

Ke Ruan

List of Publications by Year in descending order

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43
papers

1,048
citations

471509

17
h-index

434195

31
g-index

48
all docs

48
docs citations

48
times ranked

1626
citing authors

#	ARTICLE	IF	CITATIONS
1	Recent progress in fragment-based drug discovery facilitated by NMR spectroscopy. <i>Magnetic Resonance Letters</i> , 2022, 2, 107-118.	1.3	5
2	Structures of human bile acid exporter ABCB11 reveal a transport mechanism facilitated by two tandem substrate-binding pockets. <i>Cell Research</i> , 2022, 32, 501-504.	12.0	17
3	Fragment-Based Discovery of AF9 YEATS Domain Inhibitors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3893.	4.1	3
4	The acyl-CoA-binding protein Acb1 regulates mitochondria, lipid droplets, and cell proliferation. <i>FEBS Letters</i> , 2022, 596, 1795-1808.	2.8	3
5	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. <i>Nature Chemical Biology</i> , 2021, 17, 1314-1323.	8.0	29
6	Mitotic motor CENP-E cooperates with PRC1 in temporal control of central spindle assembly. <i>Journal of Molecular Cell Biology</i> , 2020, 12, 654-665.	3.3	22
7	DeSiphering receptor core-induced and ligand-dependent conformational changes in arrestin via genetic encoded trimethylsilyl ¹ H-NMR probe. <i>Nature Communications</i> , 2020, 11, 4857.	12.8	25
8	Repurposing Low-Molecular-Weight Drugs against the Main Protease of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 7267-7272.	4.6	24
9	Phase separation drives decision making in cell division. <i>Journal of Biological Chemistry</i> , 2020, 295, 13419-13431.	3.4	41
10	Conformational Selection in Ligand Recognition by the First Tudor Domain of PHF20L1. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 7932-7938.	4.6	3
11	NMR Fragment-Based Screening against Tandem RNA Recognition Motifs of TDP-43. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3230.	4.1	8
12	Structural Insights into ceNAP1 Chaperoning Activity toward ceH2A-H2B. <i>Structure</i> , 2019, 27, 1798-1810.e3.	3.3	9
13	BubR1 phosphorylates CENP-E as a switch enabling the transition from lateral association to end-on capture of spindle microtubules. <i>Cell Research</i> , 2019, 29, 562-578.	12.0	46
14	Structural insight into the unique dsDNA binding topology of the human <sc>ORC</sc>2 wing helix domain. <i>FEBS Journal</i> , 2019, 286, 2726-2736.	4.7	2
15	Dynamic acetylation of the kinetochore-associated protein HEC1 ensures accurate microtubule-kinetochore attachment. <i>Journal of Biological Chemistry</i> , 2019, 294, 576-592.	3.4	20
16	A novel inhibitor of the new antibiotic resistance protein OptrA. <i>Chemical Biology and Drug Design</i> , 2018, 92, 1458-1467.	3.2	9
17	Structural plasticity of the TDRD3 Tudor domain probed by a fragment screening hit. <i>FEBS Journal</i> , 2018, 285, 2091-2103.	4.7	18
18	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 18-32.	3.3	32

