

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	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014, 510, 172-175.	13.7	665
2	Atomic View of a Toxic Amyloid Small Oligomer. <i>Science</i> , 2012, 335, 1228-1231.	6.0	518
3	Molecular basis for amyloid- β polymorphism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16938-16943.	3.3	383
4	Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013, 8, 639-651.	5.5	354
5	Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014, 6, 1065-1071.	6.6	267
6	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010, 19, 1031-1043.	3.1	264
7	A conserved PLPLRT/SD motif of STING mediates the recruitment and activation of TBK1. <i>Nature</i> , 2019, 569, 718-722.	13.7	221
8	Towards a Pharmacophore for Amyloid. <i>PLoS Biology</i> , 2011, 9, e1001080.	2.6	184
9	The structured core domain of β -crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1562-70.	3.3	181
10	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.	9.0	152
11	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.	5.8	136
12	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
13	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
14	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
15	Origin of complexity in haemoglobin evolution. <i>Nature</i> , 2020, 581, 480-485.	13.7	89
16	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
17	A hydrophobic ratchet entrenches molecular complexes. <i>Nature</i> , 2020, 588, 503-508.	13.7	75
18	A Novel 3-Methylhistidine Modification of Yeast Ribosomal Protein Rpl3 Is Dependent upon the YIL110W Methyltransferase. <i>Journal of Biological Chemistry</i> , 2010, 285, 37598-37606.	1.6	74

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19	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
20	Structure and mechanism of human diacylglycerol O-acyltransferase \hat{A} 1. <i>Nature</i> , 2020, 581, 329-332.	13.7	72
21	C-terminal interactions mediate the quaternary dynamics of \hat{I} \pm B-crystallin. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20110405.	1.8	70
22	Allosteric modulation of protein-protein interactions by individual lipid binding events. <i>Nature Communications</i> , 2017, 8, 2203.	5.8	65
23	An approach to crystallizing proteins by metal \hat{A} -mediated synthetic symmetrization. <i>Protein Science</i> , 2011, 20, 1876-1890.	3.1	63
24	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
25	Hydroponics on a chip: Analysis of the Fe deficient <i>Arabidopsis</i> thylakoid membrane proteome. <i>Journal of Proteomics</i> , 2009, 72, 397-415.	1.2	52
26	Structural principles that enable oligomeric small heat-shock protein paralogs to evolve distinct functions. <i>Science</i> , 2018, 359, 930-935.	6.0	51
27	Identification of Two SET Domain Proteins Required for Methylation of Lysine Residues in Yeast Ribosomal Protein Rpl42ab. <i>Journal of Biological Chemistry</i> , 2008, 283, 35561-35568.	1.6	42
28	Characterization of Membrane Protein \hat{A} “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
29	Structural basis of ion transport and inhibition in ferroportin. <i>Nature Communications</i> , 2020, 11, 5686.	5.8	42
30	Sequencing covalent modifications of membrane proteins. <i>Journal of Experimental Botany</i> , 2006, 57, 1515-1522.	2.4	35
31	Surface induced dissociation as a tool to study membrane protein complexes. <i>Chemical Communications</i> , 2017, 53, 3106-3109.	2.2	34
32	Native IM-Orbitrap MS: Resolving what was hidden. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 124, 115533.	5.8	33
33	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
34	Selective binding of a toxin and phosphatidylinositides to a mammalian potassium channel. <i>Nature Communications</i> , 2019, 10, 1352.	5.8	27
35	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
36	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

