

John R Yates 3rd

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

#	Paper	IF	Citations
497	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
496	Large-scale analysis of the yeast proteome by multidimensional protein identification technology. <i>Nature Biotechnology</i> , 2001 , 19, 242-7	44.5	4123
495	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
494	Direct analysis of protein complexes using mass spectrometry. <i>Nature Biotechnology</i> , 1999 , 17, 676-82	44.5	1983
493	An automated multidimensional protein identification technology for shotgun proteomics. <i>Analytical Chemistry</i> , 2001 , 73, 5683-90	7.8	1674
492	Microglia promote learning-dependent synapse formation through brain-derived neurotrophic factor. <i>Cell</i> , 2013 , 155, 1596-609	56.2	1422
491	DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. <i>Journal of Proteome Research</i> , 2002 , 1, 21-6	5.6	1156
490	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
489	A proteomic view of the Plasmodium falciparum life cycle. <i>Nature</i> , 2002 , 419, 520-6	50.4	1066
488	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	56.2	1009
487	Protein analysis by shotgun/bottom-up proteomics. <i>Chemical Reviews</i> , 2013 , 113, 2343-94	68.1	902
486	Proteomics by mass spectrometry: approaches, advances, and applications. <i>Annual Review of Biomedical Engineering</i> , 2009 , 11, 49-79	12	803
485	A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses. <i>Science</i> , 2005 , 307, 82-6	33.3	662
484	A method for the comprehensive proteomic analysis of membrane proteins. <i>Nature Biotechnology</i> , 2003 , 21, 532-8	44.5	603
483	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. <i>Nature</i> , 2002 , 419, 512-9	50.4	591
482	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007 , 25, 887-93	44.5	583
481	The biological impact of mass-spectrometry-based proteomics. <i>Nature</i> , 2007 , 450, 991-1000	50.4	564

480	Mass spectrometry and the age of the proteome. <i>Journal of Mass Spectrometry</i> , 1998 , 33, 1-19	2.2	557
479	Nuclear membrane proteins with potential disease links found by subtractive proteomics. <i>Science</i> , 2003 , 301, 1380-2	33.3	543
478	The human CENP-A centromeric nucleosome-associated complex. <i>Nature Cell Biology</i> , 2006 , 8, 458-69	23.4	539
477	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	11.5	525
476	Mass spectrometry for proteomics. <i>Current Opinion in Chemical Biology</i> , 2008 , 12, 483-90	9.7	514
475	Automated approach for quantitative analysis of complex peptide mixtures from tandem mass spectra. <i>Nature Methods</i> , 2004 , 1, 39-45	21.6	512
474	Phospho-regulation of kinetochore-microtubule attachments by the Aurora kinase Ipl1p. <i>Cell</i> , 2002 , 111, 163-72	56.2	510
473	Hsp90 cochaperone Aha1 downregulation rescues misfolding of CFTR in cystic fibrosis. <i>Cell</i> , 2006 , 127, 803-15	56.2	498
472	Centromere-specific assembly of CENP-a nucleosomes is mediated by HJURP. <i>Cell</i> , 2009 , 137, 472-84	56.2	476
471	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
470	Analyzing marginal cases in differential shotgun proteomics. <i>Bioinformatics</i> , 2011 , 27, 275-6	7.2	454
469	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
468	Neural palmitoyl-proteomics reveals dynamic synaptic palmitoylation. <i>Nature</i> , 2008 , 456, 904-9	50.4	422
467	Isobaric labeling-based relative quantification in shotgun proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 5293-309	5.6	403
466	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , 2010 , 7, 681-5	51.6	390
465	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
464	Analysis of quantitative proteomic data generated via multidimensional protein identification technology. <i>Analytical Chemistry</i> , 2002 , 74, 1650-7	7.8	366
463	Aurora B phosphorylates spatially distinct targets to differentially regulate the kinetochore-microtubule interface. <i>Molecular Cell</i> , 2010 , 38, 383-92	17.6	360

