

Akhilesh Pandey

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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	2.2	
419	Deciphering the Interactions of SARS-CoV-2 Proteins with Human Ion Channels Using Machine-Learning-Based Methods.. <i>Pathogens</i> , 2022 , 11,	4.5	1
418	TMT-Based Multiplexed Quantitation of -Glycopeptides Reveals Glycoproteome Remodeling Induced by Oncogenic Mutations.. <i>ACS Omega</i> , 2022 , 7, 11023-11032	3.9	0
417	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		
416	CN: glucagon-based novel isotope dilution mass spectrometry method for measurement of glucagon metabolism in humans.. <i>Clinical Proteomics</i> , 2022 , 19, 16	5	
415	Targeted Detection of SARS-CoV-2 Nucleocapsid Sequence Variants by Mass Spectrometric Analysis of Tryptic Peptides. <i>Journal of Proteome Research</i> , 2021 ,	5.6	2
414	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021 , 18, 25	5	1
413	Sorbitol Is a Severity Biomarker for PMM2-CDG with Therapeutic Implications. <i>Annals of Neurology</i> , 2021 , 90, 887-900	9.4	4
412	Automated data-driven mass spectrometry for improved analysis of lipids with dual dissociation techniques.. <i>Journal of Mass Spectrometry and Advances in the Clinical Lab</i> , 2021 , 22, 43-49		1
411	Shukla-Vernon Syndrome: A Second Family with a Novel Variant in the Gene. <i>Genes</i> , 2021 , 12,	4.2	1
410	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. <i>Life Science Alliance</i> , 2021 , 4,	5.8	12
409	The mitochondrial carrier SFXN1 is critical for complex III integrity and cellular metabolism. <i>Cell Reports</i> , 2021 , 34, 108869	10.6	9
408	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021 , 81, 2094-2111.e9	17.6	5
407	Ethylmalonic encephalopathy ETHE1 p. D165H mutation alters the mitochondrial function in human skeletal muscle proteome. <i>Mitochondrion</i> , 2021 , 58, 64-71	4.9	1
406	Mitochondrial localization and moderated activity are key to murine erythroid enucleation. <i>Blood Advances</i> , 2021 , 5, 2490-2504	7.8	5
405	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	5.6	9
404	Complement and Coagulation Cascades are Potentially Involved in Dopaminergic Neurodegeneration in Eynuclein-Based Mouse Models of Parkinson's Disease. <i>Journal of Proteome Research</i> , 2021 , 20, 3428-3443	5.6	4

403	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	1.8	0
402	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021 , 69, 103465	8.8	16
401	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021 , 20, 4165-4175	5.6	5
400	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021 , 156, 988-1002	6	12
399	Expanding the clinical and metabolic phenotype of DPM2 deficient congenital disorders of glycosylation. <i>Molecular Genetics and Metabolism</i> , 2021 , 132, 27-37	3.7	1
398	Mutation-Specific and Common Phosphotyrosine Signatures of G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021 , 20, 670-683	5.6	7
397	Persistently Elevated mTOR Complex 1-S6 Kinase 1 Disrupts DARPP-32-Dependent D Dopamine Receptor Signaling and Behaviors. <i>Biological Psychiatry</i> , 2021 , 89, 1058-1072	7.9	4
396	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100069	7.6	5
395	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. <i>Indian Journal of Ophthalmology</i> , 2021 , 69, 647-654	1.6	0
394	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. <i>Molecular Omics</i> , 2021 , 17, 939-947	4.4	3
393	Maternal serum lipidomics identifies lysophosphatidic acid as a predictor of small for gestational age neonates. <i>Molecular Omics</i> , 2021 , 17, 956-966	4.4	0
392	Integrated Proteomic and Phosphoproteomics Analysis of DKK3 Signaling Reveals Activated Kinase in the Most Aggressive Gallbladder Cancer. <i>Cells</i> , 2021 , 10,	7.9	1
391	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	5.5	8
390	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. <i>Journal of Proteome Research</i> , 2021 , 20, 4566-4577	5.6	0
389	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. <i>Mitochondrion</i> , 2021 , 60, 27-32	4.9	0
388	A pathway map of signaling events triggered upon SARS-CoV infection. <i>Journal of Cell Communication and Signaling</i> , 2021 , 15, 595-600	5.2	1
387	Acute Kidney Injury in Severe COVID-19 Has Similarities to Sepsis-Associated Kidney Injury: A Multi-Omics Study. <i>Mayo Clinic Proceedings</i> , 2021 , 96, 2561-2575	6.4	4
386	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100134	7.6	0

385	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021 , 17, 454-463.	4.4	6
384	A Novel LINS1 Truncating Mutation in Autosomal Recessive Nonsyndromic Intellectual Disability. <i>Frontiers in Psychiatry</i> , 2020 , 11, 354	5	2
383	A Novel Missense Variant in PHF6 Gene Causing Björkeson-Forsman-Lehman Syndrome. <i>Journal of Molecular Neuroscience</i> , 2020 , 70, 1403-1409	3.3	2
382	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	3.8	11
381	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 394-404	3.5	3
380	Phosphoproteomic analysis identifies CLK1 as a novel therapeutic target in gastric cancer. <i>Gastric Cancer</i> , 2020 , 23, 796-810	7.6	8
379	Extra-cellular vesicles carry proteome of cancer hallmarks. <i>Frontiers in Bioscience - Landmark</i> , 2020 , 25, 398-436	2.8	6
378	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	5.6	6
377	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020 , 92, 14466-14475	7.8	8
376	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	4.8	7
375	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	10.5	21
374	Is the Proteome of Bronchoalveolar Lavage Extracellular Vesicles a Marker of Advanced Lung Cancer?. <i>Cancers</i> , 2020 , 12,	6.6	5
373	Integrated genomic analysis reveals mutated ELF3 as a potential gallbladder cancer vaccine candidate. <i>Nature Communications</i> , 2020 , 11, 4225	17.4	19
372	The PAX-SIX-EYA-DACH network modulates GATA-FOG function in fly hematopoiesis and human erythropoiesis. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	3
371	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	2.6	8
370	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020 , 34, 301-305	10.7	6
369	A Novel Splice Site Mutation in Patients With Primary Immunodeficiency Exhibiting Susceptibility to Mycobacterial Diseases. <i>Frontiers in Immunology</i> , 2019 , 10, 1964	8.4	13
368	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	6.9	7