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37	Intrinsic GTPase Activity of K-RAS Monitored by Native Mass Spectrometry. <i>Biochemistry</i> , 2019, 58, 3396-3405.	1.2	25
38	First-Principles Collision Cross Section Measurements of Large Proteins and Protein Complexes. <i>Analytical Chemistry</i> , 2020, 92, 11155-11163.	3.2	24
39	Selective regulation of human TRAAK channels by biologically active phospholipids. <i>Nature Chemical Biology</i> , 2021, 17, 89-95.	3.9	24
40	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
41	Topological Analysis of Transthyretin Disassembly Mechanism: Surface-Induced Dissociation Reveals Hidden Reaction Pathways. <i>Analytical Chemistry</i> , 2019, 91, 2345-2351.	3.2	22
42	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
43	Enhanced Characterization of Membrane Protein Complexes by Ultraviolet Photodissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 899-907.	3.2	21
44	Discovery of Potent Charge-Reducing Molecules for Native Ion Mobility Mass Spectrometry Studies. <i>Analytical Chemistry</i> , 2020, 92, 11242-11249.	3.2	21
45	Melting of Hemoglobin in Native Solutions as measured by IMS-MS. <i>Analytical Chemistry</i> , 2020, 92, 3440-3446.	3.2	20
46	Dimerization and Heme Binding Are Conserved in Amphibian and Starfish Homologues of the microRNA Processing Protein DGCR8. <i>PLoS ONE</i> , 2012, 7, e39688.	1.1	20
47	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
48	Ag ⁺ Ion Binding to Human Metallothionein-2A Is Cooperative and Domain Specific. <i>Analytical Chemistry</i> , 2020, 92, 8923-8932.	3.2	19
49	Self-Masked Aldehyde Inhibitors: A Novel Strategy for Inhibiting Cysteine Proteases. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 11267-11287.	2.9	19
50	New insights into the metal-induced oxidative degradation pathways of transthyretin. <i>Chemical Communications</i> , 2019, 55, 4091-4094.	2.2	18
51	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
52	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
53	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
54	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

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55	Molecular assemblies of the catalytic domain of SOS with KRas and oncogenic mutants. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
56	Development of native MS capabilities on an extended mass range Q-TOF MS. International Journal of Mass Spectrometry, 2020, 458, 116451.	0.7	13
57	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. Jacs Au, 2021, 1, 2385-2393.	3.6	12
58	Insight into the Selectivity of Kir3.2 toward Phosphatidylinositides. Biochemistry, 2020, 59, 2089-2099.	1.2	10
59	A Sec14-like phosphatidylinositol transfer protein paralog defines a novel class of heme-binding proteins. ELife, 2020, 9, .	2.8	10
60	Entropy in the Molecular Recognition of Membrane Proteinâ€“Lipid Interactions. Journal of Physical Chemistry Letters, 2021, 12, 12218-12224.	2.1	10
61	Implementing Digital-Waveform Technology for Extended <i>m/z</i> Range Operation on a Native Dual-Quadrupole FT-IM-Orbitrap Mass Spectrometer. Journal of the American Society for Mass Spectrometry, 2021, 32, 2812-2820.	1.2	9
62	Thermal Analysis of a Mixture of Ribosomal Proteins by vT-ESI-MS: Toward a Parallel Approach for Characterizing the Stabilitome. Analytical Chemistry, 2021, 93, 8484-8492.	3.2	8
63	Structural Analysis of the Effect of a Dual-FLAG Tag on Transthyretin. Biochemistry, 2020, 59, 1013-1022.	1.2	7
64	Covalent Inactivation of <i>Mycobacterium tuberculosis</i> Isocitrate Lyase by <i>cis</i> -2,3-Epoxy-Succinic Acid. ACS Chemical Biology, 2021, 16, 463-470.	1.6	6
65	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. Journal of the American Chemical Society, 2021, 143, 17666-17676.	6.6	4
66	Investigation of Proteinâ€“Lipid Interactions Using Native Mass Spectrometry. Methods in Molecular Biology, 2022, 2349, 41-64.	0.4	4
67	Insight into the Phospholipid-Binding Preferences of Kir3.4. Biochemistry, 2021, 60, 3813-3821.	1.2	4
68	Cupric Ions Selectively Modulate TRAAKâ€“Phosphatidylserine Interactions. Journal of the American Chemical Society, 2022, 144, 7048-7053.	6.6	4
69	Probing Heterogeneous Lipid Interactions with Membrane Proteins Using Mass Spectrometry. Methods in Molecular Biology, 2019, 2003, 175-190.	0.4	3
70	Ag ⁺ Ion Binding to Human Metallothionein-2A Is Cooperative and Domain Specific. , 0, .		1
71	Small Molecule Peptidomimetic Trypsin Inhibitors: Validation Of An EKO Binding Mode, But With A Twist. Organic and Biomolecular Chemistry, 2022, , .	1.5	1