

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

2440

100
h-index

1875

215
g-index

449
all docs

449
docs citations

449
times ranked

71418
citing authors

#	ARTICLE	IF	CITATIONS
1	Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 376-386.	2.5	4,931
2	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. <i>Neoplasia</i> , 2004, 6, 1-6.	2.3	3,212
3	Human Protein Reference Database--2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	6.5	2,882
4	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	13.7	2,173
5	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	13.7	1,948
6	Pyruvate Kinase M2 Is a PHD3-Stimulated Coactivator for Hypoxia-Inducible Factor 1. <i>Cell</i> , 2011, 145, 732-744.	13.5	1,210
7	Vesiclepedia: A Compendium for Extracellular Vesicles with Continuous Community Annotation. <i>PLoS Biology</i> , 2012, 10, e1001450.	2.6	1,064
8	Analysis of Proteins and Proteomes by Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2001, 70, 437-473.	5.0	1,044
9	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. <i>Genome Research</i> , 2003, 13, 2363-2371.	2.4	954
10	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	4.9	877
11	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.	3.3	874
12	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
13	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. <i>Nature</i> , 2014, 507, 195-200.	13.7	779
14	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. <i>Proteomics</i> , 2005, 5, 3226-3245.	1.3	766
15	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
16	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.	9.4	581
17	Human protein reference database--2006 update. <i>Nucleic Acids Research</i> , 2006, 34, D411-D414.	6.5	536
18	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004, 32, 497D-501.	6.5	534

#	ARTICLE	IF	CITATIONS
19	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
20	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.	3.3	489
21	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	13.9	456
22	Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. <i>Nature Genetics</i> , 2006, 38, 285-293.	9.4	433
23	Biomarker Discovery from Pancreatic Cancer Secretome Using a Differential Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 157-171.	2.5	421
24	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.	3.3	410
25	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	6.0	398
26	Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin. <i>Nature Immunology</i> , 2000, 1, 59-64.	7.0	393
27	GCN5 acetyltransferase complex controls glucose metabolism through transcriptional repression of PGC-1 α . <i>Cell Metabolism</i> , 2006, 3, 429-438.	7.2	383
28	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005, 23, 951-959.	9.4	380
29	A Mass Spectrometry-based Proteomic Approach for Identification of Serine/Threonine-phosphorylated Proteins by Enrichment with Phospho-specific Antibodies. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 517-527.	2.5	353
30	Role of B61, the ligand for the Eck receptor tyrosine kinase, in TNF-alpha-induced angiogenesis. <i>Science</i> , 1995, 268, 567-569.	6.0	345
31	A curated compendium of phosphorylation motifs. <i>Nature Biotechnology</i> , 2007, 25, 285-286.	9.4	345
32	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. <i>Analytical Chemistry</i> , 2001, 73, 1440-1448.	3.2	306
33	Sequential phosphorylation of CCAAT enhancer-binding protein β by MAPK and glycogen synthase kinase 3 β is required for adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9766-9771.	3.3	293
34	Plasma Proteome Database as a resource for proteomics research: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D959-D965.	6.5	273
35	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
36	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. <i>Genome Biology</i> , 2018, 19, 208.	3.8	263

#	ARTICLE	IF	CITATIONS
37	A Compendium of Potential Biomarkers of Pancreatic Cancer. <i>PLoS Medicine</i> , 2009, 6, e1000046.	3.9	260
38	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. <i>Methods in Molecular Biology</i> , 2009, 577, 67-79.	0.4	245
39	Ribosomal Protein s15 Phosphorylation Mediates LRRK2 Neurodegeneration in Parkinson's Disease. <i>Cell</i> , 2014, 157, 472-485.	13.5	239
40	A Proteomic Approach for Identification of Secreted Proteins during the Differentiation of 3T3-L1 Preadipocytes to Adipocytes. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 213-222.	2.5	227
41	Insights into the Role of Histone H3 and Histone H4 Core Modifiable Residues in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2005, 25, 10060-10070.	1.1	215
42	A Role for Thymic Stromal Lymphopoietin in CD4+ T Cell Development. <i>Journal of Experimental Medicine</i> , 2004, 200, 159-168.	4.2	208
43	Tackling the phosphoproteome: tools and strategies. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 64-69.	2.8	206
44	An evaluation of human protein-protein interaction data in the public domain. <i>BMC Bioinformatics</i> , 2006, 7, S19.	1.2	201
45	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.	1.6	201
46	Transcriptomic and proteomic profiling of KEAP1 disrupted and sulforaphane-treated human breast epithelial cells reveals common expression profiles. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 175-187.	1.1	199
47	Histone demethylase JMJD2C is a coactivator for hypoxia-inducible factor 1 that is required for breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3367-76.	3.3	196
48	Comprehensive Proteomic Analysis of Human Pancreatic Juice. <i>Journal of Proteome Research</i> , 2004, 3, 1042-1055.	1.8	194
49	Phosphoproteomic analysis of Her2/neu signaling and inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9773-9778.	3.3	193
50	K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Pdh1. <i>EMBO Journal</i> , 2009, 28, 621-631.	3.5	193
51	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008, 3, 505-516.	5.5	190
52	Protein pyrophosphorylation by inositol pyrophosphates is a posttranslational event. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15305-15310.	3.3	189
53	Dynamic Interplay between O-Linked N-Acetylglucosaminylation and Glycogen Synthase Kinase-3-dependent Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1365-1379.	2.5	183
54	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. <i>Molecular BioSystems</i> , 2012, 8, 453-463.	2.9	179

#	ARTICLE	IF	CITATIONS
55	A Comprehensive Map of the Human Urinary Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 2734-2743.	1.8	176
56	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 1031-1039.	1.6	175
57	A Proteomic Approach for Quantitation of Phosphorylation Using Stable Isotope Labeling in Cell Culture. <i>Analytical Chemistry</i> , 2003, 75, 6043-6049.	3.2	167
58	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.	3.3	165
59	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.	3.3	163
60	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	2.1	159
61	Mutant proteins as cancer-specific biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2444-2449.	3.3	157
62	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
63	Loss of C9orf72 Enhances Autophagic Activity via Deregulated mTOR and TFEB Signaling. <i>PLoS Genetics</i> , 2016, 12, e1006443.	1.5	154
64	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	3.2	153
65	GPMAW – a software tool for analyzing proteins and peptides. <i>Trends in Biochemical Sciences</i> , 2001, 26, 687-689.	3.7	145
66	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	2.5	145
67	An evaluation of the use of two-dimensional gel electrophoresis in proteomics. <i>New Biotechnology</i> , 2001, 18, 195-205.	2.7	143
68	A Proteomic Analysis of Human Bile. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 715-728.	2.5	142
69	Toward the human cellular microRNAome. <i>Genome Research</i> , 2017, 27, 1769-1781.	2.4	142
70	Context-specific Effects of Fibulin-5 (DANCE/EVEC) on Cell Proliferation, Motility, and Invasion. <i>Journal of Biological Chemistry</i> , 2002, 277, 27367-27377.	1.6	141
71	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015, 12, 1197-1204.	9.0	140
72	GBA1 deficiency negatively affects physiological β -synuclein tetramers and related multimers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 798-803.	3.3	139