367	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	5.2	8
366	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 8453-8460	7.8	3
365	Family-Based Next-Generation Sequencing Study Identifies an Variant in an Infant with Primary Immunodeficiency. <i>OMICS A Journal of Integrative Biology</i> , 2019 , 23, 285-290	3.8	2
364	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
363	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019 , 19, e1800315	4.8	8
362	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	7.6	10
361	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	5.6	27
360	Proteomic Analysis of Merosomes: The Link between Liver and Blood Stages in Malaria. <i>Journal of Proteome Research</i> , 2019 , 18, 3404-3418	5.6	12
359	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. <i>Journal of Clinical Investigation</i> , 2019 , 129, 4708-4723	15.9	21
358	Dickkopf Homolog 3 Acts as a Potential Tumor Suppressor in Gallbladder Cancer. <i>Frontiers in Oncology</i> , 2019 , 9, 1121	5.3	7
357	Mapping Keratoconus Molecular Substrates by Multiplexed High-Resolution Proteomics of Unpooled Corneas. <i>OMICS A Journal of Integrative Biology</i> , 2019 , 23, 583-597	3.8	11
356	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
355	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018 , 18, e1700386	4.8	10
354	Analysis of Cellular Tyrosine Phosphorylation via Chemical Rescue of Conditionally Active Abl Kinase. <i>Biochemistry</i> , 2018 , 57, 1390-1398	3.2	2
353	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
352	GBA1 deficiency negatively affects physiological Bsynuclein 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
351	USP9X controls translation efficiency via deubiquitination of eukaryotic translation initiation factor 4A1. <i>Nucleic Acids Research</i> , 2018 , 46, 823-839	20.1	12
350	A network map of IL-33 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2018 , 12, 615-624	4.2	49

349	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
348	Integrated Stress Response and Decreased ECM in Cultured Stromal Cells From Keratoconus Corneas 2018 , 59, 2977-2986		19
347	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018 , 23,	4.8	9
346	Quantitative phosphoproteomic analysis reveals reciprocal activation of receptor tyrosine kinases between cancer epithelial cells and stromal fibroblasts. <i>Clinical Proteomics</i> , 2018 , 15, 21	5	10
345	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018 , 12, e1700101	3.1	13
344	A Next-Generation Sequencing-Based Molecular Approach to Characterize a Tick Vector in Lyme Disease. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 565-574	3.8	1
343	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	4.3	21
342	Identification of spleen tyrosine kinase as a potential therapeutic target for esophageal squamous cell carcinoma using reverse phase protein arrays. <i>Oncotarget</i> , 2018 , 9, 18422-18434	3.3	2
341	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. <i>Genome Research</i> , 2018 , 28, 25-36	9.7	41
340	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	0.8	9
339	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
338	Proteomic Analysis of the Human Anterior Pituitary Gland. <i>OMICS A Journal of Integrative Biology</i> , 2018 , 22, 759-769	3.8	8
337	CHES: 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
336	Testican 1 (SPOCK1) and protein tyrosine phosphatase, receptor type S (PTPRS) show significant increase in saliva of tobacco users with oral cancer. <i>Translational Research in Oral Oncology</i> , 2018 , 3, 2057-2063	7.8	188053
335	Phosphotyrosine profiling of human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2018 , 15, 29	5	12
334	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017 , 355, 511-515	3.3	254
333	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	11.5	15
332	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	3.8	6

331	Mass Spectrometry Reveals Respiratory Viral Infection Biomarkers. <i>EBioMedicine</i> , 2017 , 18, 21-22	8.8	
330	Human adenine nucleotide translocases physically and functionally interact with respirasomes. <i>Molecular Biology of the Cell</i> , 2017 , 28, 1489-1506	3.5	23
329	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. <i>OMICS A Journal of Integrative Biology</i> , 2017 , 21, 295-303	3.8	24
328	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
327	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	7.6	25
326	Toward the human cellular microRNAome. <i>Genome Research</i> , 2017 , 27, 1769-1781	9.7	95
325	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	3.8	10
324	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017 , 27, 133-144	9.7	43
323	The non-receptor tyrosine kinase TNK2/ACK1 is a novel therapeutic target in triple negative breast cancer. <i>Oncotarget</i> , 2017 , 8, 2971-2983	3.3	17
322	Small molecule inhibitor screening identified HSP90 inhibitor 17-AAG as potential therapeutic agent for gallbladder cancer. <i>Oncotarget</i> , 2017 , 8, 26169-26184	3.3	14
321	A network map of Interleukin-10 signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2016 , 10, 61-7	5.2	47
320	Identification of GAPDH on the surface of Plasmodium sporozoites as a new candidate for targeting malaria liver invasion. <i>Journal of Experimental Medicine</i> , 2016 , 213, 2099-112	16.6	31
319	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2016 , 13, 29	5	23
318	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	3.8	19
317	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2016 , 6, 36132	4.9	28
316	Synovial fluid proteome in rheumatoid arthritis. <i>Clinical Proteomics</i> , 2016 , 13, 12	5	38
315	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
314	Long non-coding RNA expression in primary human monocytes. <i>Genomics</i> , 2016 , 108, 37-45	4.3	17

