

Thomas R Kislinger

List of Publications by Citations

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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.

154
papers

15,127
citations

54
h-index

122
g-index

159
ext. papers

18,285
ext. citations

10.2
avg, IF

5.72
L-index

#	Paper	IF	Citations
154	Minimal information for studies of extracellular vesicles 2018 (MISEV2018): a position statement of the International Society for Extracellular Vesicles and update of the MISEV2014 guidelines. <i>Journal of Extracellular Vesicles</i> , 2018 , 7, 1535750	16.4	3642
153	Blockade of RAGE-amphotericin signalling suppresses tumour growth and metastases. <i>Nature</i> , 2000 , 405, 354-60	50.4	1022
152	N(epsilon)-(carboxymethyl)lysine adducts of proteins are ligands for receptor for advanced glycation end products that activate cell signaling pathways and modulate gene expression. <i>Journal of Biological Chemistry</i> , 1999 , 274, 31740-9	5.4	687
151	Characterization of the proteins released from activated platelets leads to localization of novel platelet proteins in human atherosclerotic lesions. <i>Blood</i> , 2004 , 103, 2096-104	2.2	619
150	RAGE blockade stabilizes established atherosclerosis in diabetic apolipoprotein E-null mice. <i>Circulation</i> , 2002 , 106, 2827-35	16.7	486
149	RAGE drives the development of glomerulosclerosis and implicates podocyte activation in the pathogenesis of diabetic nephropathy. <i>American Journal of Pathology</i> , 2003 , 162, 1123-37	5.8	476
148	Advanced glycation end products activate endothelium through signal-transduction receptor RAGE: a mechanism for amplification of inflammatory responses. <i>Circulation</i> , 2002 , 105, 816-22	16.7	454
147	Global survey of organ and organelle protein expression in mouse: combined proteomic and transcriptomic profiling. <i>Cell</i> , 2006 , 125, 173-86	56.2	400
146	Expression of advanced glycation end products and their cellular receptor RAGE in diabetic nephropathy and nondiabetic renal disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2000 , 11, 1656-1666	12.7	350
145	Blockade of receptor for advanced glycation end-products restores effective wound healing in diabetic mice. <i>American Journal of Pathology</i> , 2001 , 159, 513-25	5.8	345
144	Blockade of RAGE suppresses periodontitis-associated bone loss in diabetic mice. <i>Journal of Clinical Investigation</i> , 2000 , 105, 1117-24	15.9	259
143	EVpedia: a community web portal for extracellular vesicles research. <i>Bioinformatics</i> , 2015 , 31, 933-9	7.2	256
142	Receptor for advanced glycation end products mediates inflammation and enhanced expression of tissue factor in vasculature of diabetic apolipoprotein E-null mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2001 , 21, 905-10	9.4	245
141	The emerging role of extracellular vesicles as biomarkers for urogenital cancers. <i>Nature Reviews Urology</i> , 2014 , 11, 688-701	5.5	201
140	A novel community driven software for functional enrichment analysis of extracellular vesicles data. <i>Journal of Extracellular Vesicles</i> , 2017 , 6, 1321455	16.4	200
139	Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. <i>Nature Genetics</i> , 2014 , 46, 1166-9	36.3	150
138	Loss of the Timp gene family is sufficient for the acquisition of the CAF-like cell state. <i>Nature Cell Biology</i> , 2014 , 16, 889-901	23.4	139

