

Andrew J Baldwin

List of Publications by Year in descending order

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64
papers

7,773
citations

109137

35
h-index

118652

62
g-index

76
all docs

76
docs citations

76
times ranked

9505
citing authors

#	ARTICLE	IF	CITATIONS
1	Phase Transition of a Disordered Nuage Protein Generates Environmentally Responsive Membraneless Organelles. <i>Molecular Cell</i> , 2015, 57, 936-947.	4.5	1,408
2	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014, 510, 172-175.	13.7	665
3	Bayesian Deconvolution of Mass and Ion Mobility Spectra: From Binary Interactions to Polydisperse Ensembles. <i>Analytical Chemistry</i> , 2015, 87, 4370-4376.	3.2	663
4	NMR spectroscopy brings invisible protein states into focus. <i>Nature Chemical Biology</i> , 2009, 5, 808-814.	3.9	403
5	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8194-E8203.	3.3	381
6	Metastability of Native Proteins and the Phenomenon of Amyloid Formation. <i>Journal of the American Chemical Society</i> , 2011, 133, 14160-14163.	6.6	369
7	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017, 541, 421-424.	13.7	344
8	Membraneless organelles can melt nucleic acid duplexes and act as biomolecular filters. <i>Nature Chemistry</i> , 2016, 8, 569-575.	6.6	278
9	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. <i>Science</i> , 2016, 354, .	6.0	247
10	Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2007-2012.	3.3	231
11	Collision Cross Sections for Structural Proteomics. <i>Structure</i> , 2015, 23, 791-799.	1.6	231
12	The structured core domain of α -crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1562-70.	3.3	181
13	Cytochrome Display on Amyloid Fibrils. <i>Journal of the American Chemical Society</i> , 2006, 128, 2162-2163.	6.6	146
14	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.	5.8	136
15	α -Crystallin Polydispersity Is a Consequence of Unbiased Quaternary Dynamics. <i>Journal of Molecular Biology</i> , 2011, 413, 297-309.	2.0	122
16	Perturbation of the Stability of Amyloid Fibrils through Alteration of Electrostatic Interactions. <i>Biophysical Journal</i> , 2011, 100, 2783-2791.	0.2	121
17	The Polydispersity of α -Crystallin Is Rationalized by an Interconverting Polyhedral Architecture. <i>Structure</i> , 2011, 19, 1855-1863.	1.6	116
18	Small Heat-Shock Proteins: Paramedics of the Cell. <i>Topics in Current Chemistry</i> , 2012, 328, 69-98.	4.0	116

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19	Selective Radical Trifluoromethylation of Native Residues in Proteins. <i>Journal of the American Chemical Society</i> , 2018, 140, 1568-1571.	6.6	102
20	Light-driven post-translational installation of reactive protein side chains. <i>Nature</i> , 2020, 585, 530-537.	13.7	100
21	Characterisation of Amyloid Fibril Formation by Small Heat-shock Chaperone Proteins Human α -A-, α -B- and R120G α -B-Crystallins. <i>Journal of Molecular Biology</i> , 2007, 372, 470-484.	2.0	93
22	Local unfolding of the HSP27 monomer regulates chaperone activity. <i>Nature Communications</i> , 2019, 10, 1068.	5.8	93
23	Quaternary Dynamics of α -B-Crystallin as a Direct Consequence of Localised Tertiary Fluctuations in the C-Terminus. <i>Journal of Molecular Biology</i> , 2011, 413, 310-320.	2.0	89
24	Dissecting Heterogeneous Molecular Chaperone Complexes Using a Mass Spectrum Deconvolution Approach. <i>Chemistry and Biology</i> , 2012, 19, 599-607.	6.2	70
25	C-terminal interactions mediate the quaternary dynamics of α -B-crystallin. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20110405.	1.8	70
26	Probing Dynamic Conformations of the High-Molecular-Weight α -B-Crystallin Heat Shock Protein Ensemble by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2012, 134, 15343-15350.	6.6	63
27	¹³ C ₂ Methyl Group Probes of Millisecond Time Scale Exchange in Proteins by ¹ H Relaxation Dispersion: An Application to Proteasome Gating Residue Dynamics. <i>Journal of the American Chemical Society</i> , 2010, 132, 10992-10995.	6.6	60
28	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. <i>Science Advances</i> , 2019, 5, eaav8421.	4.7	52
29	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018, 359, 930-935.	6.0	51
30	Twisting Transition between Crystalline and Fibrillar Phases of Aggregated Peptides. <i>Physical Review Letters</i> , 2012, 109, 158101.	2.9	48
31	Automatic Assignment of Methyl-NMR Spectra of Supramolecular Machines Using Graph Theory. <i>Journal of the American Chemical Society</i> , 2017, 139, 9523-9533.	6.6	48
32	Measurement of Amyloid Fibril Length Distributions by Inclusion of Rotational Motion in Solution NMR Diffusion Measurements. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 3385-3387.	7.2	47
33	The Quaternary Organization and Dynamics of the Molecular Chaperone HSP26 Are Thermally Regulated. <i>Chemistry and Biology</i> , 2010, 17, 1008-1017.	6.2	45
34	Investigating the Mechanisms of Amylolysis of Starch Granules by Solution-State NMR. <i>Biomacromolecules</i> , 2015, 16, 1614-1621.	2.6	44
35	An exact solution for R _{2,eff} in CPMG experiments in the case of two site chemical exchange. <i>Journal of Magnetic Resonance</i> , 2014, 244, 114-124.	1.2	42
36	Accommodating Protein Dynamics in the Modeling of Chemical Crosslinks. <i>Structure</i> , 2017, 25, 1751-1757.e5.	1.6	36

