

Yuri E M Van Der Burgt

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.

80
papers

2,428
citations

26
h-index

46
g-index

81
ext. papers

2,728
ext. citations

4.5
avg, IF

4.72
L-index

#	Paper	IF	Citations
80	New Diphosphine Ligands Based on Heterocyclic Aromatics Inducing Very High Regioselectivity in Rhodium-Catalyzed Hydroformylation: Effect of the Bite Angle. <i>Organometallics</i> , 1995 , 14, 3081-3089	3.8	710
79	Imaging of peptides in the rat brain using MALDI-FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 145-51	3.5	135
78	Mass spectrometric glycan rearrangements. <i>Mass Spectrometry Reviews</i> , 2011 , 30, 664-80	11	106
77	Automated Multiplex LC-MS/MS Assay for Quantifying Serum Apolipoproteins A-I, B, C-I, C-II, C-III, and E with Qualitative Apolipoprotein E Phenotyping. <i>Clinical Chemistry</i> , 2016 , 62, 188-97	5.5	66
76	Automation of High-Throughput Mass Spectrometry-Based Plasma N-Glycome Analysis with Linkage-Specific Sialic Acid Esterification. <i>Journal of Proteome Research</i> , 2015 , 14, 4080-6	5.6	64
75	Fibronectin is a serum biomarker for Duchenne muscular dystrophy. <i>Proteomics - Clinical Applications</i> , 2014 , 8, 269-78	3.1	55
74	Structural analysis of an intact monoclonal antibody by online electrochemical reduction of disulfide bonds and Fourier transform ion cyclotron resonance mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 5376-82	7.8	45
73	Distribution of methyl substituents over branched and linear regions in methylated starches. <i>Carbohydrate Research</i> , 1998 , 312, 201-208	2.9	45
72	Alterations of the serum peptidome in renal cell carcinoma discriminating benign and malignant kidney tumors. <i>Journal of Proteomics</i> , 2012 , 76 Spec No., 125-40	3.9	38
71	Top-down MALDI-in-source decay-FTICR mass spectrometry of isotopically resolved proteins. <i>Analytical Chemistry</i> , 2015 , 87, 3429-37	7.8	37
70	Identification of new apolipoprotein-CIII glycoforms with ultrahigh resolution MALDI-FTICR mass spectrometry of human sera. <i>Journal of Proteome Research</i> , 2013 , 12, 2260-8	5.6	37
69	Evaluation of interspecimen trypsin digestion efficiency prior to multiple reaction monitoring-based absolute protein quantification with native protein calibrators. <i>Journal of Proteome Research</i> , 2013 , 12, 5760-74	5.6	36
68	Structural Characterization of Biofunctionalized Gold Nanoparticles by Ultrahigh-Resolution Mass Spectrometry. <i>ACS Nano</i> , 2017 , 11, 8257-8264	16.7	36
67	Quantifying protein measurands by peptide measurements: where do errors arise?. <i>Journal of Proteome Research</i> , 2015 , 14, 928-42	5.6	34
66	Disulfide bond cleavages observed in SORI-CID of three nonapeptides complexed with divalent transition-metal cations. <i>Journal of Mass Spectrometry</i> , 2007 , 42, 450-8	2.2	34
65	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	4.6	32
64	Serum Protein -Glycosylation Changes with Rheumatoid Arthritis Disease Activity during and after Pregnancy. <i>Frontiers in Medicine</i> , 2017 , 4, 241	4.9	32

