

Albert Sickmann

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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	The proteome of <i>Saccharomyces cerevisiae</i> mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13207-12	11.5	753
284	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
283	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
282	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015 , 33, 22-4	44.5	344
281	State-of-the-art in phosphoproteomics. <i>Proteomics</i> , 2005 , 5, 4052-61	4.8	314
280	Toward the complete yeast mitochondrial proteome: multidimensional separation techniques for mitochondrial proteomics. <i>Journal of Proteome Research</i> , 2006 , 5, 1543-54	5.6	311
279	Mitochondrial presequence translocase: switching between TOM tethering and motor recruitment involves Tim21 and Tim17. <i>Cell</i> , 2005 , 120, 817-29	56.2	285
278	SearchGUI: An open-source graphical user interface for simultaneous OMSSA and X!Tandem searches. <i>Proteomics</i> , 2011 , 11, 996-9	4.8	261
277	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
276	Multiple pathways for sorting mitochondrial precursor proteins. <i>EMBO Reports</i> , 2008 , 9, 42-9	6.5	248
275	Protein insertion into the mitochondrial inner membrane by a twin-pore translocase. <i>Science</i> , 2003 , 299, 1747-51	33.3	242
274	The mitochondrial presequence translocase: an essential role of Tim50 in directing preproteins to the import channel. <i>Cell</i> , 2002 , 111, 507-18	56.2	221
273	Endothelial nitric-oxide synthase (type III) is activated and becomes calcium independent upon phosphorylation by cyclic nucleotide-dependent protein kinases. <i>Journal of Biological Chemistry</i> , 2000 , 275, 5179-87	5.4	220
272	Pex8p: an intraperoxisomal organizer of the peroxisomal import machinery. <i>Molecular Cell</i> , 2003 , 11, 635-46	17.6	202
271	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
270	Application of electron transfer dissociation (ETD) for the analysis of posttranslational modifications. <i>Proteomics</i> , 2008 , 8, 4466-83	4.8	194
269	Regulation of mitochondrial protein import by cytosolic kinases. <i>Cell</i> , 2011 , 144, 227-39	56.2	186

268	A J-protein is an essential subunit of the presequence translocase-associated protein import motor of mitochondria. <i>Journal of Cell Biology</i> , 2003 , 163, 707-13	7.3	179
267	Proteomic analysis of the yeast mitochondrial outer membrane reveals accumulation of a subclass of preproteins. <i>Molecular Biology of the Cell</i> , 2006 , 17, 1436-50	3.5	174
266	Pam16 has an essential role in the mitochondrial protein import motor. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 226-33	17.6	174
265	An assembly chaperone collaborates with the SMN complex to generate spliceosomal SnRNPs. <i>Cell</i> , 2008 , 135, 497-509	56.2	157
264	Challenges in mass spectrometry-based proteomics. <i>Proteomics</i> , 2004 , 4, 3686-703	4.8	149
263	Phosphoamino acid analysis. <i>Proteomics</i> , 2001 , 1, 200-6	4.8	146
262	Protein import channel of the outer mitochondrial membrane: a highly stable Tom40-Tom22 core structure differentially interacts with preproteins, small tom proteins, and import receptors. <i>Molecular and Cellular Biology</i> , 2001 , 21, 2337-48	4.8	144
261	Phosphoproteome of resting human platelets. <i>Journal of Proteome Research</i> , 2008 , 7, 526-34	5.6	140
260	Amyloid- β peptide induces mitochondrial dysfunction by inhibition of preprotein maturation. <i>Cell Metabolism</i> , 2014 , 20, 662-9	24.6	137
259	The human platelet membrane proteome reveals several new potential membrane proteins. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1754-61	7.6	129
258	The La-related protein LARP7 is a component of the 7SK ribonucleoprotein and affects transcription of cellular and viral polymerase II genes. <i>EMBO Reports</i> , 2008 , 9, 569-75	6.5	128
257	Elucidation of N-glycosylation sites on human platelet proteins: a glycoproteomic approach. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 226-33	7.6	127
256	Composition and topology of the endoplasmic reticulum-mitochondria encounter structure. <i>Journal of Molecular Biology</i> , 2011 , 413, 743-50	6.5	124
255	Profiling phosphoproteins of yeast mitochondria reveals a role of phosphorylation in assembly of the ATP synthase. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1896-906	7.6	124
254	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
253	Intermembrane space proteome of yeast mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1840-52	10.5	120
252	The mitochondrial proteome: from inventory to function. <i>Cell</i> , 2008 , 134, 22-4	56.2	119
251	Role of thioredoxin reductase 1 and thioredoxin interacting protein in prognosis of breast cancer. <i>Breast Cancer Research</i> , 2010 , 12, R44	8.3	118

