

Akhilesh Pandey

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420
papers

42,857
citations

92
h-index

200
g-index

447
ext. papers

48,632
ext. citations

8.1
avg. IF

6.98
L-index

#	Paper	IF	Citations
420	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, 376-86	7.6	4355
419	ONCOMINE: a cancer microarray database and integrated data-mining platform. <i>Neoplasia</i> , 2004 , 6, 1-6	6.4	2548
418	Human Protein Reference Database--2009 update. <i>Nucleic Acids Research</i> , 2009 , 37, D767-72	20.1	2372
417	Proteomics to study genes and genomes. <i>Nature</i> , 2000 , 405, 837-46	50.4	1907
416	A draft map of the human proteome. <i>Nature</i> , 2014 , 509, 575-81	50.4	1520
415	Pyruvate kinase M2 is a PHD3-stimulated coactivator for hypoxia-inducible factor 1. <i>Cell</i> , 2011 , 145, 732-44	44.2	922
414	Analysis of proteins and proteomes by mass spectrometry. <i>Annual Review of Biochemistry</i> , 2001 , 70, 437-73	31	906
413	Development of human protein reference database as an initial platform for approaching systems biology in humans. <i>Genome Research</i> , 2003 , 13, 2363-71	9.7	823
412	Vesiclepedia: a compendium for extracellular vesicles with continuous community annotation. <i>PLoS Biology</i> , 2012 , 10, e1001450	9.7	800
411	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002 , 20, 261-8	15.1	791
410	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, 9309-14	11.5	790
409	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, 3226-45	4.8	672
408	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. <i>Nature</i> , 2014 , 507, 195-200	50.4	630
407	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
406	The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004 , 22, 177-83	44.5	504
405	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010 , 28, 935-42	44.5	499
404	Human protein reference database--2006 update. <i>Nucleic Acids Research</i> , 2006 , 34, D411-4	20.1	481

403	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, 2199-204	11.5	469
402	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004 , 32, D497-501	20.1	441
401	Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. <i>Nature Genetics</i> , 2006 , 38, 285-93	36.3	381
400	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, 179-84	11.5	380
399	Biomarker discovery from pancreatic cancer secretome using a differential proteomic approach. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 157-71	7.6	372
398	GCN5 acetyltransferase complex controls glucose metabolism through transcriptional repression of PGC-1alpha. <i>Cell Metabolism</i> , 2006 , 3, 429-38	24.6	349
397	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005 , 23, 951-9	44.5	338
396	Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin. <i>Nature Immunology</i> , 2000 , 1, 59-64	19.1	338
395	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010 , 11, R3	18.3	331
394	A mass spectrometry-based proteomic approach for identification of serine/threonine-phosphorylated proteins by enrichment with phospho-specific antibodies: identification of a novel protein, Frigg, as a protein kinase A substrate. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 517-27	7.6	318
393	Role of B61, the ligand for the Eck receptor tyrosine kinase, in TNF-alpha-induced angiogenesis. <i>Science</i> , 1995 , 268, 567-9	33.3	315
392	A curated compendium of phosphorylation motifs. <i>Nature Biotechnology</i> , 2007 , 25, 285-6	44.5	300
391	Detection of tyrosine phosphorylated peptides by precursor ion scanning quadrupole TOF mass spectrometry in positive ion mode. <i>Analytical Chemistry</i> , 2001 , 73, 1440-8	7.8	286
390	Sequential phosphorylation of CCAAT enhancer-binding protein beta by MAPK and glycogen synthase kinase 3beta is required for adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 9766-71	11.5	266
389	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017 , 355, 511-515	35.3	254
388	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
387	A compendium of potential biomarkers of pancreatic cancer. <i>PLoS Medicine</i> , 2009 , 6, e1000046	11.6	217
386	Human Protein Reference Database and Human Proteinpedia as discovery tools for systems biology. <i>Methods in Molecular Biology</i> , 2009 , 577, 67-79	1.4	215

