

# Detlev Suckau

## List of Publications by Year in descending order

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48  
papers

3,253  
citations

186209

28  
h-index

206029

48  
g-index

50  
all docs

50  
docs citations

50  
times ranked

4026  
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of PASEF for Accelerated Protein Sequence Confirmation and De Novo Sequencing with High Data Quality. <i>Methods in Molecular Biology</i> , 2022, 2313, 207-217.	0.4	4
2	Top-Down Identification and Sequence Analysis of Small Membrane Proteins Using MALDI-MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 1293-1302.	1.2	7
3	Structural and Functional Characterization of SARS-CoV-2 RBD Domains Produced in Mammalian Cells. <i>Analytical Chemistry</i> , 2021, 93, 6839-6847.	3.2	39
4	Screening for potential interaction partners with surface plasmon resonance imaging coupled to MALDI mass spectrometry. <i>Analytical Biochemistry</i> , 2021, 624, 114195.	1.1	3
5	NIST Interlaboratory Study on Glycosylation Analysis of Monoclonal Antibodies: Comparison of Results from Diverse Analytical Methods. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 11-30.	2.5	87
6	LC-Trapped Ion Mobility Spectrometry-TOF MS Differentiation of 2- and 3-Disulfide-Bonded Isomers of the Î¼-Conotoxin PIIIA. <i>Analytical Chemistry</i> , 2020, 92, 10920-10924.	3.2	9
7	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
8	Avoiding H/D Scrambling with Minimal Ion Transmission Loss for HDX-MS/MS-ETD Analysis on a High-Resolution Q-TOF Mass Spectrometer. <i>Analytical Chemistry</i> , 2020, 92, 7453-7461.	3.2	22
9	Conformational Î¼-Conotoxin PIIIA Isomers Revisited: Impact of Cysteine Pairing on Disulfide-Bond Assignment and Structure Elucidation. <i>Analytical Chemistry</i> , 2018, 90, 3321-3327.	3.2	27
10	Identification of multiple proteoforms biomarkers on clinical samples by routine Top-Down approaches. <i>Data in Brief</i> , 2018, 18, 1013-1021.	0.5	12
11	Towards a routine application of Top-Down approaches for label-free discovery workflows. <i>Journal of Proteomics</i> , 2018, 175, 12-26.	1.2	17
12	Rapid, automated characterization of disulfide bond scrambling and IgG2 isoform determination. <i>MAbs</i> , 2018, 10, 1200-1213.	2.6	13
13	SPRi-MALDI MS: characterization and identification of a kinase from cell lysate by specific interaction with different designed ankyrin repeat proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 1827-1836.	1.9	13
14	Cross Reactive Material 197 glycoconjugate vaccines contain privileged conjugation sites. <i>Scientific Reports</i> , 2016, 6, 20488.	1.6	38
15	Full validation of therapeutic antibody sequences by middle-up mass measurements and middle-down protein sequencing. <i>MAbs</i> , 2016, 8, 318-330.	2.6	55
16	Deep serum discoveries: <sc>SDF</sc> and <sc>HSA</sc> fragments in myelodysplastic syndromes. <i>American Journal of Hematology</i> , 2015, 90, E185-7.	2.0	3
17	Imaging mass spectrometry analysis of renal amyloidosis biopsies reveals protein co-localization with amyloid deposits. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 5323-5331.	1.9	34
18	High-resolution MALDI mass spectrometric imaging of lipids in the mammalian retina. <i>Histochemistry and Cell Biology</i> , 2015, 143, 453-462.	0.8	26