63	Proteomic serum biomarkers and their potential application in cancer screening programs. <i>International Journal of Molecular Sciences</i> , 2010 , 11, 4175-93	6.3	32
62	Distribution of methyl substituents in amylose and amylopectin from methylated potato starches. <i>Carbohydrate Research</i> , 2000 , 325, 183-91	2.9	32
61	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	3.5	32
60	Automated Plasma Glycomics with Linkage-Specific Sialic Acid Esterification and Ultrahigh Resolution MS. <i>Analytical Chemistry</i> , 2018 , 90, 11955-11961	7.8	31
59	Serum -glycome alterations in colorectal cancer associate with survival. <i>Oncotarget</i> , 2018 , 9, 30610-30623	3.3	29
58	Longitudinal monitoring of immunoglobulin A glycosylation during pregnancy by simultaneous MALDI-FTICR-MS analysis of N- and O-glycopeptides. <i>Scientific Reports</i> , 2016 , 6, 27955	4.9	29
57	Structural Analysis of Monoclonal Antibodies by Ultrahigh Resolution MALDI In-Source Decay FT-ICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 2079-2085	7.8	28
56	Metrological traceability in mass spectrometry-based targeted protein quantitation: a proof-of-principle study for serum apolipoproteins A-I and B100. <i>Journal of Proteomics</i> , 2014 , 109, 143-61	6.9	26
55	Urinary signatures of Renal Cell Carcinoma investigated by peptidomic approaches. <i>PLoS ONE</i> , 2014 , 9, e106684	3.7	26
54	Solid-phase extraction strategies to surmount body fluid sample complexity in high-throughput mass spectrometry-based proteomics. <i>Journal of Analytical Methods in Chemistry</i> , 2015 , 2015, 250131	2	24
53	Mass spectrometry analysis of hepcidin peptides in experimental mouse models. <i>PLoS ONE</i> , 2011 , 6, e16362	3.62	24
52	Distribution of methyl substituents over crystalline and amorphous domains in methylated starches. <i>Carbohydrate Research</i> , 1999 , 320, 100-107	2.9	24
51	Mapping O-glycosylation of apolipoprotein C-III in MALDI-FT-ICR protein profiles. <i>Proteomics</i> , 2013 , 13, 992-1001	4.8	23
50	Combined infrared multiphoton dissociation and electron-capture dissociation using co-linear and overlapping beams in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 1838-44	2.2	22
49	On-line electrochemical reduction of disulfide bonds: improved FTICR-CID and -ETD coverage of oxytocin and hepcidin. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1980-7	3.5	21
48	Quality control based on isotopic distributions for high-throughput MALDI-TOF and MALDI-FTICR serum peptide profiling. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 1515-25	3.5	21
47	Comparative mass spectrometric and immunoassay-based proteome analysis in serum of Duchenne muscular dystrophy patients. <i>Proteomics - Clinical Applications</i> , 2016 , 10, 290-9	3.1	21
46	Standardized and automated solid-phase extraction procedures for high-throughput proteomics of body fluids. <i>Journal of Proteomics</i> , 2012 , 77, 144-53	3.9	20

45	Monitoring glycation levels of a bispecific monoclonal antibody at subunit level by ultrahigh-resolution MALDI FT-ICR mass spectrometry. <i>MAbs</i> , 2020 , 12, 1682403	6.6	20
44	Structural Studies on Methylated Starch Granules. <i>Starch/Staerke</i> , 2000 , 52, 40-43	2.3	18
43	Developments in FTICR-MS and Its Potential for Body Fluid Signatures. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 27133-44	6.3	17
42	IgA N- and O-glycosylation profiling reveals no association with the pregnancy-related improvement in rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2017 , 19, 160	5.7	16
41	In-Depth Characterization of Protein Disulfide Bonds by Online Liquid Chromatography-Electrochemistry-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 50-8	3.5	16
40	Electron capture dissociation of peptide hormone changes upon opening of the tocin ring and complexation with transition metal cations. <i>Rapid Communications in Mass Spectrometry</i> , 2009 , 23, 31-8	2.2	16
39	Robust and Accurate 2-Year Performance of a Quantitative Mass Spectrometry-Based Apolipoprotein Test in a Clinical Chemistry Laboratory. <i>Clinical Chemistry</i> , 2018 , 64, 747-749	5.5	15
38	Precision profiling and identification of human serum peptides using Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2011 , 25, 3457-63	2.2	15
37	Improving mass measurement accuracy in mass spectrometry based proteomics by combining open source tools for chromatographic alignment and internal calibration. <i>Journal of Proteomics</i> , 2009 , 72, 722-4	3.9	15
36	Novel lipochitin oligosaccharide structures produced by <i>Rhizobium etli</i> KIM5s. <i>Carbohydrate Research</i> , 2002 , 337, 1193-202	2.9	15
35	Biomarkers discovery by peptide and protein profiling in biological fluids based on functionalized magnetic beads purification and mass spectrometry. <i>Blood Transfusion</i> , 2010 , 8 Suppl 3, s92-7	3.6	15
34	Typing <i>Pseudomonas aeruginosa</i> Isolates with Ultrahigh Resolution MALDI-FTICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 5996-6003	7.8	15
33	Parallel processing of large datasets from NanoLC-FTICR-MS measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 152-61	3.5	14
32	Improved classification of breast cancer peptide and protein profiles by combining two serum workup procedures. <i>Journal of Cancer Research and Clinical Oncology</i> , 2012 , 138, 1983-92	4.9	13
31	Detection and structural elucidation of esterified oxylipids in human synovial fluid by electrospray ionization-fourier transform ion-cyclotron mass spectrometry and liquid chromatography-ion trap-MS(3): detection of esterified hydroxylated docosapentaenoic acid containing phospholipids. <i>Analytical Chemistry</i> , 2013 , 85, 6003-10	7.8	13
30	HILIC-MRM-MS for Linkage-Specific Separation of Sialylated Glycopeptides to Quantify Prostate-Specific Antigen Proteoforms. <i>Journal of Proteome Research</i> , 2020 , 19, 2708-2716	5.6	12
29	Dried blood spot N-glycome analysis by MALDI mass spectrometry. <i>Talanta</i> , 2019 , 205, 120104	6.2	12
28	A novel workflow control system for Fourier transform ion cyclotron resonance mass spectrometry allows for unique on-the-fly data-dependent decisions. <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 1245-56	2.2	12