462	Identification of long-lived proteins reveals exceptional stability of essential cellular structures. <i>Cell</i> , 2013 , 154, 971-982	56.2	351
461	Proteomics of organelles and large cellular structures. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 702-14	48.7	351
460	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
459	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
458	A quantitative analysis software tool for mass spectrometry-based proteomics. <i>Nature Methods</i> , 2008 , 5, 319-22	21.6	335
457	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
456	Metabolic labeling of mammalian organisms with stable isotopes for quantitative proteomic analysis. <i>Analytical Chemistry</i> , 2004 , 76, 4951-9	7.8	322
455	Isogenic human iPSC Parkinson's model shows nitrosative stress-induced dysfunction in MEF2-PGC1 β transcription. <i>Cell</i> , 2013 , 155, 1351-64	56.2	314
454	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
453	High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry. <i>Protein Science</i> , 1998 , 7, 706-19	6.3	265
452	Quantitative mass spectrometry identifies insulin signaling targets in <i>C. elegans</i> . <i>Science</i> , 2007 , 317, 660-3	33.3	260
451	Mass spectral analysis in proteomics. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004 , 33, 297-316		237
450	Assigning function to yeast proteins by integration of technologies. <i>Molecular Cell</i> , 2003 , 12, 1353-65	17.6	236
449	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
448	Extremely long-lived nuclear pore proteins in the rat brain. <i>Science</i> , 2012 , 335, 942	33.3	206
447	Reduced histone deacetylase 7 activity restores function to misfolded CFTR in cystic fibrosis. <i>Nature Chemical Biology</i> , 2010 , 6, 25-33	11.7	204
446	Database searching using mass spectrometry data. <i>Electrophoresis</i> , 1998 , 19, 893-900	3.6	199
445	Arginylation of beta-actin regulates actin cytoskeleton and cell motility. <i>Science</i> , 2006 , 313, 192-6	33.3	197

444	The quadrupole ion trap mass spectrometer--a small solution to a big challenge. <i>Analytical Biochemistry</i> , 1997 , 244, 1-15	3.1	194
443	O-GlcNAc transferase/host cell factor C1 complex regulates gluconeogenesis by modulating PGC-1 β stability. <i>Cell Metabolism</i> , 2012 , 16, 226-37	24.6	188
442	Proteomic analysis of mammalian primary cilia. <i>Current Biology</i> , 2012 , 22, 414-9	6.3	187
441	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
440	Code developments to improve the efficiency of automated MS/MS spectra interpretation. <i>Journal of Proteome Research</i> , 2002 , 1, 211-5	5.6	181
439	Optimization of mass spectrometry-compatible surfactants for shotgun proteomics. <i>Journal of Proteome Research</i> , 2007 , 6, 2529-38	5.6	176
438	Method to compare collision-induced dissociation spectra of peptides: potential for library searching and subtractive analysis. <i>Analytical Chemistry</i> , 1998 , 70, 3557-65	7.8	168
437	B508 CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015 , 528, 510-6	50.4	163
436	Extracting Accurate Precursor Information for Tandem Mass Spectra by RawConverter. <i>Analytical Chemistry</i> , 2015 , 87, 11361-7	7.8	159
435	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. <i>Nature Protocols</i> , 2016 , 11, 102-17	18.8	156
434	Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143. <i>Electrophoresis</i> , 1997 , 18, 1314-34	3.6	156
433	Performance of a linear ion trap-Orbitrap hybrid for peptide analysis. <i>Analytical Chemistry</i> , 2006 , 78, 4937-500	7.8	155
432	Implication of a novel multiprotein Dam1p complex in outer kinetochore function. <i>Journal of Cell Biology</i> , 2001 , 155, 1137-45	7.3	155
431	A two-step mechanism for TRF2-mediated chromosome-end protection. <i>Nature</i> , 2013 , 494, 502-5	50.4	154
430	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
429	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
428	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
427	Sperm chromatin proteomics identifies evolutionarily conserved fertility factors. <i>Nature</i> , 2006 , 443, 101-5	50.4	146

426	Proximity interactions among centrosome components identify regulators of centriole duplication. <i>Current Biology</i> , 2014 , 24, 664-70	6.3	145
425	Transnitrosylation of XIAP regulates caspase-dependent neuronal cell death. <i>Molecular Cell</i> , 2010 , 39, 184-95	17.6	144
424	Protein identification using 2D-LC-MS/MS. <i>Methods</i> , 2005 , 35, 248-55	4.6	144
423	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	11.5	142
422	In vivo activation of a conserved microRNA program induces mammalian heart regeneration. <i>Cell Stem Cell</i> , 2014 , 15, 589-604	18	141
421	Large-scale protein identification using mass spectrometry. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1646, 1-10	4	137
420	CPSF30 and Wdr33 directly bind to AAUAAA in mammalian mRNA 3Pprocessing. <i>Genes and Development</i> , 2014 , 28, 2370-80	12.6	135
419	Global site-specific N-glycosylation analysis of HIV envelope glycoprotein. <i>Nature Communications</i> , 2017 , 8, 14954	17.4	133
418	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
417	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2270-8	7.8	128
416	Analysis of the microbial proteome. <i>Current Opinion in Microbiology</i> , 2000 , 3, 292-7	7.9	127
415	Argonautes promote male fertility and provide a paternal memory of germline gene expression in <i>C. elegans</i> . <i>Cell</i> , 2013 , 155, 1532-44	56.2	123
414	PatternLab for proteomics: a tool for differential shotgun proteomics. <i>BMC Bioinformatics</i> , 2008 , 9, 316	3.6	122
413	TFG-1 function in protein secretion and oncogenesis. <i>Nature Cell Biology</i> , 2011 , 13, 550-8	23.4	121
412	Optimizing TiO ₂ -based phosphopeptide enrichment for automated multidimensional liquid chromatography coupled to tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 4666-73	7.8	121
411	Monoclonal 1- and 3-Phosphohistidine Antibodies: New Tools to Study Histidine Phosphorylation. <i>Cell</i> , 2015 , 162, 198-210	56.2	117
410	Applicability of tandem affinity purification MudPIT to pathway proteomics in yeast. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 226-37	7.6	116
409	IRE1 β s an endogenous substrate of endoplasmic-reticulum-associated degradation. <i>Nature Cell Biology</i> , 2015 , 17, 1546-55	23.4	115

