

# Bruno Kieffer

## List of Publications by Year in descending order

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64  
papers

1,942  
citations

257450

24  
h-index

265206

42  
g-index

66  
all docs

66  
docs citations

66  
times ranked

2743  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and distribution of modules in extracellular proteins. Quarterly Reviews of Biophysics, 1996, 29, 119-167.	5.7	307
2	Structural and Functional Analysis of E6 Oncoprotein: Insights in the Molecular Pathways of Human Papillomavirus-Mediated Pathogenesis. Molecular Cell, 2006, 21, 665-678.	9.7	162
3	Solution Structure Analysis of the HPV16 E6 Oncoprotein Reveals a Self-Association Mechanism Required for E6-Mediated Degradation of p53. Structure, 2012, 20, 604-617.	3.3	104
4	Structural and Biological Characterization of Chromofungin, the Antifungal Chromogranin A-(47-66)-derived Peptide. Journal of Biological Chemistry, 2001, 276, 35875-35882.	3.4	87
5	TFIIH contains a PH domain involved in DNA nucleotide excision repair. Nature Structural and Molecular Biology, 2004, 11, 616-622.	8.2	78
6	Efficient denoising algorithms for large experimental datasets and their applications in Fourier transform ion cyclotron resonance mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1385-1390.	7.1	63
7	Thermodynamics of Zn <sup>2+</sup> Binding to Cys <sub>2</sub> His <sub>2</sub> and Cys <sub>2</sub> HisCys Zinc Fingers and a Cys <sub>4</sub> Transcription Factor Site. Journal of the American Chemical Society, 2012, 134, 10405-10418.	13.7	62
8	Structures and dynamics of hibernating ribosomes from <i>Staphylococcus aureus</i> mediated by intermolecular interactions of HPF. EMBO Journal, 2017, 36, 2073-2087.	7.8	62
9	Characterization of Antibacterial COOH-terminal Proenkephalin-A-derived Peptides (PEAP) in Infectious Fluids. Journal of Biological Chemistry, 1998, 273, 29847-29856.	3.4	61
10	Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. Nature Communications, 2016, 7, 12621.	12.8	48
11	Solution Structure of the N-terminal Domain of the Human TFIIH MAT1 Subunit. Journal of Biological Chemistry, 2001, 276, 7457-7464.	3.4	44
12	The role of protein motions in molecular recognition: insights from heteronuclear NMR relaxation measurements. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 44, 141-187.	7.5	44
13	The Structural and Dynamic Response of MAGI-1 PDZ1 with Noncanonical Domain Boundaries to the Binding of Human Papillomavirus E6. Journal of Molecular Biology, 2011, 406, 745-763.	4.2	43
14	Putting into Practice Domain-Linear Motif Interaction Predictions for Exploration of Protein Networks. PLoS ONE, 2011, 6, e25376.	2.5	37
15	The Solution Structure and Self-Association Properties of the Cyclic Lipodepsipeptide Pseudodesmin Support Its Pore-Forming Potential. Chemistry - A European Journal, 2009, 15, 12653-12662.	3.3	34
16	Surface plasmon resonance analysis of the binding of high-risk mucosal HPV E6 oncoproteins to the PDZ1 domain of the tight junction protein MAGI-1. Journal of Molecular Recognition, 2011, 24, 511-523.	2.1	34
17	Effects of temperature on the dynamic behaviour of the HIV-1 nucleocapsid NCp7 and its DNA complex. Journal of Molecular Biology, 2002, 316, 611-627.	4.2	31
18	Solution Structure and Self-association Properties of the p8 TFIIH Subunit Responsible for Trichothiodystrophy. Journal of Molecular Biology, 2007, 368, 473-480.	4.2	31

