

Carla Schmidt

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

1,351

citations

18

h-index

36

g-index

66

ext. papers

1,682

ext. citations

7.9

avg, IF

5.03

L-index

#	Paper	IF	Citations
62	Structure of the human MHC-I peptide-loading complex. <i>Nature</i> , 2017 , 551, 525-528	50.4	182
61	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013 , 4, 1985	17.4	113
60	Atomic model for the membrane-embedded V motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016 , 539, 118-122	32.4	104
59	A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014 , 9, 2224-36	18.8	86
58	Hsp70 forms antiparallel dimers stabilized by post-translational modifications to position clients for transfer to Hsp90. <i>Cell Reports</i> , 2015 , 11, 759-69	10.6	83
57	Determination of protein stoichiometry within protein complexes using absolute quantification and multiple reaction monitoring. <i>Analytical Chemistry</i> , 2010 , 82, 2784-96	7.8	71
56	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
55	eIF2B is a decameric guanine nucleotide exchange factor with a $\alpha\alpha$ tetrameric core. <i>Nature Communications</i> , 2014 , 5, 3902	17.4	52
54	Dynamic protein ligand interactions--insights from MS. <i>FEBS Journal</i> , 2014 , 281, 1950-64	5.7	50
53	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	8.1	46
52	Investigation of protein-RNA interactions by mass spectrometry--Techniques and applications. <i>Journal of Proteomics</i> , 2012 , 75, 3478-94	3.9	37
51	Topological models of heteromeric protein assemblies from mass spectrometry: application to the yeast eIF3:eIF5 complex. <i>Chemistry and Biology</i> , 2015 , 22, 117-28		34
50	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. <i>Analytical Chemistry</i> , 2017 , 89, 1459-1468	7.8	32
49	Accommodating Protein Dynamics in the Modeling of Chemical Crosslinks. <i>Structure</i> , 2017 , 25, 1751-1757	3.5	30
48	Dimer interface of bovine cytochrome c 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, 8230-5	11.5	30
47	Structure based biophysical characterization of the PROPPIN Atg18 shows Atg18 oligomerization upon membrane binding. <i>Scientific Reports</i> , 2017 , 7, 14008	4.9	27
46	Uncovering the Early Assembly Mechanism for Amyloidogenic β -Microglobulin Using Cross-linking and Native Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4626-37	5.4	22

45	iTRAQ-labeling of in-gel digested proteins for relative quantification. <i>Methods in Molecular Biology</i> , 2009 , 564, 207-26	1.4	19
44	eIF2 interactions with initiator tRNA and eIF2B are regulated by post-translational modifications and conformational dynamics. <i>Cell Discovery</i> , 2015 , 1, 15020	22.3	18
43	An automated in-gel digestion/iTRAQ-labeling workflow for robust quantification of gel-separated proteins. <i>Proteomics</i> , 2013 , 13, 1417-22	4.8	17
42	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	3.7	16
41	Structural characterisation of medically relevant protein assemblies by integrating mass spectrometry with computational modelling. <i>Journal of Proteomics</i> , 2018 , 175, 34-41	3.9	16
40	Acetylation and phosphorylation control both local and global stability of the chloroplast F ATP synthase. <i>Scientific Reports</i> , 2017 , 7, 44068	4.9	14
39	Native mass spectrometry-A valuable tool in structural biology. <i>Journal of Mass Spectrometry</i> , 2020 , 55, e4578	2.2	14
38	Cross-linking mass spectrometry uncovers protein interactions and functional assemblies in synaptic vesicle membranes. <i>Nature Communications</i> , 2021 , 12, 858	17.4	14
37	Insights into Eukaryotic Translation Initiation from Mass Spectrometry of Macromolecular Protein Assemblies. <i>Journal of Molecular Biology</i> , 2016 , 428, 344-356	6.5	13
36	Protein-Lipid Interactions Stabilize the Oligomeric State of BOR1p from. <i>Analytical Chemistry</i> , 2019 , 91, 13071-13079	7.8	12
35	Mass spectrometry of membrane protein complexes. <i>Biological Chemistry</i> , 2019 , 400, 813-829	4.5	12
34	Small-Molecule-Induced Soluble Oligomers of E5ynuclein with Helical Structure. <i>Chemistry - A European Journal</i> , 2017 , 23, 13010-13014	4.8	12
33	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	5.2	10
32	Absolute quantification of proteins using standard peptides and multiple reaction monitoring. <i>Methods in Molecular Biology</i> , 2012 , 893, 249-65	1.4	10
31	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	3.5	9
30	Quantitative Mass Spectrometry-Based Proteomics: An Overview. <i>Methods in Molecular Biology</i> , 2021 , 2228, 85-116	1.4	9
29	A novel sample preparation strategy for shotgun lipidomics of phospholipids employing multilamellar vesicles. <i>Analytical and Bioanalytical Chemistry</i> , 2018 , 410, 4253-4258	4.4	7
28	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 ,	1.6	7

