John R Yates 3rd

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/127864/john-r-yates-3rd-publications-by-year.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

54,603 96 497 227 h-index g-index citations papers 62,038 657 10.4 7.73 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
497	Proteomic screen reveals diverse protein transport between connected neurons in the visual system <i>Cell Reports</i> , 2022 , 38, 110287	10.6	2
496	Intercepting IRE1 kinase-FMRP signaling prevents atherosclerosis progression <i>EMBO Molecular Medicine</i> , 2022 , e15344	12	2
495	Cancer Conformational Landscape Shape Tumorigenesis Journal of Proteome Research, 2022,	5.6	1
494	Quantitative BONCAT (QBONCAT) allows identification of newly synthesized proteins after optic nerve injury <i>Journal of Neuroscience</i> , 2022 ,	6.6	2
493	Targeted protein S-nitrosylation of ACE2 as potential treatment to prevent spread of SARS-CoV-2 infection. 2022 ,		1
492	Hexokinase 3 enhances myeloid cell survival via non-glycolytic functions <i>Cell Death and Disease</i> , 2022 , 13, 448	9.8	2
491	SMG1 and CDK12 Link Np63Phosphorylation to RNA Surveillance in Keratinocytes. <i>Journal of Proteome Research</i> , 2021 , 20, 5347-5358	5.6	1
490	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPS cell-derived neural progenitor cells. <i>IScience</i> , 2021 , 24, 103321	6.1	
489	Glycoengineering of NK Cells with Glycan Ligands of CD22 and Selectins for B-Cell Lymphoma Therapy. <i>Angewandte Chemie</i> , 2021 , 133, 3647-3654	3.6	O
488	An APEX2 proximity ligation method for mapping interactions with the nuclear lamina. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	9
487	Regulation of ex-translational activities is the primary function of the multi-tRNA synthetase complex. <i>Nucleic Acids Research</i> , 2021 , 49, 3603-3616	20.1	7
486	S-nitrosylated TDP-43 triggers aggregation, cell-to-cell spread, and neurotoxicity in hiPSCs and in vivo models of ALS/FTD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	10
485	Site-Specific O-Glycosylation Analysis of SARS-CoV-2 Spike Protein Produced in Insect and Human Cells. <i>Viruses</i> , 2021 , 13,	6.2	23
484	Identification of sulfenylation patterns in trophozoite stage Plasmodium falciparum using a non-dimedone based probe. <i>Molecular and Biochemical Parasitology</i> , 2021 , 242, 111362	1.9	2
483	Borrelia burgdorferi infection modifies protein content in saliva of Ixodes scapularis nymphs. <i>BMC Genomics</i> , 2021 , 22, 152	4.5	3
482	Autism-linked Cullin3 germline haploinsufficiency impacts cytoskeletal dynamics and cortical neurogenesis through RhoA signaling. <i>Molecular Psychiatry</i> , 2021 , 26, 3586-3613	15.1	1
481	Altered network and rescue of human neurons derived from individuals with early-onset genetic epilepsy. <i>Molecular Psychiatry</i> , 2021 ,	15.1	11

(2021-2021)

480	Ciliary extracellular vesicles are distinct from the cytosolic extracellular vesicles. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12086	16.4	5
479	Protein Footprinting via Covalent Protein Painting Reveals Structural Changes of the Proteome in Alzheimerß Disease. <i>Journal of Proteome Research</i> , 2021 , 20, 2762-2771	5.6	9
478	Aurora Kinase A proximity map reveals centriolar satellites as regulators of its ciliary function. <i>EMBO Reports</i> , 2021 , 22, e51902	6.5	2
477	Temporal Quantitative Profiling of Newly Synthesized Proteins during Alaccumulation. <i>Journal of Proteome Research</i> , 2021 , 20, 763-775	5.6	3
476	Penicillium oxalicum secretomic analysis identify plant cell wall degrading enzymes important for fruit juice extraction. <i>Journal of Food Science and Technology</i> , 2021 , 58, 1764-1775	3.3	O
475	Noncanonical transnitrosylation network contributes to synapse loss in Alzheimerß disease. <i>Science</i> , 2021 , 371,	33.3	12
474	Glycoengineering of NK Cells with Glycan Ligands of CD22 and Selectins for B-Cell Lymphoma Therapy. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 3603-3610	16.4	13
473	HSP70 chaperones RNA-free TDP-43 into anisotropic intranuclear liquid spherical shells. <i>Science</i> , 2021 , 371,	33.3	73
472	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. <i>Nature Communications</i> , 2021 , 12, 502	17.4	101
471	Site-specific O-glycosylation analysis of SARS-CoV-2 spike protein produced in insect and human cells 2021 ,		2
470	The RNA phosphatase PIR-1 regulates endogenous small RNA pathways in C. elegans. <i>Molecular Cell</i> , 2021 , 81, 546-557.e5	17.6	7
47° 469		17.6 8.9	7
	Cell, 2021 , 81, 546-557.e5	·	,
469	Cell, 2021, 81, 546-557.e5 SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. ELife, 2021, 10, Exposure to a sublethal menadione concentration modifies the mycelial secretome and conidial enzyme activities of Metarhizium anisopliae sensu lato and increases its virulence against	8.9	,
469 468	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. <i>ELife</i> , 2021 , 10, Exposure to a sublethal menadione concentration modifies the mycelial secretome and conidial enzyme activities of Metarhizium anisopliae sensu lato and increases its virulence against Rhipicephalus microplus. <i>Microbiological Research</i> , 2021 , 248, 126753 Phenotypic and functional variation in venom and venom resistance of two sympatric rattlesnakes	8.9 5·3	2
469 468 467	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. <i>ELife</i> , 2021 , 10, Exposure to a sublethal menadione concentration modifies the mycelial secretome and conidial enzyme activities of Metarhizium anisopliae sensu lato and increases its virulence against Rhipicephalus microplus. <i>Microbiological Research</i> , 2021 , 248, 126753 Phenotypic and functional variation in venom and venom resistance of two sympatric rattlesnakes and their prey. <i>Journal of Evolutionary Biology</i> , 2021 , 34, 1447-1465 Cortical organoids model early brain development disrupted by 16p11.2 copy number variants in	8.9 5·3 2.3	3
469 468 467 466	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in. <i>ELife</i> , 2021 , 10, Exposure to a sublethal menadione concentration modifies the mycelial secretome and conidial enzyme activities of Metarhizium anisopliae sensu lato and increases its virulence against Rhipicephalus microplus. <i>Microbiological Research</i> , 2021 , 248, 126753 Phenotypic and functional variation in venom and venom resistance of two sympatric rattlesnakes and their prey. <i>Journal of Evolutionary Biology</i> , 2021 , 34, 1447-1465 Cortical organoids model early brain development disrupted by 16p11.2 copy number variants in autism. <i>Molecular Psychiatry</i> , 2021 , Clathrin packets move in slow axonal transport and deliver functional payloads to synapses. <i>Neuron</i>	8.9 5.3 2.3	3

462	Cross-editing by a tRNA synthetase allows vertebrates to abundantly express mischargeable tRNA without causing mistranslation. <i>Nucleic Acids Research</i> , 2020 , 48, 6445-6457	20.1	7
461	HIV-1 Envelope and MPER Antibody Structures in Lipid Assemblies. <i>Cell Reports</i> , 2020 , 31, 107583	10.6	29
460	Proteomic Identification Reveals the Role of Ciliary Extracellular-Like Vesicle in Cardiovascular Function. <i>Advanced Science</i> , 2020 , 7, 1903140	13.6	3
459	Confronting Racism in Chemistry Journals. ACS Applied Nano Materials, 2020, 3, 6131-6133	5.6	
458	Confronting Racism in Chemistry Journals. ACS Applied Polymer Materials, 2020, 2, 2496-2498	4.3	
457	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. <i>Journal of Proteome Research</i> , 2020 , 19, 3153-3161	5.6	14
456	Confronting Racism in Chemistry Journals. <i>Organometallics</i> , 2020 , 39, 2331-2333	3.8	
455	PTPN22 phosphorylation acts as a molecular rheostat for the inhibition of TCR signaling. <i>Science Signaling</i> , 2020 , 13,	8.8	5
454	National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. <i>Journal of Proteome Research</i> , 2020 , 19, 1900-1912	5.6	4
453	Proteomics of Select Neglected Tropical Diseases. Annual Review of Analytical Chemistry, 2020, 13, 315-	·3 i3:6 5	3
452	Unbiased Identification of trans Regulators of ADAR and A-to-I RNA Editing. <i>Cell Reports</i> , 2020 , 31, 1076	5 56 .6	11
451	Proteomics Profiling of KAIMRC1 in Comparison to MDA-MB231 and MCF-7. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	6
450	Update to Our Reader, Reviewer, and Author CommunitiesApril 2020. <i>Energy & amp; Fuels</i> , 2020 , 34, 5107-5108	4.1	
449	EThcD and 213 nm UVPD for Top-Down Analysis of Bovine Seminal Plasma Proteoforms on Electrophoretic and Chromatographic Time Frames. <i>Analytical Chemistry</i> , 2020 , 92, 2979-2987	7.8	13
448	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. <i>Cell</i> , 2020 , 180, 263-277.e20	56.2	46
447	The Journey Is the Reward, a Taoist Proverb: John B. Fenn Award for Distinguished Contribution in Mass Spectrometry Lecture. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1327-1336	3.5	
446	Amblyomma americanum serpin 41 (AAS41) inhibits inflammation by targeting chymase and chymotrypsin. <i>International Journal of Biological Macromolecules</i> , 2020 , 156, 1007-1021	7.9	8
445	Update to Our Reader, Reviewer, and Author CommunitiesApril 2020. Organometallics, 2020 , 39, 1665-	16,86	

(2020-2020)

