

Janne Lehti

List of Publications by Year in descending order

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Version: 2024-02-01

149
papers

8,759
citations

53794

45
h-index

54911

84
g-index

172
all docs

172
docs citations

172
times ranked

16466
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides. <i>Bioinformatics</i> , 2022, 38, 1470-1472.	4.1	16
2	The Molecular Tumor Board Portal supports clinical decisions and automated reporting for precision oncology. <i>Nature Cancer</i> , 2022, 3, 251-261.	13.2	44
3	A novel immunopeptidomic-based pipeline for the generation of personalized oncolytic cancer vaccines. <i>ELife</i> , 2022, 11, .	6.0	21
4	Integrative multi-omics and drug response profiling of childhood acute lymphoblastic leukemia cell lines. <i>Nature Communications</i> , 2022, 13, 1691.	12.8	20
5	The transcriptome-wide landscape of molecular subtype-specific <scp>mRNA</scp> expression profiles in acute myeloid leukemia. <i>American Journal of Hematology</i> , 2021, 96, 580-588.	4.1	9
6	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	159
7	Correcting for Naturally Occurring Mass Isotopologue Abundances in Stable-Isotope Tracing Experiments with PolyMID. <i>Metabolites</i> , 2021, 11, 310.	2.9	3
8	Therapeutic Cancer Vaccination with Immunopeptidomics-Discovered Antigens Confers Protective Antitumor Efficacy. <i>Cancers</i> , 2021, 13, 3408.	3.7	16
9	PeptiCHIP: A Microfluidic Platform for Tumor Antigen Landscape Identification. <i>ACS Nano</i> , 2021, 15, 15992-16010.	14.6	17
10	Reprogrammed transsulfuration promotes basal-like breast tumor progression via realigning cellular cysteine persulfidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
11	Proteogenomics of non-small cell lung cancer reveals molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. <i>Nature Cancer</i> , 2021, 2, 1224-1242.	13.2	37
12	PCSK6 Is a Key Protease in the Control of Smooth Muscle Cell Function in Vascular Remodeling. <i>Circulation Research</i> , 2020, 126, 571-585.	4.5	38
13	Mutation-independent Proteomic Signatures of Pathological Progression in Murine Models of Duchenne Muscular Dystrophy. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2047-2068.	3.8	25
14	Ex vivo assessment of targeted therapies in a rare metastatic epithelial-“myoepithelial carcinoma. <i>Neoplasia</i> , 2020, 22, 390-398.	5.3	9
15	Combined transcriptome and proteome profiling of the pancreatic β -cell response to palmitate unveils key pathways of β -cell lipotoxicity. <i>BMC Genomics</i> , 2020, 21, 590.	2.8	35
16	Novel Broad-Spectrum Antiviral Inhibitors Targeting Host Factors Essential for Replication of Pathogenic RNA Viruses. <i>Viruses</i> , 2020, 12, 1423.	3.3	22
17	DEqMS: A Method for Accurate Variance Estimation in Differential Protein Expression Analysis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1047-1057.	3.8	127
18	In-depth plasma proteomics reveals increase in circulating PD-1 during anti-PD-1 immunotherapy in patients with metastatic cutaneous melanoma. , 2020, 8, e000204.		35

