

# David Fenyo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/23652/publications.pdf>

Version: 2024-02-01

187  
papers

18,134  
citations

22153

59  
h-index

16650

123  
g-index

227  
all docs

227  
docs citations

227  
times ranked

24830  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Learning and Pathomics Analyses Reveal Cell Nuclei as Important Features for Mutation Prediction of BRAF-Mutated Melanomas. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1650-1658.e6.	0.7	22
2	Deep Learning and Its Applications in Computational Pathology. <i>BioMedInformatics</i> , 2022, 2, 159-168.	2.0	7
3	Predicting and Visualizing STK11 Mutation in Lung Adenocarcinoma Histopathology Slides Using Deep Learning. <i>BioMedInformatics</i> , 2022, 2, 101-105.	2.0	3
4	LINE-1 expression in cancer correlates with p53 mutation, copy number alteration, and S phase checkpoint. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	36
5	USP1-trapping lesions as a source of DNA replication stress and genomic instability. <i>Nature Communications</i> , 2022, 13, 1740.	12.8	15
6	Prediction of Maternal Hemorrhage Using Machine Learning: Retrospective Cohort Study. <i>Journal of Medical Internet Research</i> , 2022, 24, e34108.	4.3	3
7	When blockchain meets artificial intelligence: An application to cancer histopathology. <i>Cell Reports Medicine</i> , 2022, 3, 100666.	6.5	0
8	Dissecting the Structural Dynamics of the Nuclear Pore Complex. <i>Molecular Cell</i> , 2021, 81, 153-165.e7.	9.7	31
9	Structural and Functional Characterization of a Na <sup>v</sup> 1.5-Mitochondrial Couplon. <i>Circulation Research</i> , 2021, 128, 419-432.	4.5	15
10	Monitoring genome-wide replication fork directionality by Okazaki fragment sequencing in mammalian cells. <i>Nature Protocols</i> , 2021, 16, 1193-1218.	12.0	5
11	RIP-seq reveals LINE-1 ORF1p association with p-body enriched mRNAs. <i>Mobile DNA</i> , 2021, 12, 5.	3.6	20
12	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
13	Discovery of Protein Modifications Using Differential Tandem Mass Spectrometry Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 1835-1848.	3.7	13
14	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
15	CRL4AMBRA1 is a master regulator of D-type cyclins. <i>Nature</i> , 2021, 592, 789-793.	27.8	78
16	Spatially interacting phosphorylation sites and mutations in cancer. <i>Nature Communications</i> , 2021, 12, 2313.	12.8	12
17	Diversity of Functionally Distinct Clonal Sets of Human Conventional Memory B Cells That Bind Staphylococcal Protein A. <i>Frontiers in Immunology</i> , 2021, 12, 662782.	4.8	6
18	A predictive model for vertebrate bone identification from collagen using proteomic mass spectrometry. <i>Scientific Reports</i> , 2021, 11, 10900.	3.3	4

