

# 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	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
2	The Proteomes of Human Parotid and Submandibular/Sublingual Gland Salivas Collected as the Ductal Secretions. <i>Journal of Proteome Research</i> , 2008, 7, 1994-2006.	1.8	376
3	Large-scale identification of proteins in human salivary proteome by liquid chromatography/mass spectrometry and two-dimensional gel electrophoresis-mass spectrometry. <i>Proteomics</i> , 2005, 5, 1714-1728.	1.3	339
4	Digital Microfluidics with In-Line Sample Purification for Proteomics Analyses with MALDI-MS. <i>Analytical Chemistry</i> , 2005, 77, 534-540.	3.2	301
5	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
6	Enhanced FASP (eFASP) to Increase Proteome Coverage and Sample Recovery for Quantitative Proteomic Experiments. <i>Journal of Proteome Research</i> , 2014, 13, 1885-1895.	1.8	275
7	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
8	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
9	Proinflammatory Stimuli Induce IKK $\beta$ -Mediated Phosphorylation of PIAS1 to Restrict Inflammation and Immunity. <i>Cell</i> , 2007, 129, 903-914.	13.5	145
10	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
11	Structure of <i>Tetrahymena</i> telomerase reveals previously unknown subunits, functions, and interactions. <i>Science</i> , 2015, 350, aab4070.	6.0	134
12	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
13	The cell-shape protein MreC interacts with extracytoplasmic proteins including cell wall assembly complexes in <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18602-18607.	3.3	119
14	Multiply charged negative ions by electrospray ionization of polypeptides and proteins. <i>Analytical Chemistry</i> , 1992, 64, 81-88.	3.2	112
15	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
16	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
17	Mass Spectrometry of Proteins Directly from Polyacrylamide Gels. <i>Analytical Chemistry</i> , 1996, 68, 1910-1917.	3.2	95
18	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

#	ARTICLE	IF	CITATIONS
19	Synthesis of Maleimide-End-Functionalized Star Polymers and Multimeric Protein~Polymer Conjugates. <i>Macromolecules</i> , 2009, 42, 8028-8033.	2.2	90
20	Amyloid fibrils in FTL-D-TDP are composed of TMEM106B and not TDP-43. <i>Nature</i> , 2022, 605, 304-309.	13.7	85
21	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
22	Amino Acid Position-specific Contributions to Amyloid $\beta$ -Protein Oligomerization. <i>Journal of Biological Chemistry</i> , 2009, 284, 23580-23591.	1.6	79
23	Synthetic approach to homodimeric protein~polymer conjugates. <i>Chemical Communications</i> , 2009, , 2148.	2.2	78
24	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
25	Salt Bridge Rearrangement (SaBRe) Explains the Dissociation Behavior of Noncovalent Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 975-990.	1.2	73
26	CryoEM structure of the <i>Methanospirillum hungatei</i> archaeum reveals structural features distinct from the bacterial flagellum and type IV pilus. <i>Nature Microbiology</i> , 2017, 2, 16222.	5.9	72
27	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
28	Reactive-Electrospray-Assisted Laser Desorption/Ionization for Characterization of Peptides and Proteins. <i>Analytical Chemistry</i> , 2008, 80, 6995-7003.	3.2	71
29	Virtual 2-D Gel Electrophoresis: Visualization and Analysis of the <i>E. coli</i> Proteome by Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 4063-4070.	3.2	70
30	Connecting actin monomers by iso-peptide bond is a toxicity mechanism of the <i>Vibrio cholerae</i> MARTX toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18537-18542.	3.3	68
31	High sensitivity mass spectrometric methods for obtaining intact molecular weights from gel-separated proteins. <i>Electrophoresis</i> , 1999, 20, 743-748.	1.3	66
32	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
33	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
34	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
35	Electrospray-assisted laser desorption/ionization and tandem mass spectrometry of peptides and proteins. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2541-2546.	0.7	58
36	Comprehensive Phosphoprotein Analysis of Linker Histone H1 from <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1593-1609.	2.5	55

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	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
41	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
42	Electrospray-assisted laser desorption ionization mass spectrometry (ELDI-MS) with an infrared laser for characterizing peptides and proteins. <i>Analyst</i> , 2010, 135, 767.	1.7	44
43	Recommended criteria for the mass spectrometric identification of target peptides and proteins (<math>< 8\text{kDa}</math>) in sports drug testing. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 297-304.	0.7	41
44	Doping Control Analysis of Bovine Hemoglobin-Based Oxygen Therapeutics in Human Plasma by LC-MS/MS. <i>Analytical Chemistry</i> , 2003, 75, 3287-3293.	3.2	40
45	Application of mass spectrometry for target identification and characterization. <i>Medicinal Research Reviews</i> , 1999, 19, 307-319.	5.0	39
46	Mapping the Cofilin Binding Site on Yeast G-Actin by Chemical Cross-Linking. <i>Journal of Molecular Biology</i> , 2008, 377, 395-409.	2.0	39
47	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
48	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
49	In-Gel Derivatization of Proteins for Cysteine-Specific Cleavages and their Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2003, 2, 163-172.	1.8	36
50	Enhancing protein disulfide bond cleavage by UV excitation and electron capture dissociation for top-down mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 137-145.	0.7	36
51	Mass spectrometric characterization of transferrins and their fragments derived by reduction of disulfide bonds. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 635-647.	1.2	35
52	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
53	Membrane Complexes of <i>Syntrophomonas wolfei</i> Involved in Syntrophic Butyrate Degradation and Hydrogen Formation. <i>Frontiers in Microbiology</i> , 2016, 7, 1795.	1.5	34
54	Morphology of the archaeellar motor and associated cytoplasmic cone in <i>Thermococcus kodakaraensis</i> . <i>EMBO Reports</i> , 2017, 18, 1660-1670.	2.0	34