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19	Dynamic Nature of CTCF Tandem 11 Zinc Fingers in Multivalent Recognition of DNA As Revealed by NMR Spectroscopy. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 4020-4028.	4.6	18
20	Allosteric mechanisms underlie GPCR signaling to SH3-domain proteins through arrestin. <i>Nature Chemical Biology</i> , 2018, 14, 876-886.	8.0	50
21	Ligand Proton Pseudocontact Shifts Determined from Paramagnetic Relaxation Dispersion in the Limit of NMR Intermediate Exchange. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 3361-3367.	4.6	17
22	The polar warhead of a TRIM 24 bromodomain inhibitor rearranges a water-mediated interaction network. <i>FEBS Journal</i> , 2017, 284, 1082-1095.	4.7	15
23	Fluorine Pseudocontact Shifts Used for Characterizing the Protein-Ligand Interaction Mode in the Limit of NMR Intermediate Exchange. <i>Angewandte Chemie</i> , 2017, 129, 13162-13166.	2.0	0
24	Fluorine Pseudocontact Shifts Used for Characterizing the Protein-Ligand Interaction Mode in the Limit of NMR Intermediate Exchange. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 12982-12986.	13.8	23
25	Structural insight into the recognition of acetylated histone H3K56ac mediated by the bromodomain of CREB-binding protein. <i>FEBS Journal</i> , 2017, 284, 3422-3436.	4.7	16
26	NMR characterization of weak interactions between RhoGDI2 and fragment screening hits. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3061-3070.	2.4	15
27	Process of Fragment-Based Lead Discovery—A Perspective from NMR. <i>Molecules</i> , 2016, 21, 854.	3.8	23
28	NMR Backbone Assignment of Large Proteins by Using ¹³ C-Only Triple-Resonance Experiments. <i>Chemistry - A European Journal</i> , 2016, 22, 9556-9564.	3.3	6
29	Frontispiece: NMR Backbone Assignment of Large Proteins by Using ¹³ C-Only Triple-Resonance Experiments. <i>Chemistry - A European Journal</i> , 2016, 22, .	3.3	0
30	NMR Fragment Screening Hit Induces Plasticity of BRD7/9 Bromodomains. <i>ChemBioChem</i> , 2016, 17, 1456-1463.	2.6	18
31	Structural and Functional Insights into the Human Björjeson-Forsman-Lehmann Syndrome-associated Protein PHF6. <i>Journal of Biological Chemistry</i> , 2014, 289, 10069-10083.	3.4	59
32	Automated NMR Fragment Based Screening Identified a Novel Interface Blocker to the LARG/RhoA Complex. <i>PLoS ONE</i> , 2014, 9, e88098.	2.5	17
33	Structure and Catalytic Mechanism of Yeast 4-Amino-4-deoxychorismate Lyase. <i>Journal of Biological Chemistry</i> , 2013, 288, 22985-22992.	3.4	5
34	Structural analysis of Stc1 provides insights into the coupling of RNAi and chromatin modification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1879-88.	7.1	16
35	Multiplexed NMR: An Automated CapNMR Dual-Sample Probe. <i>Analytical Chemistry</i> , 2010, 82, 7227-7236.	6.5	12
36	Application of Hadamard spectroscopy to automated structure verification in high-throughput NMR. <i>Magnetic Resonance in Chemistry</i> , 2009, 47, 693-700.	1.9	3

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37	De novo determination of internuclear vector orientations from residual dipolar couplings measured in three independent alignment media. <i>Journal of Biomolecular NMR</i> , 2008, 41, 61-76.	2.8	46
38	Interfacial tension of the aqueous two-phase systems of cationic-anionic surfactant mixtures. <i>Acta Physico-chimica Sinica</i> , 2006, 22, 1451-1455.	0.6	7
39	NMR Residual Dipolar Couplings as Probes of Biomolecular Dynamics. <i>Chemical Reviews</i> , 2006, 106, 1720-1736.	47.7	235
40	Multiple Alignment Tensors from a Denatured Protein. <i>Journal of the American Chemical Society</i> , 2006, 128, 9310-9311.	13.7	5
41	Interfacial Tension of Aqueous Three-Phase Systems Formed by Triton X100/PEG/Dextran. <i>Journal of Dispersion Science and Technology</i> , 2006, 27, 927-930.	2.4	5
42	Composite Alignment Media for the Measurement of Independent Sets of NMR Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2005, 127, 15032-15033.	13.7	48
43	Homogeneous Solutions of Equimolar Mixed Cationic~Anionic Surfactants. <i>Langmuir</i> , 2002, 18, 7250-7252.	3.5	73