

Akhilesh Pandey

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2367467/publications.pdf>

Version: 2024-02-01

430
papers

52,589
citations

2101

100
h-index

1634

215
g-index

449
all docs

449
docs citations

449
times ranked

64465
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeted Detection of SARS-CoV-2 Nucleocapsid Sequence Variants by Mass Spectrometric Analysis of Tryptic Peptides. <i>Journal of Proteome Research</i> , 2022, 21, 142-150.	3.7	9
2	Preclinical evaluation of LCK as a novel therapeutic target in YAP-activated and FGFR2-altered cholangiocarcinoma.. <i>Journal of Clinical Oncology</i> , 2022, 40, 463-463.	1.6	1
3	Deciphering the Interactions of SARS-CoV-2 Proteins with Human Ion Channels Using Machine-Learning-Based Methods. <i>Pathogens</i> , 2022, 11, 259.	2.8	3
4	TMT-Based Multiplexed Quantitation of <i>N</i> -Glycopeptides Reveals Glycoproteome Remodeling Induced by Oncogenic Mutations. <i>ACS Omega</i> , 2022, 7, 11023-11032.	3.5	7
5	In Silico Analysis of Ion Channels and Their Correlation with Epithelial to Mesenchymal Transition in Breast Cancer. <i>Cancers</i> , 2022, 14, 1444.	3.7	6
6	Metallothionein immunohistochemistry has high sensitivity and specificity for detection of Wilson disease. <i>Modern Pathology</i> , 2022, 35, 946-955.	5.5	4
7	Comparison of anti-peptide and anti-protein antibody-based purification techniques for detection of SARS-CoV-2 by targeted LC-MS/MS. <i>Advances in Sample Preparation</i> , 2022, 2, 100018.	3.0	0
8	¹³ C ¹⁵ N: glucagon-based novel isotope dilution mass spectrometry method for measurement of glucagon metabolism in humans. <i>Clinical Proteomics</i> , 2022, 19, 16.	2.1	1
9	Machine Learning-Based Fragment Selection Improves the Performance of Qualitative PRM Assays. <i>Journal of Proteome Research</i> , 2022, 21, 2045-2054.	3.7	2
10	Neuronal activity induces glucosylceramide that is secreted via exosomes for lysosomal degradation in glia. <i>Science Advances</i> , 2022, 8, .	10.3	21
11	Development of a multiomics model for identification of predictive biomarkers for COVID-19 severity: a retrospective cohort study. <i>The Lancet Digital Health</i> , 2022, 4, e632-e645.	12.3	37
12	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021, 156, 988-1002.	3.9	32
13	Expanding the clinical and metabolic phenotype of DPM2 deficient congenital disorders of glycosylation. <i>Molecular Genetics and Metabolism</i> , 2021, 132, 27-37.	1.1	10
14	Mutation-Specific and Common Phosphotyrosine Signatures of <i>KRAS</i> G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021, 20, 670-683.	3.7	12
15	Persistently Elevated mTOR Complex 1-S6 Kinase 1 Disrupts DARPP-32-Dependent D1 Dopamine Receptor Signaling and Behaviors. <i>Biological Psychiatry</i> , 2021, 89, 1058-1072.	1.3	8
16	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100069.	3.8	21
17	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. <i>Indian Journal of Ophthalmology</i> , 2021, 69, 647.	1.1	7
18	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. <i>Molecular Omics</i> , 2021, 17, 939-947.	2.8	15

#	ARTICLE	IF	CITATIONS
19	Maternal serum lipidomics identifies lysophosphatidic acid as a predictor of small for gestational age neonates. <i>Molecular Omics</i> , 2021, 17, 956-966.	2.8	3
20	Integrated Proteomic and Phosphoproteomics Analysis of DKK3 Signaling Reveals Activated Kinase in the Most Aggressive Gallbladder Cancer. <i>Cells</i> , 2021, 10, 511.	4.1	9
21	Shukla-Vernon Syndrome: A Second Family with a Novel Variant in the BCORL1 Gene. <i>Genes</i> , 2021, 12, 452.	2.4	5
22	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. <i>Life Science Alliance</i> , 2021, 4, e202000774.	2.8	26
23	The mitochondrial carrier SFXN1 is critical for complex III integrity and cellular metabolism. <i>Cell Reports</i> , 2021, 34, 108869.	6.4	30
24	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021, 81, 2094-2111.e9.	9.7	17
25	Ethylmalonic encephalopathy ETHE1 p. D165H mutation alters the mitochondrial function in human skeletal muscle proteome. <i>Mitochondrion</i> , 2021, 58, 64-71.	3.4	4
26	Mitochondrial localization and moderated activity are key to murine erythroid enucleation. <i>Blood Advances</i> , 2021, 5, 2490-2504.	5.2	16
27	Mass Spectrometric Analysis of Urine from COVID-19 Patients for Detection of SARS-CoV-2 Viral Antigen and to Study Host Response. <i>Journal of Proteome Research</i> , 2021, 20, 3404-3413.	3.7	35
28	Complement and Coagulation Cascades are Potentially Involved in Dopaminergic Neurodegeneration in α -Synuclein-Based Mouse Models of Parkinson's Disease. <i>Journal of Proteome Research</i> , 2021, 20, 3428-3443.	3.7	21
29	Digging deeper into the immunopeptidome: characterization of post-translationally modified peptides presented by MHC I. <i>Journal of Proteins and Proteomics</i> , 2021, 12, 151-160.	1.5	8
30	Tyrosine Phosphoproteomics of Patient-Derived Xenografts Reveals Ephrin Type-B Receptor 4 Tyrosine Kinase as a Therapeutic Target in Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 3404.	3.7	2
31	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021, 69, 103465.	6.1	44
32	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021, 20, 4165-4175.	3.7	21
33	Analytical Sensitivity and Specificity of Four Point of Care Rapid Antigen Diagnostic Tests for SARS-CoV-2 Using Real-Time Quantitative PCR, Quantitative Droplet Digital PCR, and a Mass Spectrometric Antigen Assay as Comparator Methods. <i>Clinical Chemistry</i> , 2021, 67, 1545-1553.	3.2	22
34	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. <i>Cancers</i> , 2021, 13, 4234.	3.7	1
35	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. <i>Journal of Proteome Research</i> , 2021, 20, 4566-4577.	3.7	3
36	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. <i>Mitochondrion</i> , 2021, 60, 27-32.	3.4	2

#	ARTICLE	IF	CITATIONS
37	A pathway map of signaling events triggered upon SARS-CoV infection. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 595-600.	3.4	4
38	Acute Kidney Injury in Severe COVID-19 Has Similarities to Sepsis-Associated Kidney Injury. <i>Mayo Clinic Proceedings</i> , 2021, 96, 2561-2575.	3.0	41
39	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100134.	3.8	25
40	Very long-chain acyl-CoA synthetase 3 mediates onco-sphingolipid metabolism in malignant glioma. <i>Medical Research Archives</i> , 2021, 9, .	0.2	5
41	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021, 17, 454-463.	2.8	21
42	Reinspection of a Clinical Proteomics Tumor Analysis Consortium (CPTAC) Dataset with Cloud Computing Reveals Abundant Post-Translational Modifications and Protein Sequence Variants. <i>Cancers</i> , 2021, 13, 5034.	3.7	9
43	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021, 18, 25.	2.1	10
44	Sorbitol Is a Severity Biomarker for <scp>PMM2â€CDG</scp> with Therapeutic Implications. <i>Annals of Neurology</i> , 2021, 90, 887-900.	5.3	22
45	Automated data-driven mass spectrometry for improved analysis of lipids with dual dissociation techniques. <i>Journal of Mass Spectrometry and Advances in the Clinical Lab</i> , 2021, 22, 43-49.	2.4	5
46	Proteomic Signatures of Diffuse and Intestinal Subtypes of Gastric Cancer. <i>Cancers</i> , 2021, 13, 5930.	3.7	9
47	Exome sequencing reveals a novel splice site variant in HUWE1 gene in patients with suspected Say-Meyer syndrome. <i>European Journal of Medical Genetics</i> , 2020, 63, 103635.	1.3	14
48	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020, 34, 301-305.	7.2	10
49	Center of Mass Calculation in Combination with MS/MS Allows Robust Identification of Single Amino Acid Polymorphisms in Clinical Measurements of Insulin-Like Growth Factor-1. <i>Journal of Proteome Research</i> , 2020, 19, 186-193.	3.7	10
50	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020, 92, 14466-14475.	6.5	19
51	High-quality nuclear genome for <i>Sarcoptes scabiei</i> â€”A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	3.0	25
52	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
53	Is the Proteome of Bronchoalveolar Lavage Extracellular Vesicles a Marker of Advanced Lung Cancer?. <i>Cancers</i> , 2020, 12, 3450.	3.7	14
54	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. <i>Nature Communications</i> , 2020, 11, 4225.	12.8	47

