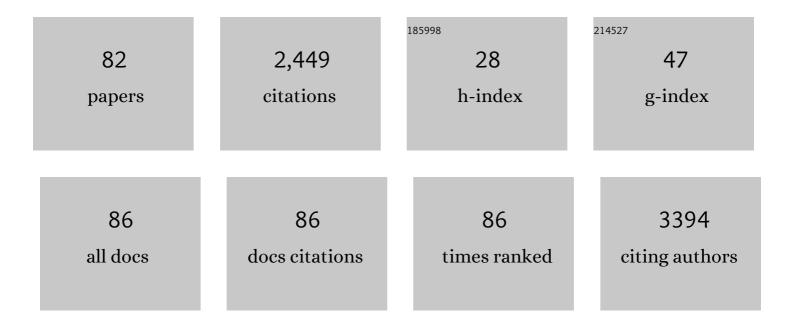
## R Andrew Atkinson

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Three-dimensional structure of echistatin, the smallest active RGD protein. Biochemistry, 1991, 30, 7369-7372.	1.2	215
2	TCTP protects from apoptotic cell death by antagonizing bax function. Cell Death and Differentiation, 2008, 15, 1211-1220.	5.0	184
3	Structural and Functional Analysis of E6 Oncoprotein: Insights in the Molecular Pathways of Human Papillomavirus-Mediated Pathogenesis. Molecular Cell, 2006, 21, 665-678.	4.5	162
4	Solution Structure Analysis of the HPV16 E6 Oncoprotein Reveals a Self-Association Mechanism Required for E6-Mediated Degradation of p53. Structure, 2012, 20, 604-617.	1.6	104
5	Mechanism and consequence of the autoactivation of p38α mitogen-activated protein kinase promoted by TAB1. Nature Structural and Molecular Biology, 2013, 20, 1182-1190.	3.6	95
6	The assembly of immunoglobulin-like modules in titin: implications for muscle elasticity. Journal of Molecular Biology, 1998, 284, 761-777.	2.0	78
7	Conformational Flexibility Determines Selectivity and Antibacterial, Antiplasmodial, and Anticancer Potency of Cationic α-Helical Peptides*. Journal of Biological Chemistry, 2012, 287, 34120-34133.	1.6	78
8	Ca2+-independent binding of an EF-hand domain to a novel motif in the alpha-actinin-titin complex. Nature Structural Biology, 2001, 8, 853-857.	9.7	76
9	Proton NMR and circular dichroism studies of the N-terminal domain of cyclic GMP dependent protein kinase: a leucine/isoleucine zipper. Biochemistry, 1991, 30, 9387-9395.	1.2	71
10	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. Nucleic Acids Research, 2015, 43, 645-660.	6.5	68
11	Microbial functional change is linked with clinical outcomes after capsular fecal transplant in cirrhosis. JCI Insight, 2019, 4, .	2.3	49
12	Binding of α-Actinin to Titin: Implications for Z-Disk Assembly. Biochemistry, 2000, 39, 5255-5264.	1.2	47
13	Conformational study of cyclo[D-Trp-D-Asp-Pro-D-Val-Leu], an endothelin-A receptor-selective antagonist. FEBS Letters, 1992, 296, 1-6.	1.3	46
14	Solution structure of the kringle 4 domain from human plasminogen by 1H nuclear magnetic resonance spectroscopy and distance geometry. Journal of Molecular Biology, 1990, 212, 541-552.	2.0	45
15	Solution Structure of ZASP PDZ Domain. Structure, 2004, 12, 611-622.	1.6	45
16	The role of protein motions in molecular recognition: insights from heteronuclear NMR relaxation measurements. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 44, 141-187.	3.9	44
17	The secondary structure of echistatin from 1H-NMR, circular-dichroism and Raman spectroscopy. FEBS Journal, 1991, 202, 329-338.	0.2	43
18	The Structural and Dynamic Response of MAGI-1 PDZ1 with Noncanonical Domain Boundaries to the Binding of Human Papillomavirus E6. Journal of Molecular Biology, 2011, 406, 745-763.	2.0	43

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19	Bacterial Iron Transport:Â1H NMR Determination of the Three-Dimensional Structure of the Gallium Complex of Pyoverdin G4R, the Peptidic Siderophore ofPseudomonas putidaG4Râ€,‡. Biochemistry, 1998, 37, 15965-15973.	1.2	42
20	A Structural Characterization of the Interactions between Titin Z-Repeats and the α-Actinin C-Terminal Domain. Biochemistry, 2001, 40, 4957-4965.	1.2	41
