

Carla Schmidt

List of Publications by Year in descending order

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59
papers

1,974
citations

304368

22
h-index

276539

41
g-index

66
all docs

66
docs citations

66
times ranked

3352
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the human MHC-I peptide-loading complex. <i>Nature</i> , 2017, 551, 525-528.	13.7	284
2	Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016, 539, 118-122.	13.7	141
3	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013, 4, 1985.	5.8	122
4	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
5	A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014, 9, 2224-2236.	5.5	93
6	Hsp70 Forms Antiparallel Dimers Stabilized by Post-translational Modifications to Position Clients for Transfer to Hsp90. <i>Cell Reports</i> , 2015, 11, 759-769.	2.9	93
7	Quantitative Mass Spectrometry-Based Proteomics: An Overview. <i>Methods in Molecular Biology</i> , 2021, 2228, 85-116.	0.4	84
8	Determination of Protein Stoichiometry within Protein Complexes Using Absolute Quantification and Multiple Reaction Monitoring. <i>Analytical Chemistry</i> , 2010, 82, 2784-2796.	3.2	79
9	eIF2B is a decameric guanine nucleotide exchange factor with a $\beta_2\beta_2$ tetrameric core. <i>Nature Communications</i> , 2014, 5, 3902.	5.8	71
10	Combining cryo-electron microscopy (cryo-EM) and cross-linking mass spectrometry (CX-MS) for structural elucidation of large protein assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 46, 157-168.	2.6	69
11	Dynamic protein ligand interactions—Insights from sc^2MS . <i>FEBS Journal</i> , 2014, 281, 1950-1964.	2.2	61
12	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. <i>Analytical Chemistry</i> , 2017, 89, 1459-1468.	3.2	46
13	Native mass spectrometry—A valuable tool in structural biology. <i>Journal of Mass Spectrometry</i> , 2020, 55, e4578.	0.7	45
14	Investigation of protein–RNA interactions by mass spectrometry—Techniques and applications. <i>Journal of Proteomics</i> , 2012, 75, 3478-3494.	1.2	43
15	Dimer interface of bovine cytochrome <i>c</i> oxidase is influenced by local posttranslational modifications and lipid binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8230-8235.	3.3	40
16	Topological Models of Heteromeric Protein Assemblies from Mass Spectrometry: Application to the Yeast eIF3:eIF5 Complex. <i>Chemistry and Biology</i> , 2015, 22, 117-128.	6.2	38
17	Structure based biophysical characterization of the PROPPIN Atg18 shows Atg18 oligomerization upon membrane binding. <i>Scientific Reports</i> , 2017, 7, 14008.	1.6	38
18	Accommodating Protein Dynamics in the Modeling of Chemical Crosslinks. <i>Structure</i> , 2017, 25, 1751-1757.e5.	1.6	36

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19	eIF2 interactions with initiator tRNA and eIF2B are regulated by post-translational modifications and conformational dynamics. <i>Cell Discovery</i> , 2015, 1, 15020.	3.1	29
20	Cross-linking mass spectrometry uncovers protein interactions and functional assemblies in synaptic vesicle membranes. <i>Nature Communications</i> , 2021, 12, 858.	5.8	26
21	Uncovering the Early Assembly Mechanism for Amyloidogenic β 2-Microglobulin Using Cross-linking and Native Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2016, 291, 4626-4637.	1.6	24
22	Assembly defects of human tRNA splicing endonuclease contribute to impaired pre-tRNA processing in pontocerebellar hypoplasia. <i>Nature Communications</i> , 2021, 12, 5610.	5.8	24
23	An automated in-gel digestion/iTRAQ-labeling workflow for robust quantification of gel-separated proteins. <i>Proteomics</i> , 2013, 13, 1417-1422.	1.3	23
24	Structural and Functional Analyses of the Human PDH Complex Suggest a "Division-of-Labor" Mechanism by Local E1 and E3 Clusters. <i>Structure</i> , 2019, 27, 1124-1136.e4.	1.6	23
25	Mass spectrometry – A versatile tool for characterising the lipid environment of membrane protein assemblies. <i>Chemistry and Physics of Lipids</i> , 2019, 221, 145-157.	1.5	23
26	iTRAQ-Labeling of In-Gel Digested Proteins for Relative Quantification. <i>Methods in Molecular Biology</i> , 2009, 564, 207-226.	0.4	23
27	Structural characterisation of medically relevant protein assemblies by integrating mass spectrometry with computational modelling. <i>Journal of Proteomics</i> , 2018, 175, 34-41.	1.2	19
28	Mass spectrometry of membrane protein complexes. <i>Biological Chemistry</i> , 2019, 400, 813-829.	1.2	19
29	Acetylation and phosphorylation control both local and global stability of the chloroplast F1 ATP synthase. <i>Scientific Reports</i> , 2017, 7, 44068.	1.6	18
30	Liposomes as Carriers of Membrane-Associated Proteins and Peptides for Mass Spectrometric Analysis. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 11523-11530.	7.2	16
31	Decision-Making in Cascade Complexes Harboring crRNAs of Altered Length. <i>Cell Reports</i> , 2019, 28, 3157-3166.e4.	2.9	15
32	Absolute Quantification of Proteins Using Standard Peptides and Multiple Reaction Monitoring. <i>Methods in Molecular Biology</i> , 2012, 893, 249-265.	0.4	14
33	Insights into Eukaryotic Translation Initiation from Mass Spectrometry of Macromolecular Protein Assemblies. <i>Journal of Molecular Biology</i> , 2016, 428, 344-356.	2.0	14
34	Small-Molecule-Induced Soluble Oligomers of β -Synuclein with Helical Structure. <i>Chemistry - A European Journal</i> , 2017, 23, 13010-13014.	1.7	14
35	Oligomerisation of Synaptobrevin-2 Studied by Native Mass Spectrometry and Chemical Cross-Linking. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 149-160.	1.2	14
36	Protein-Lipid Interactions Stabilize the Oligomeric State of BOR1p from <i>Saccharomyces cerevisiae</i> . <i>Analytical Chemistry</i> , 2019, 91, 13071-13079.	3.2	14