408	15N metabolic labeling of mammalian tissue with slow protein turnover. <i>Journal of Proteome Research</i> , 2007 , 6, 2005-10	5.6	115
407	Proteomic analysis of cattle tick <i>Rhipicephalus (Boophilus) microplus</i> saliva: a comparison between partially and fully engorged females. <i>PLoS ONE</i> , 2014 , 9, e94831	3.7	114
406	Global analysis of posttranslational protein arginylation. <i>PLoS Biology</i> , 2007 , 5, e258	9.7	109
405	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
404	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
403	Protein kinase C- ζ controls CTLA-4-mediated regulatory T cell function. <i>Nature Immunology</i> , 2014 , 15, 465-72	19.1	97
402	Product binding enforces the genomic specificity of a yeast polycomb repressive complex. <i>Cell</i> , 2015 , 160, 204-18	56.2	96
401	The IRE1 α -XBP1s Pathway Is Essential for the Glucose Response and Protection of β Cells. <i>PLoS Biology</i> , 2015 , 13, e1002277	9.7	94
400	Circadian Amplitude Regulation via FBXW7-Targeted REV-ERB α Degradation. <i>Cell</i> , 2016 , 165, 1644-1657	56.2	94
399	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	11.5	93
398	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
397	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. <i>Nature Communications</i> , 2015 , 6, 7623	17.4	92
396	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
395	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
394	Differential processing of HIV envelope glycans on the virus and soluble recombinant trimer. <i>Nature Communications</i> , 2018 , 9, 3693	17.4	87
393	Quantification of the synaptosomal proteome of the rat cerebellum during post-natal development. <i>Genome Research</i> , 2007 , 17, 1378-88	9.7	86
392	Protein S-glutathionylation in malaria parasites. <i>Antioxidants and Redox Signaling</i> , 2011 , 15, 2855-65	8.4	83
391	Search engine processor: Filtering and organizing peptide spectrum matches. <i>Proteomics</i> , 2012 , 12, 944-54	2.8	82

390	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
389	A cell cycle phosphoproteome of the yeast centrosome. <i>Science</i> , 2011 , 332, 1557-61	33.3	80
388	Capillary electrophoresis applied to proteomic analysis. <i>Journal of Separation Science</i> , 2009 , 32, 1175-88	3.4	78
387	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
386	Glycolytic Enzymes Coalesce in G Bodies under Hypoxic Stress. <i>Cell Reports</i> , 2017 , 20, 895-908	10.6	77
385	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
384	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
383	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. <i>Analytical Chemistry</i> , 2016 , 88, 3967-75	7.8	73
382	HSP70 chaperones RNA-free TDP-43 into anisotropic intranuclear liquid spherical shells. <i>Science</i> , 2021 , 371,	33.3	73
381	Pervasive and dynamic protein binding sites of the mRNA transcriptome in Saccharomyces cerevisiae. <i>Genome Biology</i> , 2013 , 14, R13	18.3	71
380	Strategies for shotgun identification of post-translational modifications by mass spectrometry. <i>Journal of Chromatography A</i> , 2004 , 1053, 7-14	4.5	71
379	Proteomic analysis of two functional states of the Golgi complex in mammary epithelial cells. <i>Traffic</i> , 2000 , 1, 769-82	5.7	71
378	Reduced pachytene piRNAs and translation underlie spermiogenic arrest in Maelstrom mutant mice. <i>EMBO Journal</i> , 2014 , 33, 1999-2019	13	70
377	S-Nitrosylation of PINK1 Attenuates PINK1/Parkin-Dependent Mitophagy in hiPSC-Based Parkinson's Disease Models. <i>Cell Reports</i> , 2017 , 21, 2171-2182	10.6	70
376	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
375	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
374	Comparisons of mass spectrometry compatible surfactants for global analysis of the mammalian brain proteome. <i>Analytical Chemistry</i> , 2008 , 80, 8694-701	7.8	69
373	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