137	PRISM, a generic large scale proteomic investigation strategy for mammals. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 96-106	7.6	133
136	Integrating gene and protein expression data: pattern analysis and profile mining. <i>Methods</i> , 2005 , 35, 303-14	4.6	132
135	A proteome resource of ovarian cancer ascites: integrated proteomic and bioinformatic analyses to identify putative biomarkers. <i>Journal of Proteome Research</i> , 2008 , 7, 339-51	5.6	123
134	RAGE limits regeneration after massive liver injury by coordinated suppression of TNF-alpha and NF-kappaB. <i>Journal of Experimental Medicine</i> , 2005 , 201, 473-84	16.6	123
133	Cell-surface proteomics identifies lineage-specific markers of embryo-derived stem cells. <i>Developmental Cell</i> , 2012 , 22, 887-901	10.2	120
132	Comparative systems biology of human and mouse as a tool to guide the modeling of human placental pathology. <i>Molecular Systems Biology</i> , 2009 , 5, 279	12.2	115
131	Cancer cells induced to express mesenchymal phenotype release exosome-like extracellular vesicles carrying tissue factor. <i>Journal of Biological Chemistry</i> , 2012 , 287, 43565-72	5.4	111
130	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine. <i>Proteomics</i> , 2013 , 13, 1667-1671	4.8	109
129	Cardiovascular proteomics: tools to develop novel biomarkers and potential applications. <i>Journal of the American College of Cardiology</i> , 2006 , 48, 1733-41	15.1	109
128	Multidimensional protein identification technology (MudPIT): technical overview of a profiling method optimized for the comprehensive proteomic investigation of normal and diseased heart tissue. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 1207-20	3.5	107
127	Proteome dynamics during C2C12 myoblast differentiation. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 887-901	7.6	104
126	Onco-proteogenomics: cancer proteomics joins forces with genomics. <i>Nature Methods</i> , 2014 , 11, 1107-13	11.6	102
125	The Proteogenomic Landscape of Curable Prostate Cancer. <i>Cancer Cell</i> , 2019 , 35, 414-427.e6	24.3	97
124	Tumor-derived exosomes and microvesicles in head and neck cancer: implications for tumor biology and biomarker discovery. <i>Proteomics</i> , 2013 , 13, 1608-23	4.8	91
123	The Glc7 phosphatase subunit of the cleavage and polyadenylation factor is essential for transcription termination on snoRNA genes. <i>Molecular Cell</i> , 2008 , 29, 577-87	17.6	85
122	Comparative proteomics profiling of a phospholamban mutant mouse model of dilated cardiomyopathy reveals progressive intracellular stress responses. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 519-33	7.6	85
121	In-depth proteomic analyses of ovarian cancer cell line exosomes reveals differential enrichment of functional categories compared to the NCI 60 proteome. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 694-701	3.4	80
120	Impaired tRNA nuclear export links DNA damage and cell-cycle checkpoint. <i>Cell</i> , 2007 , 131, 915-26	56.2	77

119	MicroRNA networks in mouse lung organogenesis. <i>PLoS ONE</i> , 2010 , 5, e10854	3.7	73
118	A combination of H2A.Z and H4 acetylation recruits Brd2 to chromatin during transcriptional activation. <i>PLoS Genetics</i> , 2012 , 8, e1003047	6	70
117	Genes, proteins and complexes: the multifaceted nature of FHL family proteins in diverse tissues. <i>Journal of Cellular and Molecular Medicine</i> , 2010 , 14, 2702-20	5.6	70
116	Cardiac-specific overexpression of sarcolipin in phospholamban null mice impairs myocyte function that is restored by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 2446-51	11.5	69
115	An acetylated form of histone H2A.Z regulates chromosome architecture in <i>Schizosaccharomyces pombe</i> . <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1286-93	17.6	68
114	Glycoprotein 2 is a specific cell surface marker of human pancreatic progenitors. <i>Nature Communications</i> , 2017 , 8, 331	17.4	67
113	Integrated omic analysis of lung cancer reveals metabolism proteome signatures with prognostic impact. <i>Nature Communications</i> , 2014 , 5, 5469	17.4	67
112	Targeted proteomics by selected reaction monitoring mass spectrometry: applications to systems biology and biomarker discovery. <i>Molecular BioSystems</i> , 2011 , 7, 292-303		66
111	Recent advances in mass spectrometry based clinical proteomics: applications to cancer research. <i>Clinical Proteomics</i> , 2020 , 17, 17	5	65
110	Qualitative changes in the proteome of extracellular vesicles accompanying cancer cell transition to mesenchymal state. <i>Experimental Cell Research</i> , 2013 , 319, 2747-57	4.2	64
109	Isolation of cell surface proteins for mass spectrometry-based proteomics. <i>Expert Review of Proteomics</i> , 2010 , 7, 141-54	4.2	64
108	Divergent evolution of temozolomide resistance in glioblastoma stem cells is reflected in extracellular vesicles and coupled with radiosensitization. <i>Neuro-Oncology</i> , 2018 , 20, 236-248	1	64
107	In-depth proteomics of ovarian cancer ascites: combining shotgun proteomics and selected reaction monitoring mass spectrometry. <i>Journal of Proteome Research</i> , 2011 , 10, 2286-99	5.6	63
106	Identification of differentially expressed proteins in direct expressed prostatic secretions of men with organ-confined versus extracapsular prostate cancer. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1870-84	7.6	62
105	Targeted proteomics identifies liquid-biopsy signatures for extracapsular prostate cancer. <i>Nature Communications</i> , 2016 , 7, 11906	17.4	59
104	Automated 2D peptide separation on a 1D nano-LC-MS system. <i>Journal of Proteome Research</i> , 2009 , 8, 1610-6	5.6	56
103	Peptide separations by on-line MudPIT compared to isoelectric focusing in an off-gel format: application to a membrane-enriched fraction from C2C12 mouse skeletal muscle cells. <i>Journal of Proteome Research</i> , 2009 , 8, 4860-9	5.6	56
102	Integrated proteomic and transcriptomic profiling of mouse lung development and Nmyc target genes. <i>Molecular Systems Biology</i> , 2007 , 3, 109	12.2	56

