

Ole N Jensen

List of Publications by Year in Descending Order

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

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	Distinct and diverse chromatin proteomes of ageing mouse organs reveal protein signatures that correlate with physiological functions.. <i>ELife</i> , 2022 , 11,	8.9	2
333	Complex-dependent histone acetyltransferase activity of KAT8 determines its role in transcription and cellular homeostasis. <i>Molecular Cell</i> , 2021 , 81, 1749-1765.e8	17.6	7
332	Inactivation of the Schizophrenia-associated BRD1 gene in Brain Causes Failure-to-thrive, Seizure Susceptibility and Abnormal Histone H3 Acetylation and N-tail Clipping. <i>Molecular Neurobiology</i> , 2021 , 58, 4495-4505	6.2	1
331	Fast and Accurate Quantification of Nitrogen and Phosphorus Constituents in Animal Slurries Using NMR Sensor Technology. <i>ACS Omega</i> , 2021 , 6, 17335-17341	3.9	1
330	Proteoform Differentiation using Tandem Trapped Ion Mobility, Electron Capture Dissociation, and ToF Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 9575-9582	7.8	4
329	Zirconium(IV)-IMAC Revisited: Improved Performance and Phosphoproteome Coverage by Magnetic Microparticles for Phosphopeptide Affinity Enrichment. <i>Journal of Proteome Research</i> , 2021 , 20, 453-462	5.6	10
328	White adipose remodeling during browning in mice involves YBX1 to drive thermogenic commitment. <i>Molecular Metabolism</i> , 2021 , 44, 101137	8.8	2
327	Lipid molecular timeline profiling reveals diurnal crosstalk between the liver and circulation. <i>Cell Reports</i> , 2021 , 34, 108710	10.6	7
326	Selective Enrichment of Histidine Phosphorylated Peptides Using Molecularly Imprinted Polymers. <i>Analytical Chemistry</i> , 2021 , 93, 3857-3866	7.8	12
325	A conserved, buried cysteine near the P-site is accessible to cysteine modifications and increases ROS stability in the P-type plasma membrane H ⁺ -ATPase. <i>Biochemical Journal</i> , 2021 , 478, 619-632	3.8	3
324	Real-world particulate matters induce lung toxicity in rats fed with a high-fat diet: Evidence of histone modifications. <i>Journal of Hazardous Materials</i> , 2021 , 416, 126182	12.8	1
323	Silencing of ceramide synthase 2 in hepatocytes modulates plasma ceramide biomarkers predictive of cardiovascular death. <i>Molecular Therapy</i> , 2021 ,	11.7	1
322	PolySTest: Robust Statistical Testing of Proteomics Data with Missing Values Improves Detection of Biologically Relevant Features. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1396-1408	7.6	6
321	The effect of phytoalbumin overexpression on the plant proteome during nonhost response of barley (<i>Hordeum vulgare</i>) to wheat powdery mildew (<i>Blumeria graminis</i> f. sp. <i>tritici</i>). <i>Scientific Reports</i> , 2020 , 10, 9192	4.9	
320	Mutant FOXL2 Hijacks SMAD4 and SMAD2/3 to Drive Adult Granulosa Cell Tumors. <i>Cancer Research</i> , 2020 , 80, 3466-3479	10.1	12
319	The Hypoxic Proteome and Metabolome of Barley (<i>L.</i>) with and without Phytoalbumin Priming. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5
318	Visualization of the dynamics of histone modifications and their crosstalk using PTM-CrossTalkMapper. <i>Methods</i> , 2020 , 184, 78-85	4.6	8

