

Lukas Zidek

List of Publications by Year in descending order

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67
papers

2,156
citations

236925

25
h-index

243625

44
g-index

70
all docs

70
docs citations

70
times ranked

2262
citing authors

#	ARTICLE	IF	CITATIONS
1	Increased protein backbone conformational entropy upon hydrophobic ligand binding. <i>Nature Structural Biology</i> , 1999, 6, 1118-1121.	9.7	224
2	Positive identification of the puberty-accelerating pheromone of the house mouse: the volatile ligands associating with the major urinary protein. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 2017-2022.	2.6	194
3	Pheromone binding by polymorphic mouse major urinary proteins. <i>Protein Science</i> , 2002, 11, 2247-2256.	7.6	109
4	Structural basis of pheromone binding to mouse major urinary protein (MUP). <i>Protein Science</i> , 2001, 10, 997-1004.	7.6	101
5	Strategy for complete NMR assignment of disordered proteins with highly repetitive sequences based on resolution-enhanced 5D experiments. <i>Journal of Biomolecular NMR</i> , 2010, 48, 169-177.	2.8	99
6	5D ¹³ C-detected experiments for backbone assignment of unstructured proteins with a very low signal dispersion. <i>Journal of Biomolecular NMR</i> , 2011, 50, 1-11.	2.8	77
7	Structure of <i>Bombyx mori</i> chemosensory protein 1 in solution. <i>Archives of Insect Biochemistry and Physiology</i> , 2007, 66, 135-145.	1.5	74
8	NMR methodology for the study of nucleic acids. <i>Current Opinion in Structural Biology</i> , 2001, 11, 275-281.	5.7	71
9	NMR Mapping of the Recombinant Mouse Major Urinary Protein I Binding Site Occupied by the Pheromone 2-sec-Butyl-4,5-dihydrothiazole. <i>Biochemistry</i> , 1999, 38, 9850-9861.	2.5	65
10	Refinement of d(GCGAAGC) hairpin structure using one- and two-bond residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2002, 24, 1-14.	2.8	61
11	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins. <i>Chemical Reviews</i> , 2022, 122, 9331-9356.	47.7	51
12	Temperature-dependent spectral density analysis applied to monitoring backbone dynamics of major urinary protein-I complexed with the pheromone 2-sec-butyl-4,5-dihydrothiazole*. <i>Journal of Biomolecular NMR</i> , 2004, 28, 369-384.	2.8	50
13	Structure and binding specificity of the receiver domain of sensor histidine kinase CKII from <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2011, 67, 827-839.	5.7	50
14	The $\hat{\Gamma}$ Subunit of RNA Polymerase Is Required for Rapid Changes in Gene Expression and Competitive Fitness of the Cell. <i>Journal of Bacteriology</i> , 2013, 195, 2603-2611.	2.2	44
15	Structure and Functions of Microtubule Associated Proteins Tau and MAP2c: Similarities and Differences. <i>Biomolecules</i> , 2019, 9, 105.	4.0	41
16	4D Non-uniformly sampled HCBCACON and 1 J(NC $\hat{\pm}$)-selective HCBCANCO experiments for the sequential assignment and chemical shift analysis of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2012, 53, 139-148.	2.8	40
17	Role of SH3b binding domain in a natural deletion mutant of Kayvirus endolysin LysF1 with a broad range of lytic activity. <i>Virus Genes</i> , 2018, 54, 130-139.	1.6	40
18	Reaction of N-Acetylglycyllysine Methyl Ester with 2-Alkenals: An Alternative Model for Covalent Modification of Proteins. <i>Chemical Research in Toxicology</i> , 1998, 11, 730-740.	3.3	39