101	PTP1B controls non-mitochondrial oxygen consumption by regulating RNF213 to promote tumour survival during hypoxia. <i>Nature Cell Biology</i> , 2016 , 18, 803-813	23.4	55
100	Qualitative determination of specific protein glycation products by matrix-assisted laser desorption/ionization mass spectrometry Peptide mapping. <i>Journal of Agricultural and Food Chemistry</i> , 2002 , 50, 2153-60	5.7	54
99	In-depth proteomic analyses of direct expressed prostatic secretions. <i>Journal of Proteome Research</i> , 2010 , 9, 2109-16	5.6	52
98	Potentially novel candidate biomarkers for head and neck squamous cell carcinoma identified using an integrated cell line-based discovery strategy. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1404-15	7.6	51
97	The proteomics of prostate cancer exosomes. <i>Expert Review of Proteomics</i> , 2014 , 11, 167-77	4.2	50
96	Identification of prostate-enriched proteins by in-depth proteomic analyses of expressed prostatic secretions in urine. <i>Journal of Proteome Research</i> , 2012 , 11, 2386-96	5.6	50
95	Proteomic Analysis of Cancer-Associated Fibroblasts Reveals a Paracrine Role for MFAP5 in Human Oral Tongue Squamous Cell Carcinoma. <i>Journal of Proteome Research</i> , 2018 , 17, 2045-2059	5.6	47
94	The replication-independent histone H3-H4 chaperones HIR, ASF1, and RTT106 co-operate to maintain promoter fidelity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 1709-18	5.4	47
93	Constitutively active calcineurin induces cardiac endoplasmic reticulum stress and protects against apoptosis that is mediated by alpha-crystallin-B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18481-6	11.5	47
92	Extracellular vesicles in ovarian cancer: applications to tumor biology, immunotherapy and biomarker discovery. <i>Expert Review of Proteomics</i> , 2016 , 13, 395-409	4.2	46
91	Identification of pathways associated with invasive behavior by ovarian cancer cells using multidimensional protein identification technology (MudPIT). <i>Molecular BioSystems</i> , 2008 , 4, 762-73		45
90	Relative quantification of N(epsilon)-(Carboxymethyl)lysine, imidazolone A, and the Amadori product in glycated lysozyme by MALDI-TOF mass spectrometry. <i>Journal of Agricultural and Food Chemistry</i> , 2003 , 51, 51-7	5.7	45
89	Molecular heterogeneity of non-small cell lung carcinoma patient-derived xenografts closely reflect their primary tumors. <i>International Journal of Cancer</i> , 2017 , 140, 662-673	7.5	44
88	Large-scale characterization and analysis of the murine cardiac proteome. <i>Journal of Proteome Research</i> , 2009 , 8, 1887-901	5.6	43
87	Analysis of protein glycation products by MALDI-TOF/MS. <i>Annals of the New York Academy of Sciences</i> , 2005 , 1043, 249-59	6.5	43
86	Novel insights into head and neck cancer using next-generation "omic" technologies. <i>Cancer Research</i> , 2015 , 75, 480-6	10.1	42
85	Sarcoplipin retention in the endoplasmic reticulum depends on its C-terminal RSYQY sequence and its interaction with sarco(endo)plasmic Ca(2+)-ATPases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 16807-12	11.5	42
84	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. <i>Cell Stem Cell</i> , 2016 , 19, 383-96	18	40