317	Middle-Down Proteomic Analyses with Ion Mobility Separations of Endogenous Isomeric Proteoforms. <i>Analytical Chemistry</i> , 2020 , 92, 2364-2368	7.8	9
316	Histo-molecular differentiation of renal cancer subtypes by mass spectrometry imaging and rapid proteome profiling of formalin-fixed paraffin-embedded tumor tissue sections. <i>Oncotarget</i> , 2020 , 11, 3998-4015	3.3	3
315	Combinatory Treatment of Canavanine and Arginine Deprivation Efficiently Targets Human Glioblastoma Cells via Pleiotropic Mechanisms. <i>Cells</i> , 2020 , 9,	7.9	3
314	Yeast Ppz1 protein phosphatase toxicity involves the alteration of multiple cellular targets. <i>Scientific Reports</i> , 2020 , 10, 15613	4.9	6
313	Phosphoproteomic Analysis across the Yeast Life Cycle Reveals Control of Fatty Acyl Chain Length by Phosphorylation of the Fatty Acid Synthase Complex. <i>Cell Reports</i> , 2020 , 32, 108024	10.6	5
312	High-Resolution Differential Ion Mobility Separations/Orbitrap Mass Spectrometry without Buffer Gas Limitations. <i>Analytical Chemistry</i> , 2019 , 91, 6918-6925	7.8	10
311	Selective Enrichment of Phosphorylated Peptides by Monolithic Polymers Surface Imprinted with -Imidazolium Moieties by UV-Initiated Cryopolymerization. <i>Analytical Chemistry</i> , 2019 , 91, 10188-10196	7.8	18
310	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
309	FlashPack: Fast and Simple Preparation of Ultrahigh-performance Capillary Columns for LC-MS. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 383-390	7.6	35
308	Differential Ion Mobility Separations/Mass Spectrometry with High Resolution in Both Dimensions. <i>Analytical Chemistry</i> , 2019 , 91, 1479-1485	7.8	13
307	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
306	VSclust: feature-based variance-sensitive clustering of omics data. <i>Bioinformatics</i> , 2018 , 34, 2965-2972	7.2	14
305	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
304	Linear and Differential Ion Mobility Separations of Middle-Down Proteoforms. <i>Analytical Chemistry</i> , 2018 , 90, 2918-2925	7.8	31
303	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
302	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. <i>Analytical Chemistry</i> , 2018 , 90, 10425-10433 ¹⁶	7.8	16
301	Proteomic Analysis of Post-Translational Modifications by Mass Spectrometry 2018 , 33-53		
300	Distinct Roles of Two Histone Methyltransferases in Transmitting H3K36me3-Based Epigenetic Memory Across Generations in. <i>Genetics</i> , 2018 , 210, 969-982	4	16

299	Phosphoproteomics in Microbiology: Protocols for Studying <i>Streptomyces coelicolor</i> Differentiation. <i>Methods in Molecular Biology</i> , 2018 , 1841, 249-260	1.4	
298	Maximizing Sequence Coverage in Top-Down Proteomics By Automated Multimodal Gas-Phase Protein Fragmentation. <i>Analytical Chemistry</i> , 2018 , 90, 12519-12526	7.8	12
297	Evaluation of sample preparation methods for mass spectrometry-based proteomic analysis of barley leaves. <i>Plant Methods</i> , 2018 , 14, 72	5.8	21
296	Quantitative Proteome and Phosphoproteome Analyses of Reveal Proteins and Phosphoproteins Modulating Differentiation and Secondary Metabolism. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1591-1611 ¹⁸	7.6	18
295	The Tumor Suppressor CIC Directly Regulates MAPK Pathway Genes via Histone Deacetylation. <i>Cancer Research</i> , 2018 , 78, 4114-4125	10.1	30
294	A biotin enrichment strategy identifies novel carbonylated amino acids in proteins from human plasma. <i>Journal of Proteomics</i> , 2017 , 156, 40-51	3.9	20
293	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017 , 23, 483-492	50.5	278
292	Characterization of Complete Histone Tail Proteoforms Using Differential Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 5461-5466	7.8	35
291	Abnormal levels of histone methylation in the retinas of diabetic rats are reversed by minocycline treatment. <i>Scientific Reports</i> , 2017 , 7, 45103	4.9	14
290	Hierarchically templated beads with tailored pore structure for phosphopeptide capture and phosphoproteomics. <i>RSC Advances</i> , 2017 , 7, 17154-17163	3.7	13
289	Phosphotyrosine Biased Enrichment of Tryptic Peptides from Cancer Cells by Combining pY-MIP and TiO Affinity Resins. <i>Analytical Chemistry</i> , 2017 , 89, 11332-11340	7.8	17
288	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
287	Molecularly Imprinted Porous Monolithic Materials from Melamine-Formaldehyde for Selective Trapping of Phosphopeptides. <i>Analytical Chemistry</i> , 2017 , 89, 9491-9501	7.8	27
286	Nuclear phosphoproteome analysis of 3T3-L1 preadipocyte differentiation reveals system-wide phosphorylation of transcriptional regulators. <i>Proteomics</i> , 2017 , 17, 1600248	4.8	7
285	Subcompartmentalization by cross-membranes during early growth of <i>Streptomyces</i> hyphae. <i>Nature Communications</i> , 2016 , 7, 12467	17.4	20
284	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
283	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016 , 16, 907-14	4.8	53
282	Dynamic changes of histone H3 marks during <i>Caenorhabditis elegans</i> lifecycle revealed by middle-down proteomics. <i>Proteomics</i> , 2016 , 16, 459-64	4.8	13