444	Loss of MAGEL2 in Prader-Willi syndrome leads to decreased secretory granule and neuropeptide production. <i>JCI Insight</i> , 2020 , 5,	9.9	15
443	Time-resolved proteomic profile of Amblyomma americanum tick saliva during feeding. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0007758	4.8	22
442	RNA promotes phase separation of glycolysis enzymes into yeast G bodies in hypoxia. <i>ELife</i> , 2020 , 9,	8.9	30
441	Confronting Racism in Chemistry Journals. <i>Journal of Chemical Health and Safety</i> , 2020 , 27, 198-200	1.7	
440	The INO80 Complex Regulates Epigenetic Inheritance of Heterochromatin. <i>Cell Reports</i> , 2020 , 33, 1085	6 61 0.6	5
439	Structural analysis of full-length SARS-CoV-2 spike protein from an advanced vaccine candidate 2020 ,		8
438	Function of the MYND Domain and C-Terminal Region in Regulating the Subcellular Localization and Catalytic Activity of the SMYD Family Lysine Methyltransferase Set5. <i>Molecular and Cellular Biology</i> , 2020 , 40,	4.8	7
437	Improving Proteomics Data Reproducibility with a Dual-Search Strategy. <i>Analytical Chemistry</i> , 2020 , 92, 1697-1701	7.8	3
436	Intracellular amyloid toxicity induces oxytosis/ferroptosis regulated cell death. <i>Cell Death and Disease</i> , 2020 , 11, 828	9.8	21
435	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020 , 92, 14466-14475	7.8	8
434	Structural analysis of full-length SARS-CoV-2 spike protein from an advanced vaccine candidate. <i>Science</i> , 2020 , 370, 1089-1094	33.3	153
433	Expression of Amyloidogenic Transthyretin Drives Hepatic Proteostasis Remodeling in an Induced Pluripotent Stem Cell Model of Systemic Amyloid Disease. <i>Stem Cell Reports</i> , 2020 , 15, 515-528	8	4
432	Changes in porcine cauda epididymal fluid proteome by disrupting the HPT axis: Unveiling potential mechanisms of male infertility. <i>Molecular Reproduction and Development</i> , 2020 , 87, 952-965	2.6	0
431	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1783-1802	3.5	32
430	Visualization of the HIV-1 Env glycan shield across scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28014-28025	11.5	29
429	Quantitative analysis of global protein stability rates in tissues. <i>Scientific Reports</i> , 2020 , 10, 15983	4.9	5
428	Protein signatures of seminal plasma from bulls with contrasting frozen-thawed sperm viability. <i>Scientific Reports</i> , 2020 , 10, 14661	4.9	10
427	O-GlcNAcase targets pyruvate kinase M2 to regulate tumor growth. <i>Oncogene</i> , 2020 , 39, 560-573	9.2	16

426	Ready for the journey: a comparative proteome profiling of porcine cauda epididymal fluid and spermatozoa. <i>Cell and Tissue Research</i> , 2020 , 379, 389-405	4.2	5
425	Human Influenza Virus Hemagglutinins Contain Conserved Oligomannose N-Linked Glycans Allowing Potent Neutralization by Lectins. <i>Cell Host and Microbe</i> , 2020 , 27, 725-735.e5	23.4	12
424	A Hetero-Multimeric Chitinase-Containing and Ookinete-Secreted Protein Complex Involved in Mosquito Midgut Invasion. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 615343	5.9	3
423	Proteomics of Rat Lungs Infected by Reveals a Potential Warburg-like Effect. <i>Journal of Proteome Research</i> , 2019 , 18, 3885-3895	5.6	10
422	The interactome of 2-Cys peroxiredoxins in Plasmodium falciparum. <i>Scientific Reports</i> , 2019 , 9, 13542	4.9	4
421	Mitogenic Signals Stimulate the CREB Coactivator CRTC3 through PP2A Recruitment. <i>IScience</i> , 2019 , 11, 134-145	6.1	10
420	The circadian E3 ligase complex SCF targets TLK2. <i>Scientific Reports</i> , 2019 , 9, 198	4.9	16
419	Proteomics INTegrator (PINT): An Online Tool To Store, Query, and Visualize Large Proteomics Experiment Results. <i>Journal of Proteome Research</i> , 2019 , 18, 2999-3008	5.6	
418	Exploring protein myristoylation in Toxoplasma gondii. Experimental Parasitology, 2019, 203, 8-18	2.1	4
417	DNA replication acts as an error correction mechanism to maintain centromere identity by restricting CENP-A to centromeres. <i>Nature Cell Biology</i> , 2019 , 21, 743-754	23.4	43
416	Identification of new transmembrane proteins concentrated at the nuclear envelope using organellar proteomics of mesenchymal cells. <i>Nucleus</i> , 2019 , 10, 126-143	3.9	13
415	A Non-Dicer RNase III and Four Other Novel Factors Required for RNAi-Mediated Transposon Suppression in the Human Pathogenic Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2235-2244	3.2	11
414	A quantitation module for isotope-labeled peptides integrated into PatternLab for proteomics. Journal of Proteomics, 2019 , 202, 103371	3.9	0
413	Large-Scale Phosphoproteomics 2019 , 291-309		1
412	Protein P rotein Interactions 2019 , 125-144		1
411	Comparative Proteomic Analysis of Murine Cutaneous Lesions Induced by or. <i>ACS Infectious Diseases</i> , 2019 , 5, 1295-1305	5.5	4
410	A proteomic comparison of excretion/secretion products in Fasciola hepatica newly excysted juveniles (NEJ) derived from Lymnaea viatrix or Pseudosuccinea columella. <i>Experimental Parasitology</i> , 2019 , 201, 11-20	2.1	6
409	Phosphotyrosine-dependent interaction between the kinases PKCland Zap70 promotes proximal TCR signaling. <i>Science Signaling</i> , 2019 , 12,	8.8	8

408	Paip2 cooperates with Cbp80 at an active promoter and participates in RNA Polymerase II phosphorylation in Drosophila. <i>FEBS Letters</i> , 2019 , 593, 1102-1112	3.8	5
407	Proteomics of Communities: Metaproteomics. <i>Journal of Proteome Research</i> , 2019 , 18, 2359	5.6	5
406	Blood anticlotting activity of a Rhipicephalus microplus cathepsin L-like enzyme. <i>Biochimie</i> , 2019 , 163, 12-20	4.6	9
405	Tick Gen B organ engagement in lipid metabolism revealed by a combined transcriptomic and proteomic approach. <i>Ticks and Tick-borne Diseases</i> , 2019 , 10, 787-797	3.6	9
404	Perm1 regulates CaMKII activation and shapes skeletal muscle responses to endurance exercise training. <i>Molecular Metabolism</i> , 2019 , 23, 88-97	8.8	12
403	Venom Composition in a Phenotypically Variable Pit Viper (Trimeresurus insularis) across the Lesser Sunda Archipelago. <i>Journal of Proteome Research</i> , 2019 , 18, 2206-2220	5.6	13
402	Label-Free Proteomic Analysis Reveals Parasite-Specific Protein Alterations in Macrophages Following Leishmania amazonensis, Leishmania major, or Leishmania infantum Infection. <i>ACS Infectious Diseases</i> , 2019 , 5, 851-862	5.5	8
401	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPK Interactome. <i>Journal of Proteome Research</i> , 2019 , 18, 3703-3714	5.6	3
400	Recent technical advances in proteomics. F1000Research, 2019, 8,	3.6	33
399	Recent trends of capillary electrophoresis-mass spectrometry in proteomics research. <i>Mass Spectrometry Reviews</i> , 2019 , 38, 445-460	11	42
398	The Retinal Ganglion Cell Transportome Identifies Proteins Transported to Axons and Presynaptic Compartments in the Visual System In Vivo. <i>Cell Reports</i> , 2019 , 28, 1935-1947.e5	10.6	10
397	Dataset supporting the proteomic differences found between excretion/secretion products from two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019 , 25, 104272	1.2	O
397	two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. Data in Brief, 2019	1.2	o 93
	two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019 , 25, 104272 Exosomes regulate neurogenesis and circuit assembly. <i>Proceedings of the National Academy of</i>		
396	two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019 , 25, 104272 Exosomes regulate neurogenesis and circuit assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16086-16094 Tandem Mass Tag Proteomic Analysis of and Models of Cutaneous Leishmaniasis Reveals Parasite-Specific and Nonspecific Modulation of Proteins in the Host. <i>ACS Infectious Diseases</i> , 2019 ,	11.5	93
396 395	two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019 , 25, 104272 Exosomes regulate neurogenesis and circuit assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16086-16094 Tandem Mass Tag Proteomic Analysis of and Models of Cutaneous Leishmaniasis Reveals Parasite-Specific and Nonspecific Modulation of Proteins in the Host. <i>ACS Infectious Diseases</i> , 2019 , 5, 2136-2147	11.5	93
396 395 394	two isolates of newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019 , 25, 104272 Exosomes regulate neurogenesis and circuit assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16086-16094 Tandem Mass Tag Proteomic Analysis of and Models of Cutaneous Leishmaniasis Reveals Parasite-Specific and Nonspecific Modulation of Proteins in the Host. <i>ACS Infectious Diseases</i> , 2019 , 5, 2136-2147 Protein Analysis by Shotgun Proteomics 2019 , 1-38 Proteomic analyses reveal misregulation of LIN28 expression and delayed timing of glial	11. 5	9353

390	The KLDpT activation loop motif is critical for MARK kinase activity. <i>PLoS ONE</i> , 2019 , 14, e0225727	3.7	O
389	Characterization of a novel antioxidant peptide from feather keratin hydrolysates. <i>New Biotechnology</i> , 2019 , 49, 71-76	6.4	36
388	A posttranslational modification code for CFTR maturation is altered in cystic fibrosis. <i>Science Signaling</i> , 2019 , 12,	8.8	16
387	Secretomic analysis of Beauveria bassiana related to cattle tick, Rhipicephalus microplus, infection. <i>Folia Microbiologica</i> , 2019 , 64, 361-372	2.8	4
386	Zika Virus Infection of Human Mesenchymal Stem Cells Promotes Differential Expression of Proteins Linked to Several Neurological Diseases. <i>Molecular Neurobiology</i> , 2019 , 56, 4708-4717	6.2	24
385	ComPIL 2.0: An Updated Comprehensive Metaproteomics Database. <i>Journal of Proteome Research</i> , 2019 , 18, 616-622	5.6	12
384	Understanding molecular mechanisms of disease through spatial proteomics. <i>Current Opinion in Chemical Biology</i> , 2019 , 48, 19-25	9.7	11
383	Mitogen-activated kinase kinase kinase 1 inhibits hedgehog signaling and medulloblastoma growth through GLI1 phosphorylation. <i>International Journal of Oncology</i> , 2019 , 54, 505-514	4.4	14
382	Increased proteomic complexity in hybrids during development. Science Advances, 2018, 4, eaao3424	14.3	8
381	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. <i>Cell</i> , 2018 , 173, 1014-1030.e17	56.2	27
380	Global site-specific analysis of glycoprotein N-glycan processing. <i>Nature Protocols</i> , 2018 , 13, 1196-1212	18.8	40
379	PACOM: A Versatile Tool for Integrating, Filtering, Visualizing, and Comparing Multiple Large Mass Spectrometry Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2018 , 17, 1547-1558	5.6	6
378	A proteomic insight into vitellogenesis during tick ovary maturation. Scientific Reports, 2018, 8, 4698	4.9	21
377	Expression profile of Rhipicephalus microplus vitellogenin receptor during oogenesis. <i>Ticks and Tick-borne Diseases</i> , 2018 , 9, 72-81	3.6	19
376	The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	62
375	Quantitative analysis of newly synthesized proteins. <i>Nature Protocols</i> , 2018 , 13, 1744-1762	18.8	18
374	An overview of Phoneutria nigriventer spider venom using combined transcriptomic and proteomic approaches. <i>PLoS ONE</i> , 2018 , 13, e0200628	3.7	22
373	Proteomics and pulse azidohomoalanine labeling of newly synthesized proteins: what are the potential applications?. <i>Expert Review of Proteomics</i> , 2018 , 15, 545-554	4.2	15