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19	ZMIZ1 Variants Cause a Syndromic Neurodevelopmental Disorder. <i>American Journal of Human Genetics</i> , 2019, 104, 319-330.	6.2	30
20	Structural Characterization of the Cysteine-rich Domain of TFIIH p44 Subunit. <i>Journal of Biological Chemistry</i> , 2000, 275, 31963-31971.	3.4	28
21	Two-Point Self-Coordination of a Dizinc(II) Bispyridylporphyrin Ruthenium Complex Leading Selectively to a Discrete Molecular Assembly: Solution and Solid-State Characterization. <i>Chemistry - A European Journal</i> , 2002, 8, 4670-4674.	3.3	28
22	Solution Structure of the C-terminal Domain of TFIIH P44 Subunit Reveals a Novel Type of C4C4 Ring Domain Involved in Protein-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2005, 280, 20785-20792.	3.4	28
23	The structural plasticity of SCA7 domains defines their differential nucleosome-binding properties. <i>EMBO Reports</i> , 2010, 11, 612-618.	4.5	28
24	Minimising conformational bias in fluoroprolines through vicinal difluorination. <i>Chemical Communications</i> , 2018, 54, 5118-5121.	4.1	28
25	Vinexin <sup>2</sup> , an atypical co-sensor of retinoic acid receptor <sup>3</sup> signaling: union and sequestration, separation, and phosphorylation. <i>FASEB Journal</i> , 2010, 24, 4523-4534.	0.5	26
26	Solution structure of the 5'-terminal hairpin of the 7SK small nuclear RNA. <i>Rna</i> , 2016, 22, 1844-1858.	3.5	26
27	A fully enzymatic method for site-directed spin labeling of long RNA. <i>Nucleic Acids Research</i> , 2014, 42, e117-e117.	14.5	25
28	Combining inducible protein overexpression with NMR-grade triple isotope labeling in the cyanobacterium <i>Anabaena</i> sp. PCC 7120. <i>BioTechniques</i> , 2005, 39, 405-411.	1.8	23
29	Dynamics and Metal Exchange Properties of C4C4 RING Domains from CNOT4 and the p44 Subunit of TFIIH. <i>Journal of Molecular Biology</i> , 2005, 349, 621-637.	4.2	21
30	DNA Binding by Sgf11 Protein Affects Histone H2B Ubiquitination by Spt-Ada-Gcn5-Acetyltransferase (SAGA). <i>Journal of Biological Chemistry</i> , 2014, 289, 8989-8999.	3.4	21
31	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor <sup>1</sup> in the Context of the Full-Length Protein. <i>Biochemistry</i> , 2016, 55, 1741-1748.	2.5	19
32	Molecular determinants of MED1 interaction with the DNA bound VDR-RXR heterodimer. <i>Nucleic Acids Research</i> , 2020, 48, 11199-11213.	14.5	17
33	<sup>1</sup> H and <sup>15</sup> N resonance assignment, secondary structure and dynamic behaviour of the C-terminal domain of human papillomavirus oncoprotein E6. <i>Journal of Biomolecular NMR</i> , 2005, 31, 129-141.	2.8	16
34	Defining the minimal interacting regions of the tight junction protein MAGI-1 and HPV16 E6 oncoprotein for solution structure studies. <i>Protein Expression and Purification</i> , 2008, 60, 64-73.	1.3	16
35	Structural studies of two antiaggregant RGDW peptides by <sup>1</sup> H and <sup>13</sup> C NMR. <i>International Journal of Peptide and Protein Research</i> , 1994, 44, 70-79.	0.1	16
36	Synthesis and Conformational Properties of 3,4-Difluoro- <i>l</i> -prolines. <i>Journal of Organic Chemistry</i> , 2019, 84, 3100-3120.	3.2	16