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37	Measurement of Methyl Axis Orientations in Invisible, Excited States of Proteins by Relaxation Dispersion NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 11939-11948.	6.6	33
38	An R1 ρ expression for a spin in chemical exchange between two sites with unequal transverse relaxation rates. <i>Journal of Biomolecular NMR</i> , 2013, 55, 211-218.	1.6	32
39	Proline isomerization in the C-terminal region of HSP27. <i>Cell Stress and Chaperones</i> , 2017, 22, 639-651.	1.2	24
40	Pathogen-sugar interactions revealed by universal saturation transfer analysis. <i>Science</i> , 2022, 377, .	6.0	24
41	Contribution of rotational diffusion to pulsed field gradient diffusion measurements. <i>Journal of Chemical Physics</i> , 2007, 127, 114505.	1.2	23
42	Monitoring the Disassembly of Virus-like Particles by ¹⁹ F-NMR. <i>Journal of the American Chemical Society</i> , 2017, 139, 5277-5280.	6.6	23
43	Fast Molecular Compression by a Hyperthermal Collision Gives Bond-Selective Mechanochemistry. <i>Physical Review Letters</i> , 2021, 126, 056001.	2.9	22
44	Conditional Disorder in Small Heat-shock Proteins. <i>Journal of Molecular Biology</i> , 2020, 432, 3033-3049.	2.0	21
45	The Morphology of Decorated Amyloid Fibers is Controlled by the Conformation and Position of the Displayed Protein. <i>ACS Nano</i> , 2012, 6, 1332-1346.	7.3	19
46	Measurement of the signs of methyl ¹³ C chemical shift differences between interconverting ground and excited protein states by R1 ρ : an application to β -crystallin. <i>Journal of Biomolecular NMR</i> , 2012, 53, 1-12.	1.6	18
47	Measuring Diffusion Constants of Invisible Protein Conformers by Triple α Quantum ¹ H CPMG Relaxation Dispersion. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16777-16780.	7.2	17
48	Combining tandem mass spectrometry with ion mobility separation to determine the architecture of polydisperse proteins. <i>International Journal of Mass Spectrometry</i> , 2015, 377, 663-671.	0.7	16
49	Dynamic design: manipulation of millisecond timescale motions on the energy landscape of cyclophilin A. <i>Chemical Science</i> , 2020, 11, 2670-2680.	3.7	16
50	Post-translational insertion of boron in proteins to probe and modulate function. <i>Nature Chemical Biology</i> , 2021, 17, 1245-1261.	3.9	15
51	A weakened interface in the P182L variant of HSP27 associated with severe Charcot α Marie α Tooth neuropathy causes aberrant binding to interacting proteins. <i>EMBO Journal</i> , 2021, 40, e103811.	3.5	14
52	Local frustration determines loop opening during the catalytic cycle of an oxidoreductase. <i>ELife</i> , 2020, 9, .	2.8	13
53	Determination of an optimally sensitive and specific chemical exchange saturation transfer MRI quantification metric in relevant biological phantoms. <i>NMR in Biomedicine</i> , 2016, 29, 1624-1633.	1.6	12
54	INDIANA: An in-cell diffusion method to characterize the size, abundance and permeability of cells. <i>Journal of Magnetic Resonance</i> , 2019, 302, 1-13.	1.2	11

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55	Dynamic binding. <i>Nature</i> , 2012, 488, 165-166.	13.7	10
56	Harnessing NMR relaxation interference effects to characterise supramolecular assemblies. <i>Chemical Communications</i> , 2016, 52, 7450-7453.	2.2	6
57	Cell-permeable lanthanide- ^{IV} platinum anti-cancer prodrugs. <i>Dalton Transactions</i> , 2021, 50, 8761-8767.	1.6	6
58	Measuring Diffusion Constants of Invisible Protein Conformers by Triple-Quantum ¹ H CPMG Relaxation Dispersion. <i>Angewandte Chemie</i> , 2018, 130, 17019-17022.	1.6	5
59	Formation of a Secretion-Competent Protein Complex by a Dynamic Wrap-around Binding Mechanism. <i>Journal of Molecular Biology</i> , 2018, 430, 3157-3169.	2.0	5
60	Quantitative chemical exchange saturation transfer imaging of nuclear overhauser effects in acute ischemic stroke. <i>Magnetic Resonance in Medicine</i> , 2022, , .	1.9	2
61	Phase Separation of Disordered Protein in the Formation of Membrane-Less Organelles. <i>Biophysical Journal</i> , 2014, 106, 35a.	0.2	1
62	Reductive site-selective atypical C ₁ , C ₂ -type N ₂ -C ₂ cleavage allows C-terminal protein amidation. <i>Science Advances</i> , 2022, 8, eabl8675.	4.7	1
63	Studying the Conformational Equilibrium of the N-Terminal Domain of Dsbd by NMR and Computer Simulation. <i>Biophysical Journal</i> , 2015, 108, 184a.	0.2	0
64	AB-Crystallin Binds to Titin Ig Domains and Increases Stiffness of Skinned Cardiac Trabeculae. <i>Biophysical Journal</i> , 2015, 108, 444a.	0.2	0