(2018-2018)

372	Quantitative temporal analysis of protein dynamics in cardiac remodeling. <i>Journal of Molecular and Cellular Cardiology</i> , 2018 , 121, 163-172	5.8	16	
371	PML Recruits TET2 to Regulate DNA Modification and Cell Proliferation in Response to Chemotherapeutic Agent. <i>Cancer Research</i> , 2018 , 78, 2475-2489	10.1	11	
370	Regulated nuclear accumulation of a histone methyltransferase times the onset of heterochromatin formation in embryos. <i>Science Advances</i> , 2018 , 4, eaat6224	14.3	35	
369	Structural Analysis of Hippocampal Kinase Signal Transduction. ACS Chemical Neuroscience, 2018, 9, 30)72 , . 3 08	5 ₂	
368	CBD-1 organizes two independent complexes required for eggshell vitelline layer formation and egg activation in C. elegans. <i>Developmental Biology</i> , 2018 , 442, 288-300	3.1	5	•
367	NRDE-2, the human homolog of fission yeast Nrl1, prevents DNA damage accumulation in human cells. <i>RNA Biology</i> , 2018 , 15, 868-876	4.8	9	
366	Control of seed dormancy and germination by DOG1-AHG1 PP2C phosphatase complex via binding to heme. <i>Nature Communications</i> , 2018 , 9, 2132	17.4	77	
365	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018 , 9, 2320	17.4	13	
364	SHMT2 and the BRCC36/BRISC deubiquitinase regulate HIV-1 Tat K63-ubiquitylation and destruction by autophagy. <i>PLoS Pathogens</i> , 2018 , 14, e1007071	7.6	23	
363	Interactome analysis of the lymphocytic choriomeningitis virus nucleoprotein in infected cells reveals ATPase Na+/K+ transporting subunit Alpha 1 and prohibitin as host-cell factors involved in the life cycle of mammarenaviruses. <i>PLoS Pathogens</i> , 2018 , 14, e1006892	7.6	22	
362	Defective RNA polymerase III is negatively regulated by the SUMO-Ubiquitin-Cdc48 pathway. <i>ELife</i> , 2018 , 7,	8.9	15	
361	Validation of In Vivo Protein Surface Accessibility Method. FASEB Journal, 2018, 32, 802.12	0.9		
360	Identification and characterization of proteins in the Amblyomma americanum tick cement cone. <i>International Journal for Parasitology</i> , 2018 , 48, 211-224	4.3	17	
359	From Synapse to Function: A Perspective on the Role of Neuroproteomics in Elucidating Mechanisms of Drug Addiction. <i>Proteomes</i> , 2018 , 6,	4.6	4	
358	Content Is King: Databases Preserve the Collective Information of Science. <i>Journal of Biomolecular Techniques</i> , 2018 , 29, 1-3	1.1		
357	Integrated In Vivo Quantitative Proteomics and Nutrient Tracing Reveals Age-Related Metabolic Rewiring of Pancreatic ICell Function. <i>Cell Reports</i> , 2018 , 25, 2904-2918.e8	10.6	29	
356	Proteomic analysis identifies highly expressed plasma membrane proteins for detection and therapeutic targeting of specific breast cancer subtypes. <i>Clinical Proteomics</i> , 2018 , 15, 30	5	6	
355	DAF-16/FOXO and HLH-30/TFEB function as combinatorial transcription factors to promote stress resistance and longevity. <i>Nature Communications</i> , 2018 , 9, 4400	17.4	66	

354	MIEF1 Microprotein Regulates Mitochondrial Translation. <i>Biochemistry</i> , 2018 , 57, 5564-5575	3.2	37
353	Differential processing of HIV envelope glycans on the virus and soluble recombinant trimer. <i>Nature Communications</i> , 2018 , 9, 3693	17.4	87
352	Proteins that control the geometry of microtubules at the ends of cilia. <i>Journal of Cell Biology</i> , 2018 , 217, 4298-4313	7.3	25
351	Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer. <i>Molecular Cell</i> , 2018 , 70, 842-853.e7	17.6	57
350	ANKRD16 prevents neuron loss caused by an editing-defective tRNA synthetase. <i>Nature</i> , 2018 , 557, 510)-551.54	16
349	Role of the visual experience-dependent nascent proteome in neuronal plasticity. <i>ELife</i> , 2018 , 7,	8.9	11
348	Evidence for opposing roles of Celsr3 and Vangl2 in glutamatergic synapse formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E610-E618	11.5	33
347	The centriolar satellite protein CCDC66 interacts with CEP290 and functions in cilium formation and trafficking. <i>Journal of Cell Science</i> , 2017 , 130, 1450-1462	5.3	29
346	Targeting BMK1 Impairs the Drug Resistance to Combined Inhibition of BRAF and MEK1/2 in Melanoma. <i>Scientific Reports</i> , 2017 , 7, 46244	4.9	14
345	Mechanism of ubiquitin chain synthesis employed by a HECT domain ubiquitin ligase. <i>Journal of Biological Chemistry</i> , 2017 , 292, 10398-10413	5.4	34
344	Matchmaking in Proteomics. Clinical Chemistry, 2017, 63, 1297-1298	5.5	1
343	HILAQ: A Novel Strategy for Newly Synthesized Protein Quantification. <i>Journal of Proteome Research</i> , 2017 , 16, 2213-2220	5.6	21
342	MEF2D haploinsufficiency downregulates the NRF2 pathway and renders photoreceptors susceptible to light-induced oxidative stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E4048-E4056	11.5	24
341	Identification of Microprotein-Protein Interactions via APEX Tagging. <i>Biochemistry</i> , 2017 , 56, 3299-3306	3.2	26
340	Hsc70 chaperone activity is required for the cytosolic slow axonal transport of synapsin. <i>Journal of Cell Biology</i> , 2017 , 216, 2059-2074	7.3	16
339	Global site-specific N-glycosylation analysis of HIV envelope glycoprotein. <i>Nature Communications</i> , 2017 , 8, 14954	17.4	133
338	Global Analysis of Protein Expression of Inner Ear Hair Cells. <i>Journal of Neuroscience</i> , 2017 , 37, 1320-133	3 0 .6	33
337	Secreted Glioblastoma Nanovesicles Contain Intracellular Signaling Proteins and Active Ras Incorporated in a Farnesylation-dependent Manner. <i>Journal of Biological Chemistry</i> , 2017 , 292, 611-628	5.4	28

336	High infestation levels of Schizotetranychus oryzae severely affects rice metabolism. <i>Journal of Plant Physiology</i> , 2017 , 219, 100-111	3.6	9
335	Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. <i>Journal of Proteome Research</i> , 2017 , 16, 4425-4434	5.6	11
334	Analysis of a cAMP regulated coactivator family reveals an alternative phosphorylation motif for AMPK family members. <i>PLoS ONE</i> , 2017 , 12, e0173013	3.7	19
333	The GAGA factor regulatory network: Identification of GAGA factor associated proteins. <i>PLoS ONE</i> , 2017 , 12, e0173602	3.7	22
332	An SMC-like protein binds and regulates Caenorhabditis elegans condensins. <i>PLoS Genetics</i> , 2017 , 13, e1006614	6	5
331	TFG facilitates outer coat disassembly on COPII transport carriers to promote tethering and fusion with ER-Golgi intermediate compartments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E7707-E7716	11.5	40
330	Proteomic Analysis of Peripheral Blood Mononuclear Cells after a High-Fat, High-Carbohydrate Meal with Orange Juice. <i>Journal of Proteome Research</i> , 2017 , 16, 4086-4092	5.6	13
329	Protein arginylation targets alpha synuclein, facilitates normal brain health, and prevents neurodegeneration. <i>Scientific Reports</i> , 2017 , 7, 11323	4.9	18
328	Quantitative Analysis of the Proteome Response to the Histone Deacetylase Inhibitor (HDACi) Vorinostat in Niemann-Pick Type C1 disease. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1938-1957	7.6	18
327	An Mtr4/ZFC3H1 complex facilitates turnover of unstable nuclear RNAs to prevent their cytoplasmic transport and global translational repression. <i>Genes and Development</i> , 2017 , 31, 1257-1271	12.6	63
326	Glycolytic Enzymes Coalesce in G Bodies under Hypoxic Stress. Cell Reports, 2017, 20, 895-908	10.6	77
325	S-Nitrosylation of PINK1 Attenuates PINK1/Parkin-Dependent Mitophagy in hiPSC-Based Parkinson B Disease Models. <i>Cell Reports</i> , 2017 , 21, 2171-2182	10.6	70
324	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimerß Disease-like Pathology. <i>Cell Reports</i> , 2017 , 21, 2614-2627	10.6	35
323	Profiling of Protein O-GlcNAcylation in Murine CD8 Effector- and Memory-like T Cells. <i>ACS Chemical Biology</i> , 2017 , 12, 3031-3038	4.9	14
322	Ist1 regulates ESCRT-III assembly and function during multivesicular endosome biogenesis in Caenorhabditis elegans embryos. <i>Nature Communications</i> , 2017 , 8, 1439	17.4	21
321	A post-transcriptional program coordinated by CSDE1 prevents intrinsic neural differentiation of human embryonic stem cells. <i>Nature Communications</i> , 2017 , 8, 1456	17.4	38
320	Chemoproteomic profiling and discovery of protein electrophiles in human cells. <i>Nature Chemistry</i> , 2017 , 9, 234-243	17.6	46
319	DCLK1 phosphorylates the microtubule-associated protein MAP7D1 to promote axon elongation in cortical neurons. <i>Developmental Neurobiology</i> , 2017 , 77, 493-510	3.2	16