#	ARTICLE	IF	CITATIONS
55	A Novel LINS1 Truncating Mutation in Autosomal Recessive Nonsyndromic Intellectual Disability. <i>Frontiers in Psychiatry</i> , 2020, 11, 354.	2.6	2
56	A Novel Missense Variant in PHF6 Gene Causing Batten-Jones-Forssman-Lehman Syndrome. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1403-1409.	2.3	8
57	Multiplexed Phosphoproteomic Study of Brain in Patients with Alzheimer's Disease and Age-Matched Cognitively Healthy Controls. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 216-227.	2.0	22
58	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 394-404.	2.8	8
59	Phosphoproteomic analysis identifies CLK1 as a novel therapeutic target in gastric cancer. <i>Gastric Cancer</i> , 2020, 23, 796-810.	5.3	26
60	Extra-cellular vesicles carry proteome of cancer hallmarks. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 398-436.	3.0	14
61	Surgery, Octreotide, Temozolomide, Bevacizumab, Radiotherapy, and Pegvisomant Treatment of an AIP Mutation-Positive Child. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 3539-3544.	3.6	41
62	Proteomic Analysis of <i>Plasmodium</i> Merozoites: The Link between Liver and Blood Stages in Malaria. <i>Journal of Proteome Research</i> , 2019, 18, 3404-3418.	3.7	29
63	A Novel Splice Site Mutation in IFNGR2 in Patients With Primary Immunodeficiency Exhibiting Susceptibility to Mycobacterial Diseases. <i>Frontiers in Immunology</i> , 2019, 10, 1964.	4.8	19
64	Multi-omics studies in cellular models of methylmalonic acidemia and propionic acidemia reveal dysregulation of serine metabolism. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 165538.	3.8	17
65	PIM1 kinase promotes gallbladder cancer cell proliferation via inhibition of proline-rich Akt substrate of 40 kDa (PRAS40). <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 163-177.	3.4	12
66	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 8453-8460.	6.5	7
67	Family-Based Next-Generation Sequencing Study Identifies an <i>IL2RG</i> Variant in an Infant with Primary Immunodeficiency. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 285-290.	2.0	2
68	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
69	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	2.2	16
70	Integrated Transcriptomic and Proteomic Analysis of Human Eccrine Sweat Glands Identifies Missing and Novel Proteins. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1382-1395.	3.8	25
71	PAX-SIX-EYA-DACH Network modulates GATA-FOG function in fly hematopoiesis and human erythropoiesis. <i>Development (Cambridge)</i> , 2019, 147, .	2.5	5
72	Dickkopf Homolog 3 (DKK3) Acts as a Potential Tumor Suppressor in Gallbladder Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1121.	2.8	18

#	ARTICLE	IF	CITATIONS
73	Mapping Keratoconus Molecular Substrates by Multiplexed High-Resolution Proteomics of Unpooled Corneas. OMICS A Journal of Integrative Biology, 2019, 23, 583-597.	2.0	19
74	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. Proteomics - Clinical Applications, 2019, 13, e1800105.	1.6	82
75	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. Journal of Clinical Investigation, 2019, 129, 4708-4723.	8.2	41
76	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. Proteomics, 2018, 18, e1700386.	2.2	13
77	Analysis of Cellular Tyrosine Phosphorylation via Chemical Rescue of Conditionally Active Abl Kinase. Biochemistry, 2018, 57, 1390-1398.	2.5	4
78	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. Journal of Proteome Research, 2018, 17, 759-769.	3.7	70
79	GBA1 deficiency negatively affects physiological α -synuclein tetramers and related multimers. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 798-803.	7.1	139
80	USP9X controls translation efficiency via deubiquitination of eukaryotic translation initiation factor 4A1. Nucleic Acids Research, 2018, 46, 823-839.	14.5	20
81	A network map of IL-33 signaling pathway. Journal of Cell Communication and Signaling, 2018, 12, 615-624.	3.4	90
82	Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3827-E3836.	7.1	122
83	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. Genome Research, 2018, 28, 25-36.	5.5	75
84	Targeting focal adhesion kinase overcomes erlotinib resistance in smoke induced lung cancer by altering phosphorylation of epidermal growth factor receptor. Oncoscience, 2018, 5, 21-38.	2.2	14
85	Ubiquilin 2 modulates ALS/FTD-linked FUS-RNA complex dynamics and stress granule formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11485-E11494.	7.1	100
86	Proteomic Analysis of the Human Anterior Pituitary Gland. OMICS A Journal of Integrative Biology, 2018, 22, 759-769.	2.0	23
87	CHES: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. Genome Biology, 2018, 19, 208.	8.8	263
88	Testican 1 (SPOCK1) and protein tyrosine phosphatase, receptor type S (PTPRS) show significant increase in saliva of tobacco users with oral cancer. Translational Research in Oral Oncology, 2018, 3, 2057178X1880053.	3.3	1
89	Phosphotyrosine profiling of human cerebrospinal fluid. Clinical Proteomics, 2018, 15, 29.	2.1	18
90	Integrated Stress Response and Decreased ECM in Cultured Stromal Cells From Keratoconus Corneas. , 2018, 59, 2977.		31

#	ARTICLE	IF	CITATIONS
91	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	3.8	12
92	Quantitative phosphoproteomic analysis reveals reciprocal activation of receptor tyrosine kinases between cancer epithelial cells and stromal fibroblasts. <i>Clinical Proteomics</i> , 2018, 15, 21.	2.1	15
93	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1700101.	1.6	15
94	A Next-Generation Sequencing-Based Molecular Approach to Characterize a Tick Vector in Lyme Disease. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 565-574.	2.0	2
95	Proteome-wide changes in primary skin keratinocytes exposed to diesel particulate extract—A role for antioxidants in skin health. <i>Journal of Dermatological Science</i> , 2018, 91, 239-249.	1.9	25
96	Identification of spleen tyrosine kinase as a potential therapeutic target for esophageal squamous cell carcinoma using reverse phase protein arrays. <i>Oncotarget</i> , 2018, 9, 18422-18434.	1.8	4
97	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	12.6	398
98	H3K4me3 induces allosteric conformational changes in the DNA-binding and catalytic regions of the V(D)J recombinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1904-1909.	7.1	24
99	Understanding Epstein-Barr Virus Life Cycle with Proteomics: A Temporal Analysis of Ubiquitination During Virus Reactivation. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 27-37.	2.0	9
100	Mass Spectrometry Reveals Respiratory Viral Infection Biomarkers. <i>EBioMedicine</i> , 2017, 18, 21-22.	6.1	0
101	Human adenine nucleotide translocases physically and functionally interact with respirasomes. <i>Molecular Biology of the Cell</i> , 2017, 28, 1489-1506.	2.1	37
102	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 295-303.	2.0	34
103	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017, 29, 14-23.	5.6	73
104	Quantitative Tyrosine Phosphoproteomics of Epidermal Growth Factor Receptor (EGFR) Tyrosine Kinase Inhibitor-treated Lung Adenocarcinoma Cells Reveals Potential Novel Biomarkers of Therapeutic Response. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 891-910.	3.8	42
105	Moving to Translational Proteomics. <i>Proteomics</i> , 2017, 17, 1770042.	2.2	0
106	Toward the human cellular microRNAome. <i>Genome Research</i> , 2017, 27, 1769-1781.	5.5	142
107	Mosquito-Borne Diseases and Omics: Tissue-Restricted Expression and Alternative Splicing Revealed by Transcriptome Profiling of <i>Anopheles stephensi</i> . <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 488-497.	2.0	23
108	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017, 27, 133-144.	5.5	60