313	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. <i>Cancer Immunology Research</i> , 2016 , 4, 225-33	12.5	19
312	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. <i>Cancer Biology and Therapy</i> , 2016 , 17, 219-29	4.6	20
311	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	3.3	23
310	Loss of C9orf72 Enhances Autophagic Activity via Deregulated mTOR and TFEB Signaling. <i>PLoS Genetics</i> , 2016 , 12, e1006443	6	115
309	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016 , 16, 700-14	4.8	75
308	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	5.8	13
307	Unbiased identification of substrates of protein tyrosine phosphatase ptp-3 in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016 , 10, 910-20	7.9	12
306	PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2829-38	7.6	18
305	A phosphoproteomic screen demonstrates differential dependence on HER3 for MAP kinase pathway activation by distinct PIK3CA mutations. <i>Proteomics</i> , 2015 , 15, 318-26	4.8	12
304	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
303	Ablation of Dicer leads to widespread perturbation of signaling pathways. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 389-94	3.4	6
302	A knowledgebase resource for interleukin-17 family mediated signaling. <i>Journal of Cell Communication and Signaling</i> , 2015 , 9, 291-6	5.2	20
301	Proteomics of human aqueous humor. <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 283-93	3.8	43
300	Calcium calmodulin dependent kinase kinase 2 - a novel therapeutic target for gastric adenocarcinoma. <i>Cancer Biology and Therapy</i> , 2015 , 16, 336-45	4.6	41
299	Identification of differentially expressed serum proteins in gastric adenocarcinoma. <i>Journal of Proteomics</i> , 2015 , 127, 80-8	3.9	43
298	Identifying novel targets of oncogenic EGF receptor signaling in lung cancer through global phosphoproteomics. <i>Proteomics</i> , 2015 , 15, 340-55	4.8	34
297	Integrated analysis of CRLF2 signaling in acute lymphoblastic leukemia identifies Polo-like kinase 1 as a potential therapeutic target. <i>Leukemia and Lymphoma</i> , 2015 , 56, 1524-7	1.9	2
296	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, 2466-79	5.6	24

295	Chronic exposure to chewing tobacco selects for overexpression of stearyl-CoA desaturase in normal oral keratinocytes. <i>Cancer Biology and Therapy</i> , 2015 , 16, 1593-603	4.6	27
294	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. <i>Genome Research</i> , 2015 , 25, 1536-45	9.7	92
293	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015 , 12, 1197-204	21.6	115
292	Activating Mutations in PIK3CA Lead to Widespread Modulation of the Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , 2015 , 14, 3882-3891	5.6	7
291	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, 2887-900	7.6	18
290	Quantitative phosphoproteomic analysis of IL-33-mediated signaling. <i>Proteomics</i> , 2015 , 15, 532-44	4.8	42
289	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, 383-93	4.8	27
288	Identification of miR-145 targets through an integrated omics analysis. <i>Molecular BioSystems</i> , 2015 , 11, 197-207		18
287	Macrophage migration inhibitory factor - a therapeutic target in gallbladder cancer. <i>BMC Cancer</i> , 2015 , 15, 843	4.8	24
286	A multi-omic analysis of human naïve CD4+ T cells. <i>BMC Systems Biology</i> , 2015 , 9, 75	3.5	30
285	Phosphoproteomic profiling of tumor tissues identifies HSP27 Ser82 phosphorylation as a robust marker of early ischemia. <i>Scientific Reports</i> , 2015 , 5, 13660	4.9	11
284	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. <i>PLoS ONE</i> , 2015 , 10, e0143066	3.7	66
283	Downregulation of S100 Calcium Binding Protein A9 in Esophageal Squamous Cell Carcinoma. <i>Scientific World Journal, The</i> , 2015 , 2015, 325721	2.2	6
282	Comprehensive proteomics analysis of glycosomes from <i>Leishmania donovani</i> . <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 157-70	3.8	24
281	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
280	LC-MS-based serum metabolomic analysis reveals dysregulation of phosphatidylcholines in esophageal squamous cell carcinoma. <i>Journal of Proteomics</i> , 2015 , 127, 96-102	3.9	26
279	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous-cell carcinoma. <i>Proteomics</i> , 2015 , 15, 374-82	4.8	17
278	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

277	Differential Signaling through p190 and p210 Forms of BCR-ABL Fusion Proteins Revealed By Proteomic Analysis. <i>Blood</i> , 2015 , 126, 3651-3651	2.2	1
276	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. <i>PLoS Pathogens</i> , 2015 , 11, e1005346	7.6	40
275	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. <i>Oncotarget</i> , 2015 , 6, 29143-60	3.3	34
274	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. <i>Nature</i> , 2014 , 507, 195-200	50.4	630
273	A network map of the gastrin signaling pathway. <i>Journal of Cell Communication and Signaling</i> , 2014 , 8, 165-70	5.2	9
272	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2014 , 11, 5	5	16
271	Ribosomal protein s15 phosphorylation mediates LRRK2 neurodegeneration in Parkinson's disease. <i>Cell</i> , 2014 , 157, 472-485	56.2	182
270	A draft map of the human proteome. <i>Nature</i> , 2014 , 509, 575-81	50.4	1520
269	Proteomic analysis and genome annotation of <i>Pichia pastoris</i> , a recombinant protein expression host. <i>Proteomics</i> , 2014 , 14, 2769-79	4.8	13
268	Annotation of the zebrafish genome through an integrated transcriptomic and proteomic analysis. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3184-98	7.6	40
267	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
266	Brain proteomics of <i>Anopheles gambiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 421-37	3.8	12
265	PHD3-mediated prolyl hydroxylation of nonmuscle actin impairs polymerization and cell motility. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2788-96	3.5	23
264	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014 , 5, 4961	17.4	53
263	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, 3166-77	5.6	11
262	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014 , 11, 29	5	90
261	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	3.8	23
260	Chromosome-centric human proteome project: deciphering proteins associated with glioma and neurodegenerative disorders on chromosome 12. <i>Journal of Proteome Research</i> , 2014 , 13, 3178-90	5.6	18