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19	Immunometabolic Network Interactions of the Kynurenine Pathway in Cutaneous Malignant Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 51.	2.8	5
20	Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. <i>Nature Medicine</i> , 2020, 26, 992-994.	30.7	56
21	Ribonucleotide reductase inhibitors suppress SAMHD1 and CTPase activity enhancing cytarabine efficacy. <i>EMBO Molecular Medicine</i> , 2020, 12, e10419.	6.9	35
22	Cell Cycle Profiling Reveals Protein Oscillation, Phosphorylation, and Localization Dynamics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 608-623.	3.8	22
23	PTEN and DNA-PK determine sensitivity and recovery in response to WEE1 inhibition in human breast cancer. <i>ELife</i> , 2020, 9, .	6.0	15
24	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. <i>Blood</i> , 2020, 136, 10-11.	1.4	0
25	MYCN-enhanced Oxidative and Glycolytic Metabolism Reveals Vulnerabilities for Targeting Neuroblastoma. <i>IScience</i> , 2019, 21, 188-204.	4.1	50
26	Early symptoms and sensations as predictors of lung cancer: a machine learning multivariate model. <i>Scientific Reports</i> , 2019, 9, 16504.	3.3	12
27	Voluntary exercise normalizes the proteomic landscape in muscle and brain and improves the phenotype of progeroid mice. <i>Aging Cell</i> , 2019, 18, e13029.	6.7	25
28	Ultrasensitive Immunoprofiling of Plasma Extracellular Vesicles Identifies Syndecan-1 as a Potential Tool for Minimally Invasive Diagnosis of Glioma. <i>Clinical Cancer Research</i> , 2019, 25, 3115-3127.	7.0	72
29	The viral protein corona directs viral pathogenesis and amyloid aggregation. <i>Nature Communications</i> , 2019, 10, 2331.	12.8	160
30	Ouabain-regulated phosphoproteome reveals molecular mechanisms for Na ⁺ , K ⁺ ATPase control of cell adhesion, proliferation, and survival. <i>FASEB Journal</i> , 2019, 33, 10193-10206.	0.5	17
31	Systematic assessment of antibody selectivity in plasma based on a resource of enrichment profiles. <i>Scientific Reports</i> , 2019, 9, 8324.	3.3	29
32	Breast cancer quantitative proteome and proteogenomic landscape. <i>Nature Communications</i> , 2019, 10, 1600.	12.8	152
33	Proteogenomics and Hi-C reveal transcriptional dysregulation in high hyperdiploid childhood acute lymphoblastic leukemia. <i>Nature Communications</i> , 2019, 10, 1519.	12.8	61
34	Two subgroups in systemic lupus erythematosus with features of antiphospholipid or Sjögren's syndrome differ in molecular signatures and treatment perspectives. <i>Arthritis Research and Therapy</i> , 2019, 21, 62.	3.5	24
35	A Mitochondrial LYR Protein Is Required for Complex I Assembly. <i>Plant Physiology</i> , 2019, 181, 1632-1650.	4.8	22
36	TcellSubC: An Atlas of the Subcellular Proteome of Human T Cells. <i>Frontiers in Immunology</i> , 2019, 10, 2708.	4.8	14

