

Sarah Cianferani

List of Publications by Year in descending order

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143
papers

3,724
citations

147566

31
h-index

182168

51
g-index

151
all docs

151
docs citations

151
times ranked

5163
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic analysis of <i>Rhodospirillum rubrum</i> after carbon monoxide exposure reveals an important effect on metallic cofactor biosynthesis. <i>Journal of Proteomics</i> , 2022, 250, 104389.	1.2	3
2	Probing the mechanism of peroxiredoxin decamer interaction with its reductase sulfiredoxin from the single molecule to the solution scale. <i>Nanoscale Horizons</i> , 2022, , .	4.1	0
3	A Confinementâ€Driven Nucleation Mechanism of Metal Oxide Nanoparticles Obtained via Thermal Decomposition in Organic Media. <i>Small</i> , 2022, 18, e2200414.	5.2	5
4	Repeated Exposure of Macrophages to Synthetic Amorphous Silica Induces Adaptive Proteome Changes and a Moderate Cell Activation. <i>Nanomaterials</i> , 2022, 12, 1424.	1.9	3
5	Combination of IM-Based Approaches to Unravel the Coexistence of Two Conformers on a Therapeutic Multispecific mAb. <i>Analytical Chemistry</i> , 2022, 94, 7981-7989.	3.2	9
6	Does size matter? A proteomics-informed comparison of the effects of polystyrene beads of different sizes on macrophages. <i>Environmental Science: Nano</i> , 2022, 9, 2827-2840.	2.2	4
7	Upconversion in a dâ€f [RuYb₃] Supramolecular Assembly. <i>Journal of the American Chemical Society</i> , 2022, 144, 13356-13365.	6.6	16
8	Structural and Biochemical Investigation of the Heterodimeric Murine tRNA-Guanine Transglycosylase. <i>ACS Chemical Biology</i> , 2022, 17, 2229-2247.	1.6	7
9	Optimized Sample Preparation and Data Processing of Data-Independent Acquisition Methods for the Robust Quantification of Trace-Level Host Cell Protein Impurities in Antibody Drug Products. <i>Journal of Proteome Research</i> , 2021, 20, 923-931.	1.8	17
10	Fast Afucosylation Profiling of Glycoengineered Antibody Subunits by Middle-Up Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2271, 73-83.	0.4	2
11	Structural studies of RNase M5 reveal two-metal-ion supported two-step dsRNA cleavage for 5S rRNA maturation. <i>RNA Biology</i> , 2021, 18, 1-11.	1.5	1
12	Combining labelâ€free and labelâ€based accurate quantifications with SWATHâ€MS: Comparison with SRM and PRM for the evaluation of bovine muscle type effects. <i>Proteomics</i> , 2021, 21, e2000214.	1.3	5
13	Pushing the limits of native MS: Online SEC-native MS for structural biology applications. <i>International Journal of Mass Spectrometry</i> , 2021, 461, 116502.	0.7	22
14	A structural signature motif enlightens the origin and diversification of nuclear receptors. <i>PLoS Genetics</i> , 2021, 17, e1009492.	1.5	8
15	A Class of Valuable (Pro-)Activity-Based Protein Profiling Probes: Application to the Redox-Active Antiplasmodial Agent, Plasmodione. <i>Jacs Au</i> , 2021, 1, 669-689.	3.6	4
16	Temporal multiomic modeling reveals a B-cell receptor proliferative program in chronic lymphocytic leukemia. <i>Leukemia</i> , 2021, 35, 1463-1474.	3.3	6
17	Proteo3Dnet: a web server for the integration of structural information with interactomics data. <i>Nucleic Acids Research</i> , 2021, 49, W567-W572.	6.5	5
18	A proteomic view of cellular responses of macrophages to copper when added as ion or as copper-polyacrylate complex. <i>Journal of Proteomics</i> , 2021, 239, 104178.	1.2	1