259	Functional annotation of proteome encoded by human chromosome 22. <i>Journal of Proteome Research</i> , 2014 , 13, 2749-60	5.6	17
258	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014 , 11, 6	5	85
257	Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. <i>Journal of Proteomics</i> , 2014 , 108, 306-15	3.9	15
256	Botch is a Eglutamyl cyclotransferase that deglycinates and antagonizes Notch. <i>Cell Reports</i> , 2014 , 7, 681-8	10.6	23
255	Identification of targets of miR-200b by a SILAC-based quantitative proteomic approach. <i>EuPA Open Proteomics</i> , 2014 , 4, 10-17	0.1	1
254	Prediction of Gene Activity in Early B Cell Development Based on an Integrative Multi-Omics Analysis. <i>Journal of Proteomics and Bioinformatics</i> , 2014 , 7,	2.1	11
253	A breast cancer cell microarray (CMA) as a rapid method to characterize candidate biomarkers. <i>Cancer Biology and Therapy</i> , 2014 , 15, 1593-9	4.6	10
252	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
251	Plasma Proteome Database as a resource for proteomics research: 2014 update. <i>Nucleic Acids Research</i> , 2014 , 42, D959-65	20.1	212
250	Pancreatic Cancer Database: an integrative resource for pancreatic cancer. <i>Cancer Biology and Therapy</i> , 2014 , 15, 963-7	4.6	37
249	Identification of candidate substrates for the Golgi Tul1 E3 ligase using quantitative diGly proteomics in yeast. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2871-82	7.6	25
248	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. <i>Clinical Proteomics</i> , 2014 , 11, 39	5	14
247	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
246	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014 , 11, 1	5	82
245	Signaling Network Map of Endothelial TEK Tyrosine Kinase. <i>Journal of Signal Transduction</i> , 2014 , 2014, 173026		24
244	A Network Map of FGF-1/FGFR Signaling System. <i>Journal of Signal Transduction</i> , 2014 , 2014, 962962		65
243	Identification of prosaposin and transgelin as potential biomarkers for gallbladder cancer using quantitative proteomics. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 446, 863-9	3.4	24
242	Phosphoproteome of Cryptococcus neoformans. <i>Journal of Proteomics</i> , 2014 , 97, 287-95	3.9	37

241	Moving from unsequenced to sequenced genome: reanalysis of the proteome of <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2014 , 97, 48-61	3.9	26
240	Proteomic analysis of human follicular fluid: a new perspective towards understanding folliculogenesis. <i>Journal of Proteomics</i> , 2013 , 87, 68-77	3.9	85
239	Proteomic analysis of purified protein derivative of <i>Mycobacterium tuberculosis</i> . <i>Clinical Proteomics</i> , 2013 , 10, 8	5	22
238	Quantitative proteomics for identifying biomarkers for Rabies. <i>Clinical Proteomics</i> , 2013 , 10, 3	5	24
237	A multicellular signal transduction network of AGE/RAGE signaling. <i>Journal of Cell Communication and Signaling</i> , 2013 , 7, 19-23	5.2	35
236	SILAC-based quantitative proteomic analysis of gastric cancer secretome. <i>Proteomics - Clinical Applications</i> , 2013 , 7, 355-66	3.1	44
235	The keratoconus corneal proteome: loss of epithelial integrity and stromal degeneration. <i>Journal of Proteomics</i> , 2013 , 87, 122-31	3.9	95
234	A multilectin affinity approach for comparative glycoprotein profiling of rheumatoid arthritis and spondyloarthritis. <i>Clinical Proteomics</i> , 2013 , 10, 11	5	13
233	Characterizing the normal proteome of human ciliary body. <i>Clinical Proteomics</i> , 2013 , 10, 9	5	30
232	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. <i>Malaria Journal</i> , 2013 , 12, 216	3.6	33
231	Proteomic strategies to characterize signaling pathways. <i>Methods in Molecular Biology</i> , 2013 , 1007, 359-774		9
230	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013 , 9, 655	12.2	134
229	Proteomics for understanding miRNA biology. <i>Proteomics</i> , 2013 , 13, 558-67	4.8	19
228	FAM190A deficiency creates a cell division defect. <i>American Journal of Pathology</i> , 2013 , 183, 296-303	5.8	15
227	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
226	Downregulation of cornulin in esophageal squamous cell carcinoma. <i>Acta Histochemica</i> , 2013 , 115, 89-992		17
225	Access guide to human proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013 , Chapter 1, Unit 1.21	24.2	18
224	IL-11/IL11RA receptor mediated signaling: a web accessible knowledgebase. <i>Cell Communication and Adhesion</i> , 2013 , 20, 81-6		6

