

# Julia Chamot-Rooke

## List of Publications by Year in descending order

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90  
papers

4,626  
citations

126858

33  
h-index

114418

63  
g-index

101  
all docs

101  
docs citations

101  
times ranked

6141  
citing authors

#	ARTICLE	IF	CITATIONS
1	Top-down and Bottom-up Approaches Revealed New Categories of Peptides from the Venom of Moroccan Scorpion <i>Androctonus mauretanicus</i> . <i>Venoms and Toxins</i> , 2022, 2, .	0.3	1
2	The ion-coupling mechanism of human excitatory amino acid transporters. <i>EMBO Journal</i> , 2022, 41, e108341.	3.5	13
3	TDFragmenter: a visualization tool for evaluating experimental parameters in top-down proteomics. <i>Bioinformatics</i> , 2022, 38, 1136-1138.	1.8	3
4	Structural and molecular determinants for the interaction of ExbB from <i>Serratia marcescens</i> and HasB, a TonB paralog. <i>Communications Biology</i> , 2022, 5, 355.	2.0	5
5	ProteoCombiner: integrating bottom-up with top-down proteomics data for improved proteoform assessment. <i>Bioinformatics</i> , 2021, 37, 2206-2208.	1.8	5
6	Optimization of a Top-Down Proteomics Platform for Closely Related Pathogenic Bacterial Discrimination. <i>Journal of Proteome Research</i> , 2021, 20, 202-211.	1.8	24
7	Advanced <i>In Vivo</i> Cross-Linking Mass Spectrometry Platform to Characterize Proteome-Wide Protein Interactions. <i>Analytical Chemistry</i> , 2021, 93, 4166-4174.	3.2	22
8	DiagnoTop: A Computational Pipeline for Discriminating Bacterial Pathogens without Database Search. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1295-1299.	1.2	4
9	Mass spectrometry-based top-down and bottom-up approaches for proteomic analysis of the Moroccan <i>Buthus occitanus</i> scorpion venom. <i>FEBS Open Bio</i> , 2021, 11, 1867-1892.	1.0	9
10	<i>De Novo</i> Sequencing of Antibody Light Chain Proteoforms from Patients with Multiple Myeloma. <i>Analytical Chemistry</i> , 2021, 93, 10627-10634.	3.2	14
11	Leveraging the partition selection bias to achieve a high-quality clustering of mass spectra. <i>Journal of Proteomics</i> , 2021, 245, 104282.	1.2	0
12	Mass spectrometry analysis of the human pineal proteome during night and day and in autism. <i>Journal of Pineal Research</i> , 2021, 70, e12713.	3.4	4
13	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021, 7, eabk0734.	4.7	106
14	Mounting, structure and autocleavage of a type VI secretion-associated Rhs polymorphic toxin. <i>Nature Communications</i> , 2021, 12, 6998.	5.8	27
15	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	1.2	67
16	Structural basis for loading and inhibition of a bacterial T6 <i>ss</i> phospholipase effector by the VgrG spike. <i>EMBO Journal</i> , 2020, 39, e104129.	3.5	31
17	The Flemmingsome reveals an ESCRT-to-membrane coupling via ALIX/syntenin/syndecan-4 required for completion of cytokinesis. <i>Nature Communications</i> , 2020, 11, 1941.	5.8	61
18	Extensive flavivirus E trimer breathing accompanies stem zippering of the post-fusion hairpin. <i>EMBO Reports</i> , 2020, 21, e50069.	2.0	8