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19	A proteomic-informed view of the changes induced by loss of cellular adherence: The example of mouse macrophages. <i>PLoS ONE</i> , 2021, 16, e0252450.	1.1	2
20	State-of-the-Art Native Mass Spectrometry and Ion Mobility Methods to Monitor Homogeneous Site-Specific Antibody-Drug Conjugates Synthesis. <i>Pharmaceuticals</i> , 2021, 14, 498.	1.7	16
21	High-Resolution IMS-MS to Assign Additional Disulfide Bridge Pairing in Complementarity-Determining Regions of an IgG4 Monoclonal Antibody. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2505-2512.	1.2	13
22	Iron Stearate Structures: An Original Tool for Nanoparticles Design. <i>Inorganic Chemistry</i> , 2021, 60, 12445-12456.	1.9	14
23	Rab7-harboring vesicles are carriers of the transferrin receptor through the biosynthetic secretory pathway. <i>Science Advances</i> , 2021, 7, .	4.7	11
24	Strongly Adhesive and Antimicrobial Peptide-Loaded, Alginate-Catechol-Based Gels for Application against Periimplantitis. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 10050.	1.3	2
25	Hands on Native Mass Spectrometry Analysis of Multi-protein Complexes. <i>Methods in Molecular Biology</i> , 2021, 2247, 173-191.	0.4	1
26	Bicyclo[6.1.0]nonyne carboxylic acid for the production of stable molecular probes. <i>RSC Advances</i> , 2021, 11, 36777-36780.	1.7	0
27	<i>Toxoplasma gondii</i> ROP16 kinase silences the cyclin B1 gene promoter by hijacking host cell UHRF1-dependent epigenetic pathways. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 2141-2156.	2.4	15
28	VHH characterization. Recombinant VHHs: Production, characterization and affinity. <i>Analytical Biochemistry</i> , 2020, 589, 113491.	1.1	9
29	Homogeneous antibody-drug conjugates: DAR 2 anti-HER2 obtained by conjugation on isolated light chain followed by mAb assembly. <i>MAbs</i> , 2020, 12, 1702262.	2.6	9
30	Automated linkage of proteins and payloads producing monodisperse conjugates. <i>Chemical Science</i> , 2020, 11, 1210-1215.	3.7	19
31	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR-RXR. <i>Nucleic Acids Research</i> , 2020, 48, 9969-9985.	6.5	17
32	Molecular determinants of MED1 interaction with the DNA bound VDR-RXR heterodimer. <i>Nucleic Acids Research</i> , 2020, 48, 11199-11213.	6.5	17
33	Structures of <i>B. subtilis</i> Maturation RNases Captured on 50S Ribosome with Pre-rRNAs. <i>Molecular Cell</i> , 2020, 80, 227-236.e5.	4.5	12
34	How Reversible Are the Effects of Fumed Silica on Macrophages? A Proteomics-Informed View. <i>Nanomaterials</i> , 2020, 10, 1939.	1.9	7
35	Software Requirements for the Analysis and Interpretation of Native Ion Mobility Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 10881-10890.	3.2	17
36	Computational Strategies and Challenges for Using Native Ion Mobility Mass Spectrometry in Biophysics and Structural Biology. <i>Analytical Chemistry</i> , 2020, 92, 10872-10880.	3.2	24