#	ARTICLE	IF	CITATIONS
73	Systematic Interactome Mapping and Genetic Perturbation Analysis of a <i>C. elegans</i> TGF- β Signaling Network. <i>Molecular Cell</i> , 2004, 13, 469-482.	4.5	136
74	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005, 5, 3531-3536.	1.3	135
75	Temporal Profiling of the Adipocyte Proteome during Differentiation Using a Five-Plex SILAC Based Strategy. <i>Journal of Proteome Research</i> , 2009, 8, 48-58.	1.8	133
76	Proteomic analysis of human follicular fluid: A new perspective towards understanding folliculogenesis. <i>Journal of Proteomics</i> , 2013, 87, 68-77.	1.2	129
77	The keratoconus corneal proteome: Loss of epithelial integrity and stromal degeneration. <i>Journal of Proteomics</i> , 2013, 87, 122-131.	1.2	125
78	Inhibition of Spleen Tyrosine Kinase Potentiates Paclitaxel-Induced Cytotoxicity in Ovarian Cancer Cells by Stabilizing Microtubules. <i>Cancer Cell</i> , 2015, 28, 82-96.	7.7	125
79	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014, 11, 6.	1.1	122
80	Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3827-E3836.	3.3	122
81	Phosphoproteome Analysis of HeLa Cells Using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC). <i>Journal of Proteome Research</i> , 2005, 4, 1661-1671.	1.8	121
82	A Quantitative Proteomic Approach for Identification of Potential Biomarkers in Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 4289-4298.	1.8	121
83	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.	2.1	121
84	Genomewide mRNA profiling of esophageal squamous cell carcinoma for identification of cancer biomarkers. <i>Cancer Biology and Therapy</i> , 2009, 8, 36-46.	1.5	121
85	Proteogenomics. <i>Proteomics</i> , 2011, 11, 620-630.	1.3	121
86	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. <i>Genome Research</i> , 2015, 25, 1536-1545.	2.4	121
87	The Ret Receptor Protein Tyrosine Kinase Associates with the SH2-containing Adapter Protein Grb10. <i>Journal of Biological Chemistry</i> , 1995, 270, 21461-21463.	1.6	118
88	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.	2.1	117
89	Cloning and characterization of PAK5, a novel member of mammalian p21-activated kinase-II subfamily that is predominantly expressed in brain. <i>Oncogene</i> , 2002, 21, 3939-3948.	2.6	114
90	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014, 11, 29.	1.1	114

#	ARTICLE	IF	CITATIONS
91	Oncogenic RET Receptors Display Different Autophosphorylation Sites and Substrate Binding Specificities. <i>Journal of Biological Chemistry</i> , 1996, 271, 5309-5312.	1.6	113
92	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.	3.3	113
93	Identification of miR-21 targets in breast cancer cells using a quantitative proteomic approach. <i>Proteomics</i> , 2009, 9, 1374-1384.	1.3	113
94	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014, 11, 1.	1.1	113
95	Src-like Adaptor Protein (Slap) Is a Negative Regulator of T Cell Receptor Signaling. <i>Journal of Experimental Medicine</i> , 2000, 191, 463-474.	4.2	111
96	Use of mass spectrometry-derived data to annotate nucleotide and protein sequence databases. <i>Trends in Biochemical Sciences</i> , 2001, 26, 54-61.	3.7	111
97	Chemical Rescue of a Mutant Enzyme in Living Cells. <i>Science</i> , 2006, 311, 1293-1297.	6.0	111
98	Proteomics of Follicular Fluid From Women With Polycystic Ovary Syndrome Suggests Molecular Defects in Follicular Development. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, 744-753.	1.8	109
99	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.	1.6	108
100	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	1.3	106
101	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.	1.6	103
102	The dynamic stress-induced O-GlcNAc highlights functions for O-GlcNAc in regulating DNA damage/repair and other cellular pathways. <i>Amino Acids</i> , 2011, 40, 793-808.	1.2	103
103	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011, 12, 510-522.	1.5	102
104	Temporal Profiling of the Secretome during Adipogenesis in Humans. <i>Journal of Proteome Research</i> , 2010, 9, 5228-5238.	1.8	100
105	Ubiquilin 2 modulates ALS/FTD-linked FUS-RNA complex dynamics and stress granule formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11485-E11494.	3.3	100
106	Electron transfer dissociation mass spectrometry in proteomics. <i>Proteomics</i> , 2012, 12, 530-542.	1.3	99
107	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001, 17, 685-687.	2.9	98
108	Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2008, 80, 4825-4835.	3.2	97

#	ARTICLE	IF	CITATIONS
109	A Novel Proteomic Approach for Specific Identification of Tyrosine Kinase Substrates Using [13C]Tyrosine. <i>Journal of Biological Chemistry</i> , 2004, 279, 15805-15813.	1.6	96
110	Mac-2-binding protein is a diagnostic marker for biliary tract carcinoma. <i>Cancer</i> , 2004, 101, 1609-1615.	2.0	95
111	Global Impact of Oncogenic Src on a Phosphotyrosine Proteome. <i>Journal of Proteome Research</i> , 2008, 7, 3447-3460.	1.8	90
112	A network map of IL-33 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2018, 12, 615-624.	1.8	90
113	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. <i>Molecular Biotechnology</i> , 2011, 48, 87-95.	1.3	87
114	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. <i>PLoS ONE</i> , 2015, 10, e0143066.	1.1	87
115	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.	1.5	85
116	A network map of Interleukin-10 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2016, 10, 61-67.	1.8	85
117	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005, 5, 3506-3519.	1.3	82
118	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800105.	0.8	82
119	A Network Map of FGF-1/FGFR Signaling System. <i>Journal of Signal Transduction</i> , 2014, 2014, 1-16.	2.0	80
120	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.	1.5	79
121	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.	1.9	77
122	LC-MS/MS Analysis of Differentially Expressed Glioblastoma Membrane Proteome Reveals Altered Calcium Signaling and Other Protein Groups of Regulatory Functions. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013565.	2.5	76
123	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.	1.6	75
124	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	6.5	75
125	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. <i>Genome Research</i> , 2018, 28, 25-36.	2.4	75
126	Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) for Studying Dynamics of Protein Abundance and Posttranslational Modifications. <i>Science Signaling</i> , 2005, 2005, pl2-pl2.	1.6	74

