Garry L Corthals

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Evaluation of two-dimensional gel electrophoresis-based proteome analysis technology. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9390-9395.	7.1	1,250
2	The dynamic range of protein expression: A challenge for proteomic research. Electrophoresis, 2000, 21, 1104-1115.	2.4	603
3	A panel of cerebrospinal fluid potential biomarkers for the diagnosis of Alzheimer's disease. Proteomics, 2003, 3, 1486-1494.	2.2	344
4	Identification of Flow-dependent Endothelial Nitric-oxide Synthase Phosphorylation Sites by Mass Spectrometry and Regulation of Phosphorylation and Nitric Oxide Production by the Phosphatidylinositol 3-Kinase Inhibitor LY294002. Journal of Biological Chemistry, 1999, 274, 30101-30108.	3.4	296
5	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
6	A gene encoding a novel RFX-associated transactivator is mutated in the majority of MHC class II deficiency patients. Nature Genetics, 1998, 20, 273-277.	21.4	262
7	A Cortactin-CD2-associated Protein (CD2AP) Complex Provides a Novel Link between Epidermal Growth Factor Receptor Endocytosis and the Actin Cytoskeleton. Journal of Biological Chemistry, 2003, 278, 21805-21813.	3.4	192
8	Peptide and protein imaging mass spectrometry in cancer research. Journal of Proteomics, 2010, 73, 1921-1944.	2.4	143
9	ApoC-I and ApoC-III as potential plasmatic markers to distinguish between ischemic and hemorrhagic stroke. Proteomics, 2004, 4, 2242-2251.	2.2	119
10	Vimentin–ERK Signaling Uncouples Slug Gene Regulatory Function. Cancer Research, 2015, 75, 2349-2362.	0.9	112
11	Cystatin C as a potential cerebrospinal fluid marker for the diagnosis of Creutzfeldt-Jakob disease. Proteomics, 2004, 4, 2229-2233.	2.2	95
12	Comprehensive analyses of prostate gene expression: Convergence of expressed sequence tag databases, transcript profiling and proteomics. Electrophoresis, 2000, 21, 1823-1831.	2.4	86
13	Prefractionation of protein samples prior to two-dimensional electrophoresis. Electrophoresis, 1997, 18, 317-323.	2.4	84
14	Identification of Protein Interactions Involved in Cellular Signaling. Molecular and Cellular Proteomics, 2013, 12, 1752-1763.	3.8	84
15	Size distributions of droplets produced by ultrasonic nebulizers. Scientific Reports, 2019, 9, 6128.	3.3	79
16	Akt Mediates Insulin-stimulated Phosphorylation of Ndrg2. Journal of Biological Chemistry, 2004, 279, 18623-18632.	3.4	76
17	Exploitation of specific properties of trifluoroethanol for extraction and separation of membrane proteins. Proteomics, 2003, 3, 1418-1424.	2.2	74
18	Reference-facilitated Phosphoproteomics. Molecular and Cellular Proteomics, 2007, 6, 1380-1391.	3.8	72

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19	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. PLoS ONE, 2016, 11, e0153294.	2.5	70
20	Phosphoproteomics to Characterize Host Response During Influenza A Virus Infection of Human Macrophages. Molecular and Cellular Proteomics, 2016, 15, 3203-3219.	3.8	66
21	Multifunctional apparatus for electrokinetic processing of proteins. Electrophoresis, 1994, 15, 968-971.	2.4	63
22	Data-Dependent Modulation of Solid-Phase Extraction Capillary Electrophoresis for the Analysis of Complex Peptide and Phosphopeptide Mixtures by Tandem Mass Spectrometry:Â Application to Endothelial Nitric Oxide Synthase. Analytical Chemistry, 1999, 71, 2279-2287.	6.5	63
23	Identification of miR-193b Targets in Breast Cancer Cells and Systems Biological Analysis of Their Functional Impact. Molecular and Cellular Proteomics, 2011, 10, M110.005322.	3.8	60
24	Correlation of proteomic and transcriptomic profiles of Staphylococcus aureus during the post-exponential phase of growth. Journal of Microbiological Methods, 2005, 60, 247-257.	1.6	59
25	Quantitative Proteomics Analysis of the Nuclear Fraction of Human CD4+ Cells in the Early Phases of IL-4-induced Th2 Differentiation. Molecular and Cellular Proteomics, 2010, 9, 1937-1953.	3.8	55