250	Defective glycosylation of coagulation factor XII underlies hereditary angioedema type III. <i>Journal of Clinical Investigation</i> , 2015 , 125, 3132-46	15.9	116
249	Inhibition of proinflammatory and innate immune signaling pathways by a cytomegalovirus RIP1-interacting protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 3094-9	11.5	110
248	Platelet membrane proteomics: a novel repository for functional research. <i>Blood</i> , 2009 , 114, e10-9	2.2	106
247	A comprehensive interaction map of the human survival of motor neuron (SMN) complex. <i>Journal of Biological Chemistry</i> , 2007 , 282, 5825-33	5.4	102
246	Overexpression of LASP-1 mediates migration and proliferation of human ovarian cancer cells and influences zyxin localisation. <i>British Journal of Cancer</i> , 2007 , 96, 296-305	8.7	101
245	Cytoskeleton assembly at endothelial cell-cell contacts is regulated by alphaII-spectrin-VASP complexes. <i>Journal of Cell Biology</i> , 2008 , 180, 205-19	7.3	99
244	Pam17 is required for architecture and translocation activity of the mitochondrial protein import motor. <i>Molecular and Cellular Biology</i> , 2005 , 25, 7449-58	4.8	97
243	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
242	Proteomic analysis of brain plasma membranes isolated by affinity two-phase partitioning. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 390-400	7.6	92
241	Peptide and protein quantification: a map of the minefield. <i>Proteomics</i> , 2010 , 10, 650-70	4.8	89
240	Identification of peroxisomal membrane proteins of <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Electrophoresis</i> , 2001 , 22, 2955-68	3.6	88
239	Identification of proteins from human cerebrospinal fluid, separated by two-dimensional polyacrylamide gel electrophoresis. <i>Electrophoresis</i> , 2000 , 21, 2721-8	3.6	88
238	RioK1, a new interactor of protein arginine methyltransferase 5 (PRMT5), competes with pICln for binding and modulates PRMT5 complex composition and substrate specificity. <i>Journal of Biological Chemistry</i> , 2011 , 286, 1976-86	5.4	87
237	Silver- and Coomassie-staining protocols: detection limits and compatibility with ESI MS. <i>Electrophoresis</i> , 2007 , 28, 2095-9	3.6	87
236	Precise protein quantification based on peptide quantification using iTRAQ. <i>BMC Bioinformatics</i> , 2007 , 8, 214	3.6	87
235	Conformational switch and role of phosphorylation in PAK activation. <i>Molecular and Cellular Biology</i> , 2001 , 21, 5179-89	4.8	87
234	Catch me if you can: mass spectrometry-based phosphoproteomics and quantification strategies. <i>Proteomics</i> , 2011 , 11, 554-70	4.8	84
233	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018 , 28, 866-880.e15	24.6	83

