

Donghan Lee

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

1,744
citations

279798

23
h-index

289244

40
g-index

62
all docs

62
docs citations

62
times ranked

2199
citing authors

#	ARTICLE	IF	CITATIONS
1	Effective rotational correlation times of proteins from NMR relaxation interference. <i>Journal of Magnetic Resonance</i> , 2006, 178, 72-76.	2.1	238
2	Weak Long-Range Correlated Motions in a Surface Patch of Ubiquitin Involved in Molecular Recognition. <i>Journal of the American Chemical Society</i> , 2011, 133, 10336-10339.	13.7	155
3	NMR structure of the unliganded <i>Bombyx mori</i> pheromone-binding protein at physiological pH. <i>FEBS Letters</i> , 2002, 531, 314-318.	2.8	91
4	Bilayer in Small Bicelles Revealed by Lipid-Protein Interactions Using NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 13822-13823.	13.7	81
5	Modular architecture of Munc13/calmodulin complexes: dual regulation by Ca ²⁺ and possible function in short-term synaptic plasticity. <i>EMBO Journal</i> , 2010, 29, 680-691.	7.8	65
6	Exceeding the limit of dynamics studies on biomolecules using high spin-lock field strengths with a cryogenically cooled probehead. <i>Journal of Magnetic Resonance</i> , 2012, 221, 1-4.	2.1	60
7	RAP Uses a Histidine Switch to Regulate Its Interaction with LRP in the ER and Golgi. <i>Molecular Cell</i> , 2006, 22, 423-430.	9.7	59
8	Kinetics of Conformational Sampling in Ubiquitin. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 11437-11440.	13.8	59
9	Population Shuffling of Protein Conformations. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 207-210.	13.8	57
10	Allosteric switch regulates protein-protein binding through collective motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3269-3274.	7.1	57
11	Unusual Heme-Histidine Bond in the Active Site of a Chaperone. <i>Journal of the American Chemical Society</i> , 2005, 127, 3716-3717.	13.7	55
12	A Designed Conformational Shift To Control Protein Binding Specificity. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 10367-10371.	13.8	45
13	Structure and Interactions of the First Three RNA Recognition Motifs of Splicing Factor Prp24. <i>Journal of Molecular Biology</i> , 2007, 367, 1447-1458.	4.2	36
14	Measuring Dynamic and Kinetic Information in the Previously Inaccessible Supra-tc Window of Nanoseconds to Microseconds by Solution NMR Spectroscopy. <i>Molecules</i> , 2013, 18, 11904-11937.	3.8	35
15	Detection of C ^α , C ^β correlations in proteins using a new time- and sensitivity-optimal experiment. <i>Journal of Biomolecular NMR</i> , 2005, 31, 273-278.	2.8	33
16	The Structure of Free L11 and Functional Dynamics of L11 in Free, L11-rRNA(58 nt) Binary and L11-rRNA(58) Tj ETQp 0 0 rgBT /Overloc	4.2	32
17	Measuring membrane protein bond orientations in nanodiscs via residual dipolar couplings. <i>Protein Science</i> , 2014, 23, 851-856.	7.6	32
18	Hyperpolarized Binding Pocket Nuclear Overhauser Effect for Determination of Competitive Ligand Binding. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5179-5182.	13.8	31

#	ARTICLE	IF	CITATIONS
19	Recent advances in measuring the kinetics of biomolecules by NMR relaxation dispersion spectroscopy. Archives of Biochemistry and Biophysics, 2017, 628, 81-91.	3.0	30
20	Dynamic Conformational Equilibria in the Physiological Function of the Bombyx mori Pheromone-Binding Protein. Journal of Molecular Biology, 2011, 408, 922-931.	4.2	29
21	Quantum mechanical NMR simulation algorithm for protein-size spin systems. Journal of Magnetic Resonance, 2014, 243, 107-113.	2.1	28
22	Simultaneous determination of fast and slow dynamics in molecules using extreme CPMG relaxation dispersion experiments. Journal of Biomolecular NMR, 2018, 70, 1-9.	2.8	27
23	Solution NMR views of dynamical ordering of biomacromolecules. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 287-306.	2.4	26
24	The structure of receptor-associated protein (RAP). Protein Science, 2007, 16, 1628-1640.	7.6	23
25	Kinetics of the Antibody Recognition Site in the Third IgG-binding Domain of Protein G. Angewandte Chemie - International Edition, 2016, 55, 9567-9570.	13.8	21
26	pH-responsive delivery of Griffithsin from electrospun fibers. European Journal of Pharmaceutics and Biopharmaceutics, 2019, 138, 64-74.	4.3	21
27	Enhanced accuracy of kinetic information from CT-CPMG experiments by transverse rotating-frame spectroscopy. Journal of Biomolecular NMR, 2013, 57, 73-82.	2.8	20
28	Thermal coefficients of the methyl groups within ubiquitin. Protein Science, 2012, 21, 562-570.	7.6	18
29	A Combination of Spin Diffusion Methods for the Determination of Protein-Ligand Complex Structural Ensembles. Angewandte Chemie - International Edition, 2015, 54, 6511-6515.	13.8	18
30	ShereKhan-calculating exchange parameters in relaxation dispersion data from CPMG experiments. Bioinformatics, 2013, 29, 1819-1820.	4.1	17
31	ORIU: Optimized RDC-based Iterative and Unified Model-free analysis. Journal of Biomolecular NMR, 2014, 58, 287-301.	2.8	17
32	Detection and Identification of Protein Phosphorylation Sites in Histidines through HNP Correlation Patterns. Angewandte Chemie - International Edition, 2010, 49, 8971-8974.	13.8	15
33	Solution structure and functional investigation of human guanylate kinase reveals allosteric networking and a crucial role for the enzyme in cancer. Journal of Biological Chemistry, 2019, 294, 11920-11933.	3.4	15
34	Characteristic Analysis of Homo- and Heterodimeric Complexes of Human Mitochondrial Pyruvate Carrier Related to Metabolic Diseases. International Journal of Molecular Sciences, 2020, 21, 3403.	4.1	15
35	Polychromatic Selective Population Inversion for TROSY Experiments with Large Proteins. Journal of the American Chemical Society, 2005, 127, 405-411.	13.7	13
36	Peptide Ligands Selected with CD4-Induced Epitopes on Native Dualtropic HIV-1 Envelope Proteins Mimic Extracellular Coreceptor Domains and Bind to HIV-1 gp120 Independently of Coreceptor Usage. Journal of Virology, 2010, 84, 10131-10138.	3.4	13

