

Albert Sickmann

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.

285
papers

14,905
citations

69
h-index

112
g-index

302
ext. papers

16,822
ext. citations

7.3
avg, IF

6.34
L-index

#	Paper	IF	Citations
285	Novel insights into PORCN mutations, associated phenotypes and pathophysiological aspects.. <i>Orphanet Journal of Rare Diseases</i> , 2022 , 17, 29	4.2	0
284	Toward Zero Variance in Proteomics Sample Preparation: Positive-Pressure FASP in 96-Well Format (PF96) Enables Highly Reproducible, Time- and Cost-Efficient Analysis of Sample Cohorts.. <i>Journal of Proteome Research</i> , 2022 , 21, 1181-1188	5.6	2
283	The key features of SARS-CoV-2 leader and NSP1 required for viral escape of NSP1-mediated repression.. <i>Rna</i> , 2022 ,	5.8	1
282	Inhibition of Src but not Syk causes weak reversal of GPVI-mediated platelet aggregation measured by light transmission aggregometry.. <i>Platelets</i> , 2022 , 1-8	3.6	
281	Homozygous WASHC4 variant in two sisters causes a syndromic phenotype defined by dysmorphisms, intellectual disability, profound developmental disorder, and skeletal muscle involvement. <i>Journal of Pathology</i> , 2021 ,	9.4	1
280	Exercise prevents fatty liver by modifying the compensatory response of mitochondrial metabolism to excess substrate availability. <i>Molecular Metabolism</i> , 2021 , 101359	8.8	0
279	MARCKS affects cell motility and response to BTK inhibitors in CLL. <i>Blood</i> , 2021 , 138, 544-556	2.2	2
278	Regulatory Function of Sympathetic Innervation on the Endo/Lysosomal Trafficking of Acetylcholine Receptor. <i>Frontiers in Physiology</i> , 2021 , 12, 626707	4.6	2
277	eIF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. <i>Cell Reports</i> , 2021 , 35, 108941	10.6	12
276	Divergent Proteomic Responses Offer Insights into Resistant Physiological Responses of a Reef-Foraminifera to Climate Change Scenarios. <i>Oceans</i> , 2021 , 2, 281-314	1.3	1
275	Proteomics: A Tool to Study Platelet Function. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
274	Targeted Phosphoinositides Analysis Using High-Performance Ion Chromatography-Coupled Selected Reaction Monitoring Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021 , 20, 3114-3123	5.6	0
273	Targeted Quantification of Phosphorylation Sites Identifies STRIPAK-Dependent Phosphorylation of the Hippo Pathway-Related Kinase SmKIN3. <i>MBio</i> , 2021 , 12,	7.8	1
272	Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions. <i>Scientific Reports</i> , 2021 , 11, 12358	4.9	6
271	Exome reanalysis and proteomic profiling identified TRIP4 as a novel cause of cerebellar hypoplasia and spinal muscular atrophy (PCH1). <i>European Journal of Human Genetics</i> , 2021 , 29, 1348-1353	5.3	3
270	Lymphocyte transformation test: History and current approaches. <i>Journal of Immunological Methods</i> , 2021 , 493, 113036	2.5	3
269	Xenotropic and polytropic retrovirus receptor 1 regulates procoagulant platelet polyphosphate. <i>Blood</i> , 2021 , 137, 1392-1405	2.2	11