#	ARTICLE	IF	CITATIONS
127	Differentially expressed genes in pancreatic ductal adenocarcinomas identified through serial analysis of gene expression. <i>Cancer Biology and Therapy</i> , 2004, 3, 1254-1261.	1.5	73
128	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017, 29, 14-23.	2.7	73
129	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	3.7	72
130	A network map of BDNF/TRKB and BDNF/p75NTR signaling system. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 301-307.	1.8	72
131	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	5.8	72
132	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.	0.4	71
133	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.	1.4	71
134	Calcium calmodulin dependent kinase kinase 2 - a novel therapeutic target for gastric adenocarcinoma. <i>Cancer Biology and Therapy</i> , 2015, 16, 336-345.	1.5	71
135	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018, 17, 759-769.	1.8	70
136	Src-like adaptor protein (Slap) is a negative regulator of mitogenesis. <i>Current Biology</i> , 1998, 8, 975-978.	1.8	67
137	O-Linked N-Acetylglucosamine Modification on CCAAT Enhancer-binding Protein β . <i>Journal of Biological Chemistry</i> , 2009, 284, 19248-19254.	1.6	66
138	Identification of Src tyrosine kinase substrates in platelet-derived growth factor receptor signaling. <i>Molecular Oncology</i> , 2009, 3, 439-450.	2.1	65
139	A pathway map of prolactin signaling. <i>Journal of Cell Communication and Signaling</i> , 2012, 6, 169-173.	1.8	65
140	The Escherichia coli Phosphotyrosine Proteome Relates to Core Pathways and Virulence. <i>PLoS Pathogens</i> , 2013, 9, e1003403.	2.1	65
141	Proteomics goes quantitative: measuring protein abundance. <i>Trends in Biotechnology</i> , 2002, 20, 361-364.	4.9	64
142	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005, 5, 3765-3777.	1.3	63
143	Identification of c-Src Tyrosine Kinase Substrates Using Mass Spectrometry and Peptide Microarrays. <i>Journal of Proteome Research</i> , 2008, 7, 3900-3910.	1.8	62
144	Synovial fluid proteome in rheumatoid arthritis. <i>Clinical Proteomics</i> , 2016, 13, 12.	1.1	62

#	ARTICLE	IF	CITATIONS
145	Inhibition of Adipocyte Differentiation by Resistin-like Molecule $\hat{\pm}$. Journal of Biological Chemistry, 2002, 277, 42011-42016.	1.6	61
146	Multiple pathways for <i>Plasmodium</i> ookinete invasion of the mosquito midgut. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E492-500.	3.3	61
147	A Proteomic Analysis of Human Hemodialysis Fluid. Molecular and Cellular Proteomics, 2005, 4, 637-650.	2.5	60
148	Quantitative phosphoproteomics reveals crosstalk between phosphorylation and O^6GlcNAc in the DNA damage response pathway. Proteomics, 2015, 15, 591-607.	1.3	60
149	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. Genome Research, 2017, 27, 133-144.	2.4	60
150	Architectural Organization of the Metabolic Regulatory Enzyme Ghrelin O-Acyltransferase. Journal of Biological Chemistry, 2013, 288, 32211-32228.	1.6	59
151	Genome annotation of <i>Anopheles gambiae</i> using mass spectrometry-derived data. BMC Genomics, 2005, 6, 128.	1.2	58
152	Identifying targets of miR-143 using a SILAC-based proteomic approach. Molecular BioSystems, 2010, 6, 1873.	2.9	58
153	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. Genome Research, 2011, 21, 1872-1881.	2.4	58
154	SILAC -based quantitative proteomic analysis of gastric cancer secretome. Proteomics - Clinical Applications, 2013, 7, 355-366.	0.8	57
155	Pancreatic Cancer Database. Cancer Biology and Therapy, 2014, 15, 963-967.	1.5	57
156	A multicellular signal transduction network of AGE/RAGE signaling. Journal of Cell Communication and Signaling, 2013, 7, 19-23.	1.8	54
157	Characterization of B61, the Ligand for the Eck Receptor Protein-Tyrosine Kinase. Journal of Biological Chemistry, 1995, 270, 5636-5641.	1.6	53
158	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.	1.6	53
159	Temporal Analysis of Neural Differentiation Using Quantitative Proteomics. Journal of Proteome Research, 2009, 8, 1315-1326.	1.8	53
160	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. PLoS Pathogens, 2015, 11, e1005346.	2.1	53
161	Identification of novel highly expressed genes in pancreatic ductal adenocarcinomas through a bioinformatics analysis of expressed sequence tags. Cancer Biology and Therapy, 2004, 3, 1081-1089.	1.5	52
162	Identification of head and neck squamous cell carcinoma biomarker candidates through proteomic analysis of cancer cell secretome. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2308-2316.	1.1	52

