

David Ban

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,021
citations

687363

13
h-index

610901

24
g-index

25
all docs

25
docs citations

25
times ranked

1536
citing authors

#	ARTICLE	IF	CITATIONS
1	EGCG binds intrinsically disordered N-terminal domain of p53 and disrupts p53-MDM2 interaction. <i>Nature Communications</i> , 2021, 12, 986.	12.8	77
2	Evolving Role of Conformational Dynamics in Understanding Fundamental Biomolecular Behavior. <i>ACS Symposium Series</i> , 2020, , 57-81.	0.5	1
3	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
4	¹ H, ¹³ C and ¹⁵ N resonance assignment of human guanylate kinase. <i>Biomolecular NMR Assignments</i> , 2018, 12, 11-14.	0.8	3
5	Solution NMR views of dynamical ordering of biomacromolecules. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 287-306.	2.4	26
6	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
7	A Small Molecule Causes a Population Shift in the Conformational Landscape of an Intrinsically Disordered Protein. <i>Journal of the American Chemical Society</i> , 2017, 139, 13692-13700.	13.7	37
8	Deciphering Conformational Changes Associated with the Maturation of Thrombin Anion Binding Exosite I. <i>Biochemistry</i> , 2017, 56, 6343-6354.	2.5	2
9	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
10	Kinetics of the Antibody Recognition Site in the Third IgGâ€œBinding Domain of Protein G. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 9567-9570.	13.8	21
11	Kinetics of the Antibody Recognition Site in the Third IgGâ€œBinding Domain of Protein G. <i>Angewandte Chemie</i> , 2016, 128, 9719-9722.	2.0	6
12	Nucleophosmin integrates within the nucleolus via multi-modal interactions with proteins displaying R-rich linear motifs and rRNA. <i>ELife</i> , 2016, 5, .	6.0	395
13	High-power ¹ 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
14	Monitoring Ligand-Induced Protein Ordering in Drug Discovery. <i>Journal of Molecular Biology</i> , 2016, 428, 1290-1303.	4.2	29
15	Allosteric switch regulates proteinâ€œprotein 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
16	Discovery of Small Molecules that Inhibit the Disordered Protein, p27Kip1. <i>Scientific Reports</i> , 2015, 5, 15686.	3.3	70
17	Sampling of Glycanâ€œBound Conformers by the Antiâ€œHIV Lectin <i>Oscillatoria agardhii</i> agglutinin in the Absence of Sugar. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 6462-6465.	13.8	11
18	Population Shuffling of Protein Conformations. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 207-210.	13.8	57

#	ARTICLE	IF	CITATIONS
19	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
20	Kinetics of Conformational Sampling in Ubiquitin. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 11437-11440.	13.8	59