

Kris Gevaert

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4424548/kris-gevaert-publications-by-citations.pdf>

Version: 2024-04-27

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

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

404
papers

20,922
citations

79
h-index

125
g-index

441
ext. papers

24,880
ext. citations

8
avg, IF

6.63
L-index

#	Paper	IF	Citations
404	Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides. <i>Nature Biotechnology</i> , 2003 , 21, 566-9	44.5	507
403	Improved visualization of protein consensus sequences by iceLogo. <i>Nature Methods</i> , 2009 , 6, 786-7	21.6	496
402	PRIDE: the proteomics identifications database. <i>Proteomics</i> , 2005 , 5, 3537-45	4.8	454
401	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013 , 41, D246-51	20.1	400
400	Proteomics analyses reveal the evolutionary conservation and divergence of N-terminal acetyltransferases from yeast and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 8157-62	11.5	368
399	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016 , 531, 518-22	50.4	355
398	Global analysis of the mitochondrial N-proteome identifies a processing peptidase critical for protein stability. <i>Cell</i> , 2009 , 139, 428-39	56.2	351
397	Cdc42 induces filopodia by promoting the formation of an IRSp53:Mena complex. <i>Current Biology</i> , 2001 , 11, 1645-55	6.3	308
396	Morphological and biochemical characterization of a human liver in a uPA-SCID mouse chimera. <i>Hepatology</i> , 2005 , 41, 847-56	11.2	301
395	Protein identification methods in proteomics. <i>Electrophoresis</i> , 2000 , 21, 1145-54	3.6	289
394	The serine protease Omi/HtrA2 is released from mitochondria during apoptosis. Omi interacts with caspase-inhibitor XIAP and induces enhanced caspase activity. <i>Cell Death and Differentiation</i> , 2002 , 9, 20-6	12.7	270
393	LRRK2 controls an EndoA phosphorylation cycle in synaptic endocytosis. <i>Neuron</i> , 2012 , 75, 1008-21	13.9	261
392	Endonuclease G: a mitochondrial protein released in apoptosis and involved in caspase-independent DNA degradation. <i>Cell Death and Differentiation</i> , 2001 , 8, 1136-42	12.7	260
391	The miR-17-92 microRNA cluster regulates multiple components of the TGF- β pathway in neuroblastoma. <i>Molecular Cell</i> , 2010 , 40, 762-73	17.6	247
390	PINK1 loss-of-function mutations affect mitochondrial complex I activity via NdufA10 ubiquinone uncoupling. <i>Science</i> , 2014 , 344, 203-7	33.3	238
389	Caspase-14 protects against epidermal UVB photodamage and water loss. <i>Nature Cell Biology</i> , 2007 , 9, 666-74	23.4	234
388	Rac/Cdc42 and p65PAK regulate the microtubule-destabilizing protein stathmin through phosphorylation at serine 16. <i>Journal of Biological Chemistry</i> , 2001 , 276, 1677-80	5.4	223

387	Targeted peptidecentric proteomics reveals caspase-7 as a substrate of the caspase-1 inflammasomes. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2350-63	7.6	221
386	The deubiquitinase USP15 antagonizes Parkin-mediated mitochondrial ubiquitination and mitophagy. <i>Human Molecular Genetics</i> , 2014 , 23, 5227-42	5.6	204
385	Parkin interacts with Ambra1 to induce mitophagy. <i>Journal of Neuroscience</i> , 2011 , 31, 10249-61	6.6	204
384	Protein N-terminal acetyltransferases: when the start matters. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 152-61	10.3	199
383	Caspase-specific and nonspecific in vivo protein processing during Fas-induced apoptosis. <i>Nature Methods</i> , 2005 , 2, 771-7	21.6	195
382	Chromatographic isolation of methionine-containing peptides for gel-free proteome analysis: identification of more than 800 Escherichia coli proteins. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 896-903	7.6	191
381	Identification of a novel mechanism of blood-brain communication during peripheral inflammation via choroid plexus-derived extracellular vesicles. <i>EMBO Molecular Medicine</i> , 2016 , 8, 1162-1183	12	184
380	The TPLATE adaptor complex drives clathrin-mediated endocytosis in plants. <i>Cell</i> , 2014 , 156, 691-704	56.2	167
379	T-cell receptor-induced JNK activation requires proteolytic inactivation of CYLD by MALT1. <i>EMBO Journal</i> , 2011 , 30, 1742-52	13	165
378	Listeria monocytogenes impairs SUMOylation for efficient infection. <i>Nature</i> , 2010 , 464, 1192-5	50.4	162
377	Selecting protein N-terminal peptides by combined fractional diagonal chromatography. <i>Nature Protocols</i> , 2011 , 6, 1130-41	18.8	139
376	ANGUSTIFOLIA3 binds to SWI/SNF chromatin remodeling complexes to regulate transcription during Arabidopsis leaf development. <i>Plant Cell</i> , 2014 , 26, 210-29	11.6	138
375	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
374	Caspase-14 is required for filaggrin degradation to natural moisturizing factors in the skin. <i>Journal of Investigative Dermatology</i> , 2011 , 131, 2233-41	4.3	136
373	Sulfenome mining in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11545-50	11.5	131
372	Deep proteome coverage based on ribosome profiling aids mass spectrometry-based protein and peptide discovery and provides evidence of alternative translation products and near-cognate translation initiation events. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1780-90	7.6	131
371	The neural cell adhesion molecules L1 and CHL1 are cleaved by BACE1 protease in vivo. <i>Journal of Biological Chemistry</i> , 2012 , 287, 25927-40	5.4	130
370	Improved recovery of proteome-informative, protein N-terminal peptides by combined fractional diagonal chromatography (COFRADIC). <i>Proteomics</i> , 2008 , 8, 1362-70	4.8	128

369	Identification and functional characterization of N-terminally acetylated proteins in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2009 , 7, e1000236	9.7	125
368	NatF contributes to an evolutionary shift in protein N-terminal acetylation and is important for normal chromosome segregation. <i>PLoS Genetics</i> , 2011 , 7, e1002169	6	121
367	N-terminal acetylome analyses and functional insights of the N-terminal acetyltransferase NatB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 12449-54	11.5	121
366	The human platelet proteome mapped by peptide-centric proteomics: a functional protein profile. <i>Proteomics</i> , 2005 , 5, 3193-204	4.8	120
365	DBToolkit: processing protein databases for peptide-centric proteomics. <i>Bioinformatics</i> , 2005 , 21, 3584-5	5.2	120
364	Global differential non-gel proteomics by quantitative and stable labeling of tryptic peptides with oxygen-18. <i>Journal of Proteome Research</i> , 2004 , 3, 786-91	5.6	117
363	A plant plasma membrane H ⁺ -ATPase expressed in yeast is activated by phosphorylation at its penultimate residue and binding of 14-3-3 regulatory proteins in the absence of fusicoccin. <i>Journal of Biological Chemistry</i> , 2000 , 275, 17762-70	5.4	115
362	Confounding factors of ultrafiltration and protein analysis in extracellular vesicle research. <i>Scientific Reports</i> , 2017 , 7, 2704	4.9	112
361	LRRK2 functions in synaptic vesicle endocytosis through a kinase-dependent mechanism. <i>Journal of Cell Science</i> , 2015 , 128, 541-52	5.3	112
360	Citrullinated glucose-regulated protein 78 is an autoantigen in type 1 diabetes. <i>Diabetes</i> , 2015 , 64, 573-8	6.9	111
359	Stable isotopic labeling in proteomics. <i>Proteomics</i> , 2008 , 8, 4873-85	4.8	110
358	Toll-like Receptor 4 Engagement on Dendritic Cells Restrains Phago-Lysosome Fusion and Promotes Cross-Presentation of Antigens. <i>Immunity</i> , 2015 , 43, 1087-100	32.3	108
357	Analysis of the gamma-secretase interactome and validation of its association with tetraspanin-enriched microdomains. <i>Nature Cell Biology</i> , 2009 , 11, 1340-6	23.4	108
356	Listeria comet tails: the actin-based motility machinery at work. <i>Trends in Cell Biology</i> , 2008 , 18, 220-7	18.3	108
355	Redox proteomics of protein-bound methionine oxidation. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006866	7.6	103
354	Proteome-wide Identification of HtrA2/Omi Substrates. <i>Journal of Proteome Research</i> , 2007 , 6, 1006-15	5.6	101
353	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019 , 5, 316-327	11.5	100
352	Large-scale identification of N-terminal peptides in the halophilic archaea <i>Halobacterium salinarum</i> and <i>Natronomonas pharaonis</i> . <i>Journal of Proteome Research</i> , 2007 , 6, 2195-204	5.6	100