223	Signaling network of Oncostatin M pathway. <i>Journal of Cell Communication and Signaling</i> , 2013 , 7, 103-8	5.2	37
222	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
221	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, 3128-38	5.6	15
220	The Escherichia coli phosphotyrosine proteome relates to core pathways and virulence. <i>PLoS Pathogens</i> , 2013 , 9, e1003403	7.6	56
219	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 32211-32228	5.4	48
218	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. <i>Clinical Proteomics</i> , 2013 , 10, 14	5	20
217	Integrated proteomic and metabolic analysis of breast cancer progression. <i>PLoS ONE</i> , 2013 , 8, e76220	3.7	21
216	The role of cardiolipin in defining the mammalian ANT interactome. <i>FASEB Journal</i> , 2013 , 27, 1026.3	0.9	
215	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
214	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> , 2012 , 12, 1-9	3.8	15
213	Differences in signaling through the B-cell leukemia oncoprotein CRLF2 in response to TSLP and through mutant JAK2. <i>Blood</i> , 2012 , 120, 2853-63	2.2	36
212	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. <i>Molecular BioSystems</i> , 2012 , 8, 453-63		137
211	TSLP signaling network revealed by SILAC-based phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M112.017764	7.6	44
210	Proteomic analysis of an unsequenced plant--Mangifera indica. <i>Journal of Proteomics</i> , 2012 , 75, 5793-6	3.9	16
209	Rapid characterization of candidate biomarkers for pancreatic cancer using cell microarrays (CMAs). <i>Journal of Proteome Research</i> , 2012 , 11, 5556-63	5.6	13
208	Identification of targets of c-Src tyrosine kinase by chemical complementation and phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 355-69	7.6	37
207	Regulation of lipid metabolism by Dicer revealed through SILAC mice. <i>Journal of Proteome Research</i> , 2012 , 11, 2193-205	5.6	22
206	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	7.6	65

205	Unbiased discovery of interactions at a control locus driving expression of the cancer-specific therapeutic and diagnostic target, mesothelin. <i>Journal of Proteome Research</i> , 2012 , 11, 5301-10	5.6	5
204	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, 2141-52	3.9	21
203	Overexpression of ribosome binding protein 1 (RRBP1) in breast cancer. <i>Clinical Proteomics</i> , 2012 , 9, 7	5	20
202	A pathway map of prolactin signaling. <i>Journal of Cell Communication and Signaling</i> , 2012 , 6, 169-73	5.2	47
201	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. <i>Clinical Proteomics</i> , 2012 , 9, 12	5	21
200	Proteogenomic analysis of <i>Candida glabrata</i> using high resolution mass spectrometry. <i>Journal of Proteome Research</i> , 2012 , 11, 247-60	5.6	38
199	Transcriptomic Profiling of Medial Temporal Lobe Epilepsy. <i>Journal of Proteomics and Bioinformatics</i> , 2012 , 5,	2.1	15
198	Overexpression of Kinesin Associated Protein 3 (KIFAP3) in Breast Cancer. <i>Journal of Proteomics and Bioinformatics</i> , 2012 , 5, 122-126	2.1	3
197	A proteogenomic approach to map the proteome of an unsequenced pathogen - <i>Leishmania donovani</i> . <i>Proteomics</i> , 2012 , 12, 832-44	4.8	39
196	Electron transfer dissociation mass spectrometry in proteomics. <i>Proteomics</i> , 2012 , 12, 530-42	4.8	83
195	Secretome analysis of the fungus <i>Trichoderma harzianum</i> grown on cellulose. <i>Proteomics</i> , 2012 , 12, 2716-28	4.28	45
194	Vesiclepedia: a compendium for extracellular vesicles with continuous community annotation. <i>PLoS Biology</i> , 2012 , 10, e1001450	9.7	800
193	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
192	A Bioinformatics Resource for TWEAK-Fn14 Signaling Pathway. <i>Journal of Signal Transduction</i> , 2012 , 2012, 376470		21
191	Gene Expression Profiling of Tuberculous Meningitis Co-infected with HIV. <i>Journal of Proteomics and Bioinformatics</i> , 2012 , 5, 235-244	2.1	9
190	A comprehensive curated resource for follicle stimulating hormone signaling. <i>BMC Research Notes</i> , 2011 , 4, 408	2.3	19
189	A comprehensive map of the human urinary proteome. <i>Journal of Proteome Research</i> , 2011 , 10, 2734-43	5.6	141
188	Pyruvate kinase M2 is a PHD3-stimulated coactivator for hypoxia-inducible factor 1. <i>Cell</i> , 2011 , 145, 732-44	4.2	922

187	Proteome profiling of wild type and lumican-deficient mouse corneas. <i>Journal of Proteomics</i> , 2011 , 74, 1895-905	3.9	17
186	A Signaling Network of Thyroid-Stimulating Hormone. <i>Journal of Proteomics and Bioinformatics</i> , 2011 , 4,	2.1	6
185	Identification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. <i>Journal of Proteomics and Bioinformatics</i> , 2011 , 4, 22-35	2.1	27
184	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
183	Human protein reference database and human proteinpedia as discovery resources for molecular biotechnology. <i>Molecular Biotechnology</i> , 2011 , 48, 87-95	3	63
182	Systematic evaluation of alternating CID and ETD fragmentation for phosphorylated peptides. <i>Proteomics</i> , 2011 , 11, 2568-72	4.8	30
181	Proteogenomics. <i>Proteomics</i> , 2011 , 11, 620-30	4.8	100
180	Quantitative temporal proteomic analysis of human embryonic stem cell differentiation into oligodendrocyte progenitor cells. <i>Proteomics</i> , 2011 , 11, 4007-20	4.8	33
179	Comprehensive proteomic analysis of human bile. <i>Proteomics</i> , 2011 , 11, 4443-53	4.8	38
178	Monoclonal antibody cocktail as an enrichment tool for acetylome analysis. <i>Analytical Chemistry</i> , 2011 , 83, 3623-6	7.8	24
177	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
176	Proteogenomic analysis of <i>Mycobacterium tuberculosis</i> by high resolution mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.011627	7.6	119
175	The interactome of a PTB domain-containing adapter protein, Odin, revealed by SILAC. <i>Journal of Proteomics</i> , 2011 , 74, 294-303	3.9	11
174	NetSlim: high-confidence curated signaling maps. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar032	5	27
173	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011 , 21, 1872-81	9.7	47
172	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
171	A comprehensive manually curated reaction map of RANKL/RANK-signaling pathway. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar021	5	33
170	An evolutionarily 'young' lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2011 , 25, 1306-19	12.6	19

