

Konstantinos Thalassinos

List of Publications by Year in descending order

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69
papers

3,626
citations

159585
30
h-index

138484
58
g-index

74
all docs

74
docs citations

74
times ranked

4303
citing authors

#	ARTICLE	IF	CITATIONS
1	An investigation of the mobility separation of some peptide and protein ions using a new hybrid quadrupole/travelling wave IMS/oa-ToF instrument. <i>International Journal of Mass Spectrometry</i> , 2007, 261, 1-12.	1.5	749
2	Recommendations for reporting ion mobility Mass Spectrometry measurements. <i>Mass Spectrometry Reviews</i> , 2019, 38, 291-320.	5.4	315
3	A Comparison of Labeling and Label-Free Mass Spectrometry-Based Proteomics Approaches. <i>Journal of Proteome Research</i> , 2009, 8, 3752-3759.	3.7	245
4	Characterization of Phosphorylated Peptides Using Traveling Wave-Based and Drift Cell Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 248-254.	6.5	223
5	Travelling wave ion mobility mass spectrometry studies of protein structure: biological significance and comparison with X-ray crystallography and nuclear magnetic resonance spectroscopy measurements. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 3297-3304.	1.5	164
6	Structure of the VirB4 ATPase, alone and bound to the core complex of a type IV secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11348-11353.	7.1	86
7	The Importance of Non-accessible Crosslinks and Solvent Accessible Surface Distance in Modeling Proteins with Restraints From Crosslinking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2491-2500.	3.8	79
8	Structure of a VirD4 coupling protein bound to a VirB type <scp>IV</scp> secretion machinery. <i>EMBO Journal</i> , 2017, 36, 3080-3095.	7.8	79
9	Structural Analysis of Synthetic Polymer Mixtures Using Ion Mobility and Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2008, 80, 9720-9725.	6.5	72
10	Probing hemoglobin structure by means of traveling-wave ion mobility mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 625-631.	2.8	67
11	Ion Mobility Mass Spectrometry for Extracting Spectra <i>of N</i>-Glycans Directly from Incubation Mixtures Following Glycan Release: Application to Glycans from Engineered Glycoforms of Intact, Folded HIV gp120. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 568-581.	2.8	65
12	Gas Phase Stability of Protein Ions in a Cyclic Ion Mobility Spectrometry Traveling Wave Device. <i>Analytical Chemistry</i> , 2019, 91, 7554-7561.	6.5	58
13	The Effect of Calcium Ions and Peptide Ligands on the Relative Stabilities of the Calmodulin Dumbbell and Compact Structures. <i>Journal of Physical Chemistry B</i> , 2010, 114, 437-447.	2.6	56
14	Methodology for measuring conformation of solvent-disrupted protein subunits using T-WAVE ion mobility MS: An investigation into eukaryotic initiation factors. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1699-1706.	2.8	54
15	Newly folded substrates inside the molecular cage of the HtrA chaperone DegQ. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 152-157.	8.2	53
16	Amphitrite: A program for processing travelling wave ion mobility mass spectrometry data. <i>International Journal of Mass Spectrometry</i> , 2013, 345-347, 54-62.	1.5	53
17	Modeling Protein Complexes Using Restraints from Crosslinking Mass Spectrometry. <i>Structure</i> , 2018, 26, 1015-1024.e2.	3.3	50
18	Archaeal TFE \pm $\hat{\mu}$ ² is a hybrid of TFIIE and the RNA polymerase III subcomplex hRPC62/39. <i>ELife</i> , 2015, 4, e08378.	6.0	50