351	Proteome-derived peptide libraries allow detailed analysis of the substrate specificities of N(alpha)-acetyltransferases and point to hNaa10p as the post-translational actin N(alpha)-acetyltransferase. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.004580	7.6	99
350	Damage on plants activates Ca-dependent metacaspases for release of immunomodulatory peptides. <i>Science</i> , 2019 , 363,	33.3	98
349	FYVE1/FREE1 Interacts with the PYL4 ABA Receptor and Mediates Its Delivery to the Vacuolar Degradation Pathway. <i>Plant Cell</i> , 2016 , 28, 2291-2311	11.6	97
348	Proteome analysis of the Chlamydia pneumoniae elementary body. <i>Electrophoresis</i> , 2001 , 22, 1204-23	3.6	95
347	SitePredicting the cleavage of proteinase substrates. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 319-23	10.3	94
346	The ROS Wheel: Refining ROS Transcriptional Footprints. <i>Plant Physiology</i> , 2016 , 171, 1720-33	6.6	92
345	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010 , 7, 512-5	21.6	92
344	An improved toolbox to unravel the plant cellular machinery by tandem affinity purification of Arabidopsis protein complexes. <i>Nature Protocols</i> , 2015 , 10, 169-87	18.8	90
343	Analysis of protein processing by N-terminal proteomics reveals novel species-specific substrate determinants of granzyme B orthologs. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 258-72	7.6	90
342	The Arabidopsis metacaspase9 degradome. <i>Plant Cell</i> , 2013 , 25, 2831-47	11.6	89
341	A protein phosphatase 2A complex spatially controls plant cell division. <i>Nature Communications</i> , 2013 , 4, 1863	17.4	88
340	Reversible labeling of cysteine-containing peptides allows their specific chromatographic isolation for non-gel proteome studies. <i>Proteomics</i> , 2004 , 4, 897-908	4.8	88
339	Multiple mechanisms limit meiotic crossovers: TOP3 and two BLM homologs antagonize crossovers in parallel to FANCM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 4713-8	11.5	87
338	The chaperone-like protein HYPK acts together with NatA in cotranslational N-terminal acetylation and prevention of Huntingtin aggregation. <i>Molecular and Cellular Biology</i> , 2010 , 30, 1898-909	4.8	87
337	Mutations in LZTR1 drive human disease by dysregulating RAS ubiquitination. <i>Science</i> , 2018 , 362, 1177-1183	13.3	87
336	Protein Language: Post-Translational Modifications Talking to Each Other. <i>Trends in Plant Science</i> , 2018 , 23, 1068-1080	13.1	87
335	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015 , 27, 1605-19	11.6	86
334	Matrix metalloproteinase 13 modulates intestinal epithelial barrier integrity in inflammatory diseases by activating TNF. <i>EMBO Molecular Medicine</i> , 2013 , 5, 1000-16	12	86

333	Tumor necrosis factor-induced modulation of glyoxalase I activities through phosphorylation by PKA results in cell death and is accompanied by the formation of a specific methylglyoxal-derived AGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 949-54	11.5	86
332	Genetic predisposition for beta cell fragility underlies type 1 and type 2 diabetes. <i>Nature Genetics</i> , 2016 , 48, 519-27	36.3	83
331	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018 , 28, 866-880.e15	24.6	83
330	NAA80 is actin@N-terminal acetyltransferase and regulates cytoskeleton assembly and cell motility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4399-4404	11.5	82
329	Synaptogyrin-3 Mediates Presynaptic Dysfunction Induced by Tau. <i>Neuron</i> , 2018 , 97, 823-835.e8	13.9	80
328	Chronic Kidney Disease Circulating Calciprotein Particles and Extracellular Vesicles Promote Vascular Calcification: A Role for GRP (Gla-Rich Protein). <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018 , 38, 575-587	9.4	79
327	Small heat-shock protein HSPB1 mutants stabilize microtubules in Charcot-Marie-Tooth neuropathy. <i>Journal of Neuroscience</i> , 2011 , 31, 15320-8	6.6	79
326	A la carte proteomics with an emphasis on gel-free techniques. <i>Proteomics</i> , 2007 , 7, 2698-718	4.8	79
325	Vpr content of HIV-1 virions determines infection of resting peripheral blood CD4+ lymphocytes. <i>Retrovirology</i> , 2013 , 10,	3.6	78
324	The human N-alpha-acetyltransferase 40 (hNaa40p/hNatD) is conserved from yeast and N-terminally acetylates histones H2A and H4. <i>PLoS ONE</i> , 2011 , 6, e24713	3.7	77
323	Cysteines under ROS attack in plants: a proteomics view. <i>Journal of Experimental Botany</i> , 2015 , 66, 2935-44	4.4	76
322	In vitro and in vivo protein-bound tyrosine nitration characterized by diagonal chromatography. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2642-52	7.6	76
321	A matrix-assisted laser desorption ionization post-source decay (MALDI-PSD) analysis of proteins released from isolated liver mitochondria treated with recombinant truncated Bid. <i>Cell Death and Differentiation</i> , 2002 , 9, 301-8	12.7	76
320	clAP1/2 are direct E3 ligases conjugating diverse types of ubiquitin chains to receptor interacting proteins kinases 1 to 4 (RIP1-4). <i>PLoS ONE</i> , 2011 , 6, e22356	3.7	74
319	Comparative proteome analysis of Chlamydia trachomatis serovar A, D and L2. <i>Proteomics</i> , 2002 , 2, 164-86	4.8	73
318	An organellar N-acetyltransferase, naa60, acetylates cytosolic N termini of transmembrane proteins and maintains Golgi integrity. <i>Cell Reports</i> , 2015 , 10, 1362-74	10.6	71
317	A Repressor Protein Complex Regulates Leaf Growth in Arabidopsis. <i>Plant Cell</i> , 2015 , 27, 2273-87	11.6	71
316	Proteome studies of bacterial antibiotic resistance mechanisms. <i>Journal of Proteomics</i> , 2014 , 97, 88-99	3.9	70

315	Constitutively active UVR8 photoreceptor variant in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 20326-31	11.5	70
314	Variable Glutamine-Rich Repeats Modulate Transcription Factor Activity. <i>Molecular Cell</i> , 2015 , 59, 615-27	7.6	69
313	Protein Methionine Sulfoxide Dynamics in Arabidopsis thaliana under Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1217-29	7.6	68
312	Proteomic Identification of Cysteine Cathepsin Substrates Shed from the Surface of Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2213-28	7.6	68
311	The deubiquitylase USP33 discriminates between RALB functions in autophagy and innate immune response. <i>Nature Cell Biology</i> , 2013 , 15, 1220-30	23.4	68
310	Improving the reliability and throughput of mass spectrometry-based proteomics by spectrum quality filtering. <i>Proteomics</i> , 2006 , 6, 2086-94	4.8	68
309	Zebrafish Collagen Type I: Molecular and Biochemical Characterization of the Major Structural Protein in Bone and Skin. <i>Scientific Reports</i> , 2016 , 6, 21540	4.9	67
308	A nanobody targeting the F-actin capping protein CapG restrains breast cancer metastasis. <i>Breast Cancer Research</i> , 2013 , 15, R116	8.3	67
307	GRIM REAPER peptide binds to receptor kinase PRK5 to trigger cell death in Arabidopsis. <i>EMBO Journal</i> , 2015 , 34, 55-66	13	66
306	Recessive osteogenesis imperfecta caused by LEPRE1 mutations: clinical documentation and identification of the splice form responsible for prolyl 3-hydroxylation. <i>Journal of Medical Genetics</i> , 2009 , 46, 233-41	5.8	66
305	Biochemical and cellular analysis of Ogden syndrome reveals downstream Nt-acetylation defects. <i>Human Molecular Genetics</i> , 2015 , 24, 1956-76	5.6	65
304	ms_lims, a simple yet powerful open source laboratory information management system for MS-driven proteomics. <i>Proteomics</i> , 2010 , 10, 1261-4	4.8	65
303	Cells lacking F-actin are genetically reprogrammed and maintain conditional migratory capacity. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 255-71	7.6	64
302	A novel approach to analyze lysosomal dysfunctions through subcellular proteomics and lipidomics: the case of NPC1 deficiency. <i>Scientific Reports</i> , 2017 , 7, 41408	4.9	63
301	Protein alpha-N-acetylation studied by N-terminomics. <i>FEBS Journal</i> , 2011 , 278, 3822-34	5.7	63
300	Diagonal reverse-phase chromatography applications in peptide-centric proteomics: ahead of catalogue-omics?. <i>Analytical Biochemistry</i> , 2005 , 345, 18-29	3.1	63
299	A peptide concentration and purification method for protein characterization in the subpicomole range using matrix assisted laser desorption/ionization-postsorce decay (MALDI-PSD) sequencing. <i>Electrophoresis</i> , 1998 , 19, 909-17	3.6	62
298	The MAGUK protein MPP7 binds to the polarity protein hDlg1 and facilitates epithelial tight junction formation. <i>Molecular Biology of the Cell</i> , 2007 , 18, 1744-55	3.5	62