#	ARTICLE	IF	CITATIONS
109	The non-receptor tyrosine kinase TNK2/ACK1 is a novel therapeutic target in triple negative breast cancer. <i>Oncotarget</i> , 2017, 8, 2971-2983.	1.8	42
110	Small molecule inhibitor screening identified HSP90 inhibitor 17-AAG as potential therapeutic agent for gallbladder cancer. <i>Oncotarget</i> , 2017, 8, 26169-26184.	1.8	21
111	Loss of C9orf72 Enhances Autophagic Activity via Deregulated mTOR and TFEB Signaling. <i>PLoS Genetics</i> , 2016, 12, e1006443.	3.5	154
112	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	2.2	106
113	A sequence upstream of canonical PDZ-binding motif within CFTR COOH-terminus enhances NHERF1 interaction. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2016, 311, L1170-L1182.	2.9	13
114	Unbiased identification of substrates of protein tyrosine phosphatase ptp β in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	4.6	16
115	PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2829-2838.	3.8	24
116	Identification of GAPDH on the surface of <i>Plasmodium</i> sporozoites as a new candidate for targeting malaria liver invasion. <i>Journal of Experimental Medicine</i> , 2016, 213, 2099-2112.	8.5	45
117	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2016, 13, 29.	2.1	30
118	How Does Chronic Cigarette Smoke Exposure Affect Human Skin? A Global Proteomics Study in Primary Human Keratinocytes. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 615-626.	2.0	26
119	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2016, 6, 36132.	3.3	36
120	Synovial fluid proteome in rheumatoid arthritis. <i>Clinical Proteomics</i> , 2016, 13, 12.	2.1	62
121	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
122	Long non-coding RNA expression in primary human monocytes. <i>Genomics</i> , 2016, 108, 37-45.	2.9	20
123	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 225-233.	3.4	21
124	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. <i>Cancer Biology and Therapy</i> , 2016, 17, 219-229.	3.4	25
125	A network map of Interleukin-10 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2016, 10, 61-67.	3.4	85
126	Chronic exposure to cigarette smoke leads to activation of p21 (RAC1)-activated kinase 6 (PAK6) in non-small cell lung cancer cells. <i>Oncotarget</i> , 2016, 7, 61229-61245.	1.8	45

#	ARTICLE	IF	CITATIONS
127	Macrophage migration inhibitory factor - a therapeutic target in gallbladder cancer. BMC Cancer, 2015, 15, 843.	2.6	33
128	A multi-omic analysis of human naïve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
129	Phosphoproteomic profiling of tumor tissues identifies HSP27 Ser82 phosphorylation as a robust marker of early ischemia. Scientific Reports, 2015, 5, 13660.	3.3	11
130	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. PLoS ONE, 2015, 10, e0143066.	2.5	87
131	Downregulation of S100 Calcium Binding Protein A9 in Esophageal Squamous Cell Carcinoma. Scientific World Journal, The, 2015, 2015, 1-10.	2.1	8
132	Comprehensive Proteomics Analysis of Glycosomes from <i>Leishmania donovani</i> . OMICS A Journal of Integrative Biology, 2015, 19, 157-170.	2.0	27
133	Quantitative phosphoproteomics reveals crosstalk between phosphorylation and O-GlcNAc in the DNA damage response pathway. Proteomics, 2015, 15, 591-607.	2.2	60
134	LC-MS-based serum metabolomic analysis reveals dysregulation of phosphatidylcholines in esophageal squamous cell carcinoma. Journal of Proteomics, 2015, 127, 96-102.	2.4	38
135	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous cell carcinoma. Proteomics, 2015, 15, 374-382.	2.2	38
136	Proteomics of Follicular Fluid From Women With Polycystic Ovary Syndrome Suggests Molecular Defects in Follicular Development. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 744-753.	3.6	109
137	A phosphoproteomic screen demonstrates differential dependence on HER3 for MAP kinase pathway activation by distinct PIK3CA mutations. Proteomics, 2015, 15, 318-326.	2.2	13
138	Inhibition of Spleen Tyrosine Kinase Potentiates Paclitaxel-Induced Cytotoxicity in Ovarian Cancer Cells by Stabilizing Microtubules. Cancer Cell, 2015, 28, 82-96.	16.8	125
139	Ablation of Dicer leads to widespread perturbation of signaling pathways. Biochemical and Biophysical Research Communications, 2015, 463, 389-394.	2.1	7
140	A knowledgebase resource for interleukin-17 family mediated signaling. Journal of Cell Communication and Signaling, 2015, 9, 291-296.	3.4	25
141	Proteomics of Human Aqueous Humor. OMICS A Journal of Integrative Biology, 2015, 19, 283-293.	2.0	46
142	Calcium calmodulin dependent kinase kinase 2 - a novel therapeutic target for gastric adenocarcinoma. Cancer Biology and Therapy, 2015, 16, 336-345.	3.4	71
143	Identification of differentially expressed serum proteins in gastric adenocarcinoma. Journal of Proteomics, 2015, 127, 80-88.	2.4	51
144	Identifying novel targets of oncogenic EGF receptor signaling in lung cancer through global phosphoproteomics. Proteomics, 2015, 15, 340-355.	2.2	42

#	ARTICLE	IF	CITATIONS
145	Integrated analysis of CRLF2 signaling in acute lymphoblastic leukemia identifies Polo-like kinase 1 as a potential therapeutic target. <i>Leukemia and Lymphoma</i> , 2015, 56, 1524-1527.	1.3	2
146	Proteomic Signature of Endothelial Dysfunction Identified in the Serum of Acute Ischemic Stroke Patients by the iTRAQ-Based LC-MS Approach. <i>Journal of Proteome Research</i> , 2015, 14, 2466-2479.	3.7	31
147	Chronic exposure to chewing tobacco selects for overexpression of stearyl-CoA desaturase in normal oral keratinocytes. <i>Cancer Biology and Therapy</i> , 2015, 16, 1593-1603.	3.4	31
148	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. <i>Genome Research</i> , 2015, 25, 1536-1545.	5.5	121
149	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015, 12, 1197-1204.	19.0	140
150	Activating Mutations in <i>PIK3CA</i> Lead to Widespread Modulation of the Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , 2015, 14, 3882-3891.	3.7	7
151	Phosphoproteomic Analysis Identifies Focal Adhesion Kinase 2 (FAK2) as a Potential Therapeutic Target for Tamoxifen Resistance in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2887-2900.	3.8	26
152	Quantitative phosphoproteomic analysis of IL-3-mediated signaling. <i>Proteomics</i> , 2015, 15, 532-544.	2.2	50
153	Silencing of high-mobility group box 2 (HMGB2) modulates cisplatin and 5-fluorouracil sensitivity in head and neck squamous cell carcinoma. <i>Proteomics</i> , 2015, 15, 383-393.	2.2	30
154	Identification of miR-145 targets through an integrated omics analysis. <i>Molecular BioSystems</i> , 2015, 11, 197-207.	2.9	21
155	Differential Signaling through p190 and p210 Forms of BCR-ABL Fusion Proteins Revealed By Proteomic Analysis. <i>Blood</i> , 2015, 126, 3651-3651.	1.4	1
156	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. <i>PLoS Pathogens</i> , 2015, 11, e1005346.	4.7	53
157	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. <i>Oncotarget</i> , 2015, 6, 29143-29160.	1.8	44
158	Prediction of Gene Activity in Early B Cell Development Based on an Integrative Multi-Omics Analysis. <i>Journal of Proteomics and Bioinformatics</i> , 2014, 07, .	0.4	13
159	A breast cancer cell microarray (CMA) as a rapid method to characterize candidate biomarkers. <i>Cancer Biology and Therapy</i> , 2014, 15, 1593-1599.	3.4	12
160	Multiple pathways for <i>Plasmodium</i> ookinete invasion of the mosquito midgut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E492-500.	7.1	61
161	Plasma Proteome Database as a resource for proteomics research: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D959-D965.	14.5	273
162	Pancreatic Cancer Database. <i>Cancer Biology and Therapy</i> , 2014, 15, 963-967.	3.4	57

