

Albert Sickmann

List of Publications by Year in descending order

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Version: 2024-02-01

295
papers

18,350
citations

9756

73
h-index

18075

120
g-index

302
all docs

302
docs citations

302
times ranked

20870
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting early stages of cardiotoxicity from anti-PD1 immune checkpoint inhibitor therapy. <i>European Heart Journal</i> , 2022, 43, 316-329.	1.0	84
2	ERK1/2 Activity Is Critical for the Outcome of Ischemic Stroke. <i>International Journal of Molecular Sciences</i> , 2022, 23, 706.	1.8	3
3	Novel insights into PORCN mutations, associated phenotypes and pathophysiological aspects. <i>Orphanet Journal of Rare Diseases</i> , 2022, 17, 29.	1.2	3
4	Identification of a novel homozygous <i>c10orf150</i> variant in siblings with early-onset axonal Charcot-Marie-Tooth disease. <i>Human Mutation</i> , 2022, 43, 477-486.	1.1	3
5	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.	1.8	12
6	The key features of SARS-CoV-2 leader and NSP1 required for viral escape of NSP1-mediated repression. <i>Rna</i> , 2022, 28, 766-779.	1.6	30
7	Mono-ADP-ribosylation sites of human CD73 inhibit its adenosine-generating enzymatic activity. <i>Purinergic Signalling</i> , 2022, 18, 115-121.	1.1	3
8	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.	1.1	1
9	The potential of remdesivir to affect function, metabolism and proliferation of cardiac and kidney cells in vitro. <i>Archives of Toxicology</i> , 2022, 96, 2341-2360.	1.9	11
10	Skeletal muscle provides the immunological micro-milieu for specific plasma cells in anti-synthetase syndrome-associated myositis. <i>Acta Neuropathologica</i> , 2022, 144, 353-372.	3.9	19
11	Proteomic and morphological insights and clinical presentation of two young patients with novel mutations of BVES (POPDC1). <i>Molecular Genetics and Metabolism</i> , 2022, 136, 226-237.	0.5	11
12	Endoplasmic reticulum stress and unfolded protein response activation in immune-mediated necrotizing myopathy. <i>Brain Pathology</i> , 2022, 32, .	2.1	7
13	Xenotropic and polytropic retrovirus receptor 1 regulates procoagulant platelet polyphosphate. <i>Blood</i> , 2021, 137, 1392-1405.	0.6	21
14	Tandem Mass Tags for Comparative and Discovery Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2228, 117-131.	0.4	6
15	Quantitative Proteome Data Analysis of Tandem Mass Tags Labeled Samples. <i>Methods in Molecular Biology</i> , 2021, 2228, 409-417.	0.4	1
16	Mouse Quantitative Proteomics Knowledgebase: reference protein concentration ranges in 20 mouse tissues using 5000 quantitative proteomics assays. <i>Bioinformatics</i> , 2021, 37, 1900-1908.	1.8	6
17	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.	1.2	18
18	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.	1.7	2

