

Akhilesh Pandey

List of Publications by Year in descending order

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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	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.	3.8	4,931
2	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. <i>Neoplasia</i> , 2004, 6, 1-6.	5.3	3,212
3	Human Protein Reference Database--2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	14.5	2,882
4	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	27.8	2,173
5	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	27.8	1,948
6	Pyruvate Kinase M2 Is a PHD3-Stimulated Coactivator for Hypoxia-Inducible Factor 1. <i>Cell</i> , 2011, 145, 732-744.	28.9	1,210
7	Vesiclepedia: A Compendium for Extracellular Vesicles with Continuous Community Annotation. <i>PLoS Biology</i> , 2012, 10, e1001450.	5.6	1,064
8	Analysis of Proteins and Proteomes by Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2001, 70, 437-473.	11.1	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.	5.5	954
10	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	9.3	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.	7.1	874
12	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
13	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. <i>Nature</i> , 2014, 507, 195-200.	27.8	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.	2.2	766
15	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
16	The HUPO PSI's Molecular Interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
17	Human protein reference database--2006 update. <i>Nucleic Acids Research</i> , 2006, 34, D411-D414.	14.5	536
18	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004, 32, 497D-501.	14.5	534

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19	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	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.	7.1	489
21	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	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.	21.4	433
23	Biomarker Discovery from Pancreatic Cancer Secretome Using a Differential Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 157-171.	3.8	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.	7.1	410
25	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	12.6	398
26	Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin. <i>Nature Immunology</i> , 2000, 1, 59-64.	14.5	393
27	GCN5 acetyltransferase complex controls glucose metabolism through transcriptional repression of PGC-1 α . <i>Cell Metabolism</i> , 2006, 3, 429-438.	16.2	383
28	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005, 23, 951-959.	17.5	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.	3.8	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.	12.6	345
31	A curated compendium of phosphorylation motifs. <i>Nature Biotechnology</i> , 2007, 25, 285-286.	17.5	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.	6.5	306
33	Sequential phosphorylation of CCAAT enhancer-binding protein β by MAPK and glycogen synthase kinase 3 α is required for adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9766-9771.	7.1	293
34	Plasma Proteome Database as a resource for proteomics research: 2014 update. <i>Nucleic Acids Research</i> , 2014, 42, D959-D965.	14.5	273
35	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	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.	8.8	263

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37	A Compendium of Potential Biomarkers of Pancreatic Cancer. PLoS Medicine, 2009, 6, e1000046.	8.4	260
38	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. Methods in Molecular Biology, 2009, 577, 67-79.	0.9	245
39	Ribosomal Protein s15 Phosphorylation Mediates LRRK2 Neurodegeneration in Parkinson's Disease. Cell, 2014, 157, 472-485.	28.9	239
40	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
41	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
42	A Role for Thymic Stromal Lymphopoietin in CD4+ T Cell Development. Journal of Experimental Medicine, 2004, 200, 159-168.	8.5	208
43	Tackling the phosphoproteome: tools and strategies. Current Opinion in Chemical Biology, 2003, 7, 64-69.	6.1	206
44	An evaluation of human protein-protein interaction data in the public domain. BMC Bioinformatics, 2006, 7, S19.	2.6	201
45	Hsp70 and CHIP Selectively Mediate Ubiquitination and Degradation of Hypoxia-inducible Factor (HIF)-1 α but Not HIF-2 α . Journal of Biological Chemistry, 2010, 285, 3651-3663.	3.4	201
46	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
47	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
48	Comprehensive Proteomic Analysis of Human Pancreatic Juice. Journal of Proteome Research, 2004, 3, 1042-1055.	3.7	194
49	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
50	K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Pdh1. EMBO Journal, 2009, 28, 621-631.	7.8	193
51	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. Nature Protocols, 2008, 3, 505-516.	12.0	190
52	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
53	Dynamic Interplay between O-Linked N-Acetylglucosaminylation and Glycogen Synthase Kinase-3-dependent Phosphorylation. Molecular and Cellular Proteomics, 2007, 6, 1365-1379.	3.8	183
54	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. Molecular BioSystems, 2012, 8, 453-463.	2.9	179

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55	A Comprehensive Map of the Human Urinary Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 2734-2743.	3.7	176
56	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 1031-1039.	3.4	175
57	A Proteomic Approach for Quantitation of Phosphorylation Using Stable Isotope Labeling in Cell Culture. <i>Analytical Chemistry</i> , 2003, 75, 6043-6049.	6.5	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.	7.1	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.	7.1	163
60	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	4.6	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.	7.1	157
62	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
63	Loss of C9orf72 Enhances Autophagic Activity via Deregulated mTOR and TFEB Signaling. <i>PLoS Genetics</i> , 2016, 12, e1006443.	3.5	154
64	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	7.2	153
65	GPMAW – a software tool for analyzing proteins and peptides. <i>Trends in Biochemical Sciences</i> , 2001, 26, 687-689.	7.5	145
66	Proteogenomic Analysis of <i>Mycobacterium tuberculosis</i> By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	3.8	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.	3.8	142
69	Toward the human cellular microRNAome. <i>Genome Research</i> , 2017, 27, 1769-1781.	5.5	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.	3.4	141
71	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015, 12, 1197-1204.	19.0	140
72	GBA1 deficiency negatively affects physiological α -synuclein tetramers and related multimers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 798-803.	7.1	139

