

Rachel R Ogorzalek Loo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2672493/publications.pdf>

Version: 2024-02-01

96
papers

6,259
citations

71061

41
h-index

71651

76
g-index

100
all docs

100
docs citations

100
times ranked

6584
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards understanding the formation of internal fragments generated by collisionally activated dissociation for top-down mass spectrometry. <i>Analytica Chimica Acta</i> , 2022, 1194, 339400.	2.6	11
2	Amyloid fibrils in FTL-D-TDP are composed of TMEM106B and not TDP-43. <i>Nature</i> , 2022, 605, 304-309.	13.7	85
3	The Acyl-Proteome of <i>Syntrophus aciditrophicus</i> Reveals Metabolic Relationships in Benzoate Degradation. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100215.	2.5	5
4	Leveraging Immonium Ions for Targeting Acyl-Lysine Modifications in Proteomic Datasets. <i>Proteomics</i> , 2021, 21, e2000111.	1.3	9
5	ClipsMS: An Algorithm for Analyzing Internal Fragments Resulting from Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 1928-1935.	1.8	35
6	Internal Fragments Generated from Different Top-Down Mass Spectrometry Fragmentation Methods Extend Protein Sequence Coverage. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1752-1758.	1.2	22
7	N-terminal autoprocessing and acetylation of multifunctional autoprocessing repeats toxins (MARTX) Makes Caterpillars Floppy-like effector is stimulated by adenosine diphosphate (ADP) Ribosylation Factor 1 in advance of Golgi fragmentation. <i>Cellular Microbiology</i> , 2020, 22, e13133.	1.1	9
8	Internal Fragments Generated by Electron Ionization Dissociation Enhance Protein Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1896-1902.	1.2	30
9	Kinetics and Optimization of the Lysine-Isopeptide Bond Forming Sortase Enzyme from <i>Corynebacterium diphtheriae</i> . <i>Bioconjugate Chemistry</i> , 2020, 31, 1624-1634.	1.8	9
10	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 3779-3791.	1.8	49
11	<i>Syntrophus aciditrophicus</i> uses the same enzymes in a reversible manner to degrade and synthesize aromatic and alicyclic acids. <i>Environmental Microbiology</i> , 2019, 21, 1833-1846.	1.8	17
12	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
13	Enhancing sensitivity of liquid chromatography-mass spectrometry of peptides and proteins using supercharging agents. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 157-164.	0.7	52
14	An integrated native mass spectrometry and top-down proteomics method that connects sequence to structure and function of macromolecular complexes. <i>Nature Chemistry</i> , 2018, 10, 139-148.	6.6	170
15	Proteomics identification of radiation-induced changes of membrane proteins in the rat model of arteriovenous malformation in pursuit of targets for brain AVM molecular therapy. <i>Clinical Proteomics</i> , 2018, 15, 43.	1.1	7
16	In vitro reconstitution of sortase-catalyzed pilin polymerization reveals structural elements involved in pilin cross-linking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5477-E5486.	3.3	27
17	Protein Labeling via a Specific Lysine-Isopeptide Bond Using the Pilin Polymerizing Sortase from <i>Corynebacterium diphtheriae</i> . <i>Journal of the American Chemical Society</i> , 2018, 140, 8420-8423.	6.6	37
18	Improving Proteome Coverage and Sample Recovery with Enhanced FASP (eFASP) for Quantitative Proteomic Experiments. <i>Methods in Molecular Biology</i> , 2017, 1550, 11-18.	0.4	33

