

Dobrin Nedelkov

List of Publications by Year in descending order

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66
papers

3,113
citations

109321

35
h-index

155660

55
g-index

68
all docs

68
docs citations

68
times ranked

2145
citing authors

#	ARTICLE	IF	CITATIONS
1	Complexity, cost, and content – three important factors for translation of clinical protein mass spectrometry tests, and the case for apolipoprotein C-III proteoform testing. <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, 858-863.	2.3	2
2	Top-down mass spectrometric immunoassay for human insulin and its therapeutic analogs. <i>Journal of Proteomics</i> , 2018, 175, 27-33.	2.4	25
3	Human proteoforms as new targets for clinical mass spectrometry protein tests. <i>Expert Review of Proteomics</i> , 2017, 14, 691-699.	3.0	11
4	Mass Spectrometric Studies of Apolipoprotein Proteoforms and Their Role in Lipid Metabolism and Type 2 Diabetes. <i>Proteomes</i> , 2017, 5, 27.	3.5	12
5	Mass Spectrometric Immunoassays in Characterization of Clinically Significant Proteoforms. <i>Proteomes</i> , 2016, 4, 13.	3.5	29
6	Association of cystatin C proteoforms with estimated glomerular filtration rate. <i>Clinical Mass Spectrometry</i> , 2016, 1, 27-31.	1.9	5
7	Mass spectrometric immunoassays for discovery, screening and quantification of clinically relevant proteoforms. <i>Bioanalysis</i> , 2016, 8, 1623-1633.	1.5	17
8	Development of quantitative mass spectrometric immunoassay for serum amyloid A. <i>Biomarkers</i> , 2016, 21, 743-751.	1.9	8
9	Posttranslational modifications of apolipoprotein A-II proteoforms in type 2 diabetes. <i>Journal of Clinical Lipidology</i> , 2016, 10, 808-815.	1.5	10
10	Serum Amyloid A Truncations in Type 2 Diabetes Mellitus. <i>PLoS ONE</i> , 2015, 10, e0115320.	2.5	30
11	Quantitative mass spectrometric immunoassay for the chemokine RANTES and its variants. <i>Journal of Proteomics</i> , 2015, 116, 15-23.	2.4	18
12	Development of multiplex mass spectrometric immunoassay for detection and quantification of apolipoproteins C-I, C-II, C-III and their proteoforms. <i>Methods</i> , 2015, 81, 86-92.	3.8	42
13	An automated, high-throughput 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 (MSIA-HR/AM). <i>Proteomics</i> , 2014, 14, 1445-1456.	2.2	54
14	Mass Spectrometric Immunoassay for the qualitative and quantitative analysis of the cytokine Macrophage Migration Inhibitory Factor (MIF). <i>Proteome Science</i> , 2014, 12, 52.	1.7	25
15	Parallel Workflow for High-Throughput (>1,000 Samples/Day) Quantitative Analysis of Human Insulin-Like Growth Factor 1 Using Mass Spectrometric Immunoassay. <i>PLoS ONE</i> , 2014, 9, e92801.	2.5	48
16	Delineation of Concentration Ranges and Longitudinal Changes of Human Plasma Protein Variants. <i>PLoS ONE</i> , 2014, 9, e100713.	2.5	20
17	Rapid development of sensitive, high-throughput, quantitative and highly selective mass spectrometric targeted immunoassays for clinically important proteins in human plasma and serum. <i>Clinical Biochemistry</i> , 2013, 46, 399-410.	1.9	98
18	Targeted Selected Reaction Monitoring Mass Spectrometric Immunoassay for Insulin-like Growth Factor 1. <i>PLoS ONE</i> , 2013, 8, e81125.	2.5	40

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19	Mass spectrometry-based protein assays for <i>in vitro</i> diagnostic testing. Expert Review of Molecular Diagnostics, 2012, 12, 235-239.	3.1	19
20	Proteomics and Host-Pathogen Interactions. , 2011, , 263-303.		4
21	Targeted quantitative mass spectrometric immunoassay for human protein variants. Proteome Science, 2011, 9, 19.	1.7	31
22	Mass spectrometric immunoassay for quantitative determination of transthyretin and its variants. Proteomics, 2011, 11, 3633-3641.	2.2	28
23	Quantitative Mass Spectrometry Evaluation of Human Retinol Binding Protein 4 and Related Variants. PLoS ONE, 2011, 6, e17282.	2.5	37
24	Integration of SPR Biosensors with Mass Spectrometry (SPR-MS). Methods in Molecular Biology, 2010, 627, 261-268.	0.9	16
25	Mass Spectrometric Immunoassay for Quantitative Determination of Protein Biomarker Isoforms. Journal of Proteome Research, 2010, 9, 5969-5973.	3.7	49
26	Population proteomics: Investigation of protein diversity in human populations. Proteomics, 2008, 8, 779-786.	2.2	42
27	Investigation of Human Protein Variants and Their Frequency in the General Population. Molecular and Cellular Proteomics, 2007, 6, 1183-1187.	3.8	51
28	Development of Surface Plasmon Resonance Mass Spectrometry Array Platform. Analytical Chemistry, 2007, 79, 5987-5990.	6.5	70
29	Proteomics of Human Urine. , 2007, , 225-268.		0
30	Volumetric Mass Spectrometry Protein Arrays. Methods in Molecular Biology, 2007, 382, 333-343.	0.9	1
31	Mass spectrometry-based immunoassays for the next phase of clinical applications. Expert Review of Proteomics, 2006, 3, 631-640.	3.0	43
32	Quantitative Multiplexed C-Reactive Protein Mass Spectrometric Immunoassay. Journal of Proteome Research, 2006, 5, 1682-1687.	3.7	47
33	Multiplexed Mass Spectrometric Immunoassay in Biomarker Research: A Novel Approach to the Determination of a Myocardial Infarct. Journal of Proteome Research, 2006, 5, 2928-2934.	3.7	48
34	High-Throughput Affinity Mass Spectrometry. , 2006, 328, 141-150.		12
35	Development of Recombinant-Based Mass Spectrometric Immunoassay with Application to Resistin Expression Profiling. Analytical Chemistry, 2006, 78, 3271-3276.	6.5	25
36	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

