

Arthur Laganowsky

List of Publications by Year in descending order

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71
papers

5,314
citations

147726

31
h-index

88593

70
g-index

75
all docs

75
docs citations

75
times ranked

6396
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of Protein-Lipid Interactions Using Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2022, 2349, 41-64.	0.4	4
2	Small Molecule Peptidomimetic Trypsin Inhibitors: Validation Of An EKO Binding Mode, But With A Twist. <i>Organic and Biomolecular Chemistry</i> , 2022, , .	1.5	1
3	Temperature Regulates Stability, Ligand Binding (Mg ²⁺ and ATP), and Stoichiometry of GroEL-GroES Complexes. <i>Journal of the American Chemical Society</i> , 2022, 144, 2667-2678.	6.6	18
4	Variable-Temperature Native Mass Spectrometry for Studies of Protein Folding, Stabilities, Assembly, and Molecular Interactions. <i>Annual Review of Biophysics</i> , 2022, 51, 63-77.	4.5	18
5	Cupric Ions Selectively Modulate TRAAK-Phosphatidylserine Interactions. <i>Journal of the American Chemical Society</i> , 2022, 144, 7048-7053.	6.6	4
6	Selective regulation of human TRAAK channels by biologically active phospholipids. <i>Nature Chemical Biology</i> , 2021, 17, 89-95.	3.9	24
7	Covalent Inactivation of <i>Mycobacterium tuberculosis</i> Isocitrate Lyase by <i>cis</i> -2,3-Epoxy-Succinic Acid. <i>ACS Chemical Biology</i> , 2021, 16, 463-470.	1.6	6
8	Molecular assemblies of the catalytic domain of SOS with KRas and oncogenic mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
9	Variable-Temperature Electrospray Ionization for Temperature-Dependent Folding/Refolding Reactions of Proteins and Ligand Binding. <i>Analytical Chemistry</i> , 2021, 93, 6924-6931.	3.2	33
10	Thermal Analysis of a Mixture of Ribosomal Proteins by vT-ESI-MS: Toward a Parallel Approach for Characterizing the Stabilitome. <i>Analytical Chemistry</i> , 2021, 93, 8484-8492.	3.2	8
11	Protons Are Fast and Smart; Proteins Are Slow and Dumb: On the Relationship of Electrospray Ionization Charge States and Conformations. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1553-1561.	1.2	17
12	Self-Masked Aldehyde Inhibitors: A Novel Strategy for Inhibiting Cysteine Proteases. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 11267-11287.	2.9	19
13	Mechanism-Based Inactivation of <i>Mycobacterium tuberculosis</i> Isocitrate Lyase 1 by (2 <i>R</i> ,3 <i>S</i>)-2-Hydroxy-3-(nitromethyl)succinic acid. <i>Journal of the American Chemical Society</i> , 2021, 143, 17666-17676.	6.6	4
14	Implementing Digital-Waveform Technology for Extended <i>m/z</i> Range Operation on a Native Dual-Quadrupole FT-IM-Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2812-2820.	1.2	9
15	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. <i>Jacs Au</i> , 2021, 1, 2385-2393.	3.6	12
16	Insight into the Phospholipid-Binding Preferences of Kir3.4. <i>Biochemistry</i> , 2021, 60, 3813-3821.	1.2	4
17	Entropy in the Molecular Recognition of Membrane Protein-Lipid Interactions. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 12218-12224.	2.1	10
18	Native IM-Orbitrap MS: Resolving what was hidden. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 124, 115533.	5.8	33

