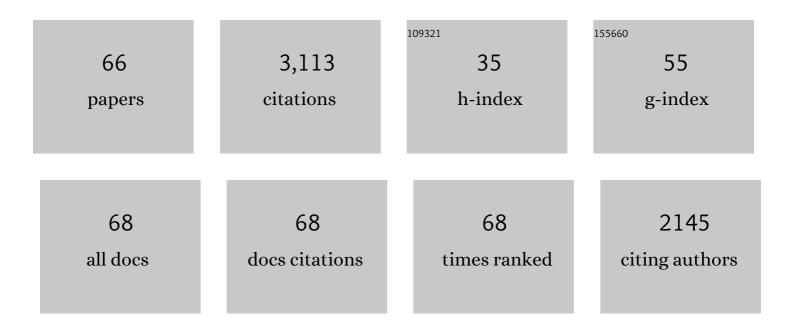
## Dobrin Nedelkov

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Biosensor chip mass spectrometry: A chip-based proteomics approach. Electrophoresis, 2000, 21, 1155-1163.	2.4	196
2	Investigating diversity in human plasma proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10852-10857.	7.1	169
3	Surface Plasmon Resonance Imaging Measurements of Antibody Arrays for the Multiplexed Detection of Low Molecular Weight Protein Biomarkers. Analytical Chemistry, 2006, 78, 6504-6510.	6.5	159
4	Multitoxin biosensor–mass spectrometry analysis: a new approach for rapid, real-time, sensitive analysis of staphylococcal toxins in food. International Journal of Food Microbiology, 2000, 60, 1-13.	4.7	115
5	Surface plasmon resonance mass spectrometry: recent progress and outlooks. Trends in Biotechnology, 2003, 21, 301-305.	9.3	107
6	Rapid development of sensitive, high-throughput, quantitative and highly selective mass spectrometric targeted immunoassays for clinically important proteins in human plasma and serum. Clinical Biochemistry, 2013, 46, 399-410.	1.9	98
7	Determination of β-2 Microglobulin Levels in Plasma Using a High-Throughput Mass Spectrometric Immunoassay System. Analytical Chemistry, 2001, 73, 3294-3299.	6.5	86
8	Quantitative Mass Spectrometric Immunoassay of Insulin Like Growth Factor 1. Journal of Proteome Research, 2004, 3, 851-855.	3.7	78
9	High-Throughput Protein Characterization Using Mass Spectrometric Immunoassay. Analytical Biochemistry, 2002, 301, 49-56.	2.4	76
10	Detection of novel truncated forms of human serum amyloid A protein in human plasma. FEBS Letters, 2003, 537, 166-170.	2.8	76
11	Detection and Quantification of β-2-Microglobulin Using Mass Spectrometric Immunoassay. Analytical Biochemistry, 2001, 289, 26-35.	2.4	73
12	Population Proteomics. Molecular and Cellular Proteomics, 2006, 5, 1811-1818.	3.8	73
13	High-Throughput Comprehensive Analysis of Human Plasma Proteins:Â A Step toward Population Proteomics. Analytical Chemistry, 2004, 76, 1733-1737.	6.5	70
14	Development of Surface Plasmon Resonance Mass Spectrometry Array Platform. Analytical Chemistry, 2007, 79, 5987-5990.	6.5	70
15	Practical considerations in BIA/MS: optimizing the biosensor-mass spectrometry interface. Journal of Molecular Recognition, 2000, 13, 140-145.	2.1	69
16	Novel mass spectrometric immunoassays for the rapid structural characterization of plasma apolipoproteins. Journal of Lipid Research, 2003, 44, 630-639.	4.2	66
17	Comparative Urine Protein Phenotyping Using Mass Spectrometric Immunoassay. Journal of Proteome Research, 2003, 2, 191-197.	3.7	65
18	Comparative phenotypic analyses of human plasma and urinary retinol binding protein using mass spectrometric immunoassay. Biochemical and Biophysical Research Communications, 2002, 297, 401-405.	2.1	64

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19	Detection of Staphylococcal Enterotoxin B via Biomolecular Interaction Analysis Mass Spectrometry. Applied and Environmental Microbiology, 2003, 69, 5212-5215.	3.1	64
20	Analysis of human urine protein biomarkers via biomolecular interaction analysis mass spectrometry. American Journal of Kidney Diseases, 2001, 38, 481-487.	1.9	59
21	Analysis of native proteins from biological fluids by biomolecular interaction analysis mass spectrometry (BIA/MS): exploring the limit of detection, identification of non-specific binding and detection of multi-protein complexes. Biosensors and Bioelectronics, 2001, 16, 1071-1078.	10.1	54