#	ARTICLE	IF	CITATIONS
163	Identification of Candidate Substrates for the Golgi Tul1 E3 Ligase Using Quantitative diGly Proteomics in Yeast. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2871-2882.	3.8	32
164	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. <i>Clinical Proteomics</i> , 2014, 11, 39.	2.1	18
165	TSLP signaling pathway map: a platform for analysis of TSLP-mediated signaling. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau007-bau007.	3.0	71
166	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014, 11, 1.	2.1	113
167	Signaling Network Map of Endothelial TEK Tyrosine Kinase. <i>Journal of Signal Transduction</i> , 2014, 2014, 1-6.	2.0	46
168	A Network Map of FGF-1/FGFR Signaling System. <i>Journal of Signal Transduction</i> , 2014, 2014, 1-16.	2.0	80
169	Identification of prosaposin and transgelin as potential biomarkers for gallbladder cancer using quantitative proteomics. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 863-869.	2.1	35
170	Phosphoproteome of <i>Cryptococcus neoformans</i> . <i>Journal of Proteomics</i> , 2014, 97, 287-295.	2.4	41
171	Moving from unsequenced to sequenced genome: Reanalysis of the proteome of <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2014, 97, 48-61.	2.4	40
172	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. <i>Nature</i> , 2014, 507, 195-200.	27.8	779
173	A network map of the gastrin signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2014, 8, 165-170.	3.4	11
174	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2014, 11, 5.	2.1	18
175	Ribosomal Protein s15 Phosphorylation Mediates LRRK2 Neurodegeneration in Parkinson's Disease. <i>Cell</i> , 2014, 157, 472-485.	28.9	239
176	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	27.8	1,948
177	Proteomic analysis and genome annotation of <i>Pichia pastoris</i> , a recombinant protein expression host. <i>Proteomics</i> , 2014, 14, 2769-2779.	2.2	14
178	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3184-3198.	3.8	52
179	Heterogeneity of Pancreatic Cancer Metastases in a Single Patient Revealed by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2803-2811.	3.8	52
180	Brain Proteomics of <i>Anopheles gambiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 421-437.	2.0	14

#	ARTICLE	IF	CITATIONS
181	PHD3-mediated prolyl hydroxylation of nonmuscle actin impairs polymerization and cell motility. <i>Molecular Biology of the Cell</i> , 2014, 25, 2788-2796.	2.1	27
182	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	12.8	72
183	Identification and Characterization of Proteins Encoded by Chromosome 12 as Part of Chromosome-centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2014, 13, 3166-3177.	3.7	11
184	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014, 11, 29.	2.1	114
185	Neglected Tropical Diseases and Omics Science: Proteogenomics Analysis of the Promastigote Stage of <i>Leishmania major</i> Parasite. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 499-512.	2.0	35
186	Chromosome-centric Human Proteome Project: Deciphering Proteins Associated with Glioma and Neurodegenerative Disorders on Chromosome 12. <i>Journal of Proteome Research</i> , 2014, 13, 3178-3190.	3.7	23
187	Functional Annotation of Proteome Encoded by Human Chromosome 22. <i>Journal of Proteome Research</i> , 2014, 13, 2749-2760.	3.7	22
188	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014, 11, 6.	2.1	122
189	Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. <i>Journal of Proteomics</i> , 2014, 108, 306-315.	2.4	15
190	Botch Is a Γ^3 -Glutamyl Cyclotransferase that Deglycinates and Antagonizes Notch. <i>Cell Reports</i> , 2014, 7, 681-688.	6.4	29
191	Identification of targets of miR-200b by a SILAC-based quantitative proteomic approach. <i>EuPA Open Proteomics</i> , 2014, 4, 10-17.	2.5	1
192	Proteomic analysis of human follicular fluid: A new perspective towards understanding folliculogenesis. <i>Journal of Proteomics</i> , 2013, 87, 68-77.	2.4	129
193	Proteomic analysis of purified protein derivative of <i>Mycobacterium tuberculosis</i> . <i>Clinical Proteomics</i> , 2013, 10, 8.	2.1	26
194	Quantitative proteomics for identifying biomarkers for Rabies. <i>Clinical Proteomics</i> , 2013, 10, 3.	2.1	27
195	A multicellular signal transduction network of AGE/RAGE signaling. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 19-23.	3.4	54
196	SILAC-based quantitative proteomic analysis of gastric cancer secretome. <i>Proteomics - Clinical Applications</i> , 2013, 7, 355-366.	1.6	57
197	Evaluation of protein expression pattern of stanniocalcin 2, insulin-like growth factor-binding protein 7, inhibin beta A and four and a half LIM domains 1 in esophageal squamous cell carcinoma. <i>Cancer Biomarkers</i> , 2013, 12, 1-9.	1.7	17
198	The keratoconus corneal proteome: Loss of epithelial integrity and stromal degeneration. <i>Journal of Proteomics</i> , 2013, 87, 122-131.	2.4	125

#	ARTICLE	IF	CITATIONS
199	A multilectin affinity approach for comparative glycoprotein profiling of rheumatoid arthritis and spondyloarthropathy. <i>Clinical Proteomics</i> , 2013, 10, 11.	2.1	18
200	Characterizing the normal proteome of human ciliary body. <i>Clinical Proteomics</i> , 2013, 10, 9.	2.1	37
201	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. <i>Malaria Journal</i> , 2013, 12, 216.	2.3	39
202	Proteomic Strategies to Characterize Signaling Pathways. <i>Methods in Molecular Biology</i> , 2013, 1007, 359-377.	0.9	9
203	Construction of human activityâ€based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	7.2	153
204	Proteomics for understanding miRNA biology. <i>Proteomics</i> , 2013, 13, 558-567.	2.2	21
205	FAM190A Deficiency Creates a Cell Division Defect. <i>American Journal of Pathology</i> , 2013, 183, 296-303.	3.8	25
206	Identification of head and neck squamous cell carcinoma biomarker candidates through proteomic analysis of cancer cell secretome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2308-2316.	2.3	52
207	Downregulation of cornulin in esophageal squamous cell carcinoma. <i>Acta Histochemica</i> , 2013, 115, 89-99.	1.8	23
208	Access Guide to Human Proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 1.21.	25.8	19
209	IL-11/IL11RA receptor mediated signaling: a web accessible knowledgebase. <i>Cell Communication and Adhesion</i> , 2013, 20, 81-86.	1.0	8
210	Signaling network of Oncostatin M pathway. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 103-108.	3.4	46
211	A network map of BDNF/TRKB and BDNF/p75NTR signaling system. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 301-307.	3.4	72
212	Heterogeneous Nuclear Ribonucleoproteins and Their Interactors Are a Major Class of Deregulated Proteins in Anaplastic Astrocytoma: A Grade III Malignant Glioma. <i>Journal of Proteome Research</i> , 2013, 12, 3128-3138.	3.7	15
213	The Escherichia coli Phosphotyrosine Proteome Relates to Core Pathways and Virulence. <i>PLoS Pathogens</i> , 2013, 9, e1003403.	4.7	65
214	Architectural Organization of the Metabolic Regulatory Enzyme Ghrelin O-Acyltransferase. <i>Journal of Biological Chemistry</i> , 2013, 288, 32211-32228.	3.4	59
215	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. <i>Clinical Proteomics</i> , 2013, 10, 14.	2.1	25
216	Integrated Proteomic and Metabolic Analysis of Breast Cancer Progression. <i>PLoS ONE</i> , 2013, 8, e76220.	2.5	24

