

Rainer Cramer

List of Publications by Year in descending order

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122
papers

6,324
citations

57719

44
h-index

71651

76
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125
all docs

125
docs citations

125
times ranked

7480
citing authors

#	ARTICLE	IF	CITATIONS
1	LAP-MALDI MS coupled with machine learning: an ambient mass spectrometry approach for high-throughput diagnostics. <i>Chemical Science</i> , 2022, 13, 1746-1758.	3.7	9
2	Ultra-high-Throughput Sample Analysis Using Liquid Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 4141-4145.	3.2	17
3	Advances in ionisation techniques for mass spectrometry-based omics research. <i>Proteomics</i> , 2022, 22, .	1.3	4
4	Production and analysis of multiply charged negative ions by liquid atmospheric pressure matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e8246.	0.7	9
5	Speciation and milk adulteration analysis by rapid ambient liquid MALDI mass spectrometry profiling using machine learning. <i>Scientific Reports</i> , 2021, 11, 3305.	1.6	21
6	UHPLC-MS/MS analysis of cocoa bean proteomes from four different genotypes. <i>Food Chemistry</i> , 2020, 303, 125244.	4.2	11
7	Bacterial identification by lipid profiling using liquid atmospheric pressure matrix-assisted laser desorption/ionization mass spectrometry. <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, 930-938.	1.4	18
8	Proteomic and peptidomic UHPLC-ESI MS/MS analysis of cocoa beans fermented using the Styrofoam-box method. <i>Food Chemistry</i> , 2020, 316, 126350.	4.2	9
9	High-speed Analysis of Large Sample Sets – How Can This Key Aspect of the Omics Be Achieved?. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1760-1766.	2.5	4
10	Rapid Liquid AP-MALDI MS Profiling of Lipids and Proteins from Goat and Sheep Milk for Speciation and Colostrum Analysis. <i>Proteomes</i> , 2020, 8, 20.	1.7	13
11	Raw Cow Milk Bacterial Consortium as Bioindicator of Circulating Anti-Microbial Resistance (AMR). <i>Animals</i> , 2020, 10, 2378.	1.0	11
12	Advancing Liquid Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Toward Ultra-high-Throughput Analysis. <i>Analytical Chemistry</i> , 2020, 92, 2931-2936.	3.2	29
13	Analysis of Barley Leaf Epidermis and Extrahaustorial Proteomes During Powdery Mildew Infection Reveals That the PR5 Thaumatin-Like Protein TLP5 Is Required for Susceptibility Towards <i>Blumeria graminis</i> f. sp. <i>hordei</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1138.	1.7	19
14	Liquid Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Adds Enhanced Functionalities to MALDI MS Profiling for Disease Diagnostics. <i>ACS Omega</i> , 2019, 4, 12759-12765.	1.6	16
15	Atmospheric Pressure Ultraviolet Laser Desorption and Ionization from Liquid Samples for Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 14192-14197.	3.2	6
16	Melanin production by tyrosinase activity on a tyrosine-rich peptide fragment and pH-dependent self-assembly of its lipidated analogue. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 4543-4553.	1.5	12
17	The composition of liquid atmospheric pressure matrix-assisted laser desorption/ionization matrices and its effect on ionization in mass spectrometry. <i>Analytica Chimica Acta</i> , 2018, 1013, 43-53.	2.6	19
18	Characterization of the Proteome of <i>Theobroma cacao</i> Beans by Nano-UHPLC-ESI MS/MS. <i>Proteomics</i> , 2018, 18, 1700339.	1.3	12