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19	Defective lytic transglycosylase disrupts cell morphogenesis by hindering cell wall de-O-acetylation in <i>Neisseria meningitidis</i> . <i>ELife</i> , 2020, 9, .	2.8	7
20	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	9.0	55
21	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	9.0	241
22	Top-Down Garbage Collector: a tool for selecting high-quality top-down proteomics mass spectra. <i>Bioinformatics</i> , 2019, 35, 3489-3490.	1.8	4
23	Deep mutational scanning of the <i>Neisseria meningitidis</i> major pilin reveals the importance of pilus tip-mediated adhesion. <i>EMBO Journal</i> , 2019, 38, e102145.	3.5	12
24	Characterization of homodimer interfaces with cross-linking mass spectrometry and isotopically labeled proteins. <i>Nature Protocols</i> , 2018, 13, 431-458.	5.5	47
25	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	1.8	35
26	Calcium-dependent disorder-to-order transitions are central to the secretion and folding of the CyaA toxin of <i>Bordetella pertussis</i> , the causative agent of whooping cough. <i>Toxicon</i> , 2018, 149, 37-44.	0.8	29
27	A step-by-step guide to bond cleavage and 1,6-anhydro-sugar product synthesis by a peptidoglycan-degrading lytic transglycosylase. <i>Journal of Biological Chemistry</i> , 2018, 293, 6000-6010.	1.6	18
28	The stress sigma factor of RNA polymerase RpoS/ $\sigma$ S is a solvent-exposed open molecule in solution. <i>Biochemical Journal</i> , 2018, 475, 341-354.	1.7	7
29	Biogenesis and structure of a type VI secretion baseplate. <i>Nature Microbiology</i> , 2018, 3, 1404-1416.	5.9	76
30	Glycosylphosphatidylinositol Anchors from Galactomannan and GPI-Anchored Protein Are Synthesized by Distinct Pathways in <i>Aspergillus fumigatus</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2018, 4, 19.	1.5	19
31	Characterization of LE3 and LE4, the only lytic phages known to infect the spirochete <i>Leptospira</i> . <i>Scientific Reports</i> , 2018, 8, 11781.	1.6	10
32	eXL-MS: An Enhanced Cross-Linking Mass Spectrometry Workflow To Study Protein Complexes. <i>Analytical Chemistry</i> , 2018, 90, 10707-10714.	3.2	12
33	Consensus designs and thermal stability determinants of a human glutamate transporter. <i>ELife</i> , 2018, 7, .	2.8	23
34	Prepore Stability Controls Productive Folding of the BAM-independent Multimeric Outer Membrane Secretin PulD. <i>Journal of Biological Chemistry</i> , 2017, 292, 328-338.	1.6	11
35	Stability, structural and functional properties of a monomeric, calcium-loaded adenylate cyclase toxin, CyaA, from <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2017, 7, 42065.	1.6	38
36	Structure and allosteric inhibition of excitatory amino acid transporter 1. <i>Nature</i> , 2017, 544, 446-451.	13.7	179

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37	DiagnoProt: a tool for discovery of new molecules by mass spectrometry. <i>Bioinformatics</i> , 2017, 33, 1883-1885.	1.8	7
38	Structural Characterization of Whirlin Reveals an Unexpected and Dynamic Supramodule Conformation of Its PDZ Tandem. <i>Structure</i> , 2017, 25, 1645-1656.e5.	1.6	22
39	Characterization of Post-Translational Modifications and Cytotoxic Properties of the Adenylate-Cyclase Hemolysin Produced by Various <i>Bordetella pertussis</i> and <i>Bordetella parapertussis</i> Isolates. <i>Toxins</i> , 2017, 9, 304.	1.5	6
40	Calmodulin fishing with a structurally disordered bait triggers CyaA catalysis. <i>PLoS Biology</i> , 2017, 15, e2004486.	2.6	31
41	Regulation of NF- $\kappa$ B by the p105-ABIN2-TPL2 complex and RelA $\kappa$ 43 during rabies virus infection. <i>PLoS Pathogens</i> , 2017, 13, e1006697.	2.1	32
42	Pseudopilin residue E5 is essential for recruitment by the type 2 secretion system assembly platform. <i>Molecular Microbiology</i> , 2016, 101, 924-941.	1.2	32
43	Abundant Lysine Methylation and N-Terminal Acetylation in <i>Sulfolobus islandicus</i> Revealed by Bottom-Up and Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3388-3404.	2.5	36
44	MEMHDX: an interactive tool to expedite the statistical validation and visualization of large HDX-MS datasets. <i>Bioinformatics</i> , 2016, 32, 3413-3419.	1.8	52
45	Changes in markers associated with dendritic cells driving the differentiation of either TH2 cells or regulatory T cells correlate with clinical benefit during allergen immunotherapy. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 545-558.	1.5	110
46	Bio-guided identification of proteins for the diagnosis of cysticercosis in swine. <i>Veterinary Parasitology</i> , 2016, 220, 23-27.	0.7	3
47	R vs. S fluoroproline ring substitution: trans/cis effects on the formation of b <sub>2</sub> ions in gas-phase peptide fragmentation. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 2202-2209.	1.3	6
48	Structural models of intrinsically disordered and calcium-bound folded states of a protein adapted for secretion. <i>Scientific Reports</i> , 2015, 5, 14223.	1.6	46
49	The COPII complex and lysosomal VAMP7 determine intracellular <i>Salmonella</i> localization and growth. <i>Cellular Microbiology</i> , 2015, 17, 1699-1720.	1.1	46
50	Conserved <i>Streptococcus pneumoniae</i> Spirosomes Suggest a Single Type of Transformation Pilus in Competence. <i>PLoS Pathogens</i> , 2015, 11, e1004835.	2.1	26
51	A Novel Bio-Orthogonal Cross-Linker for Improved Protein/Protein Interaction Analysis. <i>Analytical Chemistry</i> , 2015, 87, 1853-1860.	3.2	24
52	<i>Paenibacillus faecis</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4621-4626.	0.8	25
53	<i>Neisseria meningitidis</i> Type IV Pili Composed of Sequence Invariable Pilins Are Masked by Multisite Glycosylation. <i>PLoS Pathogens</i> , 2015, 11, e1005162.	2.1	55
54	Evolution of <i>Helicobacter</i> : Acquisition by Gastric Species of Two Histidine-Rich Proteins Essential for Colonization. <i>PLoS Pathogens</i> , 2015, 11, e1005312.	2.1	40