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19	MARCKS affects cell motility and response to BTK inhibitors in CLL. <i>Blood</i> , 2021, 138, 544-556.	0.6	14
20	Regulatory Function of Sympathetic Innervation on the Endo/Lysosomal Trafficking of Acetylcholine Receptor. <i>Frontiers in Physiology</i> , 2021, 12, 626707.	1.3	6
21	eIF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. <i>Cell Reports</i> , 2021, 35, 108941.	2.9	56
22	Divergent Proteomic Responses Offer Insights into Resistant Physiological Responses of a Reef-Foraminifera to Climate Change Scenarios. <i>Oceans</i> , 2021, 2, 281-314.	0.6	16
23	Proteomics: A Tool to Study Platelet Function. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4776.	1.8	12
24	Targeted Phosphoinositides Analysis Using High-Performance Ion Chromatography-Coupled Selected Reaction Monitoring Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 3114-3123.	1.8	8
25	Targeted Quantification of Phosphorylation Sites Identifies STRIPAK-Dependent Phosphorylation of the Hippo Pathway-Related Kinase SmKIN3. <i>MBio</i> , 2021, 12, .	1.8	4
26	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.	1.6	40
27	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.	1.4	10
28	Lymphocyte transformation test: History and current approaches. <i>Journal of Immunological Methods</i> , 2021, 493, 113036.	0.6	38
29	Muscular and Molecular Pathology Associated with SPATA5 Deficiency in a Child with EHLMRS. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7835.	1.8	4
30	Global kinome profiling reveals DYRK1A as critical activator of the human mitochondrial import machinery. <i>Nature Communications</i> , 2021, 12, 4284.	5.8	15
31	Future perspectives on in-vitro diagnosis of drug allergy by the lymphocyte transformation test. <i>Journal of Immunological Methods</i> , 2021, 495, 113072.	0.6	7
32	ANXA7 Regulates Platelet Lipid Metabolism and Ca ²⁺ Release in Arterial Thrombosis. <i>Circulation Research</i> , 2021, 129, 494-507.	2.0	16
33	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.	1.9	1
34	Identification of the factor XII contact activation site enables sensitive coagulation diagnostics. <i>Nature Communications</i> , 2021, 12, 5596.	5.8	23
35	Molecular Proteomics and Signalling of Human Platelets in Health and Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9860.	1.8	19
36	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, , .	2.1	5

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37	Exercise prevents fatty liver by modifying the compensatory response of mitochondrial metabolism to excess substrate availability. <i>Molecular Metabolism</i> , 2021, 54, 101359.	3.0	11
38	Phenotypical and Myopathological Consequences of Compound Heterozygous Missense and Nonsense Variants in SLC18A3. <i>Cells</i> , 2021, 10, 3481.	1.8	1
39	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.	5.9	39
40	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	5.8	49
41	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.	1.6	16
42	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. <i>Blood</i> , 2020, 136, 1956-1967.	0.6	34
43	Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 13672-13676.	3.2	1
44	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.	1.0	3
45	Mild hyperlipidemia in mice aggravates platelet responsiveness in thrombus formation and exploration of platelet proteome and lipidome. <i>Scientific Reports</i> , 2020, 10, 21407.	1.6	13
46	First clinical and myopathological description of a myofibrillar myopathy with congenital onset and homozygous mutation in <i>FLNC</i> . <i>Human Mutation</i> , 2020, 41, 1600-1614.	1.1	11
47	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. <i>Plant Physiology</i> , 2020, 184, 148-164.	2.3	26
48	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.	1.5	1
49	Targeted Approach to Distinguish and Determine Absolute Levels of GDF8 and GDF11 in Mouse Serum. <i>Proteomics</i> , 2020, 20, e1900104.	1.3	6
50	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.	1.2	15
51	Improving Identification of In-organello 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.	2.5	34
52	Coactosin-like 1 integrates signaling critical for shear-dependent thrombus formation in mouse platelets. <i>Haematologica</i> , 2020, 105, 1667-1676.	1.7	8
53	BIN2 orchestrates platelet calcium signaling in thrombosis and thrombo-inflammation. <i>Journal of Clinical Investigation</i> , 2020, 130, 6064-6079.	3.9	20
54	The STRIPAK signaling complex regulates dephosphorylation of GUL1, an RNA-binding protein that shuttles on endosomes. <i>PLoS Genetics</i> , 2020, 16, e1008819.	1.5	13