385	Plasma Proteome Database as a resource for proteomics research: 2014 update. <i>Nucleic Acids Research</i> , 2014 , 42, D959-65	20.1	212
384	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, 213-22	7.6	202
383	Tackling the phosphoproteome: tools and strategies. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 64-9	9.7	192
382	A role for thymic stromal lymphopoietin in CD4(+) T cell development. <i>Journal of Experimental Medicine</i> , 2004 , 200, 159-68	16.6	191
381	Ribosomal protein s15 phosphorylation mediates LRRK2 neurodegeneration in Parkinson's disease. <i>Cell</i> , 2014 , 157, 472-485	56.2	182
380	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, 10060-70	4.8	179
379	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, 9773-8	11.5	175
378	Comprehensive proteomic analysis of human pancreatic juice. <i>Journal of Proteome Research</i> , 2004 , 3, 1042-55	5.6	173
377	K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Poh1. <i>EMBO Journal</i> , 2009 , 28, 621-31	13	171
376	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008 , 3, 505-16	18.8	170
375	An evaluation of human protein-protein interaction data in the public domain. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 5, S19	3.6	168
374	Tyrosine phosphorylation mapping of the epidermal growth factor receptor signaling pathway. <i>Journal of Biological Chemistry</i> , 2002 , 277, 1031-9	5.4	165
373	Hsp70 and CHIP selectively mediate ubiquitination and degradation of hypoxia-inducible factor (HIF)-1alpha but Not HIF-2alpha. <i>Journal of Biological Chemistry</i> , 2010 , 285, 3651-3663	5.4	164
372	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	11.5	164
371	Dynamic interplay between O-linked N-acetylglucosamylation and glycogen synthase kinase-3-dependent phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1365-79	7.6	162
370	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, 15305-10	11.5	161
369	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	18.3	158
368	A proteomic approach for quantitation of phosphorylation using stable isotope labeling in cell culture. <i>Analytical Chemistry</i> , 2003 , 75, 6043-9	7.8	155

367	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, 175-87	4.4	148
366	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, 16653-8	11.5	143
365	A comprehensive map of the human urinary proteome. <i>Journal of Proteome Research</i> , 2011 , 10, 2734-43	5.6	141
364	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
363	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. <i>Molecular BioSystems</i> , 2012 , 8, 453-63		137
362	Mutant proteins as cancer-specific biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2444-9	11.5	136
361	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013 , 9, 655	12.2	134
360	Disruption of Plasmodium falciparum 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, 13461-6	11.5	130
359	A proteomic analysis of human bile. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 715-28	7.6	130
358	Context-specific effects of fibulin-5 (DANCE/EVEC) on cell proliferation, motility, and invasion. Fibulin-5 is induced by transforming growth factor-beta and affects protein kinase cascades. <i>Journal of Biological Chemistry</i> , 2002 , 277, 27367-77	5.4	127
357	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	5.6	125
356	GPMAW--a software tool for analyzing proteins and peptides. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 687-9	10.3	125
355	Proteogenomic analysis of Mycobacterium tuberculosis by high resolution mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.011627	7.6	119
354	An evaluation of the use of two-dimensional gel electrophoresis in proteomics. <i>New Biotechnology</i> , 2001 , 18, 195-205		119
353	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010 , 4, 482-95	7.9	118
352	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005 , 5, 3531-6	4.8	118
351	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015 , 12, 1197-204	21.6	115
350	Systematic interactome mapping and genetic perturbation analysis of a C. elegans TGF-beta signaling network. <i>Molecular Cell</i> , 2004 , 13, 469-82	17.6	115

349	Loss of C9orf72 Enhances Autophagic Activity via Deregulated mTOR and TFEB Signaling. <i>PLoS Genetics</i> , 2016 , 12, e1006443	6	115
348	A quantitative proteomic approach for identification of potential biomarkers in hepatocellular carcinoma. <i>Journal of Proteome Research</i> , 2008 , 7, 4289-98	5.6	112
347	Phosphoproteome analysis of HeLa cells using stable isotope labeling with amino acids in cell culture (SILAC). <i>Journal of Proteome Research</i> , 2005 , 4, 1661-71	5.6	108
346	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	11.5	106
345	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, 3939-48	9.2	106
344	The Ret receptor protein tyrosine kinase associates with the SH2-containing adapter protein Grb10. <i>Journal of Biological Chemistry</i> , 1995 , 270, 21461-3	5.4	104
343	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, 14112-7	11.5	103
342	Use of mass spectrometry-derived data to annotate nucleotide and protein sequence databases. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 54-61	10.3	103
341	Oncogenic RET receptors display different autophosphorylation sites and substrate binding specificities. <i>Journal of Biological Chemistry</i> , 1996 , 271, 5309-12	5.4	102
340	Proteogenomics. <i>Proteomics</i> , 2011 , 11, 620-30	4.8	100
339	Identification of miR-21 targets in breast cancer cells using a quantitative proteomic approach. <i>Proteomics</i> , 2009 , 9, 1374-84	4.8	100
338	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, 188-96	6.7	100
337	Inhibition of Spleen Tyrosine Kinase Potentiates Paclitaxel-Induced Cytotoxicity in Ovarian Cancer Cells by Stabilizing Microtubules. <i>Cancer Cell</i> , 2015 , 28, 82-96	24.3	96
336	Temporal profiling of the secretome during adipogenesis in humans. <i>Journal of Proteome Research</i> , 2010 , 9, 5228-38	5.6	96
335	Chemical rescue of a mutant enzyme in living cells. <i>Science</i> , 2006 , 311, 1293-7	33.3	96
334	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001 , 17, 685-7	8.5	96
333	The keratoconus corneal proteome: loss of epithelial integrity and stromal degeneration. <i>Journal of Proteomics</i> , 2013 , 87, 122-31	3.9	95
332	Toward the human cellular microRNAome. <i>Genome Research</i> , 2017 , 27, 1769-1781	9.7	95

