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. *Journal of the American Society for Mass Spectrometry*, **1994**, 5, 976-89	3.5	5082
496	Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nature Biotechnology*, **2001**, 19, 242-7	44.5	4123
495	A model for random sampling and estimation of relative protein abundance in shotgun proteomics. *Analytical Chemistry*, **2004**, 76, 4193-201	7.8	2080
494	Direct analysis of protein complexes using mass spectrometry. *Nature Biotechnology*, **1999**, 17, 676-82	44.5	1983
493	An automated multidimensional protein identification technology for shotgun proteomics. *Analytical Chemistry*, **2001**, 73, 5683-90	7.8	1674
492	Microglia promote learning-dependent synapse formation through brain-derived neurotrophic factor. *Cell*, **2013**, 155, 1596-609	56.2	1422
491	DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. *Journal of Proteome Research*, **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. *Analytical Chemistry*, **1995**, 67, 1426-36	7.8	1117
489	A proteomic view of the Plasmodium falciparum life cycle. *Nature*, **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. *Cell*, **1998**, 93, 477-86	56.2	1009
487	Protein analysis by shotgun/bottom-up proteomics. *Chemical Reviews*, **2013**, 113, 2343-94	68.1	902
486	Proteomics by mass spectrometry: approaches, advances, and applications. *Annual Review of Biomedical Engineering*, **2009**, 11, 49-79	12	803
485	A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses. *Science*, **2005**, 307, 82-6	33.3	662
484	A method for the comprehensive proteomic analysis of membrane proteins. *Nature Biotechnology*, **2003**, 21, 532-8	44.5	603
483	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. *Nature*, **2002**, 419, 512-9	50.4	591
482	The minimum information about a proteomics experiment (MIAPE). *Nature Biotechnology*, **2007**, 25, 887-93	44.5	583
481	The biological impact of mass-spectrometry-based proteomics. *Nature*, **2007**, 450, 991-1000	50.4	564

480	Mass spectrometry and the age of the proteome. *Journal of Mass Spectrometry*, **1998**, 33, 1-19	2.2	557
479	Nuclear membrane proteins with potential disease links found by subtractive proteomics. *Science*, **2003**, 301, 1380-2	33.3	543
478	The human CENP-A centromeric nucleosome-associated complex. *Nature Cell Biology*, **2006**, 8, 458-69	23.4	539
477	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	11.5	525
476	Mass spectrometry for proteomics. *Current Opinion in Chemical Biology*, **2008**, 12, 483-90	9.7	514
475	Automated approach for quantitative analysis of complex peptide mixtures from tandem mass spectra. *Nature Methods*, **2004**, 1, 39-45	21.6	512
474	Phospho-regulation of kinetochore-microtubule attachments by the Aurora kinase Ipl1p. *Cell*, **2002**, 111, 163-72	56.2	510
473	Hsp90 cochaperone Aha1 downregulation rescues misfolding of CFTR in cystic fibrosis. *Cell*, **2006**, 127, 803-15	56.2	498
472	Centromere-specific assembly of CENP-a nucleosomes is mediated by HJURP. *Cell*, **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. *Analytical Chemistry*, **1997**, 69, 767-76	7.8	456
470	Analyzing marginal cases in differential shotgun proteomics. *Bioinformatics*, **2011**, 27, 275-6	7.2	454
469	Analysis of the myosin-II-responsive focal adhesion proteome reveals a role for β-Pix in negative regulation of focal adhesion maturation. *Nature Cell Biology*, **2011**, 13, 383-93	23.4	425
468	Neural palmitoyl-proteomics reveals dynamic synaptic palmitoylation. *Nature*, **2008**, 456, 904-9	50.4	422
467	Isobaric labeling-based relative quantification in shotgun proteomics. *Journal of Proteome Research* , **2014**, 13, 5293-309	5.6	403
466	Mass spectrometry in high-throughput proteomics: ready for the big time. *Nature Methods*, **2010**, 7, 681-5	21.6	390
465	The CENP-H-I complex is required for the efficient incorporation of newly synthesized CENP-A into centromeres. *Nature Cell Biology*, **2006**, 8, 446-57	23.4	376
464	Analysis of quantitative proteomic data generated via multidimensional protein identification technology. *Analytical Chemistry*, **2002**, 74, 1650-7	7.8	366
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462	Identification of long-lived proteins reveals exceptional stability of essential cellular structures. *Cell* , **2013**, 154, 971-982	56.2	351
461	Proteomics of organelles and large cellular structures. *Nature Reviews Molecular Cell Biology*, **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. *Plant Journal*, **2010**, 61, 290-9	6.9	350
459	Mining genomes: correlating tandem mass spectra of modified and unmodified peptides to sequences in nucleotide databases. *Analytical Chemistry*, **1995**, 67, 3202-10	7.8	350
458	A quantitative analysis software tool for mass spectrometry-based proteomics. *Nature Methods*, **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. *PLoS Pathogens*, **2012**, 8, e1002623	7.6	329
