

R Andrew Atkinson

List of Publications by Year in descending order

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82
papers

2,449
citations

186265

28
h-index

214800

47
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86
all docs

86
docs citations

86
times ranked

3394
citing authors

#	ARTICLE	IF	CITATIONS
1	Dipeptide inhibitors of the prostate specific membrane antigen (PSMA): A comparison of urea and thiourea derivatives. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021, 42, 128044.	2.2	3
2	One-step, kit-based radiopharmaceuticals for molecular SPECT imaging: a versatile diphosphine chelator for ^{99m}Tc radiolabelling of peptides. <i>Dalton Transactions</i> , 2021, 50, 16156-16165.	3.3	6
3	Metabolomics and microbial composition increase insight into the impact of dietary differences in cirrhosis. <i>Liver International</i> , 2020, 40, 416-427.	3.9	13
4	Organocatalytic Access to a <i>cis</i> -Cyclopentyl- ^{13}C -amino Acid: An Intriguing Model of Selectivity and Formation of a Stable 10/12-Helix from the Corresponding ^{13}C -Peptide. <i>Journal of the American Chemical Society</i> , 2020, 142, 1382-1393.	13.7	11
5	A pleurocidin analogue with greater conformational flexibility, enhanced antimicrobial potency and in vivo therapeutic efficacy. <i>Communications Biology</i> , 2020, 3, 697.	4.4	14
6	NMR of proteins and nucleic acids. <i>Nuclear Magnetic Resonance</i> , 2020, , 250-271.	0.2	1
7	Temporin L and aurein 2.5 have identical conformations but subtly distinct membrane and antibacterial activities. <i>Scientific Reports</i> , 2019, 9, 10934.	3.3	22
8	PS-082-Plasma metabolomic changes modulate the impact of Middle Eastern versus Western Diet in an international cirrhosis cohort. <i>Journal of Hepatology</i> , 2019, 70, e52-e53.	3.7	0
9	Resonance assignment of human LARP4A La module. <i>Biomolecular NMR Assignments</i> , 2019, 13, 169-172.	0.8	4
10	15-deoxy- $^{12,14}\text{C}$ -Prostaglandin J2 inhibits human soluble epoxide hydrolase by a dual orthosteric and allosteric mechanism. <i>Communications Biology</i> , 2019, 2, 188.	4.4	16
11	THU-052-Immunometabolic profiling of ascites from patients with acute-on-chronic liver failure reveals increased MerTK+ immunosuppressive myeloid cells and cell death markers with preferential lipid metabolism compared to cirrhosis without organ failure. <i>Journal of Hepatology</i> , 2019, 70, e183.	3.7	1
12	LARP4A recognizes polyA RNA via a novel binding mechanism mediated by disordered regions and involving the PAM2w motif, revealing interplay between PABP, LARP4A and mRNA. <i>Nucleic Acids Research</i> , 2019, 47, 4272-4291.	14.5	23
13	Controlling the dynamics of the Nek2 leucine zipper by engineering of ϵ -disulphide bonds. <i>PLoS ONE</i> , 2019, 14, e0210352.	2.5	3
14	Metabolomic and lipidomic plasma profile changes in human participants ascending to Everest Base Camp. <i>Scientific Reports</i> , 2019, 9, 2297.	3.3	31
15	Minor sequence modifications in temporin B cause drastic changes in antibacterial potency and selectivity by fundamentally altering membrane activity. <i>Scientific Reports</i> , 2019, 9, 1385.	3.3	26
16	Microbial functional change is linked with clinical outcomes after capsular fecal transplant in cirrhosis. <i>JCI Insight</i> , 2019, 4, .	5.0	49
17	Structural and Functional Insights into Bacillus subtilis Sigma Factor Inhibitor, CsfB. <i>Structure</i> , 2018, 26, 640-648.e5.	3.3	12
18	Human physiological and metabolic responses to an attempted winter crossing of Antarctica: the effects of prolonged hypobaric hypoxia. <i>Physiological Reports</i> , 2018, 6, e13613.	1.7	18