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19	Collision-induced dissociation of doubly-charged barium-cationized lipids generated from liquid samples by atmospheric pressure matrix-assisted laser desorption/ionization provides structurally diagnostic product ions. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 1435-1444.	1.9	19
20	Protein identification using a nanoUHPLC-AP-MALDI MS/MS workflow with CID of multiply charged proteolytic peptides. <i>International Journal of Mass Spectrometry</i> , 2017, 416, 20-28.	0.7	12
21	Advances in mass spectrometry-based cancer research and analysis: from cancer proteomics to clinical diagnostics. <i>Expert Review of Proteomics</i> , 2016, 13, 593-607.	1.3	12
22	Investigation and optimization of parameters affecting the multiply charged ion yield in AP-MALDI MS. <i>Methods</i> , 2016, 104, 11-20.	1.9	31
23	â€œNext generationâ€™ laser-based biological mass spectrometry. <i>Methods</i> , 2016, 104, 1-2.	1.9	1
24	Liquid MALDI MS Analysis of Complex Peptide and Proteome Samples. <i>Journal of Proteome Research</i> , 2016, 15, 2998-3008.	1.8	8
25	Interactions between the Powdery Mildew Effector BEC1054 and Barley Proteins Identify Candidate Host Targets. <i>Journal of Proteome Research</i> , 2016, 15, 826-839.	1.8	85
26	Ionic Liquids and Other Liquid Matrices for Sensitive MALDI MS Analysis. , 2016, , 51-64.		4
27	Proteomic analysis of the medicinal plant <i>Artemisia annua</i> : Data from leaf and trichome extracts. <i>Data in Brief</i> , 2016, 7, 325-331.	0.5	16
28	Coupling Liquid MALDI MS to Liquid Chromatography. , 2016, , 65-76.		0
29	Sample Preparation: A Crucial Factor for the Analytical Performance of Rationally Designed MALDI Matrices. <i>Analytical Chemistry</i> , 2015, 87, 1485-1488.	3.2	20
30	Distribution analysis of the putative cancer marker S100A4 across invasive squamous cell carcinoma penile tissue. <i>EuPA Open Proteomics</i> , 2015, 7, 1-10.	2.5	2
31	Proteomic analysis of <i>Artemisia annua</i> â€œ towards elucidating the biosynthetic pathways of the antimalarial pro-drug artemisinin. <i>BMC Plant Biology</i> , 2015, 15, 175.	1.6	41
32	Multiprobabilistic prediction in early medical diagnoses. <i>Annals of Mathematics and Artificial Intelligence</i> , 2015, 74, 203-222.	0.9	9
33	MALDI mass spectrometry in prostate cancer biomarker discovery. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 940-949.	1.1	32
34	Enhanced MALDI MS Sensitivity by Weak Base Additives and Glycerol Sample Coating. <i>Analytical Chemistry</i> , 2014, 86, 744-751.	3.2	14
35	MALDI MS profiling of postâ€œRE urine samples highlights the potential of Î²â€œmicroseminoprotein as a marker for prostatic diseases. <i>Prostate</i> , 2014, 74, 103-111.	1.2	22
36	Plant Proteomics in Crop Improvement. <i>Proteomics</i> , 2013, 13, 1771-1771.	1.3	5

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37	Mutual binding of polymer end-groups by complementary π - π -stacking: a molecular π - π Handshake. <i>Chemical Communications</i> , 2013, 49, 454-456.	2.2	33
38	Analysis of tyrosine phosphorylation and phosphotyrosine-binding proteins in germinating seeds from Scots pine. <i>Plant Physiology and Biochemistry</i> , 2013, 67, 33-40.	2.8	10
39	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. <i>Mass Spectrometry Reviews</i> , 2013, 32, 335-365.	2.8	70
40	INPPO Actions and Recognition as a Driving Force for Progress in Plant Proteomics: Change of Guard, INPPO Update, and Upcoming Activities. <i>Proteomics</i> , 2013, 13, 3093-3100.	1.3	0
41	Liquid AP- μ -MALDI Enables Stable Ion Yields of Multiply Charged Peptide and Protein Ions for Sensitive Analysis by Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 2364-2367.	7.2	63
42	Application of DIGE and Mass Spectrometry in the Study of Type 2 Diabetes Mellitus Mouse Models. <i>Methods in Molecular Biology</i> , 2012, 854, 299-318.	0.4	0
43	Hydroponic Isotope Labeling of Entire Plants and High-Performance Mass Spectrometry for Quantitative Plant Proteomics. <i>Methods in Molecular Biology</i> , 2012, 893, 155-173.	0.4	3
44	Translational plant proteomics: A perspective. <i>Journal of Proteomics</i> , 2012, 75, 4588-4601.	1.2	63
45	Functional Proteomic Analysis of Long-term Growth Factor Stimulation and Receptor Tyrosine Kinase Coactivation in Swiss 3T3 Fibroblasts. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1690-1708.	2.5	3
46	Conformal predictors in early diagnostics of ovarian and breast cancers. <i>Progress in Artificial Intelligence</i> , 2012, 1, 245-257.	1.5	14
47	Structure and evolution of barley powdery mildew effector candidates. <i>BMC Genomics</i> , 2012, 13, 694.	1.2	238
48	Boosting the Globalization of Plant Proteomics through INPPO: Current Developments and Future Prospects. <i>Proteomics</i> , 2012, 12, 359-368.	1.3	10
49	Mass spectrometry imaging of glucosinolates in Arabidopsis flowers and siliques. <i>Phytochemistry</i> , 2012, 77, 110-118.	1.4	50
50	Multiprobabilistic Venn Predictors with Logistic Regression. <i>International Federation for Information Processing</i> , 2012, , 224-233.	0.4	5
51	Deciphering the Complexity of Sainfoin (<i>Onobrychis viciifolia</i>) Proanthocyanidins by MALDI-TOF Mass Spectrometry with a Judicious Choice of Isotope Patterns and Matrixes. <i>Analytical Chemistry</i> , 2011, 83, 4147-4153.	3.2	27
52	MALDI MS-Based Biomarker Profiling of Blood Samples. , 2011, , 733-747.		0
53	Proteogenomics and in silico structural and functional annotation of the barley powdery mildew <i>Blumeria graminis</i> f. sp. <i>hordei</i> . <i>Methods</i> , 2011, 54, 432-441.	1.9	57
54	Single-cell proteomic analysis of glucosinolate-rich S-cells in Arabidopsis thaliana. <i>Methods</i> , 2011, 54, 413-423.	1.9	52