#	ARTICLE	IF	CITATIONS
217	The role of cardiolipin in defining the mammalian ANT interactome. FASEB Journal, 2013, 27, 1026.3.	0.5	0
218	Vesiclepedia: A Compendium for Extracellular Vesicles with Continuous Community Annotation. PLoS Biology, 2012, 10, e1001450.	5.6	1,064
219	Histone demethylase JMJD2C is a coactivator for hypoxia-inducible factor 1 that is required for breast cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3367-76.	7.1	196
220	A Bioinformatics Resource for TWEAK-Fn14 Signaling Pathway. Journal of Signal Transduction, 2012, 2012, 1-10.	2.0	24
221	Differences in signaling through the B-cell leukemia oncoprotein CRLF2 in response to TSLP and through mutant JAK2. Blood, 2012, 120, 2853-2863.	1.4	41
222	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. Molecular BioSystems, 2012, 8, 453-463.	2.9	179
223	TSLP Signaling Network Revealed by SILAC-Based Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M112.017764.	3.8	47
224	Proteomic analysis of an unsequenced plant "Mangifera indica. Journal of Proteomics, 2012, 75, 5793-5796.	2.4	17
225	Rapid Characterization of Candidate Biomarkers for Pancreatic Cancer Using Cell Microarrays (CMAs). Journal of Proteome Research, 2012, 11, 5556-5563.	3.7	14
226	Identification of Targets of c-Src Tyrosine Kinase by Chemical Complementation and Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, 355-369.	3.8	47
227	Regulation of Lipid Metabolism by Dicer Revealed through SILAC Mice. Journal of Proteome Research, 2012, 11, 2193-2205.	3.7	26
228	LC-MS/MS Analysis of Differentially Expressed Glioblastoma Membrane Proteome Reveals Altered Calcium Signaling and Other Protein Groups of Regulatory Functions. Molecular and Cellular Proteomics, 2012, 11, M111.013565.	3.8	76
229	Unbiased Discovery of Interactions at a Control Locus Driving Expression of the Cancer-Specific Therapeutic and Diagnostic Target, Mesothelin. Journal of Proteome Research, 2012, 11, 5301-5310.	3.7	6
230	Proteomic analysis of the abomasal mucosal response following infection by the nematode, Haemonchus contortus, in genetically resistant and susceptible sheep. Journal of Proteomics, 2012, 75, 2141-2152.	2.4	24
231	Overexpression of ribosome binding protein 1 (RRBP1) in breast cancer. Clinical Proteomics, 2012, 9, 7.	2.1	25
232	A pathway map of prolactin signaling. Journal of Cell Communication and Signaling, 2012, 6, 169-173.	3.4	65
233	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. Clinical Proteomics, 2012, 9, 12.	2.1	26
234	Proteogenomic Analysis of <i>Candida glabrata</i> using High Resolution Mass Spectrometry. Journal of Proteome Research, 2012, 11, 247-260.	3.7	42

#	ARTICLE	IF	CITATIONS
235	Transcriptomic Profiling of Medial Temporal Lobe Epilepsy. Journal of Proteomics and Bioinformatics, 2012, 05, .	0.4	20
236	Overexpression of Kinesin Associated Protein 3 (KIFAP3) in Breast Cancer. Journal of Proteomics and Bioinformatics, 2012, 05, 122-126.	0.4	4
237	A proteogenomic approach to map the proteome of an unsequenced pathogen “ <i>Leishmania donovani</i> ”. Proteomics, 2012, 12, 832-844.	2.2	42
238	Electron transfer dissociation mass spectrometry in proteomics. Proteomics, 2012, 12, 530-542.	2.2	99
239	Secretome analysis of the fungus <i>Trichoderma harzianum</i> grown on cellulose. Proteomics, 2012, 12, 2716-2728.	2.2	51
240	Transcriptomic and proteomic profiling of KEAP1 disrupted and sulforaphane-treated human breast epithelial cells reveals common expression profiles. Breast Cancer Research and Treatment, 2012, 132, 175-187.	2.5	199
241	Gene Expression Profiling of Tuberculous Meningitis Co-infected with HIV. Journal of Proteomics and Bioinformatics, 2012, 05, 235-244.	0.4	14
242	Monoclonal Antibody Cocktail as an Enrichment Tool for Acetylome Analysis. Analytical Chemistry, 2011, 83, 3623-3626.	6.5	30
243	Mutant proteins as cancer-specific biomarkers. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2444-2449.	7.1	157
244	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.011445.	3.8	145
245	A comprehensive curated resource for follicle stimulating hormone signaling. BMC Research Notes, 2011, 4, 408.	1.4	20
246	A Comprehensive Map of the Human Urinary Proteome. Journal of Proteome Research, 2011, 10, 2734-2743.	3.7	176
247	Pyruvate Kinase M2 Is a PHD3-Stimulated Coactivator for Hypoxia-Inducible Factor 1. Cell, 2011, 145, 732-744.	28.9	1,210
248	Proteome profiling of wild type and lumican-deficient mouse corneas. Journal of Proteomics, 2011, 74, 1895-1905.	2.4	18
249	A Signaling Network of Thyroid-Stimulating Hormone. Journal of Proteomics and Bioinformatics, 2011, 04, .	0.4	11
250	Identification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. Journal of Proteomics and Bioinformatics, 2011, 04, 22-35.	0.4	31
251	The dynamic stress-induced “O-GlcNAc” highlights functions for O-GlcNAc in regulating DNA damage/repair and other cellular pathways. Amino Acids, 2011, 40, 793-808.	2.7	103
252	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. Molecular Biotechnology, 2011, 48, 87-95.	2.4	87

#	ARTICLE	IF	CITATIONS
253	Systematic evaluation of alternating CID and ETD fragmentation for phosphorylated peptides. <i>Proteomics</i> , 2011, 11, 2568-2572.	2.2	36
254	Proteogenomics. <i>Proteomics</i> , 2011, 11, 620-630.	2.2	121
255	Quantitative temporal proteomic analysis of human embryonic stem cell differentiation into oligodendrocyte progenitor cells. <i>Proteomics</i> , 2011, 11, 4007-4020.	2.2	39
256	Comprehensive proteomic analysis of human bile. <i>Proteomics</i> , 2011, 11, 4443-4453.	2.2	44
257	The interactome of a PTB domain-containing adapter protein, Odin, revealed by SILAC. <i>Journal of Proteomics</i> , 2011, 74, 294-303.	2.4	15
258	NetSlim: high-confidence curated signaling maps. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar032-bar032.	3.0	29
259	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011, 21, 1872-1881.	5.5	58
260	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011, 12, 510-522.	3.4	102
261	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar021-bar021.	3.0	39
262	An evolutionarily "young" lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2011, 25, 1306-1319.	5.9	27
263	Quantitative Proteomic Profiling Unravels Dynamic Changes in the Myeloma Cell Proteome Treated with Valproic Acid (VPA). <i>Blood</i> , 2011, 118, 1847-1847.	1.4	1
264	Gene Expression Profiling of Gastric Cancer. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 4, 74-82.	0.4	14
265	Assessment of resolution parameters for CID-based shotgun proteomic experiments on the LTQ-Orbitrap mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1606-1611.	2.8	26
266	Comparative Proteomic Analysis of <i>Candida albicans</i> and <i>Candida glabrata</i> . <i>Clinical Proteomics</i> , 2010, 6, 163-173.	2.1	3
267	Site-directed mutagenesis reveals a unique requirement for tyrosine residues in IL-7R α and TSLPR cytoplasmic domains in TSLP-dependent cell proliferation. <i>BMC Immunology</i> , 2010, 11, 5.	2.2	12
268	Comparative proteomics of human embryonic stem cells and embryonal carcinoma cells. <i>Proteomics</i> , 2010, 10, 1359-1373.	2.2	48
269	Screening for therapeutic targets of vorinostat by SILAC-based proteomic analysis in human breast cancer cells. <i>Proteomics</i> , 2010, 10, 1029-1039.	2.2	43
270	Proteomic characterization of Her2/neu-overexpressing breast cancer cells. <i>Proteomics</i> , 2010, 10, 3800-3810.	2.2	32