83	Genome-wide analysis of the maternal-to-zygotic transition in <i>Drosophila</i> primordial germ cells. <i>Genome Biology</i> , 2012 , 13, R11	18.3	39
82	Structural determination of the phosphorylation domain of the ryanodine receptor. <i>FEBS Journal</i> , 2012 , 279, 3952-64	5.7	38
81	Analysis of protein glycation products by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. <i>Current Medicinal Chemistry</i> , 2004 , 11, 2185-93	4.3	38
80	A live zebrafish-based screening system for human nuclear receptor ligand and cofactor discovery. <i>PLoS ONE</i> , 2010 , 5, e9797	3.7	38
79	System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. <i>Clinical Cancer Research</i> , 2010 , 16, 4572-82	12.9	36
78	Translational analysis of mouse and human placental protein and mRNA reveals distinct molecular pathologies in human preeclampsia. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.012526	7.6	36
77	Multidimensional protein identification technology: current status and future prospects. <i>Expert Review of Proteomics</i> , 2005 , 2, 27-39	4.2	32
76	Global protein shotgun expression profiling of proliferating mcf-7 breast cancer cells. <i>Journal of Proteome Research</i> , 2005 , 4, 674-89	5.6	31
75	Determination of Nε-carboxymethyllysine in heated milk products by immunochemical methods. <i>European Food Research and Technology</i> , 1999 , 209, 72-76	3.4	31
74	Proteotranscriptomic Analysis Reveals Stage Specific Changes in the Molecular Landscape of Clear-Cell Renal Cell Carcinoma. <i>PLoS ONE</i> , 2016 , 11, e0154074	3.7	31
73	CHCHD2 Is Coamplified with EGFR in NSCLC and Regulates Mitochondrial Function and Cell Migration. <i>Molecular Cancer Research</i> , 2015 , 13, 1119-29	6.6	30
72	Detecting protein variants by mass spectrometry: a comprehensive study in cancer cell-lines. <i>Genome Medicine</i> , 2017 , 9, 62	14.4	30
71	Cell-surface proteomics for the identification of novel therapeutic targets in cancer. <i>Expert Review of Proteomics</i> , 2018 , 15, 259-275	4.2	29
70	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2241-6	11.5	29
69	Spatially confined sub-tumor microenvironments in pancreatic cancer. <i>Cell</i> , 2021 , 184, 5577-5592.e18	56.2	29
68	Endoplasmic reticulum protein targeting of phospholamban: a common role for an N-terminal di-arginine motif in ER retention?. <i>PLoS ONE</i> , 2010 , 5, e11496	3.7	28
67	VennDIS: a JavaFX-based Venn and Euler diagram software to generate publication quality figures. <i>Proteomics</i> , 2015 , 15, 1239-44	4.8	27
66	A cost-benefit analysis of multidimensional fractionation of affinity purification-mass spectrometry samples. <i>Proteomics</i> , 2011 , 11, 2603-12	4.8	27

65	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <i>Nature Medicine</i> , 2019 , 25, 1615-1626	50.5	25
64	Qualitative determination of early Maillard-products by MALDI-TOF mass spectrometry peptide mapping. <i>European Food Research and Technology</i> , 2002 , 215, 65-71	3.4	25
63	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021 , 597, 119-125	50.4	25
62	Proteomic profiles of human lung adeno and squamous cell carcinoma using super-SILAC and label-free quantification approaches. <i>Proteomics</i> , 2014 , 14, 795-803	4.8	24
61	Expansion of stem cells counteracts age-related mammary regression in compound Timp1/Timp3 null mice. <i>Nature Cell Biology</i> , 2015 , 17, 217-27	23.4	24
60	Global proteome analysis identifies active immunoproteasome subunits in human platelets. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3308-19	7.6	24
59	Proteomic profiling of the planarian <i>Schmidtea mediterranea</i> and its mucous reveals similarities with human secretions and those predicted for parasitic flatworms. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 681-91	7.6	24
58	Evolutionarily conserved intercalated disc protein Tmem65 regulates cardiac conduction and connexin 43 function. <i>Nature Communications</i> , 2015 , 6, 8391	17.4	23
57	Proteomic analysis of human fetal atria and ventricle. <i>Journal of Proteome Research</i> , 2014 , 13, 5869-78	5.6	23
56	Primary tumor xenografts of human lung adeno and squamous cell carcinoma express distinct proteomic signatures. <i>Journal of Proteome Research</i> , 2011 , 10, 161-74	5.6	23
55	HLA-DP constitutively presents endogenous peptides generated by the class I antigen processing pathway. <i>Nature Communications</i> , 2017 , 8, 15244	17.4	22
54	Choice of biological source material supersedes oxidative stress in its influence on DJ-1 in vivo interactions with Hsp90. <i>Journal of Proteome Research</i> , 2011 , 10, 4388-404	5.6	22
53	Proteogenomics: Opportunities and Caveats. <i>Clinical Chemistry</i> , 2016 , 62, 551-7	5.5	21
52	A Genome Scale Screen for Mutants with Delayed Exit from Mitosis: Ire1-Independent Induction of Autophagy Integrates ER Homeostasis into Mitotic Lifespan. <i>PLoS Genetics</i> , 2015 , 11, e1005429	6	21
51	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , 2018 , 217, 2951-2974	7.3	20
50	Identification of an FHL1 protein complex containing ACTN1, ACTN4, and PDLIM1 using affinity purifications and MS-based protein-protein interaction analysis. <i>Molecular BioSystems</i> , 2011 , 7, 1185-96		20
49	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015 , 12, 183-9	10.6	17
48	Use of colloidal silica-beads for the isolation of cell-surface proteins for mass spectrometry-based proteomics. <i>Methods in Molecular Biology</i> , 2011 , 748, 227-41	1.4	17

