Detlev Suckau

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Use of PASEF for Accelerated Protein Sequence Confirmation and De Novo Sequencing with High Data Quality. Methods in Molecular Biology, 2022, 2313, 207-217.	0.9	4
2	Top-Down Identification and Sequence Analysis of Small Membrane Proteins Using MALDI-MS/MS. Journal of the American Society for Mass Spectrometry, 2022, 33, 1293-1302.	2.8	7
3	Structural and Functional Characterization of SARS-CoV-2 RBD Domains Produced in Mammalian Cells. Analytical Chemistry, 2021, 93, 6839-6847.	6.5	39
4	Screening for potential interaction partners with surface plasmon resonance imaging coupled to MALDI mass spectrometry. Analytical Biochemistry, 2021, 624, 114195.	2.4	3
5	NIST Interlaboratory Study on Glycosylation Analysis of Monoclonal Antibodies: Comparison of Results from Diverse Analytical Methods. Molecular and Cellular Proteomics, 2020, 19, 11-30.	3.8	87
6	LC-Trapped Ion Mobility Spectrometry-TOF MS Differentiation of 2- and 3-Disulfide-Bonded Isomers of the μ-Conotoxin PIIIA. Analytical Chemistry, 2020, 92, 10920-10924.	6.5	9
7	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2020, 31, 1783-1802.	2.8	67
8	Avoiding H/D Scrambling with Minimal Ion Transmission Loss for HDX-MS/MS-ETD Analysis on a High-Resolution Q-TOF Mass Spectrometer. Analytical Chemistry, 2020, 92, 7453-7461.	6.5	22
9	Conformational Î1⁄4-Conotoxin PIIIA Isomers Revisited: Impact of Cysteine Pairing on Disulfide-Bond Assignment and Structure Elucidation. Analytical Chemistry, 2018, 90, 3321-3327.	6.5	27
10	Identification of multiple proteoforms biomarkers on clinical samples by routine Top-Down approaches. Data in Brief, 2018, 18, 1013-1021.	1.0	12
11	Towards a routine application of Top-Down approaches for label-free discovery workflows. Journal of Proteomics, 2018, 175, 12-26.	2.4	17
12	Rapid, automated characterization of disulfide bond scrambling and IgG2 isoform determination. MAbs, 2018, 10, 1200-1213.	5.2	13
13	SPRi-MALDI MS: characterization and identification of a kinase from cell lysate by specific interaction with different designed ankyrin repeat proteins. Analytical and Bioanalytical Chemistry, 2017, 409, 1827-1836.	3.7	13
14	Cross Reactive Material 197 glycoconjugate vaccines contain privileged conjugation sites. Scientific Reports, 2016, 6, 20488.	3.3	38
15	Full validation of therapeutic antibody sequences by middle-up mass measurements and middle-down protein sequencing. MAbs, 2016, 8, 318-330.	5.2	55
16	Deep serum discoveries: <scp>SDF</scp> â€lî± and <scp>HSA</scp> fragments in myelodysplastic syndromes. American Journal of Hematology, 2015, 90, E185-7.	4.1	3
17	Imaging mass spectrometry analysis of renal amyloidosis biopsies reveals protein co-localization with amyloid deposits. Analytical and Bioanalytical Chemistry, 2015, 407, 5323-5331.	3.7	34
18	High-resolution MALDI mass spectrometric imaging of lipids in the mammalian retina. Histochemistry and Cell Biology, 2015, 143, 453-462.	1.7	26

