

Ole N Jensen

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334 papers	28,475 citations	86 h-index	161 g-index
349 ext. papers	31,275 ext. citations	7 avg, IF	7.05 L-index

#	Paper	IF	Citations
334	Proteomic analysis of post-translational modifications. <i>Nature Biotechnology</i> , 2003 , 21, 255-61	44.5	1566
333	Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996 , 93, 14440-5	11.5	1292
332	Highly selective enrichment of phosphorylated peptides from peptide mixtures using titanium dioxide microcolumns. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 873-86	7.6	1257
331	Development of human protein reference database as an initial platform for approaching systems biology in humans. <i>Genome Research</i> , 2003 , 13, 2363-71	9.7	823
330	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002 , 20, 261-8	15.1	791
329	Quantitative phosphoproteomics applied to the yeast pheromone signaling pathway. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 310-27	7.6	665
328	Highly selective enrichment of phosphorylated peptides using titanium dioxide. <i>Nature Protocols</i> , 2006 , 1, 1929-35	18.8	509
327	Large-scale analysis of in vivo phosphorylated membrane proteins by immobilized metal ion affinity chromatography and mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 1234-43	7.6	492
326	Modification-specific proteomics: characterization of post-translational modifications by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2004 , 8, 33-41	9.7	454
325	A new strategy for identification of N-glycosylated proteins and unambiguous assignment of their glycosylation sites using HILIC enrichment and partial deglycosylation. <i>Journal of Proteome Research</i> , 2004 , 3, 556-66	5.6	425
324	Phosphoproteomics of the Arabidopsis plasma membrane and a new phosphorylation site database. <i>Plant Cell</i> , 2004 , 16, 2394-405	11.6	394
323	Analytical strategies for phosphoproteomics. <i>Proteomics</i> , 2009 , 9, 1451-68	4.8	392
322	Interpreting the protein language using proteomics. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 391-403	4.8	392
321	Biomarker discovery from pancreatic cancer secretome using a differential proteomic approach. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 157-71	7.6	372
320	SIMAC (sequential elution from IMAC), a phosphoproteomics strategy for the rapid separation of monophosphorylated from multiply phosphorylated peptides. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 661-71	7.6	355
319	Identification of proteins in the postsynaptic density fraction by mass spectrometry. <i>Journal of Neuroscience</i> , 2000 , 20, 4069-80	6.6	348
318	Characterization of phosphoproteins from electrophoretic gels by nanoscale Fe(III) affinity chromatography with off-line mass spectrometry analysis. <i>Proteomics</i> , 2001 , 1, 207-22	4.8	339

317	Electron capture dissociation of singly and multiply phosphorylated peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2000 , 14, 1793-800	2.2	325
316	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
315	A mass spectrometry-based proteomic approach for identification of serine/threonine-phosphorylated proteins by enrichment with phospho-specific antibodies: identification of a novel protein, Frigg, as a protein kinase A substrate. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 517-27	7.6	318
314	High-oxygen packaging atmosphere influences protein oxidation and tenderness of porcine longissimus dorsi during chill storage. <i>Meat Science</i> , 2007 , 77, 295-303	6.4	298
313	Delayed extraction improves specificity in database searches by matrix-assisted laser desorption/ionization peptide maps. <i>Rapid Communications in Mass Spectrometry</i> , 1996 , 10, 1371-8	2.2	279
312	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017 , 23, 483-492	50.5	278
311	Analysis of the <i>Saccharomyces</i> spindle pole by matrix-assisted laser desorption/ionization (MALDI) mass spectrometry. <i>Journal of Cell Biology</i> , 1998 , 141, 967-77	7.3	277
310	Phosphoric acid as a matrix additive for MALDI MS analysis of phosphopeptides and phosphoproteins. <i>Analytical Chemistry</i> , 2004 , 76, 5109-17	7.8	276
309	Modification-specific proteomics: strategies for characterization of post-translational modifications using enrichment techniques. <i>Proteomics</i> , 2009 , 9, 4632-41	4.8	275
308	Characterization of an antagonistic switch between histone H3 lysine 27 methylation and acetylation in the transcriptional regulation of Polycomb group target genes. <i>Nucleic Acids Research</i> , 2010 , 38, 4958-69	20.1	251
307	Binding of 14-3-3 protein to the plasma membrane H(+)-ATPase AHA2 involves the three C-terminal residues Tyr(946)-Thr-Val and requires phosphorylation of Thr(947). <i>Journal of Biological Chemistry</i> , 1999 , 274, 36774-80	5.4	251
306	A specific p47phox -serine phosphorylated by convergent MAPKs mediates neutrophil NADPH oxidase priming at inflammatory sites. <i>Journal of Clinical Investigation</i> , 2006 , 116, 2033-43	15.9	237
305	Identification of the components of simple protein mixtures by high-accuracy peptide mass mapping and database searching. <i>Analytical Chemistry</i> , 1997 , 69, 4741-50	7.8	230
304	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015 , 29, 585-90	12.6	226
303	Identification by a differential proteomic approach of heat shock protein 27 as a potential marker of atherosclerosis. <i>Circulation</i> , 2004 , 110, 2216-9	16.7	199
302	The pseudokinase domain of JAK2 is a dual-specificity protein kinase that negatively regulates cytokine signaling. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 971-6	17.6	195
301	A strategy for identifying gel-separated proteins in sequence databases by MS alone. <i>Biochemical Society Transactions</i> , 1996 , 24, 893-6	5.1	192
300	Protein hydrogen exchange measured at single-residue resolution by electron transfer dissociation mass spectrometry. <i>Analytical Chemistry</i> , 2009 , 81, 5577-84	7.8	186

