Lukas Zidek

List of Publications by Year
in descending order

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67 papers	2,156 citations	236612 25 h-index	243296 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. Nature Structural Biology, 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. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 2017-2022.	1.2	194
3	Pheromone binding by polymorphic mouse major urinary proteins. Protein Science, 2009, 11, 2247-2256.	3.1	109
4	Structural basis of pheromone binding to mouse major urinary protein (MUP-I). Protein Science, 2001, 10, 997-1004.	3.1	101
5	Strategy for complete NMR assignment of disordered proteins with highly repetitive sequences based on resolution-enhanced 5D experiments. Journal of Biomolecular NMR, 2010, 48, 169-177.	1.6	99
6	5D 13C-detected experiments for backbone assignment of unstructured proteins with a very low signal dispersion. Journal of Biomolecular NMR, 2011, 50, 1-11.	1.6	77
7	Structure of Bombyx mori chemosensory protein 1 in solution. Archives of Insect Biochemistry and Physiology, 2007, 66, 135-145.	0.6	74
8	NMR methodology for the study of nucleic acids. Current Opinion in Structural Biology, 2001, 11, 275-281.	2.6	71
9	NMR Mapping of the Recombinant Mouse Major Urinary Protein I Binding Site Occupied by the Pheromone 2-sec-Butyl-4,5-dihydrothiazoleâ€. Biochemistry, 1999, 38, 9850-9861.	1.2	65
10	Refinement of d(GCGAAGC) hairpin structure using one- and two-bond residual dipolar couplings. Journal of Biomolecular NMR, 2002, 24, 1-14.	1.6	61
11	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins. Chemical Reviews, 2022, 122, 9331-9356.	23.0	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*. Journal of Biomolecular NMR, 2004, 28, 369-384.	1.6	50
13	Structure and binding specificity of the receiver domain of sensor histidine kinase CKI1 from Arabidopsis thaliana. Plant Journal, 2011, 67, 827-839.	2.8	50
14	The Î´ Subunit of RNA Polymerase Is Required for Rapid Changes in Gene Expression and Competitive Fitness of the Cell. Journal of Bacteriology, 2013, 195, 2603-2611.	1.0	44
15	Structure and Functions of Microtubule Associated Proteins Tau and MAP2c: Similarities and Differences. Biomolecules, 2019, 9, 105.	1.8	41
16	4D Non-uniformly sampled HCBCACON and 1 J(NCÎ±)-selective HCBCANCO experiments for the sequential assignment and chemical shift analysis of intrinsically disordered proteins. Journal of Biomolecular NMR, 2012, 53, 139-148.	1.6	40
17	Role of SH3b binding domain in a natural deletion mutant of Kayvirus endolysin LysF1 with a broad range of lytic activity. Virus Genes, 2018, 54, 130-139.	0.7	40
18	Reaction of N-Acetylglycyllysine Methyl Ester with 2-Alkenals:â€‰ An Alternative Model for Covalent Modification of Proteins. Chemical Research in Toxicology, 1998, 11, 730-740.	1.7	39