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19	Structural analysis of prion proteins by means of drift cell and traveling wave ion mobility mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 845-854.	2.8	47
20	The C-terminal portion of the cleaved HT motif is necessary and sufficient to mediate export of proteins from the malaria parasite into its host cell. <i>Molecular Microbiology</i> , 2013, 87, 835-850.	2.5	46
21	The Respiratory Arsenite Oxidase: Structure and the Role of Residues Surrounding the Rieske Cluster. <i>PLoS ONE</i> , 2013, 8, e72535.	2.5	45
22	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. <i>Molecular Immunology</i> , 2013, 56, 794-803.	2.2	43
23	Solution structure of the major factor VIII binding region on von Willebrand factor. <i>Blood</i> , 2014, 123, 4143-4151.	1.4	41
24	The Role of Disulfide Bond Replacements in Analogues of the Tarantula Toxin ProTx-II and Their Effects on Inhibition of the Voltage-Gated Sodium Ion Channel Na _v 1.7. <i>Journal of the American Chemical Society</i> , 2017, 139, 13063-13075.	13.7	41
25	An integrative approach combining ion mobility mass spectrometry, X-ray crystallography, and nuclear magnetic resonance spectroscopy to study the conformational dynamics of I κ B1 antitrypsin upon ligand binding. <i>Protein Science</i> , 2015, 24, 1301-1312.	7.6	37
26	Autophosphorylation Activity of a Soluble Hexameric Histidine Kinase Correlates with the Shift in Protein Conformational Equilibrium. <i>Chemistry and Biology</i> , 2013, 20, 1411-1420.	6.0	36
27	Integration of Mass Spectrometry Data for Structural Biology. <i>Chemical Reviews</i> , 2022, 122, 7952-7986.	47.7	36
28	Inhibition of the Staphylococcus aureus c-di-AMP cyclase DacA by direct interaction with the phosphoglucosamine mutase GlmM. <i>PLoS Pathogens</i> , 2019, 15, e1007537.	4.7	35
29	Comparative analysis of interactions of RASSF1-10. <i>Advances in Biological Regulation</i> , 2013, 53, 190-201.	2.3	34
30	Travelling-wave ion mobility and negative ion fragmentation of high-mannose N-glycans. <i>Journal of Mass Spectrometry</i> , 2016, 51, 219-235.	1.6	34
31	Developments in tandem ion mobility mass spectrometry. <i>Biochemical Society Transactions</i> , 2020, 48, 2457-2466.	3.4	34
32	Structural Dynamics Associated with Intermediate Formation in an Archetypal Conformational Disease. <i>Structure</i> , 2012, 20, 504-512.	3.3	33
33	Expansion of Lysine-rich Repeats in Plasmodium Proteins Generates Novel Localization Sequences That Target the Periphery of the Host Erythrocyte. <i>Journal of Biological Chemistry</i> , 2016, 291, 26188-26207.	3.4	32
34	FAN1 controls mismatch repair complex assembly via MLH1 retention to stabilize CAG repeat expansion in Huntington's disease. <i>Cell Reports</i> , 2021, 36, 109649.	6.4	32
35	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. <i>Structure</i> , 2013, 21, 1500-1508.	3.3	29
36	Travelling-wave ion mobility mass spectrometry and negative ion fragmentation of hybrid and complex N-glycans. <i>Journal of Mass Spectrometry</i> , 2016, 51, 1064-1079.	1.6	28

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37	Cyclic Ion Mobilityâ€“Collision Activation Experiments Elucidate Protein Behavior in the Gas Phase. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1545-1552.	2.8	27
38	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
39	Cdk5 and GSK3 ^{Î²} inhibit fast endophilin-mediated endocytosis. <i>Nature Communications</i> , 2021, 12, 2424.	12.8	24
40	Jwalk and MNXL web server: model validation using restraints from crosslinking mass spectrometry. <i>Bioinformatics</i> , 2018, 34, 3584-3585.	4.1	23
41	Novel software for the assignment of peaks from tandem mass spectrometry spectra of synthetic polymers. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1324-1331.	2.8	21
42	Analysis of Baboon IAPP Provides Insight into Amyloidogenicity and Cytotoxicity of Human IAPP. <i>Biophysical Journal</i> , 2020, 118, 1142-1151.	0.5	19
43	End-group characterisation of poly(propylene glycol)s by means of electrospray ionisationâ€“tandem mass spectrometry (ESI-MS/MS). <i>Analytical and Bioanalytical Chemistry</i> , 2008, 392, 643-650.	3.7	18
44	Deconvolution of ion mobility mass spectrometry arrival time distributions using a genetic algorithm approach: Application to Î±1-antitrypsin peptide binding. <i>International Journal of Mass Spectrometry</i> , 2018, 426, 29-37.	1.5	18
45	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
46	Combining Information from Crosslinks and Monolinks in the Modeling of Protein Structures. <i>Structure</i> , 2020, 28, 1061-1070.e3.	3.3	17
47	Crystal Structure of Reduced MsAcp, a Putative Nitroreductase from <i>Mycobacterium smegmatis</i> and a Close Homologue of <i>Mycobacterium tuberculosis</i> Acp. <i>Journal of Biological Chemistry</i> , 2012, 287, 44372-44383.	3.4	16
48	Comparison of One- and Two-dimensional Liquid Chromatography Approaches in the Label-free Quantitative Analysis of <i>Methylocella silvestris</i> . <i>Journal of Proteome Research</i> , 2012, 11, 4755-4763.	3.7	16
49	A proteomic approach to the identification of the major virion structural proteins of the marine cyanomyovirus S-PM2. <i>Microbiology (United Kingdom)</i> , 2008, 154, 1775-1782.	1.8	15
50	Targeting Serpins in High-Throughput and Structure-Based Drug Design. <i>Methods in Enzymology</i> , 2011, 501, 139-175.	1.0	15
51	The crystal structure of the Sgt1-Skp1 complex: the link between Hsp90 and both SCF E3 ubiquitin ligases and kinetochores. <i>Scientific Reports</i> , 2017, 7, 41626.	3.3	14
52	The solution structure of the human IgG2 subclass is distinct from those for human IgG1 and IgG4 providing an explanation for their discrete functions. <i>Journal of Biological Chemistry</i> , 2019, 294, 10789-10806.	3.4	14
53	Design and Application of a Data-Independent Precursor and Product Ion Repository. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1808-1820.	2.8	13
54	Characterization of the UK anthrax vaccine and human immunogenicity. <i>Human Vaccines and Immunotherapeutics</i> , 2021, 17, 747-758.	3.3	12

