Andrew L Lee

List of Publications by Year
in descending order

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53 papers	2,998 citations	186265 28 h-index	175258 52 g-index
68 all docs	68 docs citations	68 times ranked	2651 citing authors

#	Article	IF	Citations
1	Backbone and ILVM methyl resonance assignments of human thymidylate synthase in apo and substrate bound forms. Biomolecular NMR Assignments, 2021, 15, 197-202.	0.8	3
2	Quality of Life in Vulvar Lichen Sclerosus Patients Treated With Long-Term Topical Corticosteroids. Journal of Lower Genital Tract Disease, 2021, 25, 158-165.	1.9	8
3	Balancing the benefits of antimicrobial therapy with the threat of antimicrobial resistanceÂdevelopment. Journal of Cystic Fibrosis, 2021, 20, 377-378.	0.7	1
4	Visualizing an Allosteric Intermediate Using CuAAC Stabilization of an NMR Mixed Labeled Dimer. ACS Chemical Biology, 2021, 16, 2766-2775.	3.4	4
5	Mapping allosteric communications within individual proteins. Nature Communications, 2020, 11, 3862.	12.8	101
6	Inter-Active Site Communication Mediated by the Dimer Interface Î²-Sheet in the Half-the-Sites Enzyme, Thymidylate Synthase. Biochemistry, 2019, 58, 3302-3313.	2.5	9
7	Isotopic Labeling of Formate Dehydrogenase Perturbs the Protein Dynamics. Journal of Physical Chemistry B, 2019, 123, 10403-10409.	2.6	14
8	Positive Cooperativity in Substrate Binding by Human Thymidylate Synthase. Biophysical Journal, 2019, 117, 1074-1084.	0.5	11
9	Thermodynamic and NMR Assessment of Ligand Cooperativity and Intersubunit Communication in Symmetric Dimers: Application to Thymidylate Synthase. Frontiers in Molecular Biosciences, 2018, 5, 47.	3.5	11
10	Protein Mass Effects on Formate Dehydrogenase. Journal of the American Chemical Society, 2017, 139, 17405-17413.	13.7	17
11	An Ancestral Tryptophanyl-tRNA Synthetase Precursor Achieves High Catalytic Rate Enhancement without Ordered Ground-State Tertiary Structures. ACS Chemical Biology, 2016, 11, 1661-1668.	3.4	21
12	Chemical shift imprint of intersubunit communication in a symmetric homodimer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9533-9538.	7.1	17
13	Widespread Perturbation of Function, Structure, and Dynamics by a Conservative Single-Atom Substitution in Thymidylate Synthase. Biochemistry, 2016, 55, 5702-5713.	2.5	9
14	The Effect of Protein Mass Modulation on Human Dihydrofolate Reductase. Biochemistry, 2016, 55, 1100-1106.	2.5	27
15	Contrasting roles of dynamics in protein allostery: NMR and structural studies of CheY and the third PDZ domain from PSD-95. Biophysical Reviews, 2015, 7, 217-226.	3.2	21
16	Bacterial Thymidylate Synthase Binds Two Molecules of Substrate and Cofactor without Cooperativity. Journal of the American Chemical Society, 2015, 137, 14260-14263.	13.7	18
17	Chronic Hepatitis C Infection in Children: Current Treatment and New Therapies. Journal of Clinical and Translational Hepatology, 2015, 3, 36-41.	1.4	8
18	Backbone and ILV methyl resonance assignments of E. coli thymidylate synthase bound to cofactor and a nucleotide analogue. Biomolecular NMR Assignments, 2014, 8, 195-199.	0.8	8