299	Plasmin in nephrotic urine activates the epithelial sodium channel. <i>Journal of the American Society of Nephrology: JASN</i> , 2009 , 20, 299-310	12.7	184
298	ER-60, a chaperone with thiol-dependent reductase activity involved in MHC class I assembly. <i>EMBO Journal</i> , 1998 , 17, 2186-95	13	184
297	Sample preparation methods for mass spectrometric peptide mapping directly from 2-DE gels. <i>Methods in Molecular Biology</i> , 1999 , 112, 513-30	1.4	181
296	The histone methyltransferase SET8 is required for S-phase progression. <i>Journal of Cell Biology</i> , 2007 , 179, 1337-45	7.3	179
295	Hybridisation based DNA screening on peptide nucleic acid (PNA) oligomer arrays. <i>Nucleic Acids Research</i> , 1997 , 25, 2792-9	20.1	176
294	Differential expression profiling of membrane proteins by quantitative proteomics in a human mesenchymal stem cell line undergoing osteoblast differentiation. <i>Stem Cells</i> , 2005 , 23, 1367-77	5.8	175
293	Comprehensive proteomic analysis of human pancreatic juice. <i>Journal of Proteome Research</i> , 2004 , 3, 1042-55	5.6	173
292	The Rac-RhoGDI complex and the structural basis for the regulation of Rho proteins by RhoGDI. <i>Nature Structural Biology</i> , 2000 , 7, 122-6		171
291	Quantitative assessment of in-solution digestion efficiency identifies optimal protocols for unbiased protein analysis. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2992-3005	7.6	168
290	Stable isotope labeling of Arabidopsis thaliana cells and quantitative proteomics by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1697-709	7.6	165
289	Transcription factor cooperativity in early adipogenic hotspots and super-enhancers. <i>Cell Reports</i> , 2014 , 7, 1443-1455	10.6	163
288	Dynamic histone H3 epigenome marking during the intraerythrocytic cycle of Plasmodium falciparum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9655-60	11.5	162
287	Analysis of posttranslational modifications of proteins by tandem mass spectrometry. <i>BioTechniques</i> , 2006 , 40, 790-8	2.5	161
286	Proteomic analysis of glycosylphosphatidylinositol-anchored membrane proteins. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 1261-70	7.6	158
285	Quantitative proteomic analysis of post-translational modifications of human histones. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1314-25	7.6	153
284	Three v-SNAREs and two t-SNAREs, present in a pentameric cis-SNARE complex on isolated vacuoles, are essential for homotypic fusion. <i>Journal of Cell Biology</i> , 1999 , 145, 1435-42	7.3	147
283	Mass spectrometric identification and microcharacterization of proteins from electrophoretic gels: Strategies and applications. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 33, 74-89	4.2	140
282	Electron transfer dissociation facilitates the measurement of deuterium incorporation into selectively labeled peptides with single residue resolution. <i>Journal of the American Chemical Society</i> , 2008 , 130, 17453-9	16.4	139