26	Protein phosphatase 2A (<scp>PP</scp> 2A) regulatory subunit B′γ interacts with cytoplasmic <scp>ACONITASE</scp> 3 and modulates the abundance of <scp>AOX</scp> 1A and <scp>AOX</scp> 1D in <i>Arabidopsis thaliana</i> . New Phytologist, 2015, 205, 1250-1263.	7.3	55
27	Optimization of Statistical Methods Impact on Quantitative Proteomics Data. Journal of Proteome Research, 2015, 14, 4118-4126.	3.7	54
28	Microarray profiling of host-extract-induced genes and characterization of the type VI secretion cluster in the potato pathogen Pectobacterium atrosepticum. Microbiology (United Kingdom), 2008, 154, 2387-2396.	1.8	53
29	Selenoprotein biosynthesis defect causes progressive encephalopathy with elevated lactate. Neurology, 2015, 85, 306-315.	1.1	52
30	Discussion point: reporting guidelines for mass spectrometry imaging. Analytical and Bioanalytical Chemistry, 2015, 407, 2035-2045.	3.7	51
31	Identification of Phosphorylation Sites Using Microimmobilized Metal Affinity Chromatography. Methods in Enzymology, 2005, 405, 66-81.	1.0	49
32	Label-free quantitative phosphoproteomics with novel pairwise abundance normalization reveals synergistic RAS and CIP2A signaling. Scientific Reports, 2015, 5, 13099.	3.3	49
33	Phosphorylation of Notch1 by Pim kinases promotes oncogenic signaling in breast and prostate cancer cells. Oncotarget, 2016, 7, 43220-43238.	1.8	49
34	Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. Journal of Biological Chemistry, 2020, 295, 4194-4211.	3.4	48
35	Preparative reflux electrophoresis. Electrophoresis, 1995, 16, 98-100.	2.4	45
36	In-Culture Cross-Linking of Bacterial Cells Reveals Large-Scale Dynamic Protein–Protein Interactions at the Peptide Level. Journal of Proteome Research, 2017, 16, 2457-2471.	3.7	44

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37	Expression of a tyrosine phosphorylated, DNA binding Stat3β dimer in bacteria. FEBS Letters, 1998, 441, 141-147.	2.8	42
38	Tumor protein D52 (TPD52): a novel B-cell/plasma-cell molecule with unique expression pattern and Ca2+-dependent association with annexin VI. Blood, 2005, 105, 2812-2820.	1.4	41
39	MSiMass List: A Public Database of Identifications for Protein MALDI MS Imaging. Journal of Proteome Research, 2014, 13, 1138-1142.	3.7	40
40	Using Peptide-Level Proteomics Data for Detecting Differentially Expressed Proteins. Journal of Proteome Research, 2015, 14, 4564-4570.	3.7	40
41	Quantitative Site-Specific Phosphoproteomics of <i>Trichoderma reesei</i> Signaling Pathways upon Induction of Hydrolytic Enzyme Production. Journal of Proteome Research, 2016, 15, 457-467.	3.7	40
42	N-t-butyliodoacetamide and iodoacetanilide: two new cysteine alkylating reagents for relative quantitation of proteins. Rapid Communications in Mass Spectrometry, 2004, 18, 117-127.	1.5	37
43	Gradiflow as a prefractionation tool for two-dimensional electrophoresis. Proteomics, 2002, 2, 1254-1260.	2.2	36
44	Identification of new Golgi complex specific proteins by direct organelle proteomic analysis. Proteomics, 2006, 6, 3502-3508.	2.2	35
45	Nonredundant mass spectrometry: A strategy to integrate mass spectrometry acquisition and analysis. Proteomics, 2004, 4, 917-927.	2.2	34
46	Proteomic tools for biomedicine. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 771, 33-48.	2.3	33
47	Proteome analysis of tissues by mass spectrometry. Mass Spectrometry Reviews, 2019, 38, 403-441.	5.4	31
48	The molecular scanner: concept and developments. Current Opinion in Biotechnology, 2004, 15, 17-23.	6.6	28
49	Murine cathepsin D deficiency is associated with dysmyelination/myelin disruption and accumulation of cholesteryl esters in the brain. Journal of Neurochemistry, 2010, 112, 193-203.	3.9	28
50	Proprotein Convertase FURIN Constrains Th2 Differentiation and Is Critical for Host Resistance against <i>Toxoplasma gondii</i> . Journal of Immunology, 2014, 193, 5470-5479.	0.8	28
51	Characterization of heat shock protein 27 phosphorylation sites in renal cell carcinoma. Proteomics, 2005, 5, 788-795.	2.2	27