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19	Proteomic and metabolomic changes driven by elevating myocardial creatine suggest novel metabolic feedback mechanisms. <i>Amino Acids</i> , 2016, 48, 1969-1981.	2.7	15
20	¹ H, ¹⁵ N and ¹³ C chemical shift assignments of the La motif and RRM1 from human LARP6. <i>Biomolecular NMR Assignments</i> , 2015, 9, 337-340.	0.8	1
21	Disorder-To-Order Transition of MAGI-1 PDZ1 C-Terminal Extension upon Peptide Binding: Thermodynamic and Dynamic Insights. <i>Biochemistry</i> , 2015, 54, 1327-1337.	2.5	10
22	Synergic interplay of the La motif, RRM1 and the interdomain linker of LARP6 in the recognition of collagen mRNA expands the RNA binding repertoire of the La module. <i>Nucleic Acids Research</i> , 2015, 43, 645-660.	14.5	68
23	Mechanism and consequence of the autoactivation of p38 ^α mitogen-activated protein kinase promoted by TAB1. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1182-1190.	8.2	95
24	Insight into the HIV-1 Vif SOCS-box ^α ElonginBC interaction. <i>Open Biology</i> , 2013, 3, 130100.	3.6	8
25	The Asymmetric Binding of PGC-1 ^α to the ERR ^α and ERR ^β Nuclear Receptor Homodimers Involves a Similar Recognition Mechanism. <i>PLoS ONE</i> , 2013, 8, e67810.	2.5	34
26	Conformational Flexibility Determines Selectivity and Antibacterial, Antiplasmodial, and Anticancer Potency of Cationic α -Helical Peptides*. <i>Journal of Biological Chemistry</i> , 2012, 287, 34120-34133.	3.4	78
27	Solution Structure of RING Finger-like Domain of Retinoblastoma-binding Protein-6 (RBBP6) Suggests It Functions as a U-box. <i>Journal of Biological Chemistry</i> , 2012, 287, 7146-7158.	3.4	18
28	Solution Structure Analysis of the HPV16 E6 Oncoprotein Reveals a Self-Association Mechanism Required for E6-Mediated Degradation of p53. <i>Structure</i> , 2012, 20, 604-617.	3.3	104
29	The Structural and Dynamic Response of MAGI-1 PDZ1 with Noncanonical Domain Boundaries to the Binding of Human Papillomavirus E6. <i>Journal of Molecular Biology</i> , 2011, 406, 745-763.	4.2	43
30	The structural plasticity of SCA7 domains defines their differential nucleosome ^α binding properties. <i>EMBO Reports</i> , 2010, 11, 612-618.	4.5	28
31	Automated overexpression and isotopic labelling of biologically active oncoproteins in the cyanobacterium <i>Anabaena</i> sp. PCC 7120. <i>Biotechnology and Applied Biochemistry</i> , 2008, 51, 53.	3.1	7
32	TCTP protects from apoptotic cell death by antagonizing bax function. <i>Cell Death and Differentiation</i> , 2008, 15, 1211-1220.	11.2	184
33	Multiple Conformations of the Metal-Bound Pyoverdine PvdI, a Siderophore of <i>Pseudomonas aeruginosa</i> : A Nuclear Magnetic Resonance Study. <i>Biochemistry</i> , 2008, 47, 3397-3406.	2.5	19
34	Defining the minimal interacting regions of the tight junction protein MAGI-1 and HPV16 E6 oncoprotein for solution structure studies. <i>Protein Expression and Purification</i> , 2008, 60, 64-73.	1.3	16
35	Solution Structure and Self-association Properties of the p8 TFIID Subunit Responsible for Trichothiodystrophy. <i>Journal of Molecular Biology</i> , 2007, 368, 473-480.	4.2	31
36	Biophysical characterization of an indolinone inhibitor in the ATP-binding site of DNA gyrase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 1206-1213.	2.1	14