281	Detection and differentiation of 22 kDa and 20 kDa Growth Hormone proteoforms in human plasma by LC-MS/MS. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 284-90	4	7
280	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015 , 29, 585-90	12.6	226
279	Quantitative analysis of proteome and lipidome dynamics reveals functional regulation of global lipid metabolism. <i>Chemistry and Biology</i> , 2015 , 22, 412-25		55
278	NADH-Cytochrome b5 Reductase 3 Promotes Colonization and Metastasis Formation and Is a Prognostic Marker of Disease-Free and Overall Survival in Estrogen Receptor-Negative Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2988-99	7.6	12
277	H3K23me2 is a new heterochromatic mark in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 9694-710	20.1	28
276	Tumor suppressor ASXL1 is essential for the activation of INK4B expression in response to oncogene activity and anti-proliferative signals. <i>Cell Research</i> , 2015 , 25, 1205-18	24.7	28
275	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
274	Targeted mass spectrometry analysis of the proteins IGF1, IGF2, IBP2, IBP3 and A2GL by blood protein precipitation. <i>Journal of Proteomics</i> , 2015 , 113, 29-37	3.9	26
273	The human oral metaproteome reveals potential biomarkers for caries disease. <i>Proteomics</i> , 2015 , 15, 3497-507	4.8	51
272	A laser ablation ICP-MS based method for multiplexed immunoblot analysis: applications to manganese-dependent protein dynamics of photosystem II in barley (<i>Hordeum vulgare</i> L.). <i>Plant Journal</i> , 2015 , 83, 555-65	6.9	13
271	Modulation of cell metabolic pathways and oxidative stress signaling contribute to acquired melphalan resistance in multiple myeloma cells. <i>PLoS ONE</i> , 2015 , 10, e0119857	3.7	37
270	Comparative proteomic analysis of histone post-translational modifications upon ischemia/reperfusion-induced retinal injury. <i>Journal of Proteome Research</i> , 2014 , 13, 2175-86	5.6	14
269	Depletion of abundant plasma proteins by poly(N-isopropylacrylamide-acrylic acid) hydrogel particles. <i>Analytical Chemistry</i> , 2014 , 86, 1543-50	7.8	22
268	Insulin increases phosphorylation of mitochondrial proteins in human skeletal muscle in vivo. <i>Journal of Proteome Research</i> , 2014 , 13, 2359-69	5.6	20
267	Proteomic comparison between maturation drying and prematurely imposed drying of Zea mays seeds reveals a potential role of maturation drying in preparing proteins for seed germination, seedling vigor, and pathogen resistance. <i>Journal of Proteome Research</i> , 2014 , 13, 606-26	5.6	21
266	Tousled-like kinases phosphorylate Asf1 to promote histone supply during DNA replication. <i>Nature Communications</i> , 2014 , 5, 3394	17.4	43
265	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
264	Acute phencyclidine treatment induces extensive and distinct protein phosphorylation in rat frontal cortex. <i>Journal of Proteome Research</i> , 2014 , 13, 1578-92	5.6	11