47	REEP5 depletion causes sarco-endoplasmic reticulum vacuolization and cardiac functional defects. <i>Nature Communications</i> , 2020 , 11, 965	17.4	16
46	Identification of novel ryanodine receptor 1 (RyR1) protein interaction with calcium homeostasis endoplasmic reticulum protein (CHERP). <i>Journal of Biological Chemistry</i> , 2011 , 286, 17060-8	5.4	16
45	Interactome and interface protocol (ZIP): a novel strategy for high sensitivity topology mapping of protein complexes. <i>Proteomics</i> , 2007 , 7, 3835-52	4.8	15
44	Going global: protein expression profiling using shotgun mass spectrometry. <i>Current Opinion in Molecular Therapeutics</i> , 2003 , 5, 285-93		15
43	Metalloprotease inhibitor TIMP proteins control FGF-2 bioavailability and regulate skeletal growth. <i>Journal of Cell Biology</i> , 2019 , 218, 3134-3152	7.3	13
42	Integrated omic analysis of oropharyngeal carcinomas reveals human papillomavirus (HPV)-dependent regulation of the activator protein 1 (AP-1) pathway. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3572-84	7.6	13
41	Lung cancer: developmental networks gone awry?. <i>Cancer Biology and Therapy</i> , 2009 , 8, 312-8	4.6	13
40	Analyzing the cardiac muscle proteome by liquid chromatography-mass spectrometry-based expression proteomics. <i>Methods in Molecular Biology</i> , 2007 , 357, 15-31	1.4	13
39	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020 , 11, 5248	17.4	13
38	Proteomic Profiling of Secreted Proteins, Exosomes, and Microvesicles in Cell Culture Conditioned Media. <i>Methods in Molecular Biology</i> , 2018 , 1722, 91-102	1.4	12
37	High-throughput approaches for precision medicine in high-grade serous ovarian cancer. <i>Journal of Hematology and Oncology</i> , 2020 , 13, 134	22.4	12
36	N-Glycoproteomics of Patient-Derived Xenografts: A Strategy to Discover Tumor-Associated Proteins in High-Grade Serous Ovarian Cancer. <i>Cell Systems</i> , 2019 , 8, 345-351.e4	10.6	11
35	Characterization of Protein Content Present in Exosomes Isolated from Conditioned Media and Urine. <i>Current Protocols in Protein Science</i> , 2017 , 87, 24.9.1-24.9.12	3.1	10
34	Reporters to mark and eliminate basal or luminal epithelial cells in culture and in vivo. <i>PLoS Biology</i> , 2018 , 16, e2004049	9.7	10
33	Proteome analysis of mouse model systems: A tool to model human disease and for the investigation of tissue-specific biology. <i>Journal of Proteomics</i> , 2010 , 73, 2205-18	3.9	10
32	Barbiturate induced benzophenanthridine alkaloid formation proceeds by gene transcript accumulation in the California poppy. <i>Biochemical and Biophysical Research Communications</i> , 1997 , 241, 606-10	3.4	10
31	Scribble is required for pregnancy-induced alveologenesis in the adult mammary gland. <i>Journal of Cell Science</i> , 2016 , 129, 2307-15	5.3	10
30	Identification of a BET family bromodomain/casein kinase II/TAF-containing complex as a regulator of mitotic condensin function. <i>Cell Reports</i> , 2014 , 6, 892-905	10.6	9