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37	Engineering, Biophysical Characterisation and Binding Properties of a Soluble Mutant form of Annexin A2 Domain IV that Adopts a Partially Folded Conformation. <i>Journal of Molecular Biology</i> , 2006, 363, 469-481.	4.2	14
38	Structural and Functional Analysis of E6 Oncoprotein: Insights in the Molecular Pathways of Human Papillomavirus-Mediated Pathogenesis. <i>Molecular Cell</i> , 2006, 21, 665-678.	9.7	162
39	NMR in the SPINE Structural Proteomics project. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1150-1161.	2.5	12
40	¹³ C, ¹⁵ N and ¹ H Resonance Assignment of the PDZ1 domain of MAGI-1 using QUASI. <i>Journal of Biomolecular NMR</i> , 2006, 36, 33-33.	2.8	5
41	A low-temperature heteronuclear NMR study of two exchanging conformations of metal-bound pyoverdin PaA from <i>Pseudomonas aeruginosa</i> . <i>Biopolymers</i> , 2005, 79, 139-149.	2.4	7
42	¹ H and ¹⁵ N resonance assignment, secondary structure and dynamic behaviour of the C-terminal domain of human papillomavirus oncoprotein E6. <i>Journal of Biomolecular NMR</i> , 2005, 31, 129-141.	2.8	16
43	Biochemical and NMR Mapping of the Interface between CREB-binding Protein and Ligand Binding Domains of Nuclear Receptor. <i>Journal of Biological Chemistry</i> , 2005, 280, 5682-5692.	3.4	17
44	The Structure-Activity Relationship of Ferric Pyoverdine Bound to Its Outer Membrane Transporter: Implications for the Mechanism of Iron Uptake. <i>Biochemistry</i> , 2005, 44, 14069-14079.	2.5	21
45	Dynamics and Metal Exchange Properties of C4C4 RING Domains from CNOT4 and the p44 Subunit of TFIIF. <i>Journal of Molecular Biology</i> , 2005, 349, 621-637.	4.2	21
46	Solution Structure of ZASP PDZ Domain. <i>Structure</i> , 2004, 12, 611-622.	3.3	45
47	The role of protein motions in molecular recognition: insights from heteronuclear NMR relaxation measurements. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 141-187.	7.5	44
48	QUASI: Quick Access to Spectral Interpretation. <i>Comptes Rendus Chimie</i> , 2004, 7, 335-341.	0.5	3
49	Domain Architecture of the p62 Subunit from the Human Transcription/Repair Factor TFIIF Deduced by Limited Proteolysis and Mass Spectrometry Analysis. <i>Biochemistry</i> , 2004, 43, 14420-14430.	2.5	26
50	The Three-Dimensional Structure of the Gallium Complex of Azoverdin, a Siderophore of <i>Azomonas macrocytogenes</i> ATCC 12334, Determined by NMR Using Residual Dipolar Coupling Constants. <i>Biochemistry</i> , 2002, 41, 12488-12497.	2.5	15
51	Effects of temperature on the dynamic behaviour of the HIV-1 nucleocapsid NCp7 and its DNA complex. <i>Journal of Molecular Biology</i> , 2002, 316, 611-627.	4.2	31
52	The direct determination of protein structure by NMR without assignment. <i>FEBS Letters</i> , 2002, 510, 1-4.	2.8	15
53	A Structural Characterization of the Interactions between Titin Z-Repeats and the β -Actinin C-Terminal Domain. <i>Biochemistry</i> , 2001, 40, 4957-4965.	2.5	41
54	Ca ²⁺ -independent binding of an EF-hand domain to a novel motif in the alpha-actinin-titin complex. <i>Nature Structural Biology</i> , 2001, 8, 853-857.	9.7	76