#	ARTICLE	IF	CITATIONS
19	Adenosine A2A receptor null chondrocyte transcriptome resembles that of human osteoarthritic chondrocytes. <i>Purinergic Signalling</i> , 2021, 17, 439-448.	2.2	3
20	BlackSheep: A Bioconductor and Bioconda Package for Differential Extreme Value Analysis. <i>Journal of Proteome Research</i> , 2021, 20, 3767-3773.	3.7	6
21	The human melanoma proteome atlasâ€™ Defining the molecular pathology. <i>Clinical and Translational Medicine</i> , 2021, 11, e473.	4.0	14
22	The Human Melanoma Proteome Atlasâ€™ Complementing the melanoma transcriptome. <i>Clinical and Translational Medicine</i> , 2021, 11, e451.	4.0	20
23	Predictive Modeling of Morbidity and Mortality in Patients Hospitalized With COVID-19 and its Clinical Implications: Algorithm Development and Interpretation. <i>Journal of Medical Internet Research</i> , 2021, 23, e29514.	4.3	14
24	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
25	The role of retrotransposable elements in ageing and age-associated diseases. <i>Nature</i> , 2021, 596, 43-53.	27.8	156
26	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
27	Predicting endometrial cancer subtypes and molecular features from histopathology images using multi-resolution deep learning models. <i>Cell Reports Medicine</i> , 2021, 2, 100400.	6.5	50
28	511â€™...Disease flares in lupus are concordant with <i>Ruminococcus Blautia Gnavus</i> blooms arising within unstable gut microbiota communities. , 2021, , .		0
29	Highly synergistic combinations of nanobodies that target SARS-CoV-2 and are resistant to escape. <i>ELife</i> , 2021, 10, .	6.0	36
30	L1EM: a tool for accurate locus specific LINE-1 RNA quantification. <i>Bioinformatics</i> , 2020, 36, 1167-1173.	4.1	31
31	LINE-1 ORF2p expression is nearly imperceptible in human cancers. <i>Mobile DNA</i> , 2020, 11, 1.	3.6	51
32	SINGLE CELL TIPSEQ, A NEW METHOD TO MAP LINE-1 INSERTIONS, PROVIDES INFORMATION ABOUT SUB CHROMOSOMAL GENETIC VARIATION IN HUMAN EMBRYOS. <i>Fertility and Sterility</i> , 2020, 114, e524.	1.0	0
33	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
34	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
35	Intraarticular injection of liposomal adenosine reduces cartilage damage in established murine and rat models of osteoarthritis. <i>Scientific Reports</i> , 2020, 10, 13477.	3.3	18
36	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	6.2	19

#	ARTICLE	IF	CITATIONS
37	Affinity proteomic dissection of the human nuclear cap-binding complex interactome. <i>Nucleic Acids Research</i> , 2020, 48, 10456-10469.	14.5	18
38	Distinct Features of Human Myeloid Cell Cytokine Response Profiles Identify Neutrophil Activation by Cytokines as a Prognostic Feature during Tuberculosis and Cancer. <i>Journal of Immunology</i> , 2020, 204, 3389-3399.	0.8	4
39	Clinical decision support tool and rapid point-of-care platform for determining disease severity in patients with COVID-19. <i>Lab on A Chip</i> , 2020, 20, 2075-2085.	6.0	82
40	Human transposon insertion profiling by sequencing (TIPseq) to map LINE-1 insertions in single cells. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190335.	4.0	6
41	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
42	Cell fitness screens reveal a conflict between LINE-1 retrotransposition and DNA replication. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 168-178.	8.2	74
43	BRCA1 and S phase DNA repair pathways restrict LINE-1 retrotransposition in human cells. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 179-191.	8.2	60
44	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
45	TranspoScope: interactive visualization of retrotransposon insertions. <i>Bioinformatics</i> , 2020, 36, 3877-3878.	4.1	0
46	Phylogenetic debugging of a complete human biosynthetic pathway transplanted into yeast. <i>Nucleic Acids Research</i> , 2020, 48, 486-499.	14.5	11
47	Abstract 6580: Proteogenomic characterization of endometrial carcinoma. <i>Cancer Research</i> , 2020, 80, 6580-6580.	0.9	7
48	Managing COVID-19 With a Clinical Decision Support Tool in a Community Health Network: Algorithm Development and Validation. <i>Journal of Medical Internet Research</i> , 2020, 22, e22033.	4.3	33
49	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1893-1898.	3.8	106
50	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
51	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	3.8	14
52	Extracting Pathway-level Signatures from Proteogenomic Data in Breast Cancer Using Independent Component Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S169-S182.	3.8	15
53	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
54	Transposon insertion profiling by sequencing (TIPseq) for mapping LINE-1 insertions in the human genome. <i>Mobile DNA</i> , 2019, 10, 8.	3.6	22