27	The joining of the Hsp90 and Hsp70 chaperone cycles yields transient interactions and stable intermediates: insights from mass spectrometry. <i>Oncotarget</i> , 2015 , 6, 18276-81	3.3	6
26	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	7.2	5
25	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	3.7	4
24	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	3.5	4
23	Cross-linking/Mass Spectrometry: A Community-Wide, Comparative Study Towards Establishing Best Practice Guidelines		4
22	Liposomes as Carriers of Membrane-Associated Proteins and Peptides for Mass Spectrometric Analysis. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 11523-11530	16.4	4
21	Analyzing the protein assembly and dynamics of the human spliceosome with SILAC. <i>Methods in Molecular Biology</i> , 2014 , 1188, 227-44	1.4	3
20	Control of p21Cip by BRCA1-associated protein is critical for cardiomyocyte cell cycle progression and survival. <i>Cardiovascular Research</i> , 2020 , 116, 592-604	9.9	3
19	Assembly defects of human tRNA splicing endonuclease contribute to impaired pre-tRNA processing in pontocerebellar hypoplasia. <i>Nature Communications</i> , 2021 , 12, 5610	17.4	3
18	Decision-Making in Cascade Complexes Harboring crRNAs of Altered Length. <i>Cell Reports</i> , 2019 , 28, 3157-3166	13.1	4
17	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	3.9	2
16	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	5.4	2
15	Alternatively spliced isoforms of AUF1 regulate a miRNA-mRNA interaction differentially through their YGG motif. <i>RNA Biology</i> , 2021 , 18, 843-853	4.8	2
14	Assembly defects of the human tRNA splicing endonuclease contribute to impaired pre-tRNA processing in pontocerebellar hypoplasia		1
13	Nanoscale Model System for the Human Myelin Sheath. <i>Biomacromolecules</i> , 2021 , 22, 3901-3912	6.9	1
12	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	1.9	1
11	Quantitative Cross-Linking of Proteins and Protein Complexes. <i>Methods in Molecular Biology</i> , 2021 , 2228, 385-400	1.4	1
10	Viral immune evasins impact antigen presentation by allele-specific trapping of MHCI at the peptide-loading complex.. <i>Scientific Reports</i> , 2022 , 12, 1516	4.9	0

- 9 Disorder-to-order transition of Synaptobrevin-2: Tracing the conformational diversity of a synaptic SNARE protein.. *Journal of Structural Biology*, **2021**, 214, 107824 3.4 0
- 8 Massenspektrometrische Analyse von Phospholipiden aus Liposomen. *BioSpektrum*, **2019**, 25, 167-169 0.1
- 7 Analysis of Protein (-RNA) Complexes by (Quantitative) Mass Spectrometric Analysis **2012**, 366-379
- 6 Proteomic basics Quantification and post-translational modifications of proteins: The 3rd European Summer School in Kloster Neustift. *Journal of Proteomics*, **2010**, 73, 697-700 3.9
- 5 Thin-Layer Chromatography and Coomassie Staining of Phospholipids for Fast and Simple Lipidomics Sample Preparation. *Analysis & Sensing*, **2021**, 1, 134
- 4 Liposomen als Träger membranassoziierter Proteine und Peptide für die massenspektrometrische Analyse. *Angewandte Chemie*, **2021**, 133, 11624-11632 3.6
- 3 Titelbild: Liposomen als Träger membranassoziierter Proteine und Peptide für die massenspektrometrische Analyse (Angew. Chem. 20/2021). *Angewandte Chemie*, **2021**, 133, 11097-11097 3.6
- 2 Thin-Layer Chromatography and Coomassie Staining of Phospholipids for Fast and Simple Lipidomics Sample Preparation. *Analysis & Sensing*, **2021**, 1, 171
- 1 Exploring Phosphoinositide Binding Using Native Mass Spectrometry. *Methods in Molecular Biology*, **2021**, 2251, 157-175 1.4