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19	Efficient protocol for backbone and side-chain assignments of large, intrinsically disordered proteins: transient secondary structure analysis of 49.2ÂkDa microtubule associated protein 2c. Journal of Biomolecular NMR, 2013, 56, 291-301.	1.6	38
20	Multiple Recognition Motifs in Nucleoporin Nup159 Provide a Stable and Rigid Nup159-Dyn2 Assembly. Journal of Biological Chemistry, 2013, 288, 2614-2622.	1.6	35
21	Spectral density mapping protocols for analysis of molecular motions in disordered proteins. Journal of Biomolecular NMR, 2014, 58, 193-207.	1.6	34
22	Measurement of small scalar and dipolar couplings in purine and pyrimidine bases. Journal of Biomolecular NMR, 2001, 21, 153-160.	1.6	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. Journal of Magnetic Resonance, 2014, 241, 41-52.	1.2	29
25	NMR Structure of the N-Terminal Domain of Capsid Protein from the Masonâ€“Pfizer Monkey Virus. Journal of Molecular Biology, 2009, 392, 100-114.	2.0	28
26	Structural Aspects of Multistep Phosphorelay-Mediated Signaling in Plants. Molecular Plant, 2016, 9, 71-85.	3.9	28
27	Choice of Force Field for Proteins Containing Structured and Intrinsically Disordered Regions. Biophysical Journal, 2020, 118, 1621-1633.	0.2	28
28	Conformational Dynamics and Antigenicity in the Disordered Malaria Antigen Merozoite Surface Protein 2. PLoS ONE, 2015, 10, e0119899.	1.1	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. FEBS Journal, 2008, 275, 5589-5606.	2.2	26
30	Glycosylated major urinary protein of the house mouse: characterization of its N-linked oligosaccharides. Glycobiology, 2000, 10, 231-235.	1.3	25
31	NMR Determines Transient Structure and Dynamics in the Disordered C-Terminal Domain of WASp Interacting Protein. Biophysical Journal, 2013, 105, 481-493.	0.2	25
32	Solution structure of the Nâ€terminal domain of Bacillus subtilis Î´ subunit of RNA polymerase and its classification based on structural homologs. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1807-1810.	1.5	24
33	Exploring the Structure of a DNA Hairpin with the Help of NMR Spinâ^'Spin Coupling Constants:Â An Experimental and Quantum Chemical Investigation. Journal of Physical Chemistry B, 2002, 106, 10242-10250.	1.2	22
34	Modification of Horse Heart Cytochrome c with trans-2-Hexenal. Chemical Research in Toxicology, 1997, 10, 702-710.	1.7	21
35	The effect of water on NMR spinâ€“spin couplings in DNA: Improvement of calculated values by application of two solvent models. Physical Chemistry Chemical Physics, 2003, 5, 734.	1.3	18
36	Structural Study of the Partially Disordered Fullâ€Length Î´ Subunit of RNA Polymerase from Bacillus subtilis. ChemBioChem, 2013, 14, 1772-1779.	1.3	18

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37	Quantitative mapping of microtubule-associated protein 2c (MAP2c) phosphorylation and regulatory protein 14-3-3Î¶-binding sites reveals key differences between MAP2c and its homolog Tau. Journal of Biological Chemistry, 2017, 292, 6715-6727.	1.6	16
38	Quantitative Conformational Analysis of Functionally Important Electrostatic Interactions in the Intrinsically Disordered Region of Delta Subunit of Bacterial RNA Polymerase. Journal of the American Chemical Society, 2019, 141, 16817-16828.	6.6	16
39	Internal consistency of NMR data obtained in partially aligned biomacromolecules. Journal of Magnetic Resonance, 2003, 162, 385-395.	1.2	15
40	SyntheticN-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. Journal of Medicinal Chemistry, 2010, 53, 4050-4065.	2.9	13
41	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. Journal of Biological Chemistry, 2018, 293, 13297-13309.	1.6	13
42	1H, 13C, and 15N Resonance Assignment of Bombyx mori Chemosensory Protein 1 (BmorCSP1). Journal of Biomolecular NMR, 2006, 36, 47-47.	1.6	11
43	Backbone Motions of Free and Pheromone-Bound Major Urinary Protein I Studied by Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2007, 111, 5731-5739.	1.2	11
44	Investigation of Thermal Denaturation of Barley Nonspecific Lipid Transfer Protein 1 (ns-LTP1b) by Nuclear Magnetic Resonance and Differential Scanning Calorimetry. Journal of Agricultural and Food Chemistry, 2009, 57, 8444-8452.	2.4	11
45	Cooperation between Subunits Is Essential for High-Affinity Binding of N-Acetyl-<scp>d</scp>-hexosamines to Dimeric Soluble and Dimeric Cellular Forms of Human CD69. Biochemistry, 2010, 49, 4060-4067.	1.2	11
46	Triple resonance 15N NMR relaxation experiments for studies of intrinsically disordered proteins. Journal of Biomolecular NMR, 2017, 69, 133-146.	1.6	11
47	Molecular dynamics study of major urinary protein-pheromone interactions: A structural model for ligand-induced flexibility increase. FEBS Letters, 2006, 580, 682-684.	1.3	9
48	Conformational dynamics are a key factor in signaling mediated by the receiver domain of a sensor histidine kinase from Arabidopsis thaliana. Journal of Biological Chemistry, 2017, 292, 17525-17540.	1.6	9
49	X-ray vs. NMR structure of N-terminal domain of Î´-subunit of RNA polymerase. Journal of Structural Biology, 2014, 187, 174-186.	1.3	8
50	Stabilization of the Î²-hairpin in Mason-Pfizer monkey virus capsid protein- a critical step for infectivity. Retrovirology, 2014, 11, 94.	0.9	7
51	Spectral density mapping at multiple magnetic fields suitable for <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" overflow="scroll"><mml:mrow><mml:msup><mml:mrow /><mml:mrow><mml:mn>13</mml:mn></mml:mrow></mml:msup><mml:mtext>C</mml:mtext></mml:mrow></mml:math> NMR relaxation studies. Journal of Magnetic Resonance, 2016, 266, 23-40.	1.2	7
52	Solution structure of domain 1.1 of the ÏƒA factor from Bacillus subtilis is preformed for binding to the RNA polymerase core. Journal of Biological Chemistry, 2017, 292, 11610-11617.	1.6	7
53	Cross-correlated relaxation measurements under adiabatic sweeps: determination of local order in proteins. Journal of Biomolecular NMR, 2015, 63, 353-365.	1.6	6
54	Inactivation of colicinâ€ƒY by intramembrane helixâ€“helix interaction with its immunity protein. FEBS Journal, 2008, 275, 5325-5331.	2.2	5