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55	Editorial for "Advances in Biological Mass Spectrometry and Proteomics" Methods, 2011, 54, 349-350.	1.9	2
56	Biomarker Discovery and Redundancy Reduction towards Classification using a Multi-factorial MALDI-TOF MS T2DM Mouse Model Dataset. BMC Bioinformatics, 2011, 12, 140.	1.2	5
57	Quantitative plant proteomics. Proteomics, 2011, 11, 756-775.	1.3	70
58	Fully automated software solution for protein quantitation by global metabolic labeling with stable isotopes. Rapid Communications in Mass Spectrometry, 2011, 25, 1461-1471.	0.7	11
59	Evaluation of Peak-Picking Algorithms for Protein Mass Spectrometry. Methods in Molecular Biology, 2011, 696, 341-352.	0.4	17
60	Quantitative Plant Proteomics Using Hydroponic Isotope Labeling of Entire Plants (HILEP). , 2011, , 363-380.		0
61	Early detection of ovarian cancer in samples pre-diagnosis using CA125 and MALDI-MS peaks. Cancer Genomics and Proteomics, 2011, 8, 289-305.	1.0	6
62	A well-characterised peak identification list of MALDI MS profile peaks for human blood serum. Proteomics, 2010, 10, 3388-3392.	1.3	32
63	Glucosinolate-accumulating S-cells in Arabidopsis leaves and flower stalks undergo programmed cell death at early stages of differentiation. Plant Journal, 2010, 64, 456-469.	2.8	112
64	Peptides Generated Ex Vivo from Serum Proteins by Tumor-Specific Exopeptidases Are Not Useful Biomarkers in Ovarian Cancer. Clinical Chemistry, 2010, 56, 262-271.	1.5	31
65	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	6.0	725
66	Introduction of 4-Chloro- β -cyanocinnamic Acid Liquid Matrices for High Sensitivity UV-MALDI MS. Journal of Proteome Research, 2010, 9, 1931-1940.	1.8	32
67	S6K1 is acetylated at lysine 516 in response to growth factor stimulation. Biochemical and Biophysical Research Communications, 2010, 398, 400-405.	1.0	19
68	Serum Proteomic Abnormality Predating Screen Detection of Ovarian Cancer. Computer Journal, 2009, 52, 326-333.	1.5	15
69	In Planta Proteomics and Proteogenomics of the Biotrophic Barley Fungal Pathogen Blumeria graminis f. sp. hordei. Molecular and Cellular Proteomics, 2009, 8, 2368-2381.	2.5	75
70	Mass spectrometry in clinical proteomics " from the present to the future. Proteomics - Clinical Applications, 2009, 3, 6-17.	0.8	71
71	Purification and molecular cloning of antimicrobial peptides from Scots pine seedlings. Peptides, 2009, 30, 2136-2143.	1.2	27
72	Production of novel ACE inhibitory peptides from β -lactoglobulin using Protease N Amano. International Dairy Journal, 2009, 19, 69-76.	1.5	48