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37	Human H4 tail stimulates HIV-1 integration through binding to the carboxy-terminal domain of integrase. <i>Nucleic Acids Research</i> , 2019, 47, 3607-3618.	14.5	15
38	Solution Conformation of the Synthetic Bovine Proenkephalin-A209-237 by 1H NMR Spectroscopy. <i>Journal of Biological Chemistry</i> , 1998, 273, 33517-33523.	3.4	13
39	Prevalence of intrinsic disorder in the hepatitis C virus ARFP/Core+1/S protein. <i>FEBS Journal</i> , 2010, 277, 774-789.	4.7	13
40	Cost-Effective and Uniform 13C- and 15N-Labeling of the 24-kDa N-Terminal Domain of the Escherichia coli Gyrase B by Overexpression in the Photoautotrophic Cyanobacterium Anabaena sp. PCC 7120. <i>Protein Expression and Purification</i> , 2001, 23, 207-217.	1.3	11
41	Strategies for bacterial expression of protein-peptide complexes: Application to solubilization of papillomavirus E6. <i>Protein Expression and Purification</i> , 2011, 80, 8-16.	1.3	11
42	Insight into peptide self-assembly from anisotropic rotational diffusion derived from 13C NMR relaxation. <i>Chemical Science</i> , 2012, 3, 1284.	7.4	11
43	SECIS-binding protein 2, a key player in selenoprotein synthesis, is an intrinsically disordered protein. <i>Biochimie</i> , 2009, 91, 1003-1009.	2.6	10
44	Unraveling Complex Small-Molecule Binding Mechanisms by Using Simple NMR Spectroscopy. <i>Chemistry - A European Journal</i> , 2012, 18, 3969-3974.	3.3	10
45	Disorder-To-Order Transition of MAGI-1 PDZ1 C-Terminal Extension upon Peptide Binding: Thermodynamic and Dynamic Insights. <i>Biochemistry</i> , 2015, 54, 1327-1337.	2.5	10
46	Modulation of RXR-DNA complex assembly by DNA context. <i>Molecular and Cellular Endocrinology</i> , 2019, 481, 44-52.	3.2	9
47	Automated overexpression and isotopic labelling of biologically active oncoproteins in the cyanobacterium Anabaena sp. PCC 7120. <i>Biotechnology and Applied Biochemistry</i> , 2008, 51, 53.	3.1	7
48	Thermal stability of chicken brain $\beta$ -spectrin repeat 17: a spectroscopic study. <i>Journal of Biomolecular NMR</i> , 2012, 53, 71-83.	2.8	7
49	Structural and dynamic studies of two antigenic loops from haemagglutinin: A relaxation matrix approach. <i>Journal of Biomolecular NMR</i> , 1993, 3, 91-112.	2.8	6
50	Structure-function studies of CD2 by n.m.r. and mutagenesis. <i>Biochemical Society Transactions</i> , 1993, 21, 947-952.	3.4	6
51	Total chemical synthesis and biophysical properties of a designed soluble 24 kDa amyloid analogue. <i>Chemical Science</i> , 2018, 9, 5594-5599.	7.4	6
52	NMR WaterLOGSY Reveals Weak Binding of Bisphenol A with Amyloid Fibers of a Conserved 11 Residue Peptide from Androgen Receptor. <i>PLoS ONE</i> , 2016, 11, e0161948.	2.5	6
53	13C, 15N and 1H Resonance Assignment of the PDZ1 domain of MAGI-1 using QUASI. <i>Journal of Biomolecular NMR</i> , 2006, 36, 33-33.	2.8	5
54	Chemical synthesis of transactivation domain (TAD) of tumor suppressor protein p53 by native chemical ligation of three peptide segments. <i>Tetrahedron</i> , 2019, 75, 703-708.	1.9	5

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55	A chemical probe for BAG1 targets androgen receptor-positive prostate cancer through oxidative stress signaling pathway. <i>IScience</i> , 2022, 25, 104175.	4.1	5
56	Structure determination of the minimal complex between Tfb5 and Tfb2, two subunits of the yeast transcription/DNA-repair factor TFIIH: a retrospective study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 745-755.	2.5	4
57	Production and characterization of a retinoic acid receptor RAR $\beta$ 3 construction encompassing the DNA binding domain and the disordered N-terminal proline rich domain. <i>Protein Expression and Purification</i> , 2014, 95, 113-120.	1.3	4
58	An Amyloidogenic Sequence at the N-Terminus of the Androgen Receptor Impacts Polyglutamine Aggregation. <i>Biomolecules</i> , 2017, 7, 44.	4.0	4
59	Conformational editing of intrinsically disordered protein by $\beta$ -methylation. <i>Chemical Science</i> , 2021, 12, 1080-1089.	7.4	4
60	QUASIA: Quick Access to Spectral Interpretation. <i>Comptes Rendus Chimie</i> , 2004, 7, 335-341.	0.5	3
61	Self-Organization Properties of a GPCR-Binding Peptide with a Fluorinated Tail Studied by Fluorine NMR Spectroscopy. <i>ChemBioChem</i> , 2021, 22, 657-661.	2.6	3
62	A practical guide to teaching with Proteopedia. <i>Biochemistry and Molecular Biology Education</i> , 2021, 49, 707-719.	1.2	3
63	Fluorine NMR study of proline-rich sequences using fluoroprolines. <i>Magnetic Resonance</i> , 2021, 2, 795-813.	1.9	3
64	Backbone $^1\text{H}$ , $^{15}\text{N}$ , $^{13}\text{C}$ NMR assignment of the 518-627 fragment of the androgen receptor encompassing N-terminal and DNA binding domains. <i>Biomolecular NMR Assignments</i> , 2016, 10, 175-178.	0.8	2