318	Double mimicry evades tRNA synthetase editing by toxic vegetable-sourced non-proteinogenic amino acid. <i>Nature Communications</i> , 2017 , 8, 2281	17.4	30
317	Tick-Host Range Adaptation: Changes in Protein Profiles in Unfed Adult and Saliva Stimulated to Feed on Different Hosts. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 517	5.9	40
316	CKS Proteins Promote Checkpoint Recovery by Stimulating Phosphorylation of Treslin. <i>Molecular and Cellular Biology</i> , 2017 , 37,	4.8	4
315	Proteasome activity regulates CD8+ T lymphocyte metabolism and fate specification. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3609-3623	15.9	24
314	Cleavage of the SUN-domain protein Mps3 at its N-terminus regulates centrosome disjunction in budding yeast meiosis. <i>PLoS Genetics</i> , 2017 , 13, e1006830	6	13
313	The protein kinase MBK-1 contributes to lifespan extension in mutant and germline-deficient. <i>Aging</i> , 2017 , 9, 1414-1432	5.6	6
312	Integrated Proteomic Pipeline Using Multiple Search Engines for a Proteogenomic Study with a Controlled Protein False Discovery Rate. <i>Journal of Proteome Research</i> , 2016 , 15, 4082-4090	5.6	28
311	Deep interactome profiling of membrane proteins by co-interacting protein identification technology. <i>Nature Protocols</i> , 2016 , 11, 2515-2528	18.8	32
310	URI Regulates KAP1 Phosphorylation and Transcriptional Repression via PP2A Phosphatase in Prostate Cancer Cells. <i>Journal of Biological Chemistry</i> , 2016 , 291, 25516-25528	5.4	16
309	The pseudokinase CaMKv is required for the activity-dependent maintenance of dendritic spines. <i>Nature Communications</i> , 2016 , 7, 13282	17.4	19
308	Role of sulfiredoxin as a peroxiredoxin-2 denitrosylase in human iPSC-derived dopaminergic neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7	564-€7	5 7 3
307	Fimbrin phosphorylation by metaphase Cdk1 regulates actin cable dynamics in budding yeast. <i>Nature Communications</i> , 2016 , 7, 11265	17.4	19
306	Across intra-mammalian stages of the liver f luke Fasciola hepatica: a proteomic study. <i>Scientific Reports</i> , 2016 , 6, 32796	4.9	39
305	Reduced passive force in skeletal muscles lacking protein arginylation. <i>American Journal of Physiology - Cell Physiology</i> , 2016 , 310, C127-35	5.4	15
304	A butterfly effect in cancer. <i>Molecular and Cellular Oncology</i> , 2016 , 3, e1029063	1.2	3
303	Ccdc11 is a novel centriolar satellite protein essential for ciliogenesis and establishment of left-right asymmetry. <i>Molecular Biology of the Cell</i> , 2016 , 27, 48-63	3.5	29
302	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. <i>Nature Protocols</i> , 2016 , 11, 102-17	18.8	156
301	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. Analytical Chemistry, 2016 , 88, 3967-75	7.8	73

(2016-2016)

300	The proper connection between shelterin components is required for telomeric heterochromatin assembly. <i>Genes and Development</i> , 2016 , 30, 827-39	12.6	35
299	Venomous extract protein profile of Brazilian tarantula Grammostola iheringi: searching for potential biotechnological applications. <i>Journal of Proteomics</i> , 2016 , 136, 35-47	3.9	19
298	Comprehensive data analysis of human ureter proteome. <i>Data in Brief</i> , 2016 , 6, 853-7	1.2	
297	Physiological and Molecular Alterations Promoted by Schizotetranychus oryzae Mite Infestation in Rice Leaves. <i>Journal of Proteome Research</i> , 2016 , 15, 431-46	5.6	10
296	Ixodes scapularis Tick Saliva Proteins Sequentially Secreted Every 24 h during Blood Feeding. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004323	4.8	81
295	The Rqc2/Tae2 subunit of the ribosome-associated quality control (RQC) complex marks ribosome-stalled nascent polypeptide chains for aggregation. <i>ELife</i> , 2016 , 5, e11794	8.9	92
294	A histone H3K9M mutation traps histone methyltransferase Clr4 to prevent heterochromatin spreading. <i>ELife</i> , 2016 , 5,	8.9	26
293	Proteomic Analysis of Protein Turnover by Metabolic Whole Rodent Pulse-Chase Isotopic Labeling and Shotgun Mass Spectrometry Analysis. <i>Methods in Molecular Biology</i> , 2016 , 1410, 293-304	1.4	11
292	Ck2-Dependent Phosphorylation Is Required to Maintain Pax7 Protein Levels in Proliferating Muscle Progenitors. <i>PLoS ONE</i> , 2016 , 11, e0154919	3.7	16
291	Integration of Breast Cancer Secretomes with Clinical Data Elucidates Potential Serum Markers for Disease Detection, Diagnosis, and Prognosis. <i>PLoS ONE</i> , 2016 , 11, e0158296	3.7	21
290	Using PSEA-Quant for Protein Set Enrichment Analysis of Quantitative Mass Spectrometry-Based Proteomics. <i>Current Protocols in Bioinformatics</i> , 2016 , 53, 13.28.1-13.28.16	24.2	6
289	P1-038: Proteomic Analysis of Hippocampal Cell Culture With Low Doses of Lithium Treatment 2016 , 12, P415-P415		
288	Circadian Amplitude Regulation via FBXW7-Targeted REV-ERB Degradation. <i>Cell</i> , 2016 , 165, 1644-1657	56.2	94
287	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016 , 19, 849-64	23.4	59
286	Nonsense-mediated decay regulates key components of homologous recombination. <i>Nucleic Acids Research</i> , 2016 , 44, 5218-30	20.1	9
285	A proteomic glimpse into human ureter proteome. <i>Proteomics</i> , 2016 , 16, 80-4	4.8	6
284	Spindle-E cycling between nuage and cytoplasm is controlled by Qin and PIWI proteins. <i>Journal of Cell Biology</i> , 2016 , 213, 201-11	7.3	8
283	A TRAF-like motif of the inducible costimulator ICOS controls development of germinal center TFH cells via the kinase TBK1. <i>Nature Immunology</i> , 2016 , 17, 825-33	19.1	44

282	Poly(ADP-ribose) Polymerase 1 Represses Liver X Receptor-mediated ABCA1 Expression and Cholesterol Efflux in Macrophages. <i>Journal of Biological Chemistry</i> , 2016 , 291, 11172-84	5.4	30
281	A comprehensive and scalable database search system for metaproteomics. <i>BMC Genomics</i> , 2016 , 17, 642	4.5	34
280	Identification of Open Stomata1-Interacting Proteins Reveals Interactions with Sucrose Non-fermenting1-Related Protein Kinases2 and with Type 2A Protein Phosphatases That Function in Abscisic Acid Responses. <i>Plant Physiology</i> , 2015 , 169, 760-79	6.6	59
279	The Deubiquitylase MATH-33 Controls DAF-16 Stability and Function in Metabolism and Longevity. <i>Cell Metabolism</i> , 2015 , 22, 151-63	24.6	26
278	Monoclonal 1- and 3-Phosphohistidine Antibodies: New Tools to Study Histidine Phosphorylation. <i>Cell</i> , 2015 , 162, 198-210	56.2	117
277	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemann-Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1734-49	7.6	33
276	The VPS-20 subunit of the endosomal sorting complex ESCRT-III exhibits an open conformation in the absence of upstream activation. <i>Biochemical Journal</i> , 2015 , 466, 625-37	3.8	15
275	Proteomic analysis reveals a role for Bcl2-associated athanogene 3 and major vault protein in resistance to apoptosis in senescent cells by regulating ERK1/2 activation. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1-14	7.6	23
274	Harnessing the heart of big data. Circulation Research, 2015, 116, 1115-9	15.7	47
273	Phosphorylation-dependent inhibition of Cdc42 GEF Gef1 by 14-3-3 protein Rad24 spatially regulates Cdc42 GTPase activity and oscillatory dynamics during cell morphogenesis. <i>Molecular Biology of the Cell</i> , 2015 , 26, 3520-34	3.5	31
272	Extracting Accurate Precursor Information for Tandem Mass Spectra by RawConverter. <i>Analytical Chemistry</i> , 2015 , 87, 11361-7	7.8	159
271	Fmr1 deficiency promotes age-dependent alterations in the cortical synaptic proteome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4697-706	11.5	48
270	Non-canonical Hedgehog/AMPK-Mediated Control of Polyamine Metabolism Supports Neuronal and Medulloblastoma Cell Growth. <i>Developmental Cell</i> , 2015 , 35, 21-35	10.2	43
269	Pulsed Azidohomoalanine Labeling in Mammals (PALM) Detects Changes in Liver-Specific LKB1 Knockout Mice. <i>Journal of Proteome Research</i> , 2015 , 14, 4815-22	5.6	48
268	Noncanoncial signal recognition particle RNAs in a major eukaryotic phylum revealed by purification of SRP from the human pathogen Cryptococcus neoformans. <i>Nucleic Acids Research</i> , 2015 , 43, 9017-27	20.1	4
267	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. <i>Nature Communications</i> , 2015 , 6, 7623	17.4	92
266	Gene replacement and quantitative mass spectrometry approaches validate guanosine monophosphate synthetase as essential for growth. <i>Biochemistry and Biophysics Reports</i> , 2015 , 4, 277-2	8 ² 2 ²	4
265	Pivotal role of computers and software in mass spectrometry - SEQUEST and 20 years of tandem MS database searching. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1804-13	3.5	20

(2015-2015)