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37	SubCellBarCode: Proteome-wide Mapping of Protein Localization and Relocalization. <i>Molecular Cell</i> , 2019, 73, 166-182.e7.	9.7	165
38	High-Throughput Functional Ex-Vivo Drug Testing and Multi-Omics Profiling in Patients with Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 4641-4641.	1.4	1
39	Plasma proteomic analyses and treatment predictive biomarker candidates in melanoma patients receiving immune checkpoint blockade or targeted therapy.. <i>Journal of Clinical Oncology</i> , 2019, 37, 9574-9574.	1.6	2
40	In-depth human plasma proteome analysis captures tissue proteins and transfer of protein variants across the placenta. <i>ELife</i> , 2019, 8, .	6.0	56
41	Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. <i>Nature Communications</i> , 2018, 9, 903.	12.8	108
42	<i>MYCN</i> -amplified neuroblastoma maintains an aggressive and undifferentiated phenotype by deregulation of estrogen and NGF signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1229-E1238.	7.1	46
43	Splicing of platelet resident pre-mRNAs upon activation by physiological stimuli results in functionally relevant proteome modifications. <i>Scientific Reports</i> , 2018, 8, 498.	3.3	65
44	Normalization of mass spectrometry data (NOMAD). <i>Advances in Biological Regulation</i> , 2018, 67, 128-133.	2.3	16
45	Synaptic markers of cognitive decline in neurodegenerative diseases: a proteomic approach. <i>Brain</i> , 2018, 141, 582-595.	7.6	172
46	Molecular profiles of oxyphilic and chief cell parathyroid adenoma. <i>Molecular and Cellular Endocrinology</i> , 2018, 470, 84-95.	3.2	10
47	Mechanism of Peptide Binding and Cleavage by the Human Mitochondrial Peptidase Neurolysin. <i>Journal of Molecular Biology</i> , 2018, 430, 348-362.	4.2	29
48	A Common Peptidolytic Mechanism for Targeting Peptide Degradation in Mitochondria and Chloroplasts. <i>Molecular Plant</i> , 2018, 11, 342-345.	8.3	16
49	Accumulation of endogenous peptides triggers a pathogen stress response in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2018, 96, 705-715.	5.7	18
50	Single-Stranded Nucleic Acids Regulate TLR3/4/7 Activation through Interference with Clathrin-Mediated Endocytosis. <i>Scientific Reports</i> , 2018, 8, 15841.	3.3	12
51	Novel Multiomics Profiling of Human Carotid Atherosclerotic Plaques and Plasma Reveals Biliverdin Reductase B as a Marker of Intraplaque Hemorrhage. <i>JACC Basic To Translational Science</i> , 2018, 3, 464-480.	4.1	42
52	Metabolic reprogramming of acute lymphoblastic leukemia cells in response to glucocorticoid treatment. <i>Cell Death and Disease</i> , 2018, 9, 846.	6.3	44
53	A protein activity assay to measure global transcription factor activity reveals determinants of chromatin accessibility. <i>Nature Biotechnology</i> , 2018, 36, 521-529.	17.5	28
54	Heterogeneity and interplay of the extracellular vesicle small RNA transcriptome and proteome. <i>Scientific Reports</i> , 2018, 8, 10813.	3.3	118

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55	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. <i>BMC Biology</i> , 2018, 16, 47.	3.8	23
56	Extracellular nanovesicles released from the commensal yeast <i>Malassezia sympodialis</i> are enriched in allergens and interact with cells in human skin. <i>Scientific Reports</i> , 2018, 8, 9182.	3.3	59
57	Optimizing Analytical Depth and Cost Efficiency of IEF-LC/MS Proteomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 272-281.	3.0	0
58	Discrimination of pancreatic cancer and pancreatitis by LC-MS metabolomics. <i>Metabolomics</i> , 2017, 13, 61.	3.0	42
59	Comparative proteomics reveals signature metabolisms of exponentially growing and stationary phase marine bacteria. <i>Environmental Microbiology</i> , 2017, 19, 2301-2319.	3.8	30
60	Tuning Metabolome Coverage in Reversed Phase LC-MS Metabolomics of MeOH Extracted Samples Using the Reconstitution Solvent Composition. <i>Analytical Chemistry</i> , 2017, 89, 7356-7364.	6.5	29
61	Female mice lacking <i>Pald1</i> exhibit endothelial cell apoptosis and emphysema. <i>Scientific Reports</i> , 2017, 7, 15453.	3.3	12
62	Isoelectric point-based fractionation by HiRIEF coupled to LC-MS allows for in-depth quantitative analysis of the phosphoproteome. <i>Scientific Reports</i> , 2017, 7, 4513.	3.3	21
63	A multi-step peptidolytic cascade for amino acid recovery in chloroplasts. <i>Nature Chemical Biology</i> , 2017, 13, 15-17.	8.0	24
64	Silencing <i>FLI</i> or targeting <i>CD13/ANPEP</i> lead to dephosphorylation of <i>EPHA2</i> , a mediator of <i>BRAF</i> inhibitor resistance, and induce growth arrest or apoptosis in melanoma cells. <i>Cell Death and Disease</i> , 2017, 8, e3029-e3029.	6.3	35
65	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx006.	14.5	47
66	Tartrate-resistant acid phosphatase (TRAP/ACP5) promotes metastasis-related properties via $TGF\beta 2/T\beta R$ and <i>CD44</i> in MDA-MB-231 breast cancer cells. <i>BMC Cancer</i> , 2017, 17, 650.	2.6	28
67	Identification of the <i>PAK4</i> interactome reveals <i>PAK4</i> phosphorylation of <i>N-WASP</i> and promotion of <i>Arp2/3</i> -dependent actin polymerization. <i>Oncotarget</i> , 2017, 8, 77061-77074.	1.8	23
68	Genetic and epigenetic background and protein expression profiles in relation to telomerase activation in medullary thyroid carcinoma. <i>Oncotarget</i> , 2016, 7, 21332-21346.	1.8	37
69	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. <i>Nucleic Acids Research</i> , 2016, 44, 6756-6769.	14.5	15
70	Phenotypic Modulation of Smooth Muscle Cells in Atherosclerosis Is Associated With Downregulation of <i>LMOD1</i> , <i>SYNPO2</i> , <i>PDLIM7</i> , <i>PLN</i> , and <i>SYNM</i> . <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1947-1961.	2.4	64
71	Comprehensive Proteomic Analysis of Mesenchymal Stem Cell Exosomes Reveals Modulation of Angiogenesis via Nuclear Factor-KappaB Signaling. <i>Stem Cells</i> , 2016, 34, 601-613.	3.2	407
72	Cells release subpopulations of exosomes with distinct molecular and biological properties. <i>Scientific Reports</i> , 2016, 6, 22519.	3.3	728