#	ARTICLE	IF	CITATIONS
163	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3184-3198.	2.5	52
164	Heterogeneity of Pancreatic Cancer Metastases in a Single Patient Revealed by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2803-2811.	2.5	52
165	Role of p38 in Replication of <i>Trypanosoma brucei</i> Kinetoplast DNA. <i>Molecular and Cellular Biology</i> , 2006, 26, 5382-5393.	1.1	51
166	Secretome analysis of the fungus <i>Trichoderma harzianum</i> grown on cellulose. <i>Proteomics</i> , 2012, 12, 2716-2728.	1.3	51
167	Identification of differentially expressed serum proteins in gastric adenocarcinoma. <i>Journal of Proteomics</i> , 2015, 127, 80-88.	1.2	51
168	Evaluation of Several MS/MS Search Algorithms for Analysis of Spectra Derived from Electron Transfer Dissociation Experiments. <i>Analytical Chemistry</i> , 2009, 81, 7170-7180.	3.2	50
169	Quantitative phosphoproteomic analysis of IL-3-mediated signaling. <i>Proteomics</i> , 2015, 15, 532-544.	1.3	50
170	Toll and interleukin-1 receptor (TIR) domain-containing proteins in plants: a genomic perspective. <i>Trends in Plant Science</i> , 2002, 7, 388-391.	4.3	49
171	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.	0.9	49
172	Cloning of a novel phosphotyrosine binding domain containing molecule, Odin, involved in signaling by receptor tyrosine kinases. <i>Oncogene</i> , 2002, 21, 8029-8036.	2.6	48
173	Computational and experimental analysis reveals a novel Src family kinase in the <i>C. elegans</i> genome. <i>Bioinformatics</i> , 2003, 19, 169-172.	1.8	48
174	Comparative proteomics of human embryonic stem cells and embryonal carcinoma cells. <i>Proteomics</i> , 2010, 10, 1359-1373.	1.3	48
175	TSLP Signaling Network Revealed by SILAC-Based Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M112.017764.	2.5	47
176	Identification of Targets of c-Src Tyrosine Kinase by Chemical Complementation and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 355-369.	2.5	47
177	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. <i>Nature Communications</i> , 2020, 11, 4225.	5.8	47
178	Phosphotyrosine Mapping in Bcr/Abl Oncoprotein Using Phosphotyrosine-specific Immunium Ion Scanning. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 138-145.	2.5	46
179	Signaling network of Oncostatin M pathway. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 103-108.	1.8	46
180	Signaling Network Map of Endothelial TEK Tyrosine Kinase. <i>Journal of Signal Transduction</i> , 2014, 2014, 1-6.	2.0	46

#	ARTICLE	IF	CITATIONS
181	Proteomics of Human Aqueous Humor. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 283-293.	1.0	46
182	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.	4.2	45
183	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.	0.8	45
184	Comprehensive proteomic analysis of human bile. <i>Proteomics</i> , 2011, 11, 4443-4453.	1.3	44
185	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021, 69, 103465.	2.7	44
186	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. <i>Oncotarget</i> , 2015, 6, 29143-29160.	0.8	44
187	Differential Membrane Proteomics Using ¹⁸ O-Labeling To Identify Biomarkers for Cholangiocarcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 4670-4677.	1.8	43
188	Screening for therapeutic targets of vorinostat by SILAC-based proteomic analysis in human breast cancer cells. <i>Proteomics</i> , 2010, 10, 1029-1039.	1.3	43
189	A multi-omic analysis of human naïve CD4+ T cells. <i>BMC Systems Biology</i> , 2015, 9, 75.	3.0	43
190	Activated Epidermal Growth Factor Receptor as a Novel Target in Pancreatic Cancer Therapy. <i>Journal of Proteome Research</i> , 2008, 7, 4651-4658.	1.8	42
191	Proteogenomic Analysis of <i>Candida glabrata</i> using High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 247-260.	1.8	42
192	A proteogenomic approach to map the proteome of an unsequenced pathogen – <i>Leishmania donovani</i> . <i>Proteomics</i> , 2012, 12, 832-844.	1.3	42
193	Identifying novel targets of oncogenic EGF receptor signaling in lung cancer through global phosphoproteomics. <i>Proteomics</i> , 2015, 15, 340-355.	1.3	42
194	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.	2.5	42
195	The non-receptor tyrosine kinase TNK2/ACK1 is a novel therapeutic target in triple negative breast cancer. <i>Oncotarget</i> , 2017, 8, 2971-2983.	0.8	42
196	Differences in signaling through the B-cell leukemia oncoprotein CRLF2 in response to TSLP and through mutant JAK2. <i>Blood</i> , 2012, 120, 2853-2863.	0.6	41
197	Phosphoproteome of <i>Cryptococcus neoformans</i> . <i>Journal of Proteomics</i> , 2014, 97, 287-295.	1.2	41
198	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.	1.8	41

#	ARTICLE	IF	CITATIONS
199	Acute Kidney Injury in Severe COVID-19 Has Similarities to Sepsis-Associated Kidney Injury. Mayo Clinic Proceedings, 2021, 96, 2561-2575.	1.4	41
200	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. Journal of Clinical Investigation, 2019, 129, 4708-4723.	3.9	41
201	PathBuilder™ open source software for annotating and developing pathway resources. Bioinformatics, 2009, 25, 2860-2862.	1.8	40
202	Moving from unsequenced to sequenced genome: Reanalysis of the proteome of Leishmania donovani. Journal of Proteomics, 2014, 97, 48-61.	1.2	40
203	Common pitfalls in bioinformatics-based analyses: look before you leap. Trends in Genetics, 2001, 17, 541-545.	2.9	39
204	Applications of Proteomics to Lab Diagnosis. Annual Review of Pathology: Mechanisms of Disease, 2008, 3, 485-498.	9.6	39
205	Quantitative temporal proteomic analysis of human embryonic stem cell differentiation into oligodendrocyte progenitor cells. Proteomics, 2011, 11, 4007-4020.	1.3	39
206	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar021-bar021.	1.4	39
207	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. Malaria Journal, 2013, 12, 216.	0.8	39
208	Analysis of Tyrosine Phosphorylation Sites in Signaling Molecules by a Phosphotyrosine-Specific Immonium Ion Scanning Method. Science Signaling, 2002, 2002, pl16-pl16.	1.6	38
209	LC-MS-based serum metabolomic analysis reveals dysregulation of phosphatidylcholines in esophageal squamous cell carcinoma. Journal of Proteomics, 2015, 127, 96-102.	1.2	38
210	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous cell carcinoma. Proteomics, 2015, 15, 374-382.	1.3	38
211	Cloning of a novel signaling molecule, AMSH-2, that potentiates transforming growth factor beta signaling. BMC Cell Biology, 2004, 5, 2.	3.0	37
212	RAPID: Resource of Asian Primary Immunodeficiency Diseases. Nucleic Acids Research, 2009, 37, D863-D867.	6.5	37
213	Characterizing the normal proteome of human ciliary body. Clinical Proteomics, 2013, 10, 9.	1.1	37
214	Human adenine nucleotide translocases physically and functionally interact with respirasomes. Molecular Biology of the Cell, 2017, 28, 1489-1506.	0.9	37
215	Development of a multiomics model for identification of predictive biomarkers for COVID-19 severity: a retrospective cohort study. The Lancet Digital Health, 2022, 4, e632-e645.	5.9	37
216	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.	1.6	36