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37	Frontispiece: Investigating Ugi/Passerini Multicomponent Reactions for the Site-Selective Conjugation of Native Trastuzumab. <i>Chemistry - A European Journal</i> , 2020, 26, .	1.7	0
38	The Importance of Charge in Perturbing the Aromatic Glue Stabilizing the Protein-Protein Interface of Homodimeric tRNA-Guanine Transglycosylase. <i>ACS Chemical Biology</i> , 2020, 15, 3021-3029.	1.6	3
39	Toward Automation of Collision-Induced Unfolding Experiments through Online Size Exclusion Chromatography Coupled to Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 12900-12908.	3.2	18
40	On the use of DNA as a linker in antibody-drug conjugates: synthesis, stability and in vitro potency. <i>Scientific Reports</i> , 2020, 10, 7691.	1.6	20
41	Middle Level IM-MS and CIU Experiments for Improved Therapeutic Immunoglobulin Subclass Fingerprinting. <i>Analytical Chemistry</i> , 2020, 92, 8827-8835.	3.2	14
42	Glycan-Mediated Technology for Obtaining Homogeneous Site-Specific Conjugated Antibody-Drug Conjugates: Synthesis and Analytical Characterization by Using Complementary Middle-up LC/HRMS Analysis. <i>Analytical Chemistry</i> , 2020, 92, 8170-8177.	3.2	17
43	$\text{A}\beta^2(1-42)$ tetramer and octamer structures reveal edge conductivity pores as a mechanism for membrane damage. <i>Nature Communications</i> , 2020, 11, 3014.	5.8	162
44	Ethnylation of Cysteine Residues: From Peptides to Proteins in Vitro and in Living Cells. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 10961-10970.	7.2	46
45	The longer the worse: a combined proteomic and targeted study of the long-term versus short-term effects of silver nanoparticles on macrophages. <i>Environmental Science: Nano</i> , 2020, 7, 2032-2046.	2.2	11
46	Investigating Ugi/Passerini Multicomponent Reactions for the Site-Selective Conjugation of Native Trastuzumab**. <i>Chemistry - A European Journal</i> , 2020, 26, 13797-13805.	1.7	17
47	Proline: an efficient and user-friendly software suite for large-scale proteomics. <i>Bioinformatics</i> , 2020, 36, 3148-3155.	1.8	155
48	(Thia)calixarenephosphonic Acids as Potent Inhibitors of the Nucleic Acid Chaperone Activity of the HIV-1 Nucleocapsid Protein with a New Binding Mode and Multitarget Antiviral Activity. <i>ACS Infectious Diseases</i> , 2020, 6, 687-702.	1.8	9
49	Determination of size variants by CE-SDS for approved therapeutic antibodies: Key implications of subclasses and light chain specificities. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 184, 113166.	1.4	30
50	Probing Protein Interaction Networks by Combining MS-Based Proteomics and Structural Data Integration. <i>Journal of Proteome Research</i> , 2020, 19, 2807-2820.	1.8	6
51	Insight on the Impact of the Reduction Step on the Site-Directed Conjugation of an Anti-HER2 Cysteine-Engineered Antibody. <i>ChemistrySelect</i> , 2020, 5, 3187-3190.	0.7	0
52	Drug Loading and Distribution of ADCs After Reduction or IdeS Digestion and Reduction. <i>Methods in Molecular Biology</i> , 2020, 2078, 187-195.	0.4	2
53	Analysis of ADCs by Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020, 2078, 197-211.	0.4	2
54	VHH characterization. Comparison of recombinant with chemically synthesized anti-HER2 VHH. <i>Protein Science</i> , 2019, 28, 1865-1879.	3.1	16