268	Tandem Mass Tags for Comparative and Discovery Proteomics. <i>Methods in Molecular Biology</i> , 2021 , 2228, 117-131	1.4	0
267	Quantitative Proteome Data Analysis of Tandem Mass Tags Labeled Samples. <i>Methods in Molecular Biology</i> , 2021 , 2228, 409-417	1.4	1
266	Mouse Quantitative Proteomics Knowledgebase: reference protein concentration ranges in 20 mouse tissues using 5000 quantitative proteomics assays. <i>Bioinformatics</i> , 2021 ,	7.2	1
265	Protein signature of human skin fibroblasts allows the study of the molecular etiology of rare neurological diseases. <i>Orphanet Journal of Rare Diseases</i> , 2021 , 16, 73	4.2	6
264	Tracking changes in adaptation to suspension growth for MDCK cells: cell growth correlates with levels of metabolites, enzymes and proteins. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 1861-1874	5.7	0
263	Muscular and Molecular Pathology Associated with SPATA5 Deficiency in a Child with EHLMRS. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	0
262	Global kinome profiling reveals DYRK1A as critical activator of the human mitochondrial import machinery. <i>Nature Communications</i> , 2021 , 12, 4284	17.4	3
261	Targeting early stages of cardiotoxicity from anti-PD1 immune checkpoint inhibitor therapy. <i>European Heart Journal</i> , 2021 ,	9.5	14
260	Future perspectives on in-vitro diagnosis of drug allergy by the lymphocyte transformation test. <i>Journal of Immunological Methods</i> , 2021 , 495, 113072	2.5	1
259	ANXA7 Regulates Platelet Lipid Metabolism and Ca Release in Arterial Thrombosis. <i>Circulation Research</i> , 2021 , 129, 494-507	15.7	2
258	Generation of a humanized FXII knock-in mouse-A powerful model system to test novel anti-thrombotic agents. <i>Journal of Thrombosis and Haemostasis</i> , 2021 , 19, 2835-2840	15.4	
257	Identification of the factor XII contact activation site enables sensitive coagulation diagnostics. <i>Nature Communications</i> , 2021 , 12, 5596	17.4	6
256	Mono-ADP-ribosylation sites of human CD73 inhibit its adenosine-generating enzymatic activity.. <i>Purinergic Signalling</i> , 2021 , 18, 115	3.8	3
255	Mild hyperlipidemia in mice aggravates platelet responsiveness in thrombus formation and exploration of platelet proteome and lipidome. <i>Scientific Reports</i> , 2020 , 10, 21407	4.9	1
254	First clinical and myopathological description of a myofibrillar myopathy with congenital onset and homozygous mutation in FLNC. <i>Human Mutation</i> , 2020 , 41, 1600-1614	4.7	4
253	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. <i>Plant Physiology</i> , 2020 , 184, 148-164	6.6	10
252	Exposure of Patient-Derived Mesenchymal Stromal Cells to TGFB1 Supports Fibrosis Induction in a Pediatric Acute Megakaryoblastic Leukemia Model. <i>Molecular Cancer Research</i> , 2020 , 18, 1603-1612	6.6	0
251	Targeted Approach to Distinguish and Determine Absolute Levels of GDF8 and GDF11 in Mouse Serum. <i>Proteomics</i> , 2020 , 20, e1900104	4.8	3