169	Gene Expression Profiling of Gastric Cancer. <i>Journal of Proteomics and Bioinformatics</i> , 2011 , 4, 74-82	2.1	12
168	Quantitative Proteomic Profiling Unravels Dynamic Changes in the Myeloma Cell Proteome Treated with Valproic Acid (VPA). <i>Blood</i> , 2011 , 118, 1847-1847	2.2	1
167	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010 , 28, 935-42	44.5	499
166	Overexpression of periostin and lumican in esophageal squamous cell carcinoma. <i>Cancers</i> , 2010 , 2, 133-426		14
165	Mutation@A Glance: an integrative web application for analysing mutations from human genetic diseases. <i>DNA Research</i> , 2010 , 17, 197-208	4.5	21
164	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
163	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
162	Temporal profiling of the secretome during adipogenesis in humans. <i>Journal of Proteome Research</i> , 2010 , 9, 5228-38	5.6	96
161	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
160	Effects of transmembrane and juxtamembrane domains on proliferative ability of TSLP receptor. <i>Molecular Immunology</i> , 2010 , 47, 1207-15	4.3	3
159	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010 , 4, 482-95	7.9	118
158	Identifying targets of miR-143 using a SILAC-based proteomic approach. <i>Molecular BioSystems</i> , 2010 , 6, 1873-82		56
157	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010 , 11, R3	18.3	331
156	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, 1606-17	3.5	26
155	Comparative Proteomic Analysis of <i>Candida albicans</i> and <i>Candida glabrata</i> . <i>Clinical Proteomics</i> , 2010 , 6, 163-173	5	3
154	Site-directed mutagenesis reveals a unique requirement for tyrosine residues in IL-7Ralpha and TSLPR cytoplasmic domains in TSLP-dependent cell proliferation. <i>BMC Immunology</i> , 2010 , 11, 5	3.7	10
153	Comparative proteomics of human embryonic stem cells and embryonal carcinoma cells. <i>Proteomics</i> , 2010 , 10, 1359-73	4.8	41
152	Screening for therapeutic targets of vorinostat by SILAC-based proteomic analysis in human breast cancer cells. <i>Proteomics</i> , 2010 , 10, 1029-39	4.8	41

151	Proteomic characterization of Her2/neu-overexpressing breast cancer cells. <i>Proteomics</i> , 2010 , 10, 3800-108	28
150	Bone Marrow Hypoplasia Induced by Conditional Knockout of the RNase III Domain of Dicer-1. <i>Blood</i> , 2010 , 116, 2226-2226	2.2
149	Human Protein Reference Database--2009 update. <i>Nucleic Acids Research</i> , 2009 , 37, D767-72	20.1 2372
148	A compendium of potential biomarkers of pancreatic cancer. <i>PLoS Medicine</i> , 2009 , 6, e1000046	11.6 217
147	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
146	Prediction of candidate primary immunodeficiency disease genes using a support vector machine learning approach. <i>DNA Research</i> , 2009 , 16, 345-51	4.5 23
145	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009 , 37, D773-81	20.1 72
144	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
143	RAPID: Resource of Asian Primary Immunodeficiency Diseases. <i>Nucleic Acids Research</i> , 2009 , 37, D863-7	20.1 34
142	PathBuilder--open source software for annotating and developing pathway resources. <i>Bioinformatics</i> , 2009 , 25, 2860-2	7.2 35
141	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
140	Identification of miR-21 targets in breast cancer cells using a quantitative proteomic approach. <i>Proteomics</i> , 2009 , 9, 1374-84	4.8 100
139	K63-specific deubiquitination by two JAMM/MPN+ complexes: BRISC-associated Brcc36 and proteasomal Poh1. <i>EMBO Journal</i> , 2009 , 28, 621-31	13 171
138	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
137	Temporal analysis of neural differentiation using quantitative proteomics. <i>Journal of Proteome Research</i> , 2009 , 8, 1315-26	5.6 48
136	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
135	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
134	SILAC for global phosphoproteomic analysis. <i>Methods in Molecular Biology</i> , 2009 , 527, 107-16, x	1.4 28

133	Comparison of peptide array substrate phosphorylation of c-Raf and mitogen activated protein kinase kinase kinase 8. <i>PLoS ONE</i> , 2009 , 4, e6440	3.7	16
132	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. <i>Annals of Indian Academy of Neurology</i> , 2009 , 12, 3-11	0.9	9
131	Molecular alterations in exocrine neoplasms of the pancreas. <i>Archives of Pathology and Laboratory Medicine</i> , 2009 , 133, 405-12	5	12
130	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
129	A panel of biomarkers for esophageal squamous cell carcinoma. <i>FASEB Journal</i> , 2009 , 23, 925.11	0.9	
128	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
127	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008 , 3, 505-16	18.8	170
126	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
125	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
124	Differential membrane proteomics using ¹⁸ O-labeling to identify biomarkers for cholangiocarcinoma. <i>Journal of Proteome Research</i> , 2008 , 7, 4670-7	5.6	38
123	Activated epidermal growth factor receptor as a novel target in pancreatic cancer therapy. <i>Journal of Proteome Research</i> , 2008 , 7, 4651-8	5.6	37
122	Comprehensive comparison of collision induced dissociation and electron transfer dissociation. <i>Analytical Chemistry</i> , 2008 , 80, 4825-35	7.8	90
121	Global impact of oncogenic Src on a phosphotyrosine proteome. <i>Journal of Proteome Research</i> , 2008 , 7, 3447-60	5.6	80
120	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
119	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
118	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
117	Human Proteinpedia as a resource for clinical proteomics. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2038-47	7.6	14
116	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