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55	A Case Study to Identify the Drug Conjugation Site of a Site-Specific Antibody-Drug-Conjugate Using Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2419-2429.	1.2	23
56	An Investigation into the Stephensâ€Castro Synthesis of Dehydrotriaryl[12]annulenes: Factors Influencing the Cyclotrimerization. <i>European Journal of Organic Chemistry</i> , 2019, 2019, 6783-6795.	1.2	1
57	Cutting-edge multi-level analytical and structural characterization of antibody-drug conjugates: present and future. <i>Expert Review of Proteomics</i> , 2019, 16, 337-362.	1.3	47
58	A Proteomic View of Cellular Responses to Anticancer Quinoline-Copper Complexes. <i>Proteomes</i> , 2019, 7, 26.	1.7	12
59	A Combined N-terminomics and Shotgun Proteomics Approach to Investigate the Responses of Human Cells to Rapamycin and Zinc at the Mitochondrial Level. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1085-1095.	2.5	3
60	How reversible are the effects of silver nanoparticles on macrophages? A proteomic-instructed view. <i>Environmental Science: Nano</i> , 2019, 6, 3133-3157.	2.2	21
61	Synthesis and biological evaluation of 2.4 nm thiolate-protected gold nanoparticles conjugated to Cetuximab for targeting glioblastoma cancer cells via the EGFR. <i>Nanotechnology</i> , 2019, 30, 184005.	1.3	24
62	Recurrent activating mutations of PPARÎ³ associated with luminal bladder tumors. <i>Nature Communications</i> , 2019, 10, 253.	5.8	44
63	Reductionâ€rebridging strategy for the preparation of ADPN-based antibodyâ€drug conjugates. <i>MedChemComm</i> , 2018, 9, 827-830.	3.5	24
64	Hyphenation of size exclusion chromatography to native ion mobility mass spectrometry for the analytical characterization of therapeutic antibodies and related products. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1086, 176-183.	1.2	69
65	Arginine-selective bioconjugation with 4-azidophenyl glyoxal: application to the single and dual functionalisation of native antibodies. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 1305-1311.	1.5	30
66	An Online Four-Dimensional HICâ€SEC-IMâ€MS Methodology for Proof-of-Concept Characterization of Antibody Drug Conjugates. <i>Analytical Chemistry</i> , 2018, 90, 1578-1586.	3.2	75
67	Adding a new separation dimension to MS and LCâ€MS: What is the utility of ion mobility spectrometry?. <i>Journal of Separation Science</i> , 2018, 41, 20-67.	1.3	140
68	Peptide deformylases from <i>Vibrio parahaemolyticus</i> phage and bacteria display similar deformylase activity and inhibitor binding clefts. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 348-355.	1.1	4
69	Dual Data-Independent Acquisition Approach Combining Global HCP Profiling and Absolute Quantification of Key Impurities during Bioprocess Development. <i>Analytical Chemistry</i> , 2018, 90, 1241-1247.	3.2	26
70	Structure-Based Identification of HIV-1 Nucleocapsid Protein Inhibitors Active against Wild-Type and Drug-Resistant HIV-1 Strains. <i>ACS Chemical Biology</i> , 2018, 13, 253-266.	1.6	13
71	Combinatorial regulation of hepatic cytoplasmic signaling and nuclear transcriptional events by the OGT/REV-ERBÎ± complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11033-E11042.	3.3	35
72	A quantitative proteomic analysis of cofilin phosphorylation in myeloid cells and its modulation using the LIM kinase inhibitor Pyr1. <i>PLoS ONE</i> , 2018, 13, e0208979.	1.1	11

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73	Morphine Binds Creatine Kinase B and Inhibits Its Activity. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 464.	1.8	7
74	A Novel Online Four-Dimensional SEC-SEC-IM-MS Methodology for Characterization of Monoclonal Antibody Size Variants. <i>Analytical Chemistry</i> , 2018, 90, 13929-13937.	3.2	49
75	The H ₂ O ₂ -Resistant Fe ^S Redox Switch MitoNEET Acts as a pH Sensor To Repair Stress-Damaged Fe ^S Protein. <i>Biochemistry</i> , 2018, 57, 5616-5628.	1.2	16
76	The RPAP3-Cterminal domain identifies R2TP-like quaternary chaperones. <i>Nature Communications</i> , 2018, 9, 2093.	5.8	59
77	Extended investigation of tube-gel sample preparation: a versatile and simple choice for high throughput quantitative proteomics. <i>Scientific Reports</i> , 2018, 8, 8260.	1.6	3
78	Formation of Mono- and Polynuclear Luminescent Lanthanide Complexes based on the Coordination of Preorganized Phosphonated Pyridines. <i>Inorganic Chemistry</i> , 2018, 57, 6095-6106.	1.9	21
79	Native Mass Spectrometry, Ion Mobility, and Collision-Induced Unfolding for Conformational Characterization of IgG4 Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 8865-8872.	3.2	51
80	Stable isotope-labelled morphine to study <i>in vivo</i> central and peripheral morphine glucuronidation and brain transport in tolerant mice. <i>British Journal of Pharmacology</i> , 2018, 175, 3844-3856.	2.7	10
81	Austausch der Proteinkontaktflächen in der homodimeren tRNA-Guanin-Transglycosylase: ein Weg der funktionellen Regulation. <i>Angewandte Chemie</i> , 2018, 130, 10242-10247.	1.6	2
82	Multi-OMICS analyses unveil <i>STAT1</i> as a potential modifier gene in mevalonate kinase deficiency. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1675-1687.	0.5	19
83	The ESCRT-III Protein CHMP1A Mediates Secretion of Sonic Hedgehog on a Distinctive Subtype of Extracellular Vesicles. <i>Cell Reports</i> , 2018, 24, 973-986.e8.	2.9	79
84	Deep Structural Analysis of RPAP3 and PIH1D1, Two Components of the HSP90 Co-chaperone R2TP Complex. <i>Structure</i> , 2018, 26, 1196-1209.e8.	1.6	36
85	Cytosolic Diffusion and Peptide-Assisted Nuclear Shuttling of Peptide-Substituted Circa 102 Gold Atom Nanoclusters in Living Cells. <i>ACS Applied Nano Materials</i> , 2018, 1, 4236-4246.	2.4	10
86	The nuclear bile acid receptor FXR is a PKA- and FOXA2-sensitive activator of fasting hepatic gluconeogenesis. <i>Journal of Hepatology</i> , 2018, 69, 1099-1109.	1.8	40
87	Evolutionary insights into Trm112-methyltransferase holoenzymes involved in translation between archaea and eukaryotes. <i>Nucleic Acids Research</i> , 2018, 46, 8483-8499.	6.5	37
88	Homodimer Architecture of QTRT2, the Noncatalytic Subunit of the Eukaryotic tRNA-Guanine Transglycosylase. <i>Biochemistry</i> , 2018, 57, 3953-3965.	1.2	8
89	Swapping Interface Contacts in the Homodimeric tRNA-Guanine Transglycosylase: An Option for Functional Regulation. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 10085-10090.	7.2	10
90	Activation mode of the eukaryotic m ² G ¹⁰ tRNA methyltransferase Trm11 by its partner protein Trm112. <i>Nucleic Acids Research</i> , 2017, 45, gkw1271.	6.5	23