#	ARTICLE	IF	CITATIONS
217	Copy-number variants in patients with a strong family history of pancreatic cancer. <i>Cancer Biology and Therapy</i> , 2007, 6, 1592-1599.	1.5	36
218	Systematic evaluation of alternating CID and ETD fragmentation for phosphorylated peptides. <i>Proteomics</i> , 2011, 11, 2568-2572.	1.3	36
219	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2016, 6, 36132.	1.6	36
220	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.	1.0	35
221	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.	1.0	35
222	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.	1.8	35
223	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 295-303.	1.0	34
224	Macrophage migration inhibitory factor - a therapeutic target in gallbladder cancer. <i>BMC Cancer</i> , 2015, 15, 843.	1.1	33
225	Proteomic characterization of Her2/neu overexpressing breast cancer cells. <i>Proteomics</i> , 2010, 10, 3800-3810.	1.3	32
226	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.	2.5	32
227	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021, 156, 988-1002.	2.1	32
228	cDNA Cloning and Characterization of a Cdk7 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.	1.6	32
229	Identification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, 22-35.	0.4	31
230	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.	1.8	31
231	Chronic exposure to chewing tobacco selects for overexpression of stearoyl-CoA desaturase in normal oral keratinocytes. <i>Cancer Biology and Therapy</i> , 2015, 16, 1593-1603.	1.5	31
232	Integrated Stress Response and Decreased ECM in Cultured Stromal Cells From Keratoconus Corneas. <i>Journal of Cellular Biochemistry</i> , 2018, 59, 2977.		31
233	SILAC for Global Phosphoproteomic Analysis. <i>Methods in Molecular Biology</i> , 2009, 527, 107-116.	0.4	30
234	Monoclonal Antibody Cocktail as an Enrichment Tool for Acetylome Analysis. <i>Analytical Chemistry</i> , 2011, 83, 3623-3626.	3.2	30

#	ARTICLE	IF	CITATIONS
235	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.	1.3	30
236	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2016, 13, 29.	1.1	30
237	The mitochondrial carrier SFXN1 is critical for complex III integrity and cellular metabolism. <i>Cell Reports</i> , 2021, 34, 108869.	2.9	30
238	Quantitative proteomics for identification of cancer biomarkers. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1080-1089.	0.8	29
239	NetSlim: high-confidence curated signaling maps. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar032-bar032.	1.4	29
240	Botch Is a β -Glutamyl Cyclotransferase that Deglycinates and Antagonizes Notch. <i>Cell Reports</i> , 2014, 7, 681-688.	2.9	29
241	Proteomic Analysis of <i>Plasmodium</i> Merosomes: The Link between Liver and Blood Stages in Malaria. <i>Journal of Proteome Research</i> , 2019, 18, 3404-3418.	1.8	29
242	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.	2.7	27
243	Quantitative proteomics for identifying biomarkers for Rabies. <i>Clinical Proteomics</i> , 2013, 10, 3.	1.1	27
244	PHD3-mediated prolyl hydroxylation of nonmuscle actin impairs polymerization and cell motility. <i>Molecular Biology of the Cell</i> , 2014, 25, 2788-2796.	0.9	27
245	Comprehensive Proteomics Analysis of Glycosomes from <i>Leishmania donovani</i> . <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 157-170.	1.0	27
246	Prediction of Candidate Primary Immunodeficiency Disease Genes Using a Support Vector Machine Learning Approach. <i>DNA Research</i> , 2009, 16, 345-351.	1.5	26
247	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.	1.2	26
248	Mutation@A Glance: An Integrative Web Application for Analysing Mutations from Human Genetic Diseases. <i>DNA Research</i> , 2010, 17, 197-208.	1.5	26
249	Regulation of Lipid Metabolism by Dicer Revealed through SILAC Mice. <i>Journal of Proteome Research</i> , 2012, 11, 2193-2205.	1.8	26
250	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. <i>Clinical Proteomics</i> , 2012, 9, 12.	1.1	26
251	Proteomic analysis of purified protein derivative of <i>Mycobacterium tuberculosis</i> . <i>Clinical Proteomics</i> , 2013, 10, 8.	1.1	26
252	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.	2.5	26

#	ARTICLE	IF	CITATIONS
253	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.	1.0	26
254	Phosphoproteomic analysis identifies CLK1 as a novel therapeutic target in gastric cancer. <i>Gastric Cancer</i> , 2020, 23, 796-810.	2.7	26
255	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. <i>Life Science Alliance</i> , 2021, 4, e202000774.	1.3	26
256	From biological databases to platforms for biomedical discovery. <i>Trends in Biotechnology</i> , 2003, 21, 263-268.	4.9	25
257	Assessing Reproducibility of a Protein Dynamics Study Using in Vivo Labeling and Liquid Chromatography Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 2739-2744.	3.2	25
258	Overexpression of ribosome binding protein 1 (RRBP1) in breast cancer. <i>Clinical Proteomics</i> , 2012, 9, 7.	1.1	25
259	FAM190A Deficiency Creates a Cell Division Defect. <i>American Journal of Pathology</i> , 2013, 183, 296-303.	1.9	25
260	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. <i>Clinical Proteomics</i> , 2013, 10, 14.	1.1	25
261	A knowledgebase resource for interleukin-17 family mediated signaling. <i>Journal of Cell Communication and Signaling</i> , 2015, 9, 291-296.	1.8	25
262	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. <i>Cancer Biology and Therapy</i> , 2016, 17, 219-229.	1.5	25
263	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.	1.0	25
264	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.	2.5	25
265	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
266	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100134.	2.5	25
267	Utility of Bile Duct Brushings for the Early Detection of Cholangiocarcinoma in Patients With Primary Sclerosing Cholangitis. <i>Journal of Clinical Gastroenterology</i> , 2006, 40, 336-341.	1.1	24
268	A Bioinformatics Resource for TWEAK-Fn14 Signaling Pathway. <i>Journal of Signal Transduction</i> , 2012, 2012, 1-10.	2.0	24
269	Proteomic analysis of the abomasal mucosal response following infection by the nematode, <i>Haemonchus contortus</i> , in genetically resistant and susceptible sheep. <i>Journal of Proteomics</i> , 2012, 75, 2141-2152.	1.2	24
270	PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2829-2838.	2.5	24