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55	Linking bioenergetic function of mitochondria to tissue-specific molecular fingerprints. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E374-E387.	1.8	29
56	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.	1.6	26
57	O-GlcNAcylation of Histone Deacetylase 4 Protects the Diabetic Heart From Failure. <i>Circulation</i> , 2019, 140, 580-594.	1.6	77
58	Cannabinoid synthases and osmoprotective metabolites accumulate in the exudates of <i>Cannabis sativa</i> L. glandular trichomes. <i>Plant Science</i> , 2019, 284, 108-116.	1.7	43
59	Phosphorylation of the Bruchpilot N-terminus unlocks axonal transport of active zone building blocks. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	5
60	Combination of Proteogenomics with Peptide <i>De Novo</i> Sequencing Identifies New Genes and Hidden Posttranscriptional Modifications. <i>MBio</i> , 2019, 10, .	1.8	40
61	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. <i>Cancers</i> , 2019, 11, 1907.	1.7	12
62	Short Peptides with Uncleavable Peptide Bond Mimetics as Photoactivatable Caspase-3 Inhibitors. <i>Molecules</i> , 2019, 24, 206.	1.7	5
63	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.	0.8	3
64	Disentangling thermal stress responses in a reef-calcifier and its photosymbionts by shotgun proteomics. <i>Scientific Reports</i> , 2018, 8, 3524.	1.6	24
65	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 826-834.	2.5	36
66	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.	1.2	77
67	Tracking Effects of SIL1 Increase: Taking a Closer Look Beyond the Consequences of Elevated Expression Level. <i>Molecular Neurobiology</i> , 2018, 55, 2524-2546.	1.9	15
68	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.	0.8	33
69	Combined inhibition of receptor tyrosine and p21-activated kinases as a therapeutic strategy in childhood ALL. <i>Blood Advances</i> , 2018, 2, 2554-2567.	2.5	14
70	Activation of E2F-dependent transcription by the mouse cytomegalovirus M117 protein affects the viral host range. <i>PLoS Pathogens</i> , 2018, 14, e1007481.	2.1	8
71	Analysis of new growth promoting black market products. <i>Growth Hormone and IGF Research</i> , 2018, 41, 1-6.	0.5	11
72	Identification of key lipids critical for platelet activation by comprehensive analysis of the platelet lipidome. <i>Blood</i> , 2018, 132, e1-e12.	0.6	76

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73	Advanced tools for the analysis of protein phosphorylation in yeast mitochondria. <i>Analytical Biochemistry</i> , 2018, 554, 23-27.	1.1	6
74	Platelet proteomics: from discovery to diagnosis. <i>Expert Review of Proteomics</i> , 2018, 15, 467-476.	1.3	20
75	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018, 92, 1939-1952.	1.9	34
76	Molecular phenotyping of laboratory mouse strains using 500 multiple reaction monitoring mass spectrometry plasma assays. <i>Communications Biology</i> , 2018, 1, 78.	2.0	22
77	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	7.2	154
78	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 515-535.	1.3	69
79	Integrated Proteomic and Phosphoproteomic Analysis Reveal Novel Targets and Suggest Rationale for Ibrutinib Efficacy in UM-CLL. <i>Blood</i> , 2018, 132, 583-583.	0.6	0
80	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.	1.2	5
81	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017, 129, e1-e12.	0.6	97
82	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.	2.9	88
83	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.	1.2	29
84	PeptideMapper: efficient and versatile amino acid sequence and tag mapping. <i>Bioinformatics</i> , 2017, 33, 2042-2044.	1.8	11
85	LILY-lipidome isotope labeling of yeast: in vivo synthesis of ^{13}C labeled reference lipids for quantification by mass spectrometry. <i>Analyst</i> , 2017, 142, 1891-1899.	1.7	49
86	Activity-based protein profiling as a robust method for enzyme identification and screening in extremophilic Archaea. <i>Nature Communications</i> , 2017, 8, 15352.	5.8	45
87	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.	3.3	54
88	Enrichment of Cross-Linked Peptides Using Charge-Based Fractional Diagonal Chromatography (ChaFRADIC). <i>Journal of Proteome Research</i> , 2017, 16, 459-469.	1.8	31
89	Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2017, 16, 4035-4044.	1.8	10
90	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017, 8, 290.	5.8	123