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55	Structural Characterisation of Non-Deamidated Acidic Variants of <i>Erwinia chrysanthemi</i> L-asparaginase Using Small-Angle X-ray Scattering and Ion-Mobility Mass Spectrometry. <i>Pharmaceutical Research</i> , 2015, 32, 3636-3648.	3.5	11
56	Optimization Workflow for the Analysis of Cross-Linked Peptides Using a Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2019, 91, 1808-1814.	6.5	10
57	Analysis of Proline Substitutions Reveals the Plasticity and Sequence Sensitivity of Human IAPP Amyloidogenicity and Toxicity. <i>Biochemistry</i> , 2020, 59, 742-754.	2.5	9
58	Structure of the stationary phase survival protein YuiC from <i>B.subtilis</i> . <i>BMC Structural Biology</i> , 2015, 15, 12.	2.3	7
59	Structural and functional adaptation of <i>Haloferax volcanii</i> TFE \pm /I 2 . <i>Nucleic Acids Research</i> , 2018, 46, 2308-2320.	14.5	7
60	A Chemical Biology Approach to Probing the Folding Pathways of the Inhibitory Cystine Knot (ICK) Peptide ProTx-II. <i>Frontiers in Chemistry</i> , 2020, 8, 228.	3.6	7
61	Characterisation of end groups in poly(2-hydroxyethyl methacrylate) by means of electrospray ionisation-mass spectrometry/mass spectrometry (ESI-MS/MS). <i>Polymer</i> , 2010, 51, 1418-1424.	3.8	6
62	Concentration \hat{c} dependent coulombic effects in travelling wave ion mobility spectrometry collision cross section calibration. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8613.	1.5	6
63	Dynamic changes in the brain protein interaction network correlates with progression of A β 242 pathology in <i>Drosophila</i> . <i>Scientific Reports</i> , 2020, 10, 18517.	3.3	6
64	Reference Protocol to Assess Analytical Performance of Higher Order Structural Analysis Measurements: Results from an Interlaboratory Comparison. <i>Analytical Chemistry</i> , 2021, 93, 9041-9048.	6.5	4
65	Applications of Traveling Wave Ion Mobility-Mass Spectrometry. , 2009, , 205-236.		3
66	Evaluation of acquisition modes for semi \hat{c} quantitative analysis by targeted and untargeted mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, e9308.	1.5	3
67	Mechanistic insights into the activation of the IKK kinase complex by the Kaposi \hat{c} s sarcoma herpes virus oncoprotein vFLIP. <i>Journal of Biological Chemistry</i> , 2022, 298, 102012.	3.4	1
68	Building GABAA Receptors for Structural Determination. <i>Biophysical Journal</i> , 2015, 108, 433a.	0.5	0
69	Structural mass spectrometry decodes domain interaction and dynamics of the full-length Human Histone Deacetylase 2. <i>Bioch\hat{c}mica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140759.	2.3	0