27	Proteoform Analysis to Fulfill Unmet Clinical Needs and Reach Global Standardization of Protein Measurands in Clinical Chemistry Proteomics. <i>Clinics in Laboratory Medicine</i> , 2018 , 38, 487-497	2.1	11
26	Prospective applications of ultrahigh resolution proteomics in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2016 , 13, 1063-1071	4.2	10
25	Ultrahigh resolution profiles lead to more detailed serum peptidome signatures of pancreatic cancer. <i>Translational Proteomics</i> , 2014 , 2, 39-51		10
24	A novel mass spectrometry cluster for high-throughput quantitative proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 1002-11	3.5	10
23	Substituent distribution in highly branched dextrans from methylated starches. <i>Carbohydrate Research</i> , 2000 , 327, 423-9	2.9	10
22	FAB CIDMS/MS analysis of partially methylated maltotrioses derived from methylated amylose: a study of the substituent distribution. <i>Carbohydrate Research</i> , 2000 , 329, 341-9	2.9	10
21	Top-down FTICR MS for the identification of fluorescent labeling efficiency and specificity of the Cu-protein azurin. <i>Analytical Chemistry</i> , 2012 , 84, 2512-20	7.8	9
20	Serum N-Glycome analysis reveals pancreatic cancer disease signatures. <i>Cancer Medicine</i> , 2020 , 9, 8519-8529	5.8	9
19	Application of a Serum Protein Signature for Pancreatic Cancer to Separate Cases from Controls in a Pancreatic Surveillance Cohort. <i>Translational Oncology</i> , 2016 , 9, 242-7	4.9	9
18	Serum peptide signatures for pancreatic cancer based on mass spectrometry: a comparison to CA19-9 levels and routine imaging techniques. <i>Journal of Cancer Research and Clinical Oncology</i> , 2015 , 141, 531-41	4.9	7
17	Detection of pancreatic cancer using serum protein profiling. <i>Hpb</i> , 2013 , 15, 602-10	3.8	7
16	Analysis of Synthetic Monodisperse Polysaccharides by Wide Mass Range Ultrahigh-Resolution MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 4666-4675	7.8	7
15	The Time Has Come for Quantitative Protein Mass Spectrometry Tests That Target Unmet Clinical Needs. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 636-647	3.5	5
14	Clinical Perspective on Proteomic and Glycomic Biomarkers for Diagnosis, Prognosis, and Prediction of Pancreatic Cancer. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
13	Structure characterization of unexpected covalent O-sulfonation and ion-pairing on an extremely hydrophilic peptide with CE-MS and FT-ICR-MS. <i>Analytical and Bioanalytical Chemistry</i> , 2015 , 407, 6637-55	4.4	4
12	Identification of human serum peptides in fourier transform ion cyclotron resonance precision profiles. <i>International Journal of Proteomics</i> , 2012 , 2012, 804036		4
11	O- and N-glycosylation analysis of cell lines by ultrahigh resolution MALDI-FTICR-MS. <i>International Journal of Mass Spectrometry</i> , 2020 , 448, 116267	1.9	4
10	Accounting for isotopic clustering in Fourier transform mass spectrometry data analysis for clinical diagnostic studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016 , 15, 415-430	1.2	4

9	SPE-MALDI Profiling of Serum Peptides and Proteins by Ultrahigh Resolution FTICR-MS. <i>Chromatographia</i> , 2015 , 78, 445-449	2.1	3
8	Evaluation of Sibling and Twin Fragment Ions Improves the Structural Characterization of Proteins by Top-Down MALDI In-Source Decay Mass Spectrometry. <i>Analytical Chemistry</i> , 2020 , 92, 5871-5881	7.8	3
7	Protein biomarker discovery is still relevant and has entered a new phase. <i>EBioMedicine</i> , 2019 , 43, 15	8.8	2
6	Temperature-dependent instability of the cTnI subunit in NIST SRM2921 characterized by tryptic peptide mapping. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2012 , 902, 147-50	3.2	2
5	"Lossless" compression of high resolution mass spectra of small molecules. <i>Metabolomics</i> , 2010 , 6, 335-349	3.9	2
4	Improved N- and C-Terminal Sequencing of Proteins by Combining Positive and Negative Ion MALDI In-Source Decay Mass Spectrometry. <i>Analytical Chemistry</i> , 2020 , 92, 12429-12436	7.8	2
3	Differentiating samples and experimental protocols by direct comparison of tandem mass spectra. <i>Rapid Communications in Mass Spectrometry</i> , 2016 , 30, 731-8	2.2	2
2	Serum N-glycan profiles differ for various breast cancer subtypes. <i>Glycoconjugate Journal</i> , 2021 , 38, 387-395	3.9	1
1	On-the-fly targeted selection of labeled peptides in liquid chromatography/mass spectrometry based quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2010 , 24, 239-41	2.2	0