232	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017 , 8, 290	17.4	82
231	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
230	The multisubunit chloroplast RNA polymerase A from mustard (<i>Sinapis alba</i> L.). Integration of a prokaryotic core into a larger complex with organelle-specific functions. <i>FEBS Journal</i> , 2000 , 267, 253-61		79
229	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
228	What can proteomics tell us about platelets?. <i>Circulation Research</i> , 2014 , 114, 1204-19	15.7	76
227	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
226	compomics-utilities: an open-source Java library for computational proteomics. <i>BMC Bioinformatics</i> , 2011 , 12, 70	3.6	75
225	Tyrosine phosphorylation modulates the activity of TRPV4 in response to defined stimuli. <i>Journal of Biological Chemistry</i> , 2009 , 284, 2923-2933	5.4	75
224	Evolution of an RNP assembly system: a minimal SMN complex facilitates formation of UsnRNPs in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 10045-50	11.5	75
223	Towards a high resolution separation of human cerebrospinal fluid. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002 , 771, 167-96	3.2	73
222	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
221	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
220	The Wuerzburg hybridoma library against <i>Drosophila</i> brain. <i>Journal of Neurogenetics</i> , 2009 , 23, 78-91	1.6	70
219	Enhanced N-glycosylation site analysis of sialoglycopeptides by strong cation exchange prefractionation applied to platelet plasma membranes. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1933-41	7.6	70
218	IGHMBP2 is a ribosome-associated helicase inactive in the neuromuscular disorder distal SMA type 1 (DSMA1). <i>Human Molecular Genetics</i> , 2009 , 18, 1288-300	5.6	69
217	The catalytic activity of protein-disulfide isomerase requires a conformationally flexible molecule. <i>Journal of Biological Chemistry</i> , 2008 , 283, 33630-40	5.4	69
216	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
215	Phosphorylation-independent activity of atypical response regulators of <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 3100-9	3.5	66

214	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
213	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
212	Two-dimensional benzyldimethyl-n-hexadecylammonium chloride/SDS-PAGE for membrane proteomics. <i>Proteomics</i> , 2005 , 5, 3581-8	4.8	64
211	Purification and characterization of a magnesium-dependent neutral sphingomyelinase from bovine brain. <i>Journal of Biological Chemistry</i> , 2000 , 275, 7641-7	5.4	64
210	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015 , 11, 1487-93		63
209	Platelet protein interactions: map, signaling components, and phosphorylation groundstate. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2008 , 28, 1326-31	9.4	63
208	Ribosome-associated complex binds to ribosomes in close proximity of Rpl31 at the exit of the polypeptide tunnel in yeast. <i>Molecular Biology of the Cell</i> , 2008 , 19, 5279-88	3.5	63
207	Modificomics: posttranslational modifications beyond protein phosphorylation and glycosylation. <i>New Biotechnology</i> , 2007 , 24, 169-77		62
206	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
205	Laser-induced dissociation/high-energy collision-induced dissociation fragmentation using MALDI-TOF/TOF-MS instrumentation for the analysis of neutral and acidic oligosaccharides. <i>Analytical Chemistry</i> , 2005 , 77, 3274-83	7.8	56
204	Multidimensional nano-HPLC for analysis of protein complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2003 , 14, 1003-11	3.5	56
203	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
202	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
201	Proteome analysis of Apis mellifera royal jelly. <i>Analytical and Bioanalytical Chemistry</i> , 2007 , 389, 1087-93	4.4	51
200	Identification of major tyrosine phosphorylation sites in the human insulin receptor substrate Gab-1 by insulin receptor kinase in vitro. <i>Biochemistry</i> , 2000 , 39, 10898-907	3.2	50
199	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
198	Identification of novel centrosomal proteins in Dictyostelium discoideum by comparative proteomic approaches. <i>Journal of Proteome Research</i> , 2006 , 5, 589-98	5.6	49
197	Identification of new tyrosine phosphorylated proteins in rat brain mitochondria. <i>FEBS Letters</i> , 2008 , 582, 1104-10	3.8	48