#	ARTICLE	IF	CITATIONS
55	Comprehensive Scanning Mutagenesis of Human Retrotransposon LINE-1 Identifies Motifs Essential for Function. <i>Genetics</i> , 2019, 213, 1401-1414.	2.9	22
56	Informatics Approaches to Forensic Body Fluid Identification by Proteomic Mass Spectrometry. <i>ACS Symposium Series</i> , 2019, , 81-90.	0.5	1
57	The Hidden Story of Heterogeneous B-raf V600E Mutation Quantitative Protein Expression in Metastatic Melanoma—Association with Clinical Outcome and Tumor Phenotypes. <i>Cancers</i> , 2019, 11, 1981.	3.7	16
58	Transcription shapes DNA replication initiation and termination in human cells. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 67-77.	8.2	118
59	Quantitative Mass Spectrometry to Interrogate Proteomic Heterogeneity in Metastatic Lung Adenocarcinoma and Validate a Novel Somatic Mutation CDK12-G879V. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 622-641.	3.8	15
60	Mass Spectrometry—Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. <i>Cancer Research</i> , 2018, 78, 2732-2746.	0.9	52
61	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
62	Large Scale Identification of Variant Proteins in Glioma Stem Cells. <i>ACS Chemical Neuroscience</i> , 2018, 9, 73-79.	3.5	12
63	Human Memory B Cells Targeting <i>Staphylococcus aureus</i> Exotoxins Are Prevalent with Skin and Soft Tissue Infection. <i>MBio</i> , 2018, 9, .	4.1	27
64	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. <i>Nature Methods</i> , 2018, 15, 330-338.	19.0	58
65	Macrophage-derived netrin-1 promotes abdominal aortic aneurysm formation by activating MMP3 in vascular smooth muscle cells. <i>Nature Communications</i> , 2018, 9, 5022.	12.8	109
66	Spatiotemporal dynamics of homologous recombination repair at single collapsed replication forks. <i>Nature Communications</i> , 2018, 9, 3882.	12.8	46
67	Classification and mutation prediction from non—small cell lung cancer histopathology images using deep learning. <i>Nature Medicine</i> , 2018, 24, 1559-1567.	30.7	1,768
68	Transcription factor profiling reveals molecular choreography and key regulators of human retrotransposon expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5526-E5535.	7.1	77
69	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018, 7, .	6.0	63
70	LINE-1 protein localization and functional dynamics during the cell cycle. <i>ELife</i> , 2018, 7, .	6.0	99
71	UXT is required for spermatogenesis in mice. <i>PLoS ONE</i> , 2018, 13, e0195747.	2.5	5
72	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018, 19, 12.	8.8	21

#	ARTICLE	IF	CITATIONS
73	Abstract 5309: Determining EGFR and STK11 mutational status in lung adenocarcinoma histopathology images using deep learning. , 2018, , .		2
74	The ULK1-FBXW5-SEC23B nexus controls autophagy. <i>ELife</i> , 2018, 7, .	6.0	63
75	Proteogenomics from a bioinformatics angle: A growing field. <i>Mass Spectrometry Reviews</i> , 2017, 36, 584-599.	5.4	65
76	Human transposon insertion profiling: Analysis, visualization and identification of somatic LINE-1 insertions in ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E733-E740.	7.1	86
77	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. <i>Science</i> , 2017, 355, .	12.6	184
78	Low escape-rate genome safeguards with minimal molecular perturbation of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1470-E1479.	7.1	26
79	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	3.8	130
80	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. <i>Genome Research</i> , 2017, 27, 1450-1459.	5.5	15
81	A Systems Biology Approach Identifies FUT8 as a Driver of Melanoma Metastasis. <i>Cancer Cell</i> , 2017, 31, 804-819.e7.	16.8	233
82	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	12.8	112
83	Adaptive Multiview Nonnegative Matrix Factorization Algorithm for Integration of Multimodal Biomedical Data. <i>Cancer Informatics</i> , 2017, 16, 117693511772572.	1.9	6
84	Breast tumors educate the proteome of stromal tissue in an individualized but coordinated manner. <i>Science Signaling</i> , 2017, 10, .	3.6	25
85	A Method for Quantifying Molecular Interactions Using Stochastic Modelling and Super-Resolution Microscopy. <i>Scientific Reports</i> , 2017, 7, 14882.	3.3	28
86	Endothelium-Independent Primitive Myxoid Vascularization Creates Invertebrate-Like Channels to Maintain Blood Supply in Optic Gliomas. <i>American Journal of Pathology</i> , 2017, 187, 1867-1878.	3.8	4
87	[O1â€“14â€“04]: RAGE AND DIAPHâ€“1 REGULATE CRITICAL PHENOTYPES OF MICROGLIA IN HEALTHY AGING AND ALZHEIMER'S DISEASE. <i>Alzheimer's and Dementia</i> , 2017, 13, P229.	0.8	0
88	Single Molecule Localization Microscopy of DNA Damage Response Pathways in Cancer.. <i>Microscopy and Microanalysis</i> , 2016, 22, 1016-1017.	0.4	4
89	Somatic retrotransposition is infrequent in glioblastomas. <i>Mobile DNA</i> , 2016, 7, 22.	3.6	17
90	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	27.8	1,384