297	Characterization of a secreted Chlamydia protease. <i>Cellular Microbiology</i> , 2002 , 4, 411-24	3.9	61
296	Global phosphoproteome analysis on human HepG2 hepatocytes using reversed-phase diagonal LC. <i>Proteomics</i> , 2005 , 5, 3589-99	4.8	61
295	Protein identification based on matrix assisted laser desorption/ionization-post source decay-mass spectrometry. <i>Electrophoresis</i> , 2001 , 22, 1645-51	3.6	61
294	The mTOR and PP2A Pathways Regulate PHD2 Phosphorylation to Fine-Tune HIF1 α Levels and Colorectal Cancer Cell Survival under Hypoxia. <i>Cell Reports</i> , 2017 , 18, 1699-1712	10.6	60
293	Mining for protein S-sulfenylation in uncovers redox-sensitive sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21256-21261	11.5	59
292	DYn-2 Based Identification of Arabidopsis Sulfenomes. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1183-200	200	58
291	Angiotensin I-converting enzyme inhibitory activity of gelatin hydrolysates and identification of bioactive peptides. <i>Journal of Agricultural and Food Chemistry</i> , 2011 , 59, 552-8	5.7	58
290	Proteome-wide substrate analysis indicates substrate exclusion as a mechanism to generate caspase-7 versus caspase-3 specificity. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2700-14	7.6	57
289	Proteome-wide characterization of N-glycosylation events by diagonal chromatography. <i>Journal of Proteome Research</i> , 2006 , 5, 2438-47	5.6	56
288	Structural analysis and identification of gel-purified proteins, available in the femtomole range, using a novel computer program for peptide sequence assignment, by matrix-assisted laser desorption ionization-reflectron time-of-flight-mass spectrometry. <i>Electrophoresis</i> , 1996 , 17, 918-24	3.6	56
287	Feeling the Heat: Searching for Plant Thermosensors. <i>Trends in Plant Science</i> , 2019 , 24, 210-219	13.1	56
286	CEP5 and XIP1/CEPR1 regulate lateral root initiation in Arabidopsis. <i>Journal of Experimental Botany</i> , 2016 , 67, 4889-99	7	54
285	It's Time for Some "Site"-Seeing: Novel Tools to Monitor the Ubiquitin Landscape in Arabidopsis thaliana. <i>Plant Cell</i> , 2016 , 28, 6-16	11.6	54
284	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019 , 10, 3288	17.4	54
283	A proteogenomics approach integrating proteomics and ribosome profiling increases the efficiency of protein identification and enables the discovery of alternative translation start sites. <i>Proteomics</i> , 2014 , 14, 2688-98	4.8	54
282	Plant proteins under oxidative attack. <i>Proteomics</i> , 2013 , 13, 932-40	4.8	52
281	MS-driven protease substrate degradomics. <i>Proteomics</i> , 2010 , 10, 1284-96	4.8	52
280	A review of COFRADIC techniques targeting protein N-terminal acetylation. <i>BMC Proceedings</i> , 2009 , 3 Suppl 6, S6	2.3	51

279	Peptides adsorbed on reverse-phase chromatographic beads as targets for femtomole sequencing by post-source decay matrix assisted laser desorption ionization-reflectron time of flight mass spectrometry (MALDI-RETOF-MS). <i>Electrophoresis</i> , 1997 , 18, 2950-60	3.6	51
278	Positional proteomics reveals differences in N-terminal proteoform stability. <i>Molecular Systems Biology</i> , 2016 , 12, 858	12.2	51
277	The RING E3 Ligase KEEP ON GOING Modulates JASMONATE ZIM-DOMAIN12 Stability. <i>Plant Physiology</i> , 2015 , 169, 1405-17	6.6	50
276	Diversity in protein glycosylation among insect species. <i>PLoS ONE</i> , 2011 , 6, e16682	3.7	50
275	The Plant PTM Viewer, a central resource for exploring plant protein modifications. <i>Plant Journal</i> , 2019 , 99, 752-762	6.9	49
274	A complex interaction pattern of CIS and SOCS2 with the leptin receptor. <i>Journal of Cell Science</i> , 2006 , 119, 2214-24	5.3	49
273	A quantitative proteomics design for systematic identification of protease cleavage events. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2327-33	7.6	48
272	Do we want our data raw? Including binary mass spectrometry data in public proteomics data repositories. <i>Proteomics</i> , 2005 , 5, 3501-5	4.8	48
271	Look Closely, the Beautiful May Be Small: Precursor-Derived Peptides in Plants. <i>Annual Review of Plant Biology</i> , 2019 , 70, 153-186	30.7	48
270	The transcriptional repressor Glis2 is a novel binding partner for p120 catenin. <i>Molecular Biology of the Cell</i> , 2007 , 18, 1918-27	3.5	46
269	De novo design of a biologically active amyloid. <i>Science</i> , 2016 , 354,	33.3	44
268	Bioinformatics analysis of a <i>Saccharomyces cerevisiae</i> N-terminal proteome provides evidence of alternative translation initiation and post-translational N-terminal acetylation. <i>Journal of Proteome Research</i> , 2011 , 10, 3578-89	5.6	44
267	Peptizer, a tool for assessing false positive peptide identifications and manually validating selected results. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2364-72	7.6	44
266	MascotDatfile: an open-source library to fully parse and analyse MASCOT MS/MS search results. <i>Proteomics</i> , 2007 , 7, 364-6	4.8	44
265	An agarose-based gel-concentration system for microsequence and mass spectrometric characterization of proteins previously purified in polyacrylamide gels starting at low picomole levels. <i>FEBS Journal</i> , 1995 , 230, 258-65		44
264	C-terminomics: Targeted analysis of natural and posttranslationally modified protein and peptide C-termini. <i>Proteomics</i> , 2015 , 15, 903-14	4.8	43
263	Distinct branches of the N-end rule pathway modulate the plant immune response. <i>New Phytologist</i> , 2019 , 221, 988-1000	9.8	42
262	Mapping proteolytic processing in the secretome of gastric cancer-associated myofibroblasts reveals activation of MMP-1, MMP-2, and MMP-3. <i>Journal of Proteome Research</i> , 2013 , 12, 3413-22	5.6	42