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73	Proteomics Suggests a Role for APC-Survivin in Response to Somatostatin Analog Treatment of Neuroendocrine Tumors. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 3616-3627.	3.6	10
74	Mesenchymal state of intimal cells may explain higher propensity to ascending aortic aneurysm in bicuspid aortic valves. <i>Scientific Reports</i> , 2016, 6, 35712.	3.3	36
75	Multi-level omics analysis in a murine model of dystrophin loss and therapeutic restoration. <i>Human Molecular Genetics</i> , 2015, 24, 6756-6768.	2.9	42
76	Identifying and Assessing Interesting Subgroups in a Heterogeneous Population. <i>BioMed Research International</i> , 2015, 2015, 1-13.	1.9	3
77	RIFINs are adhesins implicated in severe <i>Plasmodium falciparum</i> malaria. <i>Nature Medicine</i> , 2015, 21, 314-317.	30.7	166
78	Secretome protein signature of human gastrointestinal stromal tumor cells. <i>Experimental Cell Research</i> , 2015, 336, 158-170.	2.6	6
79	Structural Basis for Oxygen Activation at a Heterodinuclear Manganese/Iron Cofactor. <i>Journal of Biological Chemistry</i> , 2015, 290, 25254-25272.	3.4	29
80	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	17.5	140
81	Ultrafiltration with size-exclusion liquid chromatography for high yield isolation of extracellular vesicles preserving intact biophysical and functional properties. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2015, 11, 879-883.	3.3	487
82	Proteomics profiling identify CAPS as a potential predictive marker of tamoxifen resistance in estrogen receptor positive breast cancer. <i>Clinical Proteomics</i> , 2015, 12, 8.	2.1	31
83	Rewired Metabolism in Drug-resistant Leukemia Cells. <i>Journal of Biological Chemistry</i> , 2015, 290, 8348-8359.	3.4	63
84	In Vivo Effects of Mesenchymal Stromal Cells in Two Patients With Severe Acute Respiratory Distress Syndrome. <i>Stem Cells Translational Medicine</i> , 2015, 4, 1199-1213.	3.3	131
85	Differential Protein Expression Profiles of Cyst Fluid from Papillary Thyroid Carcinoma and Benign Thyroid Lesions. <i>PLoS ONE</i> , 2015, 10, e0126472.	2.5	22
86	Proteomics Analysis Reveals Distinct Corona Composition on Magnetic Nanoparticles with Different Surface Coatings: Implications for Interactions with Primary Human Macrophages. <i>PLoS ONE</i> , 2015, 10, e0129008.	2.5	61
87	Serum-free culture alters the quantity and protein composition of neuroblastoma-derived extracellular vesicles. <i>Journal of Extracellular Vesicles</i> , 2015, 4, 26883.	12.2	131
88	SpliceVista, a Tool for Splice Variant Identification and Visualization in Shotgun Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1552-1562.	3.8	28
89	Mass spectrometry-based plasma proteomics: state of the art and future outlook. <i>Expert Review of Proteomics</i> , 2014, 11, 431-448.	3.0	58
90	Optimizing analytical depth and cost efficiency of IEF-LC/MS proteomics. , 2014, , .		0