#	ARTICLE	IF	CITATIONS
91	Next Generation Sequencing Data and Proteogenomics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 11-19.	1.6	6
92	OpenSlice: Quantitative data sharing from HyperPeaks to global ion chromatograms (GICs). <i>Proteomics</i> , 2016, 16, 2495-2501.	2.2	1
93	Nanoscale visualization of functional adhesion/excitability nodes at the intercalated disc. <i>Nature Communications</i> , 2016, 7, 10342.	12.8	76
94	Cyclin F-Mediated Degradation of SLBP Limits H2A.X Accumulation and Apoptosis upon Genotoxic Stress in G2. <i>Molecular Cell</i> , 2016, 64, 507-519.	9.7	64
95	HIV host interactome revealed directly from infected cells. <i>Nature Microbiology</i> , 2016, 1, 16068.	13.3	49
96	Fluorescence ImmunoPrecipitation (FLIP): a Novel Assay for High-Throughput IP. <i>Biological Procedures Online</i> , 2016, 18, 16.	2.9	6
97	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
98	Optimizing selection of large animals for antibody production by screening immune response to standard vaccines. <i>Journal of Immunological Methods</i> , 2016, 430, 56-60.	1.4	17
99	Selenocysteine: Wherefore Art Thou?. <i>Journal of Proteome Research</i> , 2016, 15, 677-678.	3.7	4
100	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1060-1071.	3.8	104
101	PGx: Putting Peptides to BED. <i>Journal of Proteome Research</i> , 2016, 15, 795-799.	3.7	20
102	g2pDB: A Database Mapping Protein Post-Translational Modifications to Genomic Coordinates. <i>Journal of Proteome Research</i> , 2016, 15, 983-990.	3.7	5
103	Separable roles for <i>Mycobacterium tuberculosis</i> ESX-3 effectors in iron acquisition and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E348-57.	7.1	166
104	Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 45-56.	3.8	68
105	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016, 1410, 223-236.	0.9	33
106	A Complex Systems Approach to Causal Discovery in Psychiatry. <i>PLoS ONE</i> , 2016, 11, e0151174.	2.5	29
107	Breast Cancer Prognostics Using Multi-Omics Data. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 52-9.	0.4	6
108	A First Step towards a Clinical Decision Support System for Post-traumatic Stress Disorders. <i>AMIA ... Annual Symposium proceedings</i> , 2016, 2016, 837-843.	0.2	3