#	ARTICLE	IF	CITATIONS
19	CryoEM structure of the Methanospirillum hungatei archaeellum reveals structural features distinct from the bacterial flagellum and type IV pilus. Nature Microbiology, 2017, 2, 16222.	5.9	72
20	Keystone predation and molecules of keystone significance. Ecology, 2017, 98, 1710-1721.	1.5	15
21	Morphology of the archaeellar motor and associated cytoplasmic cone in <i>Thermococcus kodakaraensis</i> . EMBO Reports, 2017, 18, 1660-1670.	2.0	34
22	Top-down/Bottom-up Mass Spectrometry Workflow Using Dissolvable Polyacrylamide Gels. Analytical Chemistry, 2017, 89, 8244-8250.	3.2	18
23	Structural Characterization of a Thrombin-Aptamer Complex by High Resolution Native Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 1815-1822.	1.2	24
24	Identification of protein targets in cerebral endothelial cells for brain arteriovenous malformation (AVMs) molecular therapies. Clinical Proteomics, 2017, 14, 17.	1.1	7
25	Membrane Complexes of Syntrophomonas wolfei Involved in Syntrophic Butyrate Degradation and Hydrogen Formation. Frontiers in Microbiology, 2016, 7, 1795.	1.5	34
26	Salt Bridge Rearrangement (SaBRE) Explains the Dissociation Behavior of Noncovalent Complexes. Journal of the American Society for Mass Spectrometry, 2016, 27, 975-990.	1.2	73
27	Pyrophosphate-Dependent ATP Formation from Acetyl Coenzyme A in Syntrophus aciditrophicus, a New Twist on ATP Formation. MBio, 2016, 7, .	1.8	29
28	Focus on Mass Spectrometry as a Probe of Higher Order Protein Structure, Honoring Prof. Brian T. Chait, Recipient of the 2015 ASMS Award for a Distinguished Contribution in Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2016, 27, 949-951.	1.2	4
29	Combining high-throughput MALDI-TOF mass spectrometry and isoelectric focusing gel electrophoresis for virtual 2D gel-based proteomics. Methods, 2016, 104, 163-169.	1.9	19
30	Simultaneously Revealing All Lysine Acylations in an Organism to Elucidate Substrate Metabolism. FASEB Journal, 2016, 30, 831.1.	0.2	0
31	Metabolite-Driven Modifications: Protein Acylations Elucidate Substrate Metabolism in Syntrophic Bacteria. FASEB Journal, 2016, 30, 864.1.	0.2	0
32	Enhancing protein disulfide bond cleavage by UV excitation and electron capture dissociation for top-down mass spectrometry. International Journal of Mass Spectrometry, 2015, 390, 137-145.	0.7	36
33	Increasing fragmentation of disulfide-bonded proteins for top-down mass spectrometry by supercharging. International Journal of Mass Spectrometry, 2015, 377, 546-556.	0.7	27
34	Mining proteomic data to expose protein modifications in Methanosarcina mazei strain GÅ1. Frontiers in Microbiology, 2015, 6, 149.	1.5	8
35	Structure of <i>Tetrahymena</i> telomerase reveals previously unknown subunits, functions, and interactions. Science, 2015, 350, aab4070.	6.0	134
36	Enhanced FASP (eFASP) to Increase Proteome Coverage and Sample Recovery for Quantitative Proteomic Experiments. Journal of Proteome Research, 2014, 13, 1885-1895.	1.8	275

#	ARTICLE	IF	CITATIONS
37	What Protein Charging (and Supercharging) Reveal about the Mechanism of Electrospray Ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1675-1693.	1.2	122
38	Revealing Ligand Binding Sites and Quantifying Subunit Variants of Noncovalent Protein Complexes in a Single Native Top-Down FTICR MS Experiment. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2060-2068.	1.2	63
39	Addressing the needs of traumatic brain injury with clinical proteomics. <i>Clinical Proteomics</i> , 2014, 11, 11.	1.1	19
40	Radical-directed dissociation of peptides and proteins by infrared multiphoton dissociation and sustained off-resonance irradiation collision-induced dissociation with Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 2729-2734.	0.7	7
41	Protein Complexes: Breaking Up Is Hard to Do Well. <i>Structure</i> , 2013, 21, 1265-1266.	1.6	1
42	Cofilin-Induced Changes in F-Actin Detected via Cross-Linking with Benzophenone-4-maleimide. <i>Biochemistry</i> , 2013, 52, 5503-5509.	1.2	4
43	Signal and charge enhancement for protein analysis by liquid chromatography-mass spectrometry with desorption electrospray ionization. <i>International Journal of Mass Spectrometry</i> , 2012, 325-327, 161-166.	0.7	28
44	Identification of the Major Expressed S-Layer and Cell Surface-Layer-Related Proteins in the Model Methanogenic Archaea: <i>Methanosarcina barkeri</i> Fusaro and <i>Methanosarcina acetivorans</i> C2A. <i>Archaea</i> , 2012, 2012, 1-10.	2.3	12
45	Characterization of Morphine-Glucose-6-phosphate Dehydrogenase Conjugates by Mass Spectrometry. <i>Bioconjugate Chemistry</i> , 2011, 22, 1595-1604.	1.8	6
46	Concomitant inhibition of HSP90, its mitochondrial localized homologue TRAP1 and HSP27 by green tea in pancreatic cancer HPAF-II cells. <i>Proteomics</i> , 2011, 11, 4638-4647.	1.3	24
47	New reagents for increasing ESI multiple charging of proteins and protein complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 127-131.	1.2	156
48	Ion mobility-mass spectrometry of phosphorylase B ions generated with supercharging reagents but in charge-reducing buffer. <i>Physical Chemistry Chemical Physics</i> , 2010, 12, 13476.	1.3	52
49	Electrospray-assisted laser desorption ionization mass spectrometry (ELDI-MS) with an infrared laser for characterizing peptides and proteins. <i>Analyst</i> , The, 2010, 135, 767.	1.7	44
50	Amino Acid Position-specific Contributions to Amyloid β -Protein Oligomerization. <i>Journal of Biological Chemistry</i> , 2009, 284, 23580-23591.	1.6	79
51	Increasing charge while preserving noncovalent protein complexes for ESI-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 593-596.	1.2	136
52	S-layer, Surface-Accessible, and Concanavalin A Binding Proteins of <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> . <i>Journal of Proteome Research</i> , 2009, 8, 1972-1982.	1.8	31
53	Synthesis of Maleimide-End-Functionalized Star Polymers and Multimeric Protein-Polymer Conjugates. <i>Macromolecules</i> , 2009, 42, 8028-8033.	2.2	90
54	Synthetic approach to homodimeric protein-polymer conjugates. <i>Chemical Communications</i> , 2009, , 2148.	2.2	78

