

# 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	Repositioning Food and Drug Administration-Approved Drugs for Inhibiting Biliverdin IX $\alpha$ Reductase B as a Novel Thrombocytopenia Therapeutic Target. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 2548-2557.	6.4	1
2	A litmus test for classifying recognition mechanisms of transiently binding proteins. <i>Nature Communications</i> , 2022, 13, .	12.8	13
3	A screen of FDA-approved drugs identifies inhibitors of protein tyrosine phosphatase 4A3 (PTP4A3 or) Tj ETQq1 1 0.784314 rgBT /Ove	3.3	7
4	Recombinant expression and purification of AF1q and its interaction with T-cell Factor 7. <i>Protein Expression and Purification</i> , 2020, 165, 105499.	1.3	1
5	Enhancing NMR derived ensembles with kinetics on multiple timescales. <i>Journal of Biomolecular NMR</i> , 2020, 74, 27-43.	2.8	12
6	Characteristic Analysis of Homo- and Heterodimeric Complexes of Human Mitochondrial Pyruvate Carrier Related to Metabolic Diseases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3403.	4.1	15
7	Solution structure and functional investigation of human guanylate kinase reveals allosteric networking and a crucial role for the enzyme in cancer. <i>Journal of Biological Chemistry</i> , 2019, 294, 11920-11933.	3.4	15
8	pH-responsive delivery of Griffithsin from electrospun fibers. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2019, 138, 64-74.	4.3	21
9	Utilizing dipole-dipole cross-correlated relaxation for the measurement of angles between pairs of opposing C-H...C-H bonds in anti-parallel $\beta$ -sheets. <i>Methods</i> , 2018, 138-139, 85-92.	3.8	8
10	$^1\text{H}$ , $^{13}\text{C}$ and $^{15}\text{N}$ resonance assignment of human guanylate kinase. <i>Biomolecular NMR Assignments</i> , 2018, 12, 11-14.	0.8	3
11	Solution NMR views of dynamical ordering of biomacromolecules. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 287-306.	2.4	26
12	Simultaneous determination of fast and slow dynamics in molecules using extreme CPMG relaxation dispersion experiments. <i>Journal of Biomolecular NMR</i> , 2018, 70, 1-9.	2.8	27
13	Label-free NMR-based dissociation kinetics determination. <i>Journal of Biomolecular NMR</i> , 2017, 69, 229-235.	2.8	9
14	Recent advances in measuring the kinetics of biomolecules by NMR relaxation dispersion spectroscopy. <i>Archives of Biochemistry and Biophysics</i> , 2017, 628, 81-91.	3.0	30
15	Kinetics of the Antibody Recognition Site in the Third IgG Binding Domain of Protein G. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 9567-9570.	13.8	21
16	Kinetics of the Antibody Recognition Site in the Third IgG Binding Domain of Protein G. <i>Angewandte Chemie</i> , 2016, 128, 9719-9722.	2.0	6
17	High-power $^1\text{H}$ 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
18	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