264	The Sorting Receptor SorCS1 Regulates Trafficking of Neurexin and AMPA Receptors. <i>Neuron</i> , 2015 , 87, 764-80	13.9	47
263	Degradation of HK2 by chaperone-mediated autophagy promotes metabolic catastrophe and cell death. <i>Journal of Cell Biology</i> , 2015 , 210, 705-16	7.3	73
262	Mechanism-Based Post-Translational Modification and Inactivation in Terpene Synthases. <i>ACS Chemical Biology</i> , 2015 , 10, 2501-11	4.9	16
261	B 508 CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015 , 528, 510-6	50.4	163
260	ProteinInferencer: Confident protein identification and multiple experiment comparison for large scale proteomics projects. <i>Journal of Proteomics</i> , 2015 , 129, 25-32	3.9	15
259	IRE1Hs an endogenous substrate of endoplasmic-reticulum-associated degradation. <i>Nature Cell Biology</i> , 2015 , 17, 1546-55	23.4	115
258	Phosphoregulation of the C. elegans cadherin-catenin complex. <i>Biochemical Journal</i> , 2015 , 472, 339-52	3.8	5
257	Characterization of the 26S proteasome network in Plasmodium falciparum. <i>Scientific Reports</i> , 2015 , 5, 17818	4.9	18
256	NEDD4 Regulates PAX7 Levels Promoting Activation of the Differentiation Program in Skeletal Muscle Precursors. <i>Stem Cells</i> , 2015 , 33, 3138-51	5.8	22
255	Saliva from nymph and adult females of Haemaphysalis longicornis: a proteomic study. <i>Parasites and Vectors</i> , 2015 , 8, 338	4	57
254	Curation of the Mammalian Palmitoylome Indicates a Pivotal Role for Palmitoylation in Diseases and Disorders of the Nervous System and Cancers. <i>PLoS Computational Biology</i> , 2015 , 11, e1004405	5	69
253	From raw data to biological discoveries: a computational analysis pipeline for mass spectrometry-based proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1820-	6 ^{3.5}	11
252	Chromosome-Based Proteomic Study for Identifying Novel Protein Variants from Human Hippocampal Tissue Using Customized neXtProt and GENCODE Databases. <i>Journal of Proteome Research</i> , 2015 , 14, 5028-37	5.6	4
251	Casein kinase II promotes target silencing by miRISC through direct phosphorylation of the DEAD-box RNA helicase CGH-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E7213-22	11.5	10
250	Product binding enforces the genomic specificity of a yeast polycomb repressive complex. <i>Cell</i> , 2015 , 160, 204-18	56.2	96
249	A ribonuclease coordinates siRNA amplification and mRNA cleavage during RNAi. <i>Cell</i> , 2015 , 160, 407-1	956.2	50
248	The butterfly effect in cancer: a single base mutation can remodel the cell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 1131-6	11.5	49
247	The Pallbearer E3 ligase promotes actin remodeling via RAC in efferocytosis by degrading the ribosomal protein S6. <i>Developmental Cell</i> , 2015 , 32, 19-30	10.2	18

246	The IRE1¶XBP1s Pathway Is Essential for the Glucose Response and Protection of ICells. <i>PLoS Biology</i> , 2015 , 13, e1002277	9.7	94
245	DNA damage shifts circadian clock time via Hausp-dependent Cry1 stabilization. <i>ELife</i> , 2015 , 4,	8.9	63
244	Mass spectrometry-based quantification of the cellular response to methyl methanesulfonate treatment in human cells. <i>DNA Repair</i> , 2014 , 15, 29-38	4.3	3
243	In vivo activation of a conserved microRNA program induces mammalian heart regeneration. <i>Cell Stem Cell</i> , 2014 , 15, 589-604	18	141
242	PSEA-Quant: a protein set enrichment analysis on label-free and label-based protein quantification data. <i>Journal of Proteome Research</i> , 2014 , 13, 5496-509	5.6	41
241	Drosophila TRF2 is a preferential core promoter regulator. <i>Genes and Development</i> , 2014 , 28, 2163-74	12.6	36
240	A gene-specific role for the Ssu72 RNAPII CTD phosphatase in HIV-1 Tat transactivation. <i>Genes and Development</i> , 2014 , 28, 2261-75	12.6	15
239	Isobaric labeling-based relative quantification in shotgun proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 5293-309	5.6	403
238	Sel1L is indispensable for mammalian endoplasmic reticulum-associated degradation, endoplasmic reticulum homeostasis, and survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E582-91	11.5	101
237	Reduced pachytene piRNAs and translation underlie spermiogenic arrest in Maelstrom mutant mice. <i>EMBO Journal</i> , 2014 , 33, 1999-2019	13	70
236	Quantitative phosphoproteomic profiling of PINK1-deficient cells identifies phosphorylation changes in nuclear proteins. <i>Molecular BioSystems</i> , 2014 , 10, 1719-29		8
235	Brain Proteome Changes Induced by Olfactory Learning in Drosophila. <i>Journal of Proteome Research</i> , 2014 , 13, 3763-3770	5.6	5
234	Off-Line Multidimensional Liquid Chromatography and Auto Sampling Result in Sample Loss in LC/LC-MS/MS. <i>Journal of Proteome Research</i> , 2014 , 13, 3826-36	5.6	41
233	Lysine ubiquitination and acetylation of human cardiac 20S proteasomes. <i>Proteomics - Clinical Applications</i> , 2014 , 8, 590-594	3.1	14
232	PepExplorer: a similarity-driven tool for analyzing de novo sequencing results. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2480-9	7.6	30
231	Co-opting the Fanconi anemia genomic stability pathway enables herpesvirus DNA synthesis and productive growth. <i>Molecular Cell</i> , 2014 , 55, 111-22	17.6	18
230	Census 2: isobaric labeling data analysis. <i>Bioinformatics</i> , 2014 , 30, 2208-9	7.2	35
229	ERdj3 is an endoplasmic reticulum degradation factor for mutant glucocerebrosidase variants linked to GaucherB disease. <i>Chemistry and Biology</i> , 2014 , 21, 967-76		47

(2014-2014)

228	Secretome of the biocontrol agent metarhizium anisopliae induced by the cuticle of the cotton pest Dysdercus peruvianus reveals new insights into infection. <i>Journal of Proteome Research</i> , 2014 , 13, 2282-96	5.6	27
227	Quantitative proteomic profiling reveals differentially regulated proteins in cystic fibrosis cells. Journal of Proteome Research, 2014 , 13, 4668-75	5.6	20
226	S-nitrosylation-mediated redox transcriptional switch modulates neurogenesis and neuronal cell death. <i>Cell Reports</i> , 2014 , 8, 217-28	10.6	48
225	Proteomic profile of Cryptococcus neoformans biofilm reveals changes in metabolic processes. Journal of Proteome Research, 2014 , 13, 1545-59	5.6	45
224	Interference-free proteome quantification with MS/MS-based isobaric isotopologue detection. Journal of Proteome Research, 2014 , 13, 1494-501	5.6	17
223	Direct detection of biotinylated proteins by mass spectrometry. <i>Journal of Proteome Research</i> , 2014 , 13, 3966-78	5.6	66
222	Ecto-Fc MS identifies ligand-receptor interactions through extracellular domain Fc fusion protein baits and shotgun proteomic analysis. <i>Nature Protocols</i> , 2014 , 9, 2061-74	18.8	18
221	Isolation of chromatin from dysfunctional telomeres reveals an important role for Ring1b in NHEJ-mediated chromosome fusions. <i>Cell Reports</i> , 2014 , 7, 1320-32	10.6	38
220	Arginyltransferase ATE1 catalyzes midchain arginylation of proteins at side chain carboxylates in vivo. <i>Chemistry and Biology</i> , 2014 , 21, 331-7		56
219	Polycomb- and REST-associated histone deacetylases are independent pathways toward a mature neuronal phenotype. <i>ELife</i> , 2014 , 3, e04235	8.9	30
218	Transnitrosylation from DJ-1 to PTEN attenuates neuronal cell death in parkinson® disease models. Journal of Neuroscience, 2014 , 34, 15123-31	6.6	65
217	Reelin induces Erk1/2 signaling in cortical neurons through a non-canonical pathway. <i>Journal of Biological Chemistry</i> , 2014 , 289, 20307-17	5.4	31
216	Multiple inputs control sulfur-containing amino acid synthesis in Saccharomyces cerevisiae. <i>Molecular Biology of the Cell</i> , 2014 , 25, 1653-65	3.5	25
215	The specification and global reprogramming of histone epigenetic marks during gamete formation and early embryo development in C. elegans. <i>PLoS Genetics</i> , 2014 , 10, e1004588	6	29
214	The proper splicing of RNAi factors is critical for pericentric heterochromatin assembly in fission yeast. <i>PLoS Genetics</i> , 2014 , 10, e1004334	6	21
213	Sheathless capillary electrophoresis-tandem mass spectrometry for top-down characterization of Pyrococcus furiosus proteins on a proteome scale. <i>Analytical Chemistry</i> , 2014 , 86, 11006-12	7.8	58
212	CPSF30 and Wdr33 directly bind to AAUAAA in mammalian mRNA 3Pprocessing. <i>Genes and Development</i> , 2014 , 28, 2370-80	12.6	135
211	Kinetochore biorientation in Saccharomyces cerevisiae requires a tightly folded conformation of the Ndc80 complex. <i>Genetics</i> , 2014 , 198, 1483-93	4	17

210	Dynactin integrity depends upon direct binding of dynamitin to Arp1. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2171-80	3.5	15
209	Tls1 regulates splicing of shelterin components to control telomeric heterochromatin assembly and telomere length. <i>Nucleic Acids Research</i> , 2014 , 42, 11419-32	20.1	11
208	Molecular dissection of the interaction between the AMPA receptor and cornichon homolog-3. Journal of Neuroscience, 2014 , 34, 12104-20	6.6	21
207	A separable domain of the p150 subunit of human chromatin assembly factor-1 promotes protein and chromosome associations with nucleoli. <i>Molecular Biology of the Cell</i> , 2014 , 25, 2866-81	3.5	26
206	Identification of small ubiquitin-like modifier substrates with diverse functions using the Xenopus egg extract system. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1659-75	7.6	9
205	Escargot restricts niche cell to stem cell conversion in the Drosophila testis. <i>Cell Reports</i> , 2014 , 7, 722-3	410.6	37
204	Acute synthesis of CPEB is required for plasticity of visual avoidance behavior in Xenopus. <i>Cell Reports</i> , 2014 , 6, 737-47	10.6	41
203	Proximity interactions among centrosome components identify regulators of centriole duplication. <i>Current Biology</i> , 2014 , 24, 664-70	6.3	145
202	Protein kinase C-Itontrols CTLA-4-mediated regulatory T cell function. <i>Nature Immunology</i> , 2014 , 15, 465-72	19.1	97
201	Proteomic analysis of cattle tick Rhipicephalus (Boophilus) microplus saliva: a comparison between partially and fully engorged females. <i>PLoS ONE</i> , 2014 , 9, e94831	3.7	114
200	Plasma membrane proteomics of human breast cancer cell lines identifies potential targets for breast cancer diagnosis and treatment. <i>PLoS ONE</i> , 2014 , 9, e102341	3.7	33
199	Mass spectrometry-based shotgun proteomic analysis of C. elegans protein complexes. <i>WormBook</i> , 2014 , 1-18		8
198	A single vertebrate DNA virus protein disarms invertebrate immunity to RNA virus infection. <i>ELife</i> , 2014 , 3,	8.9	12
197	Pervasive and dynamic protein binding sites of the mRNA transcriptome in Saccharomyces cerevisiae. <i>Genome Biology</i> , 2013 , 14, R13	18.3	71
196	Identification of long-lived proteins reveals exceptional stability of essential cellular structures. <i>Cell</i> , 2013 , 154, 971-982	56.2	351
195	Energy dependence of HCD on peptide fragmentation: stepped collisional energy finds the sweet spot. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1690-9	3.5	53
194	Comparative proteomic analysis of the aging soleus and extensor digitorum longus rat muscles using TMT labeling and mass spectrometry. <i>Journal of Proteome Research</i> , 2013 , 12, 4532-46	5.6	22
193	Isogenic human iPSC Parkinsonß model shows nitrosative stress-induced dysfunction in MEF2-PGC1&ranscription. <i>Cell</i> , 2013 , 155, 1351-64	56.2	314