281	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
280	Autophosphorylation is essential for the in vivo function of the Lotus japonicus Nod factor receptor 1 and receptor-mediated signalling in cooperation with Nod factor receptor 5. <i>Plant Journal</i> , 2011 , 65, 404-17	6.9	135
279	A simple and fast method to determine the parameters for fuzzy c-means cluster analysis. <i>Bioinformatics</i> , 2010 , 26, 2841-8	7.2	130
278	Phosphoproteome analysis of functional mitochondria isolated from resting human muscle reveals extensive phosphorylation of inner membrane protein complexes and enzymes. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.000299	7.6	120
277	Global histone analysis by mass spectrometry reveals a high content of acetylated lysine residues in the malaria parasite Plasmodium falciparum. <i>Journal of Proteome Research</i> , 2009 , 8, 3439-50	5.6	119
276	VEMS 3.0: algorithms and computational tools for tandem mass spectrometry based identification of post-translational modifications in proteins. <i>Journal of Proteome Research</i> , 2005 , 4, 2338-47	5.6	119
275	Erv41p and Erv46p: new components of COPII vesicles involved in transport between the ER and Golgi complex. <i>Journal of Cell Biology</i> , 2001 , 152, 503-18	7.3	116
274	A urokinase receptor-associated protein with specific collagen binding properties. <i>Journal of Biological Chemistry</i> , 2000 , 275, 1993-2002	5.4	111
273	Assessment of lectin and HILIC based enrichment protocols for characterization of serum glycoproteins by mass spectrometry. <i>Journal of Proteomics</i> , 2008 , 71, 304-17	3.9	110
272	Identification of ischemia-regulated phosphorylation sites in connexin43: A possible target for the antiarrhythmic peptide analogue rotigaptide (ZP123). <i>Journal of Molecular and Cellular Cardiology</i> , 2006 , 40, 790-8	5.8	108
271	Quantitative mass spectrometry of histones H3.2 and H3.3 in Suz12-deficient mouse embryonic stem cells reveals distinct, dynamic post-translational modifications at Lys-27 and Lys-36. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 838-50	7.6	107
270	An enzymatic deglycosylation scheme enabling identification of core fucosylated N-glycans and O-glycosylation site mapping of human plasma proteins. <i>Journal of Proteome Research</i> , 2007 , 6, 3021-31	5.6	106
269	Modification-specific proteomics of plasma membrane proteins: identification and characterization of glycosylphosphatidylinositol-anchored proteins released upon phospholipase D treatment. <i>Journal of Proteome Research</i> , 2006 , 5, 935-43	5.6	106
268	Proteomics in chromatin biology and epigenetics: Elucidation of post-translational modifications of histone proteins by mass spectrometry. <i>Journal of Proteomics</i> , 2012 , 75, 3419-33	3.9	105
267	Highly Efficient Phosphopeptide Enrichment by Calcium Phosphate Precipitation Combined with Subsequent IMAC Enrichment. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 2032-42	7.6	103
266	NetPhosYeast: prediction of protein phosphorylation sites in yeast. <i>Bioinformatics</i> , 2007 , 23, 895-7	7.2	103
265	Autophosphorylation of JAK2 on tyrosines 221 and 570 regulates its activity. <i>Molecular and Cellular Biology</i> , 2004 , 24, 4955-67	4.8	102
264	Optimized IMAC-IMAC protocol for phosphopeptide recovery from complex biological samples. <i>Journal of Proteome Research</i> , 2010 , 9, 3561-73	5.6	100

