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	NMR Provides Unique Insight into the Functional Dynamics and Interactions of Intrinsically Disordered Proteins. Chemical Reviews, 2022, 122, 9331-9356.	47.7	51
2	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.	2.8	0
3	Structural Basis of Ca 2+ -Dependent Self-Processing Activity of Repeat-in-Toxin Proteins. MBio, 2020, 11, .	4.1	5
4	Choice of Force Field for Proteins Containing Structured and Intrinsically Disordered Regions. Biophysical Journal, 2020, 118, 1621-1633.	0.5	28
5	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.	2.8	5
6	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.	13.7	16
7	Structure and Functions of Microtubule Associated Proteins Tau and MAP2c: Similarities and Differences. Biomolecules, 2019, 9, 105.	4.0	41
8	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.	2.8	3
9	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.	1.6	40
10	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. Journal of Biological Chemistry, 2018, 293, 13297-13309.	3.4	13
11	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.	3.4	16
12	Solution structure of domain 1.1 of the Ïƒ A factor from Bacillus subtilis is preformed for binding to the RNA polymerase core. Journal of Biological Chemistry, 2017, 292, 11610-11617.	3.4	7
13	Triple resonance 15N NMR relaxation experiments for studies of intrinsically disordered proteins. Journal of Biomolecular NMR, 2017, 69, 133-146.	2.8	11
14	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.	2.6	4
15	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.	3.4	9
16	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.	2.6	3
17	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.	2.1	7
18	Structural Aspects of Multistep Phosphorelay-Mediated Signaling in Plants. Molecular Plant, 2016, 9, 71-85.	8.3	28

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19	Cross-correlated relaxation measurements under adiabatic sweeps: determination of local order in proteins. Journal of Biomolecular NMR, 2015, 63, 353-365.	2.8	6
20	NMR assignment of intrinsically disordered self-processing module of the FrpC protein of Neisseria meningitidis. Biomolecular NMR Assignments, 2015, 9, 435-440.	0.8	5
21	Conformational Dynamics and Antigenicity in the Disordered Malaria Antigen Merozoite Surface Protein 2. PLoS ONE, 2015, 10, e0119899.	2.5	27
22	Stabilization of the Î²-hairpin in Mason-Pfizer monkey virus capsid protein- a critical step for infectivity. Retrovirology, 2014, 11, 94.	2.0	7
23	Spectral density mapping protocols for analysis of molecular motions in disordered proteins. Journal of Biomolecular NMR, 2014, 58, 193-207.	2.8	34
24	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.	2.1	3
25	X-ray vs. NMR structure of N-terminal domain of Î´-subunit of RNA polymerase. Journal of Structural Biology, 2014, 187, 174-186.	2.8	8
26	Toward optimal-resolution NMR of intrinsically disordered proteins. Journal of Magnetic Resonance, 2014, 241, 41-52.	2.1	29
27	NMR Determines Transient Structure and Dynamics in the Disordered C-Terminal Domain of WASp Interacting Protein. Biophysical Journal, 2013, 105, 481-493.	0.5	25
28	Multiple Recognition Motifs in Nucleoporin Nup159 Provide a Stable and Rigid Nup159-Dyn2 Assembly. Journal of Biological Chemistry, 2013, 288, 2614-2622.	3.4	35
29	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.	2.8	38
30	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.	2.2	44
31	Structural Study of the Partially Disordered Fullâ€Length Î´ Subunit of RNA Polymerase from Bacillus subtilis. ChemBioChem, 2013, 14, 1772-1779.	2.6	18
32	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.	2.8	40
33	Structure and binding specificity of the receiver domain of sensor histidine kinase CKI1 from Arabidopsis thaliana. Plant Journal, 2011, 67, 827-839.	5.7	50
34	5D 13C-detected experiments for backbone assignment of unstructured proteins with a very low signal dispersion. Journal of Biomolecular NMR, 2011, 50, 1-11.	2.8	77
35	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.	2.8	4
36	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.	2.8	99

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37	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.	2.6	24
38	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.	2.5	11
39	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.	6.4	13
40	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.	0.8	4
41	NMR Structure of the N-Terminal Domain of Capsid Protein from the Masonâ€“Pfizer Monkey Virus. Journal of Molecular Biology, 2009, 392, 100-114.	4.2	28
42	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.	5.2	11
43	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.	0.8	2
44	Inactivation of colicinâ€ƒY by intramembrane helixâ€“helix interaction with its immunity protein. FEBS Journal, 2008, 275, 5325-5331.	4.7	5
45	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.	4.7	26
46	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.	2.6	11
47	Structure of Bombyx mori chemosensory protein 1 in solution. Archives of Insect Biochemistry and Physiology, 2007, 66, 135-145.	1.5	74
48	Molecular dynamics study of major urinary protein-pheromone interactions: A structural model for ligand-induced flexibility increase. FEBS Letters, 2006, 580, 682-684.	2.8	9
49	1H, 13C, and 15N Resonance Assignment of Bombyx mori Chemosensory Protein 1 (BmorCSP1). Journal of Biomolecular NMR, 2006, 36, 47-47.	2.8	11
50	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.	2.8	50
51	Internal consistency of NMR data obtained in partially aligned biomacromolecules. Journal of Magnetic Resonance, 2003, 162, 385-395.	2.1	15
52	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.	2.8	18
53	Exploring the Structure of a DNA Hairpin with the Help of NMR Spinâˆ'Spin Coupling Constants:Â An Experimental and Quantum Chemical Investigation. Journal of Physical Chemistry B, 2002, 106, 10242-10250.	2.6	22
54	Refinement of d(GCGAAGC) hairpin structure using one- and two-bond residual dipolar couplings. Journal of Biomolecular NMR, 2002, 24, 1-14.	2.8	61

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55	Pheromone binding by polymorphic mouse major urinary proteins. Protein Science, 2002, 11, 2247-2256.	7.6	109
56	Measurement of small scalar and dipolar couplings in purine and pyrimidine bases. Journal of Biomolecular NMR, 2001, 21, 153-160.	2.8	33
57	Structural basis of pheromone binding to mouse major urinary protein (MUPâ€‰). Protein Science, 2001, 10, 997-1004.	7.6	101
58	NMR methodology for the study of nucleic acids. Current Opinion in Structural Biology, 2001, 11, 275-281.	5.7	71
59	Glycosylated major urinary protein of the house mouse: characterization of its N-linked oligosaccharides. Glycobiology, 2000, 10, 231-235.	2.5	25
60	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.	2.6	194
61	Increased protein backbone conformational entropy upon hydrophobic ligand binding. Nature Structural Biology, 1999, 6, 1118-1121.	9.7	224
62	NMR Mapping of the Recombinant Mouse Major Urinary Protein I Binding Site Occupied by the Pheromone 2-sec-Butyl-4,5-dihydrothiazole. Biochemistry, 1999, 38, 9850-9861.	2.5	65
63	Recent Biochemical Insights into Puberty Acceleration, Estrus Induction, and Puberty Delay in the House Mouse. , 1999, , 99-116.		32
64	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.	3.3	39
65	Modification of Horse Heart Cytochrome c with trans-2-Hexenal. Chemical Research in Toxicology, 1997, 10, 702-710.	3.3	21
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	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