#	ARTICLE	IF	CITATIONS
271	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
272	Overexpression of Periostin and Lumican in Esophageal Squamous Cell Carcinoma. <i>Cancers</i> , 2010, 2, 133-142.	3.7	15
273	Mutation@A Glance: An Integrative Web Application for Analysing Mutations from Human Genetic Diseases. <i>DNA Research</i> , 2010, 17, 197-208.	3.4	26
274	SILAC-based quantitative proteomic approach to identify potential biomarkers from the esophageal squamous cell carcinoma secretome. <i>Cancer Biology and Therapy</i> , 2010, 10, 796-810.	3.4	79
275	The Axl receptor tyrosine kinase is an adverse prognostic factor and a therapeutic target in esophageal adenocarcinoma. <i>Cancer Biology and Therapy</i> , 2010, 10, 1009-1018.	3.4	85
276	Temporal Profiling of the Secretome during Adipogenesis in Humans. <i>Journal of Proteome Research</i> , 2010, 9, 5228-5238.	3.7	100
277	Hsp70 and CHIP Selectively Mediate Ubiquitination and Degradation of Hypoxia-inducible Factor (HIF)-1 α but Not HIF-2 α . <i>Journal of Biological Chemistry</i> , 2010, 285, 3651-3663.	3.4	201
278	Effects of transmembrane and juxtamembrane domains on proliferative ability of TSLP receptor. <i>Molecular Immunology</i> , 2010, 47, 1207-1215.	2.2	3
279	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	4.6	159
280	Identifying targets of miR-143 using a SILAC-based proteomic approach. <i>Molecular BioSystems</i> , 2010, 6, 1873.	2.9	58
281	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	456
282	Bone Marrow Hypoplasia Induced by Conditional Knockout of the RNase III Domain of Dicer-1. <i>Blood</i> , 2010, 116, 2226-2226.	1.4	0
283	Human Protein Reference Database–2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	14.5	2,882
284	A Compendium of Potential Biomarkers of Pancreatic Cancer. <i>PLoS Medicine</i> , 2009, 6, e1000046.	8.4	260
285	Genomewide mRNA profiling of esophageal squamous cell carcinoma for identification of cancer biomarkers. <i>Cancer Biology and Therapy</i> , 2009, 8, 36-46.	3.4	121
286	Prediction of Candidate Primary Immunodeficiency Disease Genes Using a Support Vector Machine Learning Approach. <i>DNA Research</i> , 2009, 16, 345-351.	3.4	26
287	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	14.5	75
288	Malaria Parasite Invasion of the Mosquito Salivary Gland Requires Interaction between the Plasmodium TRAP and the Anopheles Saglin Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000265.	4.7	117

#	ARTICLE	IF	CITATIONS
289	RAPID: Resource of Asian Primary Immunodeficiency Diseases. Nucleic Acids Research, 2009, 37, D863-D867.	14.5	37
290	PathBuilder“open source software for annotating and developing pathway resources. Bioinformatics, 2009, 25, 2860-2862.	4.1	40
291	O-Linked N-Acetylglucosamine Modification on CCAAT Enhancer-binding Protein 1 ² . Journal of Biological Chemistry, 2009, 284, 19248-19254.	3.4	66
292	Identification of miR-21 targets in breast cancer cells using a quantitative proteomic approach. Proteomics, 2009, 9, 1374-1384.	2.2	113
293	K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Poh1. EMBO Journal, 2009, 28, 621-631.	7.8	193
294	Evaluation of Several MS/MS Search Algorithms for Analysis of Spectra Derived from Electron Transfer Dissociation Experiments. Analytical Chemistry, 2009, 81, 7170-7180.	6.5	50
295	Temporal Analysis of Neural Differentiation Using Quantitative Proteomics. Journal of Proteome Research, 2009, 8, 1315-1326.	3.7	53
296	Temporal Profiling of the Adipocyte Proteome during Differentiation Using a Five-Plex SILAC Based Strategy. Journal of Proteome Research, 2009, 8, 48-58.	3.7	133
297	Identification of Src tyrosine kinase substrates in platelet-derived growth factor receptor signaling. Molecular Oncology, 2009, 3, 439-450.	4.6	65
298	SILAC for Global Phosphoproteomic Analysis. Methods in Molecular Biology, 2009, 527, 107-116.	0.9	30
299	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. Methods in Molecular Biology, 2009, 577, 67-79.	0.9	245
300	Comparison of Peptide Array Substrate Phosphorylation of c-Raf and Mitogen Activated Protein Kinase Kinase 8. PLoS ONE, 2009, 4, e6440.	2.5	16
301	Molecular Alterations in Exocrine Neoplasms of the Pancreas. Archives of Pathology and Laboratory Medicine, 2009, 133, 405-412.	2.5	13
302	A panel of biomarkers for esophageal squamous cell carcinoma. FASEB Journal, 2009, 23, 925.11.	0.5	0
303	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. Annals of Indian Academy of Neurology, 2009, 12, 3-11.	0.5	9
304	18O Labeling for a Quantitative Proteomic Analysis of Glycoproteins in Hepatocellular Carcinoma. Clinical Proteomics, 2008, 4, 137-155.	2.1	18
305	Applications of Proteomics to Lab Diagnosis. Annual Review of Pathology: Mechanisms of Disease, 2008, 3, 485-498.	22.4	39
306	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	17.5	155

#	ARTICLE	IF	CITATIONS
307	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008, 3, 505-516.	12.0	190
308	A Quantitative Proteomic Approach for Identification of Potential Biomarkers in Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 4289-4298.	3.7	121
309	Significant conservation of synthetic lethal genetic interaction networks between distantly related eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16653-16658.	7.1	165
310	Differential Membrane Proteomics Using ¹⁸ O-Labeling To Identify Biomarkers for Cholangiocarcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 4670-4677.	3.7	43
311	Activated Epidermal Growth Factor Receptor as a Novel Target in Pancreatic Cancer Therapy. <i>Journal of Proteome Research</i> , 2008, 7, 4651-4658.	3.7	42
312	Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2008, 80, 4825-4835.	6.5	97
313	Global Impact of Oncogenic Src on a Phosphotyrosine Proteome. <i>Journal of Proteome Research</i> , 2008, 7, 3447-3460.	3.7	90
314	Identification of c-Src Tyrosine Kinase Substrates Using Mass Spectrometry and Peptide Microarrays. <i>Journal of Proteome Research</i> , 2008, 7, 3900-3910.	3.7	62
315	Casein Kinase 2 Binds to the C Terminus of Na ⁺ /H ⁺ exchanger 3 (NHE3) and Stimulates NHE3 Basal Activity by Phosphorylating a Separate Site in NHE3. <i>Molecular Biology of the Cell</i> , 2008, 19, 3859-3870.	2.1	49
316	Antitumor activity and molecular effects of the novel heat shock protein 90 inhibitor, IPI-504, in pancreatic cancer. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3275-3284.	4.1	77
317	Human Proteinpedia as a Resource for Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2038-2047.	3.8	17
318	Comparisons of tyrosine phosphorylated proteins in cells expressing lung cancer-specific alleles of EGFR and KRAS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14112-14117.	7.1	113
319	Identification of Secreted Proteins that Mediate Cell-Cell Interactions in an <i>In vitro</i> Model of the Lung Cancer Microenvironment. <i>Cancer Research</i> , 2008, 68, 7237-7245.	0.9	71
320	New Markers of Pancreatic Cancer Identified Through Differential Gene Expression Analyses: Claudin 18 and Annexin A8. <i>American Journal of Surgical Pathology</i> , 2008, 32, 188-196.	3.7	121
321	Copy-number variants in patients with a strong family history of pancreatic cancer. <i>Cancer Biology and Therapy</i> , 2007, 6, 1592-1599.	3.4	36
322	Global proteomic profiling of phosphopeptides using electron transfer dissociation tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2199-2204.	7.1	489
323	Disruption of <i>Plasmodium falciparum</i> development by antibodies against a conserved mosquito midgut antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13461-13466.	7.1	163
324	Dynamic Interplay between O-Linked N-Acetylglucosaminylation and Glycogen Synthase Kinase-3-dependent Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1365-1379.	3.8	183

