

Bill William Broadhurst

List of Publications by Year in descending order

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38
papers

2,454
citations

257450

24
h-index

330143

37
g-index

38
all docs

38
docs citations

38
times ranked

2840
citing authors

#	ARTICLE	IF	CITATIONS
1	Cis \leftrightarrow trans isomerization at a proline opens the pore of a neurotransmitter-gated ion channel. <i>Nature</i> , 2005, 438, 248-252.	27.8	421
2	DANGLE: A Bayesian inferential method for predicting protein backbone dihedral angles and secondary structure. <i>Journal of Magnetic Resonance</i> , 2010, 202, 223-233.	2.1	221
3	The Structure of Docking Domains in Modular Polyketide Synthases. <i>Chemistry and Biology</i> , 2003, 10, 723-731.	6.0	185
4	Photo-CIDNP of biopolymers. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1993, 25, 345-402.	7.5	171
5	Structure of the A-Domain of HMG1 and Its Interaction with DNA as Studied by Heteronuclear Three- and Four-Dimensional NMR Spectroscopy. <i>Biochemistry</i> , 1995, 34, 16596-16607.	2.5	171
6	An Approach to the Structure Determination of Larger Proteins Using Triple Resonance NMR Experiments in Conjunction with Random Fractional Deuteration. <i>Journal of the American Chemical Society</i> , 1996, 118, 407-415.	13.7	114
7	An RNA degradosome assembly in <i>Caulobacter crescentus</i> . <i>Nucleic Acids Research</i> , 2011, 39, 1449-1459.	14.5	84
8	Multienzyme docking in hybrid megasynthetases. <i>Nature Chemical Biology</i> , 2008, 4, 75-81.	8.0	80
9	Three-dimensional structure of the major autoantigen in primary biliary cirrhosis. <i>Gastroenterology</i> , 1998, 115, 139-146.	1.3	78
10	Solution Structures of Apo and Holo Biotinyl Domains from Acetyl Coenzyme A Carboxylase of <i>Escherichia coli</i> Determined by Triple-Resonance Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1999, 38, 5045-5053.	2.5	75
11	DNA-binding properties of the tandem HMG boxes of high-mobility-group protein 1 (HMG1). <i>FEBS Journal</i> , 1998, 253, 787-795.	0.2	71
12	Conformational plasticity of ligand-bound and ternary GPCR complexes studied by ^{19}F NMR of the β_2 -adrenergic receptor. <i>Nature Communications</i> , 2020, 11, 669.	12.8	67
13	Analysis of the natively unstructured RNA/protein-recognition core in the <i>Escherichia coli</i> RNA degradosome and its interactions with regulatory RNA/Hfq complexes. <i>Nucleic Acids Research</i> , 2018, 46, 387-402.	14.5	66
14	A photochemically induced dynamic nuclear polarization study of denatured state of lysozyme. <i>Biochemistry</i> , 1991, 30, 405-412.	2.5	58
15	An approach to global fold determination using limited NMR data from larger proteins selectively protonated at specific residue types. <i>Journal of Biomolecular NMR</i> , 1996, 8, 360-368.	2.8	56
16	^1H -NMR assignments and local environments of aromatic residues in bovine, human and guinea pig variants of alpha-lactalbumin. <i>FEBS Journal</i> , 1992, 210, 699-709.	0.2	51
17	Structure of the <i>Escherichia coli</i> ProQ RNA-binding protein. <i>Rna</i> , 2017, 23, 696-711.	3.5	50
18	Backbone Dynamics of the A-Domain of HMG1 As Studied by ^{15}N NMR Spectroscopy. <i>Biochemistry</i> , 1995, 34, 16608-16617.	2.5	46

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19	Probing the Interactions of Carboxy-atractyloside and Atractyloside with the Yeast Mitochondrial ADP/ATP Carrier. <i>Structure</i> , 2010, 18, 39-46.	3.3	42
20	Insights into Protein-Protein and Enzyme-Substrate Interactions in Modular Polyketide Synthases. <i>Chemistry and Biology</i> , 2010, 17, 705-716.	6.0	41
21	Broadening substrate specificity of a chain-extending ketosynthase through a single active-site mutation. <i>Chemical Communications</i> , 2016, 52, 8373-8376.	4.1	38
22	Hydrogen/deuterium exchange of hydrophobic peptides in model membranes by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 1376-1387.	2.8	30
23	Solution Structure and Backbone Dynamics of the KH-QUA2 Region of the Xenopus STAR/GSG Quaking Protein. <i>Journal of Molecular Biology</i> , 2005, 348, 265-279.	4.2	29
24	Interaction between an Amantadine Analogue and the Transmembrane Portion of the Influenza A M2 Protein in Liposomes Probed by ¹ H NMR Spectroscopy of the Ligand. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 4975-4978.	6.4	26
25	Interaction of the E2 and E3 components of the pyruvate dehydrogenase multienzyme complex of <i>Bacillus stearothermophilus</i> . <i>FEBS Journal</i> , 2004, 272, 259-268.	4.7	24
26	Equilibrium Unfolding Studies of Horse Muscle Acylphosphatase. <i>FEBS Journal</i> , 1994, 225, 811-817.	0.2	20
27	Structure and properties in solution of PsaD, an extrinsic polypeptide of photosystem I. <i>FEBS Journal</i> , 1998, 255, 309-316.	0.2	19
28	¹⁹ F NMR detection of the complex between amantadine and the receptor portion of the influenza A M2 ion channel in DPC micelles. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 3947-3952.	2.2	19
29	Sticky swinging arm dynamics: studies of an acyl carrier protein domain from the mycolactone polyketide synthase. <i>Biochemical Journal</i> , 2016, 473, 1097-1110.	3.7	19
30	Interpretation of the polarized electron paramagnetic resonance signal of plant Photosystem I. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1986, 852, 106-111.	1.0	16
31	Heteronuclear NMR studies of the specificity of the post-translational modification of biotinyl domains by biotinyl protein ligase. <i>FEBS Letters</i> , 2000, 479, 93-98.	2.8	15
32	Dissecting how modular polyketide synthase ketoreductases interact with acyl carrier protein-attached substrates. <i>Chemical Communications</i> , 2017, 53, 11457-11460.	4.1	12
33	Modular type I polyketide synthase acyl carrier protein domains share a common N-terminally extended fold. <i>Scientific Reports</i> , 2019, 9, 2325.	3.3	12
34	Solution structure of the lipoyl domain of the chimeric dihydrolipoyl dehydrogenase P64K from <i>Neisseria meningitidis</i> . <i>FEBS Journal</i> , 2001, 268, 4908-4917.	0.2	9
35	Autonomous folding of interdomain regions of a modular polyketide synthase. <i>FEBS Journal</i> , 2007, 274, 2196-2209.	4.7	9
36	Backbone dynamics of oxidised and reduced forms of human atrial natriuretic peptide. <i>Journal of Structural Biology</i> , 2004, 148, 214-225.	2.8	6

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37	Solution Structure of the QUA1 Dimerization Domain of pXqua, the Xenopus Ortholog of Quaking. PLoS ONE, 2013, 8, e57345.	2.5	3
38	Chapter 3. Making the Most of Chemical Shifts. RSC Biomolecular Sciences, 0, , 53-83.	0.4	0