(2012-2013)

192	Argonautes promote male fertility and provide a paternal memory of germline gene expression in C. elegans. <i>Cell</i> , 2013 , 155, 1532-44	56.2	123
191	Microglia promote learning-dependent synapse formation through brain-derived neurotrophic factor. <i>Cell</i> , 2013 , 155, 1596-609	56.2	1422
190	The revolution and evolution of shotgun proteomics for large-scale proteome analysis. <i>Journal of the American Chemical Society</i> , 2013 , 135, 1629-40	16.4	91
189	FKBP10 depletion enhances glucocerebrosidase proteostasis in Gaucher disease fibroblasts. <i>Chemistry and Biology</i> , 2013 , 20, 403-15		13
188	A two-step mechanism for TRF2-mediated chromosome-end protection. <i>Nature</i> , 2013 , 494, 502-5	50.4	154
187	Protein analysis by shotgun/bottom-up proteomics. <i>Chemical Reviews</i> , 2013 , 113, 2343-94	68.1	902
186	Modified MuDPIT separation identified 4488 proteins in a system-wide analysis of quiescence in yeast. <i>Journal of Proteome Research</i> , 2013 , 12, 2177-84	5.6	50
185	The interaction of CtIP and Nbs1 connects CDK and ATM to regulate HR-mediated double-strand break repair. <i>PLoS Genetics</i> , 2013 , 9, e1003277	6	154
184	Cell-cycle regulation of formin-mediated actin cable assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E4446-55	11.5	32
183	In vivo quantitative proteomics of somatosensory cortical synapses shows which protein levels are modulated by sensory deprivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E726-35	11.5	49
182	Regulation of ubiquitin-dependent cargo sorting by multiple endocytic adaptors at the plasma membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 11857-62	11.5	47
181	The FEAR protein Slk19 restricts Cdc14 phosphatase to the nucleus until the end of anaphase, regulating its participation in mitotic exit in Saccharomyces cerevisiae. <i>PLoS ONE</i> , 2013 , 8, e73194	3.7	3
180	Analysis of URI nuclear interaction with RPB5 and components of the R2TP/prefoldin-like complex. <i>PLoS ONE</i> , 2013 , 8, e63879	3.7	44
179	Proteomic analysis of mammalian primary cilia. <i>Current Biology</i> , 2012 , 22, 414-9	6.3	187
178	Single-step inline hydroxyapatite enrichment facilitates identification and quantitation of phosphopeptides from mass-limited proteomes with MudPIT. <i>Journal of Proteome Research</i> , 2012 , 11, 2697-709	5.6	45
177	Improving the TFold test for differential shotgun proteomics. <i>Bioinformatics</i> , 2012 , 28, 1652-4	7.2	48
176	Arginylation regulates myofibrils to maintain heart function and prevent dilated cardiomyopathy. Journal of Molecular and Cellular Cardiology, 2012 , 53, 333-41	5.8	38
175	Toward objective evaluation of proteomic algorithms. <i>Nature Methods</i> , 2012 , 9, 455-6	21.6	30

174	Quantitative proteomics of parotid saliva in primary Sj\u00e4ren\u00aB syndrome. Proteomics, 2012, 12, 3113-20	4.8	37
173	O-GlcNAc transferase/host cell factor C1 complex regulates gluconeogenesis by modulating PGC-1Btability. <i>Cell Metabolism</i> , 2012 , 16, 226-37	24.6	188
172	Nonmuscle myosin IIB links cytoskeleton to IRE1Bignaling during ER stress. <i>Developmental Cell</i> , 2012 , 23, 1141-52	10.2	45
171	PatternLab: from mass spectra to label-free differential shotgun proteomics. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 13, Unit13.19	24.2	36
170	Dynamics of subcellular proteomes during brain development. <i>Journal of Proteome Research</i> , 2012 , 11, 2467-79	5.6	35
169	Search engine processor: Filtering and organizing peptide spectrum matches. <i>Proteomics</i> , 2012 , 12, 944	-9 .8	82
168	Extremely long-lived nuclear pore proteins in the rat brain. Science, 2012, 335, 942	33.3	206
167	Phosphorylation-dependent interactions between Crb2 and Chk1 are essential for DNA damage checkpoint. <i>PLoS Genetics</i> , 2012 , 8, e1002817	6	11
166	The exopolysaccharide matrix modulates the interaction between 3D architecture and virulence of a mixed-species oral biofilm. <i>PLoS Pathogens</i> , 2012 , 8, e1002623	7.6	329
165	A chaperone trap contributes to the onset of cystic fibrosis. <i>PLoS ONE</i> , 2012 , 7, e37682	3.7	44
164	Affinity purification of protein complexes in C. elegans. <i>Methods in Cell Biology</i> , 2011 , 106, 289-322	1.8	26
163	Protein S-glutathionylation in malaria parasites. Antioxidants and Redox Signaling, 2011, 15, 2855-65	8.4	83
162	Chemo-resistant protein expression pattern of glioblastoma cells (A172) to perillyl alcohol. <i>Journal of Proteome Research</i> , 2011 , 10, 153-60	5.6	19
161	Mitotic spindle proteomics in Chinese hamster ovary cells. <i>PLoS ONE</i> , 2011 , 6, e20489	3.7	39
160	hnRNP A1 and hnRNP F modulate the alternative splicing of exon 11 of the insulin receptor gene. <i>PLoS ONE</i> , 2011 , 6, e27869	3.7	50
159	Analysis of the myosin-II-responsive focal adhesion proteome reveals a role for EPix in negative regulation of focal adhesion maturation. <i>Nature Cell Biology</i> , 2011 , 13, 383-93	23.4	425
158	TFG-1 function in protein secretion and oncogenesis. <i>Nature Cell Biology</i> , 2011 , 13, 550-8	23.4	121
157	Can the false-discovery rate be misleading?. <i>Proteomics</i> , 2011 , 11, 4105-8	4.8	28

156	Arginyltransferase is an ATP-independent self-regulating enzyme that forms distinct functional complexes in vivo. <i>Chemistry and Biology</i> , 2011 , 18, 121-30		56
155	Analyzing marginal cases in differential shotgun proteomics. <i>Bioinformatics</i> , 2011 , 27, 275-6	7.2	454
154	A cell cycle phosphoproteome of the yeast centrosome. <i>Science</i> , 2011 , 332, 1557-61	33.3	8o
153	Differential proteomic analysis of mammalian tissues using SILAM. <i>PLoS ONE</i> , 2011 , 6, e16039	3.7	27
152	PYR/PYL/RCAR family members are major in-vivo ABI1 protein phosphatase 2C-interacting proteins in Arabidopsis. <i>Plant Journal</i> , 2010 , 61, 290-9	6.9	350
151	Reduced histone deacetylase 7 activity restores function to misfolded CFTR in cystic fibrosis. Nature Chemical Biology, 2010 , 6, 25-33	11.7	204
150	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , 2010 , 7, 681	1 -5 1.6	390
149	T. gondii RP promoters & knockdown reveal molecular pathways associated with proliferation and cell-cycle arrest. <i>PLoS ONE</i> , 2010 , 5, e14057	3.7	22
148	Quantitative proteomics approach for identifying protein-drug interactions in complex mixtures using protein stability measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9078-82	11.5	130
147	Census for proteome quantification. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 13, Unit 13.12.1-	121 4.2	17
146	Analyzing shotgun proteomic data with PatternLab for proteomics. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 13, Unit 13.13.1-15	24.2	21
145	Aurora B phosphorylates spatially distinct targets to differentially regulate the kinetochore-microtubule interface. <i>Molecular Cell</i> , 2010 , 38, 383-92	17.6	360
144	Transnitrosylation of XIAP regulates caspase-dependent neuronal cell death. <i>Molecular Cell</i> , 2010 , 39, 184-95	17.6	144
143	Dynamic proteomic overview of glioblastoma cells (A172) exposed to perillyl alcohol. <i>Journal of Proteomics</i> , 2010 , 73, 1018-27	3.9	21
142	YADA: a tool for taking the most out of high-resolution spectra. <i>Bioinformatics</i> , 2009 , 25, 2734-6	7.2	62
141	Capillary electrophoresis applied to proteomic analysis. <i>Journal of Separation Science</i> , 2009 , 32, 1175-88	3.4	78
140	Preliminary quantitative profile of differential protein expression between rat L6 myoblasts and myotubes by stable isotope labeling with amino acids in cell culture. <i>Proteomics</i> , 2009 , 9, 1274-92	4.8	37
139	Characterisation of Plasmodium invasive organelles; an ookinete microneme proteome. <i>Proteomics</i> , 2009 , 9, 1142-51	4.8	57