196	iTRAQ protein quantification: a quality-controlled workflow. <i>Proteomics</i> , 2011 , 11, 1125-34	4.8	47
195	Method and platform standardization in MRM-based quantitative plasma proteomics. <i>Journal of Proteomics</i> , 2013 , 95, 66-76	3.9	46
194	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
193	Identification of a Protein Kinase C-dependent phosphorylation site involved in sensitization of TRPV4 channel. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 391, 1721-5	3.4	45
192	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
191	Cytomegalovirus downregulates IRE1 to repress the unfolded protein response. <i>PLoS Pathogens</i> , 2013 , 9, e1003544	7.6	44
190	Proteomic analysis of cathepsin B- and L-deficient mouse brain lysosomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007 , 1774, 1237-46	4	44
189	O-GlcNAcylation of Histone Deacetylase 4 Protects the Diabetic Heart From Failure. <i>Circulation</i> , 2019 , 140, 580-594	16.7	43
188	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
187	Application of free-flow IEF to identify protein candidates changing under microgravity conditions. <i>Proteomics</i> , 2010 , 10, 904-13	4.8	43
186	Identification of major ERK-related phosphorylation sites in Gab1. <i>Biochemistry</i> , 2004 , 43, 12133-40	3.2	43
185	Nuclear import of LASP-1 is regulated by phosphorylation and dynamic protein-protein interactions. <i>Oncogene</i> , 2013 , 32, 2107-13	9.2	42
184	Identification of proteins involved in inhibition of spheroid formation under microgravity. <i>Proteomics</i> , 2015 , 15, 2945-52	4.8	42
183	A stimulatory role for the La-related protein 4B in translation. <i>Rna</i> , 2010 , 16, 1488-99	5.8	42
182	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
181	Current methods for global proteome identification. <i>Expert Review of Proteomics</i> , 2012 , 9, 519-32	4.2	41
180	Identification of novel in vivo phosphorylation sites of the human proapoptotic protein BAD: pore-forming activity of BAD is regulated by phosphorylation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 28004-28020	5.4	39
179	XTandem Parser: an open-source library to parse and analyse X!Tandem MS/MS search results. <i>Proteomics</i> , 2010 , 10, 1522-4	4.8	39

178	Understanding platelets. Lessons from proteomics, genomics and promises from network analysis. <i>Thrombosis and Haemostasis</i> , 2005 , 94, 916-25	7	38
177	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
176	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
175	Mass spectrometry-based peptide quantification: applications and limitations. <i>Expert Review of Proteomics</i> , 2005 , 2, 381-92	4.2	36
174	Identification of modified proteins by mass spectrometry. <i>IUBMB Life</i> , 2002 , 54, 51-7	4.7	36
173	Investigation of charge variants of rViscumin by two-dimensional gel electrophoresis and mass spectrometry. <i>Electrophoresis</i> , 2001 , 22, 2888-97	3.6	36
172	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
171	Peptide identification quality control. <i>Proteomics</i> , 2011 , 11, 2105-14	4.8	35
170	Identification of phosphorylation and acetylation sites in alphaA-crystallin of the eye lens (musculus) after two-dimensional gel electrophoresis. <i>Analytical and Bioanalytical Chemistry</i> , 2003 , 376, 966-72	4.4	35
169	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
168	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
167	A complex standard for protein identification, designed by evolution. <i>Journal of Proteome Research</i> , 2012 , 11, 5065-71	5.6	33
166	The human TRPV6 channel protein is associated with cyclophilin B in human placenta. <i>Journal of Biological Chemistry</i> , 2008 , 283, 18086-98	5.4	33
165	Phosphoproteomics--more than meets the eye. <i>Electrophoresis</i> , 2013 , 34, 1483-92	3.6	32
164	Glycosylation Site Analysis of Human Platelets by Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Clinical Proteomics</i> , 2008 , 4, 25-36	5	32
163	Identification of post-translationally modified proteins in proteome studies. <i>Electrophoresis</i> , 2001 , 22, 1669-76	3.6	32
162	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 826-834	7.6	31
161	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