115	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
114	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
113	O Labeling for a Quantitative Proteomic Analysis of Glycoproteins in Hepatocellular Carcinoma. <i>Clinical Proteomics</i> , 2008 , 4, 137-155	5	15
112	Applications of proteomics to lab diagnosis. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2008 , 3, 485-98	34	33
111	Phosphoproteomics. <i>Current Protocols in Protein Science</i> , 2007 , Chapter 24, Unit 24.4	3.1	6
110	Quantitative proteomics for identification of cancer biomarkers. <i>Proteomics - Clinical Applications</i> , 2007 , 1, 1080-9	3.1	27
109	A curated compendium of phosphorylation motifs. <i>Nature Biotechnology</i> , 2007 , 25, 285-6	44.5	300
108	Copy-number variants in patients with a strong family history of pancreatic cancer. <i>Cancer Biology and Therapy</i> , 2007 , 6, 1592-9	4.6	33
107	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
106	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
105	Dynamic interplay between O-linked N-acetylglucosaminylation and glycogen synthase kinase-3-dependent phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1365-79	7.6	162
104	Upstream stimulatory factors regulate the C/EBP alpha gene during differentiation of 3T3-L1 preadipocytes. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 354, 517-21	3.4	18
103	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
102	Proteomics of Human Pancreatic Juice 2007 , 377-397		
101	Plasma Proteome Database 2007 , 129-136		1
100	Proteomics of Human Bile 2007 , 399-414		4
99	An evaluation of human protein-protein interaction data in the public domain. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 5, S19	3.6	168
98	Chemical rescue of a mutant enzyme in living cells. <i>Science</i> , 2006 , 311, 1293-7	33.3	96

97	Role of p38 in replication of <i>Trypanosoma brucei</i> kinetoplast DNA. <i>Molecular and Cellular Biology</i> , 2006 , 26, 5382-93	4.8	44
96	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
95	Human protein reference database--2006 update. <i>Nucleic Acids Research</i> , 2006 , 34, D411-4	20.1	481
94	Biomarker discovery from pancreatic cancer secretome using a differential proteomic approach. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 157-71	7.6	372
93	Identification of protein ubiquitylation by electrospray ionization tandem mass spectrometric analysis of sulfonated tryptic peptides. <i>Analytical Chemistry</i> , 2006 , 78, 3681-7	7.8	13
92	GCN5 acetyltransferase complex controls glucose metabolism through transcriptional repression of PGC-1alpha. <i>Cell Metabolism</i> , 2006 , 3, 429-38	24.6	349
91	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		3
90	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, 336-41	3	20
89	A functional annotation of subproteomes in human plasma 2006 , 329-351		
88	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
87	Defining the Dynamic O-GlcNAc Proteome. <i>FASEB Journal</i> , 2006 , 20, A56	0.9	
86	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, p12	8.8	62
85	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
84	Assessing reproducibility of a protein dynamics study using in vivo labeling and liquid chromatography tandem mass spectrometry. <i>Analytical Chemistry</i> , 2005 , 77, 2739-44	7.8	23
83	TAGmapper: a web-based tool for mapping SAGE tags. <i>Gene</i> , 2005 , 364, 123-9	3.8	8
82	Proteomic resources: integrating biomedical information in humans. <i>Gene</i> , 2005 , 364, 13-8	3.8	10
81	Probabilistic model of the human protein-protein interaction network. <i>Nature Biotechnology</i> , 2005 , 23, 951-9	44.5	338
80	A manually curated functional annotation of the human X chromosome. <i>Nature Genetics</i> , 2005 , 37, 331-236.3		13

79	Genome annotation of <i>Anopheles gambiae</i> using mass spectrometry-derived data. <i>BMC Genomics</i> , 2005 , 6, 128	4.5	52
78	Bioinformatics and proteomics approaches for aging research. <i>Biogerontology</i> , 2005 , 6, 227-32	4.5	10
77	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005 , 5, 3765-77	4.8	58
76	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005 , 5, 3531-6	4.8	118
75	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005 , 5, 3506-19	4.8	77
74	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
73	A bioinformatics analysis of protein tyrosine phosphatases in humans. <i>DNA Research</i> , 2005 , 12, 79-89	4.5	16
72	A proteomic analysis of human hemodialysis fluid. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 637-50	7.6	55
71	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
70	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
69	Possible Role of the Activation Loop Tyrosine Residue (Y842) in FLT3/ITD Signaling May Be Mediated by SHP-2.. <i>Blood</i> , 2005 , 106, 1199-1199	2.2	1
68	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
67	A role for thymic stromal lymphopoietin in CD4(+) T cell development. <i>Journal of Experimental Medicine</i> , 2004 , 200, 159-68	16.6	191
66	A novel proteomic approach for specific identification of tyrosine kinase substrates using [¹³ C]tyrosine. <i>Journal of Biological Chemistry</i> , 2004 , 279, 15805-13	5.4	84
65	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004 , 32, D497-501	20.1	441
64	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
63	A proteomic analysis of human bile. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 715-28	7.6	130
62	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