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55	Assignment of the ^1H , ^{13}C and ^{15}N resonances of the C-terminal EF-hands of alpha-actinin in a 14 kDa complex with Z-repeat 7 of titin. <i>Journal of Biomolecular NMR</i> , 2000, 16, 277-278.	2.8	3
56	Structural and Dynamic Characterization of ^1H -Conotoxin MVIIA: The Binding Loop Exhibits Slow Conformational Exchange. <i>Biochemistry</i> , 2000, 39, 3908-3919.	2.5	40
57	Binding of ^1H -Actinin to Titin: Implications for Z-Disk Assembly. <i>Biochemistry</i> , 2000, 39, 5255-5264.	2.5	47
58	Reduced spectral density mapping for proteins: Validity for studies of ^{13}C relaxation. <i>Journal of Biomolecular NMR</i> , 1999, 13, 83-88.	2.8	8
59	Mapping the active site of factor Xa by selective inhibitors: An NMR and MD study. , 1998, 30, 264-274.		11
60	Bacterial Iron Transport: ^1H NMR Determination of the Three-Dimensional Structure of the Gallium Complex of Pyoverdine G4R, the Peptidic Siderophore of <i>Pseudomonas putida</i> G4R. <i>Biochemistry</i> , 1998, 37, 15965-15973.	2.5	42
61	The assembly of immunoglobulin-like modules in titin: implications for muscle elasticity. <i>Journal of Molecular Biology</i> , 1998, 284, 761-777.	4.2	78
62	A NMR and MD study of the active site of factor Xa by selective inhibitors. <i>Journal De Chimie Physique Et De Physico-Chimie Biologique</i> , 1998, 95, 443-446.	0.2	2
63	The Investigation of Protein Dynamics Via the Spectral Density Function. , 1998, , 129-145.		0
64	Direct fitting of structure and chemical shift to NMR spectra. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1997, 93, 3319-3323.	1.7	7
65	^7Li Nuclear Magnetic Resonance Study of Lithium Binding to <i>Myo</i> -inositol Monophosphatase. <i>FEBS Journal</i> , 1996, 240, 288-291.	0.2	22
66	The Direct Determination of Protein Structure from Multidimensional NMR Spectra without Assignment. , 1996, , 49-55.		0
67	Conformational Studies of Osteocalcin in Solution. <i>FEBS Journal</i> , 1995, 232, 515-521.	0.2	14
68	Conformational Studies of Osteocalcin in Solution. <i>FEBS Journal</i> , 1995, 232, 515-521.	0.2	32
69	Stimulation of cGMP-dependent protein kinase alpha by a peptide from its own sequence. An investigation by enzymology, circular dichroism and ^1H NMR of the activity and structure of cGMP-dependent protein kinase alpha-(546-576)-peptide amide. <i>FEBS Journal</i> , 1994, 221, 581-593.	0.2	7
70	Echistatin: the refined structure of a disintegrin in solution by ^1H NMR and restrained molecular dynamics. <i>International Journal of Peptide and Protein Research</i> , 1994, 43, 563-572.	0.1	29
71	Conformational study of cyclo[D-Trp-D-Asp-Pro-D-Val-Leu], an endothelin-A receptor-selective antagonist. <i>FEBS Letters</i> , 1992, 296, 1-6.	2.8	46
72	Proton NMR and circular dichroism studies of the N-terminal domain of cyclic GMP dependent protein kinase: a leucine/isoleucine zipper. <i>Biochemistry</i> , 1991, 30, 9387-9395.	2.5	71

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73	Three-dimensional structure of echistatin, the smallest active RGD protein. <i>Biochemistry</i> , 1991, 30, 7369-7372.	2.5	215
74	The secondary structure of echistatin from ¹ H-NMR, circular-dichroism and Raman spectroscopy. <i>FEBS Journal</i> , 1991, 202, 329-338.	0.2	43
75	Topological mirror images in protein structure computation: An underestimated problem. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 22-32.	2.6	33
76	Thirty-Fourth Annual Meeting February 18-22, 1990 Baltimore Convention Center Baltimore, Maryland. <i>Biophysical Journal</i> , 1990, 57, 325a-365a.	0.5	1
77	Solution structure of the kringle 4 domain from human plasminogen by ¹ H nuclear magnetic resonance spectroscopy and distance geometry. <i>Journal of Molecular Biology</i> , 1990, 212, 541-552.	4.2	45
78	Identification and description of α -helical regions in horse muscle acylphosphatase by ¹ H nuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1989, 205, 229-239.	4.2	23
79	N.m.r. structural studies on the tyrosine kinase domain of the human insulin receptor. <i>Biochemical Society Transactions</i> , 1989, 17, 899-899.	3.4	0
80	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome <i>c</i> . <i>FEBS Journal</i> , 1988, 177, 179-185.	0.2	6
81	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome <i>c</i> . <i>FEBS Journal</i> , 1988, 177, 179-185.	0.2	23
82	AMPK is a Mechano-Metabolic Sensor Linking Mitochondrial Dynamics to Myosin II Dependent Cell Migration. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1