331	Src-like adaptor protein (SLAP) is a negative regulator of T cell receptor signaling. <i>Journal of Experimental Medicine</i> , 2000 , 191, 463-74	16.6	94
330	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. <i>Genome Research</i> , 2015 , 25, 1536-45	9.7	92
329	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, 38633-9	5.4	92
328	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014 , 11, 29	5	90
327	Genomewide mRNA profiling of esophageal squamous cell carcinoma for identification of cancer biomarkers. <i>Cancer Biology and Therapy</i> , 2009 , 8, 36-46	4.6	90
326	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	7.6	90
325	Comprehensive comparison of collision induced dissociation and electron transfer dissociation. <i>Analytical Chemistry</i> , 2008 , 80, 4825-35	7.8	90
324	Characterization of a novel Src-like adapter protein that associates with the Eck receptor tyrosine kinase. <i>Journal of Biological Chemistry</i> , 1995 , 270, 19201-4	5.4	90
323	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014 , 11, 6	5	85
322	Proteomic analysis of human follicular fluid: a new perspective towards understanding folliculogenesis. <i>Journal of Proteomics</i> , 2013 , 87, 68-77	3.9	85
321	The dynamic stress-induced "O-GlcNAc-ome" highlights functions for O-GlcNAc in regulating DNA damage/repair and other cellular pathways. <i>Amino Acids</i> , 2011 , 40, 793-808	3.5	84
320	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011 , 12, 510-22	4.6	84
319	A novel proteomic approach for specific identification of tyrosine kinase substrates using [13C]tyrosine. <i>Journal of Biological Chemistry</i> , 2004 , 279, 15805-13	5.4	84
318	Electron transfer dissociation mass spectrometry in proteomics. <i>Proteomics</i> , 2012 , 12, 530-42	4.8	83
317	Mac-2-binding protein is a diagnostic marker for biliary tract carcinoma. <i>Cancer</i> , 2004 , 101, 1609-15	6.4	83
316	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014 , 11, 1	5	82
315	Global impact of oncogenic Src on a phosphotyrosine proteome. <i>Journal of Proteome Research</i> , 2008 , 7, 3447-60	5.6	80
314	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	11.5	77

313	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005 , 5, 3506-19	4.8	77
312	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, 744-53	5.6	75
311	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, 1009-18	4.6	75
310	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016 , 16, 700-14	4.8	75
309	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009 , 37, D773-81	20.1	72
308	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-46.e31	4.56	71
307	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, 3275-84	6.1	70
306	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	4.6	69
305	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, 10607-10	5.4	68
304	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. <i>PLoS ONE</i> , 2015 , 10, e0143066	3.7	66
303	Differentially expressed genes in pancreatic ductal adenocarcinomas identified through serial analysis of gene expression. <i>Cancer Biology and Therapy</i> , 2004 , 3, 1254-61	4.6	66
302	A Network Map of FGF-1/FGFR Signaling System. <i>Journal of Signal Transduction</i> , 2014 , 2014, 962962		65
301	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, M1111.013565	7.6	65
300	Identification of secreted proteins that mediate cell-cell interactions in an in vitro model of the lung cancer microenvironment. <i>Cancer Research</i> , 2008 , 68, 7237-45	10.1	64
299	Human protein reference database and human proteinpedia as discovery resources for molecular biotechnology. <i>Molecular Biotechnology</i> , 2011 , 48, 87-95	3	63
298	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	8.8	62
297	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	11.5	61
296	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 276-80	8.03	60

