 is targeted to the mitochondrial matrix by a recently evolved prepeptide uniquely present in Hominidae. BMC Biology, 2007, 5, 37.	1.7	29
25	Structure and function of the human parvulins Pin1 and Par14/17. Biological Chemistry, 2018, 399, 101-125.	1.2	29
26	Nonenzymatic hydrolysis of adenosinetriphosphate (ATP) at high temperatures and high pressures. Biophysical Chemistry, 1995, 54, 175-180.	1.5	28
27	Cell entry of a host-targeting protein of oomycetes requires gp96. Nature Communications, 2018, 9, 2347.	5.8	28
28	Solution NMR Spectroscopy with Isotope-Labeled Cysteine ( $<$ sup $>$ 13 $<$ /sup $>$ C and $<$ sup $>$ 15 $<$ /sup $>$ N) Reveals the Surface Structure of $<$ scp $>$ 1 $<$ /scp $>$ -Cysteine-Coated Ultrasmall Gold Nanoparticles (1.8) Tj ETQq0 0	0 rgB√r/Ov	erloook 10 Tf 5
29	Phosphorylation of the N-terminal Domain Regulates Subcellular Localization and DNA Binding Properties of the Peptidyl-prolyl cis/trans Isomerase hPar14. Journal of Molecular Biology, 2003, 330, 955-966.	2.0	26
30	The N-terminal Region of the Ubiquitin Regulatory X (UBX) Domain-containing Protein 1 (UBXD1) Modulates Interdomain Communication within the Valosin-containing Protein p97. Journal of Biological Chemistry, 2015, 290, 29414-29427.	1.6	26
31	Structure-Activity Relation of NH2-terminal Human Parathyroid Hormone Fragments. Journal of Biological Chemistry, 1998, 273, 4308-4316.	1.6	25
32	Identification of hPin1 inhibitors that induce apoptosis in a mammalian Ras transformed cell line. Chemical Communications, 2005, , 516.	2.2	25
33	Equine infectious anemia virus Tat is a predominantly helical protein. FEBS Journal, 1993, 218, 973-976.	0.2	24
34	Human TPST1 Transmembrane Domain Triggers Enzyme Dimerisation and Localisation to the Golgi Compartment. Journal of Molecular Biology, 2006, 361, 436-449.	2.0	24
35	Transient Domain Interactions Enhance the Affinity of the Mitotic Regulator Pin1 toward Phosphorylated Peptide Ligands. Structure, 2013, 21, 1769-1777.	1.6	24
36	Structure and Dynamics of the First Archaeal Parvulin Reveal a New Functionally Important Loop in Parvulin-type Prolyl Isomerases. Journal of Biological Chemistry, 2011, 286, 6554-6565.	1.6	23

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37	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain fromDrosophila Staufen protein. Biopolymers, 1999, 52, 181-196.	1.2	22
38	Small Family with Key Contacts: Par14 and Par17 Parvulin Proteins, Relatives of Pin1, Now Emerge in Biomedical Research. Perspectives in Medicinal Chemistry, 2008, 2, PMC.S496.	4.6	22
39	Solution structure of the ribosome-associated cold shock response protein Yfia of Escherichia coli. Biochemical and Biophysical Research Communications, 2002, 299, 710-714.	1.0	21
40	Autoâ€inhibition of Mif2/CENPâ€C ensures centromereâ€dependent kinetochore assembly in budding yeast. EMBO Journal, 2020, 39, e102938.	3 <b>.</b> 5	21
41	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
42	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
43	Specific inhibition of the Survivin–CRM1 interaction by peptide-modified molecular tweezers. Nature Communications, 2021, 12, 1505.	5.8	18
44	Peptide-Conjugated Ultrasmall Gold Nanoparticles (2 nm) for Selective Protein Targeting. ACS Applied Bio Materials, 2021, 4, 945-965.	2.3	17
45	Structure prediction of protein complexes by an NMR-based protein docking algorithm. Journal of Biomolecular NMR, 2001, 20, 15-21.	1.6	16
46	Heterodimers of Tyrosylprotein Sulfotransferases Suggest Existence of a Higher Organization Level of Transferases in the Membrane of the trans-Golgi Apparatus. Journal of Molecular Biology, 2015, 427, 1404-1412.	2.0	16
47	Molecular tweezers target a protein–protein interface and thereby modulate complex formation. Chemical Communications, 2016, 52, 14141-14144.	2.2	16
48	Shear stress mediates tyrosylprotein sulfotransferase isoform shift in human endothelial cells. Biochemical and Biophysical Research Communications, 2002, 294, 541-546.	1.0	15
49	Isotopic labeling of recombinant proteins expressed in the protozoan host Leishmania tarentolae. Protein Expression and Purification, 2006, 48, 167-172.	0.6	15
50	Peptidyl Succinimidyl Peptides as Taspase 1 Inhibitors. ChemBioChem, 2014, 15, 2233-2237.	1.3	14
51	Identification and characterization of peptides that bind the PPlase domain of Parvulin17. Journal of Peptide Science, 2013, 19, 362-369.	0.8	13
52	Design of a Modular Protein-Based MRI Contrast Agent for Targeted Application. PLoS ONE, 2013, 8, e65346.	1.1	13
53	Multivalent Ligands with Tailorâ€Made Anion Binding Motif as Stabilizers of Protein–Protein Interactions. ChemBioChem, 2019, 20, 2921-2926.	1.3	13
54	Secondary structure of an armadillo single repeat from the APC protein. FEBS Letters, 1996, 383, 31-36.	1.3	12