263	KYSS: mass spectrometry data quality assessment for protein analysis and large-scale proteomics. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 702-7	3.4	2
262	Transcription factor cooperativity in early adipogenic hotspots and super-enhancers. <i>Cell Reports</i> , 2014 , 7, 1443-1455	10.6	163
261	Molecular architecture of transcription factor hotspots in early adipogenesis. <i>Cell Reports</i> , 2014 , 7, 1434-1442	10.6	50
260	Shotgun lipidomic analysis of chemically sulfated sterols compromises analytical sensitivity: Recommendation for large-scale global lipidome analysis. <i>European Journal of Lipid Science and Technology</i> , 2014 , 116, 1618-1620	3	9
259	FBXO22 protein is required for optimal synthesis of the N-methyl-D-aspartate (NMDA) receptor coagonist D-serine. <i>Journal of Biological Chemistry</i> , 2014 , 289, 33904-15	5.4	12
258	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
257	The potato tuber mitochondrial proteome. <i>Plant Physiology</i> , 2014 , 164, 637-53	6.6	94
256	Global mass spectrometry and transcriptomics array based drug profiling provides novel insight into glucosamine induced endoplasmic reticulum stress. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3294-307	7.6	25
255	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
254	Selective renal vasoconstriction, exaggerated natriuresis and excretion rates of exosomic proteins in essential hypertension. <i>Acta Physiologica</i> , 2014 , 212, 106-18	5.6	24
253	Integrated solid-phase extraction-capillary liquid chromatography (speLC) interfaced to ESI-MS/MS for fast characterization and quantification of protein and proteomes. <i>Journal of Proteome Research</i> , 2014 , 13, 6169-75	5.6	18
252	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
251	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
250	A proteomics approach to the identification of biomarkers for psoriasis utilising keratome biopsy. <i>Journal of Proteomics</i> , 2013 , 94, 176-85	3.9	23
249	New insights in osteogenic differentiation revealed by mass spectrometric assessment of phosphorylated substrates in murine skin mesenchymal cells. <i>BMC Cell Biology</i> , 2013 , 14, 47		10
248	Tissue specific phosphorylation of mitochondrial proteins isolated from rat liver, heart muscle, and skeletal muscle. <i>Journal of Proteome Research</i> , 2013 , 12, 4327-39	5.6	17
247	<i>Candida albicans</i> induces pro-inflammatory and anti-apoptotic signals in macrophages as revealed by quantitative proteomics and phosphoproteomics. <i>Journal of Proteomics</i> , 2013 , 91, 106-35	3.9	31
246	STAT3 activity is necessary and sufficient for the development of immune-mediated myocarditis in mice and promotes progression to dilated cardiomyopathy. <i>EMBO Molecular Medicine</i> , 2013 , 5, 572-90	12	32