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91	Proteome Screening of Pleural Effusions Identifies Galectin 1 as a Diagnostic Biomarker and Highlights Several Prognostic Biomarkers for Malignant Mesothelioma. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 701-715.	3.8	42
92	Quantitative accuracy in mass spectrometry based proteomics of complex samples: The impact of labeling and precursor interference. <i>Journal of Proteomics</i> , 2014, 96, 133-144.	2.4	82
93	HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics. <i>Nature Methods</i> , 2014, 11, 59-62.	19.0	222
94	Immunoproteomics Using Polyclonal Antibodies and Stable Isotope- ¹⁵ N-labeled Affinity-purified Recombinant Proteins. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1611-1624.	3.8	27
95	Investigating the Applicability of Antibodies Generated within the Human Protein Atlas as Capture Agents in Immunoenrichment Coupled to Mass Spectrometry. <i>Journal of Proteome Research</i> , 2014, 13, 4424-4435.	3.7	7
96	Differentially Expressed Proteins in Malignant and Benign Adrenocortical Tumors. <i>PLoS ONE</i> , 2014, 9, e87951.	2.5	18
97	Quantitative Proteomics Profiling of Primary Lung Adenocarcinoma Tumors Reveals Functional Perturbations in Tumor Metabolism. <i>Journal of Proteome Research</i> , 2013, 12, 3934-3943.	3.7	40
98	Direct observation of structurally encoded metal discrimination and ether bond formation in a heterodinuclear metalloprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17189-17194.	7.1	49
99	Retinoic acid receptor alpha is associated with tamoxifen resistance in breast cancer. <i>Nature Communications</i> , 2013, 4, 2175.	12.8	53
100	A Novel Prefractionation Method Combining Protein and Peptide Isoelectric Focusing in Immobilized pH Gradient Strips. <i>Journal of Proteome Research</i> , 2013, 12, 1014-1019.	3.7	17
101	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	4.1	118
102	Mammalian Target of Rapamycin (mTor) Mediates Tau Protein Dyshomeostasis. <i>Journal of Biological Chemistry</i> , 2013, 288, 15556-15570.	3.4	110
103	Defining, Comparing, and Improving iTRAQ Quantification in Mass Spectrometry Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2021-2031.	3.8	53
104	A Combined Proteomic and Transcriptomic Approach Shows Diverging Molecular Mechanisms in Thoracic Aortic Aneurysm Development in Patients with Tricuspid- And Bicuspid Aortic Valve. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 407-425.	3.8	43
105	Organellar oligopeptidase (OOP) provides a complementary pathway for targeting peptide degradation in mitochondria and chloroplasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3761-9.	7.1	50
106	Selectivity analysis of single binder assays used in plasma protein profiling. <i>Proteomics</i> , 2013, 13, 3406-3410.	2.2	15
107	MYC inhibition induces metabolic changes leading to accumulation of lipid droplets in tumor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10258-10263.	7.1	194
108	A10.23-Stratification of SLE Patients for Improved Diagnosis and Treatment. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, A80.2-A80.	0.9	0