263	Cell cycle-specific UNG2 phosphorylations regulate protein turnover, activity and association with RPA. <i>EMBO Journal</i> , 2008 , 27, 51-61	13	100
262	In-depth analysis of the secretome identifies three major independent secretory pathways in differentiating human myoblasts. <i>Journal of Proteomics</i> , 2012 , 77, 344-56	3.9	97
261	Peptide sequencing and characterization of post-translational modifications by enhanced ion-charging and liquid chromatography electron-transfer dissociation tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 9243-52	7.8	96
260	SET8 is degraded via PCNA-coupled CRL4(CDT2) ubiquitylation in S phase and after UV irradiation. <i>Journal of Cell Biology</i> , 2011 , 192, 43-54	7.3	95
259	The potato tuber mitochondrial proteome. <i>Plant Physiology</i> , 2014 , 164, 637-53	6.6	94
258	WAVE regulatory complex activation by cooperating GTPases Arf and Rac1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 14449-54	11.5	94
257	The sphingolipid long-chain base-Pkh1/2-Ypk1/2 signaling pathway regulates eisosome assembly and turnover. <i>Journal of Biological Chemistry</i> , 2008 , 283, 10433-44	5.4	94
256	Selenoprotein W of rat muscle binds glutathione and an unknown small molecular weight moiety. <i>Journal of Inorganic Biochemistry</i> , 1996 , 61, 117-24	4.2	94
255	Transcriptional co-activator protein p100 interacts with snRNP proteins and facilitates the assembly of the spliceosome. <i>Nucleic Acids Research</i> , 2007 , 35, 4485-94	20.1	93
254	Phosphoric acid enhances the performance of Fe(III) affinity chromatography and matrix-assisted laser desorption/ionization tandem mass spectrometry for recovery, detection and sequencing of phosphopeptides. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 1721-30	2.2	92
253	Phosphopeptide detection and sequencing by matrix-assisted laser desorption/ionization quadrupole time-of-flight tandem mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2002 , 37, 179-90	2.2	92
252	Purification and properties of selenoprotein W from rat muscle. <i>Journal of Biological Chemistry</i> , 1993 , 268, 17103-7	5.4	91
251	Metastasis-related plasma membrane proteins of human breast cancer cells identified by comparative quantitative mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1436-49	7.6	90
250	TiO(2)-based phosphoproteomic analysis of the plasma membrane and the effects of phosphatase inhibitor treatment. <i>Journal of Proteome Research</i> , 2008 , 7, 3304-13	5.6	90
249	Identification of the major membrane and core proteins of vaccinia virus by two-dimensional electrophoresis. <i>Journal of Virology</i> , 1996 , 70, 7485-97	6.6	90
248	Automation of matrix-assisted laser desorption/ionization mass spectrometry using fuzzy logic feedback control. <i>Analytical Chemistry</i> , 1997 , 69, 1706-14	7.8	86
247	Assessment and improvement of statistical tools for comparative proteomics analysis of sparse data sets with few experimental replicates. <i>Journal of Proteome Research</i> , 2013 , 12, 3874-83	5.6	83
246	Serum protein profiling by solid phase extraction and mass spectrometry: a future diagnostics tool?. <i>Proteomics</i> , 2009 , 9, 1428-41	4.8	83

245	Candidate hippocampal biomarkers of susceptibility and resilience to stress in a rat model of depression. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.016428	7.6	81
244	Accurate H3K27 methylation can be established de novo by SUZ12-directed PRC2. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 225-232	17.6	79
243	Mechanism for activation of the growth factor-activated AGC kinases by turn motif phosphorylation. <i>EMBO Journal</i> , 2007 , 26, 2251-61	13	78
242	Mechanisms of hydrazine toxicity in rat liver investigated by proteomics and multivariate data analysis. <i>Proteomics</i> , 2004 , 4, 868-80	4.8	77
241	Organic matter processing by microbial communities throughout the Atlantic water column as revealed by metaproteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E400-E408	11.5	76
240	Efficient isolation and quantitative proteomic analysis of cancer cell plasma membrane proteins for identification of metastasis-associated cell surface markers. <i>Journal of Proteome Research</i> , 2009 , 8, 3078-90	5.6	76
239	The tyrosine phosphatase Shp2 interacts with NPM-ALK and regulates anaplastic lymphoma cell growth and migration. <i>Cancer Research</i> , 2007 , 67, 4278-86	10.1	75
238	Mass spectrometric identification and microcharacterization of proteins from electrophoretic gels: Strategies and applications. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 33, 74-89	4.2	72
237	Identification and profiling of salinity stress-responsive proteins in Sorghum bicolor seedlings. <i>Journal of Proteomics</i> , 2012 , 75, 4139-50	3.9	71
236	Optimized preparation of urine samples for two-dimensional electrophoresis and initial application to patient samples. <i>Clinical Biochemistry</i> , 2002 , 35, 581-9	3.5	70
235	Functional domain analysis of the Remorin protein LjSYMREM1 in Lotus japonicus. <i>PLoS ONE</i> , 2012 , 7, e30817	3.7	69
234	Middle-down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial post-translational modifications in histones. <i>Proteomics</i> , 2014 , 14, 2200-11	4.8	68
233	Phosphorylation of formate dehydrogenase in potato tuber mitochondria. <i>Journal of Biological Chemistry</i> , 2003 , 278, 26021-30	5.4	68
232	Mass spectrometry and site-directed mutagenesis identify several autophosphorylated residues required for the activity of PrkC, a Ser/Thr kinase from Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2003 , 330, 459-72	6.5	68
231	Functional heterogeneity within the CD44 high human breast cancer stem cell-like compartment reveals a gene signature predictive of distant metastasis. <i>Molecular Medicine</i> , 2012 , 18, 1109-21	6.2	67
230	Identification of phosphorylation sites in protein kinase A substrates using artificial neural networks and mass spectrometry. <i>Journal of Proteome Research</i> , 2004 , 3, 426-33	5.6	67
229	p130Cas mediates the transforming properties of the anaplastic lymphoma kinase. <i>Blood</i> , 2005 , 106, 3907-16	2.2	66
228	Feedback inactivation of D-serine synthesis by NMDA receptor-elicited translocation of serine racemase to the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 7589-94	11.5	65