#	ARTICLE	IF	CITATIONS
55	Proteomic analysis to characterize differential mouse strain sensitivity to cadmium-induced forelimb teratogenesis. Birth Defects Research Part A: Clinical and Molecular Teratology, 2008, 82, 187-199.	1.6	13
56	Mapping the Cofilin Binding Site on Yeast G-Actin by Chemical Cross-Linking. Journal of Molecular Biology, 2008, 377, 395-409.	2.0	39
57	Reactive-Electrospray-Assisted Laser Desorption/Ionization for Characterization of Peptides and Proteins. Analytical Chemistry, 2008, 80, 6995-7003.	3.2	71
58	The Proteomes of Human Parotid and Submandibular/Sublingual Gland Salivas Collected as the Ductal Secretions. Journal of Proteome Research, 2008, 7, 1994-2006.	1.8	376
59	Connecting actin monomers by iso-peptide bond is a toxicity mechanism of the <i>Vibrio cholerae</i> MARTX toxin. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18537-18542.	3.3	68
60	Proinflammatory Stimuli Induce IKK β -Mediated Phosphorylation of PIAS1 to Restrict Inflammation and Immunity. Cell, 2007, 129, 903-914.	13.5	145
61	Mapping the Interaction of Cofilin with Subdomain 2 on Actin. Biochemistry, 2007, 46, 225-233.	1.2	12
62	Matrix-Assisted Laser Desorption/Ionization-Mass Spectrometry of Hydrophobic Proteins in Mixtures Using Formic Acid, Perfluorooctanoic Acid, and Sorbitol. Analytical Chemistry, 2007, 79, 1115-1125.	3.2	22
63	Recommended criteria for the mass spectrometric identification of target peptides and proteins (kDa) in sports drug testing. Rapid Communications in Mass Spectrometry, 2007, 21, 297-304.	0.7	41
64	Electrospray-assisted laser desorption/ionization and tandem mass spectrometry of peptides and proteins. Rapid Communications in Mass Spectrometry, 2007, 21, 2541-2546.	0.7	58
65	Comprehensive Phosphoprotein Analysis of Linker Histone H1 from <i>Tetrahymena thermophila</i> . Molecular and Cellular Proteomics, 2006, 5, 1593-1609.	2.5	55
66	Top-down, bottom-up, and side-to-side proteomics with virtual 2-D gels. International Journal of Mass Spectrometry, 2005, 240, 317-325.	0.7	22
67	Large-scale identification of proteins in human salivary proteome by liquid chromatography/mass spectrometry and two-dimensional gel electrophoresis-mass spectrometry. Proteomics, 2005, 5, 1714-1728.	1.3	339
68	The cell-shape protein MreC interacts with extracytoplasmic proteins including cell wall assembly complexes in <i>Caulobacter crescentus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18602-18607.	3.3	119
69	Digital Microfluidics with In-Line Sample Purification for Proteomics Analyses with MALDI-MS. Analytical Chemistry, 2005, 77, 534-540.	3.2	301
70	Virtual two-dimensional gel electrophoresis of high-density lipoproteins. Electrophoresis, 2004, 25, 2384-2391.	1.3	21
71	Mass spectrometric characterization of transferrins and their fragments derived by reduction of disulfide bonds. Journal of the American Society for Mass Spectrometry, 2003, 14, 635-647.	1.2	35
72	In-Gel Derivatization of Proteins for Cysteine-Specific Cleavages and their Analysis by Mass Spectrometry. Journal of Proteome Research, 2003, 2, 163-172.	1.8	36