160	Aqueous polymer two-phase systems for the proteomic analysis of plasma membranes from minute brain samples. <i>Journal of Proteome Research</i> , 2008 , 7, 432-42	5.6	31
159	N-glycoproteomics: mass spectrometry-based glycosylation site annotation. <i>Biological Chemistry</i> , 2012 , 393, 249-58	4.5	30
158	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
157	Interaction of proteins identified in human thyroid cells. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 1164-78	6.3	29
156	Homologous desensitization of guanylyl cyclase A, the receptor for atrial natriuretic peptide, is associated with a complex phosphorylation pattern. <i>FEBS Journal</i> , 2010 , 277, 2440-53	5.7	29
155	Analysis of the membrane proteome of canine pancreatic rough microsomes identifies a novel Hsp40, termed ERj7. <i>Proteomics</i> , 2009 , 9, 3463-73	4.8	29
154	OMSSA Parser: an open-source library to parse and extract data from OMSSA MS/MS search results. <i>Proteomics</i> , 2009 , 9, 3772-4	4.8	29
153	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
152	The Hsp70 homolog Ssb is essential for glucose sensing via the SNF1 kinase network. <i>Genes and Development</i> , 2009 , 23, 2102-15	12.6	28
151	Phosphoproteomics of human platelets: A quest for novel activation pathways. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 1963-76	4	28
150	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
149	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
148	Quality control of nano-LC-MS systems using stable isotope-coded peptides. <i>Proteomics</i> , 2011 , 11, 1049-58	4.8	26
147	Comprehensive proteome analysis of <i>Mycobacterium ulcerans</i> and quantitative comparison of mycolactone biosynthesis. <i>Proteomics</i> , 2008 , 8, 3124-38	4.8	26
146	Vegetative insecticidal protein (Vip1Ac) of <i>Bacillus thuringiensis</i> HD201: evidence for oligomer and channel formation. <i>Biochemistry</i> , 2006 , 45, 283-8	3.2	26
145	Extractor for ESI quadrupole TOF tandem MS data enabled for high throughput batch processing. <i>BMC Bioinformatics</i> , 2004 , 5, 162	3.6	26
144	The good, the bad, the ugly: validating the mass spectrometric analysis of modified peptides. <i>Proteomics</i> , 2011 , 11, 1099-109	4.8	25
143	Positive regulation of A-RAF by phosphorylation of isoform-specific hinge segment and identification of novel phosphorylation sites. <i>Journal of Biological Chemistry</i> , 2008 , 283, 27239-54	5.4	25

142	Identification of an obeche (<i>Triplochiton scleroxylon</i>) wood allergen as a class I chitinase. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2005 , 60, 808-14	9.3	25
141	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
140	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
139	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
138	Comparative proteomic analysis of biofilm and planktonic cells of <i>Neisseria meningitidis</i> . <i>Proteomics</i> , 2010 , 10, 4512-21	4.8	24
137	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
136	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
135	Feedback of the kinesin-1 neck-linker position on the catalytic site. <i>Journal of Biological Chemistry</i> , 2006 , 281, 18868-77	5.4	23
134	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	5.3	22
133	Integral quantification accuracy estimation for reporter ion-based quantitative proteomics (iQuARI). <i>Journal of Proteome Research</i> , 2012 , 11, 5072-80	5.6	22
132	Recent advances in yeast organelle and membrane proteomics. <i>Proteomics</i> , 2009 , 9, 4731-43	4.8	22
131	Regulation of the glucose-specific phosphotransferase system (PTS) of <i>Staphylococcus carnosus</i> by the antiterminator protein GlcT. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 9), 2333-2342	2.9	22
130	Combination of Proteogenomics with Peptide Sequencing Identifies New Genes and Hidden Posttranscriptional Modifications. <i>MBio</i> , 2019 , 10,	7.8	22
129	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018 , 92, 1939-1952	5.8	21
128	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
127	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
126	Quantitative differential proteome analysis in an animal model for human melanoma. <i>Journal of Proteome Research</i> , 2009 , 8, 1818-27	5.6	20
125	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