261	FIGL1 and its novel partner FLIP form a conserved complex that regulates homologous recombination. <i>PLoS Genetics</i> , 2018 , 14, e1007317	6	42
260	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	41
259	Disruption of endocytosis through chemical inhibition of clathrin heavy chain function. <i>Nature Chemical Biology</i> , 2019 , 15, 641-649	11.7	41
258	A COFRADIC protocol to study protein ubiquitination. <i>Journal of Proteome Research</i> , 2014 , 13, 3107-13	5.6	41
257	Identification of Chlamydia trachomatis CT621, a protein delivered through the type III secretion system to the host cell cytoplasm and nucleus. <i>FEMS Immunology and Medical Microbiology</i> , 2009 , 57, 46-58		41
256	Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. <i>Journal of Proteome Research</i> , 2016 , 15, 4304-4317	5.6	40
255	Peptide-level Robust Ridge Regression Improves Estimation, Sensitivity, and Specificity in Data-dependent Quantitative Label-free Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 657-68	7.6	40
254	Interaction of the tobacco lectin with histone proteins. <i>Plant Physiology</i> , 2011 , 155, 1091-102	6.6	40
253	Rover: a tool to visualize and validate quantitative proteomics data from different sources. <i>Proteomics</i> , 2010 , 10, 1226-9	4.8	39
252	Vaccination with an <i>Ostertagia ostertagi</i> polyprotein allergen protects calves against homologous challenge infection. <i>Infection and Immunity</i> , 2004 , 72, 2995-3001	3.7	39
251	The expression, processing and localization of polymorphic membrane proteins in <i>Chlamydia pneumoniae</i> strain CWL029. <i>BMC Microbiology</i> , 2002 , 2, 36	4.5	39
250	EXPANSIN A1-mediated radial swelling of pericycle cells positions anticlinal cell divisions during lateral root initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 8597-8602	11.5	38
249	Experimental design and data-analysis in label-free quantitative LC/MS proteomics: A tutorial with MSqRob. <i>Journal of Proteomics</i> , 2018 , 171, 23-36	3.9	38
248	The non-JAZ TIFY protein TIFY8 from <i>Arabidopsis thaliana</i> is a transcriptional repressor. <i>PLoS ONE</i> , 2014 , 9, e84891	3.7	38
247	Caspase substrates: easily caught in deep waters?. <i>Trends in Biotechnology</i> , 2009 , 27, 680-8	15.1	38
246	Vaccination against <i>Ostertagia ostertagi</i> with subfractions of the protective ES-thiol fraction. <i>Veterinary Parasitology</i> , 2007 , 149, 239-45	2.8	38
245	Identification and characterization of immunogenic proteins of <i>Mycoplasma genitalium</i> . <i>Vaccine Journal</i> , 2006 , 13, 913-22		38
244	Improved tandem mass spectrometric characterization of 3-nitrotyrosine sites in peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 2885-93	2.2	38

243	Activation-associated secreted proteins are the most abundant antigens in a host protective fraction from <i>Ostertagia ostertagi</i> . <i>Molecular and Biochemical Parasitology</i> , 2003 , 128, 111-4	1.9	38
242	A fast and convenient MALDI-MS based proteomic approach: identification of components scaffolded by the actin cytoskeleton of activated human thrombocytes. <i>Journal of Biotechnology</i> , 2000 , 78, 259-69	3.7	38
241	DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. <i>ELife</i> , 2018 , 7,	8.9	38
240	Mechanistic insight into taxol-induced cell death. <i>Oncogene</i> , 2008 , 27, 4580-91	9.2	37
239	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
238	Thermo-msf-parser: an open source Java library to parse and visualize Thermo Proteome Discoverer msf files. <i>Journal of Proteome Research</i> , 2011 , 10, 3840-3	5.6	36
237	The calcium-binding protein p54/NEFA is a novel luminal resident of medial Golgi cisternae that traffics independently of mannosidase II. <i>European Journal of Cell Biology</i> , 2002 , 81, 87-100	6.1	36
236	Functional characterization of the Arabidopsis transcription factor bZIP29 reveals its role in leaf and root development. <i>Journal of Experimental Botany</i> , 2016 , 67, 5825-5840	7	36
235	Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020 , 77, 927-929	17.6	35
234	A <i>Saccharomyces cerevisiae</i> model reveals in vivo functional impairment of the Ogden syndrome N-terminal acetyltransferase NAA10 Ser37Pro mutant. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2031-41	7.6	35
233	N-terminal acetylome analysis reveals the specificity of Naa50 (Nat5) and suggests a kinetic competition between N-terminal acetyltransferases and methionine aminopeptidases. <i>Proteomics</i> , 2015 , 15, 2436-46	4.8	34
232	Protein processing and other modifications analyzed by diagonal peptide chromatography. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 1801-10	4	34
231	Strigolactones, karrikins and beyond. <i>Plant, Cell and Environment</i> , 2017 , 40, 1691-1703	8.4	33
230	Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S. <i>Proteomics</i> , 2015 , 15, 2479-90	4.8	33
229	Degradomics reveals that cleavage specificity profiles of caspase-2 and effector caspases are alike. <i>Journal of Biological Chemistry</i> , 2012 , 287, 33983-95	5.4	33
228	N-terminal acetylation and other functions of N-acetyltransferases. <i>Biological Chemistry</i> , 2012 , 393, 291-8	4.5	32
227	Proteome-derived peptide libraries to study the substrate specificity profiles of carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2096-110	7.6	32
226	Human and mouse granzyme M display divergent and species-specific substrate specificities. <i>Biochemical Journal</i> , 2011 , 437, 431-42	3.8	32

225	A novel strategy for the comprehensive analysis of the biomolecular composition of isolated plasma membranes. <i>Molecular Systems Biology</i> , 2011 , 7, 541	12.2	32
224	The substrate specificity profile of human granzyme A. <i>Biological Chemistry</i> , 2010 , 391, 983-97	4.5	32
223	Protein aggregation as an antibiotic design strategy. <i>Molecular Microbiology</i> , 2016 , 99, 849-65	4.1	32
222	N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1064-1080	7.6	31
221	The proteome under translational control. <i>Proteomics</i> , 2014 , 14, 2647-62	4.8	31
220	Structural investigation of B-Raf paradox breaker and inducer inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 1818-31	8.3	31
219	Effect of phospholipid molecular structure on its interaction with whey proteins in aqueous solution. <i>Food Hydrocolloids</i> , 2013 , 32, 312-321	10.6	31
218	Abolition of stress-induced protein synthesis sensitizes leukemia cells to anthracycline-induced death. <i>Blood</i> , 2008 , 111, 2866-77	2.2	31
217	Glutaredoxin GRXS17 Associates with the Cytosolic Iron-Sulfur Cluster Assembly Pathway. <i>Plant Physiology</i> , 2016 , 172, 858-873	6.6	31
216	Contemporary positional proteomics strategies to study protein processing. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 66-72	9.7	30
215	Chitinase-like proteins are candidate biomarkers for sepsis-induced acute kidney injury. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.013094	7.6	30
214	Trapping mammalian protein complexes in viral particles. <i>Nature Communications</i> , 2016 , 7, 11416	17.4	30
213	Exploring the protein-protein interaction landscape in plants. <i>Plant, Cell and Environment</i> , 2019 , 42, 387-409	8.1	30
212	Proteomics methods to study methionine oxidation. <i>Mass Spectrometry Reviews</i> , 2014 , 33, 147-56	11	29
211	High entomotoxicity and mechanism of the fungal GalNAc/Gal-specific <i>Rhizoctonia solani</i> lectin in pest insects. <i>Journal of Insect Physiology</i> , 2013 , 59, 295-305	2.4	29
210	Ectopic application of the repressive histone modification H3K9me2 establishes post-zygotic reproductive isolation in. <i>Genes and Development</i> , 2017 , 31, 1272-1287	12.6	29
209	Glycosylation signatures in <i>Drosophila</i> : fishing with lectins. <i>Journal of Proteome Research</i> , 2010 , 9, 3235-42	4.2	29
208	SnRK2 Protein Kinases and mRNA Decapping Machinery Control Root Development and Response to Salt. <i>Plant Physiology</i> , 2020 , 182, 361-377	6.6	29