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91	Generic Hybrid Ligand Binding Assay Liquid Chromatography High-Resolution Mass Spectrometry-Based Workflow for Multiplexed Human Immunoglobulin G1 Quantification at the Intact Protein Level: Application to Preclinical Pharmacokinetic Studies. <i>Analytical Chemistry</i> , 2017, 89, 2628-2635.	3.2	39
92	Development of a fast workflow to screen the charge variants of therapeutic antibodies. <i>Journal of Chromatography A</i> , 2017, 1498, 147-154.	1.8	31
93	Insights from native mass spectrometry approaches for top- and middle- level characterization of site-specific antibody-drug conjugates. <i>MAbs</i> , 2017, 9, 801-811.	2.6	55
94	Acyl Fluorides: Fast, Efficient, and Versatile Lysine-Based Protein Conjugation via Plug-and-Play Strategy. <i>Bioconjugate Chemistry</i> , 2017, 28, 1452-1457.	1.8	31
95	Differential proteomics highlights macrophage-specific responses to amorphous silica nanoparticles. <i>Nanoscale</i> , 2017, 9, 9641-9658.	2.8	31
96	A Direct One-Pot Synthesis of Asymmetric Dehydrobenzopyrido[12]annulenes and Their Physicochemical Properties. <i>European Journal of Organic Chemistry</i> , 2017, 2017, 4625-4632.	1.2	1
97	The intricate network between the p34 and p44 subunits is central to the activity of the transcription/DNA repair factor TFIIH. <i>Nucleic Acids Research</i> , 2017, 45, 10872-10883.	6.5	21
98	Epitope characterization of anti-JAM-A antibodies using orthogonal mass spectrometry and surface plasmon resonance approaches. <i>MAbs</i> , 2017, 9, 1317-1326.	2.6	11
99	Development and evaluation of β -galactosidase-sensitive antibody-drug conjugates. <i>European Journal of Medicinal Chemistry</i> , 2017, 142, 376-382.	2.6	38
100	EB1-binding α -myomegalin protein complex promotes centrosomal microtubules functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10687-E10696.	3.3	28
101	Structural studies of protein arginine methyltransferase 2 reveal its interactions with potential substrates and inhibitors. <i>FEBS Journal</i> , 2017, 284, 77-96.	2.2	25
102	Structural characterization of the yeast CF IA complex through a combination of mass spectrometry approaches. <i>International Journal of Mass Spectrometry</i> , 2017, 420, 57-66.	0.7	5
103	Distinct roles of Pcf11 zinc-binding domains in pre-mRNA 3'-end processing. <i>Nucleic Acids Research</i> , 2017, 45, 10115-10131.	6.5	11
104	Importance of the Sequence-Directed DNA Shape for Specific Binding Site Recognition by the Estrogen-Related Receptor. <i>Frontiers in Endocrinology</i> , 2017, 8, 140.	1.5	12
105	Soaking suggests α -alternative facts: Only co-crystallization discloses major ligand-induced interface rearrangements of a homodimeric tRNA-binding protein indicating a novel mode-of-inhibition. <i>PLoS ONE</i> , 2017, 12, e0175723.	1.1	30
106	A ruthenium anticancer compound interacts with histones and impacts differently on epigenetic and death pathways compared to cisplatin. <i>Oncotarget</i> , 2017, 8, 2568-2584.	0.8	44
107	Probing Supramolecular Interactions between a Crown Ether Appended Zinc Phthalocyanine and an Ammonium Group Appended to a C ₆₀ Derivative. <i>Chemistry - A European Journal</i> , 2016, 22, 2051-2059.	1.7	13
108	Step by Step Assembly of Polynuclear Lanthanide Complexes with a Phosphonated Bipyridine Ligand. <i>Inorganic Chemistry</i> , 2016, 55, 12962-12974.	1.9	15