124	Integrin-dependent translocation of LASP-1 to the cytoskeleton of activated platelets correlates with LASP-1 phosphorylation at tyrosine 171 by Src-kinase. <i>Thrombosis and Haemostasis</i> , 2009 , 102, 520-8	7	19
123	Assembly of nuclear pore complexes mediated by major vault protein. <i>Journal of Cell Science</i> , 2009 , 122, 780-6	5.3	19
122	jTraqX: a free, platform independent tool for isobaric tag quantitation at the protein level. <i>Proteomics</i> , 2010 , 10, 1223-5	4.8	19
121	Protein identification using mass spectrometry: a method overview. <i>Exs</i> , 2007 , 97, 141-70		19
120	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
119	Response: platelet transcriptome and proteome--relation rather than correlation. <i>Blood</i> , 2013 , 121, 5257-8	7.8	18
118	The proteome of baker's yeast mitochondria. <i>Mitochondrion</i> , 2017 , 33, 15-21	4.9	18
117	CLP36 is a negative regulator of glycoprotein VI signaling in platelets. <i>Circulation Research</i> , 2012 , 111, 1410-20	15.7	18
116	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
115	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
114	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
113	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
112	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
111	Identification and isolation of Dictyostelium microtubule-associated protein interactors by tandem affinity purification. <i>European Journal of Cell Biology</i> , 2006 , 85, 1079-90	6.1	15
110	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. <i>BMC Bioinformatics</i> , 2005 , 6, 285	3.6	15
109	Human phosphatidylinositol 4-kinase isoform PI4K92. Expression of the recombinant enzyme and determination of multiple phosphorylation sites. <i>FEBS Journal</i> , 2001 , 268, 2099-106		15
108	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. <i>Blood</i> , 2020 , 136, 1956-1967	2.2	15
107	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

106	Disentangling thermal stress responses in a reef-calcifier and its photosymbionts by shotgun proteomics. <i>Scientific Reports</i> , 2018 , 8, 3524	4.9	14
105	PeptideTracker: A knowledge base for collecting and storing information on protein concentrations in biological tissues. <i>Proteomics</i> , 2017 , 17, 1600210	4.8	14
104	E. coli LoIP (YggG), a metalloprotease hydrolyzing Phe-Phe bonds. <i>Molecular BioSystems</i> , 2012 , 8, 1775-82		14
103	Parents' perspectives on the unforeseen finding of a fetal sex chromosomal aneuploidy. <i>Prenatal Diagnosis</i> , 2011 , 31, 286-92	3.2	14
102	Malignant transformation in a defined genetic background: proteome changes displayed by 2D-PAGE. <i>Molecular Cancer</i> , 2010 , 9, 254	42.1	14
101	Efficient analysis and extraction of MS/MS result data from Mascot result files. <i>BMC Bioinformatics</i> , 2005 , 6, 290	3.6	14
100	Proteomics of yeast mitochondria. <i>Methods in Molecular Biology</i> , 2007 , 372, 543-57	1.4	14
99	Targeting early stages of cardiotoxicity from anti-PD1 immune checkpoint inhibitor therapy. <i>European Heart Journal</i> , 2021 ,	9.5	14
98	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
97	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
96	Robust workflow for iTRAQ-based peptide and protein quantification. <i>Methods in Molecular Biology</i> , 2012 , 893, 101-13	1.4	13
95	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020 , 11, 5248	17.4	13
94	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
93	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
92	Phosphoproteome analysis of the platelet plasma membrane. <i>Methods in Molecular Biology</i> , 2011 , 728, 279-90	1.4	12
91	Online dual gradient reversed-phase/porous graphitized carbon nanoHPLC for proteomic applications. <i>Analytical Chemistry</i> , 2010 , 82, 5391-6	7.8	12
90	eIF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. <i>Cell Reports</i> , 2021 , 35, 108941	10.6	12
89	Two-dimensional BAC/SDS-PAGE for membrane proteomics. <i>Sub-Cellular Biochemistry</i> , 2007 , 43, 13-20	5.5	12