295	A network map of BDNF/TRKB and BDNF/p75NTR signaling system. <i>Journal of Cell Communication and Signaling</i> , 2013 , 7, 301-7	5.2	58
294	Proteomics goes quantitative: measuring protein abundance. <i>Trends in Biotechnology</i> , 2002 , 20, 361-4	15.1	58
293	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005 , 5, 3765-77	4.8	58
292	O-linked N-acetylglucosamine modification on CCAAT enhancer-binding protein beta: role during adipocyte differentiation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 19248-54	5.4	57
291	The <i>Escherichia coli</i> phosphotyrosine proteome relates to core pathways and virulence. <i>PLoS Pathogens</i> , 2013 , 9, e1003403	7.6	56
290	Identifying targets of miR-143 using a SILAC-based proteomic approach. <i>Molecular BioSystems</i> , 2010 , 6, 1873-82		56
289	Identification of c-Src tyrosine kinase substrates in platelet-derived growth factor receptor signaling. <i>Molecular Oncology</i> , 2009 , 3, 439-50	7.9	56
288	Src-like adaptor protein (Slap) is a negative regulator of mitogenesis. <i>Current Biology</i> , 1998 , 8, 975-8	6.3	55
287	A proteomic analysis of human hemodialysis fluid. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 637-50	7.6	55
286	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	5	54
285	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014 , 5, 4961	17.4	53
284	Identification of c-Src tyrosine kinase substrates using mass spectrometry and peptide microarrays. <i>Journal of Proteome Research</i> , 2008 , 7, 3900-10	5.6	53
283	Genome annotation of <i>Anopheles gambiae</i> using mass spectrometry-derived data. <i>BMC Genomics</i> , 2005 , 6, 128	4.5	52
282	Characterization of B61, the ligand for the Eck receptor protein-tyrosine kinase. <i>Journal of Biological Chemistry</i> , 1995 , 270, 5636-41	5.4	52
281	Inhibition of adipocyte differentiation by resistin-like molecule alpha. Biochemical characterization of its oligomeric nature. <i>Journal of Biological Chemistry</i> , 2002 , 277, 42011-6	5.4	51
280	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017 , 29, 14-23	10.7	49
279	A network map of IL-33 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2018 , 12, 615-624	4.2	49
278	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 32211-32228	5.4	48

277	Temporal analysis of neural differentiation using quantitative proteomics. <i>Journal of Proteome Research</i> , 2009 , 8, 1315-26	5.6	48
276	Cloning of MASK, a novel member of the mammalian germinal center kinase III subfamily, with apoptosis-inducing properties. <i>Journal of Biological Chemistry</i> , 2002 , 277, 5929-39	5.4	48
275	A network map of Interleukin-10 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2016 , 10, 61-7	5.2	47
274	Multiple pathways for Plasmodium ookinete invasion of the mosquito midgut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E492-500	11.5	47
273	A pathway map of prolactin signaling. <i>Journal of Cell Communication and Signaling</i> , 2012 , 6, 169-73	5.2	47
272	Evaluation of several MS/MS search algorithms for analysis of spectra derived from electron transfer dissociation experiments. <i>Analytical Chemistry</i> , 2009 , 81, 7170-80	7.8	47
271	A proteogenomic analysis of Anopheles gambiae using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011 , 21, 1872-81	9.7	47
270	Computational and experimental analysis reveals a novel Src family kinase in the C. elegans genome. <i>Bioinformatics</i> , 2003 , 19, 169-72	7.2	47
269	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018 , 17, 759-769	5.6	46
268	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. <i>Proteomics - Clinical Applications</i> , 2019 , 13, e1800105	3.1	46
267	Quantitative phosphoproteomics reveals crosstalk between phosphorylation and O-GlcNAc in the DNA damage response pathway. <i>Proteomics</i> , 2015 , 15, 591-607	4.8	45
266	Secretome analysis of the fungus Trichoderma harzianum grown on cellulose. <i>Proteomics</i> , 2012 , 12, 2716-28	4.8	45
265	Identification of novel highly expressed genes in pancreatic ductal adenocarcinomas through a bioinformatics analysis of expressed sequence tags. <i>Cancer Biology and Therapy</i> , 2004 , 3, 1081-9; discussion 1090-1	4.6	45
264	SILAC-based quantitative proteomic analysis of gastric cancer secretome. <i>Proteomics - Clinical Applications</i> , 2013 , 7, 355-66	3.1	44
263	Identification of head and neck squamous cell carcinoma biomarker candidates through proteomic analysis of cancer cell secretome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 2308-16	4	44
262	TSLP signaling network revealed by SILAC-based phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M112.017764	7.6	44
261	Role of p38 in replication of Trypanosoma brucei kinetoplast DNA. <i>Molecular and Cellular Biology</i> , 2006 , 26, 5382-93	4.8	44
260	Proteomics of human aqueous humor. <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 283-93	3.8	43

259	Identification of differentially expressed serum proteins in gastric adenocarcinoma. <i>Journal of Proteomics</i> , 2015 , 127, 80-8	3.9	43
258	Heterogeneity of pancreatic cancer metastases in a single patient revealed by quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2803-11	7.6	43
257	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017 , 27, 133-144	9.7	43
256	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, 3859-70	3.5	43
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