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109	Functional and Structural Insights of the Zinc-Finger HIT protein family members Involved in Box C/D snoRNP Biogenesis. <i>Journal of Molecular Biology</i> , 2016, 428, 2488-2506.	2.0	20
110	SMART Digest, compared with pellet digestion for analysis of human immunoglobulin G1 in rat serum by liquid chromatography tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2016, 501, 23-25.	1.1	8
111	Insights from native mass spectrometry and ion mobility-mass spectrometry for antibody and antibody-based product characterization. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 79-90.	1.2	48
112	Quantitative analysis of hlgG1 in monkey serum by LC-MS/MS using mass spectrometric immunoassay. <i>Bioanalysis</i> , 2016, 8, 1035-1049.	0.6	3
113	The flexibility of a generic LC-MS/MS method for the quantitative analysis of therapeutic proteins based on human immunoglobulin G and related constructs in animal studies. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 131, 214-222.	1.4	11
114	Culture medium associated changes in the core proteome of macrophages and in their responses to copper oxide nanoparticles. <i>Proteomics</i> , 2016, 16, 2864-2877.	1.3	2
115	Palladium-Catalyzed Chemoselective and Biocompatible Functionalization of Cysteine-Containing Molecules at Room Temperature. <i>Chemistry - A European Journal</i> , 2016, 22, 11365-11370.	1.7	51
116	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016, 15, 3998-4019.	1.8	66
117	Benchmarking sample preparation/digestion protocols reveals tube-gel being a fast and repeatable method for quantitative proteomics. <i>Proteomics</i> , 2016, 16, 2953-2961.	1.3	15
118	The use of generic surrogate peptides for the quantitative analysis of human immunoglobulin G1 in pre-clinical species with high-resolution mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 1687-1699.	1.9	20
119	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. <i>Data in Brief</i> , 2016, 6, 286-294.	0.5	30
120	A combined proteomic and targeted analysis unravels new toxic mechanisms for zinc oxide nanoparticles in macrophages. <i>Journal of Proteomics</i> , 2016, 134, 174-185.	1.2	41
121	Cutting-edge mass spectrometry methods for the multi-level structural characterization of antibody-drug conjugates. <i>Expert Review of Proteomics</i> , 2016, 13, 157-183.	1.3	91
122	Benchmarking quantitative label-free LC-MS data processing workflows using a complex spiked proteomic standard dataset. <i>Journal of Proteomics</i> , 2016, 132, 51-62.	1.2	68
123	MetAP1 and MetAP2 drive cell selectivity for a potent anti-cancer agent in synergy, by controlling glutathione redox state. <i>Oncotarget</i> , 2016, 7, 63306-63323.	0.8	32
124	Semi-synthesis of a HGF/SF kringle one (K1) domain scaffold generates a potent in vivo MET receptor agonist. <i>Chemical Science</i> , 2015, 6, 2110-2121.	3.7	26
125	Combining native MS approaches to decipher archaeal box H/ACA ribonucleoprotein particle structure and activity. <i>Proteomics</i> , 2015, 15, 2851-2861.	1.3	9
126	Towards integrative structural mass spectrometry: Benefits from hybrid approaches. <i>Methods</i> , 2015, 89, 4-12.	1.9	24