21	Structural and Dynamic Characterization of ï‰-Conotoxin MVIIA:  The Binding Loop Exhibits Slow Conformational Exchange,. Biochemistry, 2000, 39, 3908-3919.	1.2	40
22	The Asymmetric Binding of PGC-1α to the ERRα and ERRÎ <sup>3</sup> Nuclear Receptor Homodimers Involves a Similar Recognition Mechanism. PLoS ONE, 2013, 8, e67810.	1.1	34
23	Topological mirror images in protein structure computation: An underestimated problem. Proteins: Structure, Function and Bioinformatics, 1991, 10, 22-32.	1.5	33
24	Conformational Studies of Osteocalcin in Solution. FEBS Journal, 1995, 232, 515-521.	0.2	32
25	Effects of temperature on the dynamic behaviour of the HIV-1 nucleocapsid NCp7 and its DNA complex. Journal of Molecular Biology, 2002, 316, 611-627.	2.0	31
26	Solution Structure and Self-association Properties of the p8 TFIIH Subunit Responsible for Trichothiodystrophy. Journal of Molecular Biology, 2007, 368, 473-480.	2.0	31
27	Metabolomic and lipidomic plasma profile changes in human participants ascending to Everest Base Camp. Scientific Reports, 2019, 9, 2297.	1.6	31
28	Echistatin: the refined structure of a disintegrin in solution by <sup>1</sup> H NMR and restrained molecular dynamics. International Journal of Peptide and Protein Research, 1994, 43, 563-572.	0.1	29
29	The structural plasticity of SCA7 domains defines their differential nucleosomeâ€binding properties. EMBO Reports, 2010, 11, 612-618.	2.0	28
30	Domain Architecture of the p62 Subunit from the Human Transcription/Repair Factor TFIIH Deduced by Limited Proteolysis and Mass Spectrometry Analysis. Biochemistry, 2004, 43, 14420-14430.	1.2	26
31	Minor sequence modifications in temporin B cause drastic changes in antibacterial potency and selectivity by fundamentally altering membrane activity. Scientific Reports, 2019, 9, 1385.	1.6	26
32	Identification and description of α-helical regions in horse muscle acylphosphatase by 1H nuclear magnetic resonance spectroscopy. Journal of Molecular Biology, 1989, 205, 229-239.	2.0	23
33	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. Nucleic Acids Research, 2019, 47, 4272-4291.	6.5	23
34	Two-dimensional NMR as a probe of structural similarity applied to mutants of cytochrome c. FEBS Journal, 1988, 177, 179-185.	0.2	23
35	<sup>7</sup> Li Nuclearâ€Magneticâ€Resonance Study of Lithium Binding to <i>Myo</i> â€Inositol Monophosphatase. FEBS Journal, 1996, 240, 288-291.	0.2	22
36	Temporin L and aurein 2.5 have identical conformations but subtly distinct membrane and antibacterial activities. Scientific Reports, 2019, 9, 10934.	1.6	22

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37	The Structureâ^'Activity Relationship of Ferric Pyoverdine Bound to Its Outer Membrane Transporter:Â Implications for the Mechanism of Iron Uptakeâ€. Biochemistry, 2005, 44, 14069-14079.	1.2	21
38	Dynamics and Metal Exchange Properties of C4C4 RING Domains from CNOT4 and the p44 Subunit of TFIIH. Journal of Molecular Biology, 2005, 349, 621-637.	2.0	21
39	Multiple Conformations of the Metal-Bound Pyoverdine PvdI, a Siderophore of <i>Pseudomonas aeruginosa</i> : A Nuclear Magnetic Resonance Study <sup>,</sup> . Biochemistry, 2008, 47, 3397-3406.	1.2	19
40	Solution Structure of RING Finger-like Domain of Retinoblastoma-binding Protein-6 (RBBP6) Suggests It Functions as a U-box. Journal of Biological Chemistry, 2012, 287, 7146-7158.	1.6	18