250	Phosphoproteomic analysis of STRIPAK mutants identifies a conserved serine phosphorylation site in PAK kinase CLA4 to be important in fungal sexual development and polarized growth. <i>Molecular Microbiology</i> , 2020 , 113, 1053-1069	4.1	8
249	Improving Identification of Protein-Protein Interactions Using an Affinity-enrichable, Isotopically Coded, and Mass Spectrometry-cleavable Chemical Crosslinker. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 624-639	7.6	20
248	BIN2 orchestrates platelet calcium signaling in thrombosis and thrombo-inflammation. <i>Journal of Clinical Investigation</i> , 2020 , 130, 6064-6079	15.9	10
247	The STRIPAK signaling complex regulates dephosphorylation of GUL1, an RNA-binding protein that shuttles on endosomes. <i>PLoS Genetics</i> , 2020 , 16, e1008819	6	8
246	Herpesviruses induce aggregation and selective autophagy of host signalling proteins NEMO and RIPK1 as an immune-evasion mechanism. <i>Nature Microbiology</i> , 2020 , 5, 331-342	26.6	25
245	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020 , 11, 5248	17.4	13
244	Impaired iloprost-induced platelet inhibition and phosphoproteome changes in patients with confirmed pseudohypoparathyroidism type Ia, linked to genetic mutations in GNAS. <i>Scientific Reports</i> , 2020 , 10, 11389	4.9	8
243	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. <i>Blood</i> , 2020 , 136, 1956-1967	2.2	15
242	Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. <i>Analytical Chemistry</i> , 2020 , 92, 13672-13676	7.8	1
241	Cutting the Gordian knot: early and complete amino acid sequence confirmation of class II lasso peptides by HCD fragmentation. <i>Journal of Antibiotics</i> , 2020 , 73, 772-779	3.7	3
240	Coactosin-like 1 integrates signaling critical for shear-dependent thrombus formation in mouse platelets. <i>Haematologica</i> , 2020 , 105, 1667-1676	6.6	3
239	Linking bioenergetic function of mitochondria to tissue-specific molecular fingerprints. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019 , 317, E374-E387	6	16
238	A sensitive and simple targeted proteomics approach to quantify transcription factor and membrane proteins of the unfolded protein response pathway in glioblastoma cells. <i>Scientific Reports</i> , 2019 , 9, 8836	4.9	13
237	O-GlcNAcylation of Histone Deacetylase 4 Protects the Diabetic Heart From Failure. <i>Circulation</i> , 2019 , 140, 580-594	16.7	43
236	Cannabinoid synthases and osmoprotective metabolites accumulate in the exudates of Cannabis sativa L. glandular trichomes. <i>Plant Science</i> , 2019 , 284, 108-116	5.3	22
235	Investigating the Role of Mitochondria in Type 2 Diabetes - Lessons from Lipidomics and Proteomics Studies of Skeletal Muscle and Liver. <i>Advances in Experimental Medicine and Biology</i> , 2019 , 1158, 143-182	3.6	2
234	Phosphorylation of the Bruchpilot N-terminus in unlocks axonal transport of active zone building blocks. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	2
233	Combination of Proteogenomics with Peptide Sequencing Identifies New Genes and Hidden Posttranscriptional Modifications. <i>MBio</i> , 2019 , 10,	7.8	22

232	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. <i>Cancers</i> , 2019 , 11,	6.6	7
231	Short Peptides with Uncleavable Peptide Bond Mimetics as Photoactivatable Caspase-3 Inhibitors. <i>Molecules</i> , 2019 , 24,	4.8	2
230	Disentangling thermal stress responses in a reef-calcifier and its photosymbionts by shotgun proteomics. <i>Scientific Reports</i> , 2018 , 8, 3524	4.9	14
229	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 826-834	7.6	31
228	Effects of the NO/soluble guanylate cyclase/cGMP system on the functions of human platelets. <i>Nitric Oxide - Biology and Chemistry</i> , 2018 , 76, 71-80	5	49
227	Tracking Effects of SIL1 Increase: Taking a Closer Look Beyond the Consequences of Elevated Expression Level. <i>Molecular Neurobiology</i> , 2018 , 55, 2524-2546	6.2	12
226	Intersection of Proteomics and Genomics to "Solve the Unsolved" in Rare Disorders such as Neurodegenerative and Neuromuscular Diseases. <i>Proteomics - Clinical Applications</i> , 2018 , 12, 1700073	3.1	19
225	Molecular phenotyping of laboratory mouse strains using 500 multiple reaction monitoring mass spectrometry plasma assays. <i>Communications Biology</i> , 2018 , 1, 78	6.7	15
224	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018 , 28, 866-880.e15	24.6	83
223	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018 , 15, 515-535	4.2	43
222	Integrated Proteomic and Phosphoproteomic Analysis Reveal Novel Targets and Suggest Rationale for Ibrutinib Efficacy in UM-CLL. <i>Blood</i> , 2018 , 132, 583-583	2.2	
221	Combined inhibition of receptor tyrosine and p21-activated kinases as a therapeutic strategy in childhood ALL. <i>Blood Advances</i> , 2018 , 2, 2554-2567	7.8	10
220	Activation of E2F-dependent transcription by the mouse cytomegalovirus M117 protein affects the viral host range. <i>PLoS Pathogens</i> , 2018 , 14, e1007481	7.6	6
219	Analysis of new growth promoting black market products. <i>Growth Hormone and IGF Research</i> , 2018 , 41, 1-6	2	11
218	Identification of key lipids critical for platelet activation by comprehensive analysis of the platelet lipidome. <i>Blood</i> , 2018 , 132, e1-e12	2.2	45
217	Advanced tools for the analysis of protein phosphorylation in yeast mitochondria. <i>Analytical Biochemistry</i> , 2018 , 554, 23-27	3.1	6
216	Platelet proteomics: from discovery to diagnosis. <i>Expert Review of Proteomics</i> , 2018 , 15, 467-476	4.2	11
215	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018 , 92, 1939-1952	5.8	21

