

Christopher A Waudby

List of Publications by Year in descending order

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53
papers

4,294
citations

236925

25
h-index

197818

49
g-index

64
all docs

64
docs citations

64
times ranked

5854
citing authors

#	ARTICLE	IF	CITATIONS
1	An Analytical Solution to the Kinetics of Breakable Filament Assembly. <i>Science</i> , 2009, 326, 1533-1537.	12.6	970
2	Atomic structure and hierarchical assembly of a cross- β amyloid fibril. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5468-5473.	7.1	479
3	Mechanosensitive Self-Replication Driven by Self-Organization. <i>Science</i> , 2010, 327, 1502-1506.	12.6	465
4	Metastability of Native Proteins and the Phenomenon of Amyloid Formation. <i>Journal of the American Chemical Society</i> , 2011, 133, 14160-14163.	13.7	369
5	Structure and Properties of a Complex of β -Synuclein and a Single-Domain Camelid Antibody. <i>Journal of Molecular Biology</i> , 2010, 402, 326-343.	4.2	164
6	Two-Dimensional NMR Lineshape Analysis. <i>Scientific Reports</i> , 2016, 6, 24826.	3.3	161
7	Binding of the Molecular Chaperone β -Crystallin to β Amyloid Fibrils Inhibits Fibril Elongation. <i>Biophysical Journal</i> , 2011, 101, 1681-1689.	0.5	143
8	The Interaction of β -Crystallin with Mature β -Synuclein Amyloid Fibrils Inhibits Their Elongation. <i>Biophysical Journal</i> , 2010, 98, 843-851.	0.5	136
9	A structural ensemble of a ribosome-nascent chain complex during cotranslational protein folding. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 278-285.	8.2	135
10	Hsp90 Inhibits β -Synuclein Aggregation by Interacting with Soluble Oligomers. <i>Journal of Molecular Biology</i> , 2013, 425, 4614-4628.	4.2	104
11	Nature and Regulation of Protein Folding on the Ribosome. <i>Trends in Biochemical Sciences</i> , 2019, 44, 914-926.	7.5	97
12	Glial Innate Immunity Generated by Non-Aggregated Alpha-Synuclein in Mouse: Differences between Wild-type and Parkinson's Disease-Linked Mutants. <i>PLoS ONE</i> , 2010, 5, e13481.	2.5	89
13	In-Cell NMR Characterization of the Secondary Structure Populations of a Disordered Conformation of β -Synuclein within <i>E. coli</i> Cells. <i>PLoS ONE</i> , 2013, 8, e72286.	2.5	89
14	On the Mechanism of Nonspecific Inhibitors of Protein Aggregation: Dissecting the Interactions of β -Synuclein with Congo Red and Lacmoid. <i>Biochemistry</i> , 2009, 48, 8322-8334.	2.5	88
15	Inversion of the Balance between Hydrophobic and Hydrogen Bonding Interactions in Protein Folding and Aggregation. <i>PLoS Computational Biology</i> , 2011, 7, e1002169.	3.2	86
16	The H50Q Mutation Induces a 10-fold Decrease in the Solubility of β -Synuclein. <i>Journal of Biological Chemistry</i> , 2015, 290, 2395-2404.	3.4	65
17	Structural characterization of the interaction of β -synuclein nascent chains with the ribosomal surface and trigger factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5012-5017.	7.1	54
18	D25V apolipoprotein C-III variant causes dominant hereditary systemic amyloidosis and confers cardiovascular protective lipoprotein profile. <i>Nature Communications</i> , 2016, 7, 10353.	12.8	50