#	ARTICLE	IF	CITATIONS
109	The GPMDB REST interface. <i>Bioinformatics</i> , 2015, 31, 2056-2058.	4.1	25
110	Rapid, optimized interactomic screening. <i>Nature Methods</i> , 2015, 12, 553-560.	19.0	68
111	Organization and dynamics of the nonhomologous end-joining machinery during DNA double-strand break repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2575-84.	7.1	142
112	Use of ENCODE Resources to Characterize Novel Proteoforms and Missing Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 603-608.	3.7	17
113	Abstract SY44-02: Proteogenomic and phosphoproteomic analysis of breast cancer. , 2015, , .		0
114	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014, 11, 703-704.	19.0	150
115	Pathway analysis and transcriptomics improve protein identification by shotgun proteomics from samples comprising small number of cells - a benchmarking study. <i>BMC Genomics</i> , 2014, 15, S1.	2.8	22
116	A robust pipeline for rapid production of versatile nanobody repertoires. <i>Nature Methods</i> , 2014, 11, 1253-1260.	19.0	391
117	Super-resolution imaging reveals that loss of the C-terminus of connexin43 limits microtubule plus-end capture and Nav1.5 localization at the intercalated disc. <i>Cardiovascular Research</i> , 2014, 104, 371-381.	3.8	110
118	Integrated Chromosome 19 Transcriptomic and Proteomic Data Sets Derived from Glioma Cancer Stem-Cell Lines. <i>Journal of Proteome Research</i> , 2014, 13, 191-199.	3.7	27
119	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1690-1704.	3.8	323
120	Developments in biobanking workflow standardization providing sample integrity and stability. <i>Journal of Proteomics</i> , 2013, 95, 38-45.	2.4	56
121	A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17. <i>Journal of Proteome Research</i> , 2013, 12, 45-57.	3.7	35
122	Chromosome 19 Annotations with Disease Speciation: A First Report from the Global Research Consortium. <i>Journal of Proteome Research</i> , 2013, 12, 135-150.	3.7	16
123	Atypical and classical memory B cells produce <i>Plasmodium falciparum</i> neutralizing antibodies. <i>Journal of Experimental Medicine</i> , 2013, 210, 389-399.	8.5	200
124	Comparative proteomic analysis of the ATP-sensitive K <sup>+</sup> channel complex in different tissue types. <i>Proteomics</i> , 2013, 13, 368-378.	2.2	16
125	Super-resolution fluorescence microscopy of the cardiac connexome reveals plakophilin-2 inside the connexin43 plaque. <i>Cardiovascular Research</i> , 2013, 100, 231-240.	3.8	67
126	Strategy for Identifying Dendritic Cell-Processed CD4 <sup>+</sup> T Cell Epitopes from the HIV Gag p24 Protein. <i>PLoS ONE</i> , 2012, 7, e41897.	2.5	7



#	ARTICLE	IF	CITATIONS
127	High-throughput, Single-step Purification of Affinity-tagged Protein Complexes. <i>FASEB Journal</i> , 2012, 26, .	0.5	0
128	Sequence and Structural Convergence of Broad and Potent HIV Antibodies That Mimic CD4 Binding. <i>Science</i> , 2011, 333, 1633-1637.	12.6	1,046
129	High-capacity ion trap coupled to a time-of-flight mass spectrometer for comprehensive linked scans with no scanning losses. <i>International Journal of Mass Spectrometry</i> , 2011, 301, 211-219.	1.5	5
130	Modeling Mass Spectrometry-Based Protein Analysis. <i>Methods in Molecular Biology</i> , 2011, 694, 109-117.	0.9	2
131	The Asia Oceania Human Proteome Organisation Membrane Proteomics Initiative. Preparation and characterisation of the carbonate-washed membrane standard. <i>Proteomics</i> , 2010, 10, 4142-4148.	2.2	26
132	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 242-254.	3.8	148
133	GINS motion reveals replication fork progression is remarkably uniform throughout the yeast genome. <i>Molecular Systems Biology</i> , 2010, 6, 353.	7.2	116
134	Protein Quantitation Using Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2010, 673, 211-222.	0.9	59
135	Mass Spectrometric Protein Identification Using the Global Proteome Machine. <i>Methods in Molecular Biology</i> , 2010, 673, 189-202.	0.9	50
136	Modeling Experimental Design for Proteomics. <i>Methods in Molecular Biology</i> , 2010, 673, 223-230.	0.9	6
137	Four histone variants mark the boundaries of polycistronic transcription units in <i>Trypanosoma brucei</i> . <i>Genes and Development</i> , 2009, 23, 1063-1076.	5.9	312
138	Rapid sensitive analysis of cysteine rich peptide venom components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6910-6915.	7.1	103
139	Evaluation of the Variation in Sample Preparation for Comparative Proteomics Using Stable Isotope Labeling by Amino Acids in Cell Culture. <i>Journal of Proteome Research</i> , 2009, 8, 1285-1292.	3.7	50
140	Informatics development: Challenges and solutions for MALDI mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2008, 27, 1-19.	5.4	16
141	Blue Native PAGE and Mass Spectrometry Analysis of Ephrin Stimulation-Dependent Protein-Protein Interactions in NG108-EphB2 Cells. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2008, , 3-22.	0.5	23
142	Rapid Isolation and Identification of Bacteriophage T4-Encoded Modifications of <i>Escherichia coli</i> RNA Polymerase: A Generic Method to Study Bacteriophage/Host Interactions. <i>Journal of Proteome Research</i> , 2008, 7, 1244-1250.	3.7	14
143	Screening for EphB Signaling Effectors Using SILAC with a Linear Ion Trap-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2008, 7, 4715-4726.	3.7	26
144	Validation of Endogenous Peptide Identifications Using a Database of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 3049-3053.	3.7	28