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55	O-Glycosylation of the N-terminal Region of the Serine-rich Adhesin Srr1 of <i>Streptococcus agalactiae</i> Explored by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2168-2182.	2.5	24
56	Ion source parameters and hydrogen scrambling in the ECD of selectively deuterated peptides. <i>International Journal of Mass Spectrometry</i> , 2014, 367, 21-27.	0.7	2
57	Complete posttranslational modification mapping of pathogenic <i>Neisseria meningitidis</i> pilins requires top-down mass spectrometry. <i>Proteomics</i> , 2014, 14, 1141-1151.	1.3	27
58	Proteomic Analysis of Intact Flagella of Procytic <i>Trypanosoma brucei</i> Cells Identifies Novel Flagellar Proteins with Unique Sub-localization and Dynamics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1769-1786.	2.5	114
59	Robust and low cost uniform <sup>15</sup> N-labeling of proteins expressed in <i>Drosophila</i> S2 cells and <i>Spodoptera frugiperda</i> Sf9 cells for NMR applications. <i>Journal of Structural Biology</i> , 2014, 188, 71-78.	1.3	19
60	Identification and functional characterization of a novel $\hat{1}\pm$ -conotoxin (EIIA) from <i>Conus ermineus</i> . <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 5341-5351.	1.9	17
61	Influence of N-terminal Residue Composition on the Structure of Proline-Containing b <sup>2+</sup> Ions. <i>Journal of Physical Chemistry A</i> , 2013, 117, 1291-1298.	1.1	25
62	Proteform: a single term describing protein complexity. <i>Nature Methods</i> , 2013, 10, 186-187.	9.0	1,180
63	A Type IV Pilus Mediates DNA Binding during Natural Transformation in <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003473.	2.1	147
64	A combined mass spectrometry strategy for complete posttranslational modification mapping of <i>Neisseria meningitidis</i> major pilin. <i>Journal of Mass Spectrometry</i> , 2013, 48, 1199-1206.	0.7	14
65	Structural Influences on Preferential Oxazolone versus Diketopiperazine b <sub>2</sub> <sup>+</sup> Ion Formation for Histidine Analogue-Containing Peptides. <i>Journal of Physical Chemistry A</i> , 2012, 116, 4296-4304.	1.1	33
66	Assigning Structures to Gas-Phase Peptide Cations and Cation-Radicals. An Infrared Multiphoton Dissociation, Ion Mobility, Electron Transfer, and Computational Study of a Histidine Peptide Ion. <i>Journal of Physical Chemistry B</i> , 2012, 116, 3445-3456.	1.2	47
67	Ground Electronic State of Peptide Cation Radicals: A Delocalized Unpaired Electron?. <i>Journal of Physical Chemistry Letters</i> , 2011, 2, 1426-1431.	2.1	18
68	Posttranslational Modification of Pili upon Cell Contact Triggers <i>N. meningitidis</i> Dissemination. <i>Science</i> , 2011, 331, 778-782.	6.0	162
69	Dissociation Channel Dependence on Peptide Size Observed in Electron Capture Dissociation of Tryptic Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1631-1644.	1.2	16
70	Separation and identification of structural isomers by quadrupole collision-induced dissociation-hydrogen/deuterium exchange-infrared multiphoton dissociation (QCID-HDX-IRMPD). <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1329-1338.	1.2	28
71	Isolation and pharmacological characterization of AdTx1, a natural peptide displaying specific insurmountable antagonism of the $\hat{1}\pm$ $\hat{1}A$ $\hat{1}$ adrenoceptor. <i>British Journal of Pharmacology</i> , 2010, 159, 316-325.	2.7	43
72	Identification of a novel snake peptide toxin displaying high affinity and antagonist behaviour for the $\hat{1}\pm$ $\hat{2}$ $\hat{1}$ adrenoceptors. <i>British Journal of Pharmacology</i> , 2010, 161, 1361-1374.	2.7	36