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19	Position-Dependent Electrostatic Protection against Protein Aggregation. <i>ChemBioChem</i> , 2009, 10, 1309-1312.	2.6	47
20	A strategy for co-translational folding studies of ribosome-bound nascent chain complexes using NMR spectroscopy. <i>Nature Protocols</i> , 2016, 11, 1492-1507.	12.0	39
21	Systematic mapping of free energy landscapes of a growing filamin domain during biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9744-9749.	7.1	39
22	Rapid Distinction of Intracellular and Extracellular Proteins Using NMR Diffusion Measurements. <i>Journal of the American Chemical Society</i> , 2012, 134, 11312-11315.	13.7	35
23	Protein folding on the ribosome studied using NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2013, 74, 57-75.	7.5	35
24	Rapid Quantification of Protein-Ligand Binding via ¹⁹ F NMR Lineshape Analysis. <i>Biophysical Journal</i> , 2020, 118, 2537-2548.	0.5	34
25	Structural Dynamics Associated with Intermediate Formation in an Archetypal Conformational Disease. <i>Structure</i> , 2012, 20, 504-512.	3.3	33
26	Interactions between nascent proteins and the ribosome surface inhibit co-translational folding. <i>Nature Chemistry</i> , 2021, 13, 1214-1220.	13.6	27
27	Binding of Monovalent and Bivalent Ligands by Transthyretin Causes Different Short- and Long-Distance Conformational Changes. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 8274-8283.	6.4	25
28	Nascent chains can form co-translational folding intermediates that promote post-translational folding outcomes in a disease-causing protein. <i>Nature Communications</i> , 2021, 12, 6447.	12.8	22
29	Chemical documents: machine understanding and automated information extraction. <i>Organic and Biomolecular Chemistry</i> , 2004, 2, 3294.	2.8	21
30	An analysis of NMR sensitivity enhancements obtained using non-uniform weighted sampling, and the application to protein NMR. <i>Journal of Magnetic Resonance</i> , 2012, 219, 46-52.	2.1	21
31	GPU accelerated Monte Carlo simulation of pulsed-field gradient NMR experiments. <i>Journal of Magnetic Resonance</i> , 2011, 211, 67-73.	2.1	18
32	From Selection to Instruction and Back: Competing Conformational Selection and Induced Fit Pathways in Abiotic Hosts. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 19942-19948.	13.8	18
33	Two-dimensional NMR lineshape analysis of single, multiple, zero and double quantum correlation experiments. <i>Journal of Biomolecular NMR</i> , 2020, 74, 95-109.	2.8	15
34	High-resolution ex vivo NMR spectroscopy of human Z ¹ -antitrypsin. <i>Nature Communications</i> , 2020, 11, 6371.	12.8	15
35	Common sequence motifs of nascent chains engage the ribosome surface and trigger factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	13
36	Optimal design of adaptively sampled NMR experiments for measurement of methyl group dynamics with application to a ribosome-nascent chain complex. <i>Journal of Magnetic Resonance</i> , 2021, 326, 106937.	2.1	12

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37	Increasing the sensitivity of NMR diffusion measurements by paramagnetic longitudinal relaxation enhancement, with application to ribosomeâ€™ nascent chain complexes. <i>Journal of Biomolecular NMR</i> , 2015, 63, 151-163.	2.8	10
38	Probing the dynamic stalk region of the ribosome using solution NMR. <i>Scientific Reports</i> , 2019, 9, 13528.	3.3	10
39	Crossâ€™Peaks in Simple Twoâ€™Dimensional NMR Experiments from Chemical Exchange of Transverse Magnetisation. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 8784-8788.	13.8	10
40	Thermodynamics of co-translational folding and ribosomeâ€™ nascent chain interactions. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102357.	5.7	9
41	Nascent chain dynamics and ribosome interactions within folded ribosomeâ€™ nascent chain complexes observed by NMR spectroscopy. <i>Chemical Science</i> , 2021, 12, 13120-13126.	7.4	8
42	NMR Lineshape Analysis of Intrinsically Disordered Protein Interactions. <i>Methods in Molecular Biology</i> , 2020, 2141, 477-504.	0.9	8
43	Application of Lysine-specific Labeling to Detect Transient Interactions Present During Human Lysozyme Amyloid Fibril Formation. <i>Scientific Reports</i> , 2017, 7, 15018.	3.3	6
44	Dynamics of Ligand Binding to a Rigid Glycosidase**. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 20508-20514.	13.8	4
45	From Selection to Instruction and Back: Competing Conformational Selection and Induced Fit Pathways in Abiotic Hosts. <i>Angewandte Chemie</i> , 2021, 133, 20095-20101.	2.0	4
46	Distinct dissociation rates of murine and human norovirus P-domain dimers suggest a role of dimer stability in virus-host interactions. <i>Communications Biology</i> , 2022, 5, .	4.4	4
47	Crossâ€™Peaks in Simple Twoâ€™Dimensional NMR Experiments from Chemical Exchange of Transverse Magnetisation. <i>Angewandte Chemie</i> , 2019, 131, 8876-8880.	2.0	2
48	Solution-State Nuclear Magnetic Resonance Spectroscopy and Protein Folding. <i>Methods in Molecular Biology</i> , 2011, 752, 97-120.	0.9	2
49	Analysis of conformational exchange processes using methyl-TROSY-based Hahn echo measurements of quadruple-quantum relaxation. <i>Magnetic Resonance</i> , 2021, 2, 777-793.	1.9	1
50	Structural Investigation of an Immunoglobulin Domain on the Ribosome using NMR Spectroscopy. <i>Biophysical Journal</i> , 2017, 112, 41a.	0.5	0
51	Structures and Dynamics of Protein Folding on the Ribosome by NMR Spectroscopy. <i>Biophysical Journal</i> , 2018, 114, 414a.	0.5	0
52	Dynamics of Ligand Binding to a Rigid Glycosidase**. <i>Angewandte Chemie</i> , 2020, 132, 20689-20695.	2.0	0
53	Structural investigation of the folding of an immunoglobulin domain on the ribosome using NMR Spectroscopy (LB197). <i>FASEB Journal</i> , 2014, 28, LB197.	0.5	0