214	Deciphering lymphoma pathogenesis via state-of-the-art mass spectrometry-based quantitative proteomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017 , 1047, 2-14	3.2	0
213	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017 , 129, e1-e12	2.2	68
212	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
211	Multi-OMICS: a critical technical perspective on integrative lipidomics approaches. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2017 , 1862, 808-811	5	18
210	PeptideMapper: efficient and versatile amino acid sequence and tag mapping. <i>Bioinformatics</i> , 2017 , 33, 2042-2044	7.2	6
209	LILY-lipidome isotope labeling of yeast: in vivo synthesis of C labeled reference lipids for quantification by mass spectrometry. <i>Analyst, The</i> , 2017 , 142, 1891-1899	5	35
208	Activity-based protein profiling as a robust method for enzyme identification and screening in extremophilic Archaea. <i>Nature Communications</i> , 2017 , 8, 15352	17.4	27
207	The FERM protein EPB41L5 regulates actomyosin contractility and focal adhesion formation to maintain the kidney filtration barrier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E4621-E4630	11.5	33
206	Enrichment of Cross-Linked Peptides Using Charge-Based Fractional Diagonal Chromatography (ChaFRADIC). <i>Journal of Proteome Research</i> , 2017 , 16, 459-469	5.6	23
205	Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2017 , 16, 4035-4044	5.6	8
204	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017 , 8, 290	17.4	82
203	Combining De Novo Peptide Sequencing Algorithms, A Synergistic Approach to Boost Both Identifications and Confidence in Bottom-up Proteomics. <i>Journal of Proteome Research</i> , 2017 , 16, 3209-3218	5.6	10
202	Quantifying Missing (Phospho)Proteome Regions with the Broad-Specificity Protease Subtilisin. <i>Analytical Chemistry</i> , 2017 , 89, 13137-13145	7.8	9
201	Computational proteomics tools for identification and quality control. <i>Journal of Biotechnology</i> , 2017 , 261, 126-130	3.7	9
200	DISMS2: A flexible algorithm for direct proteome-wide distance calculation of LC-MS/MS runs. <i>BMC Bioinformatics</i> , 2017 , 18, 148	3.6	8
199	The proteome of baker yeast mitochondria. <i>Mitochondrion</i> , 2017 , 33, 15-21	4.9	18
198	PeptideTracker: A knowledge base for collecting and storing information on protein concentrations in biological tissues. <i>Proteomics</i> , 2017 , 17, 1600210	4.8	14
197	Alterations of the platelet proteome in type I Glanzmann thrombasthenia caused by different homozygous delG frameshift mutations in ITGA2B. <i>Thrombosis and Haemostasis</i> , 2017 , 117, 556-569	7	17

