Woonghee Lee

List of Publications by Year
in descending order

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35 papers	2,261 citations	623574 14 h-index	360920 35 g-index
37 all docs	37 docs citations	37 times ranked	3565 citing authors

#	Article	IF	Citations
1	Structural and dynamic studies of the human RNA binding protein RBM3 reveals the molecular basis of its oligomerization and RNA recognition. FEBS Journal, 2022, 289, 2847-2864.	2.2	4
2	Solution structure and dynamics of the mitochondrialâ€targeted GTPase â€activating protein (GAP) VopE by an integrated NMR / SAXS approach. Protein Science, 2022, , .	3.1	2
3	NMR Structure and Biophysical Characterization of Thermophilic Single-Stranded DNA Binding Protein from Sulfolobus Solfataricus. International Journal of Molecular Sciences, 2022, 23, 3099.	1.8	3
4	A Toolset for the Solid-State NMR-based 3D Structure Calculation of Proteins. Journal of Magnetic Resonance, 2022, 339, 107214.	1.2	3
5	Solution structures of the Shewanella woodyi<scp>Hâ€NOX</scp> protein in the presence and absence of soluble guanylyl cyclase stimulator <scp>IWP</scp>â€051. Protein Science, 2021, 30, 448-463.	3.1	4
6	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. Bioinformatics, 2021, 37, 1176-1177.	1.8	12
7	Resonance assignments and secondary structure of thermophile singleâ€stranded DNA binding protein from Sulfolobus solfataricus at 323K. Biomolecular NMR Assignments, 2021, 15, 159-164.	0.4	1
8	Solution NMR Determination of the CDHR3 Rhinovirus-C Binding Domain, EC1. Viruses, 2021, 13, 159.	1.5	1
9	POKY: a software suite for multidimensional NMR and 3D structure calculation of biomolecules. Bioinformatics, 2021, 37, 3041-3042.	1.8	61
10	iPick: Multiprocessing software for integrated NMR signal detection and validation. Journal of Magnetic Resonance, 2021, 328, 106995.	1.2	9
11	At sixes and sevens: cryptic domain in the metal binding chain of the human copper transporter ATP7A. Biophysical Journal, 2021, 120, 4600-4607.	0.2	3
12	Structural Insights into N-terminal IgV Domain of BTNL2, a T Cell Inhibitory Molecule, Suggests a Non-canonical Binding Interface for Its Putative Receptors. Journal of Molecular Biology, 2020, 432, 5938-5950.	2.0	13
13	Structural, Dynamic, and Functional Characterization of a DnaX Mini-intein Derived from Spirulina platensis Provides Important Insights into Intein-Mediated Catalysis of Protein Splicing. Biochemistry, 2020, 59, 4711-4724.	1.2	7
14	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. Bioinformatics, 2020, 36, 2915-2916.	1.8	7
15	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. PLoS ONE, 2019, 14, e0217098.	1.1	8
16	I-PINE web server: an integrative probabilistic NMR assignment system for proteins. Journal of Biomolecular NMR, 2019, 73, 213-222.	1.6	50
17	Backbone resonance assignments and secondary structure of Ebola nucleoprotein 600â€“739 construct. Biomolecular NMR Assignments, 2019, 13, 315-319.	0.4	3
18	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. Nature Communications, 2019, 10, 5612.	5.8	15

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19	PINE-SPARKY.2 for automated NMR-based protein structure research. Bioinformatics, 2018, 34, 1586-1588.	1.8	27
20	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. PLoS Genetics, 2017, 13, e1007084.	1.5	30
21	Integrative NMR for biomolecular research. Journal of Biomolecular NMR, 2016, 64, 307-332.	1.6	47
22	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. Journal of Biomolecular NMR, 2016, 65, 51-57.	1.6	36
23	Probabilistic validation of protein NMR chemical shift assignments. Journal of Biomolecular NMR, 2016, 64, 17-25.	1.6	11
24	NMRFAM-SDF: a protein structure determination framework. Journal of Biomolecular NMR, 2015, 62, 481-495.	1.6	4
25	NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. Bioinformatics, 2015, 31, 1325-1327.	1.8	1,507
26	PONDEROSA-C/S: clientâ€“server based software package for automated protein 3D structure determination. Journal of Biomolecular NMR, 2014, 60, 73-75.	1.6	49
27	A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation. Journal of Cell Biology, 2014, 207, 481-498.	2.3	44
28	Molecular Insights into the Recognition of N-Terminal Histone Modifications by the BRPF1 Bromodomain. Journal of Molecular Biology, 2014, 426, 1661-1676.	2.0	64
29	Solution Structure of the 2A Protease from a Common Cold Agent, Human Rhinovirus C2, Strain W12. PLoS ONE, 2014, 9, e97198.	1.1	7
30	Fast automated protein NMR data collection and assignment by ADAPT-NMR on Bruker spectrometers. Journal of Magnetic Resonance, 2013, 236, 83-88.	1.2	14
31	PACSY, a relational database management system for protein structure and chemical shift analysis. Journal of Biomolecular NMR, 2012, 54, 169-179.	1.6	33
32	PACSY database, a relational database management system for Protein structure and nuclear Magnetic Resonance chemical shift analysis. , 2012, , .		1
33	PONDEROSA, an automated 3D-NOESY peak picking program, enables automated protein structure determination. Bioinformatics, 2011, 27, 1727-1728.	1.8	29
34	PINE-SPARKY: graphical interface for evaluating automated probabilistic peak assignments in protein NMR spectroscopy. Bioinformatics, 2009, 25, 2085-2087.	1.8	107
35	Structural proteomics by NMR spectroscopy. Expert Review of Proteomics, 2008, 5, 589-601.	1.3	42