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19	Sampling of Glycan-Bound Conformers by the Anti-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
20	Population shuffling between ground and high energy excited states. <i>Protein Science</i> , 2015, 24, 1714-1719.	7.6	5
21	A pre-structured helix in the intrinsically disordered 4EBP1. <i>Molecular BioSystems</i> , 2015, 11, 366-369.	2.9	12
22	A Combination of Spin Diffusion Methods for the Determination of Protein-Ligand Complex Structural Ensembles. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 6511-6515.	13.8	18
23	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignment of the anti-HIV lectin from <i>Oscillatoria agardhii</i> . <i>Biomolecular NMR Assignments</i> , 2015, 9, 317-319.	0.8	4
24	Speeding-up exchange-mediated saturation transfer experiments by Fourier transform. <i>Journal of Biomolecular NMR</i> , 2015, 63, 237-244.	2.8	8
25	Population Shuffling of Protein Conformations. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 207-210.	13.8	57
26	ORIUM: Optimized RDC-based Iterative and Unified Model-free analysis. <i>Journal of Biomolecular NMR</i> , 2014, 58, 287-301.	2.8	17
27	Measuring membrane protein bond orientations in nanodiscs via residual dipolar couplings. <i>Protein Science</i> , 2014, 23, 851-856.	7.6	32
28	A Designed Conformational Shift To Control Protein Binding Specificity. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 10367-10371.	13.8	45
29	Quantum mechanical NMR simulation algorithm for protein-size spin systems. <i>Journal of Magnetic Resonance</i> , 2014, 243, 107-113.	2.1	28
30	Enhanced accuracy of kinetic information from CT-CPMG experiments by transverse rotating-frame spectroscopy. <i>Journal of Biomolecular NMR</i> , 2013, 57, 73-82.	2.8	20
31	ShereKhan-calculating exchange parameters in relaxation dispersion data from CPMG experiments. <i>Bioinformatics</i> , 2013, 29, 1819-1820.	4.1	17
32	Measuring Dynamic and Kinetic Information in the Previously Inaccessible Supra- $\mu$ s Window of Nanoseconds to Microseconds by Solution NMR Spectroscopy. <i>Molecules</i> , 2013, 18, 11904-11937.	3.8	35
33	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
34	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
35	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
36	Thermal coefficients of the methyl groups within ubiquitin. <i>Protein Science</i> , 2012, 21, 562-570.	7.6	18

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37	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
38	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
39	Dynamic Conformational Equilibria in the Physiological Function of the Bombyx mori Pheromone-Binding Protein. <i>Journal of Molecular Biology</i> , 2011, 408, 922-931.	4.2	29
40	Kinetics of Conformational Sampling in Ubiquitin. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 11437-11440.	13.8	59
41	Detection and Identification of Proteinâ€”Phosphorylation Sites in Histidines through HNP Correlation Patterns. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 8971-8974.	13.8	15
42	Modular architecture of Munc13/calmodulin complexes: dual regulation by Ca <sup>2+</sup> and possible function in short-term synaptic plasticity. <i>EMBO Journal</i> , 2010, 29, 680-691.	7.8	65
43	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. <i>Journal of Virology</i> , 2010, 84, 10131-10138.	3.4	13
44	Bilayer in Small Bicelles Revealed by Lipidâ€”Protein Interactions Using NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 13822-13823.	13.7	81
45	The Structure of Free L11 and Functional Dynamics of L11 in Free, L11-rRNA(58 nt) Binary and L11-rRNA(58) Tj ETQ <sub>1</sub> 1 0.784314 rg	4.2	32
46	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
47	The structure of receptorâ€”associated protein (RAP). <i>Protein Science</i> , 2007, 16, 1628-1640.	7.6	23
48	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
49	Effective rotational correlation times of proteins from NMR relaxation interference. <i>Journal of Magnetic Resonance</i> , 2006, 178, 72-76.	2.1	238
50	NMR assignment of domain 2 of the receptor-associated protein. <i>Journal of Biomolecular NMR</i> , 2006, 36, 54-54.	2.8	1
51	NMR assignment of domain 3 of the receptor-associated protein (RAP). <i>Journal of Biomolecular NMR</i> , 2006, 36, 56-56.	2.8	1
52	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
53	Detection of Câ€”C <sup>13</sup> correlations in proteins using a new time- and sensitivity-optimal experiment. <i>Journal of Biomolecular NMR</i> , 2005, 31, 273-278.	2.8	33
54	Unusual Hemeâ€”Histidine Bond in the Active Site of a Chaperone. <i>Journal of the American Chemical Society</i> , 2005, 127, 3716-3717.	13.7	55

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55	Polychromatic Selective Population Inversion for TROSY Experiments with Large Proteins. Journal of the American Chemical Society, 2005, 127, 405-411.	13.7	13
56	NMR structure of the unliganded Bombyx mori pheromone-binding protein at physiological pH. FEBS Letters, 2002, 531, 314-318.	2.8	91