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19	Efficient protocol for backbone and side-chain assignments of large, intrinsically disordered proteins: transient secondary structure analysis of 49.2 kDa microtubule associated protein 2c. <i>Journal of Biomolecular NMR</i> , 2013, 56, 291-301.	2.8	38
20	Multiple Recognition Motifs in Nucleoporin Nup159 Provide a Stable and Rigid Nup159-Dyn2 Assembly. <i>Journal of Biological Chemistry</i> , 2013, 288, 2614-2622.	3.4	35
21	Spectral density mapping protocols for analysis of molecular motions in disordered proteins. <i>Journal of Biomolecular NMR</i> , 2014, 58, 193-207.	2.8	34
22	Measurement of small scalar and dipolar couplings in purine and pyrimidine bases. <i>Journal of Biomolecular NMR</i> , 2001, 21, 153-160.	2.8	33
23	Recent Biochemical Insights into Puberty Acceleration, Estrus Induction, and Puberty Delay in the House Mouse. , 1999, , 99-116.		32
24	Toward optimal-resolution NMR of intrinsically disordered proteins. <i>Journal of Magnetic Resonance</i> , 2014, 241, 41-52.	2.1	29
25	NMR Structure of the N-Terminal Domain of Capsid Protein from the Mason-Pfizer Monkey Virus. <i>Journal of Molecular Biology</i> , 2009, 392, 100-114.	4.2	28
26	Structural Aspects of Multistep Phosphorelay-Mediated Signaling in Plants. <i>Molecular Plant</i> , 2016, 9, 71-85.	8.3	28
27	Choice of Force Field for Proteins Containing Structured and Intrinsically Disordered Regions. <i>Biophysical Journal</i> , 2020, 118, 1621-1633.	0.5	28
28	Conformational Dynamics and Antigenicity in the Disordered Malaria Antigen Merozoite Surface Protein 2. <i>PLoS ONE</i> , 2015, 10, e0119899.	2.5	27
29	Soluble recombinant CD69 receptors optimized to have an exceptional physical and chemical stability display prolonged circulation and remain intact in the blood of mice. <i>FEBS Journal</i> , 2008, 275, 5589-5606.	4.7	26
30	Glycosylated major urinary protein of the house mouse: characterization of its N-linked oligosaccharides. <i>Glycobiology</i> , 2000, 10, 231-235.	2.5	25
31	NMR Determines Transient Structure and Dynamics in the Disordered C-Terminal Domain of WASp Interacting Protein. <i>Biophysical Journal</i> , 2013, 105, 481-493.	0.5	25
32	Solution structure of the N-terminal domain of <i>Bacillus subtilis</i> σ^70 subunit of RNA polymerase and its classification based on structural homologs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1807-1810.	2.6	24
33	Exploring the Structure of a DNA Hairpin with the Help of NMR Spin-Spin Coupling Constants: An Experimental and Quantum Chemical Investigation. <i>Journal of Physical Chemistry B</i> , 2002, 106, 10242-10250.	2.6	22
34	Modification of Horse Heart Cytochrome c with trans-2-Hexenal. <i>Chemical Research in Toxicology</i> , 1997, 10, 702-710.	3.3	21
35	The effect of water on NMR spin-spin couplings in DNA: Improvement of calculated values by application of two solvent models. <i>Physical Chemistry Chemical Physics</i> , 2003, 5, 734.	2.8	18
36	Structural Study of the Partially Disordered Full-Length σ^70 Subunit of RNA Polymerase from <i>Bacillus subtilis</i> . <i>ChemBioChem</i> , 2013, 14, 1772-1779.	2.6	18

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37	Quantitative mapping of microtubule-associated protein 2c (MAP2c) phosphorylation and regulatory protein 14-3-3 σ -binding sites reveals key differences between MAP2c and its homolog Tau. <i>Journal of Biological Chemistry</i> , 2017, 292, 6715-6727.	3.4	16
38	Quantitative Conformational Analysis of Functionally Important Electrostatic Interactions in the Intrinsically Disordered Region of Delta Subunit of Bacterial RNA Polymerase. <i>Journal of the American Chemical Society</i> , 2019, 141, 16817-16828.	13.7	16
39	Internal consistency of NMR data obtained in partially aligned biomacromolecules. <i>Journal of Magnetic Resonance</i> , 2003, 162, 385-395.	2.1	15
40	Synthetic N-Acetyl-d-glucosamine Based Fully Branched Tetrasaccharide, a Mimetic of the Endogenous Ligand for CD69, Activates CD69+Killer Lymphocytes upon Dimerization via a Hydrophilic Flexible Linker. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 4050-4065.	6.4	13
41	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. <i>Journal of Biological Chemistry</i> , 2018, 293, 13297-13309.	3.4	13
42	¹ H, ¹³ C, and ¹⁵ N Resonance Assignment of Bombyx mori Chemosensory Protein 1 (BmorCSP1). <i>Journal of Biomolecular NMR</i> , 2006, 36, 47-47.	2.8	11
43	Backbone Motions of Free and Pheromone-Bound Major Urinary Protein I Studied by Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2007, 111, 5731-5739.	2.6	11
44	Investigation of Thermal Denaturation of Barley Nonspecific Lipid Transfer Protein 1 (ns-LTP1b) by Nuclear Magnetic Resonance and Differential Scanning Calorimetry. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 8444-8452.	5.2	11
45	Cooperation between Subunits Is Essential for High-Affinity Binding of N-Acetyl-d-hexosamines to Dimeric Soluble and Dimeric Cellular Forms of Human CD69. <i>Biochemistry</i> , 2010, 49, 4060-4067.	2.5	11
46	Triple resonance ¹⁵ N NMR relaxation experiments for studies of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2017, 69, 133-146.	2.8	11
47	Molecular dynamics study of major urinary protein-pheromone interactions: A structural model for ligand-induced flexibility increase. <i>FEBS Letters</i> , 2006, 580, 682-684.	2.8	9
48	Conformational dynamics are a key factor in signaling mediated by the receiver domain of a sensor histidine kinase from Arabidopsis thaliana. <i>Journal of Biological Chemistry</i> , 2017, 292, 17525-17540.	3.4	9
49	X-ray vs. NMR structure of N-terminal domain of β -subunit of RNA polymerase. <i>Journal of Structural Biology</i> , 2014, 187, 174-186.	2.8	8
50	Stabilization of the β ² -hairpin in Mason-Pfizer monkey virus capsid protein- a critical step for infectivity. <i>Retrovirology</i> , 2014, 11, 94.	2.0	7
51	Spectral density mapping at multiple magnetic fields suitable for $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" overflow="scroll" \rangle \langle \text{mml:mrow} \langle \text{mml:msup} \langle \text{mml:mrow} / \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mn} \rangle 13 \langle / \text{mml:mn} \rangle \langle / \text{mml:mrow} \rangle \langle / \text{mml:msup} \rangle \langle \text{mml:mtext} \rangle C \langle / \text{mml:mtext} \rangle \langle / \text{mml:mrow} \rangle \langle / \text{mml:math} \rangle$ NMR relaxation studies. <i>Journal of Magnetic Resonance</i> , 2016, 266, 23-48.	2.1	7
52	Solution structure of domain 1.1 of the β fA factor from Bacillus subtilis is preformed for binding to the RNA polymerase core. <i>Journal of Biological Chemistry</i> , 2017, 292, 11610-11617.	3.4	7
53	Cross-correlated relaxation measurements under adiabatic sweeps: determination of local order in proteins. <i>Journal of Biomolecular NMR</i> , 2015, 63, 353-365.	2.8	6
54	Inactivation of colicin ϵ by intramembrane helix-helix interaction with its immunity protein. <i>FEBS Journal</i> , 2008, 275, 5325-5331.	4.7	5