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19	Enhanced Characterization of Membrane Protein Complexes by Ultraviolet Photodissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 899-907.	3.2	21
20	Development of native MS capabilities on an extended mass range Q-TOF MS. <i>International Journal of Mass Spectrometry</i> , 2020, 458, 116451.	0.7	13
21	Structural basis of ion transport and inhibition in ferroportin. <i>Nature Communications</i> , 2020, 11, 5686.	5.8	42
22	First-Principles Collision Cross Section Measurements of Large Proteins and Protein Complexes. <i>Analytical Chemistry</i> , 2020, 92, 11155-11163.	3.2	24
23	Discovery of Potent Charge-Reducing Molecules for Native Ion Mobility Mass Spectrometry Studies. <i>Analytical Chemistry</i> , 2020, 92, 11242-11249.	3.2	21
24	Evidence for Many Unique Solution Structures for Chymotrypsin Inhibitor 2: A Thermodynamic Perspective Derived from vT-ESI-IMS-MS Measurements. <i>Journal of the American Chemical Society</i> , 2020, 142, 17372-17383.	6.6	26
25	A hydrophobic ratchet entrenches molecular complexes. <i>Nature</i> , 2020, 588, 503-508.	13.7	75
26	Origin of complexity in haemoglobin evolution. <i>Nature</i> , 2020, 581, 480-485.	13.7	89
27	Structure and mechanism of human diacylglycerol O-acyltransferase ¹ . <i>Nature</i> , 2020, 581, 329-332.	13.7	72
28	Ag ⁺ Ion Binding to Human Metallothionein-2A Is Cooperative and Domain Specific. <i>Analytical Chemistry</i> , 2020, 92, 8923-8932.	3.2	19
29	Structural Analysis of the Effect of a Dual-FLAG Tag on Transthyretin. <i>Biochemistry</i> , 2020, 59, 1013-1022.	1.2	7
30	Melting of Hemoglobin in Native Solutions as measured by IMS-MS. <i>Analytical Chemistry</i> , 2020, 92, 3440-3446.	3.2	20
31	Collision-Induced Unfolding Studies of Proteins and Protein Complexes using Drift Tube Ion Mobility-Mass Spectrometer. <i>Analytical Chemistry</i> , 2020, 92, 7218-7225.	3.2	18
32	Insight into the Selectivity of Kir3.2 toward Phosphatidylinositides. <i>Biochemistry</i> , 2020, 59, 2089-2099.	1.2	10
33	A Sec14-like phosphatidylinositol transfer protein paralog defines a novel class of heme-binding proteins. <i>ELife</i> , 2020, 9, .	2.8	10
34	Development and Evaluation of a Reverse-Entry Ion Source Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 192-198.	1.2	21
35	Intrinsic GTPase Activity of K-RAS Monitored by Native Mass Spectrometry. <i>Biochemistry</i> , 2019, 58, 3396-3405.	1.2	25
36	Topological Analysis of Transthyretin Disassembly Mechanism: Surface-Induced Dissociation Reveals Hidden Reaction Pathways. <i>Analytical Chemistry</i> , 2019, 91, 2345-2351.	3.2	22