#	ARTICLE	IF	CITATIONS
145	Efficient Identification of Phosphorylation by Mass Spectrometric Phosphopeptide Fingerprinting. <i>Analytical Chemistry</i> , 2008, 80, 2419-2425.	6.5	15
146	Use of DNA Ladders for Reproducible Protein Fractionation by Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) for Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 678-686.	3.7	7
147	Neuropeptidomics Strategies for Specific and Sensitive Identification of Endogenous Peptides. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1188-1197.	3.8	47
148	An Automated Method for Scanning LC-MS Data Sets for Significant Peptides and Proteins, Including Quantitative Profiling and Interactive Confirmation. <i>Journal of Proteome Research</i> , 2007, 6, 2888-2895.	3.7	19
149	Determining the Overall Merit of Protein Identification Data Sets: $\rho$ -Diagrams and $\rho$ -Scores. <i>Journal of Proteome Research</i> , 2007, 6, 1997-2004.	3.7	12
150	MALDI Sample Preparation: the Ultra Thin Layer Method. <i>Journal of Visualized Experiments</i> , 2007, , 192.	0.3	21
151	Improving the success rate of proteome analysis by modeling protein-abundance distributions and experimental designs. <i>Nature Biotechnology</i> , 2007, 25, 651-655.	17.5	71
152	Using Annotated Peptide Mass Spectrum Libraries for Protein Identification. <i>Journal of Proteome Research</i> , 2006, 5, 1843-1849.	3.7	286
153	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. , 2006, , 289-315.		0
154	Detection of artifacts and peptide modifications in liquid chromatography/mass spectrometry data using two-dimensional signal intensity map data visualization. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1558-1562.	1.5	22
155	Optimizing search conditions for the mass fingerprint-based identification of proteins. <i>Proteomics</i> , 2006, 6, 2079-2085.	2.2	18
156	Reproducibility of LC-MS-based protein identification. <i>Journal of Experimental Botany</i> , 2006, 57, 1509-1514.	4.8	27
157	SwePep, a Database Designed for Endogenous Peptides and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 998-1005.	3.8	121
158	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. <i>Proteomics</i> , 2005, 5, 3475-3490.	2.2	332
159	Phosphotyrosine Signaling Networks in Epidermal Growth Factor Receptor Overexpressing Squamous Carcinoma Cells. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 356-376.	3.8	121
160	Protein Identification in Complex Mixtures. <i>Journal of Proteome Research</i> , 2005, 4, 387-393.	3.7	24
161	Chapter 13 Simulation as a tool for optimizing proteome analysis. <i>Comprehensive Analytical Chemistry</i> , 2005, 46, 523-534.	1.3	0
162	Finding Protein Sequences Using PROWL. <i>Current Protocols in Bioinformatics</i> , 2004, 7, Unit 13.2.	25.8	9