#	ARTICLE	IF	CITATIONS
325	Upstream stimulatory factors regulate the C/EBP β gene during differentiation of 3T3-L1 preadipocytes. Biochemical and Biophysical Research Communications, 2007, 354, 517-521.	2.1	19
326	Protein pyrophosphorylation by inositol pyrophosphates is a posttranslational event. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15305-15310.	7.1	189
327	Phosphoproteomics. Current Protocols in Protein Science, 2007, 50, Unit 24.4.	2.8	6
328	Quantitative proteomics for identification of cancer biomarkers. Proteomics - Clinical Applications, 2007, 1, 1080-1089.	1.6	29
329	A curated compendium of phosphorylation motifs. Nature Biotechnology, 2007, 25, 285-286.	17.5	345
330	Proteomics of Human Bile. , 2007, , 399-414.		7
331	Proteomics of Human Pancreatic Juice. , 2007, , 377-397.		0
332	Plasma Proteome Database. , 2007, , 129-136.		1
333	Identification of Protein Ubiquitylation by Electrospray Ionization Tandem Mass Spectrometric Analysis of Sulfonated Tryptic Peptides. Analytical Chemistry, 2006, 78, 3681-3687.	6.5	15
334	GCN5 acetyltransferase complex controls glucose metabolism through transcriptional repression of PGC-1 β . Cell Metabolism, 2006, 3, 429-438.	16.2	383
335	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. , 2006, , 1-35.		4
336	Utility of Bile Duct Brushings for the Early Detection of Cholangiocarcinoma in Patients With Primary Sclerosing Cholangitis. Journal of Clinical Gastroenterology, 2006, 40, 336-341.	2.2	24
337	A functional annotation of subproteomes in human plasma. , 2006, , 329-351.		0
338	Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. Nature Genetics, 2006, 38, 285-293.	21.4	433
339	An evaluation of human protein-protein interaction data in the public domain. BMC Bioinformatics, 2006, 7, S19.	2.6	201
340	Chemical Rescue of a Mutant Enzyme in Living Cells. Science, 2006, 311, 1293-1297.	12.6	111
341	Role of p38 in Replication of Trypanosoma brucei Kinetoplast DNA. Molecular and Cellular Biology, 2006, 26, 5382-5393.	2.3	51
342	Phosphoproteomic analysis of Her2/neu signaling and inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9773-9778.	7.1	193

#	ARTICLE	IF	CITATIONS
343	Human protein reference database--2006 update. Nucleic Acids Research, 2006, 34, D411-D414.	14.5	536
344	Biomarker Discovery from Pancreatic Cancer Secretome Using a Differential Proteomic Approach. Molecular and Cellular Proteomics, 2006, 5, 157-171.	3.8	421
345	Defining the Dynamic Oâ€œGlcNAc Proteome. FASEB Journal, 2006, 20, A56.	0.5	0
346	Probabilistic model of the human protein-protein interaction network. Nature Biotechnology, 2005, 23, 951-959.	17.5	380
347	A manually curated functional annotation of the human X chromosome. Nature Genetics, 2005, 37, 331-332.	21.4	16
348	Genome annotation of Anopheles gambiae using mass spectrometry-derived data. BMC Genomics, 2005, 6, 128.	2.8	58
349	Bioinformatics and Proteomics Approaches for Aging Research. Biogerontology, 2005, 6, 227-232.	3.9	10
350	A proteomic analysis of salivary glands of female Anopheles gambiae mosquito. Proteomics, 2005, 5, 3765-3777.	2.2	63
351	Plasma Proteome Database as a resource for proteomics research. Proteomics, 2005, 5, 3531-3536.	2.2	135
352	A functional annotation of subproteomes in human plasma. Proteomics, 2005, 5, 3506-3519.	2.2	82
353	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35â€œcollaborating laboratories and multiple analytical groups, generating a core dataset of 3020â€œproteins and a publiclyâ€œavailable database. Proteomics, 2005, 5, 3226-3245.	2.2	766
354	A Bioinformatics Analysis of Protein Tyrosine Phosphatases in Humans. DNA Research, 2005, 12, 79-89.	3.4	18
355	A Proteomic Analysis of Human Hemodialysis Fluid. Molecular and Cellular Proteomics, 2005, 4, 637-650.	3.8	60
356	Insights into the Role of Histone H3 and Histone H4 Core Modifiable Residues in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2005, 25, 10060-10070.	2.3	215
357	Sequential phosphorylation of CCAAT enhancer-binding protein Å by MAPK and glycogen synthase kinase 3Å is required for adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9766-9771.	7.1	293
358	Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) for Studying Dynamics of Protein Abundance and Posttranslational Modifications. Science Signaling, 2005, 2005, pl2-pl2.	3.6	74
359	Phosphoproteome Analysis of HeLa Cells Using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC). Journal of Proteome Research, 2005, 4, 1661-1671.	3.7	121
360	Assessing Reproducibility of a Protein Dynamics Study Using in Vivo Labeling and Liquid Chromatography Tandem Mass Spectrometry. Analytical Chemistry, 2005, 77, 2739-2744.	6.5	25

#	ARTICLE	IF	CITATIONS
361	TAGmapper: A web-based tool for mapping SAGE tags. <i>Gene</i> , 2005, 364, 123-129.	2.2	10
362	Proteomic resources: Integrating biomedical information in humans. <i>Gene</i> , 2005, 364, 13-18.	2.2	14
363	Possible Role of the Activation Loop Tyrosine Residue (Y842) in FLT3/ITD Signaling May Be Mediated by SHP-2.. <i>Blood</i> , 2005, 106, 1199-1199.	1.4	2
364	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9309-9314.	7.1	874
365	A Role for Thymic Stromal Lymphopoietin in CD4+ T Cell Development. <i>Journal of Experimental Medicine</i> , 2004, 200, 159-168.	8.5	208
366	A Novel Proteomic Approach for Specific Identification of Tyrosine Kinase Substrates Using [13C]Tyrosine. <i>Journal of Biological Chemistry</i> , 2004, 279, 15805-15813.	3.4	96
367	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004, 32, 497D-501.	14.5	534
368	Differentially expressed genes in pancreatic ductal adenocarcinomas identified through serial analysis of gene expression. <i>Cancer Biology and Therapy</i> , 2004, 3, 1254-1261.	3.4	73
369	A Proteomic Analysis of Human Bile. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 715-728.	3.8	142
370	The HUPO PSI's Molecular Interaction formatâ€”a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
371	BioBuilder as a database development and functional annotation platform for proteins. <i>BMC Bioinformatics</i> , 2004, 5, 43.	2.6	7
372	Cloning of a novel signaling molecule, AMSH-2, that potentiates transforming growth factor beta signaling. <i>BMC Cell Biology</i> , 2004, 5, 2.	3.0	37
373	Mac-2-binding protein is a diagnostic marker for biliary tract carcinoma. <i>Cancer</i> , 2004, 101, 1609-1615.	4.1	95
374	Comprehensive Proteomic Analysis of Human Pancreatic Juice. <i>Journal of Proteome Research</i> , 2004, 3, 1042-1055.	3.7	194
375	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. <i>Neoplasia</i> , 2004, 6, 1-6.	5.3	3,212
376	Unraveling the human interactome: lessons from the yeast. <i>Drug Discovery Today: TARGETS</i> , 2004, 3, 79-84.	0.5	3
377	Systematic Interactome Mapping and Genetic Perturbation Analysis of a <i>C. elegans</i> TGF-Î² Signaling Network. <i>Molecular Cell</i> , 2004, 13, 469-482.	9.7	136
378	Identification of novel highly expressed genes in pancreatic ductal adenocarcinomas through a bioinformatics analysis of expressed sequence tags. <i>Cancer Biology and Therapy</i> , 2004, 3, 1081-1089.	3.4	52