196	Quantification of Cardiovascular Disease Biomarkers in Human Platelets by Targeted Mass Spectrometry. <i>Proteomes</i> , 2017 , 5,	4.6	8
195	Combined Quantification of the Global Proteome, Phosphoproteome, and Proteolytic Cleavage to Characterize Altered Platelet Functions in the Human Scott Syndrome. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3154-3169	7.6	31
194	Global profiling of protein complexes: current approaches and their perspective in biomedical research. <i>Expert Review of Proteomics</i> , 2016 , 13, 951-964	4.2	11
193	A Ribonucleoprotein Supercomplex Involved in trans-Splicing of Organelle Group II Introns. <i>Journal of Biological Chemistry</i> , 2016 , 291, 23330-23342	5.4	12
192	Annotated Gene and Proteome Data Support Recognition of Interconnections Between the Results of Different Experiments in Space Research. <i>Microgravity Science and Technology</i> , 2016 , 28, 357-365	1.6	13
191	A pioneer protein is part of a large complex involved in trans-splicing of a group II intron in the chloroplast of <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2016 , 85, 57-69	6.9	7
190	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1453-66	7.6	65
189	Functional Dissection of an Alternatively Spliced Herpesvirus Gene by Splice Site Mutagenesis. <i>Journal of Virology</i> , 2016 , 90, 4626-4636	6.6	8
188	Two Birds with One Stone: Parallel Quantification of Proteome and Phosphoproteome Using iTRAQ. <i>Methods in Molecular Biology</i> , 2016 , 1394, 25-41	1.4	7
187	Bottom-up proteomics suggests an association between differential expression of mitochondrial proteins and chronic fatigue syndrome. <i>Translational Psychiatry</i> , 2016 , 6, e904	8.6	15
186	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015 , 33, 22-4	44.5	344
185	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015 , 11, 1487-93		63
184	Conjugation of Ciprofloxacin with Poly(2-oxazoline)s and Polyethylene Glycol via End Groups. <i>Bioconjugate Chemistry</i> , 2015 , 26, 1950-62	6.3	54
183	Highly sensitive phosphoproteomics by tailoring solid-phase extraction to electrostatic repulsion-hydrophilic interaction chromatography. <i>Analytical Chemistry</i> , 2015 , 87, 1596-604	7.8	34
182	Identification of proteins involved in inhibition of spheroid formation under microgravity. <i>Proteomics</i> , 2015 , 15, 2945-52	4.8	42
181	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. <i>Expert Review of Proteomics</i> , 2015 , 12, 235-53	4.2	123
180	Multidimensional electrostatic repulsion-hydrophilic interaction chromatography (ERLIC) for quantitative analysis of the proteome and phosphoproteome in clinical and biomedical research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 460-8	4	20
179	Defective glycosylation of coagulation factor XII underlies hereditary angioedema type III. <i>Journal of Clinical Investigation</i> , 2015 , 125, 3132-46	15.9	116