227	Microbial stratification in low pH oxic and suboxic macroscopic growths along an acid mine drainage. <i>ISME Journal</i> , 2014 , 8, 1259-74	11.9	63
226	Analysis of protein-nucleic acid interactions by photochemical cross-linking and mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2002 , 21, 163-82	11	62
225	Modification-specific proteomics in plant biology. <i>Journal of Proteomics</i> , 2010 , 73, 2249-66	3.9	61
224	Precision mapping of coexisting modifications in histone H3 tails from embryonic stem cells by ETD-MS/MS. <i>Analytical Chemistry</i> , 2013 , 85, 8232-9	7.8	60
223	Phosphoproteome analysis of <i>Streptomyces</i> development reveals extensive protein phosphorylation accompanying bacterial differentiation. <i>Journal of Proteome Research</i> , 2011 , 10, 5481-92	5.6	60
222	Analysis of histidine phosphorylation using tandem MS and ion-electron reactions. <i>Analytical Chemistry</i> , 2007 , 79, 7450-6	7.8	59
221	Proteomic analysis of human metaphase chromosomes reveals topoisomerase II alpha as an Aurora B substrate. <i>Nucleic Acids Research</i> , 2002 , 30, 5318-27	20.1	58
220	Large scale analysis of co-existing post-translational modifications in histone tails reveals global fine structure of cross-talk. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1855-65	7.6	56
219	BRAG1, a Sec7 domain-containing protein, is a component of the postsynaptic density of excitatory synapses. <i>Brain Research</i> , 2006 , 1120, 35-45	3.7	56
218	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. <i>Proteomics</i> , 2004 , 4, 2583-93	4.8	56
217	Quantitative analysis of proteome and lipidome dynamics reveals functional regulation of global lipid metabolism. <i>Chemistry and Biology</i> , 2015 , 22, 412-25		55
216	Structural analysis and tissue localization of human C4.4A: a protein homologue of the urokinase receptor. <i>Biochemical Journal</i> , 2004 , 380, 845-57	3.8	55
215	Phosphorylation of dynamin I on Ser-795 by protein kinase C blocks its association with phospholipids. <i>Journal of Biological Chemistry</i> , 2000 , 275, 11610-7	5.4	55
214	PRMT5 methylome profiling uncovers a direct link to splicing regulation in acute myeloid leukemia. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 999-1012	17.6	54
213	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2715-29	7.6	53
212	Phosphopeptide quantitation using amine-reactive isobaric tagging reagents and tandem mass spectrometry: application to proteins isolated by gel electrophoresis. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 1127-34	2.2	53
211	Direct observation of UV-crosslinked protein-nucleic acid complexes by matrix-assisted laser desorption ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1993 , 7, 496-501	2.2	53
210	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016 , 16, 907-14	4.8	53