29	Advances in ovarian cancer proteomics: the quest for biomarkers and improved therapeutic interventions. <i>Expert Review of Proteomics</i> , 2008 , 5, 551-60	4.2	9
28	Quantitative peptide and protein profiling by mass spectrometry. <i>Methods in Molecular Biology</i> , 2009 , 492, 21-38	1.4	8
27	Proteomics-based investigations of animal models of disease. <i>Proteomics - Clinical Applications</i> , 2008 , 2, 638-53	3.1	7
26	Quantifying the influence of mutation detection on tumour subclonal reconstruction. <i>Nature Communications</i> , 2020 , 11, 6247	17.4	5
25	Novel approaches for the identification of biomarkers of aggressive prostate cancer. <i>Genome Medicine</i> , 2013 , 5, 56	14.4	5
24	Method for the affinity purification of covalently linked peptides following cyanogen bromide cleavage of proteins. <i>Analytical Chemistry</i> , 2009 , 81, 9885-95	7.8	5
23	Bioinformatic analysis of membrane and associated proteins in murine cardiomyocytes and human myocardium. <i>Scientific Data</i> , 2020 , 7, 425	8.2	5
22	PDCD4 regulates axonal growth by translational repression of neurite growth-related genes and is modulated during nerve injury responses. <i>Rna</i> , 2020 , 26, 1637-1653	5.8	5
21	Mammary epithelial cells have lineage-rooted metabolic identities. <i>Nature Metabolism</i> , 2021 , 3, 665-681	14.6	5
20	Quantitative Proteomics of Intestinal Mucosa From Male Mice Lacking Intestinal Epithelial Insulin Receptors. <i>Endocrinology</i> , 2017 , 158, 2470-2485	4.8	4
19	Targeted Mass Spectrometry of a Clinically Relevant PSA Variant from Post-DRE Urines for Quantitation and Genotype Determination. <i>Proteomics - Clinical Applications</i> , 2020 , 14, e2000012	3.1	4
18	Proteomic Response of Human Umbilical Vein Endothelial Cells to Histamine Stimulation. <i>Proteomics</i> , 2017 , 17, 1700116	4.8	4
17	Proteomic discovery of non-invasive biomarkers of localized prostate cancer using mass spectrometry. <i>Nature Reviews Urology</i> , 2021 , 18, 707-724	5.5	4
16	Clinical proteomics: getting to the heart of the matter. <i>Circulation: Cardiovascular Genetics</i> , 2012 , 5, 377		3
15	Addressing Cellular Heterogeneity in Cancer through Precision Proteomics. <i>Journal of Proteome Research</i> , 2020 ,	5.6	3
14	Glomulin: a permissivity factor for vaccinia virus infection. <i>Journal of Interferon and Cytokine Research</i> , 2012 , 32, 127-37	3.5	2
13	Mammary epithelial cells have lineage-restricted metabolic identities		2
12	Rat Sciatic Nerve Axoplasm Proteome Is Enriched with Ribosomal Proteins during Regeneration Processes. <i>Journal of Proteome Research</i> , 2021 , 20, 2506-2520	5.6	2

11	A proteomic investigation of isogenic radiation resistant prostate cancer cell lines. <i>Proteomics - Clinical Applications</i> , 2021 , 15, e2100037	3.1	2
10	Optimization of small extracellular vesicle isolation from expressed prostatic secretions in urine for in-depth proteomic analysis.. <i>Journal of Extracellular Vesicles</i> , 2022 , 11, e12184	16.4	1
9	Standardization and Harmonization of Distributed Multi-National Proteotype Analysis supporting Precision Medicine Studies		1
8	Mammary lineage dictates homologous recombination repair and PARP inhibitor vulnerability		1
7	Functionally selective activation of the dopamine receptor D is mirrored by the protein expression profiles. <i>Scientific Reports</i> , 2021 , 11, 3501	4.9	1
6	Spatially confined sub-tumor microenvironments orchestrate pancreatic cancer pathobiology		1
5	Multidimensional protein identification technology analysis highlights mitoxantrone-induced expression modulations in the primary prostate cancer cell proteome. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 347-58	3.1	0
4	Prostate cancer multiparametric magnetic resonance imaging visibility is a tumor-intrinsic phenomena.. <i>Journal of Hematology and Oncology</i> , 2022 , 15, 48	22.4	0
3	PRISM: a new strategy to analyze the mammalian proteome. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 37-42		
2	Using proteomics to probe neurons. <i>ELife</i> , 2015 , 4, e09103	8.9	
1	Proteomics and Bioinformatics in Biomedical Research. <i>Cancer Genomics and Proteomics</i> , 2006 , 3, 11-28	3.3	