52	Confident Site Localization Using a Simulated Phosphopeptide Spectral Library. Journal of Proteome Research, 2015, 14, 2348-2359.	3.7	26
53	Absence of Ataxin-3 Leads to Enhanced Stress Response in C. elegans. PLoS ONE, 2011, 6, e18512.	2.5	26
54	Ataxin-3 Plays a Role in Mouse Myogenic Differentiation through Regulation of Integrin Subunit Levels. PLoS ONE, 2010, 5, e11728.	2.5	25

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55	Development of a Quantitative SRM-Based Proteomics Method to Study Iron Metabolism of <i>Synechocystis</i> sp. PCC 6803. Journal of Proteome Research, 2016, 15, 266-279.	3.7	25
56	Going forward: Increasing the accessibility of imaging mass spectrometry. Journal of Proteomics, 2012, 75, 5113-5121.	2.4	24
57	Crossâ€species identification of proteins from proteome profiles of the marine oligotrophic ultramicrobacterium, <i>Sphingopyxis alaskensis</i> . Proteomics, 2004, 4, 1779-1788.	2.2	23
58	Cathepsin D deficiency induces cytoskeletal changes and affects cell migration pathways in the brain. Neurobiology of Disease, 2013, 50, 107-119.	4.4	23
59	A cyclic-olefin-copolymer microfluidic immobilized-enzyme reactor for rapid digestion of proteins from dried blood spots. Journal of Chromatography A, 2017, 1491, 36-42.	3.7	22
60	Fast and Simple Protocols for Mass Spectrometry-Based Proteomics of Small Fresh Frozen Uterine Tissue Sections. Analytical Chemistry, 2017, 89, 10769-10775.	6.5	22
61	Surface Acoustic Wave Nebulisation Mass Spectrometry for the Fast and Highly Sensitive Characterisation of Synthetic Dyes in Textile Samples. Journal of the American Society for Mass Spectrometry, 2017, 28, 2108-2116.	2.8	22
62	Relevance Rank Platform (RRP) for Functional Filtering of High Content Protein–Protein Interaction Data*. Molecular and Cellular Proteomics, 2015, 14, 3274-3283.	3.8	19
63	The role of pH and membrane porosity in preparative electrophoresis. Electrophoresis, 1996, 17, 771-775.	2.4	18
64	Ovarian Endometriosis Signatures Established through Discovery and Directed Mass Spectrometry Analysis. Journal of Proteome Research, 2014, 13, 4983-4994.	3.7	17
65	Phosphorylation of NFATC1 at PIM1 target sites is essential for its ability to promote prostate cancer cell migration and invasion. Cell Communication and Signaling, 2019, 17, 148.	6.5	17
66	Purification by reflux electrophoresis of whey proteins and of a recombinant protein expressed in Dictyostelium discoideum. Journal of Chromatography A, 1997, 773, 299-309.	3.7	15
67	Onâ€ŧarget ultrasonic digestion of proteins. Proteomics, 2013, 13, 1423-1427.	2.2	14
68	ATX-3, CDC-48 and UBXN-5: A new trimolecular complex in Caenorhabditis elegans. Biochemical and Biophysical Research Communications, 2009, 386, 575-581.	2.1	13
69	Solvent-mediated extraction of fatty acids in bilayer oil paint models: a comparative analysis of solvent application methods. Heritage Science, 2019, 7, .	2.3	13
70	The dynamic range of protein expression: A challenge for proteomic research. Electrophoresis, 2000, 21, 1104-1115.	2.4	13
71	Changes in Gene Expression Associated with Stable Drug and Radiation Resistance in Small Cell Lung Cancer Cells are Similar to those Caused by a Single X-Ray Dose. Radiation Research, 2004, 161, 495-503.	1.5	11
72	Matrixâ€assisted laser desorption/ionization timeâ€ofâ€flight mass spectrometry for quantitation and molecular stability assessment of insulin entrapped within PLGA nanoparticles. Journal of Pharmaceutical Sciences, 2005, 94, 688-694.	3.3	11

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73	Nitromatrix provides improved LCâ€MALDI signals and more protein identifications. Proteomics, 2009, 9, 1662-1671.	2.2	10
74	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	2.2	9
75	lsotopic labelling of peptides in tissues enhances mass spectrometric profiling. Rapid Communications in Mass Spectrometry, 2012, 26, 254-262.	1.5	8
