

# Argyris Politis

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

2,043  
citations

304743

22  
h-index

276875

41  
g-index

52  
all docs

52  
docs citations

52  
times ranked

2157  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass Spectrometry of Intact V-Type ATPases Reveals Bound Lipids and the Effects of Nucleotide Binding. <i>Science</i> , 2011, 334, 380-385.	12.6	251
2	Charge-State Dependent Compaction and Dissociation of Protein Complexes: Insights from Ion Mobility and Molecular Dynamics. <i>Journal of the American Chemical Society</i> , 2012, 134, 3429-3438.	13.7	223
3	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406.	19.0	149
4	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013, 4, 1985.	12.8	122
5	Integrating Ion Mobility Mass Spectrometry with Molecular Modelling to Determine the Architecture of Multiprotein Complexes. <i>PLoS ONE</i> , 2010, 5, e12080.	2.5	119
6	Direct protein-lipid interactions shape the conformational landscape of secondary transporters. <i>Nature Communications</i> , 2018, 9, 4151.	12.8	112
7	Structural Modeling of Heteromeric Protein Complexes from Disassembly Pathways and Ion Mobility-Mass Spectrometry. <i>Structure</i> , 2012, 20, 1596-1609.	3.3	110
8	Ion mobility mass spectrometry of a rotary ATPase reveals ATP-induced reduction in conformational flexibility. <i>Nature Chemistry</i> , 2014, 6, 208-215.	13.6	85
9	Interrogating Membrane Protein Conformational Dynamics within Native Lipid Compositions. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 15654-15657.	13.8	82
10	Specific cardiolipin-SecY interactions are required for proton-motive force stimulation of protein secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7967-7972.	7.1	65
11	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. <i>Cell Chemical Biology</i> , 2018, 25, 840-848.e4.	5.2	64
12	Deuterios: software for rapid analysis and visualization of data from differential hydrogen deuterium exchange-mass spectrometry. <i>Bioinformatics</i> , 2019, 35, 3171-3173.	4.1	60
13	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. <i>Analytical Chemistry</i> , 2017, 89, 1459-1468.	6.5	46
14	Native mass spectrometry goes more native: investigation of membrane protein complexes directly from SMALPs. <i>Chemical Communications</i> , 2018, 54, 13702-13705.	4.1	44
15	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. <i>Nature Communications</i> , 2019, 10, 3814.	12.8	40
16	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 17194-17199.	13.8	39
17	Integrating hydrogen-deuterium exchange mass spectrometry with molecular dynamics simulations to probe lipid-modulated conformational changes in membrane proteins. <i>Nature Protocols</i> , 2019, 14, 3183-3204.	12.0	39
18	Topological Models of Heteromeric Protein Assemblies from Mass Spectrometry: Application to the Yeast eIF3:eIF5 Complex. <i>Chemistry and Biology</i> , 2015, 22, 117-128.	6.0	38

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19	Hydrogen-deuterium exchange mass spectrometry captures distinct dynamics upon substrate and inhibitor binding to a transporter. <i>Nature Communications</i> , 2020, 11, 6162.	12.8	35
20	ATP-induced asymmetric pre-protein folding as a driver of protein translocation through the Sec machinery. <i>ELife</i> , 2019, 8, .	6.0	32
21	A glimpse into the molecular mechanism of integral membrane proteins through hydrogen-deuterium exchange mass spectrometry. <i>Protein Science</i> , 2020, 29, 1285-1301.	7.6	29
22	Structural basis for isoform-specific kinesin-1 recognition of Y-acidic cargo adaptors. <i>ELife</i> , 2018, 7, .	6.0	26
23	Uncovering the Early Assembly Mechanism for Amyloidogenic Î²2-Microglobulin Using Cross-linking and Native Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2016, 291, 4626-4637.	3.4	24
24	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020, 92, 10872-10880.	6.5	24
25	Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017, 45, 12025-12038.	14.5	23
26	HDX-MS reveals nucleotide-dependent, anti-correlated opening and closure of SecA and SecY channels of the bacterial translocon. <i>ELife</i> , 2019, 8, .	6.0	20
27	Structural characterisation of medically relevant protein assemblies by integrating mass spectrometry with computational modelling. <i>Journal of Proteomics</i> , 2018, 175, 34-41.	2.4	19
28	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 10881-10890.	6.5	17
29	Protein-Lipid Interactions Stabilize the Oligomeric State of BOR1p from <i>Saccharomyces cerevisiae</i> . <i>Analytical Chemistry</i> , 2019, 91, 13071-13079.	6.5	14
30	POPPeT: a New Method to Predict the Protection Factor of Backbone Amide Hydrogens. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 67-76.	2.8	13
31	Hybrid Mass Spectrometry: Towards Characterization of Protein Conformational States. <i>Trends in Biochemical Sciences</i> , 2016, 41, 650-653.	7.5	10
32	Cold Denaturation of Proteins in the Absence of Solvent: Implications for Protein Storage**. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	10
33	Combining Chemical Cross-linking and Mass Spectrometry of Intact Protein Complexes to Study the Architecture of Multi-subunit Protein Assemblies. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	9
34	Interrogating Membrane Protein Conformational Dynamics within Native Lipid Compositions. <i>Angewandte Chemie</i> , 2017, 129, 15860-15863.	2.0	7
35	Structural predictions of the functions of membrane proteins from HDX-MS. <i>Biochemical Society Transactions</i> , 2020, 48, 971-979.	3.4	7
36	Linking function to global and local dynamics in an elevator-type transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	7

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37	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie</i> , 2018, 130, 17440-17445.	2.0	5
38	An Unusually Rapid Protein Backbone Modification Stabilizes the Essential Bacterial Enzyme MurA. <i>Biochemistry</i> , 2020, 59, 3683-3695.	2.5	5
39	Integrative Mass Spectrometry-Based Approaches for Modeling Macromolecular Assemblies. <i>Methods in Molecular Biology</i> , 2021, 2247, 221-241.	0.9	5
40	Analyzing Protein Architectures and Protein-Ligand Complexes by Integrative Structural Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	3
41	Improving Peptide Fragmentation for Hydrogen-Deuterium Exchange Mass Spectrometry Using a Time-Dependent Collision Energy Calculator. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 996-999.	2.8	3
42	Cold Denaturation of Proteins in the Absence of Solvent: Implications for Protein Storage. <i>Angewandte Chemie</i> , 0, , .	2.0	1