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73	Systematic Interactome Mapping and Genetic Perturbation Analysis of a C. elegans TGF- β^2 Signaling Network. Molecular Cell, 2004, 13, 469-482.	9.7	136
74	Plasma Proteome Database as a resource for proteomics research. Proteomics, 2005, 5, 3531-3536.	2.2	135
75	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
76	Proteomic analysis of human follicular fluid: A new perspective towards understanding folliculogenesis. Journal of Proteomics, 2013, 87, 68-77.	2.4	129
77	The keratoconus corneal proteome: Loss of epithelial integrity and stromal degeneration. Journal of Proteomics, 2013, 87, 122-131.	2.4	125
78	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
79	Proteomic analysis of human osteoarthritis synovial fluid. Clinical Proteomics, 2014, 11, 6.	2.1	122
80	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
81	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
82	A Quantitative Proteomic Approach for Identification of Potential Biomarkers in Hepatocellular Carcinoma. Journal of Proteome Research, 2008, 7, 4289-4298.	3.7	121
83	New Markers of Pancreatic Cancer Identified Through Differential Gene Expression Analyses: Claudin 18 and Annexin A8. American Journal of Surgical Pathology, 2008, 32, 188-196.	3.7	121
84	Genomewide mRNA profiling of esophageal squamous cell carcinoma for identification of cancer biomarkers. Cancer Biology and Therapy, 2009, 8, 36-46.	3.4	121
85	Proteogenomics. Proteomics, 2011, 11, 620-630.	2.2	121
86	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. Genome Research, 2015, 25, 1536-1545.	5.5	121
87	The Ret Receptor Protein Tyrosine Kinase Associates with the SH2-containing Adapter Protein Grb10. Journal of Biological Chemistry, 1995, 270, 21461-21463.	3.4	118
88	Malaria Parasite Invasion of the Mosquito Salivary Gland Requires Interaction between the Plasmodium TRAP and the Anopheles Saglin Proteins. PLoS Pathogens, 2009, 5, e1000265.	4.7	117
89	Cloning and characterization of PAK5, a novel member of mammalian p21-activated kinase-II subfamily that is predominantly expressed in brain. Oncogene, 2002, 21, 3939-3948.	5.9	114
90	Proteomic analysis of human vitreous humor. Clinical Proteomics, 2014, 11, 29.	2.1	114

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91	Oncogenic RET Receptors Display Different Autophosphorylation Sites and Substrate Binding Specificities. <i>Journal of Biological Chemistry</i> , 1996, 271, 5309-5312.	3.4	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.	7.1	113
93	Identification of miR-21 targets in breast cancer cells using a quantitative proteomic approach. <i>Proteomics</i> , 2009, 9, 1374-1384.	2.2	113
94	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014, 11, 1.	2.1	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.	8.5	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.	7.5	111
97	Chemical Rescue of a Mutant Enzyme in Living Cells. <i>Science</i> , 2006, 311, 1293-1297.	12.6	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.	3.6	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.	3.4	108
100	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	2.2	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.	3.4	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.	2.7	103
103	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
104	Temporal Profiling of the Secretome during Adipogenesis in Humans. <i>Journal of Proteome Research</i> , 2010, 9, 5228-5238.	3.7	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.	7.1	100
106	Electron transfer dissociation mass spectrometry in proteomics. <i>Proteomics</i> , 2012, 12, 530-542.	2.2	99
107	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001, 17, 685-687.	6.7	98
108	Comprehensive Comparison of Collision Induced Dissociation and Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2008, 80, 4825-4835.	6.5	97