138	Proteomic analysis of mitochondria from Caenorhabditis elegans. <i>Proteomics</i> , 2009 , 9, 4539-53	4.8	50
137	Proteomic comparison of four Eimeria tenella life-cycle stages: unsporulated oocyst, sporulated oocyst, sporozoite and second-generation merozoite. <i>Proteomics</i> , 2009 , 9, 4566-76	4.8	75
136	Requirement for Nudel and dynein for assembly of the lamin B spindle matrix. <i>Nature Cell Biology</i> , 2009 , 11, 247-56	23.4	93
135	Identification of N-terminally arginylated proteins and peptides by mass spectrometry. <i>Nature Protocols</i> , 2009 , 4, 325-32	18.8	47
134	Proteomics by mass spectrometry: approaches, advances, and applications. <i>Annual Review of Biomedical Engineering</i> , 2009 , 11, 49-79	12	803
133	Centromere-specific assembly of CENP-a nucleosomes is mediated by HJURP. <i>Cell</i> , 2009 , 137, 472-84	56.2	476
132	GO Explorer: A gene-ontology tool to aid in the interpretation of shotgun proteomics data. <i>Proteome Science</i> , 2009 , 7, 6	2.6	26
131	Biomarkers for early and late stage chronic allograft nephropathy by proteogenomic profiling of peripheral blood. <i>PLoS ONE</i> , 2009 , 4, e6212	3.7	60
130	Genome-wide analysis of immune activation in human T and B cells reveals distinct classes of alternatively spliced genes. <i>PLoS ONE</i> , 2009 , 4, e7906	3.7	34
129	Neural palmitoyl-proteomics reveals dynamic synaptic palmitoylation. <i>Nature</i> , 2008 , 456, 904-9	50.4	422
128	A quantitative analysis software tool for mass spectrometry-based proteomics. <i>Nature Methods</i> , 2008 , 5, 319-22	21.6	335
127			
	PatternLab for proteomics: a tool for differential shotgun proteomics. <i>BMC Bioinformatics</i> , 2008 , 9, 316	3.6	122
126	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian brain proteome. <i>Analytical Chemistry</i> , 2008 , 80, 8694-701	3.6 7.8	69
126	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian		
	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian brain proteome. <i>Analytical Chemistry</i> , 2008 , 80, 8694-701 Quantitative proteomic analysis of primary neurons reveals diverse changes in synaptic protein content in fmr1 knockout mice. <i>Proceedings of the National Academy of Sciences of the United States</i>	7.8	69
125	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian brain proteome. <i>Analytical Chemistry</i> , 2008 , 80, 8694-701 Quantitative proteomic analysis of primary neurons reveals diverse changes in synaptic protein content in fmr1 knockout mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15281-6 Arginyltransferase regulates alpha cardiac actin function, myofibril formation and contractility	7.8	69
125	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian brain proteome. <i>Analytical Chemistry</i> , 2008 , 80, 8694-701 Quantitative proteomic analysis of primary neurons reveals diverse changes in synaptic protein content in fmr1 knockout mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15281-6 Arginyltransferase regulates alpha cardiac actin function, myofibril formation and contractility during heart development. <i>Development (Cambridge)</i> , 2008 , 135, 3881-9 Identification of Novel Integral Membrane Proteins of the Nuclear Envelope with Potential Disease	7.8	69 142 50

120	Mass spectrometry for proteomics. Current Opinion in Chemical Biology, 2008, 12, 483-90	9.7	514
119	Chromosomal instability by inefficient Mps1 auto-activation due to a weakened mitotic checkpoint and lagging chromosomes. <i>PLoS ONE</i> , 2008 , 3, e2415	3.7	67
118	The role of phosphorylations in hypotonic nuclear export of OREBP/TonEBP/NFAT5. <i>FASEB Journal</i> , 2008 , 22, 933.3	0.9	
117	Phosphorylation of the calpains. <i>FASEB Journal</i> , 2008 , 22, 793.5	0.9	4
116	Optimizing TiO2-based phosphopeptide enrichment for automated multidimensional liquid chromatography coupled to tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 4666-73	7.8	121
115	Optimization of mass spectrometry-compatible surfactants for shotgun proteomics. <i>Journal of Proteome Research</i> , 2007 , 6, 2529-38	5.6	176
114	Cancer proteomics by quantitative shotgun proteomics. <i>Molecular Oncology</i> , 2007 , 1, 144-59	7.9	59
113	Assigning in vivo carbamylation and acetylation in human lens proteins using tandem mass spectrometry and database searching. <i>International Journal of Mass Spectrometry</i> , 2007 , 259, 161-173	1.9	9
112	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007 , 25, 88	7-2923 .5	583
111	The biological impact of mass-spectrometry-based proteomics. <i>Nature</i> , 2007 , 450, 991-1000	50.4	564
110	Quantification of the synaptosomal proteome of the rat cerebellum during post-natal development. <i>Genome Research</i> , 2007 , 17, 1378-88	9.7	86
109	Global analysis of posttranslational protein arginylation. <i>PLoS Biology</i> , 2007 , 5, e258	9.7	109
108	Quantitative mass spectrometry identifies insulin signaling targets in C. elegans. <i>Science</i> , 2007 , 317, 66	0 3 3.3	260
107	15N metabolic labeling of mammalian tissue with slow protein turnover. <i>Journal of Proteome Research</i> , 2007 , 6, 2005-10	5.6	115
106	Validation of tandem mass spectrometry database search results using DTASelect. <i>Current Protocols in Bioinformatics</i> , 2007 , Chapter 13, Unit 13.4	24.2	153
105	MVB-12, a fourth subunit of metazoan ESCRT-I, functions in receptor downregulation. <i>PLoS ONE</i> , 2007 , 2, e956	3.7	43
104	Arginylation of beta-actin regulates actin cytoskeleton and cell motility. <i>Science</i> , 2006 , 313, 192-6	33.3	197
103	Isolation and angiogenesis by endothelial progenitors in the fetal liver. Stem Cells, 2006, 24, 44-54	5.8	39

102	Cross-correlation algorithm for calculation of peptide molecular weight from tandem mass spectra. Analytical Chemistry, 2006 , 78, 1921-9 7.8	25
101	Hsp90 cochaperone Aha1 downregulation rescues misfolding of CFTR in cystic fibrosis. <i>Cell</i> , 2006 , 127, 803-15	498
100	Performance of a linear ion trap-Orbitrap hybrid for peptide analysis. <i>Analytical Chemistry</i> , 2006 , 78, 493–580	155
99	Diagnostic Proteomics 2006 , 247-276	
98	Automation in Proteomics 2006, 277-288	
97	Bioinformatics Tools for Proteomics 2006 , 289-307	
96	Proteomic Analysis by Two-Dimensional Polyacrylamide Gel Electrophoresis 2006 , 19-46	1
95	Mass Spectrometric Characterization of Post-translational Modifications 2006 , 63-90	1
94	Protein Localization by Cell Imaging 2006 , 135-155	
93	Characterization of Functional Protein Complexes 2006 , 157-169	
92	Structural Proteomics by NMR 2006 , 171-185	2
91	Technologies for Large-Scale Proteomic Tandem Mass Spectrometry 2006 , 91-109	
90	Isotope Labeling in Quantitative Proteomics 2006 , 47-61	
89	Single Cell Proteomics 2006 , 225-245	1
88	Mass Spectrometry: The Foundation of Proteomics 2006 , 1-17	
87	Microfluidics-Based Proteome Analysis 2006 , 205-223	
86	Protein Microarrays 2006 , 187-204	
85	Protein Fractionation Methods for Proteomics 2006 , 111-133	1

(2004-2006)

84	The CENP-H-I complex is required for the efficient incorporation of newly synthesized CENP-A into centromeres. <i>Nature Cell Biology</i> , 2006 , 8, 446-57	23.4	376
83	The human CENP-A centromeric nucleosome-associated complex. <i>Nature Cell Biology</i> , 2006 , 8, 458-69	23.4	539
82	Sperm chromatin proteomics identifies evolutionarily conserved fertility factors. <i>Nature</i> , 2006 , 443, 10	1-5 0.4	146
81	Maspin and tumor metastasis. <i>IUBMB Life</i> , 2006 , 58, 25-9	4.7	22
80	Dissecting the Centriole Proteome. <i>FASEB Journal</i> , 2006 , 20, A493	0.9	1
79	Protein identification using 2D-LC-MS/MS. <i>Methods</i> , 2005 , 35, 248-55	4.6	144
78	A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses. <i>Science</i> , 2005 , 307, 82-6	33.3	662
77	Proteomics of organelles and large cellular structures. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 702-14	48.7	351
76	Large-scale muLC-MS/MS for silver- and Coomassie blue-stained polyacrylamide gels. <i>Electrophoresis</i> , 2005 , 26, 4495-507	3.6	9
75	Proteomic comparison of two fractions derived from the transsynaptic scaffold. <i>Journal of Neuroscience Research</i> , 2005 , 81, 762-75	4.4	64
74	Maspin alters the carcinoma proteome. FASEB Journal, 2005, 19, 1123-4	0.9	32
73	Mass spectrometry as an emerging tool for systems biology. <i>BioTechniques</i> , 2004 , 36, 917-9	2.5	30
72	Applicability of tandem affinity purification MudPIT to pathway proteomics in yeast. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 226-37	7.6	116
71	The Plasmodium falciparum clag9 gene encodes a rhoptry protein that is transferred to the host erythrocyte upon invasion. <i>Molecular Microbiology</i> , 2004 , 52, 107-18	4.1	70
70	Automated approach for quantitative analysis of complex peptide mixtures from tandem mass spectra. <i>Nature Methods</i> , 2004 , 1, 39-45	21.6	512
69	MS1, MS2, and SQT-three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 2162-8	2.2	295
68	Actin-binding proteins in a postsynaptic preparation: Lasp-1 is a component of central nervous system synapses and dendritic spines. <i>Journal of Neuroscience Research</i> , 2004 , 78, 38-48	4.4	35
67	Mass spectral analysis in proteomics. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004 , 33, 297-316		237