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55	NMR assignment of intrinsically disordered self-processing module of the FrpC protein of <i>Neisseria meningitidis</i> . <i>Biomolecular NMR Assignments</i> , 2015, 9, 435-440.	0.8	5
56	Structural Basis of Ca ²⁺ -Dependent Self-Processing Activity of Repeat-in-Toxin Proteins. <i>MBio</i> , 2020, 11, .	4.1	5
57	Boosting the resolution of low-field ¹⁵ N relaxation experiments on intrinsically disordered proteins with triple-resonance NMR. <i>Journal of Biomolecular NMR</i> , 2020, 74, 139-145.	2.8	5
58	Hydroperoxide Inhibitor of Horse Liver Alcohol Dehydrogenase Activity, Tightly Bound to the Enzyme-NAD ⁺ Complex, Characteristically Degrades the Coenzyme. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 1992, 6, 211-222.	0.5	4
59	Backbone ¹ H, ¹³ C, and ¹⁵ N NMR assignment for the inactive form of the retroviral protease of the murine intracisternal A-type particle, inMIA-14 PR. <i>Biomolecular NMR Assignments</i> , 2009, 3, 261-264.	0.8	4
60	S3EPY: a Sparky extension for determination of small scalar couplings from spin-state-selective excitation NMR experiments. <i>Journal of Biomolecular NMR</i> , 2010, 46, 191-197.	2.8	4
61	Conformational Entropy from Slowly Relaxing Local Structure Analysis of ¹⁵ N- ¹ H Relaxation in Proteins: Application to Pheromone Binding to MUP-I in the 283-308 K Temperature Range. <i>Journal of Physical Chemistry B</i> , 2017, 121, 8684-8692.	2.6	4
62	Retro operation on the Trp-cage miniprotein sequence produces an unstructured molecule capable of folding similar to the original only upon 2,2,2-trifluoroethanol addition. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 463-472.	2.1	3
63	The influence of Mg ²⁺ coordination on ¹³ C and ¹⁵ N chemical shifts in CKI _{RD} protein domain from experiment and molecular dynamics/density functional theory calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 686-699.	2.6	3
64	Protein environment affects the water-tryptophan binding mode. MD, QM/MM, and NMR studies of engrailed homeodomain mutants. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 12664-12677.	2.8	3
65	¹ H, ¹³ C, and ¹⁵ N resonance assignment of the N-terminal domain of Mason-Pfizer monkey virus capsid protein, CA1-140. <i>Biomolecular NMR Assignments</i> , 2008, 2, 43-45.	0.8	2
66	Kinetics of Inhibition of Horse Liver Alcohol Dehydrogenase by <i>p</i> -Methylbenzyl Hydroperoxide. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 1993, 7, 191-196.	0.5	0
67	Investigation of the structure and dynamics of gallium binding to high-affinity peptides elucidated by multi-scale simulation, quantum chemistry, NMR and ITC. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 8618-8632.	2.8	0