61	BioBuilder as a database development and functional annotation platform for proteins. <i>BMC Bioinformatics</i> , 2004 , 5, 43	3.6	7
60	Cloning of a novel signaling molecule, AMSH-2, that potentiates transforming growth factor beta signaling. <i>BMC Cell Biology</i> , 2004 , 5, 2		34
59	Mac-2-binding protein is a diagnostic marker for biliary tract carcinoma. <i>Cancer</i> , 2004 , 101, 1609-15	6.4	83
58	Comprehensive proteomic analysis of human pancreatic juice. <i>Journal of Proteome Research</i> , 2004 , 3, 1042-55	5.6	173
57	ONCOMINE: a cancer microarray database and integrated data-mining platform. <i>Neoplasia</i> , 2004 , 6, 1-6	6.4	2548
56	Unraveling the human interactome: lessons from the yeast. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 79-84		2
55	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
54	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
53	Proteomic Analysis of the Adipocyte Secretome. <i>Nutrition and Disease Prevention</i> , 2004 , 395-413		
52	Mouse embryonic fibroblasts derived from Odin deficient mice display a hyperproliferative phenotype. <i>DNA Research</i> , 2004 , 11, 285-92	4.5	8
51	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
50	Absolute systems biology--measuring dynamics of protein modifications. <i>Trends in Biotechnology</i> , 2003 , 21, 467-70	15.1	5
49	From biological databases to platforms for biomedical discovery. <i>Trends in Biotechnology</i> , 2003 , 21, 263-8	15.1	23
48	Tackling the phosphoproteome: tools and strategies. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 64-9	9.7	192
47	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
46	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
45	Phosphotyrosine mapping in Bcr/Abl oncoprotein using phosphotyrosine-specific immonium ion scanning. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 138-45	7.6	43
44	Multi-Protein Complexes Studied by Mass Spectrometry. <i>Scientific World Journal, The</i> , 2002 , 2, 91-92	2.2	1

43	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002 , 20, 261-8	15.1	791
42	Proteomics goes quantitative: measuring protein abundance. <i>Trends in Biotechnology</i> , 2002 , 20, 361-4	15.1	58
41	Resources for full-length cDNAs. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 266-7	10.3	6
40	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
39	Cloning of a novel phosphotyrosine binding domain containing molecule, Odin, involved in signaling by receptor tyrosine kinases. <i>Oncogene</i> , 2002 , 21, 8029-36	9.2	43
38	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
37	A novel Src homology 2 domain-containing molecule, Src-like adapter protein-2 (SLAP-2), which negatively regulates T cell receptor signaling. <i>Journal of Biological Chemistry</i> , 2002 , 277, 19131-8	5.4	29
36	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
35	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
34	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
33	Analysis of tyrosine phosphorylation sites in signaling molecules by a phosphotyrosine-specific ammonium ion scanning method. <i>Science Signaling</i> , 2002 , 2002, pl16	8.8	28
32	Tyrosine phosphorylation mapping of the epidermal growth factor receptor signaling pathway. <i>Journal of Biological Chemistry</i> , 2002 , 277, 1031-9	5.4	165
31	Overlapping of MINK and CHRNE gene loci in the course of mammalian evolution. <i>Nucleic Acids Research</i> , 2002 , 30, 2906-10	20.1	14
30	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
29	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
28	Toll and interleukin-1 receptor (TIR) domain-containing proteins in plants: a genomic perspective. <i>Trends in Plant Science</i> , 2002 , 7, 388-91	13.1	43
27	Cloning of rat thymic stromal lymphopoietin receptor (TSLPR) and characterization of genomic structure of murine Tslpr gene. <i>Gene</i> , 2002 , 284, 161-8	3.8	7
26	An evaluation of the use of two-dimensional gel electrophoresis in proteomics. <i>New Biotechnology</i> , 2001 , 18, 195-205		119

25	Analysis of proteins and proteomes by mass spectrometry. <i>Annual Review of Biochemistry</i> , 2001 , 70, 437-731	9.1	906
24	Common pitfalls in bioinformatics-based analyses: look before you leap. <i>Trends in Genetics</i> , 2001 , 17, 541-5	8.5	16
23	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001 , 17, 685-7	8.5	96
22	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
21	GPMAW--a software tool for analyzing proteins and peptides. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 687-9	10.3	125
20	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
19	Characterization of promoter region and genomic structure of the murine and human genes encoding Src like adapter protein. <i>Gene</i> , 2001 , 262, 267-73	3.8	3
18	Cloning of a receptor subunit required for signaling by thymic stromal lymphopietin. <i>Nature Immunology</i> , 2000 , 1, 59-64	19.1	338
17	Proteomics to study genes and genomes. <i>Nature</i> , 2000 , 405, 837-46	50.4	1907
16	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
15	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
14	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
13	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 276-80	10.3	60
12	Src-like adaptor protein (Slap) is a negative regulator of mitogenesis. <i>Current Biology</i> , 1998 , 8, 975-8	6.3	55
11	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
10	Oncogenic RET receptors display different autophosphorylation sites and substrate binding specificities. <i>Journal of Biological Chemistry</i> , 1996 , 271, 5309-12	5.4	102
9	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
8	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

7	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
6	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
5	Chromosomal localization of the mouse Src-like adapter protein (Slap) gene and its putative human homolog SLA. <i>Genomics</i> , 1995 , 30, 623-5	4-3	9
4	cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases. <i>Journal of Biological Chemistry</i> , 1995 , 270, 3467-70	5-4	28
3	Complement and coagulation cascades are potentially involved in dopaminergic neurodegeneration in α -synuclein-based mouse models of Parkinson's disease		2
2	Thousands of large-scale RNA sequencing experiments yield a comprehensive new human gene list and reveal extensive transcriptional noise		22
1	Mapping the micro-proteome of the nuclear lamina and lamin associated domains		5