66	A model for random sampling and estimation of relative protein abundance in shotgun proteomics. <i>Analytical Chemistry</i> , 2004 , 76, 4193-201	7.8	2080
65	Metabolic labeling of mammalian organisms with stable isotopes for quantitative proteomic analysis. <i>Analytical Chemistry</i> , 2004 , 76, 4951-9	7.8	322
64	Strategies for shotgun identification of post-translational modifications by mass spectrometry. <i>Journal of Chromatography A</i> , 2004 , 1053, 7-14	4.5	71
63	Strategies for shotgun identification of post-translational modifications by mass spectrometry. <i>Journal of Chromatography A</i> , 2004 , 1053, 7-14	4.5	31
62	A method for the comprehensive proteomic analysis of membrane proteins. <i>Nature Biotechnology</i> , 2003 , 21, 532-8	44.5	603
61	Large-scale protein identification using mass spectrometry. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1646, 1-10	4	137
60	Assigning function to yeast proteins by integration of technologies. <i>Molecular Cell</i> , 2003 , 12, 1353-65	17.6	236
59	Nuclear membrane proteins with potential disease links found by subtractive proteomics. <i>Science</i> , 2003 , 301, 1380-2	33.3	543
58	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. <i>Nature</i> , 2002 , 419, 512-9	50.4	591
57	A proteomic view of the Plasmodium falciparum life cycle. <i>Nature</i> , 2002 , 419, 520-6	50.4	1066
<i>57</i> <i>56</i>	A proteomic view of the Plasmodium falciparum life cycle. <i>Nature</i> , 2002 , 419, 520-6 Shotgun identification of protein modifications from protein complexes and lens tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7900-5	50.4	1066 525
	Shotgun identification of protein modifications from protein complexes and lens tissue.		
56	Shotgun identification of protein modifications from protein complexes and lens tissue. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7900-5 Code developments to improve the efficiency of automated MS/MS spectra interpretation. Journal	11.5	525
56 55	Shotgun identification of protein modifications from protein complexes and lens tissue. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7900-5 Code developments to improve the efficiency of automated MS/MS spectra interpretation. Journal of Proteome Research, 2002, 1, 211-5 Analysis of quantitative proteomic data generated via multidimensional protein identification	11.5 5.6	525 181
56 55 54	Shotgun identification of protein modifications from protein complexes and lens tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7900-5 Code developments to improve the efficiency of automated MS/MS spectra interpretation. <i>Journal of Proteome Research</i> , 2002 , 1, 211-5 Analysis of quantitative proteomic data generated via multidimensional protein identification technology. <i>Analytical Chemistry</i> , 2002 , 74, 1650-7 DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun	11.5 5.6 7.8	525 181 366
56 55 54 53	Shotgun identification of protein modifications from protein complexes and lens tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7900-5 Code developments to improve the efficiency of automated MS/MS spectra interpretation. <i>Journal of Proteome Research</i> , 2002 , 1, 211-5 Analysis of quantitative proteomic data generated via multidimensional protein identification technology. <i>Analytical Chemistry</i> , 2002 , 74, 1650-7 DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. <i>Journal of Proteome Research</i> , 2002 , 1, 21-6 Phospho-regulation of kinetochore-microtubule attachments by the Aurora kinase Ipl1p. <i>Cell</i> , 2002 ,	11.5 5.6 7.8 5.6	525 181 366 1156
5655545352	Shotgun identification of protein modifications from protein complexes and lens tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7900-5 Code developments to improve the efficiency of automated MS/MS spectra interpretation. <i>Journal of Proteome Research</i> , 2002 , 1, 211-5 Analysis of quantitative proteomic data generated via multidimensional protein identification technology. <i>Analytical Chemistry</i> , 2002 , 74, 1650-7 DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. <i>Journal of Proteome Research</i> , 2002 , 1, 21-6 Phospho-regulation of kinetochore-microtubule attachments by the Aurora kinase Ipl1p. <i>Cell</i> , 2002 , 111, 163-72 Identification of membrane proteins in the hyperthermophilic archaeon pyrococcus furiosus using	11.5 5.6 7.8 5.6	525 181 366 1156 510

(1998-2001)

48	Implication of a novel multiprotein Dam1p complex in outer kinetochore function. <i>Journal of Cell Biology</i> , 2001 , 155, 1137-45	7.3	155
47	An automated multidimensional protein identification technology for shotgun proteomics. <i>Analytical Chemistry</i> , 2001 , 73, 5683-90	7.8	1674
46	Searching the Porphyromonas gingivalis genome with peptide fragmentation mass spectra. <i>Analyst, The</i> , 2001 , 126, 52-7	5	25
45	Proteomics reveal a link between the endoplasmic reticulum and lipid secretory mechanisms in mammary epithelial cells. <i>Electrophoresis</i> , 2000 , 21, 3470-82	3.6	187
44	Proteomic tools for cell biology. <i>Traffic</i> , 2000 , 1, 747-54	5.7	36
43	Proteomic analysis of two functional states of the Golgi complex in mammary epithelial cells. <i>Traffic</i> , 2000 , 1, 769-82	5.7	71
42	Analysis of the microbial proteome. Current Opinion in Microbiology, 2000, 3, 292-7	7.9	127
41	Automated identification of amino acid sequence variations in proteins by HPLC/microspray tandem mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 757-63	7.8	209
40	Proteomics reveal a link between the endoplasmic reticulum and lipid secretory mechanisms in mammary epithelial cells 2000 , 21, 3470		1
39	Direct analysis of protein complexes using mass spectrometry. <i>Nature Biotechnology</i> , 1999 , 17, 676-82	44.5	1983
39 38	Direct analysis of protein complexes using mass spectrometry. <i>Nature Biotechnology</i> , 1999 , 17, 676-82 Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8	44·5 7·8	1983
	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary	7.8 3.6	
38	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8	,	128
38	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8 Database searching using mass spectrometry data. <i>Electrophoresis</i> , 1998 , 19, 893-900	3.6	128 199
38 37 36	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8 Database searching using mass spectrometry data. <i>Electrophoresis</i> , 1998 , 19, 893-900 Mass spectrometry and the age of the proteome. <i>Journal of Mass Spectrometry</i> , 1998 , 33, 1-19 High throughput protein characterization by automated reverse-phase	3.6	128 199 557
38 37 36 35	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8 Database searching using mass spectrometry data. <i>Electrophoresis</i> , 1998 , 19, 893-900 Mass spectrometry and the age of the proteome. <i>Journal of Mass Spectrometry</i> , 1998 , 33, 1-19 High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry. <i>Protein Science</i> , 1998 , 7, 706-19 The hMre11/hRad50 protein complex and Nijmegen breakage syndrome: linkage of double-strand	3.6 2.2 6.3	128 199 557 265
38 37 36 35 34	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8 Database searching using mass spectrometry data. <i>Electrophoresis</i> , 1998 , 19, 893-900 Mass spectrometry and the age of the proteome. <i>Journal of Mass Spectrometry</i> , 1998 , 33, 1-19 High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry. <i>Protein Science</i> , 1998 , 7, 706-19 The hMre11/hRad50 protein complex and Nijmegen breakage syndrome: linkage of double-strand break repair to the cellular DNA damage response. <i>Cell</i> , 1998 , 93, 477-86 Method to compare collision-induced dissociation spectra of peptides: potential for library	3.6 2.2 6.3 56.2	128 199 557 265 1009

30	Direct analysis and identification of proteins in mixtures by LC/MS/MS and database searching at the low-femtomole level. <i>Analytical Chemistry</i> , 1997 , 69, 767-76	7.8	456
29	High Throughput Analysis of Tandem Mass Spectrometry Data for Peptides. <i>Laboratory Automation News</i> , 1997 , 2, 28-31		
28	Direct analysis of protein mixtures by tandem mass spectrometry. <i>The Protein Journal</i> , 1997 , 16, 495-7		61
27	Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143. <i>Electrophoresis</i> , 1997 , 18, 1314-34	3.6	156
26	The quadrupole ion trap mass spectrometera small solution to a big challenge. <i>Analytical Biochemistry</i> , 1997 , 244, 1-15	3.1	194
25	Microcolumn Liquid Chromatography E lectrospray Ionization Tandem Mass Spectrometry. <i>ACS Symposium Series</i> , 1996 , 207-225	0.4	2
24	Search of sequence databases with uninterpreted high-energy collision-induced dissociation spectra of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 1996 , 7, 1089-98	3.5	66
23	Mining genomes: correlating tandem mass spectra of modified and unmodified peptides to sequences in nucleotide databases. <i>Analytical Chemistry</i> , 1995 , 67, 3202-10	7.8	350
22	Method to correlate tandem mass spectra of modified peptides to amino acid sequences in the protein database. <i>Analytical Chemistry</i> , 1995 , 67, 1426-36	7.8	1117
21	An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database. <i>Journal of the American Society for Mass Spectrometry</i> , 1994 , 5, 976-89	3.5	5082
20	Sequencing Peptides Derived from the Class II Major Histocompatibility Complex by Tandem Mass Spectrometry 1994 , 380-388		12
19	Analysis of oligodeoxynucleotides by negative-ion matrix-assisted laser desorption mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1993 , 4, 955-63	3.5	57
18	Matrix-assisted laser desorption of peptides and proteins on a quadrupole ion trap mass spectrometer. <i>Rapid Communications in Mass Spectrometry</i> , 1993 , 7, 20-6	2.2	45
17	The amino acid sequence of the acidic subunit B-chain of crotoxin. <i>BBA - Proteins and Proteomics</i> , 1990 , 1040, 217-24		25
16	Sequence homology in the metalloproteins; purple acid phosphatase from beef spleen and uteroferrin from porcine uterus. <i>Biochemical and Biophysical Research Communications</i> , 1987 , 144, 1154	1-g 0	54
15	Tandem quadrupole-Fourier transform mass spectrometry of oligopeptides. <i>Analytical Chemistry</i> , 1985 , 57, 2728-33	7.8	38
14	Mixed gas chemical ionization mass spectrometry of peptide derivatives. <i>Biomedical Mass Spectrometry</i> , 1983 , 10, 567-571		3
13	Amyloidogenic Proteins Drive Hepatic Proteostasis Remodeling in an Induced Pluripotent Stem Cell Model of Systemic Amyloid Disease		1

LIST OF PUBLICATIONS

12	TargetSeeker-MS: A Computational Method for Drug Target Discovery using Protein Separation Coupled to Mass Spectrometry	1
11	SNPC-1.3 is a sex-specific transcription factor that drives male piRNA expression in C. elegans	1
10	Characterization of membrane protein interactomes by Co-interacting Protein Identification Technology (CoPIT). <i>Protocol Exchange</i> ,	2
9	Covalent Protein Painting Reveals Structural Changes in the Proteome in Alzheimer Disease	2
8	Mechanistic Determinants of Slow Axonal Transport and Presynaptic Targeting of Clathrin Packets	1
7	TDP-43 and HSP70 phase separate into anisotropic, intranuclear liquid spherical annuli	2
6	Nucleus translocation of tRNA synthetase mediates late integrated stress response	2
5	Cortical Organoids Model Early Brain Development Disrupted by 16p11.2 Copy Number Variants in Autism	2
4	Targeted Searches for Novel Peptides in Big Mass Spectrometry Data Sets	2
3	Visualization of the HIV-1 Env Glycan Shield Across Scales	3
2	The Plasmodium Proteome85-94	
1	Mitotic R-loops direct Aurora B kinase to maintain centromeric cohesion	1