Argyris Politis

List of Publications by Year in descending order

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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	Cold Denaturation of Proteins in the Absence of Solvent: Implications for Protein Storage**. Angewandte Chemie - International Edition, 2022, 61, .	13.8	10
2	Integrative Mass Spectrometryâ€“Based Approaches for Modeling Macromolecular Assemblies. Methods in Molecular Biology, 2021, 2247, 221-241.	0.9	5
3	Linking function to global and local dynamics in an elevator-type transporter. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
4	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. Analytical Chemistry, 2020, 92, 10881-10890.	6.5	17
5	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. Analytical Chemistry, 2020, 92, 10872-10880.	6.5	24
6	Hydrogen-deuterium exchange mass spectrometry captures distinct dynamics upon substrate and inhibitor binding to a transporter. Nature Communications, 2020, 11, 6162.	12.8	35
7	An Unusually Rapid Protein Backbone Modification Stabilizes the Essential Bacterial Enzyme MurA. Biochemistry, 2020, 59, 3683-3695.	2.5	5
8	Improving Peptide Fragmentation for Hydrogenâ€“Deuterium Exchange Mass Spectrometry Using a Time-Dependent Collision Energy Calculator. Journal of the American Society for Mass Spectrometry, 2020, 31, 996-999.	2.8	3
9	A glimpse into the molecular mechanism of integral membrane proteins through hydrogenâ€“deuterium exchange mass spectrometry. Protein Science, 2020, 29, 1285-1301.	7.6	29
10	Structural predictions of the functions of membrane proteins from HDX-MS. Biochemical Society Transactions, 2020, 48, 971-979.	3.4	7
11	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. Nature Communications, 2019, 10, 3814.	12.8	40
12	Proteinâ€“Lipid Interactions Stabilize the Oligomeric State of BOR1p from Saccharomyces cerevisiae. Analytical Chemistry, 2019, 91, 13071-13079.	6.5	14
13	Integrating hydrogenâ€“deuterium exchange mass spectrometry with molecular dynamics simulations to probe lipid-modulated conformational changes in membrane proteins. Nature Protocols, 2019, 14, 3183-3204.	12.0	39
14	Deuteros: software for rapid analysis and visualization of data from differential hydrogen deuterium exchange-mass spectrometry. Bioinformatics, 2019, 35, 3171-3173.	4.1	60
15	POPPeT: a New Method to Predict the Protection Factor of Backbone Amide Hydrogens. Journal of the American Society for Mass Spectrometry, 2019, 30, 67-76.	2.8	13
16	ATP-induced asymmetric pre-protein folding as a driver of protein translocation through the Sec machinery. ELife, 2019, 8, .	6.0	32
17	HDX-MS reveals nucleotide-dependent, anti-correlated opening and closure of SecA and SecY channels of the bacterial translocon. ELife, 2019, 8, .	6.0	20
18	Structural characterisation of medically relevant protein assemblies by integrating mass spectrometry with computational modelling. Journal of Proteomics, 2018, 175, 34-41.	2.4	19

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19	A Massâ€Spectrometryâ€Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. Angewandte Chemie, 2018, 130, 17440-17445.	2.0	5
20	Native mass spectrometry goes more native: investigation of membrane protein complexes directly from SMALPs. Chemical Communications, 2018, 54, 13702-13705.	4.1	44
21	A Massâ€Spectrometryâ€Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. Angewandte Chemie - International Edition, 2018, 57, 17194-17199.	13.8	39
22	Direct protein-lipid interactions shape the conformational landscape of secondary transporters. Nature Communications, 2018, 9, 4151.	12.8	112
23	Analyzing Protein Architectures and Protein-Ligand Complexes by Integrative Structural Mass Spectrometry. Journal of Visualized Experiments, 2018, , .	0.3	3
24	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. Cell Chemical Biology, 2018, 25, 840-848.e4.	5.2	64
25	Specific cardiolipinâ€“SecY interactions are required for proton-motive force stimulation of protein secretion. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7967-7972.	7.1	65
26	Structural basis for isoform-specific kinesin-1 recognition of Y-acidic cargo adaptors. ELife, 2018, 7, .	6.0	26
27	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. Analytical Chemistry, 2017, 89, 1459-1468.	6.5	46
28	Interrogating Membrane Protein Conformational Dynamics within Native Lipid Compositions. Angewandte Chemie - International Edition, 2017, 56, 15654-15657.	13.8	82
29	Combining Chemical Cross-linking and Mass Spectrometry of Intact Protein Complexes to Study the Architecture of Multi-subunit Protein Assemblies. Journal of Visualized Experiments, 2017, , .	0.3	9
30	Interrogating Membrane Protein Conformational Dynamics within Native Lipid Compositions. Angewandte Chemie, 2017, 129, 15860-15863.	2.0	7
31	Mechanistic insight into the assembly of the HerAâ€“NurA helicaseâ€“nuclease DNA end resection complex. Nucleic Acids Research, 2017, 45, 12025-12038.	14.5	23
32	Hybrid Mass Spectrometry: Towards Characterization of Protein Conformational States. Trends in Biochemical Sciences, 2016, 41, 650-653.	7.5	10
33	Uncovering the Early Assembly Mechanism for Amyloidogenic Î²2-Microglobulin Using Cross-linking and Native Mass Spectrometry. Journal of Biological Chemistry, 2016, 291, 4626-4637.	3.4	24
34	Topological Models of Heteromeric Protein Assemblies from Mass Spectrometry: Application to the Yeast eIF3:eIF5 Complex. Chemistry and Biology, 2015, 22, 117-128.	6.0	38
35	A mass spectrometryâ€“based hybrid method for structural modeling of protein complexes. Nature Methods, 2014, 11, 403-406.	19.0	149
36	Ion mobilityâ€“mass spectrometry of a rotary ATPase reveals ATP-induced reduction in conformational flexibility. Nature Chemistry, 2014, 6, 208-215.	13.6	85

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37	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. Nature Communications, 2013, 4, 1985.	12.8	122
38	Structural Modeling of Heteromeric Protein Complexes from Disassembly Pathways and Ion Mobility-Mass Spectrometry. Structure, 2012, 20, 1596-1609.	3.3	110
39	Charge-State Dependent Compaction and Dissociation of Protein Complexes: Insights from Ion Mobility and Molecular Dynamics. Journal of the American Chemical Society, 2012, 134, 3429-3438.	13.7	223
40	Mass Spectrometry of Intact V-Type ATPases Reveals Bound Lipids and the Effects of Nucleotide Binding. Science, 2011, 334, 380-385.	12.6	251
41	Integrating Ion Mobility Mass Spectrometry with Molecular Modelling to Determine the Architecture of Multiprotein Complexes. PLoS ONE, 2010, 5, e12080.	2.5	119
42	Cold Denaturation of Proteins in the Absence of Solvent: Implications for Protein Storage. Angewandte Chemie, 0, , .	2.0	1