

# Woonghee Lee

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2856725/publications.pdf>

Version: 2024-02-01

35  
papers

2,261  
citations

623734

14  
h-index

361022

35  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3565  
citing authors

#	ARTICLE	IF	CITATIONS
1	NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. <i>Bioinformatics</i> , 2015, 31, 1325-1327.	4.1	1,507
2	PINE-SPARKY: graphical interface for evaluating automated probabilistic peak assignments in protein NMR spectroscopy. <i>Bioinformatics</i> , 2009, 25, 2085-2087.	4.1	107
3	Molecular Insights into the Recognition of N-Terminal Histone Modifications by the BRPF1 Bromodomain. <i>Journal of Molecular Biology</i> , 2014, 426, 1661-1676.	4.2	64
4	POKY: a software suite for multidimensional NMR and 3D structure calculation of biomolecules. <i>Bioinformatics</i> , 2021, 37, 3041-3042.	4.1	61
5	I-PINE web server: an integrative probabilistic NMR assignment system for proteins. <i>Journal of Biomolecular NMR</i> , 2019, 73, 213-222.	2.8	50
6	PONDEROSA-C/S: client-server based software package for automated protein 3D structure determination. <i>Journal of Biomolecular NMR</i> , 2014, 60, 73-75.	2.8	49
7	Integrative NMR for biomolecular research. <i>Journal of Biomolecular NMR</i> , 2016, 64, 307-332.	2.8	47
8	A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation. <i>Journal of Cell Biology</i> , 2014, 207, 481-498.	5.2	44
9	Structural proteomics by NMR spectroscopy. <i>Expert Review of Proteomics</i> , 2008, 5, 589-601.	3.0	42
10	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. <i>Journal of Biomolecular NMR</i> , 2016, 65, 51-57.	2.8	36
11	PACSY, a relational database management system for protein structure and chemical shift analysis. <i>Journal of Biomolecular NMR</i> , 2012, 54, 169-179.	2.8	33
12	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. <i>PLoS Genetics</i> , 2017, 13, e1007084.	3.5	30
13	PONDEROSA, an automated 3D-NOESY peak picking program, enables automated protein structure determination. <i>Bioinformatics</i> , 2011, 27, 1727-1728.	4.1	29
14	PINE-SPARKY.2 for automated NMR-based protein structure research. <i>Bioinformatics</i> , 2018, 34, 1586-1588.	4.1	27
15	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. <i>Nature Communications</i> , 2019, 10, 5612.	12.8	15
16	Fast automated protein NMR data collection and assignment by ADAPT-NMR on Bruker spectrometers. <i>Journal of Magnetic Resonance</i> , 2013, 236, 83-88.	2.1	14
17	Structural Insights into N-terminal IgV Domain of BTNL2, a T Cell Inhibitory Molecule, Suggests a Non-canonical Binding Interface for Its Putative Receptors. <i>Journal of Molecular Biology</i> , 2020, 432, 5938-5950.	4.2	13
18	CHESPA/CHESCA-SPARKY: automated NMR data analysis plugins for SPARKY to map protein allostery. <i>Bioinformatics</i> , 2021, 37, 1176-1177.	4.1	12

#	ARTICLE	IF	CITATIONS
19	Probabilistic validation of protein NMR chemical shift assignments. <i>Journal of Biomolecular NMR</i> , 2016, 64, 17-25.	2.8	11
20	iPick: Multiprocessing software for integrated NMR signal detection and validation. <i>Journal of Magnetic Resonance</i> , 2021, 328, 106995.	2.1	9
21	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. <i>PLoS ONE</i> , 2019, 14, e0217098.	2.5	8
22	Structural, Dynamic, and Functional Characterization of a DnaX Mini-intein Derived from <i>Spirulina platensis</i> Provides Important Insights into Intein-Mediated Catalysis of Protein Splicing. <i>Biochemistry</i> , 2020, 59, 4711-4724.	2.5	7
23	PISA-SPARKY: an interactive SPARKY plugin to analyze oriented solid-state NMR spectra of helical membrane proteins. <i>Bioinformatics</i> , 2020, 36, 2915-2916.	4.1	7
24	Solution Structure of the 2A Protease from a Common Cold Agent, Human Rhinovirus C2, Strain W12. <i>PLoS ONE</i> , 2014, 9, e97198.	2.5	7
25	NMRFAM-SDF: a protein structure determination framework. <i>Journal of Biomolecular NMR</i> , 2015, 62, 481-495.	2.8	4
26	Solution structures of the <i>Shewanella woodyi</i> $\text{H}\alpha\text{NOX}$ protein in the presence and absence of soluble guanylyl cyclase stimulator $\text{IWP}$ . <i>Protein Science</i> , 2021, 30, 448-463.	7.6	4
27	Structural and dynamic studies of the human RNA binding protein RBM3 reveals the molecular basis of its oligomerization and RNA recognition. <i>FEBS Journal</i> , 2022, 289, 2847-2864.	4.7	4
28	Backbone resonance assignments and secondary structure of Ebola nucleoprotein 600-739 construct. <i>Biomolecular NMR Assignments</i> , 2019, 13, 315-319.	0.8	3
29	At sixes and sevens: cryptic domain in the metal binding chain of the human copper transporter ATP7A. <i>Biophysical Journal</i> , 2021, 120, 4600-4607.	0.5	3
30	NMR Structure and Biophysical Characterization of Thermophilic Single-Stranded DNA Binding Protein from <i>Sulfolobus solfataricus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3099.	4.1	3
31	A Toolset for the Solid-State NMR-based 3D Structure Calculation of Proteins. <i>Journal of Magnetic Resonance</i> , 2022, 339, 107214.	2.1	3
32	Solution structure and dynamics of the mitochondrial-targeted GTPase activating protein ( GAP ) VopE by an integrated NMR / SAXS approach. <i>Protein Science</i> , 2022, , .	7.6	2
33	PACSY database, a relational database management system for Protein structure and nuclear Magnetic Resonance chemical shift analysis. , 2012, , .		1
34	Resonance assignments and secondary structure of thermophile single-stranded DNA binding protein from <i>Sulfolobus solfataricus</i> at 323K. <i>Biomolecular NMR Assignments</i> , 2021, 15, 159-164.	0.8	1
35	Solution NMR Determination of the CDHR3 Rhinovirus-C Binding Domain, EC1. <i>Viruses</i> , 2021, 13, 159.	3.3	1