372	Direct detection of biotinylated proteins by mass spectrometry. <i>Journal of Proteome Research</i> , 2014 , 13, 3966-78	5.6	66
371	A novel multiple affinity purification tag and its use in identification of proteins associated with a cyclin-CDK complex. <i>Nucleic Acids Research</i> , 2001 , 29, E24	20.1	66
370	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
369	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
368	Transnitrosylation from DJ-1 to PTEN attenuates neuronal cell death in parkinsonB disease models. <i>Journal of Neuroscience</i> , 2014 , 34, 15123-31	6.6	65
367	Proteomic comparison of two fractions derived from the transsynaptic scaffold. <i>Journal of Neuroscience Research</i> , 2005 , 81, 762-75	4.4	64
366	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
365	DNA damage shifts circadian clock time via Hausp-dependent Cry1 stabilization. <i>ELife</i> , 2015 , 4,	8.9	63
364	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
363	YADA: a tool for taking the most out of high-resolution spectra. <i>Bioinformatics</i> , 2009 , 25, 2734-6	7.2	62
362	Direct analysis of protein mixtures by tandem mass spectrometry. <i>The Protein Journal</i> , 1997 , 16, 495-7		61
361	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
360	Identification of Open Stomata1-Interacting Proteins Reveals Interactions with Sucrose Non-fermenting1-Related Protein Kinases2 and with Type 2A Protein Phosphatases That Function in Absciscic Acid Responses. <i>Plant Physiology</i> , 2015 , 169, 760-79	6.6	59
359	Cancer proteomics by quantitative shotgun proteomics. <i>Molecular Oncology</i> , 2007 , 1, 144-59	7.9	59
358	Strategies for shotgun identification of integral membrane proteins by tandem mass spectrometry. <i>Proteomics</i> , 2008 , 8, 3947-55	4.8	59
357	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016 , 19, 849-64	23.4	59
356	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
355	Saliva from nymph and adult females of Haemaphysalis longicornis: a proteomic study. <i>Parasites and Vectors</i> , 2015 , 8, 338	4	57

354	Characterisation of Plasmodium invasive organelles; an ookinete microneme proteome. <i>Proteomics</i> , 2009 , 9, 1142-51	4.8	57
353	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
352	Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer. <i>Molecular Cell</i> , 2018 , 70, 842-853.e7	17.6	57
351	Arginyltransferase ATE1 catalyzes midchain arginylation of proteins at side chain carboxylates in vivo. <i>Chemistry and Biology</i> , 2014 , 21, 331-7		56
350	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
349	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, 1154-60	3.4	54
348	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
347	A ribonuclease coordinates siRNA amplification and mRNA cleavage during RNAi. <i>Cell</i> , 2015 , 160, 407-19	56.2	50
346	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
345	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
344	Proteomic analysis of mitochondria from <i>Caenorhabditis elegans</i> . <i>Proteomics</i> , 2009 , 9, 4539-53	4.8	50
343	Arginyltransferase regulates alpha cardiac actin function, myofibril formation and contractility during heart development. <i>Development (Cambridge)</i> , 2008 , 135, 3881-9	6.6	50
342	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
341	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
340	Fmr1 deficiency promotes age-dependent alterations in the cortical synaptic proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4697-706	11.5	48
339	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
338	S-nitrosylation-mediated redox transcriptional switch modulates neurogenesis and neuronal cell death. <i>Cell Reports</i> , 2014 , 8, 217-28	10.6	48
337	Improving the TFold test for differential shotgun proteomics. <i>Bioinformatics</i> , 2012 , 28, 1652-4	7.2	48

336	Harnessing the heart of big data. <i>Circulation Research</i> , 2015 , 116, 1115-9	15.7	47
335	The Sorting Receptor SorCS1 Regulates Trafficking of Neurexin and AMPA Receptors. <i>Neuron</i> , 2015 , 87, 764-80	13.9	47
334	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
333	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 , 110, 11857-62	11.5	47
332	Identification of N-terminally arginylated proteins and peptides by mass spectrometry. <i>Nature Protocols</i> , 2009 , 4, 325-32	18.8	47
331	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
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