88	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
87	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
86	Characterization of a novel interaction between vasodilator-stimulated phosphoprotein and Abelson interactor 1 in human platelets: a concerted computational and experimental approach. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 843-50	9.4	11
85	The Hsp70 chaperone Ssa1 is essential for catabolite induced degradation of the gluconeogenic enzyme Fructose-1,6-bisphosphatase. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 397, 447-52	3.4	11
84	Applications of highly sensitive phosphopeptide derivatization methods without the need for organic solvents. <i>Proteomics</i> , 2006 , 6, 2647-9	4.8	11
83	N-glycosylation site analysis of human platelet proteins by hydrazide affinity capturing and LC-MS/MS. <i>Methods in Molecular Biology</i> , 2009 , 534, 225-38	1.4	11
82	Xenotropic and polytropic retrovirus receptor 1 regulates procoagulant platelet polyphosphate. <i>Blood</i> , 2021 , 137, 1392-1405	2.2	11
81	Analysis of new growth promoting black market products. <i>Growth Hormone and IGF Research</i> , 2018 , 41, 1-6	2	11
80	Platelet proteomics: from discovery to diagnosis. <i>Expert Review of Proteomics</i> , 2018 , 15, 467-476	4.2	11
79	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. <i>Plant Physiology</i> , 2020 , 184, 148-164	6.6	10
78	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
77	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
76	BIN2 orchestrates platelet calcium signaling in thrombosis and thrombo-inflammation. <i>Journal of Clinical Investigation</i> , 2020 , 130, 6064-6079	15.9	10
75	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
74	Quantifying Missing (Phospho)Proteome Regions with the Broad-Specificity Protease Subtilisin. <i>Analytical Chemistry</i> , 2017 , 89, 13137-13145	7.8	9
73	Computational proteomics tools for identification and quality control. <i>Journal of Biotechnology</i> , 2017 , 261, 126-130	3.7	9
72	Mass spectrometry--a key technology in proteome research. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2003 , 83, 141-76	1.7	9
71	Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2017 , 16, 4035-4044	5.6	8

70	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
69	Functional Dissection of an Alternatively Spliced Herpesvirus Gene by Splice Site Mutagenesis. <i>Journal of Virology</i> , 2016 , 90, 4626-4636	6.6	8
68	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
67	Quantification of Cardiovascular Disease Biomarkers in Human Platelets by Targeted Mass Spectrometry. <i>Proteomes</i> , 2017 , 5,	4.6	8
66	Native purification of protein and RNA-protein complexes using a novel affinity procedure. <i>Fly</i> , 2009 , 3, 223-231	1.3	8
65	Prostaglandin-induced VASP phosphorylation controls alpha II-spectrin breakdown in apoptotic cells. <i>International Immunopharmacology</i> , 2008 , 8, 319-24	5.8	8
64	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
63	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
62	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
61	Adenylation, MS, and proteomics--Introducing a "new" modification to bottom-up proteomics. <i>Proteomics</i> , 2013 , 13, 955-63	4.8	7
60	Command line tool for calculating theoretical MS spectra for given sequences. <i>Bioinformatics</i> , 2004 , 20, 2889-91	7.2	7
59	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
58	Strong cation exchange chromatography for analysis of sialylated glycopeptides. <i>Methods in Molecular Biology</i> , 2011 , 753, 299-308	1.4	7
57	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. <i>Cancers</i> , 2019 , 11,	6.6	7
56	PeptideMapper: efficient and versatile amino acid sequence and tag mapping. <i>Bioinformatics</i> , 2017 , 33, 2042-2044	7.2	6
55	Squash: A Tool for Analyzing, Tuning and Refactoring Relational Database Applications. <i>Lecture Notes in Computer Science</i> , 2009 , 82-98	0.9	6
54	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
53	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

52	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
51	Advanced tools for the analysis of protein phosphorylation in yeast mitochondria. <i>Analytical Biochemistry</i> , 2018 , 554, 23-27	3.1	6
50	Identification of the factor XII contact activation site enables sensitive coagulation diagnostics. <i>Nature Communications</i> , 2021 , 12, 5596	17.4	6
49	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
48	Ruthenium (II) tris-bathophenanthroline disulfonate is well suitable for Tris-Glycine PAGE but not for Bis-Tris gels. <i>Proteomics</i> , 2007 , 7, 524-527	4.8	5
47	A comprehensive dictionary of protein accession codes for complete protein accession identifier alias resolving. <i>Proteomics</i> , 2006 , 6, 4223-6	4.8	5
46	Identification of major histocompatibility complex class II-associated peptides derived from freshly prepared rat Langerhans cells using MALDI-PSD and Edman degradation. <i>Analyst, The</i> , 2000 , 125, 569-73 ⁵		5
45	Proteomics: A Tool to Study Platelet Function. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
44	Phosphoamino acid analysis 2001 , 1, 200		5
43	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
42	Targeted Approach to Distinguish and Determine Absolute Levels of GDF8 and GDF11 in Mouse Serum. <i>Proteomics</i> , 2020 , 20, e1900104	4.8	3
41	Analysis of tyrosine-phosphorylated proteins in rat brain mitochondria. <i>Methods in Enzymology</i> , 2009 , 457, 117-36	1.7	3
40	Platelet Proteomics: Essentials for Understanding and Application. <i>Transfusion Medicine and Hemotherapy</i> , 2006 , 33, 227-235	4.2	3
39	Nuclear envelopes from amphibian oocytes--from morphology to protein inventory. <i>European Journal of Cell Biology</i> , 2005 , 84, 151-62	6.1	3
38	Identification of Eps15 as antigen recognized by the monoclonal antibodies aa2 and ab52 of the Wuerzburg Hybridoma Library against Drosophila brain. <i>PLoS ONE</i> , 2011 , 6, e29352	3.7	3
37	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
36	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
35	Lymphocyte transformation test: History and current approaches. <i>Journal of Immunological Methods</i> , 2021 , 493, 113036	2.5	3