22	An automated, highâ€ŧhroughput method for targeted quantification of intact insulin and its therapeutic analogs in human serum or plasma coupling mass spectrometric immunoassay with high resolution and accurate mass detection (MSIAâ€HR/AM). Proteomics, 2014, 14, 1445-1456.	2.2	54
23	Proteomic characterization of novel serum amyloid P component variants from human plasma and urine. Proteomics, 2004, 4, 1825-1829.	2.2	53
24	Investigation of Human Protein Variants and Their Frequency in the General Population. Molecular and Cellular Proteomics, 2007, 6, 1183-1187.	3.8	51
25	Mass Spectrometric Immunoassay for Quantitative Determination of Protein Biomarker Isoforms. Journal of Proteome Research, 2010, 9, 5969-5973.	3.7	49
26	Multiplexed Mass Spectrometric Immunoassay in Biomarker Research:Â A Novel Approach to the Determination of a Myocardial Infarct. Journal of Proteome Research, 2006, 5, 2928-2934.	3.7	48
27	Parallel Workflow for High-Throughput (>1,000 Samples/Day) Quantitative Analysis of Human Insulin-Like Growth Factor 1 Using Mass Spectrometric Immunoassay. PLoS ONE, 2014, 9, e92801.	2.5	48
28	Quantitative Multiplexed C-Reactive Protein Mass Spectrometric Immunoassay. Journal of Proteome Research, 2006, 5, 1682-1687.	3.7	47
29	Population proteomics: addressing protein diversity in humans. Expert Review of Proteomics, 2005, 2, 315-324.	3.0	45
30	Peer Reviewed: Biomolecular Interaction Analysis Mass Spectrometry Analytical Chemistry, 2000, 72, 404 A-411 A.	6.5	44
31	Mass spectrometry-based immunoassays for the next phase of clinical applications. Expert Review of Proteomics, 2006, 3, 631-640.	3.0	43
32	Population proteomics: Investigation of protein diversity in human populations. Proteomics, 2008, 8, 779-786.	2.2	42
33	Development of multiplex mass spectrometric immunoassay for detection and quantification of apolipoproteins C-I, C-II, C-III and their proteoforms. Methods, 2015, 81, 86-92.	3.8	42
34	Targeted Selected Reaction Monitoring Mass Spectrometric Immunoassay for Insulin-like Growth Factor 1. PLoS ONE, 2013, 8, e81125.	2.5	40
35	Quantitative Mass Spectrometry Evaluation of Human Retinol Binding Protein 4 and Related Variants. PLoS ONE, 2011, 6, e17282.	2.5	37
36	Exploring the limit of detection in biomolecular interaction analysis mass spectrometry (BIA/MS): detection of attomole amounts of native proteins present in complex biological mixtures. Analytica Chimica Acta, 2000, 423, 1-7.	5.4	36

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37	Design and use of multi-affinity surfaces in biomolecular interaction analysis-mass spectrometry (BIA/MS): a step toward the design of SPR/MS arrays. Journal of Molecular Recognition, 2003, 16, 15-19.	2.1	32
38	Detection of bound and free IGF-1 and IGF-2 in human plasma via biomolecular interaction analysis mass spectrometry. FEBS Letters, 2003, 536, 130-134.	2.8	31
39	Targeted quantitative mass spectrometric immunoassay for human protein variants. Proteome Science, 2011, 9, 19.	1.7	31
40	Serum Amyloid A Truncations in Type 2 Diabetes Mellitus. PLoS ONE, 2015, 10, e0115320.	2.5	30
41	Mass Spectrometric Immunoassays in Characterization of Clinically Significant Proteoforms. Proteomes, 2016, 4, 13.	3.5	29
