

Jie-rong Huang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8940126/publications.pdf>

Version: 2024-02-01

27
papers

2,124
citations

393982

19
h-index

454577

30
g-index

32
all docs

32
docs citations

32
times ranked

2803
citing authors

#	ARTICLE	IF	CITATIONS
1	Phase separation driven by interchangeable properties in the intrinsically disordered regions of protein paralogs. <i>Communications Biology</i> , 2022, 5, 400.	2.0	13
2	The return of the rings: Evolutionary convergence of aromatic residues in the intrinsically disordered regions of RNA-binding proteins for liquid-liquid phase separation. <i>Protein Science</i> , 2022, 31, e4317.	3.1	9
3	Interactions between the Intrinsically Disordered Regions of hnRNP-A2 and TDP-43 Accelerate TDP-43's Conformational Transition. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5930.	1.8	5
4	Musashi-1: An Example of How Polyalanine Tracts Contribute to Self-Association in the Intrinsically Disordered Regions of RNA-Binding Proteins. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2289.	1.8	14
5	Liquid-liquid phase separation and extracellular multivalent interactions in the tale of galectin-3. <i>Nature Communications</i> , 2020, 11, 1229.	5.8	66
6	TAR DNA-binding protein 43 (TDP-43) liquid-liquid phase separation is mediated by just a few aromatic residues. <i>Journal of Biological Chemistry</i> , 2018, 293, 6090-6098.	1.6	195
7	The physical forces mediating self-association and phase-separation in the C-terminal domain of TDP-43. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 214-223.	1.1	89
8	The intrinsically disordered N-terminal domain of galectin-3 dynamically mediates multisite self-association of the protein through fuzzy interactions. <i>Journal of Biological Chemistry</i> , 2017, 292, 17845-17856.	1.6	54
9	Fibronectin in cell adhesion and migration via N-glycosylation. <i>Oncotarget</i> , 2017, 8, 70653-70668.	0.8	98
10	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 54.	1.6	23
11	Comprehensive structural and dynamical view of an unfolded protein from the combination of single-molecule FRET, NMR, and SAXS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5389-98.	3.3	134
12	The Nearest-Neighbor Effect on Random-Coil NMR Chemical Shifts Demonstrated Using a Low-Complexity Amino-Acid Sequence. <i>Protein and Peptide Letters</i> , 2016, 23, 967-975.	0.4	10
13	Exploring Free-Energy Landscapes of Intrinsically Disordered Proteins at Atomic Resolution Using NMR Spectroscopy. <i>Chemical Reviews</i> , 2014, 114, 6632-6660.	23.0	252
14	Transient Electrostatic Interactions Dominate the Conformational Equilibrium Sampled by Multidomain Splicing Factor U2AF65: A Combined NMR and SAXS Study. <i>Journal of the American Chemical Society</i> , 2014, 136, 7068-7076.	6.6	79
15	Direct Prediction of NMR Residual Dipolar Couplings from the Primary Sequence of Unfolded Proteins. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 687-690.	7.2	19
16	Residual dipolar couplings measured in unfolded proteins are sensitive to amino-acid-specific geometries as well as local conformational sampling. <i>Biochemical Society Transactions</i> , 2012, 40, 989-994.	1.6	10
17	Mapping the Potential Energy Landscape of Intrinsically Disordered Proteins at Amino Acid Resolution. <i>Journal of the American Chemical Society</i> , 2012, 134, 15138-15148.	6.6	113
18	Modulation of Structure and Dynamics by Disulfide Bond Formation in Unfolded States. <i>Journal of the American Chemical Society</i> , 2012, 134, 6846-6854.	6.6	33

#	ARTICLE	IF	CITATIONS
19	Sequence-Specific Mapping of the Interaction between Urea and Unfolded Ubiquitin from Ensemble Analysis of NMR and Small Angle Scattering Data. <i>Journal of the American Chemical Society</i> , 2012, 134, 4429-4436.	6.6	38
20	<i>Flexible-meccano</i> : a tool for the generation of explicit ensemble descriptions of intrinsically disordered proteins and their associated experimental observables. <i>Bioinformatics</i> , 2012, 28, 1463-1470.	1.8	324
21	Towards a robust description of intrinsic protein disorder using nuclear magnetic resonance spectroscopy. <i>Molecular BioSystems</i> , 2012, 8, 58-68.	2.9	95
22	Side-Chain ^1H Conformations in Urea-Denatured Ubiquitin and Protein G from ^3J Coupling Constants and Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2010, 132, 3196-3203.	6.6	35
23	Ensemble Calculations of Unstructured Proteins Constrained by RDC and PRE Data: A Case Study of Urea-Denatured Ubiquitin. <i>Journal of the American Chemical Society</i> , 2010, 132, 694-705.	6.6	112
24	DOTA-M8: An Extremely Rigid, High-Affinity Lanthanide Chelating Tag for PCS NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 14761-14767.	6.6	141
25	The extremely slow-exchanging core and acid-denatured state of green fluorescent protein. <i>HFSP Journal</i> , 2008, 2, 378-387.	2.5	17
26	Stable Intermediate States and High Energy Barriers in the Unfolding of GFP. <i>Journal of Molecular Biology</i> , 2007, 370, 356-371.	2.0	93
27	Understanding the folding of GFP using biophysical techniques. <i>Expert Review of Proteomics</i> , 2006, 3, 545-559.	1.3	46