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37	Probing Heterogeneous Lipid Interactions with Membrane Proteins Using Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 2003, 175-190.	0.4	3
38	A conserved PLPLRT/SD motif of STING mediates the recruitment and activation of TBK1. <i>Nature</i> , 2019, 569, 718-722.	13.7	221
39	Variable-Temperature ESI-IMS-MS Analysis of Myohemerythrin Reveals Ligand Losses, Unfolding, and a Non-Native Disulfide Bond. <i>Analytical Chemistry</i> , 2019, 91, 6808-6814.	3.2	23
40	New insights into the metal-induced oxidative degradation pathways of transthyretin. <i>Chemical Communications</i> , 2019, 55, 4091-4094.	2.2	18
41	Generation of Charge-Reduced Ions of Membrane Protein Complexes for Native Ion Mobility Mass Spectrometry Studies. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 886-892.	1.2	19
42	Selective binding of a toxin and phosphatidylinositides to a mammalian potassium channel. <i>Nature Communications</i> , 2019, 10, 1352.	5.8	27
43	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018, 359, 930-935.	6.0	51
44	Allostery revealed within lipid binding events to membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2976-2981.	3.3	91
45	Protonation state of glutamate 73 regulates the formation of a specific dimeric association of mVDAC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E172-E179.	3.3	26
46	Fourier Transform-Ion Mobility-Orbitrap Mass Spectrometer: A Next-Generation Instrument for Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 10472-10478.	3.2	59
47	Surface induced dissociation as a tool to study membrane protein complexes. <i>Chemical Communications</i> , 2017, 53, 3106-3109.	2.2	34
48	Melting Proteins: Evidence for Multiple Stable Structures upon Thermal Denaturation of Native Ubiquitin from Ion Mobility Spectrometry-Mass Spectrometry Measurements. <i>Journal of the American Chemical Society</i> , 2017, 139, 6306-6309.	6.6	86
49	Characterization of Membrane Protein-Lipid Interactions by Mass Spectrometry Ion Mobility Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 579-586.	1.2	42
50	Allosteric modulation of protein-protein interactions by individual lipid binding events. <i>Nature Communications</i> , 2017, 8, 2203.	5.8	65
51	Determining Membrane Protein-Lipid Binding Thermodynamics Using Native Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2016, 138, 4346-4349.	6.6	116
52	The Effect of Detergent, Temperature, and Lipid on the Oligomeric State of MscL Constructs: Insights from Mass Spectrometry. <i>Chemistry and Biology</i> , 2015, 22, 593-603.	6.2	72
53	The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4577-4581.	7.2	117
54	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.	5.8	136

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55	The structured core domain of $\hat{I}\pm$ B-crystallin can prevent amyloid fibrillation and associated toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1562-70.	3.3	181
56	Structure of a designed protein cage that self-assembles into a highly porous cube. Nature Chemistry, 2014, 6, 1065-1071.	6.6	267
57	Membrane proteins bind lipids selectively to modulate their structure and function. Nature, 2014, 510, 172-175.	13.7	665
58	Detergent-free mass spectrometry of membrane protein complexes. Nature Methods, 2013, 10, 1206-1208.	9.0	152
59	C-terminal interactions mediate the quaternary dynamics of $\hat{I}\pm$ B-crystallin. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20110405.	1.8	70
60	Mass spectrometry of intact membrane protein complexes. Nature Protocols, 2013, 8, 639-651.	5.5	354
61	Atomic View of a Toxic Amyloid Small Oligomer. Science, 2012, 335, 1228-1231.	6.0	518
62	Dimerization and Heme Binding Are Conserved in Amphibian and Starfish Homologues of the microRNA Processing Protein DGCR8. PLoS ONE, 2012, 7, e39688.	1.1	20
63	Molecular basis for amyloid- \hat{I}^2 polymorphism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16938-16943.	3.3	383
64	An approach to crystallizing proteins by metal-mediated synthetic symmetrization. Protein Science, 2011, 20, 1876-1890.	3.1	63
65	Towards a Pharmacophore for Amyloid. PLoS Biology, 2011, 9, e1001080.	2.6	184
66	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. Protein Science, 2010, 19, 1031-1043.	3.1	264
67	A Novel 3-Methylhistidine Modification of Yeast Ribosomal Protein Rpl3 Is Dependent upon the YIL110W Methyltransferase. Journal of Biological Chemistry, 2010, 285, 37598-37606.	1.6	74
68	Hydroponics on a chip: Analysis of the Fe deficient Arabidopsis thylakoid membrane proteome. Journal of Proteomics, 2009, 72, 397-415.	1.2	52
69	Identification of Two SET Domain Proteins Required for Methylation of Lysine Residues in Yeast Ribosomal Protein Rpl42ab. Journal of Biological Chemistry, 2008, 283, 35561-35568.	1.6	42
70	Sequencing covalent modifications of membrane proteins. Journal of Experimental Botany, 2006, 57, 1515-1522.	2.4	35
71	Ag ⁺ Ion Binding to Human Metallothionein-2A Is Cooperative and Domain Specific. , 0, .		1