42	Delineation ofin vivo assembled multiprotein complexesvia biomolecular interaction analysis mass spectrometry. Proteomics, 2001, 1, 1441-1446.	2.2	28
43	Mass spectrometric immunoassay for quantitative determination of transthyretin and its variants. Proteomics, 2011, 11, 3633-3641.	2.2	28
44	Surface plasmon resonance-enabled mass spectrometry arrays. Electrophoresis, 2006, 27, 3671-3675.	2.4	27
45	Delineating protein-protein interactions via biomolecular interaction analysis-mass spectrometry. Journal of Molecular Recognition, 2003, 16, 9-14.	2.1	26
46	Development of Recombinant-Based Mass Spectrometric Immunoassay with Application to Resistin Expression Profiling. Analytical Chemistry, 2006, 78, 3271-3276.	6.5	25
47	Mass Spectrometric Immunoassay for the qualitative and quantitative analysis of the cytokine Macrophage Migration Inhibitory Factor (MIF). Proteome Science, 2014, 12, 52.	1.7	25
48	Top-down mass spectrometric immunoassay for human insulin and its therapeutic analogs. Journal of Proteomics, 2018, 175, 27-33.	2.4	25
49	Selected expression profiling of full-length proteins and their variants in human plasma. Clinical Proteomics, 2004, 1, 7-16.	2.1	23
50	High-throughput MS-based protein phenotyping: Application to haptoglobin. Proteomics, 2005, 5, 5002-5007.	2.2	21
51	Delineation of Concentration Ranges and Longitudinal Changes of Human Plasma Protein Variants. PLoS ONE, 2014, 9, e100713.	2.5	20
52	Mass spectrometry-based protein assays for <i>in vitro</i> diagnostic testing. Expert Review of Molecular Diagnostics, 2012, 12, 235-239.	3.1	19
53	Quantitative mass spectrometric immunoassay for the chemokine RANTES and its variants. Journal of Proteomics, 2015, 116, 15-23.	2.4	18
54	Mass spectrometric immunoassays for discovery, screening and quantification of clinically relevant proteoforms. Bioanalysis, 2016, 8, 1623-1633.	1.5	17

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#	Article	IF	CITATIONS
55	Integration of SPR Biosensors with Mass Spectrometry (SPR-MS). Methods in Molecular Biology, 2010, 627, 261-268.	0.9	16
56	High-Throughput Affinity Mass Spectrometry. , 2006, 328, 141-150.		12
57	Mass Spectrometric Studies of Apolipoprotein Proteoforms and Their Role in Lipid Metabolism and Type 2 Diabetes. Proteomes, 2017, 5, 27.	3.5	12
58	Surface Plasmon Resonance Mass Spectrometry for Protein Analysis. , 2006, 328, 131-140.		11
59	Human proteoforms as new targets for clinical mass spectrometry protein tests. Expert Review of Proteomics, 2017, 14, 691-699.	3.0	11
60	Posttranslational modifications of apolipoprotein A-II proteoforms in type 2 diabetes. Journal of Clinical Lipidology, 2016, 10, 808-815.	1.5	10
61	Development of quantitative mass spectrometric immunoassay for serum amyloid A. Biomarkers, 2016, 21, 743-751.	1.9	8
62	Association of cystatin C proteoforms with estimated glomerular filtration rate. Clinical Mass Spectrometry, 2016, 1, 27-31.	1.9	5
63	Proteomics and Host—Pathogen Interactions. , 2011, , 263-303.		4
64	Complexity, cost, and content – three important factors for translation of clinical protein mass spectrometry tests, and the case for apolipoprotein C-III proteoform testing. Clinical Chemistry and Laboratory Medicine, 2020, 58, 858-863.	2.3	2
65	Volumetric Mass Spectrometry Protein Arrays. Methods in Molecular Biology, 2007, 382, 333-343.	0.9	1
66	Proteomics of Human Urine. , 2007, , 225-268.		0