207	The iceLogo web server and SOAP service for determining protein consensus sequences. <i>Nucleic Acids Research</i> , 2015 , 43, W543-6	20.1	28
206	ADAM30 Downregulates APP-Linked Defects Through Cathepsin D Activation in Alzheimer@ Disease. <i>EBioMedicine</i> , 2016 , 9, 278-292	8.8	28
205	PP2A-3 interacts with ACR4 and regulates formative cell division in the Arabidopsis root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1447-52	11.5	28
204	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017 , 7, 4676	4.9	28
203	Four stage liquid chromatographic selection of methionyl peptides for peptide-centric proteome analysis: the proteome of human multipotent adult progenitor cells. <i>Journal of Proteome Research</i> , 2006 , 5, 1415-28	5.6	28
202	A new functional, chemical proteomics technology to identify purine nucleotide binding sites in complex proteomes. <i>Journal of Proteome Research</i> , 2006 , 5, 3438-45	5.6	28
201	Investigation of rifampicin resistance mechanisms in <i>Brucella abortus</i> using MS-driven comparative proteomics. <i>Journal of Proteome Research</i> , 2012 , 11, 2374-85	5.6	27
200	The Whats, the Wheres and the Hows of strigolactone action in the roots. <i>Planta</i> , 2016 , 243, 1327-37	4.7	26
199	Developmental Plasticity at High Temperature. <i>Plant Physiology</i> , 2019 , 181, 399-411	6.6	26
198	Probing the efficiency of proteolytic events by positional proteomics. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003301	7.6	26
197	A protein-protein interaction map of the TNF-induced NF- κ B signal transduction pathway. <i>Scientific Data</i> , 2018 , 5, 180289	8.2	26
196	The transcriptional repressor complex FRS7-FRS12 regulates flowering time and growth in Arabidopsis. <i>Nature Communications</i> , 2017 , 8, 15235	17.4	25
195	NBPF1, a tumor suppressor candidate in neuroblastoma, exerts growth inhibitory effects by inducing a G1 cell cycle arrest. <i>BMC Cancer</i> , 2015 , 15, 391	4.8	25
194	A catalogue of putative HIV-1 protease host cell substrates. <i>Biological Chemistry</i> , 2012 , 393, 915-31	4.5	25
193	The actin propulsive machinery: the proteome of <i>Listeria monocytogenes</i> tails. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 375, 194-9	3.4	25
192	Implementation and application of a versatile clustering tool for tandem mass spectrometry data. <i>Proteomics</i> , 2007 , 7, 3245-58	4.8	25
191	A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <i>Proteomics</i> , 2006 , 6, 5076-86	4.8	25
190	Substrate specificities of the granzyme tryptases A and K. <i>Journal of Proteome Research</i> , 2014 , 13, 6067-76	3.6	24

189	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5587-92	11.5	24
188	Analysis of the transthyretin-like (TTL) gene family in <i>Ostertagia ostertagi</i> —comparison with other strongylid nematodes and <i>Caenorhabditis elegans</i> . <i>International Journal for Parasitology</i> , 2008 , 38, 1545-56	4.3	24
187	The Response of the Root Proteome to the Synthetic Strigolactone GR24 in <i>Arabidopsis</i> . <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2744-55	7.6	23
186	Taximin, a conserved plant-specific peptide is involved in the modulation of plant-specialized metabolism. <i>Plant Biotechnology Journal</i> , 2014 , 12, 971-83	11.6	23
185	Applications of diagonal chromatography for proteome-wide characterization of protein modifications and activity-based analyses. <i>FEBS Journal</i> , 2007 , 274, 6277-89	5.7	23
184	Compound A, a selective glucocorticoid receptor modulator, enhances heat shock protein Hsp70 gene promoter activation. <i>PLoS ONE</i> , 2013 , 8, e69115	3.7	23
183	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. <i>Journal of Proteome Research</i> , 2017 , 16, 2508-2515	5.6	22
182	C-terminomics screen for natural substrates of cytosolic carboxypeptidase 1 reveals processing of acidic protein C termini. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 177-90	7.6	22
181	<i>Arabidopsis thaliana</i> RNase H2 deficiency counteracts the needs for the WEE1 checkpoint kinase but triggers genome instability. <i>Plant Cell</i> , 2014 , 26, 3680-92	11.6	22
180	Early targets of miR-34a in neuroblastoma. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2114-31	7.6	22
179	Protein N-terminal acetyltransferases act as N-terminal propionyltransferases in vitro and in vivo. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 42-54	7.6	22
178	Natural substrates of plant proteases: how can protease degradomics extend our knowledge?. <i>Physiologia Plantarum</i> , 2012 , 145, 28-40	4.6	22
177	Analysis of proteins in <i>Chlamydia trachomatis</i> L2 outer membrane complex, COMC. <i>FEMS Immunology and Medical Microbiology</i> , 2009 , 55, 187-95		22
176	Assessing a novel microfluidic interface for shotgun proteome analyses. <i>Journal of Separation Science</i> , 2007 , 30, 1468-76	3.4	22
175	The proteome of the human neuroblastoma cell line SH-SY5Y: an enlarged proteome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008 , 1784, 983-5	4	22
174	A Role For Human N-alpha Acetyltransferase 30 (Naa30) in Maintaining Mitochondrial Integrity. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3361-3372	7.6	22
173	Xilmass: A New Approach toward the Identification of Cross-Linked Peptides. <i>Analytical Chemistry</i> , 2016 , 88, 9949-9957	7.8	21
172	Early mannitol-triggered changes in the <i>Arabidopsis</i> leaf (phospho)proteome reveal growth regulators. <i>Journal of Experimental Botany</i> , 2018 , 69, 4591-4607	7	21

171	SCX charge state selective separation of tryptic peptides combined with 2D-RP-HPLC allows for detailed proteome mapping. <i>Journal of Proteomics</i> , 2013 , 91, 164-71	3.9	21
170	The Apaf-1-binding protein Aven is cleaved by Cathepsin D to unleash its anti-apoptotic potential. <i>Cell Death and Differentiation</i> , 2012 , 19, 1435-45	12.7	21
169	Quantitative proteome profiling of <i>C. burnetii</i> under tetracycline stress conditions. <i>PLoS ONE</i> , 2012 , 7, e33599	3.7	21
168	Gender-enriched transcription of activation associated secreted proteins in <i>Ostertagia ostertagi</i> . <i>International Journal for Parasitology</i> , 2008 , 38, 455-65	4.3	21
167	Temperature-induced changes in the wheat phosphoproteome reveal temperature-regulated interconversion of phosphoforms. <i>Journal of Experimental Botany</i> , 2018 , 69, 4609-4624	7	21
166	Targeted Proteomics for Studying Pathogenic Bacteria. <i>Proteomics</i> , 2019 , 19, e1800435	4.8	20
165	Pick a Tag and Explore the Functions of Your Pet Protein. <i>Trends in Biotechnology</i> , 2019 , 37, 1078-1090	15.1	20
164	Improving the identification rate of endogenous peptides using electron transfer dissociation and collision-induced dissociation. <i>Journal of Proteome Research</i> , 2013 , 12, 5410-21	5.6	20
163	Development of an enzyme-linked immunosorbent assay for detection of cellular and in vivo LRRK2 S935 phosphorylation. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2013 , 76, 49-58	3.5	20
162	RIBAR and xRIBAR: Methods for reproducible relative MS/MS-based label-free protein quantification. <i>Journal of Proteome Research</i> , 2011 , 10, 3183-9	5.6	20
161	Novel techniques for identification and characterization of proteins loaded on gels in femtomole amounts. <i>The Protein Journal</i> , 1997 , 16, 335-42		20
160	Identification of Serpinb6b as a species-specific mouse granzyme A inhibitor suggests functional divergence between human and mouse granzyme A. <i>Journal of Biological Chemistry</i> , 2014 , 289, 9408-17	5.4	19
159	GalNAc/Gal-binding <i>Rhizoctonia solani</i> agglutinin has antiproliferative activity in <i>Drosophila melanogaster</i> S2 cells via MAPK and JAK/STAT signaling. <i>PLoS ONE</i> , 2012 , 7, e33680	3.7	19
158	A new approach for mapping sialylated N-glycosites in serum proteomes. <i>Journal of Proteome Research</i> , 2007 , 6, 4304-12	5.6	19
157	CYP707As are effectors of karrikin and strigolactone signalling pathways in <i>Arabidopsis thaliana</i> and parasitic plants. <i>Plant, Cell and Environment</i> , 2019 , 42, 2612-2626	8.4	18
156	Seed germination in parasitic plants: what insights can we expect from strigolactone research?. <i>Journal of Experimental Botany</i> , 2018 , 69, 2265-2280	7	18
155	Deregulation of focal adhesion formation and cytoskeletal tension due to loss of A-type lamins. <i>Cell Adhesion and Migration</i> , 2017 , 11, 447-463	3.2	18
154	A comparison of MS2-based label-free quantitative proteomic techniques with regards to accuracy and precision. <i>Proteomics</i> , 2011 , 11, 1110-3	4.8	18