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73	MALDI MS. Methods in Molecular Biology, 2009, 564, 85-103.	0.4	5
74	Difference gel electrophoresis. Proteomics, 2008, 8, 4886-4897.	1.3	213
75	Hydroponic isotope labelling of entire plants (HILEP) for quantitative plant proteomics; an oxidative stress case study. Phytochemistry, 2008, 69, 1962-1972.	1.4	103
76	Proteomic Profiling of Neuromas Reveals Alterations in Protein Composition and Local Protein Synthesis in Hyper-Excitable Nerves. Molecular Pain, 2008, 4, 1744-8069-4-33.	1.0	62
77	Gene and Protein Expression Profiling of Human Ovarian Cancer Cells Treated with the Heat Shock Protein 90 Inhibitor 17-Allylamino-17-Demethoxygeldanamycin. Cancer Research, 2007, 67, 3239-3253.	0.4	135
78	Liquid matrix deposition on conductive hydrophobic surfaces for tuning and quantitation in UV-MALDI mass spectrometry. Journal of the American Society for Mass Spectrometry, 2007, 18, 693-697.	1.2	40
79	Chromatographic alignment of LC-MS and LC-MS/MS datasets by genetic algorithm feature extraction. Journal of the American Society for Mass Spectrometry, 2007, 18, 1835-1843.	1.2	42
80	Quantitative proteomics using uniform ¹⁵ N-labeling, MASCOT, and the transproteomic pipeline. Proteomics, 2007, 7, 3462-3469.	1.3	41
81	Serum Peptide Profiling using MALDI Mass Spectrometry. Proteomics, 2007, 7, 77-89.	1.3	51
82	PIGOK: Linking Protein Identity to Gene Ontology and Function. Journal of Proteome Research, 2006, 5, 3429-3432.	1.8	10
83	Automatic internal calibration in liquid chromatography/Fourier transform ion cyclotron resonance mass spectrometry of protein digests. Rapid Communications in Mass Spectrometry, 2006, 20, 3076-3080.	0.7	16
84	PDGF regulates the actin cytoskeleton through hnRNP-K-mediated activation of the ubiquitin E3-ligase MIR. EMBO Journal, 2006, 25, 1871-1882.	3.5	21
85	Combined affinity labelling and mass spectrometry analysis of differential cell surface protein expression in normal and prostate cancer cells. Oncogene, 2005, 24, 5905-5913.	2.6	45
86	Proteomic analysis of plasma membrane vesicles isolated from the rat renal cortex. Proteomics, 2005, 5, 101-112.	1.3	61
87	Liquid ultraviolet matrix-assisted laser desorption/ionization - mass spectrometry for automated proteomic analysis. Proteomics, 2005, 5, 360-370.	1.3	39
88	Stress-induced changes in the Schizosaccharomyces pombe proteome using two-dimensional difference gel electrophoresis, mass spectrometry and a novel integrated robotics platform. Proteomics, 2005, 5, 1669-1685.	1.3	24
89	Proteomic analysis of redox- and ErbB2-dependent changes in mammary luminal epithelial cells using cysteine- and lysine-labelling two-dimensional difference gel electrophoresis. Proteomics, 2005, 5, 2908-2926.	1.3	100
90	Enhanced phosphopeptide isolation by Fe(III)-IMAC using 1,1,1,3,3,3-hexafluoroisopropanol. Proteomics, 2005, 5, 4376-4388.	1.3	30