178	What can proteomics tell us about platelets?. <i>Circulation Research</i> , 2014 , 114, 1204-19	15.7	76
177	The protein import machinery of mitochondria-a regulatory hub in metabolism, stress, and disease. <i>Cell Metabolism</i> , 2014 , 19, 357-72	24.6	257
176	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 12-20	4	24
175	Proteomic differences between microvascular endothelial cells and the EA.hy926 cell line forming three-dimensional structures. <i>Proteomics</i> , 2014 , 14, 689-98	4.8	29
174	Amyloid- β peptide induces mitochondrial dysfunction by inhibition of preprotein maturation. <i>Cell Metabolism</i> , 2014 , 20, 662-9	24.6	137
173	Antimicrobial poly(2-methylloxazoline)s with bioswitchable activity through satellite group modification. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 3830-4	16.4	78
172	Time-resolved characterization of cAMP/PKA-dependent signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways. <i>Blood</i> , 2014 , 123, e1-e10	2.2	71
171	Catch me if you can: challenges and applications of cross-linking approaches. <i>European Journal of Mass Spectrometry</i> , 2014 , 20, 99-116	1.1	11
170	Method and platform standardization in MRM-based quantitative plasma proteomics. <i>Journal of Proteomics</i> , 2013 , 95, 66-76	3.9	46
169	Developmental changes of the protein repertoire in the rat auditory brainstem: a comparative proteomics approach in the superior olivary complex and the inferior colliculus with DIGE and iTRAQ. <i>Journal of Proteomics</i> , 2013 , 79, 43-59	3.9	10
168	Nuclear import of LASP-1 is regulated by phosphorylation and dynamic protein-protein interactions. <i>Oncogene</i> , 2013 , 32, 2107-13	9.2	42
167	Response: platelet transcriptome and proteome--relation rather than correlation. <i>Blood</i> , 2013 , 121, 5257-8	2.8	18
166	An alternative NFAT-activation pathway mediated by IL-7 is critical for early thymocyte development. <i>Nature Immunology</i> , 2013 , 14, 127-35	19.1	45
165	Novel highly sensitive, specific, and straightforward strategy for comprehensive N-terminal proteomics reveals unknown substrates of the mitochondrial peptidase Icp55. <i>Journal of Proteome Research</i> , 2013 , 12, 3823-30	5.6	72
164	Adenylation, MS, and proteomics--Introducing a "new" modification to bottom-up proteomics. <i>Proteomics</i> , 2013 , 13, 955-63	4.8	7
163	Phosphoproteomics--more than meets the eye. <i>Electrophoresis</i> , 2013 , 34, 1483-92	3.6	32
162	Phosphorylation of CalDAG-GEFI by protein kinase A prevents Rap1b activation. <i>Journal of Thrombosis and Haemostasis</i> , 2013 , 11, 1574-82	15.4	37
161	Novel function assignment to a member of the essential HP1043 response regulator family of epsilon-proteobacteria. <i>Microbiology (United Kingdom)</i> , 2013 , 159, 880-889	2.9	5

160	Cytomegalovirus downregulates IRE1 to repress the unfolded protein response. <i>PLoS Pathogens</i> , 2013 , 9, e1003544	7.6	44
159	Interaction of proteins identified in human thyroid cells. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 1164-78	6.3	29
158	Deciphering of ADP-induced, phosphotyrosine-dependent signaling networks in human platelets by Src-homology 2 region (SH2)-profiling. <i>Proteomics</i> , 2013 , 13, 1016-27	4.8	16
157	The Bruchpilot cytomatrix determines the size of the readily releasable pool of synaptic vesicles. <i>Journal of Cell Biology</i> , 2013 , 202, 667-83	7.3	76
156	Systematic and quantitative comparison of digest efficiency and specificity reveals the impact of trypsin quality on MS-based proteomics. <i>Journal of Proteomics</i> , 2012 , 75, 1454-62	3.9	194
155	Current methods for global proteome identification. <i>Expert Review of Proteomics</i> , 2012 , 9, 519-32	4.2	41
154	N-glycoproteomics: mass spectrometry-based glycosylation site annotation. <i>Biological Chemistry</i> , 2012 , 393, 249-58	4.5	30
153	E. coli LoiP (YggG), a metalloprotease hydrolyzing Phe-Phe bonds. <i>Molecular BioSystems</i> , 2012 , 8, 1775-82		14
152	Robust workflow for iTRAQ-based peptide and protein quantification. <i>Methods in Molecular Biology</i> , 2012 , 893, 101-13	1.4	13
151	The first comprehensive and quantitative analysis of human platelet protein composition allows the comparative analysis of structural and functional pathways. <i>Blood</i> , 2012 , 120, e73-82	2.2	485
150	A complex standard for protein identification, designed by evolution. <i>Journal of Proteome Research</i> , 2012 , 11, 5065-71	5.6	33
149	Integral quantification accuracy estimation for reporter ion-based quantitative proteomics (iQuARI). <i>Journal of Proteome Research</i> , 2012 , 11, 5072-80	5.6	22
148	iTRAQ analysis of a cell culture model for malignant transformation, including comparison with 2D-PAGE and SILAC. <i>Journal of Proteome Research</i> , 2012 , 11, 2140-53	5.6	24
147	DipA, a pore-forming protein in the outer membrane of Lyme disease spirochetes exhibits specificity for the permeation of dicarboxylates. <i>PLoS ONE</i> , 2012 , 7, e36523	3.7	17
146	Metabolic enzyme diversity in different human thyroid cell lines and their sensitivity to gravitational forces. <i>Proteomics</i> , 2012 , 12, 2539-46	4.8	23
145	Well-defined amphiphilic poly(2-oxazoline) ABA-triblock copolymers and their aggregation behavior in aqueous solution. <i>Macromolecular Rapid Communications</i> , 2012 , 33, 1677-82	4.8	26
144	STEAP1 is associated with the invasive and oxidative stress phenotype of Ewing tumors. <i>Molecular Cancer Research</i> , 2012 , 10, 52-65	6.6	80
143	Raf kinases mediate the phosphorylation of eukaryotic translation elongation factor 1A and regulate its stability in eukaryotic cells. <i>Cell Death and Disease</i> , 2012 , 3, e276	9.8	29