153	Integrator restrains paraspeckles assembly by promoting isoform switching of the lncRNA. <i>Science Advances</i> , 2020 , 6, eaaz9072	14.3	17
152	Granzyme M targets topoisomerase II alpha to trigger cell cycle arrest and caspase-dependent apoptosis. <i>Cell Death and Differentiation</i> , 2014 , 21, 416-26	12.7	17
151	m-Calpain activation in vitro does not require autolysis or subunit dissociation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 864-72	4	17
150	Disentanglement of protease substrate repertoires. <i>Biological Chemistry</i> , 2008 , 389, 371-81	4.5	17
149	Selection of egg peptide biomarkers in processed food products by high resolution mass spectrometry. <i>Journal of Chromatography A</i> , 2019 , 1584, 115-125	4.5	17
148	SFINX: Straightforward Filtering Index for Affinity Purification-Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016 , 15, 332-8	5.6	16
147	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. <i>Nucleic Acids Research</i> , 2013 , 41, D333-7	20.1	16
146	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011 , 8, 481-3	21.6	16
145	Identification of potentially involved proteins in levofloxacin resistance mechanisms in <i>Coxiella burnetii</i> . <i>Journal of Proteome Research</i> , 2011 , 10, 756-62	5.6	16
144	Cell_motility: a cross-platform, open source application for the study of cell motion paths. <i>BMC Bioinformatics</i> , 2006 , 7, 289	3.6	16
143	An aspartyl protease inhibitor of <i>Ostertagia ostertagi</i> : molecular cloning, analysis of stage and tissue specific expression and vaccine trial. <i>Molecular and Biochemical Parasitology</i> , 2005 , 141, 81-8	1.9	16
142	Salmonella Typhi, Paratyphi A, Enteritidis and Typhimurium core proteomes reveal differentially expressed proteins linked to the cell surface and pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007416	4.8	15
141	N-Terminal Proteoforms in Human Disease. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 308-320	10.3	15
140	Combination of COFRADIC and high temperature-extended column length conventional liquid chromatography: a very efficient way to tackle complex protein samples, such as serum. <i>Journal of Separation Science</i> , 2007 , 30, 658-68	3.4	15
139	Evaluation of Encoded Layer-By-Layer Coated Microparticles As Protease Sensors. <i>Advanced Functional Materials</i> , 2008 , 18, 1624-1631	15.6	15
138	Identification by two-dimensional electrophoresis of a new adhesin expressed by a low-passaged strain of <i>Mycoplasma bovis</i> . <i>Research in Microbiology</i> , 2005 , 156, 713-8	4	15
137	Pollens destroy respiratory epithelial cell anchors and drive alphaherpesvirus infection. <i>Scientific Reports</i> , 2019 , 9, 4787	4.9	14
136	Resolution of protein structure by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2016 , 35, 653-665	11	14

135	A phylogenetic approach to study the origin and evolution of the CRINKLY4 family. <i>Frontiers in Plant Science</i> , 2015 , 6, 880	6.2	14
134	Interaction of Ecatulin with dystrobrevin contributes to integrity of dystrophin complex in muscle. <i>Journal of Biological Chemistry</i> , 2012 , 287, 21717-28	5.4	14
133	A case study on the comparison of different software tools for automated quantification of peptides. <i>Methods in Molecular Biology</i> , 2011 , 753, 373-98	1.4	14
132	Hybrid N-glycans on the host protective activation-associated secreted proteins of <i>Ostertagia ostertagi</i> and their importance in immunogenicity. <i>Molecular and Biochemical Parasitology</i> , 2008 , 161, 67-71	1.9	14
131	Molecular analysis of astacin-like metalloproteases of <i>Ostertagia ostertagi</i> . <i>Parasitology</i> , 2005 , 130, 89-98	2.7	14
130	A novel receptor-mediated regulation mechanism of type I inositol polyphosphate 5-phosphatase by calcium/calmodulin-dependent protein kinase II phosphorylation. <i>Journal of Biological Chemistry</i> , 2001 , 276, 38738-47	5.4	14
129	Organellar Omics-A Reviving Strategy to Untangle the Biomolecular Complexity of the Cell. <i>Proteomics</i> , 2018 , 18, e1700113	4.8	14
128	Analyzing trapped protein complexes by Virotrap and SFINX. <i>Nature Protocols</i> , 2017 , 12, 881-898	18.8	13
127	Disulfide bond formation protects <i>Arabidopsis thaliana</i> glutathione transferase tau 23 from oxidative damage. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 775-789	4	13
126	Isolation of protein complexes from the model legume <i>Medicago truncatula</i> by tandem affinity purification in hairy root cultures. <i>Plant Journal</i> , 2016 , 88, 476-489	6.9	13
125	Identification of Immune-Responsive Gene 1 (IRG1) as a Target of A20. <i>Journal of Proteome Research</i> , 2018 , 17, 2182-2191	5.6	13
124	Gold nanodome SERS platform for label-free detection of protease activity. <i>Faraday Discussions</i> , 2017 , 205, 345-361	3.6	13
123	Proteome Profiling of Wheat Shoots from Different Cultivars. <i>Frontiers in Plant Science</i> , 2017 , 8, 332	6.2	13
122	Study of the whole cell lysate of two <i>Coxiella burnetii</i> strains using N-terminomics. <i>Journal of Proteome Research</i> , 2012 , 11, 3150-9	5.6	13
121	The tandem PDZ protein Syntenin interacts with the aminoacyl tRNA synthetase complex in a lysyl-tRNA synthetase-dependent manner. <i>Journal of Proteome Research</i> , 2008 , 7, 4962-73	5.6	13
120	Dehydrin ERD14 activates glutathione transferase Phi9 in <i>Arabidopsis thaliana</i> under osmotic stress. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020 , 1864, 129506	4	13
119	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. <i>Nature Communications</i> , 2021 , 12, 2842	17.4	13
118	The autophagy receptor SQSTM1/p62 mediates anti-inflammatory actions of the selective NR3C1/glucocorticoid receptor modulator compound A (CpdA) in macrophages. <i>Autophagy</i> , 2018 , 14, 2049-2064	10.2	13

117	Study of Protein Expression in Peri-Infarct Tissue after Cerebral Ischemia. <i>Scientific Reports</i> , 2015 , 5, 12030	10	12
116	The CEP5 Peptide Promotes Abiotic Stress Tolerance, As Revealed by Quantitative Proteomics, and Attenuates the AUX/IAA Equilibrium in. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1248-1262	7.6	12
115	Simple Peptide Quantification Approach for MS-Based Proteomics Quality Control. <i>ACS Omega</i> , 2020 , 5, 6754-6762	3.9	12
114	An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics. <i>Scientific Reports</i> , 2016 , 6, 27220	4.9	12
113	Proteogenomics in Aid of Host-Pathogen Interaction Studies: A Bacterial Perspective. <i>Proteomes</i> , 2017 , 5,	4.6	12
112	A stringent approach to improve the quality of nitrotyrosine peptide identifications. <i>Proteomics</i> , 2011 , 11, 1094-8	4.8	12
111	Analysis of the translationally controlled tumour protein in the nematodes <i>Ostertagia ostertagi</i> and <i>Caenorhabditis elegans</i> suggests a pivotal role in egg production. <i>International Journal for Parasitology</i> , 2009 , 39, 1205-13	4.3	12
110	HyperISGylation of Old World monkey ISG15 in human cells. <i>PLoS ONE</i> , 2008 , 3, e2427	3.7	12
109	The Arabidopsis Iron-Sulfur Protein GRXS17 is a Target of the Ubiquitin E3 Ligases RGLG3 and RGLG4. <i>Plant and Cell Physiology</i> , 2016 , 57, 1801-13	4.9	12
108	Comparison of Free-Space and Waveguide-Based SERS Platforms. <i>Nanomaterials</i> , 2019 , 9,	5.4	11
107	N-terminal Acetylation Levels Are Maintained During Acetyl-CoA Deficiency in. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2309-2323	7.6	11
106	Proteomic approaches to identify substrates of the three Deg/HtrA proteases of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Biochemical Journal</i> , 2015 , 468, 373-84	3.8	11
105	In-gel N-acetylation for the quantification of the degree of protein in vivo N-terminal acetylation. <i>Methods in Molecular Biology</i> , 2013 , 981, 115-26	1.4	11
104	Conservation of the extended substrate specificity profiles among homologous granzymes across species. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2921-34	7.6	11
103	Multiple isoforms of the tumor suppressor myopodin are simultaneously transcribed in cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 370, 269-73	3.4	11
102	The growing story of (ARABIDOPSIS) CRINKLY 4. <i>Journal of Experimental Botany</i> , 2016 , 67, 4835-47	7	11
101	A Well-Controlled BioID Design for Endogenous Bait Proteins. <i>Journal of Proteome Research</i> , 2019 , 18, 95-106	5.6	11
100	Plant hormone signalling through the eye of the mass spectrometer. <i>Proteomics</i> , 2015 , 15, 1113-26	4.8	10