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91	Heat Shock Protein 27 Is the Major Differentially Phosphorylated Protein Involved in Renal Epithelial Cellular Stress Response and Controls Focal Adhesion Organization and Apoptosis. <i>Journal of Biological Chemistry</i> , 2005, 280, 29885-29898.	1.6	81
92	High-throughput proteomics using matrix-assisted laser desorption/ ionization mass spectrometry. <i>Expert Review of Proteomics</i> , 2005, 2, 407-420.	1.3	31
93	The urinary proteome in Fanconi syndrome implies specificity in the reabsorption of proteins by renal proximal tubule cells. <i>American Journal of Physiology - Renal Physiology</i> , 2004, 287, F353-F364.	1.3	100
94	Quantitative amino acid and proteomic analysis: Very low excretion of polypeptides >750 Da in normal urine. <i>Kidney International</i> , 2004, 66, 1994-2003.	2.6	74
95	Differential protein synthesis and expression levels in normal and neoplastic human prostate cells and their regulation by type I and II interferons. <i>Oncogene</i> , 2004, 23, 1693-1703.	2.6	52
96	Sample Preparation of Gel Electrophoretically Separated Protein Binding Partners for Analysis by Mass Spectrometry. , 2004, 261, 499-510.		5
97	On-target oxidation of methionine residues using hydrogen peroxide for composition-restricted matrix-assisted laser desorption/ionisation peptide mass mapping. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 1212-1215.	0.7	9
98	Detection and analysis of urinary peptides by on-line liquid chromatography and mass spectrometry: application to patients with renal Fanconi syndrome. <i>Clinical Science</i> , 2003, 104, 483-490.	1.8	90
99	Characterization of Protein Phosphorylation by Mass Spectrometry Using Immobilized Metal Ion Affinity Chromatography with On-Resin \hat{I}^2 -Elimination and Michael Addition. <i>Analytical Chemistry</i> , 2003, 75, 3232-3243.	3.2	86
100	Phosphorylation of the WASP-VCA Domain Increases Its Affinity for the Arp2/3 Complex and Enhances Actin Polymerization by WASP. <i>Molecular Cell</i> , 2003, 11, 1229-1239.	4.5	126
101	Protein Kinase C Phosphorylates Ribosomal Protein S6 Kinase \hat{I}^2 II and Regulates Its Subcellular Localization. <i>Molecular and Cellular Biology</i> , 2003, 23, 852-863.	1.1	65
102	Proteomics in the Analysis of Prostate Cancer. , 2003, 81, 277-298.		7
103	Urinary Proteomics of Renal Fanconi Syndrome. , 2003, 141, 155-169.		14
104	Localization of a highly active pool of type II phosphatidylinositol 4-kinase in a p97/valosin-containing-protein-rich fraction of the endoplasmic reticulum. <i>Biochemical Journal</i> , 2003, 373, 57-63.	1.7	61
105	Evaluation of Two-dimensional Differential Gel Electrophoresis for Proteomic Expression Analysis of a Model Breast Cancer Cell System. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 91-98.	2.5	255
106	Phosphorylation of Tyrosine 291 Enhances the Ability of WASp to Stimulate Actin Polymerization and Filopodium Formation. <i>Journal of Biological Chemistry</i> , 2002, 277, 45115-45121.	1.6	185
107	Differential Proteome Analysis of Replicative Senescence in Rat Embryo Fibroblasts. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 280-292.	2.5	41
108	Metabolism of the novel Ca ²⁺ -mobilizing messenger nicotinic acidâ€™adenine dinucleotide phosphate via a 2â€™-specific Ca ²⁺ -dependent phosphatase. <i>Biochemical Journal</i> , 2002, 365, 295-301.	1.7	43

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109	Chaperonin assisted overexpression, purification, and characterisation of human PP2A methyltransferase. <i>Protein Expression and Purification</i> , 2002, 26, 266-274.	0.6	4
110	Activation of the ATPase Activity of Hsp90 by the Stress-Regulated Cochaperone Aha1. <i>Molecular Cell</i> , 2002, 10, 1307-1318.	4.5	487
111	Factors governing the solubilization of phosphopeptides retained on ferric NTA IMAC beads and their analysis by MALDI TOFMS. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 1042-1051.	1.2	64
112	Identification of novel candidates for replicative senescence by functional proteomics. <i>Oncogene</i> , 2002, 21, 4403-4413.	2.6	29
113	Cloning of a Human Type II Phosphatidylinositol 4-Kinase Reveals a Novel Lipid Kinase Family. <i>Journal of Biological Chemistry</i> , 2001, 276, 16635-16640.	1.6	90
114	Proteomics – post-genomic cartography to understand gene function. <i>Trends in Pharmacological Sciences</i> , 2001, 22, 376-384.	4.0	104
115	The nature of collision-induced dissociation processes of doubly protonated peptides: comparative study for the future use of matrix-assisted laser desorption/ionization on a hybrid quadrupole time-of-flight mass spectrometer in proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 2058-2066.	0.7	49
116	High-resolution infrared laser desorption/ionization and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry of synthetic polymers. , 1999, 34, 1089-1092.		2
117	Analysis of Phospho- and Glycopolypeptides with Infrared Matrix-Assisted Laser Desorption and Ionization. <i>Analytical Chemistry</i> , 1998, 70, 4939-4944.	3.2	45
118	Matrix-assisted laser desorption and ionization in the O-H and C=O absorption bands of aliphatic and aromatic matrices: dependence on laser wavelength and temporal beam profile. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1997, 169-170, 51-67.	1.9	74
119	Infrared matrix-assisted laser desorption and ionization by using a tunable mid-infrared free-electron laser. <i>Journal of the American Society for Mass Spectrometry</i> , 1996, 7, 1187-1193.	1.2	45
120	Direct mass spectrometric sequencing of low-picomole amounts of oligodeoxynucleotides with up to 21 bases by matrix-assisted laser desorption/ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 1995, 30, 99-112.	0.7	129
121	Comparison of IR- and UV-matrix-assisted laser desorption/ionization mass spectrometry of oligodeoxynucleotides. <i>Nucleic Acids Research</i> , 1994, 22, 2460-2465.	6.5	76
122	Ion stability of nucleic acids in infrared matrix-assisted laser desorption/ionization mass spectrometry. <i>Nucleic Acids Research</i> , 1993, 21, 3347-3357.	6.5	193