456	Metabolic labeling of mammalian organisms with stable isotopes for quantitative proteomic analysis. *Analytical Chemistry*, **2004**, 76, 4951-9	7.8	322
455	Isogenic human iPSC Parkinson's model shows nitrosative stress-induced dysfunction in MEF2-PGC1α transcription. *Cell*, **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. *Rapid Communications in Mass Spectrometry*, **2004**, 18, 2162-8	2.2	295
453	High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry. *Protein Science*, **1998**, 7, 706-19	6.3	265
452	Quantitative mass spectrometry identifies insulin signaling targets in C. elegans. *Science*, **2007**, 317, 660-3	33.3	260
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450	Assigning function to yeast proteins by integration of technologies. *Molecular Cell*, **2003**, 12, 1353-65	17.6	236
449	Automated identification of amino acid sequence variations in proteins by HPLC/microspray tandem mass spectrometry. *Analytical Chemistry*, **2000**, 72, 757-63	7.8	209
448	Extremely long-lived nuclear pore proteins in the rat brain. *Science*, **2012**, 335, 942	33.3	206
447	Reduced histone deacetylase 7 activity restores function to misfolded CFTR in cystic fibrosis. *Nature Chemical Biology*, **2010**, 6, 25-33	11.7	204
446	Database searching using mass spectrometry data. *Electrophoresis*, **1998**, 19, 893-900	3.6	199
445	Arginylation of beta-actin regulates actin cytoskeleton and cell motility. *Science*, **2006**, 313, 192-6	33.3	197

444	The quadrupole ion trap mass spectrometer--a small solution to a big challenge. *Analytical Biochemistry*, **1997**, 244, 1-15	3.1	194
443	O-GlcNAc transferase/host cell factor C1 complex regulates gluconeogenesis by modulating PGC-1 stability. *Cell Metabolism*, **2012**, 16, 226-37	24.6	188
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441	Proteomics reveal a link between the endoplasmic reticulum and lipid secretory mechanisms in mammary epithelial cells. *Electrophoresis*, **2000**, 21, 3470-82	3.6	187
440	Code developments to improve the efficiency of automated MS/MS spectra interpretation. *Journal of Proteome Research*, **2002**, 1, 211-5	5.6	181
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438	Method to compare collision-induced dissociation spectra of peptides: potential for library searching and subtractive analysis. *Analytical Chemistry*, **1998**, 70, 3557-65	7.8	168
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435	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. *Nature Protocols*, **2016**, 11, 102-17	18.8	156
434	Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143. *Electrophoresis*, **1997**, 18, 1314-34	3.6	156
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431	A two-step mechanism for TRF2-mediated chromosome-end protection. *Nature*, **2013**, 494, 502-5	50.4	154
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429	Validation of tandem mass spectrometry database search results using DTASelect. *Current Protocols in Bioinformatics*, **2007**, Chapter 13, Unit 13.4	24.2	153
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422	In vivo activation of a conserved microRNA program induces mammalian heart regeneration. *Cell Stem Cell*, **2014**, 15, 589-604	18	141
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417	Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry. *Analytical Chemistry*, **1999**, 71, 2270-8	7.8	128
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415	Argonautes promote male fertility and provide a paternal memory of germline gene expression in C. elegans. *Cell*, **2013**, 155, 1532-44	56.2	123
414	PatternLab for proteomics: a tool for differential shotgun proteomics. *BMC Bioinformatics*, **2008**, 9, 316	3.6	122
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406	Global analysis of posttranslational protein arginylation. *PLoS Biology*, **2007**, 5, e258	9.7	109
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404	The SARS-CoV-2 nucleocapsid phosphoprotein forms mutually exclusive condensates with RNA and the membrane-associated M protein. *Nature Communications*, **2021**, 12, 502	17.4	101
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398	Requirement for Nudel and dynein for assembly of the lamin B spindle matrix. *Nature Cell Biology*, **2009**, 11, 247-56	23.4	93
397	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. *Nature Communications*, **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. *ELife*, **2016**, 5, e11794	8.9	92
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380	Strategies for shotgun identification of post-translational modifications by mass spectrometry. *Journal of Chromatography A*, **2004**, 1053, 7-14	4.5	71
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