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37	Combining Chemical Cross-linking and Mass Spectrometry of Intact Protein Complexes to Study the Architecture of Multi-subunit Protein Assemblies. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	9
38	Control of p21Cip by BRCA1-associated protein is critical for cardiomyocyte cell cycle progression and survival. <i>Cardiovascular Research</i> , 2020, 116, 592-604.	1.8	9
39	A novel sample preparation strategy for shotgun lipidomics of phospholipids employing multilamellar vesicles. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 4253-4258.	1.9	8
40	Alternatively spliced isoforms of AUF1 regulate a miRNA-mRNA interaction differentially through their YGG motif. <i>RNA Biology</i> , 2021, 18, 843-853.	1.5	8
41	The joining of the Hsp90 and Hsp70 chaperone cycles yields transient interactions and stable intermediates: insights from mass spectrometry. <i>Oncotarget</i> , 2015, 6, 18276-18281.	0.8	8
42	Instrument response of phosphatidylglycerol lipids with varying fatty acyl chain length in nano-ESI shotgun experiments. <i>Chemistry and Physics of Lipids</i> , 2019, 223, 104782.	1.5	7
43	The CroCo cross-link converter: a user-centred tool to convert results from cross-linking mass spectrometry experiments. <i>Bioinformatics</i> , 2020, 36, 1296-1297.	1.8	6
44	Formation and Stoichiometry of CRISPR-Cascade Complexes with Varying Spacer Lengths Revealed by Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 538-546.	1.2	6
45	Quantitative proteomics and in-cell cross-linking reveal cellular reorganisation during early neuronal differentiation of SH-SY5Y cells. <i>Communications Biology</i> , 2022, 5, .	2.0	6
46	Evaluation of NHS-Acetate and DEPC labelling for determination of solvent accessible amino acid residues in protein complexes. <i>Journal of Proteomics</i> , 2020, 222, 103793.	1.2	5
47	Polydisperse molecular architecture of connexin 26/30 heteromeric hemichannels revealed by atomic force microscopy imaging. <i>Journal of Biological Chemistry</i> , 2020, 295, 16499-16509.	1.6	4
48	Effects of non-ionic and zwitterionic detergents on soluble proteins during native mass spectrometry experiments. <i>International Journal of Mass Spectrometry</i> , 2021, 468, 116652.	0.7	4
49	Quantitative Cross-Linking of Proteins and Protein. <i>Methods in Molecular Biology</i> , 2021, 2228, 385-400.	0.4	4
50	Nanoscale Model System for the Human Myelin Sheath. <i>Biomacromolecules</i> , 2021, 22, 3901-3912.	2.6	3
51	Analyzing the Protein Assembly and Dynamics of the Human Spliceosome with SILAC. <i>Methods in Molecular Biology</i> , 2014, 1188, 227-244.	0.4	3
52	Viral immune evasins impact antigen presentation by allele-specific trapping of MHC-I at the peptide-loading complex. <i>Scientific Reports</i> , 2022, 12, 1516.	1.6	3
53	Thin-Layer Chromatography and Coomassie Staining of Phospholipids for Fast and Simple Lipidomics Sample Preparation. <i>Analysis & Sensing</i> , 2021, 1, 171-179.	1.1	2
54	Disorder-to-order transition of Synaptobrevin-2: Tracing the conformational diversity of a synaptic SNARE protein. <i>Journal of Structural Biology</i> , 2022, 214, 107824.	1.3	2

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55	Proteomic basics – quantification and post-translational modifications of proteins: The 3rd European Summer School in Kloster Neustift. Journal of Proteomics, 2010, 73, 697-700.	1.2	0
56	Liposomen als Träger membranassoziierter Proteine und Peptide für die massenspektrometrische Analyse. Angewandte Chemie, 2021, 133, 11624-11632.	1.6	0
57	Titelbild: Liposomen als Träger membranassoziierter Proteine und Peptide für die massenspektrometrische Analyse (Angew. Chem. 20/2021). Angewandte Chemie, 2021, 133, 11097-11097.	1.6	0
58	Exploring Phosphoinositide Binding Using Native Mass Spectrometry. Methods in Molecular Biology, 2021, 2251, 157-175.	0.4	0
59	Thin-Layer Chromatography and Coomassie Staining of Phospholipids for Fast and Simple Lipidomics Sample Preparation. Analysis & Sensing, 2021, 1, 134.	1.1	0