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55	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
56	Increased Backbone Flexibility in Threonine45-Phosphorylated Hirudin upon pH Change. Biochemistry, 2001, 40, 7957-7963.	1.2	11
57	Structural attributes in the conjugation of Ubiquitin, SUMO and RUB to protein substrates. Frontiers in Bioscience - Landmark, 2002, 7, a148.	3.0	11
58	Targeting the Surface of the Protein 14â€3â€3 by Ultrasmall (1.5â€nm) Gold Nanoparticles Carrying the Specific Peptide CRaf. ChemBioChem, 2021, 22, 1456-1463.	1.3	10
59	Metal–Ligand Interface and Internal Structure of Ultrasmall Silver Nanoparticles (2 nm). Journal of Physical Chemistry B, 2021, 125, 5645-5659.	1.2	10
60	A potential transcriptional regulator is out-of-frame translated from the metallothionein 2A messenger RNA. Analytical Biochemistry, 2011, 409, 159-161.	1.1	9
61	Human DNA-binding peptidyl-prolyl cis/trans isomerase Par14 is cell cycle dependently expressed and associates with chromatin in vivo. BMC Biochemistry, 2015, 16, 4.	4.4	9
62	Spectroscopic investigations of HIV-1 trans-activator and related peptides in aqueous solutions. Biophysical Chemistry, 1997, 63, 87-96.	1.5	8
63	Equine infectious anemia virus transactivator is a homeodomain-type protein 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 277, 749-755.	2.0	8
64	Expression, purification and crystallization of human 3′-phosphoadenosine-5′-phosphosulfate synthetase 1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 350-352.	2.5	8
65	Structural Model of the Bilitranslocase Transmembrane Domain Supported by NMR and FRET Data. PLoS ONE, 2015, 10, e0135455.	1.1	8
66	NmPin from the marine thaumarchaeote Nitrosopumilus maritimus is an active membrane associated prolyl isomerase. BMC Biology, 2016, 14, 53.	1.7	8
67	Structural Characterization of the Loop at the Alpha-Subunit C-Terminus of the Mixed Lineage Leukemia Protein Activating Protease Taspase1. PLoS ONE, 2016, 11, e0151431.	1.1	8
68	1H, 13C and 15N resonance assignments of the ribosome-associated cold shock response protein Yfia of Escherichia coli. Journal of Biomolecular NMR, 2002, 23, 335-336.	1.6	7
69	Structure of the corrinoid:coenzyme M methyltransferase MtaA from <i>Methanosarcina mazei</i> Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1549-1557.	2.5	7
70	Determinants of tyrosylprotein sulfation coding and substrate specificity of tyrosylprotein sulfotransferases in metazoans. Chemico-Biological Interactions, 2016, 259, 17-22.	1.7	7
71	The other side of the corona: nanoparticles inhibit the protease taspase1 in a size-dependent manner. Nanoscale, 2020, 12, 19093-19103.	2.8	7
72	15N magnetic relaxation study of backbone dynamics of the ribosome-associated cold shock response protein Yfia of Escherichia coli Acta Biochimica Polonica, 2007, 54, 769-775.	0.3	7

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73	Backbone and side-chain chemical shift assignments of full-length, apo, human Pin1, a phosphoprotein regulator with interdomain allostery. Biomolecular NMR Assignments, 2019, 13, 85-89.	0.4	6
74	Water-Based Synthesis of Ultrasmall Nanoparticles of Platinum Group Metal Oxides (1.8 nm). Inorganic Chemistry, 2022, 61, 5133-5147.	1.9	6
75	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
76	Single-Domain Parvulins Constitute a Specific Marker for Recently Proposed Deep-Branching Archaeal Subgroups. Evolutionary Bioinformatics, 2011, 7, EBO.S7683.	0.6	4
77	Binding Methylarginines and Methyllysines as Free Amino Acids: A Comparative Study of Multiple Host Classes**. ChemBioChem, 2022, 23, .	1.3	4
78	[14] Nuclear magnetic resonance methods to study RNA-protein complexes. Methods in Enzymology, 2000, 317, 198-220.	0.4	3
79	NMR Spectroscopy of supramolecular chemistry on protein surfaces. Beilstein Journal of Organic Chemistry, 2020, 16, 2505-2522.	1.3	3
80	Funktionelle Inhibition der krebsrelevanten Interaktion von Survivin und Histon H3 mit einem Guanidiniumcarbonylpyrrol‣iganden. Angewandte Chemie, 2020, 132, 5614-5619.	1.6	3
81	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. Biological Chemistry, 2009, 390, 417-426.	1.2	2
82	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain from Drosophila Staufen protein., 1999, 52, 181.		1
83	Determination of the structure of the RNA complex of a double-stranded RNA-binding domain from Drosophila Staufen protein. , 1999, 52, 181.		1
84	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
85	Structural attributes in the conjugation of Ubiquitin SUMO and RUB to protein substrates. Frontiers in Bioscience - Landmark, 2002, 7, a148-162.	3.0	O
86	Structural Analysis of the 42 kDa Parvulin of Trypanosoma brucei. Biomolecules, 2019, 9, 93.	1.8	0
87	The Structure of Lentiviral Tat Proteins in Solution. , 1996, , 287-303.		0