David Cowburn

List of Publications by Year in descending order

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28 papers 1,061 citations

623734 14 h-index 501196 28 g-index

29 all docs

29 docs citations

29 times ranked 1281 citing authors

#	Article	IF	CITATIONS
1	Direct Measurement of 15N Chemical Shift Anisotropy in Solution. Journal of the American Chemical Society, 1998, 120, 10947-10952.	13.7	154
2	The molecular mechanism of nuclear transport revealed by atomic-scale measurements. ELife, 2015, 4, .	6.0	130
3	A promiscuous split intein with expanded protein engineering applications. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8538-8543.	7.1	102
4	Model-Independent Analysis of 15N Chemical Shift Anisotropy from NMR Relaxation Data. Ubiquitin as a Test Example. Journal of the American Chemical Society, 1998, 120, 7109-7110.	13.7	88
5	An Approach to Direct Determination of Protein Dynamics from 15N NMR Relaxation at Multiple Fields, Independent of Variable 15N Chemical Shift Anisotropy and Chemical Exchange Contributions. Journal of the American Chemical Society, 1999, 121, 8577-8582.	13.7	84
6	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex. Structure, 2017, 25, 434-445.	3.3	61
7	Structural and Dynamical Features of Inteins and Implications on Protein Splicing. Journal of Biological Chemistry, 2014, 289, 14506-14511.	3.4	55
8	A Full-Length Group 1 Bacterial Sigma Factor Adopts a Compact Structure Incompatible with DNA Binding. Chemistry and Biology, 2008, 15, 1091-1103.	6.0	51
9	Thermodynamic characterization of the multivalent interactions underlying rapid and selective translocation through the nuclear pore complex. Journal of Biological Chemistry, 2018, 293, 4555-4563.	3.4	47
10	Solution Structures of FclµRI l̂±-Chain Mimics:Â A l̂²-Hairpin Peptide and Its Retroenantiomer. Journal of the American Chemical Society, 1997, 119, 5321-5328.	13.7	44
11	Chapter 8 Segmental Isotopic Labeling of Proteins for Nuclear Magnetic Resonance. Methods in Enzymology, 2009, 462, 151-175.	1.0	43
12	The Effect of Finite Sampling on the Determination of Orientational Properties:Â A Theoretical Treatment with Application to Interatomic Vectors in Proteins. Journal of the American Chemical Society, 2000, 122, 10640-10649.	13.7	35
13	Dynamic intramolecular regulation of the histone chaperone nucleoplasmin controls histone binding and release. Nature Communications, 2017, 8, 2215.	12.8	23
14	Enzymatic semisynthesis of porcine despentapeptide (B26–30) insulin using unprotected desoctapeptide (B23–30) insulin as a substrate. International Journal of Peptide and Protein Research, 1986, 27, 514-521.	0.1	22
15	Deciphering the "Fuzzy―Interaction of FG Nucleoporins and Transport Factors Using Small-Angle Neutron Scattering. Structure, 2018, 26, 477-484.e4.	3.3	19
16	Combining biophysical methods to analyze the disulfide bond in SH2 domain of C-terminal Src kinase. Biophysics Reports, 2016, 2, 33-43.	0.8	15
17	An Atypical Mechanism of Split Intein Molecular Recognition and Folding. Journal of the American Chemical Society, 2018, 140, 11791-11799.	13.7	15
18	Structural determination of biomolecular interfaces by nuclear magnetic resonance of proteins with reduced proton density. Journal of Biomolecular NMR, 2010, 47, 41-54.	2.8	14

#	Article	lF	CITATIONS
19	Anti-DNA antibody mediated catalysis is isotype dependent. Molecular Immunology, 2016, 69, 33-43.	2.2	12
20	Effects of FGFR2 kinase activation loop dynamics on catalytic activity. PLoS Computational Biology, 2017, 13, e1005360.	3.2	10
21	Segmental Isotopic Labeling of Proteins for NMR Study Using Intein Technology. Methods in Molecular Biology, 2017, 1495, 131-145.	0.9	9
22	Correlation of chemical shifts predicted by molecular dynamics simulations for partially disordered proteins. Journal of Biomolecular NMR, 2015, 61, 35-45.	2.8	8
23	Resurfaced ZIKV EDIII nanoparticle immunogens elicit neutralizing and protective responses inÂvivo. Cell Chemical Biology, 2022, 29, 811-823.e7.	5.2	6
24	Domain interactions of C-terminal Src Kinase determined through NMR spectroscopy with segmental isotope labeling. Protein and Cell, 2017, 8, 67-71.	11.0	4
25	Identification of Hydrophobic Interfaces in Protein-Ligand Complexes by Selective Saturation Transfer NMR Spectroscopy. Molecules, 2015, 20, 21992-21999.	3.8	3
26	Integrating NOE and RDC using sum-of-squares relaxation for protein structure determination. Journal of Biomolecular NMR, 2017, 68, 163-185.	2.8	3
27	ANOMALOUS EXCHANGE KINETICS OF PEPTIDE AMIDE PROTONS IN AQUEOUS SOLUTIONS. International Journal of Peptide and Protein Research, 1981, 17, 42-47.	0.1	2
28	NMR assignment through linear programming. Journal of Global Optimization, 2022, 83, 3-28.	1.8	2