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91	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.	1.8	14
92	Quantifying Missing (Phospho)Proteome Regions with the Broad-Specificity Protease Subtilisin. <i>Analytical Chemistry</i> , 2017, 89, 13137-13145.	3.2	13
93	Computational proteomics tools for identification and quality control. <i>Journal of Biotechnology</i> , 2017, 261, 126-130.	1.9	11
94	DISMS2: A flexible algorithm for direct proteome- wide distance calculation of LC-MS/MS runs. <i>BMC Bioinformatics</i> , 2017, 18, 148.	1.2	15
95	The proteome of baker's yeast mitochondria. <i>Mitochondrion</i> , 2017, 33, 15-21.	1.6	22
96	PeptideTracker: A knowledge base for collecting and storing information on protein concentrations in biological tissues. <i>Proteomics</i> , 2017, 17, 1600210.	1.3	20
97	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.	1.8	23
98	Quantification of Cardiovascular Disease Biomarkers in Human Platelets by Targeted Mass Spectrometry. <i>Proteomes</i> , 2017, 5, 31.	1.7	13
99	Bottom-up proteomics suggests an association between differential expression of mitochondrial proteins and chronic fatigue syndrome. <i>Translational Psychiatry</i> , 2016, 6, e904-e904.	2.4	19
100	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.	2.5	52
101	Global profiling of protein complexes: current approaches and their perspective in biomedical research. <i>Expert Review of Proteomics</i> , 2016, 13, 951-964.	1.3	15
102	A Ribonucleoprotein Supercomplex Involved in trans-Splicing of Organelle Group II Introns. <i>Journal of Biological Chemistry</i> , 2016, 291, 23330-23342.	1.6	16
103	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.	0.7	15
104	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.	2.8	11
105	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1435-1466.	2.5	99
106	Functional Dissection of an Alternatively Spliced Herpesvirus Gene by Splice Site Mutagenesis. <i>Journal of Virology</i> , 2016, 90, 4626-4636.	1.5	9
107	Two Birds with One Stone: Parallel Quantification of Proteome and Phosphoproteome Using iTRAQ. <i>Methods in Molecular Biology</i> , 2016, 1394, 25-41.	0.4	24
108	Identification of proteins involved in inhibition of spheroid formation under microgravity. <i>Proteomics</i> , 2015, 15, 2945-2952.	1.3	50

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109	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. <i>Expert Review of Proteomics</i> , 2015, 12, 235-253.	1.3	147
110	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, 460-468.	1.1	20
111	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015, 33, 22-24.	9.4	460
112	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015, 11, 1487-1493.	2.9	94
113	Conjugation of Ciprofloxacin with Poly(2-oxazoline)s and Polyethylene Glycol via End Groups. <i>Bioconjugate Chemistry</i> , 2015, 26, 1950-1962.	1.8	69
114	Highly Sensitive Phosphoproteomics by Tailoring Solid-Phase Extraction to Electrostatic Repulsion-Hydrophilic Interaction Chromatography. <i>Analytical Chemistry</i> , 2015, 87, 1596-1604.	3.2	34
115	Defective glycosylation of coagulation factor XII underlies hereditary angioedema type III. <i>Journal of Clinical Investigation</i> , 2015, 125, 3132-3146.	3.9	138
116	What Can Proteomics Tell Us About Platelets?. <i>Circulation Research</i> , 2014, 114, 1204-1219.	2.0	97
117	The Protein Import Machinery of Mitochondria: A Regulatory Hub in Metabolism, Stress, and Disease. <i>Cell Metabolism</i> , 2014, 19, 357-372.	7.2	316
118	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 12-20.	1.1	27
119	Proteomic differences between microvascular endothelial cells and the EA.hy926 cell line forming three-dimensional structures. <i>Proteomics</i> , 2014, 14, 689-698.	1.3	36
120	Proteomics - moving from inventory to personalized medicine?. <i>Proteomics</i> , 2014, 14, 1953-1953.	1.3	2
121	Amyloid- β Peptide Induces Mitochondrial Dysfunction by Inhibition of Preprotein Maturation. <i>Cell Metabolism</i> , 2014, 20, 662-669.	7.2	176
122	Antimicrobial Poly(2-methylloxazoline)s with Bioswitchable Activity through Satellite Group Modification. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 3830-3834.	7.2	96
123	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.	0.6	80
124	Catch Me if You Can: Challenges and Applications of Cross-Linking Approaches. <i>European Journal of Mass Spectrometry</i> , 2014, 20, 99-116.	0.5	12
125	Method and platform standardization in MRM-based quantitative plasma proteomics. <i>Journal of Proteomics</i> , 2013, 95, 66-76.	1.2	55
126	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.	1.2	10