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37	A litmus test for classifying recognition mechanisms of transiently binding proteins. <i>Nature Communications</i> , 2022, 13, .	12.8	13
38	A pre-structured helix in the intrinsically disordered 4EBP1. <i>Molecular BioSystems</i> , 2015, 11, 366-369.	2.9	12
39	Enhancing NMR derived ensembles with kinetics on multiple timescales. <i>Journal of Biomolecular NMR</i> , 2020, 74, 27-43.	2.8	12
40	Sampling of Glycanâ€Bound Conformers by the Antiâ€HIV Lectin <i>Oscillatoria agardhii</i> agglutinin in the Absence of Sugar. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 6462-6465.	13.8	11
41	Label-free NMR-based dissociation kinetics determination. <i>Journal of Biomolecular NMR</i> , 2017, 69, 229-235.	2.8	9
42	Determinants of Interaction Specificity of the <i>Bacillus subtilis</i> GlcT Antitermination Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 27731-27742.	3.4	8
43	Speeding-up exchange-mediated saturation transfer experiments by Fourier transform. <i>Journal of Biomolecular NMR</i> , 2015, 63, 237-244.	2.8	8
44	Utilizing dipole-dipole cross-correlated relaxation for the measurement of angles between pairs of opposing C-Hâ€C-H bonds in anti-parallel Î²-sheets. <i>Methods</i> , 2018, 138-139, 85-92.	3.8	8
45	High-power 1 H composite pulse decoupling provides artifact free exchange-mediated saturation transfer (EST) experiments. <i>Journal of Magnetic Resonance</i> , 2016, 269, 65-69.	2.1	7
46	A screen of FDA-approved drugs identifies inhibitors of protein tyrosine phosphatase 4A3 (PTP4A3 or Tj ETQq0 0 0,rgBT /Overlock 10 TF	3.3	7
47	Kinetics of the Antibody Recognition Site in the Third IgGâ€Binding Domain of Protein G. <i>Angewandte Chemie</i> , 2016, 128, 9719-9722.	2.0	6
48	Resonance assignments for the two N-terminal RNA recognition motifs (RRM) of the <i>S. cerevisiae</i> Pre-mRNA Processing Protein Prp24. <i>Journal of Biomolecular NMR</i> , 2006, 36, 58-58.	2.8	5
49	Population shuffling between ground and high energy excited states. <i>Protein Science</i> , 2015, 24, 1714-1719.	7.6	5
50	Standard Tensorial Analysis of Local Ordering in Proteins from Residual Dipolar Couplings. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6106-6117.	2.6	4
51	1H, 13C and 15N resonance assignment of the anti-HIV lectin from <i>Oscillatoria agardhii</i> . <i>Biomolecular NMR Assignments</i> , 2015, 9, 317-319.	0.8	4
52	1H, 13C and 15N resonance assignment of human guanylate kinase. <i>Biomolecular NMR Assignments</i> , 2018, 12, 11-14.	0.8	3
53	NMR assignment of domain 2 of the receptor-associated protein. <i>Journal of Biomolecular NMR</i> , 2006, 36, 54-54.	2.8	1
54	NMR assignment of domain 3 of the receptor-associated protein (RAP). <i>Journal of Biomolecular NMR</i> , 2006, 36, 56-56.	2.8	1

#	ARTICLE	IF	CITATIONS
55	Recombinant expression and purification of AF1q and its interaction with T-cell Factor 7. Protein Expression and Purification, 2020, 165, 105499.	1.3	1
56	Repositioning Food and Drug Administration-Approved Drugs for Inhibiting Biliverdin IX ^α Reductase B as a Novel Thrombocytopenia Therapeutic Target. Journal of Medicinal Chemistry, 2022, 65, 2548-2557.	6.4	1