#	ARTICLE	IF	CITATIONS
379	Proteomic Analysis of the Adipocyte Secretome. Nutrition and Disease Prevention, 2004, , 395-413.	0.1	0
380	Mouse embryonic fibroblasts derived from Odin deficient mice display a hyperproliferative phenotype. DNA Research, 2004, 11, 285-92.	3.4	9
381	Absolute systems biology â€” measuring dynamics of protein modifications. Trends in Biotechnology, 2003, 21, 467-470.	9.3	5
382	From biological databases to platforms for biomedical discovery. Trends in Biotechnology, 2003, 21, 263-268.	9.3	25
383	Tackling the phosphoproteome: tools and strategies. Current Opinion in Chemical Biology, 2003, 7, 64-69.	6.1	206
384	A Proteomic Approach for Quantitation of Phosphorylation Using Stable Isotope Labeling in Cell Culture. Analytical Chemistry, 2003, 75, 6043-6049.	6.5	167
385	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. Genome Research, 2003, 13, 2363-2371.	5.5	954
386	Phosphotyrosine Mapping in Bcr/Abl Oncoprotein Using Phosphotyrosine-specific Immonium Ion Scanning. Molecular and Cellular Proteomics, 2003, 2, 138-145.	3.8	46
387	Computational and experimental analysis reveals a novel Src family kinase in the C. elegans genome. Bioinformatics, 2003, 19, 169-172.	4.1	48
388	A Novel Src Homology 2 Domain-containing Molecule, Src-like Adapter Protein-2 (SLAP-2), Which Negatively Regulates T Cell Receptor Signaling. Journal of Biological Chemistry, 2002, 277, 19131-19138.	3.4	36
389	Inhibition of Adipocyte Differentiation by Resistin-like Molecule $\hat{\pm}$. Journal of Biological Chemistry, 2002, 277, 42011-42016.	3.4	61
390	Cloning of MASK, a Novel Member of the Mammalian Germinal Center Kinase III Subfamily, with Apoptosis-inducing Properties. Journal of Biological Chemistry, 2002, 277, 5929-5939.	3.4	53
391	A Proteomic Approach for Identification of Secreted Proteins during the Differentiation of 3T3-L1 Preadipocytes to Adipocytes. Molecular and Cellular Proteomics, 2002, 1, 213-222.	3.8	227
392	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. Science Signaling, 2002, 2002, pl16-pl16.	3.6	38
393	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. Journal of Biological Chemistry, 2002, 277, 1031-1039.	3.4	175
394	Overlapping of MINK and CHRNE gene loci in the course of mammalian evolution. Nucleic Acids Research, 2002, 30, 2906-2910.	14.5	16
395	Context-specific Effects of Fibulin-5 (DANCE/EVEC) on Cell Proliferation, Motility, and Invasion. Journal of Biological Chemistry, 2002, 277, 27367-27377.	3.4	141
396	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. Molecular and Cellular Proteomics, 2002, 1, 517-527.	3.8	353

#	ARTICLE	IF	CITATIONS
397	Toll and interleukin-1 receptor (TIR) domain-containing proteins in plants: a genomic perspective. Trends in Plant Science, 2002, 7, 388-391.	8.8	49
398	Cloning of rat thymic stromal lymphopoietin receptor (TSLPR) and characterization of genomic structure of murine Tslpr gene. Gene, 2002, 284, 161-168.	2.2	7
399	Multi-Protein Complexes Studied by Mass Spectrometry. Scientific World Journal, The, 2002, 2, 91-92.	2.1	1
400	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. Trends in Biotechnology, 2002, 20, 261-268.	9.3	877
401	Proteomics goes quantitative: measuring protein abundance. Trends in Biotechnology, 2002, 20, 361-364.	9.3	64
402	Resources for full-length cDNAs. Trends in Biochemical Sciences, 2002, 27, 266-267.	7.5	6
403	Cloning and characterization of PAK5, a novel member of mammalianp21-activated kinase-II subfamily that is predominantly expressed in brain. Oncogene, 2002, 21, 3939-3948.	5.9	114
404	Cloning of a novel phosphotyrosine binding domain containing molecule, Odin, involved in signaling by receptor tyrosine kinases. Oncogene, 2002, 21, 8029-8036.	5.9	48
405	Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. Molecular and Cellular Proteomics, 2002, 1, 376-386.	3.8	4,931
406	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. Analytical Chemistry, 2001, 73, 1440-1448.	6.5	306
407	Characterization of promoter region and genomic structure of the murine and human genes encoding Src like adapter protein. Gene, 2001, 262, 267-273.	2.2	3
408	An evaluation of the use of two-dimensional gel electrophoresis in proteomics. New Biotechnology, 2001, 18, 195-205.	2.7	143
409	Analysis of Proteins and Proteomes by Mass Spectrometry. Annual Review of Biochemistry, 2001, 70, 437-473.	11.1	1,044
410	Common pitfalls in bioinformatics-based analyses: look before you leap. Trends in Genetics, 2001, 17, 541-545.	6.7	39
411	A reassessment of the translation initiation codon in vertebrates. Trends in Genetics, 2001, 17, 685-687.	6.7	98
412	Use of mass spectrometry-derived data to annotate nucleotide and protein sequence databases. Trends in Biochemical Sciences, 2001, 26, 54-61.	7.5	111
413	GPMAW â€“ a software tool for analyzing proteins and peptides. Trends in Biochemical Sciences, 2001, 26, 687-689.	7.5	145
414	Microarrays go live â€“ new prospects for proteomics. Trends in Biochemical Sciences, 2001, 26, 639-641.	7.5	19

#	ARTICLE	IF	CITATIONS
415	Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin. <i>Nature Immunology</i> , 2000, 1, 59-64.	14.5	393
416	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	27.8	2,173
417	Src-like Adaptor Protein (Slap) Is a Negative Regulator of T Cell Receptor Signaling. <i>Journal of Experimental Medicine</i> , 2000, 191, 463-474.	8.5	111
418	Analysis of receptor signaling pathways by mass spectrometry: Identification of Vav-2 as a substrate of the epidermal and platelet-derived growth factor receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 179-184.	7.1	410
419	Identification of a Novel Immunoreceptor Tyrosine-based Activation Motif-containing Molecule, STAM2, by Mass Spectrometry and Its Involvement in Growth Factor and Cytokine Receptor Signaling Pathways. <i>Journal of Biological Chemistry</i> , 2000, 275, 38633-38639.	3.4	103
420	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	7.5	72
421	Src-like adaptor protein (Slap) is a negative regulator of mitogenesis. <i>Current Biology</i> , 1998, 8, 975-978.	3.9	67
422	Direct Association between the Ret Receptor Tyrosine Kinase and the Src Homology 2-containing Adapter Protein Grb7. <i>Journal of Biological Chemistry</i> , 1996, 271, 10607-10610.	3.4	75
423	Oncogenic RET Receptors Display Different Autophosphorylation Sites and Substrate Binding Specificities. <i>Journal of Biological Chemistry</i> , 1996, 271, 5309-5312.	3.4	113
424	Characterization of a Novel Src-like Adapter Protein That Associates with the Eck Receptor Tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 1995, 270, 19201-19204.	3.4	108
425	The Ret Receptor Protein Tyrosine Kinase Associates with the SH2-containing Adapter Protein Grb10. <i>Journal of Biological Chemistry</i> , 1995, 270, 21461-21463.	3.4	118
426	Role of B61, the ligand for the Eck receptor tyrosine kinase, in TNF-alpha-induced angiogenesis. <i>Science</i> , 1995, 268, 567-569.	12.6	345
427	Characterization of B61, the Ligand for the Eck Receptor Protein-Tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 1995, 270, 5636-5641.	3.4	53
428	Chromosomal Localization of the Mouse Src-like Adapter Protein (Slap) Gene and Its Putative Human Homolog SLA. <i>Genomics</i> , 1995, 30, 623-625.	2.9	13
429	cDNA Cloning and Characterization of a Cek7 Receptor Protein-tyrosine Kinase Ligand That Is Identical to the Ligand (ELF-1) for the Mek-4 and Sek Receptor Protein-tyrosine Kinases. <i>Journal of Biological Chemistry</i> , 1995, 270, 3467-3470.	3.4	32
430	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. <i>Proteomics</i> , 0, , 2200077.	2.2	2