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19	Monitoring Side-Chain Dynamics of Proteins Using 2H Relaxation. Methods in Molecular Biology, 2014, 1084, 3-27.	0.9	1
20	Supertertiary Structure of the MAGUK Core from PSD-95. Structure, 2013, 21, 402-413.	3.3	61
21	Colocalization of Fast and Slow Timescale Dynamics in the Allosteric Signaling Protein CheY. Journal of Molecular Biology, 2013, 425, 2372-2381.	4.2	30
22	Mg²⁺ Binds to the Surface of Thymidylate Synthase and Affects Hydride Transfer at the Interior Active Site. Journal of the American Chemical Society, 2013, 135, 7583-7592.	13.7	21
23	Segmental Motions, Not a Two-State Concerted Switch, Underlie Allostery in CheY. Structure, 2012, 20, 1363-1373.	3.3	40
24	Structure and Dynamics of the G121V Dihydrofolate Reductase Mutant: Lessons from a Transition-State Inhibitor Complex. PLoS ONE, 2012, 7, e33252.	2.5	24
25	Evidence for dynamics in proteins as a mechanism for ligand dissociation. Nature Chemical Biology, 2012, 8, 246-252.	8.0	79
26	Multi-Timescale Dynamics Study of FKBP12 Along the Rapamycinâ€“mTOR Binding Coordinate. Journal of Molecular Biology, 2011, 405, 378-394.	4.2	30
27	Exploring the role of structure and dynamics in the function of chymotrypsin inhibitor 2. Proteins: Structure, Function and Bioinformatics, 2011, 79, 916-924.	2.6	6
28	Phosphorylation of a PDZ Domain Extension Modulates Binding Affinity and Interdomain Interactions in Postsynaptic Density-95 (PSD-95) Protein, a Membrane-associated Guanylate Kinase (MAGUK). Journal of Biological Chemistry, 2011, 286, 41776-41785.	3.4	61
29	Nuclear Magnetic Resonance Study of the Role of M42 in the Solution Dynamics of Escherichia coli Dihydrofolate Reductase. Biochemistry, 2010, 49, 1606-1615.	2.5	30
30	Crystallographic and Nuclear Magnetic Resonance Evaluation of the Impact of Peptide Binding to the Second PDZ Domain of Protein Tyrosine Phosphatase 1E. Biochemistry, 2010, 49, 9280-9291.	2.5	64
31	Using NMR to study fast dynamics in proteins: methods and applications. Current Opinion in Pharmacology, 2010, 10, 723-730.	3.5	72
32	Detection of Native-State Nonadditivity in Double Mutant Cycles via Hydrogen Exchange. Journal of the American Chemical Society, 2010, 132, 8010-8019.	13.7	11
33	Hidden dynamic allostery in a PDZ domain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18249-18254.	7.1	296
34	Dynamic Dysfunction in Dihydrofolate Reductase Results from Antifolate Drug Binding: Modulation of Dynamics within a Structural State. Structure, 2009, 17, 386-394.	3.3	70
35	Conservation of Side-Chain Dynamics Within a Protein Family. Journal of the American Chemical Society, 2009, 131, 6322-6323.	13.7	42
36	Frameworks for Understanding Long-Range Intra-Protein Communication. Current Protein and Peptide Science, 2009, 10, 116-127.	1.4	64

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37	Monitoring Aromatic Picosecond to Nanosecond Dynamics in Proteins via ¹³C Relaxation: Expanding Perturbation Mapping of the Rigidifying Core Mutation, V54A, in Eglin c. Biochemistry, 2008, 47, 4876-4886.	2.5	35
38	Hydrophobic Core Mutations in CI2 Globally Perturb Fast Side-Chain Dynamics Similarly without Regard to Position. Biochemistry, 2008, 47, 8566-8576.	2.5	18
39	Dynamic Coupling and Allosteric Behavior in a Nonallosteric Proteinâ€. Biochemistry, 2006, 45, 7693-7699.	2.5	130
40	Evaluation of Energetic and Dynamic Coupling Networks in a PDZ Domain Protein. Journal of Molecular Biology, 2006, 364, 337-351.	4.2	118
41	Relating side-chain mobility in proteins to rotameric transitions: Insights from molecular dynamics simulations and NMR. Journal of Biomolecular NMR, 2005, 32, 151-162.	2.8	43
42	Backbone and Side Chain Dynamics of Mutant Calmodulinâ^'Peptide Complexes. Biochemistry, 2005, 44, 12627-12639.	2.5	29
43	Long-Range Dynamic Effects of Point Mutations Propagate through Side Chains in the Serine Protease Inhibitor Eglin câ€. Biochemistry, 2004, 43, 12448-12458.	2.5	81
44	Ligand-dependent Dynamics and Intramolecular Signaling in a PDZ Domain. Journal of Molecular Biology, 2004, 335, 1105-1115.	4.2	215
45	Increased Rigidity of Eglin c at Acidic pH:â€‰ Evidence from NMR Spin Relaxation and MD Simulations. Biochemistry, 2003, 42, 13856-13868.	2.5	30
46	Dynamics and Entropy of a Calmodulinâ^'Peptide Complex Studied by NMR and Molecular Dynamicsâ€. Biochemistry, 2003, 42, 562-570.	2.5	61
47	Temperature Dependence of the Internal Dynamics of a Calmodulinâ^'Peptide Complex. Biochemistry, 2002, 41, 13814-13825.	2.5	88
48	Main Chain and Side Chain Dynamics of a Heme Protein:Â15N and2H NMR Relaxation Studies ofR.capsulatusFerrocytochromec2â€. Biochemistry, 2001, 40, 6559-6569.	2.5	42
49	Dynamics of a De Novo Designed Three-Helix Bundle Protein Studied by15N,13C, and2H NMR Relaxation Methodsâ€. Biochemistry, 2001, 40, 9560-9569.	2.5	44
50	Microscopic origins of entropy, heat capacity and the glass transition in proteins. Nature, 2001, 411, 501-504.	27.8	292
51	Redistribution and loss of side chain entropy upon formation of a calmodulin-peptide complex. Nature Structural Biology, 2000, 7, 72-77.	9.7	282
52	Assessing potential bias in the determination of rotational correlation times of proteins by NMR relaxation. , 1999, 13, 101-112.		69
53	Comparison of 2H and 13C NMR Relaxation Techniques for the Study of Protein Methyl Group Dynamics in Solution. Journal of the American Chemical Society, 1999, 121, 2891-2902.	13.7	111