209	Sequence patterns produced by incomplete enzymatic digestion or one-step Edman degradation of peptide mixtures as probes for protein database searches. <i>Electrophoresis</i> , 1996 , 17, 938-44	3.6	52
208	The human oral metaproteome reveals potential biomarkers for caries disease. <i>Proteomics</i> , 2015 , 15, 3497-507	4.8	51
207	Isolation and characterization of glycosylphosphatidylinositol-anchored peptides by hydrophilic interaction chromatography and MALDI tandem mass spectrometry. <i>Analytical Chemistry</i> , 2006 , 78, 3335-41	7.8	51
206	Molecular architecture of transcription factor hotspots in early adipogenesis. <i>Cell Reports</i> , 2014 , 7, 1434-1442	10.6	50
205	The C. elegans H3K27 demethylase UTX-1 is essential for normal development, independent of its enzymatic activity. <i>PLoS Genetics</i> , 2012 , 8, e1002647	6	50
204	Correlation of acidic and basic carrier ampholyte and immobilized pH gradient two-dimensional gel electrophoresis patterns based on mass spectrometric protein identification. <i>Electrophoresis</i> , 1998 , 19, 1024-35	3.6	50
203	Accumulation of histone variant H3.3 with age is associated with profound changes in the histone methylation landscape. <i>Nucleic Acids Research</i> , 2017 , 45, 9272-9289	20.1	49
202	Serum protein profiling by miniaturized solid-phase extraction and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2005 , 19, 1578-86	2.2	48
201	Phosphosite mapping of P-type plasma membrane H ⁺ -ATPase in homologous and heterologous environments. <i>Journal of Biological Chemistry</i> , 2012 , 287, 4904-13	5.4	47
200	Allosteric activation of coagulation factor VIIa visualized by hydrogen exchange. <i>Journal of Biological Chemistry</i> , 2006 , 281, 23018-24	5.4	47
199	Reproducibility of mass spectrometry based protein profiles for diagnosis of breast cancer across clinical studies: a systematic review. <i>Journal of Proteome Research</i> , 2008 , 7, 1395-402	5.6	46
198	Distinction between human cytochrome P450 (CYP) isoforms and identification of new phosphorylation sites by mass spectrometry. <i>Journal of Proteome Research</i> , 2008 , 7, 4678-88	5.6	46
197	Phosphorylation of JAK2 at serine 523: a negative regulator of JAK2 that is stimulated by growth hormone and epidermal growth factor. <i>Molecular and Cellular Biology</i> , 2006 , 26, 4052-62	4.8	46
196	Utility of immonium ions for assignment of epsilon-N-acetyllysine-containing peptides by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2008 , 80, 3422-30	7.8	44
195	Tousled-like kinases phosphorylate Asf1 to promote histone supply during DNA replication. <i>Nature Communications</i> , 2014 , 5, 3394	17.4	43
194	Enrichment and characterization of phosphopeptides by immobilized metal affinity chromatography (IMAC) and mass spectrometry. <i>Methods in Molecular Biology</i> , 2009 , 527, 47-56, xi	1.4	43
193	Quantitative phosphoproteomics of tomato mounting a hypersensitive response reveals a swift suppression of photosynthetic activity and a differential role for hsp90 isoforms. <i>Journal of Proteome Research</i> , 2009 , 8, 1168-82	5.6	42
192	Characterization of peptide-oligonucleotide heteroconjugates by mass spectrometry. <i>Nucleic Acids Research</i> , 1996 , 24, 3866-72	20.1	42

191	Top-down and Middle-down Protein Analysis Reveals that Intact and Clipped Human Histones Differ in Post-translational Modification Patterns. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 3142-53	7.6	41
190	Unraveling the pathogenesis of type 1 diabetes with proteomics: present and future directions. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 441-57	7.6	41
189	Atorvastatin modulates the profile of proteins released by human atherosclerotic plaques. <i>European Journal of Pharmacology</i> , 2007 , 562, 119-29	5.3	40
188	In situ liquid-liquid extraction as a sample preparation method for matrix-assisted laser desorption/ionization MS analysis of polypeptide mixtures. <i>Analytical Chemistry</i> , 2003 , 75, 2362-9	7.8	40
187	Mass spectrometric analysis of a UV-cross-linked protein-DNA complex: tryptophans 54 and 88 of E. coli SSB cross-link to DNA. <i>Protein Science</i> , 2001 , 10, 1989-2001	6.3	40
186	Plasminogen-independent initiation of the pro-urokinase activation cascade in vivo. Activation of pro-urokinase by glandular kallikrein (mGK-6) in plasminogen-deficient mice. <i>Biochemistry</i> , 2000 , 39, 5083-13	3.2	40
185	Posttranslational modification of Galphao1 generates Galphao3, an abundant G protein in brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 1327-32	11.5	40
184	Quantitative proteomics identifies Gemin5, a scaffolding protein involved in ribonucleoprotein assembly, as a novel partner for eukaryotic initiation factor 4E. <i>Journal of Proteome Research</i> , 2006 , 5, 1367-78	5.6	39
183	Simplified sample preparation method for protein identification by matrix-assisted laser desorption/ionization mass spectrometry: in-gel digestion on the probe surface. <i>Proteomics</i> , 2001 , 1, 955-66	4.8	39
182	Enrichment and separation of mono- and multiply phosphorylated peptides using sequential elution from IMAC prior to mass spectrometric analysis. <i>Methods in Molecular Biology</i> , 2009 , 527, 67-78, xi	1.4	39
181	Enrichment and identification of integral membrane proteins from barley aleurone layers by reversed-phase chromatography, SDS-PAGE, and LC-MS/MS. <i>Journal of Proteome Research</i> , 2006 , 5, 3105-13	5.6	38
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