142	Proteomic and metabolomic analyses of mitochondrial complex I-deficient mouse model generated by spontaneous B2 short interspersed nuclear element (SINE) insertion into NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Ndufs4) gene. <i>Journal of Biological Chemistry</i> , 2012 , 287, 20652-63	5.4	42
141	Intermembrane space proteome of yeast mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1840-52	12.0	
140	CLP36 is a negative regulator of glycoprotein VI signaling in platelets. <i>Circulation Research</i> , 2012 , 111, 1410-20	15.7	18
139	Phosphoproteome analysis of the platelet plasma membrane. <i>Methods in Molecular Biology</i> , 2011 , 728, 279-90	1.4	12
138	Regulation of mitochondrial protein import by cytosolic kinases. <i>Cell</i> , 2011 , 144, 227-39	56.2	186
137	Dual function of Sdh3 in the respiratory chain and TIM22 protein translocase of the mitochondrial inner membrane. <i>Molecular Cell</i> , 2011 , 44, 811-8	17.6	96
136	Composition and topology of the endoplasmic reticulum-mitochondria encounter structure. <i>Journal of Molecular Biology</i> , 2011 , 413, 743-50	6.5	124
135	Subcellular Analysis of the Platelet Proteome. <i>Current Proteomics</i> , 2011 , 8, 181-192	0.7	
134	compomics-utilities: an open-source Java library for computational proteomics. <i>BMC Bioinformatics</i> , 2011 , 12, 70	3.6	75
133	Parents' perspectives on the unforeseen finding of a fetal sex chromosomal aneuploidy. <i>Prenatal Diagnosis</i> , 2011 , 31, 286-92	3.2	14
132	Catch me if you can: mass spectrometry-based phosphoproteomics and quantification strategies. <i>Proteomics</i> , 2011 , 11, 554-70	4.8	84
131	The good, the bad, the ugly: validating the mass spectrometric analysis of modified peptides. <i>Proteomics</i> , 2011 , 11, 1099-109	4.8	25
130	SearchGUI: An open-source graphical user interface for simultaneous OMSSA and X!Tandem searches. <i>Proteomics</i> , 2011 , 11, 996-9	4.8	261
129	Quality control of nano-LC-MS systems using stable isotope-coded peptides. <i>Proteomics</i> , 2011 , 11, 1049-53	4.8	26
128	Peptide identification quality control. <i>Proteomics</i> , 2011 , 11, 2105-14	4.8	35
127	iTRAQ protein quantification: a quality-controlled workflow. <i>Proteomics</i> , 2011 , 11, 1125-34	4.8	47
126	A proteomic approach to analysing spheroid formation of two human thyroid cell lines cultured on a random positioning machine. <i>Proteomics</i> , 2011 , 11, 2095-104	4.8	55
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