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127	Nuclear import of LASP-1 is regulated by phosphorylation and dynamic protein-protein interactions. <i>Oncogene</i> , 2013, 32, 2107-2113.	2.6	50
128	Response: platelet transcriptome and proteome relation rather than correlation. <i>Blood</i> , 2013, 121, 5257-5258.	0.6	21
129	An alternative NFAT-activation pathway mediated by IL-7 is critical for early thymocyte development. <i>Nature Immunology</i> , 2013, 14, 127-135.	7.0	65
130	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, 3823-3830.	1.8	82
131	196. <i>Cytokine</i> , 2013, 63, 289.	1.4	0
132	Adenylylation, MS, and proteomics: Introducing a new modification to bottom-up proteomics. <i>Proteomics</i> , 2013, 13, 955-963.	1.3	8
133	Phosphoproteomics: More than meets the eye. <i>Electrophoresis</i> , 2013, 34, 1483-1492.	1.3	32
134	Phosphorylation of CalDAG-GEFI by protein kinase A prevents Rap1b activation. <i>Journal of Thrombosis and Haemostasis</i> , 2013, 11, 1574-1582.	1.9	41
135	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.	0.7	5
136	Cytomegalovirus Downregulates IRE1 to Repress the Unfolded Protein Response. <i>PLoS Pathogens</i> , 2013, 9, e1003544.	2.1	48
137	Interaction of Proteins Identified in Human Thyroid Cells. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1164-1178.	1.8	30
138	Deciphering of ADP-induced, phosphotyrosine-dependent signaling networks in human platelets by Src homology 2 region (SH2) profiling. <i>Proteomics</i> , 2013, 13, 1016-1027.	1.3	16
139	The Bruchpilot cytomatrix determines the size of the readily releasable pool of synaptic vesicles. <i>Journal of Cell Biology</i> , 2013, 202, 667-683.	2.3	101
140	Analysis of Post-translational Modifications. <i>Proteomics</i> , 2013, 13, 901-903.	1.3	4
141	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-e276.	2.7	36
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, 20652-20663.	1.6	58
143	Intermembrane Space Proteome of Yeast Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1840-1852.	2.5	134
144	CLP36 Is a Negative Regulator of Glycoprotein VI Signaling in Platelets. <i>Circulation Research</i> , 2012, 111, 1410-1420.	2.0	22

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145	Current methods for global proteome identification. <i>Expert Review of Proteomics</i> , 2012, 9, 519-532.	1.3	43
146	N-glycoproteomics: mass spectrometry-based glycosylation site annotation. <i>Biological Chemistry</i> , 2012, 393, 249-258.	1.2	32
147	<i>E. coli</i> LoIP (YggG), a metalloprotease hydrolyzing Phe-Phe bonds. <i>Molecular BioSystems</i> , 2012, 8, 1775.	2.9	17
148	Robust Workflow for iTRAQ-Based Peptide and Protein Quantification. <i>Methods in Molecular Biology</i> , 2012, 893, 101-113.	0.4	13
149	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-e82.	0.6	623
150	A Complex Standard for Protein Identification, Designed by Evolution. <i>Journal of Proteome Research</i> , 2012, 11, 5065-5071.	1.8	51
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152	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, 2140-2153.	1.8	26
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