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	Pyrophosphate-Dependent ATP Formation from Acetyl Coenzyme A in <i>Syntrophus aciditrophicus</i> , a New Twist on ATP Formation. <i>MBio</i> , 2016, 7, .	1.8	29
59	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
60	Increasing fragmentation of disulfide-bonded proteins for top-down mass spectrometry by supercharging. <i>International Journal of Mass Spectrometry</i> , 2015, 377, 546-556.	0.7	27
61	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
62	Concomitant inhibition of HSP90, its mitochondrial localized homologue TRAP1 and HSP27 by green tea in pancreatic cancer HPAF cells. <i>Proteomics</i> , 2011, 11, 4638-4647.	1.3	24
63	Structural Characterization of a Thrombin-Aptamer Complex by High Resolution Native Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1815-1822.	1.2	24
64	Top-down, bottom-up, and side-to-side proteomics with virtual 2-D gels. <i>International Journal of Mass Spectrometry</i> , 2005, 240, 317-325.	0.7	22
65	Matrix-Assisted Laser Desorption/Ionization-Mass Spectrometry of Hydrophobic Proteins in Mixtures Using Formic Acid, Perfluorooctanoic Acid, and Sorbitol. <i>Analytical Chemistry</i> , 2007, 79, 1115-1125.	3.2	22
66	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
67	Virtual two-dimensional gel electrophoresis of high-density lipoproteins. <i>Electrophoresis</i> , 2004, 25, 2384-2391.	1.3	21
68	Addressing the needs of traumatic brain injury with clinical proteomics. <i>Clinical Proteomics</i> , 2014, 11, 11.	1.1	19
69	Combining high-throughput MALDI-TOF mass spectrometry and isoelectric focusing gel electrophoresis for virtual 2D gel-based proteomics. <i>Methods</i> , 2016, 104, 163-169.	1.9	19
70	Top-down/Bottom-up Mass Spectrometry Workflow Using Dissolvable Polyacrylamide Gels. <i>Analytical Chemistry</i> , 2017, 89, 8244-8250.	3.2	18
71	<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
72	Keystone predation and molecules of keystone significance. <i>Ecology</i> , 2017, 98, 1710-1721.	1.5	15

#	ARTICLE	IF	CITATIONS
73	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
74	Proteomic analysis to characterize differential mouse strain sensitivity to cadmium-induced forelimb teratogenesis. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2008, 82, 187-199.	1.6	13
75	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
76	Mapping the Interaction of Cofilin with Subdomain 2 on Actin. <i>Biochemistry</i> , 2007, 46, 225-233.	1.2	12
77	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
78	Conformation and Dynamics of the SH1~SH2 Helix in Scallop Myosin. <i>Biochemistry</i> , 2003, 42, 7663-7674.	1.2	11
79	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
80	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
81	N-terminal autoprocessing and acetylation of multifunctional autoprocessing repeats in 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
82	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
83	Leveraging Immonium Ions for Targeting Acyl-Lysine Modifications in Proteomic Datasets. <i>Proteomics</i> , 2021, 21, e2000111.	1.3	9
84	Mining proteomic data to expose protein modifications in <i>Methanosarcina mazei</i> strain GÅ¶1. <i>Frontiers in Microbiology</i> , 2015, 6, 149.	1.5	8
85	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
86	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
87	Identification of protein targets in cerebral endothelial cells for brain arteriovenous malformation (AVMs) molecular therapies. <i>Clinical Proteomics</i> , 2017, 14, 17.	1.1	7
88	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
89	Characterization of Morphine-Glucose-6-phosphate Dehydrogenase Conjugates by Mass Spectrometry. <i>Bioconjugate Chemistry</i> , 2011, 22, 1595-1604.	1.8	6
90	Obtaining Molecular Weights of Proteins and Their Cleavage Products by Directly Combining Gel Electrophoresis with Mass Spectrometry. , 1999, 112, 473-486.		6

#	ARTICLE	IF	CITATIONS
91	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
92	Cofilin-Induced Changes in F-Actin Detected via Cross-Linking with Benzophenone-4-maleimide. <i>Biochemistry</i> , 2013, 52, 5503-5509.	1.2	4
93	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. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 949-951.	1.2	4
94	Protein Complexes: Breaking Up Is Hard to Do Well. <i>Structure</i> , 2013, 21, 1265-1266.	1.6	1
95	Simultaneously Revealing All Lysine Acylations in an Organism to Elucidate Substrate Metabolism. <i>FASEB Journal</i> , 2016, 30, 831.1.	0.2	0
96	Metabolite-Driven Modifications: Protein Acylations Elucidate Substrate Metabolism in Syntrophic Bacteria. <i>FASEB Journal</i> , 2016, 30, 864.1.	0.2	0