#	ARTICLE	IF	CITATIONS
271	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.	3.3	24
272	Integrated Proteomic and Metabolic Analysis of Breast Cancer Progression. <i>PLoS ONE</i> , 2013, 8, e76220.	1.1	24
273	Downregulation of cornulin in esophageal squamous cell carcinoma. <i>Acta Histochemica</i> , 2013, 115, 89-99.	0.9	23
274	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.	1.8	23
275	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.	1.0	23
276	Proteomic Analysis of the Human Anterior Pituitary Gland. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 759-769.	1.0	23
277	Functional Annotation of Proteome Encoded by Human Chromosome 22. <i>Journal of Proteome Research</i> , 2014, 13, 2749-2760.	1.8	22
278	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.	1.0	22
279	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.	1.5	22
280	Sorbitol Is a Severity Biomarker for α -Mannosidosis with Therapeutic Implications. <i>Annals of Neurology</i> , 2021, 90, 887-900.	2.8	22
281	Proteomics for understanding miRNA biology. <i>Proteomics</i> , 2013, 13, 558-567.	1.3	21
282	Identification of miR-145 targets through an integrated omics analysis. <i>Molecular BioSystems</i> , 2015, 11, 197-207.	2.9	21
283	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 225-233.	1.6	21
284	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100069.	2.5	21
285	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.	1.8	21
286	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021, 20, 4165-4175.	1.8	21
287	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021, 17, 454-463.	1.4	21
288	Small molecule inhibitor screening identified HSP90 inhibitor 17-AAG as potential therapeutic agent for gallbladder cancer. <i>Oncotarget</i> , 2017, 8, 26169-26184.	0.8	21

#	ARTICLE	IF	CITATIONS
289	Neuronal activity induces glucosylceramide that is secreted via exosomes for lysosomal degradation in glia. <i>Science Advances</i> , 2022, 8, .	4.7	21
290	A comprehensive curated resource for follicle stimulating hormone signaling. <i>BMC Research Notes</i> , 2011, 4, 408.	0.6	20
291	Transcriptomic Profiling of Medial Temporal Lobe Epilepsy. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, .	0.4	20
292	Long non-coding RNA expression in primary human monocytes. <i>Genomics</i> , 2016, 108, 37-45.	1.3	20
293	USP9X controls translation efficiency via deubiquitination of eukaryotic translation initiation factor 4A1. <i>Nucleic Acids Research</i> , 2018, 46, 823-839.	6.5	20
294	Microarrays go live – new prospects for proteomics. <i>Trends in Biochemical Sciences</i> , 2001, 26, 639-641.	3.7	19
295	Upstream stimulatory factors regulate the C/EBP β gene during differentiation of 3T3-L1 preadipocytes. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 517-521.	1.0	19
296	Access Guide to Human Proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 1.21.	25.8	19
297	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.	2.2	19
298	Mapping Keratoconus Molecular Substrates by Multiplexed High-Resolution Proteomics of Unpooled Corneas. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 583-597.	1.0	19
299	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020, 92, 14466-14475.	3.2	19
300	A Bioinformatics Analysis of Protein Tyrosine Phosphatases in Humans. <i>DNA Research</i> , 2005, 12, 79-89.	1.5	18
301	¹⁸ O Labeling for a Quantitative Proteomic Analysis of Glycoproteins in Hepatocellular Carcinoma. <i>Clinical Proteomics</i> , 2008, 4, 137-155.	1.1	18
302	Proteome profiling of wild type and lumican-deficient mouse corneas. <i>Journal of Proteomics</i> , 2011, 74, 1895-1905.	1.2	18
303	A multilectin affinity approach for comparative glycoprotein profiling of rheumatoid arthritis and spondyloarthritis. <i>Clinical Proteomics</i> , 2013, 10, 11.	1.1	18
304	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. <i>Clinical Proteomics</i> , 2014, 11, 39.	1.1	18
305	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2014, 11, 5.	1.1	18
306	Phosphotyrosine profiling of human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2018, 15, 29.	1.1	18

#	ARTICLE	IF	CITATIONS
307	Dickkopf Homolog 3 (DKK3) Acts as a Potential Tumor Suppressor in Gallbladder Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1121.	1.3	18
308	Human Proteinpedia as a Resource for Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2038-2047.	2.5	17
309	Proteomic analysis of an unsequenced plant "Mangifera indica. <i>Journal of Proteomics</i> , 2012, 75, 5793-5796.	1.2	17
310	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.	0.8	17
311	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.	1.8	17
312	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021, 81, 2094-2111.e9.	4.5	17
313	Overlapping of MINK and CHRNE gene loci in the course of mammalian evolution. <i>Nucleic Acids Research</i> , 2002, 30, 2906-2910.	6.5	16
314	A manually curated functional annotation of the human X chromosome. <i>Nature Genetics</i> , 2005, 37, 331-332.	9.4	16
315	Unbiased identification of substrates of protein tyrosine phosphatase ptp ϵ 3 in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	2.1	16
316	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	1.3	16
317	Mitochondrial localization and moderated activity are key to murine erythroid enucleation. <i>Blood Advances</i> , 2021, 5, 2490-2504.	2.5	16
318	Comparison of Peptide Array Substrate Phosphorylation of c-Raf and Mitogen Activated Protein Kinase Kinase Kinase 8. <i>PLoS ONE</i> , 2009, 4, e6440.	1.1	16
319	Identification of Protein Ubiquitylation by Electrospray Ionization Tandem Mass Spectrometric Analysis of Sulfonated Tryptic Peptides. <i>Analytical Chemistry</i> , 2006, 78, 3681-3687.	3.2	15
320	Overexpression of Periostin and Lumican in Esophageal Squamous Cell Carcinoma. <i>Cancers</i> , 2010, 2, 133-142.	1.7	15
321	The interactome of a PTB domain-containing adapter protein, Odin, revealed by SILAC. <i>Journal of Proteomics</i> , 2011, 74, 294-303.	1.2	15
322	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.	1.8	15
323	Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. <i>Journal of Proteomics</i> , 2014, 108, 306-315.	1.2	15
324	Quantitative phosphoproteomic analysis reveals reciprocal activation of receptor tyrosine kinases between cancer epithelial cells and stromal fibroblasts. <i>Clinical Proteomics</i> , 2018, 15, 21.	1.1	15