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109	Thapsigargin downregulates protein levels of GRP78/BiP in INS1E cells. <i>Journal of Cellular Biochemistry</i> , 2012, 113, 1635-1644.	2.6	19
110	Proteomic profiling of follicular and papillary thyroid tumors. <i>European Journal of Endocrinology</i> , 2012, 166, 657-667.	3.7	48
111	Tumor Proteomics by Multivariate Analysis on Individual Pathway Data for Characterization of Vulvar Cancer Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M112.016998-1-M112.016998-14.	3.8	83
112	Systems biology of SLE: biochemical characterisation of subgroups within sle for improved diagnosis and treatment. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, A12.2-A12.	0.9	1
113	Proteomic screen reveals Fbw7 as a modulator of the NF- κ B pathway. <i>Nature Communications</i> , 2012, 3, 976.	12.8	82
114	In vitro oxidative inactivation of human presequence protease (hPreP). <i>Free Radical Biology and Medicine</i> , 2012, 53, 2188-2195.	2.9	23
115	Tumour suppressor p16 ^{INK4a} favours decrease in N-glycan/cell surface sialylation by downregulation of enzymes in sialic acid biosynthesis in tandem in a pancreatic carcinoma model. <i>FEBS Journal</i> , 2012, 279, 4062-4080.	4.7	108
116	Systematic Analysis of Native Membrane Protein Complexes in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2011, 10, 1848-1859.	3.7	67
117	Design of a peptide-based vector, PepFect6, for efficient delivery of siRNA in cell culture and systemically in vivo. <i>Nucleic Acids Research</i> , 2011, 39, 3972-3987.	14.5	262
118	Phosphoproteomic Profiling of NSCLC Cells Reveals that Ephrin B3 Regulates Pro-survival Signaling through Akt1-Mediated Phosphorylation of the EphA2 Receptor. <i>Journal of Proteome Research</i> , 2011, 10, 2566-2578.	3.7	32
119	Identification of Chromatophore Membrane Protein Complexes Formed under Different Nitrogen Availability Conditions in <i>Rhodospirillum rubrum</i> . <i>Journal of Proteome Research</i> , 2011, 10, 2703-2714.	3.7	12
120	Diagnostic and prognostic role of plasma levels of two forms of cytokeratin 18 in patients with non-small-cell lung cancer. <i>European Journal of Cancer</i> , 2011, 47, 131-137.	2.8	38
121	Vascular endothelial growth factor receptor 2 and downstream p38 mitogen-activated protein kinase are possible candidate markers of intrinsic resistance to adjuvant endocrine treatment in steroid receptor positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 125, 457-465.	2.5	19
122	Observed peptide pI and retention time shifts as a result of post-translational modifications in multidimensional separations using narrow-range IPG-IEF. <i>Amino Acids</i> , 2011, 40, 697-711.	2.7	27
123	Penicillin-binding protein 5 can form a homooligomeric complex in the inner membrane of <i>Escherichia coli</i> . <i>Protein Science</i> , 2011, 20, 1520-1529.	7.6	5
124	Enhanced Information Output From Shotgun Proteomics Data by Protein Quantification and Peptide Quality Control (PQPQ). <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010264.	3.8	28
125	A novel method for sample preparation of fresh lung cancer tissue for proteomics analysis by tumor cell enrichment and removal of blood contaminants. <i>Proteome Science</i> , 2010, 8, 9.	1.7	15
126	Lung cancer proteomics, clinical and technological considerations. <i>Journal of Proteomics</i> , 2010, 73, 1851-1863.	2.4	35