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37	Surface plasmon resonance-enabled mass spectrometry arrays. <i>Electrophoresis</i> , 2006, 27, 3671-3675.	2.4	27
38	Surface Plasmon Resonance Mass Spectrometry for Protein Analysis. , 2006, 328, 131-140.		11
39	Population Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1811-1818.	3.8	73
40	High-throughput MS-based protein phenotyping: Application to haptoglobin. <i>Proteomics</i> , 2005, 5, 5002-5007.	2.2	21
41	Population proteomics: addressing protein diversity in humans. <i>Expert Review of Proteomics</i> , 2005, 2, 315-324.	3.0	45
42	Investigating diversity in human plasma proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10852-10857.	7.1	169
43	Selected expression profiling of full-length proteins and their variants in human plasma. <i>Clinical Proteomics</i> , 2004, 1, 7-16.	2.1	23
44	Proteomic characterization of novel serum amyloid P component variants from human plasma and urine. <i>Proteomics</i> , 2004, 4, 1825-1829.	2.2	53
45	High-Throughput Comprehensive Analysis of Human Plasma Proteins: A Step toward Population Proteomics. <i>Analytical Chemistry</i> , 2004, 76, 1733-1737.	6.5	70
46	Quantitative Mass Spectrometric Immunoassay of Insulin Like Growth Factor 1. <i>Journal of Proteome Research</i> , 2004, 3, 851-855.	3.7	78
47	Surface plasmon resonance mass spectrometry: recent progress and outlooks. <i>Trends in Biotechnology</i> , 2003, 21, 301-305.	9.3	107
48	Delineating protein-protein interactions via biomolecular interaction analysis-mass spectrometry. <i>Journal of Molecular Recognition</i> , 2003, 16, 9-14.	2.1	26
49	Design and use of multi-affinity surfaces in biomolecular interaction analysis-mass spectrometry (BIA/MS): a step toward the design of SPR/MS arrays. <i>Journal of Molecular Recognition</i> , 2003, 16, 15-19.	2.1	32
50	Detection of bound and free IGF-1 and IGF-2 in human plasma via biomolecular interaction analysis mass spectrometry. <i>FEBS Letters</i> , 2003, 536, 130-134.	2.8	31
51	Detection of novel truncated forms of human serum amyloid A protein in human plasma. <i>FEBS Letters</i> , 2003, 537, 166-170.	2.8	76
52	Comparative Urine Protein Phenotyping Using Mass Spectrometric Immunoassay. <i>Journal of Proteome Research</i> , 2003, 2, 191-197.	3.7	65
53	Detection of Staphylococcal Enterotoxin B via Biomolecular Interaction Analysis Mass Spectrometry. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5212-5215.	3.1	64
54	Novel mass spectrometric immunoassays for the rapid structural characterization of plasma apolipoproteins. <i>Journal of Lipid Research</i> , 2003, 44, 630-639.	4.2	66

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55	Comparative phenotypic analyses of human plasma and urinary retinol binding protein using mass spectrometric immunoassay. <i>Biochemical and Biophysical Research Communications</i> , 2002, 297, 401-405.	2.1	64
56	High-Throughput Protein Characterization Using Mass Spectrometric Immunoassay. <i>Analytical Biochemistry</i> , 2002, 301, 49-56.	2.4	76
57	Determination of \hat{I}^2 -2 Microglobulin Levels in Plasma Using a High-Throughput Mass Spectrometric Immunoassay System. <i>Analytical Chemistry</i> , 2001, 73, 3294-3299.	6.5	86
58	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. <i>Biosensors and Bioelectronics</i> , 2001, 16, 1071-1078.	10.1	54
59	Detection and Quantification of \hat{I}^2 -2-Microglobulin Using Mass Spectrometric Immunoassay. <i>Analytical Biochemistry</i> , 2001, 289, 26-35.	2.4	73
60	Delineation of in vivo assembled multiprotein complexes via biomolecular interaction analysis mass spectrometry. <i>Proteomics</i> , 2001, 1, 1441-1446.	2.2	28
61	Analysis of human urine protein biomarkers via biomolecular interaction analysis mass spectrometry. <i>American Journal of Kidney Diseases</i> , 2001, 38, 481-487.	1.9	59
62	Biosensor chip mass spectrometry: A chip-based proteomics approach. <i>Electrophoresis</i> , 2000, 21, 1155-1163.	2.4	196
63	Practical considerations in BIA/MS: optimizing the biosensor-mass spectrometry interface. <i>Journal of Molecular Recognition</i> , 2000, 13, 140-145.	2.1	69
64	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. <i>Analytica Chimica Acta</i> , 2000, 423, 1-7.	5.4	36
65	Multitoxin biosensor's mass spectrometry analysis: a new approach for rapid, real-time, sensitive analysis of staphylococcal toxins in food. <i>International Journal of Food Microbiology</i> , 2000, 60, 1-13.	4.7	115
66	Peer Reviewed: Biomolecular Interaction Analysis Mass Spectrometry.. <i>Analytical Chemistry</i> , 2000, 72, 404 A-411 A.	6.5	44