34	Coactosin-like 1 integrates signaling critical for shear-dependent thrombus formation in mouse platelets. <i>Haematologica</i> , 2020 , 105, 1667-1676	6.6	3
33	Global kinome profiling reveals DYRK1A as critical activator of the human mitochondrial import machinery. <i>Nature Communications</i> , 2021 , 12, 4284	17.4	3
32	Mono-ADP-ribosylation sites of human CD73 inhibit its adenosine-generating enzymatic activity.. <i>Purinergic Signalling</i> , 2021 , 18, 115	3.8	3
31	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
30	MARCKS affects cell motility and response to BTK inhibitors in CLL. <i>Blood</i> , 2021 , 138, 544-556	2.2	2
29	Regulatory Function of Sympathetic Innervation on the Endo/Lysosomal Trafficking of Acetylcholine Receptor. <i>Frontiers in Physiology</i> , 2021 , 12, 626707	4.6	2
28	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
27	Short Peptides with Uncleavable Peptide Bond Mimetics as Photoactivatable Caspase-3 Inhibitors. <i>Molecules</i> , 2019 , 24,	4.8	2
26	ANXA7 Regulates Platelet Lipid Metabolism and Ca Release in Arterial Thrombosis. <i>Circulation Research</i> , 2021 , 129, 494-507	15.7	2
25	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
24	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
23	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
22	Interaction of Vasodilator-stimulated phosphoprotein (VASP) with β -Spectrin is crucial for the cAMP-dependent regulation of cortical actin dynamics. <i>FASEB Journal</i> , 2006 , 20, A103	0.9	1
21	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
20	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
19	Targeted Quantification of Phosphorylation Sites Identifies STRIPAK-Dependent Phosphorylation of the Hippo Pathway-Related Kinase SmKIN3. <i>MBio</i> , 2021 , 12,	7.8	1
18	Quantitative Proteome Data Analysis of Tandem Mass Tags Labeled Samples. <i>Methods in Molecular Biology</i> , 2021 , 2228, 409-417	1.4	1
17	Mouse Quantitative Proteomics Knowledgebase: reference protein concentration ranges in 20 mouse tissues using 5000 quantitative proteomics assays. <i>Bioinformatics</i> , 2021 ,	7.2	1

16	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
15	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
14	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
13	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
12	Novel insights into PORCN mutations, associated phenotypes and pathophysiological aspects.. <i>Orphanet Journal of Rare Diseases</i> , 2022 , 17, 29	4.2	0
11	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
10	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
9	Tandem Mass Tags for Comparative and Discovery Proteomics. <i>Methods in Molecular Biology</i> , 2021 , 2228, 117-131	1.4	0
8	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
7	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
6	Identification of proteins from human cerebrospinal fluid, separated by two-dimensional polyacrylamide gel electrophoresis 2000 , 21, 2721		0
5	Subcellular Analysis of the Platelet Proteome. <i>Current Proteomics</i> , 2011 , 8, 181-192	0.7	
4	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	
3	Mass-Spectrometry-Based Proteomics: General Overview and Posttranslational Modification Analysis in the Context of Platelet Research27-65		
2	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	
1	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	