#	ARTICLE	IF	CITATIONS
163	The Statistical Significance of Protein Identification Results as a Function of the Number of Protein Sequences Searched. <i>Journal of Proteome Research</i> , 2004, 3, 979-982.	3.7	22
164	Probioty:â€‰ A Protein Identification Algorithm with Accurate Assignment of the Statistical Significance of the Results. <i>Journal of Proteome Research</i> , 2004, 3, 32-36.	3.7	49
165	A Method for Assessing the Statistical Significance of Mass Spectrometry-Based Protein Identifications Using General Scoring Schemes. <i>Analytical Chemistry</i> , 2003, 75, 768-774.	6.5	448
166	A Modular Cross-Linking Approach for Exploring Protein Interactions. <i>Journal of the American Chemical Society</i> , 2003, 125, 2416-2425.	13.7	189
167	Informatics and data management in proteomics. <i>Trends in Biotechnology</i> , 2002, 20, s35-s38.	9.3	31
168	RADARS, a bioinformatics solution that automates proteome mass spectral analysis, optimises protein identification, and archives data in a relational database. <i>Proteomics</i> , 2002, 2, 36-47.	2.2	208
169	A model of random mass-matching and its use for automated significance testing in mass spectrometric proteome analysis. <i>Proteomics</i> , 2002, 2, 262.	2.2	35
170	RADARS, a bioinformatics solution that automates proteome mass spectral analysis, optimises protein identification, and archives data in a relational database. <i>Proteomics</i> , 2002, 2, 36-47.	2.2	44
171	Identifying the proteome: software tools. <i>Current Opinion in Biotechnology</i> , 2000, 11, 391-395.	6.6	134
172	Database searching with mass-spectrometric information. <i>Trends in Biotechnology</i> , 2000, 18, 22-27.	9.3	4
173	A Statistical Basis for Testing the Significance of Mass Spectrometric Protein Identification Results. <i>Analytical Chemistry</i> , 2000, 72, 999-1005.	6.5	119
174	Protein indentification using mass spectrometric information. <i>Electrophoresis</i> , 1998, 19, 998-1005.	2.4	207
175	A Strategy for Rapid, High-Confidence Protein Identification. <i>Analytical Chemistry</i> , 1997, 69, 3995-4001.	6.5	98
176	Determinants for Escherichia coli RNA polymerase assembly within the Î² subunit. <i>Journal of Molecular Biology</i> , 1997, 270, 648-662.	4.2	36
177	Laser desorption mass spectrometry of synthetic multiporphyrin arrays. <i>Journal of Porphyrins and Phthalocyanines</i> , 1997, 1, 93-99.	0.8	22
178	Peer Reviewed: Internet-Based Analytical Chemistry Resources: A Model Project. <i>Analytical Chemistry</i> , 1996, 68, 721A-726A.	6.5	40
179	Domain Organization of the Escherichia coli RNA Polymerase Î² Subunit. <i>Journal of Molecular Biology</i> , 1996, 263, 637-647.	4.2	133
180	Structural and functional properties of region II-plus of the malaria circumsporozoite protein.. <i>Journal of Experimental Medicine</i> , 1994, 180, 297-306.	8.5	132

#	ARTICLE	IF	CITATIONS
181	Crystallization of Proliferating Cell Nuclear Antigen (PCNA) from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1994, 241, 265-268.	4.2	40
182	Formation of fullerenes in MeV-ion sputtering from organic solids. <i>Physical Review B</i> , 1993, 47, 7560-7567.	3.2	42
183	Computer experiments on molecular ejection from an amorphous solid: Comparison to an analytic continuum mechanical model. <i>Physical Review B</i> , 1992, 46, 5090-5099.	3.2	62
184	Formation of fullerenes in MeV ion track plasmas. <i>Chemical Physics Letters</i> , 1992, 191, 345-350.	2.6	42
185	The influence of ion flux on defect production in MeV proton-irradiated silicon. <i>Journal of Applied Physics</i> , 1991, 70, 3025-3030.	2.5	59
186	Molecular-dynamics study of electronic sputtering of large organic molecules. <i>Physical Review B</i> , 1990, 42, 1895-1902.	3.2	70
187	Sputtering by fast ions based on a sum of impulses. <i>Physical Review B</i> , 1989, 40, 49-53.	3.2	170