76	SimPhospho: a software tool enabling confident phosphosite assignment. Bioinformatics, 2018, 34, 2690-2692.	4.1	8
77	Utilizing Surface Acoustic Wave Nebulization (SAWN) for the Rapid and Sensitive Ambient Ionization Mass Spectrometric Analysis of Organic Explosives. Journal of the American Society for Mass Spectrometry, 2019, 30, 2655-2669.	2.8	8
78	Protein Information and Knowledge Extractor: Discovering biological information from proteomics data. Proteomics, 2010, 10, 3262-3271.	2.2	7
79	Liver lipid metabolism is altered by increased circulating estrogen to androgen ratio in male mouse. Journal of Proteomics, 2016, 133, 66-75.	2.4	7
80	Evaluation of Fast and Sensitive Proteome Profiling of FF and FFPE Kidney Patient Tissues. Molecules, 2022, 27, 1137.	3.8	7
81	Identification of differentially expressed proteins in <i>Ficedula</i> flycatchers. Proteomics, 2008, 8, 2150-2153.	2.2	6
82	Enrichment and sequencing of phosphopeptides on indium tin oxide coated glass slides. Molecular BioSystems, 2011, 7, 1828.	2.9	6
83	Human serum protein enhances HIV-1 replication and up-regulates the transcription factor AP-1. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17639-17644.	7.1	6
84	Surface Acoustic Wave Nebulization–Mass Spectrometry as a New Tool to Investigate the Water Sensitivity Behavior of 20th Century Oil Paints. Journal of the American Society for Mass Spectrometry, 2021, 32, 444-454.	2.8	6
85	Concanavalin-A Induces Granulosa Cell Death and Inhibits FSH-Mediated Follicular Growth and Ovarian Maturation in Female Rats. Endocrinology, 2013, 154, 1885-1896.	2.8	5
86	Cross-Correlation of Spectral Count Ranking to Validate Quantitative Proteome Measurements. Journal of Proteome Research, 2014, 13, 1957-1968.	3.7	5
87	Report. Proteomics Education, an Important Challenge for the Scientific Community: Report on the Activities of the EuPA Education Committee. Proteomics, 2006, 6, 77-81.	2.2	4
88	Promoting Proteomics Knowledge in Europe. Proteomics, 2007, 7, 90-94.	2.2	4
89	Phosphopeptide enrichment with stable spatial coordination on a titanium dioxide coated glass slide. Rapid Communications in Mass Spectrometry, 2009, 23, 3661-3667.	1.5	4
90	The European Proteomics Association (EuPA) is in the field Report of the formal inauguration of the European Proteome Association (Munich, Germany, August 29, 2005). Proteomics, 2005, 5, 4648-4650.	2.2	3

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91	Mass Spectrometry in Laboratory Medicine. Clinical Chemistry and Laboratory Medicine, 2003, 41, 1539.	2.3	2
92	Data combination from multiple matrixâ€essisted laser desorption/ionization (MALDI) matrices: opportunities and limitations for MALDI analysis. Rapid Communications in Mass Spectrometry, 2010, 24, 3493-3495.	1.5	2
93	Preface. Journal of Proteomics, 2012, 75, 4881-4882.	2.4	2
94	Discovery of New Diagnostic Markers of Stroke. , 2004, , 57-72.		1
95	Proteomics in clinical and fundamental medicine. Scandinavian Journal of Clinical and Laboratory Investigation, 2002, 62, 7-7.	1.2	0
96	Human Cerebrospinal Fluid. , 2004, , 341-353.		0
97	STRATEGIES FOR QUANTITATIVE MEMBRANE PROTEIN PROFILING. Shock, 2004, 21, 1.	2.1	0
98	The transition of the European Proteomics Association into the future. Journal of Proteomics, 2011, 75, 18-22.	2.4	0
99	Tumor Protein D52 (TPD52): A Novel B Cell/Plasma Cell Molecule Identified through a Proteomic Approach and Characterized by Unique Expression Pattern and Ca2+-Dependent Association with Annexin VI Blood, 2004, 104, 3652-3652.	1.4	0
100	Offline Micro-IMAC Enrichment of Phosphoproteins. Cold Spring Harbor Protocols, 2007, 2007, pdb.prot4624.	0.3	0
101	Analysis of Phosphopeptides by μLC-ESI-MS/MS. Cold Spring Harbor Protocols, 2007, 2007, pdb.prot4625.	0.3	0
102	Abstract 512: Pim kinases and Pim inhibitors in the regulation of prostate cancer cell migration and invasion. , 2015, , .		0
103	Abstract 5328: Protein phosphatase 2A activity is a major determinant of therapy response in cancer cells. , 2015, , .		0