245	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
244	Glycopeptide enrichment for MALDI-TOF mass spectrometry analysis by hydrophilic interaction liquid chromatography solid phase extraction (HILIC SPE). <i>Methods in Molecular Biology</i> , 2013 , 951, 131-144	11.4	30
243	Proteomics identifies molecular networks affected by tetradecylthioacetic acid and fish oil supplemented diets. <i>Journal of Proteomics</i> , 2013 , 84, 61-77	3.9	15
242	Monitoring the native phosphorylation state of plasma membrane proteins from a single mouse cerebellum. <i>Journal of Neuroscience Methods</i> , 2013 , 213, 153-64	3	5
241	Proteomic changes and endophytic micromycota during storage of organically and conventionally grown carrots. <i>Postharvest Biology and Technology</i> , 2013 , 76, 26-33	6.2	12
240	Functional proteomics of barley and barley chloroplasts - strategies, methods and perspectives. <i>Frontiers in Plant Science</i> , 2013 , 4, 52	6.2	16
239	Composition and structure of photosystem I in the moss <i>Physcomitrella patens</i> . <i>Journal of Experimental Botany</i> , 2013 , 64, 2689-99	7	28
238	MALDI-MS in Protein Chemistry and Proteomics 2013 , 105-131		
237	Mapping of p140Cap phosphorylation sites: the EPLYA and EGLYA motifs have a key role in tyrosine phosphorylation and Csk binding, and are substrates of the Abl kinase. <i>PLoS ONE</i> , 2013 , 8, e54931	3.7	15
236	Effects of elaidic acid on lipid metabolism in HepG2 cells, investigated by an integrated approach of lipidomics, transcriptomics and proteomics. <i>PLoS ONE</i> , 2013 , 8, e74283	3.7	27
235	A computational model for histone mark propagation reproduces the distribution of heterochromatin in different human cell types. <i>PLoS ONE</i> , 2013 , 8, e73818	3.7	6
234	Reproducibility of mass spectrometry based protein profiles for diagnosis of ovarian cancer across clinical studies: A systematic review. <i>Journal of Proteomics</i> , 2012 , 75, 2758-72	3.9	12
233	Identification of a potential biomarker panel for the intake of the common dietary trans fat elaidic acid (trans- β -C18:1). <i>Journal of Proteomics</i> , 2012 , 75, 2685-96	3.9	7
232	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
231	Spatially resolved protein hydrogen exchange measured by subzero-cooled chip-based nanoelectrospray ionization tandem mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 4467-73	7.8	36
230	A probabilistic framework for peptide and protein quantification from data-dependent and data-independent LC-MS proteomics experiments. <i>OMICS A Journal of Integrative Biology</i> , 2012 , 16, 468-82	3.8	12
229	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
228	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

227	The influence of the fungal pathogen <i>Mycocentrospora acerina</i> on the proteome and polyacetylenes and 6-methoxymellein in organic and conventionally cultivated carrots (<i>Daucus carota</i>) during post harvest storage. <i>Journal of Proteomics</i> , 2012 , 75, 962-77	3.9	13
226	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
225	Identification and profiling of salinity stress-responsive proteins in <i>Sorghum bicolor</i> seedlings. <i>Journal of Proteomics</i> , 2012 , 75, 4139-50	3.9	71
224	Automated and high confidence protein phosphorylation site localization using complementary collision-activated dissociation and electron transfer dissociation tandem mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 9694-9	7.8	13
223	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
222	Quantitative proteomics of primary tumors with varying metastatic capabilities using stable isotope-labeled proteins of multiple histogenic origins. <i>Proteomics</i> , 2012 , 12, 2139-48	4.8	18
221	The <i>C. elegans</i> H3K27 demethylase UTX-1 is essential for normal development, independent of its enzymatic activity. <i>PLoS Genetics</i> , 2012 , 8, e1002647	6	50
220	Vesicular signalling and immune modulation as hedonic fingerprints: proteomic profiling in the chronic mild stress depression model. <i>Journal of Psychopharmacology</i> , 2012 , 26, 1569-83	4.6	22
219	CD163-L1 is an endocytic macrophage protein strongly regulated by mediators in the inflammatory response. <i>Journal of Immunology</i> , 2012 , 188, 2399-409	5.3	22
218	Functional domain analysis of the Remorin protein LjSYMREM1 in <i>Lotus japonicus</i> . <i>PLoS ONE</i> , 2012 , 7, e30817	3.7	69
217	Identification of markers associated with highly aggressive metastatic phenotypes using quantitative comparative proteomics. <i>Cancer Genomics and Proteomics</i> , 2012 , 9, 265-73	3.3	14
216	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
215	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
214	Quantitative profiling of PE, MMPE, DMPE, and PC lipid species by multiple precursor ion scanning: a tool for monitoring PE metabolism. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2011 , 1811, 1081-9	5	27
213	Human inter- α -inhibitor is a substrate for factor XIIIa and tissue transglutaminase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 1624-30	4	7
212	Quantitative proteomics by 2DE and MALDI MS/MS uncover the effects of organic and conventional cropping methods on vegetable products. <i>Journal of Proteomics</i> , 2011 , 74, 2810-25	3.9	23
211	Autophosphorylation is essential for the in vivo function of the <i>Lotus japonicus</i> 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
210	Analytical strategies in mass spectrometry-based phosphoproteomics. <i>Methods in Molecular Biology</i> , 2011 , 753, 183-213	1.4	16