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127	CBTF: New Amine-to-Thiol Coupling Reagent for Preparation of Antibody Conjugates with Increased Plasma Stability. <i>Bioconjugate Chemistry</i> , 2015, 26, 197-200.	1.8	53
128	Cutting-edge mass spectrometry characterization of originator, biosimilar and biobetter antibodies. <i>Journal of Mass Spectrometry</i> , 2015, 50, 285-297.	0.7	109
129	Native mass spectrometry and ion mobility characterization of trastuzumab emtansine, a lysine-linked antibody drug conjugate. <i>Protein Science</i> , 2015, 24, 1210-1223.	3.1	113
130	What Glues a Homodimer Together: Systematic Analysis of the Stabilizing Effect of an Aromatic Hot Spot in the Protein-Protein Interface of the tRNA-Modifying Enzyme Tgt. <i>ACS Chemical Biology</i> , 2015, 10, 1897-1907.	1.6	19
131	Characterization of the N-Terminal Heterogeneities of Monoclonal Antibodies Using In-Gel Charge Derivatization of ϵ -Amines and LC-MS/MS. <i>Analytical Chemistry</i> , 2015, 87, 3784-3790.	3.2	28
132	Intermolecular recognition of the non-coding RNA 7SK and HEXIM protein in perspective. <i>Biochimie</i> , 2015, 117, 63-71.	1.3	16
133	Ion mobility coupled to native mass spectrometry as a relevant tool to investigate extremely small ligand-induced conformational changes. <i>Analyst</i> , 2015, 140, 7234-7245.	1.7	32
134	Structure/Function Analysis of Protein-Protein Interactions Developed by the Yeast Pih1 Platform Protein and Its Partners in Box C/D snoRNP Assembly. <i>Journal of Molecular Biology</i> , 2015, 427, 2816-2839.	2.0	22
135	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. <i>Journal of Proteome Research</i> , 2015, 14, 3621-3634.	1.8	35
136	MAPN: First-in-Class Reagent for Kinetically Resolved Thiol-to-Thiol Conjugation. <i>Bioconjugate Chemistry</i> , 2015, 26, 1863-1867.	1.8	11
137	Multicentric Analyses of the CD148, CD180, and CD200 Combination for the Diagnosis of Mature B-Cell Neoplasm Using Flow Cytometry. <i>Blood</i> , 2015, 126, 2662-2662.	0.6	4
138	Comparative Expression Study of the Endo-G Protein Coupled Receptor (GPCR) Repertoire in Human Glioblastoma Cancer Stem-like Cells, U87-MG Cells and Non Malignant Cells of Neural Origin Unveils New Potential Therapeutic Targets. <i>PLoS ONE</i> , 2014, 9, e91519.	1.1	28
139	Innovative Native MS Methodologies for Antibody Drug Conjugate Characterization: High Resolution Native MS and IM-MS for Average DAR and DAR Distribution Assessment. <i>Analytical Chemistry</i> , 2014, 86, 10674-10683.	3.2	147
140	Interest of the CD148, CD180 and CD200 Combination in Flow Cytometry Analyses for Mature B-Cell Neoplasms Diagnosis. <i>Blood</i> , 2014, 124, 5407-5407.	0.6	0
141	Analytical characterization of biosimilar antibodies and Fc-fusion proteins. <i>TrAC - Trends in Analytical Chemistry</i> , 2013, 48, 81-95.	5.8	104
142	Time Resolved Native Ion-Mobility Mass Spectrometry to Monitor Dynamics of IgG4 Fab Arm Exchange and Bispecific Monoclonal Antibody Formation. <i>Analytical Chemistry</i> , 2013, 85, 9785-9792.	3.2	62
143	Strong Cell Surface Expression of the Toll-Like Receptor Homolog CD180 Identifies Circulating Cells of Marginal Zone Lymphoma From Other B-Cell Malignancies. <i>Blood</i> , 2012, 120, 1542-1542.	0.6	0