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55	NMR assignment of intrinsically disordered self-processing module of the FrpC protein of Neisseria meningitidis. Biomolecular NMR Assignments, 2015, 9, 435-440.	0.4	5
56	Structural Basis of Ca 2+ -Dependent Self-Processing Activity of Repeat-in-Toxin Proteins. MBio, 2020, 11, .	1.8	5
57	Boosting the resolution of low-field $$^{15}hbox {N}$$ relaxation experiments on intrinsically disordered proteins with triple-resonance NMR. Journal of Biomolecular NMR, 2020, 74, 139-145.	1.6	5
58	Hydroperoxide Inhibitor of Horse Liver Alcohol Dehydrogenase Activity, Tightly Bound to the Enzyme-Nad+Complex, Characteristically Degrades the Coenzyme. Journal of Enzyme Inhibition and Medicinal Chemistry, 1992, 6, 211-222.	0.5	4
59	Backbone 1H, 13C, and 15N NMR assignment for the inactive form of the retroviral protease of the murine intracisternal A-type particle, inMIA-14 PR. Biomolecular NMR Assignments, 2009, 3, 261-264.	0.4	4
60	S3EPY: a Sparky extension for determination of small scalar couplings from spin-state-selective excitation NMR experiments. Journal of Biomolecular NMR, 2010, 46, 191-197.	1.6	4
61	Conformational Entropy from Slowly Relaxing Local Structure Analysis of 15Nâ€“H Relaxation in Proteins: Application to Pheromone Binding to MUP-I in the 283â€“308 K Temperature Range. Journal of Physical Chemistry B, 2017, 121, 8684-8692.	1.2	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. Protein Engineering, Design and Selection, 2014, 27, 463-472.	1.0	3
63	The influence of Mg²⁺ coordination on ¹³C and ¹⁵N chemical shifts in CKI1_{RD} protein domain from experiment and molecular dynamics/density functional theory calculations. Proteins: Structure, Function and Bioinformatics, 2016, 84, 686-699.	1.5	3
64	Protein environment affects the waterâ€“tryptophan binding mode. MD, QM/MM, and NMR studies of engrailed homeodomain mutants. Physical Chemistry Chemical Physics, 2018, 20, 12664-12677.	1.3	3
65	1H, 13C, and 15N resonance assignment of the N-terminal domain of Mason-Pfizer monkey virus capsid protein, CAÂ1-140. Biomolecular NMR Assignments, 2008, 2, 43-45.	0.4	2
66	Kinetics of Inhibition of Horse Liver Alcohol Dehydrogenase byp-Methylbenzyl Hydroperoxide. Journal of Enzyme Inhibition and Medicinal Chemistry, 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. Physical Chemistry Chemical Physics, 2021, 23, 8618-8632.	1.3	0