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73	The Histidine Effect. Electron Transfer and Capture Cause Different Dissociations and Rearrangements of Histidine Peptide Cation-Radicals. <i>Journal of the American Chemical Society</i> , 2010, 132, 10728-10740.	6.6	55
74	Oxidative stress induces mainly human centrin 2 polymerisation. <i>International Journal of Radiation Biology</i> , 2010, 86, 657-668.	1.0	14
75	Synthesis of hexakis(2-keto-3,6-anhydro)cyclomaltohexaose: structural studies and Pb <sup>2+</sup> complexation evaluation. <i>Tetrahedron Letters</i> , 2009, 50, 4251-4253.	0.7	2
76	Evidence of Diketopiperazine and Oxazolone Structures for HA b <sub>2</sub> <sup>+</sup> Ion. <i>Journal of the American Chemical Society</i> , 2009, 131, 17528-17529.	6.6	94
77	IRMPD Spectroscopy Shows That AGG Forms an Oxazolone b <sub>2</sub> <sup>+</sup> Ion. <i>Journal of the American Chemical Society</i> , 2008, 130, 17644-17645.	6.6	99
78	Structure of Electron-Capture Dissociation Fragments from Charge-Tagged Peptides Probed by Tunable Infrared Multiple Photon Dissociation. <i>Journal of the American Chemical Society</i> , 2008, 130, 14916-14917.	6.6	59
79	Alternative <i>Neisseria</i> spp. type IV pilin glycosylation with a glyceramido acetamido trideoxyhexose residue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14783-14788.	3.3	77
80	The combination of electron capture dissociation and fixed charge derivatization increases sequence coverage for O-glycosylated and O-phosphorylated peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1405-1413.	1.2	41
81	Glycosylation status of the membrane protein CD9Pá€1. <i>Proteomics</i> , 2007, 7, 3880-3895.	1.3	19
82	Electron capture in charge-tagged peptides. Evidence for the role of excited electronic states. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 2146-2161.	1.2	58
83	Fourier transform mass spectrometry: A powerful tool for toxin analysis. <i>Toxicon</i> , 2006, 47, 715-726.	0.8	25
84	Proteomic analysis of the tetraspanin web using LC-ESI-MS/MS and MALDI-FTICR-MS. <i>Proteomics</i> , 2006, 6, 1437-1449.	1.3	87
85	Characterization of Toxins within Crude Venoms by Combined Use of Fourier Transform Mass Spectrometry and Cloning. <i>Analytical Chemistry</i> , 2005, 77, 6630-6639.	3.2	44
86	Electrophilic and radical reactivity of ionized aminohydroxycarbene toward alkenes. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 625-641.	0.7	6
87	Spontaneous and catalyzed isomerizations of the acetamide radical cation. <i>Journal of Mass Spectrometry</i> , 2001, 36, 102-104.	0.7	27
88	Proton Affinity and Heat of Formation of Vinyloxy [CH <sub>2</sub> CHO]. and Acetonyl [CH <sub>2</sub> COCH <sub>3</sub> ]. Radicals. <i>ChemPhysChem</i> , 2001, 2, 235-241.	1.0	40
89	A comparison of matrix-assisted laser desorption/ionization time-of-flight and liquid chromatography electrospray ionization mass spectrometry methods for the analysis of crude tarantula venoms in the Pterinochilus group. , 1999, 13, 1861-1868.		41
90	Formation of the distonic acetate radical anioná€¢CH <sub>2</sub> CO <sub>2</sub> <sup>-</sup> in reactions of O-á€¢ with lactones in the gas phase. <i>Journal of Mass Spectrometry</i> , 1998, 33, 677-679.	0.7	5