41	Human physiological and metabolic responses to an attempted winter crossing of Antarctica: the effects of prolonged hypobaric hypoxia Physiological Reports, 2018, 6, e13613.	0.7	18
42	Biochemical and NMR Mapping of the Interface between CREB-binding Protein and Ligand Binding Domains of Nuclear Receptor. Journal of Biological Chemistry, 2005, 280, 5682-5692.	1.6	17
43	1H and 15N resonance assignment, secondary structure and dynamic behaviour of the C-terminal domain of human papillomavirus oncoprotein E6. Journal of Biomolecular NMR, 2005, 31, 129-141.	1.6	16
44	Defining the minimal interacting regions of the tight junction protein MAGI-1 and HPV16 E6 oncoprotein for solution structure studies. Protein Expression and Purification, 2008, 60, 64-73.	0.6	16
45	15-deoxy-î"12,14-Prostaglandin J2 inhibits human soluble epoxide hydrolase by a dual orthosteric and allosteric mechanism. Communications Biology, 2019, 2, 188.	2.0	16
46	The Three-Dimensional Structure of the Gallium Complex of Azoverdin, a Siderophore ofAzomonas macrocytogenesATCC 12334, Determined by NMR Using Residual Dipolar Coupling Constantsâ€. Biochemistry, 2002, 41, 12488-12497.	1.2	15
47	The direct determination of protein structure by NMR without assignment. FEBS Letters, 2002, 510, 1-4.	1.3	15
48	Proteomic and metabolomic changes driven by elevating myocardial creatine suggest novel metabolic feedback mechanisms. Amino Acids, 2016, 48, 1969-1981.	1.2	15
49	Conformational Studies of Osteocalcin in Solution. FEBS Journal, 1995, 232, 515-521.	0.2	14
50	Biophysical characterization of an indolinone inhibitor in the ATP-binding site of DNA gyrase. Biochemical and Biophysical Research Communications, 2006, 349, 1206-1213.	1.0	14
51	Engineering, Biophysical Characterisation and Binding Properties of a Soluble Mutant form of Annexin A2 Domain IV that Adopts a Partially Folded Conformation. Journal of Molecular Biology, 2006, 363, 469-481.	2.0	14
52	A pleurocidin analogue with greater conformational flexibility, enhanced antimicrobial potency and in vivo therapeutic efficacy. Communications Biology, 2020, 3, 697.	2.0	14
53	Metabolomics and microbial composition increase insight into the impact of dietary differences in cirrhosis. Liver International, 2020, 40, 416-427.	1.9	13
54	NMR in the SPINE Structural Proteomics project. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1150-1161.	2.5	12

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55	Structural and Functional Insights into Bacillus subtilis Sigma Factor Inhibitor, CsfB. Structure, 2018, 26, 640-648.e5.	1.6	12
56	Mapping the active site of factor Xa by selective inhibitors: An NMR and MD study. , 1998, 30, 264-274.		11
57	Organocatalytic Access to a <i>cis</i> -Cyclopentyl-γ-amino Acid: An Intriguing Model of Selectivity and Formation of a Stable 10/12-Helix from the Corresponding γ/α-Peptide. Journal of the American Chemical Society, 2020, 142, 1382-1393.	6.6	11
58	Disorder-To-Order Transition of MAGI-1 PDZ1 C-Terminal Extension upon Peptide Binding: Thermodynamic and Dynamic Insights. Biochemistry, 2015, 54, 1327-1337.	1.2	10
59	Reduced spectral density mapping for proteins: Validity for studies of 13C relaxation. Journal of Biomolecular NMR, 1999, 13, 83-88.	1.6	8
60	Insight into the HIV-1 Vif SOCS-box–ElonginBC interaction. Open Biology, 2013, 3, 130100.	1.5	8