209	Development of novel monoclonal antibodies that define differentiation stages of human stromal (mesenchymal) stem cells. <i>Molecules and Cells</i> , 2011 , 32, 133-42	3.5	13
208	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
207	Time-resolved quantitative proteome analysis of in vivo intestinal development. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.005231	7.6	20
206	Characterization of human myotubes from type 2 diabetic and nondiabetic subjects using complementary quantitative mass spectrometric methods. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006650	7.6	34
205	PTB-associated splicing factor (PSF) functions as a repressor of STAT6-mediated Ig epsilon gene transcription by recruitment of HDAC1. <i>Journal of Biological Chemistry</i> , 2011 , 286, 3451-9	5.4	19
204	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
203	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
202	Transfer-messenger RNA controls the translation of cell-cycle and stress proteins in <i>Streptomyces</i> . <i>EMBO Reports</i> , 2010 , 11, 119-25	6.5	19
201	Ø-Syntrophin is a Cdk5 substrate that restrains the motility of insulin secretory granules. <i>PLoS ONE</i> , 2010 , 5, e12929	3.7	32
200	Quantitative proteomics analysis of <i>Streptomyces coelicolor</i> development demonstrates that onset of secondary metabolism coincides with hypha differentiation. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1423-36	7.6	36
199	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
198	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
197	Serum peptide/protein profiling by mass spectrometry provides diagnostic information independently of CA125 in women with an ovarian tumor. <i>Cancer Biomarkers</i> , 2010 , 6, 73-82	3.8	4
196	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
195	Loss of ammonia during electron-transfer dissociation of deuterated peptides as an inherent gauge of gas-phase hydrogen scrambling. <i>Analytical Chemistry</i> , 2010 , 82, 9755-62	7.8	37
194	Quantitative proteome analysis of <i>Streptomyces coelicolor</i> Nonsporulating liquid cultures demonstrates a complex differentiation process comparable to that occurring in sporulating solid cultures. <i>Journal of Proteome Research</i> , 2010 , 9, 4801-11	5.6	31
193	Optimized IMAC-IMAC protocol for phosphopeptide recovery from complex biological samples. <i>Journal of Proteome Research</i> , 2010 , 9, 3561-73	5.6	100
192	Identification of salt-tolerant <i>Sinorhizobium</i> sp. strain BL3 membrane proteins based on proteomics. <i>Microbes and Environments</i> , 2010 , 25, 275-80	2.6	2

191	Phosphorylation of mouse serine racemase regulates D-serine synthesis. <i>FEBS Letters</i> , 2010 , 584, 2937-44	3.8	31
190	LmxMPK4, an essential mitogen-activated protein kinase of <i>Leishmania mexicana</i> is phosphorylated and activated by the STE7-like protein kinase LmxMKK5. <i>International Journal for Parasitology</i> , 2010 , 40, 969-78	4.3	20
189	Characterization of sialylated and fucosylated glycopeptides of beta2-glycoprotein I by a combination of HILIC LC and MALDI MS/MS. <i>Journal of Separation Science</i> , 2010 , 33, 891-902	3.4	22
188	Modification-specific proteomics in plant biology. <i>Journal of Proteomics</i> , 2010 , 73, 2249-66	3.9	61
187	Proteomics and the dynamic plasma membrane: Quo Vadis?. <i>Proteomics</i> , 2010 , 10, 3997-4011	4.8	17
186	Dynamic histone H3 epigenome marking during the intraerythrocytic cycle of <i>Plasmodium falciparum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9655-60	11.5	162
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