99	GS, a Multifaceted Tag for Functional Protein Analysis in Monocot and Dicot Plants. <i>Plant Physiology</i> , 2018 , 177, 447-464	6.6	10
98	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. <i>Archives of Toxicology</i> , 2013 , 87, 883-94	5.8	10
97	Asn3, a reliable, robust, and universal lock mass for improved accuracy in LC-MS and LC-MS/MS. <i>Analytical Chemistry</i> , 2013 , 85, 11054-60	7.8	10
96	The C-terminus of CIS defines its interaction pattern. <i>Biochemical Journal</i> , 2007 , 401, 257-67	3.8	10
95	COFRADIC—the Hubble telescope of proteomics. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 16-22		10
94	Selection of universal peptide biomarkers for the detection of the allergen hazelnut in food through a comprehensive, high resolution mass spectrometric (HRMS) based approach. <i>Food Chemistry</i> , 2020 , 309, 125679	8.5	10
93	Importance of extracellular vesicle secretion at the blood-cerebrospinal fluid interface in the pathogenesis of Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 143	7.3	10
92	Evolutionarily conserved and species-specific glycoproteins in the N-glycoproteomes of diverse insect species. <i>Insect Biochemistry and Molecular Biology</i> , 2018 , 100, 22-29	4.5	9
91	Identification and characterization of a novel specific secreted protein family for selected members of the subfamily Ostertagiinae (Nematoda). <i>Parasitology</i> , 2008 , 135, 63-70	2.7	9
90	Expanding the Interactome of TES by Exploiting TES Modules with Different Subcellular Localizations. <i>Journal of Proteome Research</i> , 2017 , 16, 2054-2071	5.6	8
89	RIPK4 activity in keratinocytes is controlled by the SCF ubiquitin ligase to maintain cortical actin organization. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 2827-2841	10.3	8
88	Intelligent Mixing of Proteomes for Elimination of False Positives in Affinity Purification-Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016 , 15, 3929-3937	5.6	8
87	Holistic view on the extended substrate specificities of orthologous granzymes. <i>Journal of Proteome Research</i> , 2014 , 13, 1785-93	5.6	8
86	Phosphoproteomics-based peptide ligand-receptor kinase pairing. Commentary on: "A peptide hormone and its receptor protein kinase regulate plant cell expansion". <i>Frontiers in Plant Science</i> , 2015 , 6, 224	6.2	8
85	Reverse-phase diagonal chromatography for phosphoproteome research. <i>Methods in Molecular Biology</i> , 2009 , 527, 219-27, ix	1.4	8
84	High-resolution mass spectrometry-based selection of peanut peptide biomarkers considering food processing and market type variation. <i>Food Chemistry</i> , 2020 , 304, 125428	8.5	8
83	Construction and analysis of a human testis/sperm-enriched interaction network: Unraveling the PPP1CC2 interactome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 375-385	4	7
82	Protease Substrate Profiling by N-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017 , 1574, 51-76	1.4	7

81	MSqRob Takes the Missing Hurdle: Uniting Intensity- and Count-Based Proteomics. <i>Analytical Chemistry</i> , 2020 , 92, 6278-6287	7.8	7
80	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. <i>New Phytologist</i> , 2020 , 227, 1124-1137	9.8	7
79	HIV-1 Vpr N-terminal tagging affects alternative splicing of the viral genome. <i>Scientific Reports</i> , 2016 , 6, 34573	4.9	7
78	Quantitative Tandem Affinity Purification, an Effective Tool to Investigate Protein Complex Composition in Plant Hormone Signaling: Strigolactones in the Spotlight. <i>Frontiers in Plant Science</i> , 2018 , 9, 528	6.2	7
77	Selective Glucocorticoid Receptor Properties of GSK866 Analogs with Cysteine Reactive Warheads. <i>Frontiers in Immunology</i> , 2017 , 8, 1324	8.4	7
76	Proteome profiling of the green sulfur bacterium <i>Chlorobaculum tepidum</i> by N-terminal proteomics. <i>Proteomics</i> , 2012 , 12, 63-7	4.8	7
75	The chlorosome of <i>Chlorobaculum tepidum</i> : size, mass and protein composition revealed by electron microscopy, dynamic light scattering and mass spectrometry-driven proteomics. <i>Proteomics</i> , 2011 , 11, 2867-80	4.8	7
74	Who gets cut during cell death?. <i>Current Opinion in Cell Biology</i> , 2010 , 22, 859-64	9	7
73	A small heat shock protein of <i>Ostertagia ostertagi</i> : stage-specific expression, heat inducibility, and protection trial. <i>Journal of Parasitology</i> , 2006 , 92, 1244-50	0.9	7
72	Targeting of aminopeptidase I to the yeast vacuole is mediated by Ssa1p, a cytosolic member of the 70-kDa stress protein family. <i>Journal of Biological Chemistry</i> , 2000 , 275, 34054-9	5.4	7
71	New Strategies in High Sensitivity Characterization of Proteins Separated from 1-D or 2-D Gels 1995 , 15-26		7
70	Preparation of <i>Arabidopsis thaliana</i> seedling proteomes for identifying metacaspase substrates by N-terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2014 , 1133, 255-61	1.4	7
69	Unraveling the specificities of the different human methionine sulfoxide reductases. <i>Proteomics</i> , 2014 , 14, 1990-8	4.8	6
68	Activation of ADF/cofilin by phosphorylation-regulated Slingshot phosphatase is required for the meiotic spindle assembly in <i>Xenopus laevis</i> oocytes. <i>Molecular Biology of the Cell</i> , 2013 , 24, 1933-46	3.5	6
67	Unraveling persistent host cell infection with <i>Coxiella burnetii</i> by quantitative proteomics. <i>Journal of Proteome Research</i> , 2011 , 10, 4241-51	5.6	6
66	UBP12 and UBP13 negatively regulate the activity of the ubiquitin-dependent peptidases DA1, DAR1 and DAR2. <i>ELife</i> , 2020 , 9,	8.9	6
65	Protein processing characterized by a gel-free proteomics approach. <i>Methods in Molecular Biology</i> , 2008 , 484, 245-62	1.4	6
64	Protein amino-termini and how to identify them. <i>Expert Review of Proteomics</i> , 2020 , 17, 581-594	4.2	6