61	Stimulation of cGMP-dependent protein kinase lalpha 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 lalpha-(546-576)-peptide amide. FEBS Journal, 1994, 221, 581-593.	0.2	7
62	Direct fitting of structure and chemical shift to NMR spectra. Journal of the Chemical Society, Faraday Transactions, 1997, 93, 3319-3323.	1.7	7
63	A low-temperature heteronuclear NMR study of two exchanging conformations of metal-bound pyoverdin PaA fromPseudomonas aeruginosa. Biopolymers, 2005, 79, 139-149.	1.2	7
64	Automated overexpression and isotopic labelling of biologically active oncoproteins in the cyanobacterium Anabaena sp. PCC 7120. Biotechnology and Applied Biochemistry, 2008, 51, 53.	1.4	7
65	Twoâ€dimensional NMR as a probe of structural similarity applied to mutants of cytochrome <i>c</i> . FEBS Journal, 1988, 177, 179-185.	0.2	6
66	One-step, kit-based radiopharmaceuticals for molecular SPECT imaging: a versatile diphosphine chelator for <sup>99m</sup> Tc radiolabelling of peptides. Dalton Transactions, 2021, 50, 16156-16165.	1.6	6
67	13C, 15N and 1H Resonance Assignment of the PDZ1 domain of MAGI-1 using QUASI. Journal of Biomolecular NMR, 2006, 36, 33-33.	1.6	5
68	Resonance assignment of human LARP4A La module. Biomolecular NMR Assignments, 2019, 13, 169-172.	0.4	4
69	Assignment of the 1H, 13C and 15N resonances of the C-terminal EF-hands of alpha-actinin in a 14 kDa complex with Z-repeat 7 of titin. Journal of Biomolecular NMR, 2000, 16, 277-278.	1.6	3
70	QUASIÂ: Quick Access to Spectral Interpretation. Comptes Rendus Chimie, 2004, 7, 335-341.	0.2	3
71	Controlling the dynamics of the Nek2 leucine zipper by engineering of "kinetic―disulphide bonds. PLoS ONE, 2019, 14, e0210352.	1.1	3
72	Dipeptide inhibitors of the prostate specific membrane antigen (PSMA): A comparison of urea and thiourea derivatives. Bioorganic and Medicinal Chemistry Letters, 2021, 42, 128044.	1.0	3

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73	A NMR and MD study of the active site of factor Xa by selective inhibitors. Journal De Chimie Physique Et De Physico-Chimie Biologique, 1998, 95, 443-446.	0.2	2
74	Thirty-Fourth Annual Meeting February 18–22, 1990 Baltimore Convention Center Baltimore, Maryland. Biophysical Journal, 1990, 57, 325a-365a.	0.2	1
75	1H, 15N and 13C chemical shift assignments of the La motif and RRM1 from human LARP6. Biomolecular NMR Assignments, 2015, 9, 337-340.	0.4	1
76	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. Journal of Hepatology, 2019, 70, e183.	1.8	1
77	AMPK is a Mechano-Metabolic Sensor Linking Mitochondrial Dynamics to Myosin II Dependent Cell Migration. SSRN Electronic Journal, 0, , .	0.4	1
78	NMR of proteins and nucleic acids. Nuclear Magnetic Resonance, 2020, , 250-271.	0.1	1
79	N.m.r. structural studies on the tyrosine kinase domain of the human insulin receptor. Biochemical Society Transactions, 1989, 17, 899-899.	1.6	0
80	PS-082-Plasma metabolomic changes modulate the impact of Middle Eastern versus Western Diet in an international cirrhosis cohort. Journal of Hepatology, 2019, 70, e52-e53.	1.8	0
81	The Direct Determination of Protein Structure from Multidimensional NMR Spectra without Assignment. , 1996, , 49-55.		0
82	The Investigation of Protein Dynamics Via the Spectral Density Function. , 1998, , 129-145.		0