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109	A Novel Proteomic Approach for Specific Identification of Tyrosine Kinase Substrates Using [13C]Tyrosine. Journal of Biological Chemistry, 2004, 279, 15805-15813.	3.4	96
110	Mac-2-binding protein is a diagnostic marker for biliary tract carcinoma. Cancer, 2004, 101, 1609-1615.	4.1	95
111	Global Impact of Oncogenic Src on a Phosphotyrosine Proteome. Journal of Proteome Research, 2008, 7, 3447-3460.	3.7	90
112	A network map of IL-33 signaling pathway. Journal of Cell Communication and Signaling, 2018, 12, 615-624.	3.4	90
113	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. Molecular Biotechnology, 2011, 48, 87-95.	2.4	87
114	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. PLoS ONE, 2015, 10, e0143066.	2.5	87
115	The Axl receptor tyrosine kinase is an adverse prognostic factor and a therapeutic target in esophageal adenocarcinoma. Cancer Biology and Therapy, 2010, 10, 1009-1018.	3.4	85
116	A network map of Interleukin-10 signaling pathway. Journal of Cell Communication and Signaling, 2016, 10, 61-67.	3.4	85
117	A functional annotation of subproteomes in human plasma. Proteomics, 2005, 5, 3506-3519.	2.2	82
118	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. Proteomics - Clinical Applications, 2019, 13, e1800105.	1.6	82
119	A Network Map of FGF-1/FGFR Signaling System. Journal of Signal Transduction, 2014, 2014, 1-16.	2.0	80
120	SILAC-based quantitative proteomic approach to identify potential biomarkers from the esophageal squamous cell carcinoma secretome. Cancer Biology and Therapy, 2010, 10, 796-810.	3.4	79
121	Antitumor activity and molecular effects of the novel heat shock protein 90 inhibitor, IPI-504, in pancreatic cancer. Molecular Cancer Therapeutics, 2008, 7, 3275-3284.	4.1	77
122	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
123	Direct Association between the Ret Receptor Tyrosine Kinase and the Src Homology 2-containing Adapter Protein Grb7. Journal of Biological Chemistry, 1996, 271, 10607-10610.	3.4	75
124	Human Proteinpedia: a unified discovery resource for proteomics research. Nucleic Acids Research, 2009, 37, D773-D781.	14.5	75
125	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. Genome Research, 2018, 28, 25-36.	5.5	75
126	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

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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.	3.4	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.	5.6	73
129	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	7.5	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.	3.4	72
131	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	12.8	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.	0.9	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.	3.0	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.	3.4	71
135	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018, 17, 759-769.	3.7	70
136	Src-like adaptor protein (Slap) is a negative regulator of mitogenesis. <i>Current Biology</i> , 1998, 8, 975-978.	3.9	67
137	O-Linked N-Acetylglucosamine Modification on CCAAT Enhancer-binding Protein β . <i>Journal of Biological Chemistry</i> , 2009, 284, 19248-19254.	3.4	66
138	Identification of c-Src tyrosine kinase substrates in platelet-derived growth factor receptor signaling. <i>Molecular Oncology</i> , 2009, 3, 439-450.	4.6	65
139	A pathway map of prolactin signaling. <i>Journal of Cell Communication and Signaling</i> , 2012, 6, 169-173.	3.4	65
140	The Escherichia coli Phosphotyrosine Proteome Relates to Core Pathways and Virulence. <i>PLoS Pathogens</i> , 2013, 9, e1003403.	4.7	65
141	Proteomics goes quantitative: measuring protein abundance. <i>Trends in Biotechnology</i> , 2002, 20, 361-364.	9.3	64
142	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005, 5, 3765-3777.	2.2	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.	3.7	62
144	Synovial fluid proteome in rheumatoid arthritis. <i>Clinical Proteomics</i> , 2016, 13, 12.	2.1	62

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145	Inhibition of Adipocyte Differentiation by Resistin-like Molecule $\hat{\pm}$. Journal of Biological Chemistry, 2002, 277, 42011-42016.	3.4	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.	7.1	61
147	A Proteomic Analysis of Human Hemodialysis Fluid. Molecular and Cellular Proteomics, 2005, 4, 637-650.	3.8	60
148	Quantitative phosphoproteomics reveals crosstalk between phosphorylation and <i>O</i> -GlcNAc in the DNA damage response pathway. Proteomics, 2015, 15, 591-607.	2.2	60
149	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. Genome Research, 2017, 27, 133-144.	5.5	60
150	Architectural Organization of the Metabolic Regulatory Enzyme Ghrelin O-Acyltransferase. Journal of Biological Chemistry, 2013, 288, 32211-32228.	3.4	59
151	Genome annotation of <i>Anopheles gambiae</i> using mass spectrometry-derived data. BMC Genomics, 2005, 6, 128.	2.8	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.	5.5	58
154	SILAC-based quantitative proteomic analysis of gastric cancer secretome. Proteomics - Clinical Applications, 2013, 7, 355-366.	1.6	57
155	Pancreatic Cancer Database. Cancer Biology and Therapy, 2014, 15, 963-967.	3.4	57
156	A multicellular signal transduction network of AGE/RAGE signaling. Journal of Cell Communication and Signaling, 2013, 7, 19-23.	3.4	54
157	Characterization of B61, the Ligand for the Eck Receptor Protein-Tyrosine Kinase. Journal of Biological Chemistry, 1995, 270, 5636-5641.	3.4	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.	3.4	53
159	Temporal Analysis of Neural Differentiation Using Quantitative Proteomics. Journal of Proteome Research, 2009, 8, 1315-1326.	3.7	53
160	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. PLoS Pathogens, 2015, 11, e1005346.	4.7	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.	3.4	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.	2.3	52

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163	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
164	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
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