63	Proteomics in the genome engineering era. <i>Proteomics</i> , 2016 , 16, 177-87	4.8	6
62	Use of Hybrid Data-Dependent and -Independent Acquisition Spectral Libraries Empowers Dual-Proteome Profiling. <i>Journal of Proteome Research</i> , 2021 , 20, 1165-1177	5.6	6
61	A KAI2 protein perceives strigolactones and isothiocyanates enzymatically. <i>Plant Communications</i> , 2021 , 2, 100166	9	6
60	Unraveling the MAX2 Protein Network in Arabidopsis thaliana: Identification of the Protein Phosphatase PAPP5 as a Novel MAX2 Interactor. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100040	7.6	6
59	Extracellular peptide Kratos restricts cell death during vascular development and stress in Arabidopsis. <i>Journal of Experimental Botany</i> , 2019 , 70, 2199-2210	7	5
58	N-glycosylation Site Analysis Reveals Sex-related Differences in Protein N-glycosylation in the Rice Brown Planthopper (). <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 529-539	7.6	5
57	How many spots with missing values can be tolerated in quantitative two-dimensional gel electrophoresis when applying univariate statistics?. <i>Journal of Proteomics</i> , 2012 , 75, 1792-802	3.9	5
56	A reproducibility-based evaluation procedure for quantifying the differences between MS/MS peak intensity normalization methods. <i>Proteomics</i> , 2011 , 11, 1172-80	4.8	5
55	Time-dependent expression and processing of a hypothetical protein of possible importance for regulation of the Chlamydia pneumoniae developmental cycle. <i>Electrophoresis</i> , 2001 , 22, 1697-704	3.6	5
54	Improved Glucocorticoid Receptor Ligands: Fantastic Beasts, but How to Find Them?. <i>Frontiers in Endocrinology</i> , 2020 , 11, 559673	5.7	5
53	Mass spectrometry and the cellular surfaceome. <i>Mass Spectrometry Reviews</i> , 2021 ,	11	5
52	An AKT2-specific nanobody that targets the hydrophobic motif induces cell cycle arrest, autophagy and loss of focal adhesions in MDA-MB-231 cells. <i>Biomedicine and Pharmacotherapy</i> , 2021 , 133, 111055	7.5	5
51	Limited Proteolysis Combined with Stable Isotope Labeling Reveals Conformational Changes in Protein (Pseudo)kinases upon Binding Small Molecules. <i>Journal of Proteome Research</i> , 2015 , 14, 4179-93	5.6	4
50	Comparative study of concatemer efficiency as an isotope-labelled internal standard for allergen quantification. <i>Food Chemistry</i> , 2020 , 332, 127413	8.5	4
49	Transferring an optimized TAP-toolbox for the isolation of protein complexes to a portfolio of rice tissues. <i>Plant Molecular Biology</i> , 2016 , 91, 341-54	4.6	4
48	How has urinary proteomics contributed to the discovery of early biomarkers of acute kidney injury?. <i>Expert Review of Proteomics</i> , 2014 , 11, 415-24	4.2	4
47	HPLC-based quantification of in vitro N-terminal acetylation. <i>Methods in Molecular Biology</i> , 2013 , 981, 95-102	1.4	4
46	Mass spectrometry-driven proteomics: an introduction. <i>Methods in Molecular Biology</i> , 2011 , 753, 1-27	1.4	4

45	Waveguide-based surface-enhanced Raman spectroscopy detection of protease activity using non-natural aromatic amino acids. <i>Biomedical Optics Express</i> , 2020 , 11, 4800-4816	3.5	4
44	Bacterial Genetic Engineering by Means of Recombineering for Reverse Genetics. <i>Frontiers in Microbiology</i> , 2020 , 11, 548410	5.7	4
43	Development and characterization of protein kinase B/AKT isoform-specific nanobodies. <i>PLoS ONE</i> , 2020 , 15, e0240554	3.7	4
42	Challenges in the Structural-Functional Characterization of Multidomain, Partially Disordered Proteins CBP and p300: Preparing Native Proteins and Developing Nanobody Tools. <i>Methods in Enzymology</i> , 2018 , 611, 607-675	1.7	4
41	Peanut Stunt Virus and Its Satellite RNA Trigger Changes in Phosphorylation in Infected Plants at the Early Stage of the Infection. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	4
40	Prune-1 drives polarization of tumor-associated macrophages (TAMs) within the lung metastatic niche in triple-negative breast cancer. <i>iScience</i> , 2021 , 24, 101938	6.1	4
39	Identification of Carboxypeptidase Substrates by C-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017 , 1574, 115-133	1.4	3
38	Caught green-handed: methods for in vivo detection and visualization of protease activity. <i>Journal of Experimental Botany</i> , 2019 , 70, 2125-2141	7	3
37	Importance of extended protease substrate recognition motifs in steering BNIP-2 cleavage by human and mouse granzymes B. <i>BMC Biochemistry</i> , 2014 , 15, 21	4.8	3
36	Integrated proteomic analysis reveals a substantial enrichment of protein trafficking processes in hippocampus tissue after hypoxic stress. <i>Journal of Proteome Research</i> , 2010 , 9, 204-15	5.6	3
35	Membrane proteome of the green sulfur bacterium <i>Chlorobium tepidum</i> (syn. <i>Chlorobaculum tepidum</i>) analyzed by gel-based and gel-free methods. <i>Photosynthesis Research</i> , 2010 , 104, 153-62	3.7	3
34	Proteolytic cleavage of the <i>Chlamydia pneumoniae</i> major outer membrane protein in the absence of Pmp10. <i>Proteomics</i> , 2007 , 7, 4477-87	4.8	3
33	Techniques for sample preparation including methods for concentrating peptide samples. <i>Exs</i> , 2000 , 88, 29-42		3
32	The Proteolytic Landscape of an Arabidopsis Separase-Deficient Mutant Reveals Novel Substrates Associated With Plant Development		3
31	A well-ordered nanoflow LC-MS/MS approach for proteome profiling using 200 cm long micro pillar array columns		3
30	The lectin Oryzata induces phosphatase-mediated and carbohydrate-independent aggregation of insect cells. <i>Journal of Insect Physiology</i> , 2021 , 131, 104241	2.4	3
29	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12122	16.4	3
28	Proteome-wide cellular thermal shift assay reveals unexpected cross-talk between brassinosteroid and auxin signaling.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2118220119	11.5	3

27	PepShell: visualization of conformational proteomics data. <i>Journal of Proteome Research</i> , 2015 , 14, 1987-90	2
26	Proteome Analysis of Arabidopsis Roots. <i>Methods in Molecular Biology</i> , 2018 , 1761, 263-274	1.4 2
25	The Final Maturation State of F-actin Involves N-terminal Acetylation by NAA80, not N-terminal Arginylation by ATE1.. <i>Journal of Molecular Biology</i> , 2021 , 434, 167397	6.5 2
24	SAMBA controls cell division rate during maize development. <i>Plant Physiology</i> , 2021 ,	6.6 2
23	The use of hybrid data-dependent and -independent acquisition spectral libraries empower dual-proteome profiling	2
22	The Plant PTM Viewer, a central resource exploring plant protein modifications. From site-seeing to protein function	2
21	FIGL1 and its novel partner FLIP form a conserved complex that regulates homologous recombination	2
20	Mechanisms of Congenital Heart Disease Caused by NAA15 Haploinsufficiency. <i>Circulation Research</i> , 2021 , 128, 1156-1169	15.7 2
19	Design and visualization of second-generation cyanoisindole-based fluorescent strigolactone analogs. <i>Plant Journal</i> , 2019 , 98, 165-180	6.9 2
18	Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a Q-function follows form Q model of differentiation. <i>Molecular Omics</i> , 2018 , 14, 181-196	4.4 2
17	Binding of Orsata lectin induces an immune response in insect cells. <i>Insect Science</i> , 2021 ,	3.6 2
16	Protein identification methods in proteomics 2000 , 21, 1145	2
15	Sample preparation procedures for ultrasensitive protein identification by PSD-MALDI-TOF mass spectrometry. <i>The Protein Journal</i> , 1998 , 17, 560	2
14	A Phelipanche ramosa KAI2 Protein Perceives enzymatically Strigolactones and Isothiocyanates	1
13	Temperature-induced changes in wheat phosphoproteome reveal temperature-regulated interconversion of phosphoforms	1
12	Early mannitol-triggered changes in the Arabidopsis leaf (phospho)proteome	1
11	Proteome analysis of the Chlamydia pneumoniae elementary body 2001 , 22, 1204	1
10	Comparative proteome analysis of Chlamydia trachomatis serovar A, D and L2 2002 , 2, 164	1

9	A new generation of AD biomarkers: 2019 to 2021. <i>Ageing Research Reviews</i> , 2022 , 79, 101654	12	1
8	Characterization of the ß-secretase subunit interactome in <i>Arabidopsis thaliana</i> . <i>Acta Physiologiae Plantarum</i> , 2019 , 41, 1	2.6	0
7	Diagonal chromatography to study plant protein modifications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 945-51	4	
6	Mapping protein N-Glycosylation by COFRADIC. <i>Springer Protocols</i> , 2009 , 1395-1402	0.3	
5	The Use of Proteomics to Identify and Characterize Cell Death Proteins 2005 , 403-434		
4	Towards SERS-based multiplexed monitoring of protease activity using non-natural aromatic amino acids. <i>EPJ Web of Conferences</i> , 2020 , 238, 04001	0.3	
3	Platelet Proteomics and its Applications to Study Platelet-Related Disorders 2017 , 157-170		
2	N-Terminal Combined Fractional Diagonal Chromatographic (COFRADIC) Analysis of the Human Platelet Proteome 185-206		
1	A Strong Cation Exchange Chromatography Protocol for Examining N-Terminal Proteoforms.. <i>Methods in Molecular Biology</i> , 2022 , 2477, 293-309	1.4	