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19	Advanced mass spectrometry workflows for analyzing disulfide bonds in biologics. Expert Review of Proteomics, 2015, 12, 115-123.	3.0	34
20	Quantification of serum apolipoproteins A-I and B-100 in clinical samples using an automated SISCAPA–MALDI-TOF-MS workflow. Methods, 2015, 81, 74-85.	3.8	37
21	An automated assay for the clinical measurement of plasma renin activity by immuno-MALDI (iMALDI). Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 547-558.	2.3	23
22	lmaging mass spectrometry to discriminate breast from pancreatic cancer metastasis in formalinâ€fixed paraffinâ€embedded tissues. Proteomics, 2014, 14, 956-964.	2.2	66
23	Correct primary structure assessment and extensive glyco-profiling of cetuximab by a combination of intact, middle-up, middle-down and bottom-up ESI and MALDI mass spectrometry techniques. MAbs, 2013, 5, 699-710.	5.2	159
24	Interlaboratory Study on Differential Analysis of Protein Glycosylation by Mass Spectrometry: The ABRF Glycoprotein Research Multi-Institutional Study 2012. Molecular and Cellular Proteomics, 2013, 12, 2935-2951.	3.8	103
25	Precision of Heavy–Light Peptide Ratios Measured by MALDI-TOF Mass Spectrometry. Journal of Proteome Research, 2012, 11, 1868-1878.	3.7	59
26	Revisiting Rat Spermatogenesis with MALDI Imaging at 20-μm Resolution. Molecular and Cellular Proteomics, 2011, 10, M110.005991.	3.8	68
27	A simple TLC-MALDI method to monitor oxidation products of phosphatidylcholines and -ethanolamines. Acta Chromatographica, 2011, 23, 365-375.	1.3	10
28	Topâ€down labelâ€free LCâ€MALDI analysis of the peptidome during neural progenitor cell differentiation reveals complexity in cytoskeletal protein dynamics and identifies progenitor cell markers. Proteomics, 2011, 11, 3992-4006.	2.2	12
29	Tutorial: Multivariate Statistical Treatment of Imaging Data for Clinical Biomarker Discovery. Methods in Molecular Biology, 2010, 656, 385-403.	0.9	27
30	Classification of HER2 Receptor Status in Breast Cancer Tissues by MALDI Imaging Mass Spectrometry. Journal of Proteome Research, 2010, 9, 1854-1863.	3.7	256
31	Approaching MALDI molecular imaging for clinical proteomic research: current state and fields of application. Expert Review of Proteomics, 2010, 7, 927-941.	3.0	47
32	Top-Down <i>de Novo</i> Protein Sequencing of a 13.6 kDa Camelid Single Heavy Chain Antibody by Matrix-Assisted Laser Desorption Ionization-Time-of-Flight/Time-of-Flight Mass Spectrometry. Analytical Chemistry, 2010, 82, 3283-3292.	6.5	67
33	Toward top-down determination of PEGylation site using MALDI in-source decay MS analysis. Journal of the American Society for Mass Spectrometry, 2009, 20, 326-333.	2.8	42
34	Phosphatidylcholines and -ethanolamines can be easily mistaken in phospholipid mixtures: a negative ion MALDI-TOF MS study with 9-aminoacridine as matrix and egg yolk as selected example. Analytical and Bioanalytical Chemistry, 2009, 395, 2479-2487.	3.7	82
35	Capabilities and disadvantages of combined matrix-assisted laser-desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) and high-performance thin-layer chromatography (HPTLC): Analysis of egg yolk lipids. Journal of Planar Chromatography - Modern TLC, 2009, 22, 35-42.	1.2	45

Mass Spectrometry-Based Tissue Imaging. , 2009, , 131-146.

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37	MALDI Top-Down sequencing: calling N- and C-terminal protein sequences with high confidence and speed. Journal of Biomolecular Techniques, 2009, 20, 258-62.	1.5	13
38	Analysis of stem cell lipids by offline HPTLC-MALDI-TOF MS. Analytical and Bioanalytical Chemistry, 2008, 392, 849-860.	3.7	107
39	A direct and simple method of coupling matrix-assisted laser desorption and ionization time-of-flight mass spectrometry (MALDI-TOF MS) to thin-layer chromatography (TLC) for the analysis of phospholipids from egg yolk. Analytical and Bioanalytical Chemistry, 2007, 389, 827-834.	3.7	194
40	Analysis of glycoproteins in human serum by means of glycospecific magnetic bead separation and LC-MALDI-TOF/TOF analysis with automated glycopeptide detection. Journal of Biomolecular Techniques, 2007, 18, 252-8.	1.5	44
41	A novel MALDI LIFT-TOF/TOF mass spectrometer for proteomics. Analytical and Bioanalytical Chemistry, 2003, 376, 952-965.	3.7	625
42	T3-Sequencing:Â Targeted Characterization of the N- and C-Termini of Undigested Proteins by Mass Spectrometry. Analytical Chemistry, 2003, 75, 5817-5824.	6.5	122
43	Screening for Disulfide Bonds in Proteins by MALDI In-Source Decay and LIFT-TOF/TOF-MS. Analytical Chemistry, 2002, 74, 4980-4988.	6.5	109
44	MALDI-PSD-MS analysis of the phosphorylation sites of caseinomacropeptide. Peptides, 2001, 22, 1093-1098.	2.4	36
45	Molecular Characterization of Surface Topology in Protein Tertiary Structures by Amino-Acylation and Mass Spectrometric Peptide Mapping. Bioconjugate Chemistry, 1994, 5, 583-590.	3.6	127
46	Human C5a Anaphylatoxin: Gene Cloning and Expression in Escherichia coli. Immunobiology, 1992, 185, 41-52.	1.9	21
47	Protein surface topology-probing by selective chemical modification and mass spectrometric peptide mapping Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 5630-5634.	7.1	224
48	Mass spectrometric peptide mapping analysis and structural characterization of dihydrodiol dehydrogenase isoenzymes. Environmental Health Perspectives, 1990, 88, 57-62.	6.0	10