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19	Advanced mass spectrometry workflows for analyzing disulfide bonds in biologics. <i>Expert Review of Proteomics</i> , 2015, 12, 115-123.	1.3	34
20	Quantification of serum apolipoproteins A-I and B-100 in clinical samples using an automated SISCAPA-MALDI-TOF-MS workflow. <i>Methods</i> , 2015, 81, 74-85.	1.9	37
21	An automated assay for the clinical measurement of plasma renin activity by immuno-MALDI (iMALDI). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 547-558.	1.1	23
22	Imaging mass spectrometry to discriminate breast from pancreatic cancer metastasis in formalin-fixed paraffin-embedded tissues. <i>Proteomics</i> , 2014, 14, 956-964.	1.3	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. <i>MABs</i> , 2013, 5, 699-710.	2.6	159
24	Interlaboratory Study on Differential Analysis of Protein Glycosylation by Mass Spectrometry: The ABRF Glycoprotein Research Multi-Institutional Study 2012. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2935-2951.	2.5	103
25	Precision of Heavy-Light Peptide Ratios Measured by MALDI-TOF Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 1868-1878.	1.8	59
26	Revisiting Rat Spermatogenesis with MALDI Imaging at 20- $\mu$ m Resolution. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005991.	2.5	68
27	A simple TLC-MALDI method to monitor oxidation products of phosphatidylcholines and -ethanolamines. <i>Acta Chromatographica</i> , 2011, 23, 365-375.	0.7	10
28	Top-down label-free LC-MALDI analysis of the peptidome during neural progenitor cell differentiation reveals complexity in cytoskeletal protein dynamics and identifies progenitor cell markers. <i>Proteomics</i> , 2011, 11, 3992-4006.	1.3	12
29	Tutorial: Multivariate Statistical Treatment of Imaging Data for Clinical Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2010, 656, 385-403.	0.4	27
30	Classification of HER2 Receptor Status in Breast Cancer Tissues by MALDI Imaging Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 1854-1863.	1.8	256
31	Approaching MALDI molecular imaging for clinical proteomic research: current state and fields of application. <i>Expert Review of Proteomics</i> , 2010, 7, 927-941.	1.3	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. <i>Analytical Chemistry</i> , 2010, 82, 3283-3292.	3.2	67
33	Toward top-down determination of PEGylation site using MALDI in-source decay MS analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 326-333.	1.2	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. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 2479-2487.	1.9	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. <i>Journal of Planar Chromatography - Modern TLC</i> , 2009, 22, 35-42.	0.6	45
36	Mass Spectrometry-Based Tissue Imaging. , 2009, , 131-146.		2

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37	MALDI Top-Down sequencing: calling N- and C-terminal protein sequences with high confidence and speed. <i>Journal of Biomolecular Techniques</i> , 2009, 20, 258-62.	0.8	13
38	Analysis of stem cell lipids by offline HPTLC-MALDI-TOF MS. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 392, 849-860.	1.9	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. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 827-834.	1.9	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. <i>Journal of Biomolecular Techniques</i> , 2007, 18, 252-8.	0.8	44
41	A novel MALDI LIFT-TOF/TOF mass spectrometer for proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2003, 376, 952-965.	1.9	625
42	T3-Sequencing: Targeted Characterization of the N- and C-Termini of Undigested Proteins by Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 5817-5824.	3.2	122
43	Screening for Disulfide Bonds in Proteins by MALDI In-Source Decay and LIFT-TOF/TOF-MS. <i>Analytical Chemistry</i> , 2002, 74, 4980-4988.	3.2	109
44	MALDI-PSD-MS analysis of the phosphorylation sites of caseinomacropeptide. <i>Peptides</i> , 2001, 22, 1093-1098.	1.2	36
45	Molecular Characterization of Surface Topology in Protein Tertiary Structures by Amino-Acylation and Mass Spectrometric Peptide Mapping. <i>Bioconjugate Chemistry</i> , 1994, 5, 583-590.	1.8	127
46	Human C5a Anaphylatoxin: Gene Cloning and Expression in <i>Escherichia coli</i> . <i>Immunobiology</i> , 1992, 185, 41-52.	0.8	21
47	Protein surface topology-probing by selective chemical modification and mass spectrometric peptide mapping.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 5630-5634.	3.3	224
48	Mass spectrometric peptide mapping analysis and structural characterization of dihydrodiol dehydrogenase isoenzymes.. <i>Environmental Health Perspectives</i> , 1990, 88, 57-62.	2.8	10