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127	Proteomic Study of Thyroid Tumors Reveals Frequent Up-Regulation of the Ca ²⁺ -Binding Protein S100A6 in Papillary Thyroid Carcinoma. <i>Thyroid</i> , 2010, 20, 1067-1076.	4.5	32
128	N ^ε -Tosyl-L-phenylalanine Chloromethyl Ketone Induces Caspase-dependent Apoptosis in Transformed Human B Cell Lines with Transcriptional Down-regulation of Anti-apoptotic Hs1-associated Protein X-1. <i>Journal of Biological Chemistry</i> , 2009, 284, 27827-27837.	3.4	26
129	Proteomics and Pathway Analysis Identifies JNK Signaling as Critical for High Linear Energy Transfer Radiation-induced Apoptosis in Non-small Lung Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1117-1129.	3.8	20
130	Affinity prefractionation for MS-based plasma proteomics. <i>Proteomics</i> , 2009, 9, 1420-1427.	2.2	86
131	Use of narrow range peptide IEF to improve detection of lung adenocarcinoma markers in plasma and pleural effusion. <i>Proteomics</i> , 2009, 9, 3414-3424.	2.2	46
132	Robustness and accuracy of high speed LC-MS separations for global peptide quantitation and biomarker discovery. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 1306-1316.	2.3	10
133	Tumor expression of S100A6 correlates with survival of patients with stage I non-small-cell lung cancer. <i>Lung Cancer</i> , 2009, 63, 410-417.	2.0	52
134	Quantitative membrane proteomics applying narrow range peptide isoelectric focusing for studies of small cell lung cancer resistance mechanisms. <i>Proteomics</i> , 2008, 8, 3008-3018.	2.2	72
135	Multiple Ionization Mass Spectrometry Strategy Used To Reveal the Complexity of Metabolomics. <i>Analytical Chemistry</i> , 2008, 80, 421-429.	6.5	182
136	Evaluation of Three Principally Different Intact Protein Prefractionation Methods for Plasma Biomarker Discovery. <i>Journal of Proteome Research</i> , 2008, 7, 2712-2722.	3.7	46
137	Proteomic Data Analysis Workflow for Discovery of Candidate Biomarker Peaks Predictive of Clinical Outcome for Patients with Acute Myeloid Leukemia. <i>Journal of Proteome Research</i> , 2008, 7, 2332-2341.	3.7	22
138	Up-regulation, Modification, and Translocation of S100A6 Induced by Exposure to Ionizing Radiation Revealed by Proteomics Profiling. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2122-2131.	3.8	58
139	Proteomics in clinical prostate research. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1058-1065.	1.6	5
140	iTRAQ compatibility of peptide immobilized pH gradient isoelectric focusing. <i>Proteomics</i> , 2007, 7, 1746-1752.	2.2	44
141	Pre-fractionation of archival frozen tumours for proteomics applications. <i>Journal of Biotechnology</i> , 2006, 126, 582-586.	3.8	10
142	p53 is involved in clearance of ionizing radiation-induced RAD51 foci in a human colon cancer cell line. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 1211-1217.	2.1	13
143	Annotated regions of significance of SELDI-TOF-MS spectra for detecting protein biomarkers. <i>Proteomics</i> , 2006, 6, 6124-6133.	2.2	10
144	Finding regions of significance in SELDI measurements for identifying protein biomarkers. <i>Bioinformatics</i> , 2006, 22, 1515-1523.	4.1	39

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145	The binding specificity and affinity determinants of family 1 and family 3 cellulose binding modules. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 484-489.	7.1	323
146	Engineering of staphylococcal surfaces for biotechnological applications. Journal of Biotechnology, 2002, 96, 67-78.	3.8	20
147	Directed immobilization of recombinant staphylococci on cotton fibers by functional display of a fungal cellulose-binding domain. FEMS Microbiology Letters, 2001, 195, 197-204.	1.8	27
148	Trichoderma reesei cellobiohydrolase I with an endoglucanase cellulose-binding domain: action on bacterial microcrystalline cellulose. Journal of Biotechnology, 1997, 57, 49-57.	3.8	66
149	SubCellBarCode: integrated workflow for robust spatial proteomics by mass spectrometry. Nature Protocols, 0, , .	12.0	0