#	ARTICLE	IF	CITATIONS
325	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1700101.	0.8	15
326	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. <i>Molecular Omics</i> , 2021, 17, 939-947.	1.4	15
327	Proteomic resources: Integrating biomedical information in humans. <i>Gene</i> , 2005, 364, 13-18.	1.0	14
328	Rapid Characterization of Candidate Biomarkers for Pancreatic Cancer Using Cell Microarrays (CMAs). <i>Journal of Proteome Research</i> , 2012, 11, 5556-5563.	1.8	14
329	Proteomic analysis and genome annotation of <i>Pichia pastoris</i> , a recombinant protein expression host. <i>Proteomics</i> , 2014, 14, 2769-2779.	1.3	14
330	Brain Proteomics of <i>Anopheles gambiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 421-437.	1.0	14
331	Targeting focal adhesion kinase overcomes erlotinib resistance in smoke induced lung cancer by altering phosphorylation of epidermal growth factor receptor. <i>Oncoscience</i> , 2018, 5, 21-38.	0.9	14
332	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.	0.7	14
333	Is the Proteome of Bronchoalveolar Lavage Extracellular Vesicles a Marker of Advanced Lung Cancer?. <i>Cancers</i> , 2020, 12, 3450.	1.7	14
334	Extra-cellular vesicles carry proteome of cancer hallmarks. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 398-436.	3.0	14
335	Gene Expression Profiling of Tuberculous Meningitis Co-infected with HIV. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, 235-244.	0.4	14
336	Gene Expression Profiling of Gastric Cancer. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 4, 74-82.	0.4	14
337	Chromosomal Localization of the Mouse Src-like Adapter Protein (Slap) Gene and Its Putative Human Homolog SLA. <i>Genomics</i> , 1995, 30, 623-625.	1.3	13
338	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
339	A phosphoproteomic screen demonstrates differential dependence on HER3 for MAP kinase pathway activation by distinct <i>PIK3CA</i> mutations. <i>Proteomics</i> , 2015, 15, 318-326.	1.3	13
340	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.	1.3	13
341	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	1.3	13
342	Molecular Alterations in Exocrine Neoplasms of the Pancreas. <i>Archives of Pathology and Laboratory Medicine</i> , 2009, 133, 405-412.	1.2	13

#	ARTICLE	IF	CITATIONS
343	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.	0.9	12
344	A breast cancer cell microarray (CMA) as a rapid method to characterize candidate biomarkers. <i>Cancer Biology and Therapy</i> , 2014, 15, 1593-1599.	1.5	12
345	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	1.7	12
346	PIM1 kinase promotes gallbladder cancer cell proliferation via inhibition of proline-rich Akt substrate of 40kDa (PRAS40). <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 163-177.	1.8	12
347	Mutation-Specific and Common Phosphotyrosine Signatures of KRAS G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021, 20, 670-683.	1.8	12
348	A Signaling Network of Thyroid-Stimulating Hormone. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, .	0.4	11
349	A network map of the gastrin signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2014, 8, 165-170.	1.8	11
350	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.	1.8	11
351	Phosphoproteomic profiling of tumor tissues identifies HSP27 Ser82 phosphorylation as a robust marker of early ischemia. <i>Scientific Reports</i> , 2015, 5, 13660.	1.6	11
352	Bioinformatics and Proteomics Approaches for Aging Research. <i>Biogerontology</i> , 2005, 6, 227-232.	2.0	10
353	TAGmapper: A web-based tool for mapping SAGE tags. <i>Gene</i> , 2005, 364, 123-129.	1.0	10
354	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020, 34, 301-305.	3.3	10
355	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.	1.8	10
356	Expanding the clinical and metabolic phenotype of DPM2 deficient congenital disorders of glycosylation. <i>Molecular Genetics and Metabolism</i> , 2021, 132, 27-37.	0.5	10
357	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021, 18, 25.	1.1	10
358	Proteomic Strategies to Characterize Signaling Pathways. <i>Methods in Molecular Biology</i> , 2013, 1007, 359-377.	0.4	9
359	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.	1.0	9
360	Integrated Proteomic and Phosphoproteomics Analysis of DKK3 Signaling Reveals Activated Kinase in the Most Aggressive Gallbladder Cancer. <i>Cells</i> , 2021, 10, 511.	1.8	9

#	ARTICLE	IF	CITATIONS
361	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.	1.7	9
362	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. <i>Annals of Indian Academy of Neurology</i> , 2009, 12, 3-11.	0.2	9
363	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.	1.8	9
364	Proteomic Signatures of Diffuse and Intestinal Subtypes of Gastric Cancer. <i>Cancers</i> , 2021, 13, 5930.	1.7	9
365	Mouse embryonic fibroblasts derived from Odin deficient mice display a hyperproliferative phenotype. <i>DNA Research</i> , 2004, 11, 285-92.	1.5	9
366	IL-11/IL11RA receptor mediated signaling: a web accessible knowledgebase. <i>Cell Communication and Adhesion</i> , 2013, 20, 81-86.	1.0	8
367	Downregulation of S100 Calcium Binding Protein A9 in Esophageal Squamous Cell Carcinoma. <i>Scientific World Journal</i> , The, 2015, 2015, 1-10.	0.8	8
368	A Novel Missense Variant in PHF6 Gene Causing B�rjeson-Forssman-Lehman Syndrome. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1403-1409.	1.1	8
369	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 394-404.	1.2	8
370	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.	0.7	8
371	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.	1.0	8
372	Cloning of rat thymic stromal lymphopoietin receptor (TSLPR) and characterization of genomic structure of murine Tslpr gene. <i>Gene</i> , 2002, 284, 161-168.	1.0	7
373	BioBuilder as a database development and functional annotation platform for proteins. <i>BMC Bioinformatics</i> , 2004, 5, 43.	1.2	7
374	Ablation of Dicer leads to widespread perturbation of signaling pathways. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 389-394.	1.0	7
375	Activating Mutations in <i>PIK3CA</i> Lead to Widespread Modulation of the Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , 2015, 14, 3882-3891.	1.8	7
376	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 8453-8460.	3.2	7
377	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. <i>Indian Journal of Ophthalmology</i> , 2021, 69, 647.	0.5	7
378	Proteomics of Human Bile. , 2007, , 399-414.		7