#	ARTICLE	IF	CITATIONS
73	Conformation and Dynamics of the SH1~SH2 Helix in Scallop Myosin. <i>Biochemistry</i> , 2003, 42, 7663-7674.	1.2	11
74	Doping Control Analysis of Bovine Hemoglobin-Based Oxygen Therapeutics in Human Plasma by LC~Electrospray Ionization-MS/MS. <i>Analytical Chemistry</i> , 2003, 75, 3287-3293.	3.2	40
75	In vivo labeling: A glimpse of the dynamic proteome and additional constraints for protein identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 804-812.	1.2	7
76	Virtual 2-D Gel Electrophoresis: Visualization and Analysis of the E.coli Proteome by Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 4063-4070.	3.2	70
77	Application of mass spectrometry for target identification and characterization. <i>Medicinal Research Reviews</i> , 1999, 19, 307-319.	5.0	39
78	High sensitivity mass spectrometric methods for obtaining intact molecular weights from gel-separated proteins. <i>Electrophoresis</i> , 1999, 20, 743-748.	1.3	66
79	Obtaining Molecular Weights of Proteins and Their Cleavage Products by Directly Combining Gel Electrophoresis with Mass Spectrometry. , 1999, 112, 473-486.		6
80	Sensitivity and mass accuracy for proteins analyzed directly from polyacrylamide gels: Implications for proteome mapping. <i>Electrophoresis</i> , 1997, 18, 382-390.	1.3	71
81	Mass Spectrometry of Proteins Directly from Polyacrylamide Gels. <i>Analytical Chemistry</i> , 1996, 68, 1910-1917.	3.2	95
82	Chapter 32. Application of Mass Spectrometry for Characterizing and Identifying Ligands from Combinatorial Libraries. <i>Annual Reports in Medicinal Chemistry</i> , 1996, 31, 319-325.	0.5	12
83	Proton transfer reactions of multiply charged peptide and protein cations and anions. <i>Journal of Mass Spectrometry</i> , 1995, 30, 339-347.	0.7	53
84	Applying charge discrimination with electrospray ionization~mass spectrometry to protein analyses. <i>Journal of the American Society for Mass Spectrometry</i> , 1995, 6, 1098-1104.	1.2	13
85	A study of the thermal denaturation of ribonuclease S by electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1994, 5, 614-622.	1.2	44
86	Investigation of the Gas-Phase Structure of Electrosprayed Proteins Using Ion-Molecule Reactions. <i>Journal of the American Society for Mass Spectrometry</i> , 1994, 5, 207-220.	1.2	93
87	Proton transfer reaction studies of multiply charged proteins in a high mass-to-charge ratio quadrupole mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 1994, 5, 1064-1071.	1.2	59
88	Primary to quaternary protein structure determination with electrospray ionization and magnetic sector mass spectrometry. <i>Organic Mass Spectrometry</i> , 1993, 28, 1640-1649.	1.3	58
89	Observation and implications of high mass-to-charge ratio ions from electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1993, 4, 536-545.	1.2	105
90	Electrospray mass spectrometric analysis of the domains of a large enzyme: Observation of the occupied cobalamin-binding domain and redefinition of the carboxyl terminus of methionine synthase. <i>Biochemistry</i> , 1993, 32, 9282-9289.	1.2	38

#	ARTICLE	IF	CITATIONS
91	Observation of a noncovalent ribonuclease S-protein/S-peptide complex by electrospray ionization mass spectrometry. <i>Journal of the American Chemical Society</i> , 1993, 115, 4391-4392.	6.6	98
92	Multiply charged negative ions by electrospray ionization of polypeptides and proteins. <i>Analytical Chemistry</i> , 1992, 64, 81-88.	3.2	112
93	Protein structural effects in gas phase ion/molecule reactions with diethylamine. <i>Rapid Communications in Mass Spectrometry</i> , 1992, 6, 159-165.	0.7	77
94	A new approach for the study of gas-phase ion-ion reactions using electrospray ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 1992, 3, 695-705.	1.2	82
95	Application of electrospray ionization mass spectrometry and tandem mass spectrometry in combination with capillary electrophoresis for biochemical investigations. <i>Biochemical Society Transactions</i> , 1991, 19, 943-947.	1.6	9
96	Solvent-induced conformational changes of polypeptides probed by electrospray-ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1991, 5, 101-105.	0.7	279