#	ARTICLE	IF	CITATIONS
379	TMT-Based Multiplexed Quantitation of N-Glycopeptides Reveals Glycoproteome Remodeling Induced by Oncogenic Mutations. ACS Omega, 2022, 7, 11023-11032.	1.6	7
380	Resources for full-length cDNAs. Trends in Biochemical Sciences, 2002, 27, 266-267.	3.7	6
381	Phosphoproteomics. Current Protocols in Protein Science, 2007, 50, Unit 24.4.	2.8	6
382	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.	1.8	6
383	In Silico Analysis of Ion Channels and Their Correlation with Epithelial to Mesenchymal Transition in Breast Cancer. Cancers, 2022, 14, 1444.	1.7	6
384	Absolute systems biology – measuring dynamics of protein modifications. Trends in Biotechnology, 2003, 21, 467-470.	4.9	5
385	PAX-SIX-EYA-DACH Network modulates GATA-FOG function in fly hematopoiesis and human erythropoiesis. Development (Cambridge), 2019, 147, .	1.2	5
386	Shukla-Vernon Syndrome: A Second Family with a Novel Variant in the BCORL1 Gene. Genes, 2021, 12, 452.	1.0	5
387	Very long-chain acyl-CoA synthetase 3 mediates onco-sphingolipid metabolism in malignant glioma. Medical Research Archives, 2021, 9, .	0.1	5
388	Automated data-driven mass spectrometry for improved analysis of lipids with dual dissociation techniques. Journal of Mass Spectrometry and Advances in the Clinical Lab, 2021, 22, 43-49.	1.3	5
389	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
390	Overexpression of Kinesin Associated Protein 3 (KIFAP3) in Breast Cancer. Journal of Proteomics and Bioinformatics, 2012, 05, 122-126.	0.4	4
391	Analysis of Cellular Tyrosine Phosphorylation via Chemical Rescue of Conditionally Active Abl Kinase. Biochemistry, 2018, 57, 1390-1398.	1.2	4
392	Ethylmalonic encephalopathy ETHE1 p. D165H mutation alters the mitochondrial function in human skeletal muscle proteome. Mitochondrion, 2021, 58, 64-71.	1.6	4
393	A pathway map of signaling events triggered upon SARS-CoV infection. Journal of Cell Communication and Signaling, 2021, 15, 595-600.	1.8	4
394	Identification of spleen tyrosine kinase as a potential therapeutic target for esophageal squamous cell carcinoma using reverse phase protein arrays. Oncotarget, 2018, 9, 18422-18434.	0.8	4
395	Metallothionein immunohistochemistry has high sensitivity and specificity for detection of Wilson disease. Modern Pathology, 2022, 35, 946-955.	2.9	4
396	Characterization of promoter region and genomic structure of the murine and human genes encoding Src like adapter protein. Gene, 2001, 262, 267-273.	1.0	3

#	ARTICLE	IF	CITATIONS
397	Unraveling the human interactome: lessons from the yeast. Drug Discovery Today: TARGETS, 2004, 3, 79-84.	0.5	3
398	Comparative Proteomic Analysis of Candida albicans and Candida glabrata. Clinical Proteomics, 2010, 6, 163-173.	1.1	3
399	Effects of transmembrane and juxtamembrane domains on proliferative ability of TSLP receptor. Molecular Immunology, 2010, 47, 1207-1215.	1.0	3
400	Maternal serum lipidomics identifies lysophosphatidic acid as a predictor of small for gestational age neonates. Molecular Omics, 2021, 17, 956-966.	1.4	3
401	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. Journal of Proteome Research, 2021, 20, 4566-4577.	1.8	3
402	Deciphering the Interactions of SARS-CoV-2 Proteins with Human Ion Channels Using Machine-Learning-Based Methods. Pathogens, 2022, 11, 259.	1.2	3
403	Integrated analysis of CRLF2 signaling in acute lymphoblastic leukemia identifies Polo-like kinase 1 as a potential therapeutic target. Leukemia and Lymphoma, 2015, 56, 1524-1527.	0.6	2
404	A Next-Generation Sequencing-Based Molecular Approach to Characterize a Tick Vector in Lyme Disease. OMICS A Journal of Integrative Biology, 2018, 22, 565-574.	1.0	2
405	Family-Based Next-Generation Sequencing Study Identifies an <i>IL2RG</i> Variant in an Infant with Primary Immunodeficiency. OMICS A Journal of Integrative Biology, 2019, 23, 285-290.	1.0	2
406	A Novel LINS1 Truncating Mutation in Autosomal Recessive Nonsyndromic Intellectual Disability. Frontiers in Psychiatry, 2020, 11, 354.	1.3	2
407	Tyrosine Phosphoproteomics of Patient-Derived Xenografts Reveals Ephrin Type-B Receptor 4 Tyrosine Kinase as a Therapeutic Target in Pancreatic Cancer. Cancers, 2021, 13, 3404.	1.7	2
408	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. Mitochondrion, 2021, 60, 27-32.	1.6	2
409	Possible Role of the Activation Loop Tyrosine Residue (Y842) in FLT3/ITD Signaling May Be Mediated by SHP-2. Blood, 2005, 106, 1199-1199.	0.6	2
410	Machine Learning-Based Fragment Selection Improves the Performance of Qualitative PRM Assays. Journal of Proteome Research, 2022, 21, 2045-2054.	1.8	2
411	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. Proteomics, 0, , 2200077.	1.3	2
412	Multi-Protein Complexes Studied by Mass Spectrometry. Scientific World Journal, The, 2002, 2, 91-92.	0.8	1
413	Identification of targets of miR-200b by a SILAC-based quantitative proteomic approach. EuPA Open Proteomics, 2014, 4, 10-17.	2.5	1
414	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.	2.3	1

#	ARTICLE	IF	CITATIONS
415	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. <i>Cancers</i> , 2021, 13, 4234.	1.7	1
416	Differential Signaling through p190 and p210 Forms of BCR-ABL Fusion Proteins Revealed By Proteomic Analysis. <i>Blood</i> , 2015, 126, 3651-3651.	0.6	1
417	Quantitative Proteomic Profiling Unravels Dynamic Changes in the Myeloma Cell Proteome Treated with Valproic Acid (VPA). <i>Blood</i> , 2011, 118, 1847-1847.	0.6	1
418	Plasma Proteome Database. , 2007, , 129-136.		1
419	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.	0.8	1
420	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.	1.1	1
421	A functional annotation of subproteomes in human plasma. , 2006, , 329-351.		0
422	Mass Spectrometry Reveals Respiratory Viral Infection Biomarkers. <i>EBioMedicine</i> , 2017, 18, 21-22.	2.7	0
423	Moving to Translational Proteomics. <i>Proteomics</i> , 2017, 17, 1770042.	1.3	0
424	Proteomic Analysis of the Adipocyte Secretome. <i>Nutrition and Disease Prevention</i> , 2004, , 395-413.	0.1	0
425	Defining the Dynamic O α -GlcNAc Proteome. <i>FASEB Journal</i> , 2006, 20, A56.	0.2	0
426	A panel of biomarkers for esophageal squamous cell carcinoma. <i>FASEB Journal</i> , 2009, 23, 925.11.	0.2	0
427	Bone Marrow Hypoplasia Induced by Conditional Knockout of the RNase III Domain of Dicer-1. <i>Blood</i> , 2010, 116, 2226-2226.	0.6	0
428	The role of cardiolipin in defining the mammalian ANT interactome. <i>FASEB Journal</i> , 2013, 27, 1026.3.	0.2	0
429	Proteomics of Human Pancreatic Juice. , 2007, , 377-397.		0
430	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.	1.1	0