

Joao A Paulo

List of Publications by Year in descending order

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229
papers

15,507
citations

26630

56
h-index

25787

108
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257
all docs

257
docs citations

257
times ranked

23032
citing authors

#	ARTICLE	IF	CITATIONS
1	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	28.9	1,241
2	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
3	The PINK1-PARKIN Mitochondrial Ubiquitylation Pathway Drives a Program of OPTN/NDP52 Recruitment and TBK1 Activation to Promote Mitophagy. <i>Molecular Cell</i> , 2015, 60, 7-20.	9.7	658
4	Autophagy promotes immune evasion of pancreatic cancer by degrading MHC-I. <i>Nature</i> , 2020, 581, 100-105.	27.8	628
5	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
6	Detection and Quantitation of Circulating Human Irisin by Tandem Mass Spectrometry. <i>Cell Metabolism</i> , 2015, 22, 734-740.	16.2	414
7	Excessive Cell Growth Causes Cytoplasm Dilution And Contributes to Senescence. <i>Cell</i> , 2019, 176, 1083-1097.e18.	28.9	347
8	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. <i>Nature Methods</i> , 2020, 17, 399-404.	19.0	276
9	Streamlined Tandem Mass Tag (SL-TMT) Protocol: An Efficient Strategy for Quantitative (Phospho)proteome Profiling Using Tandem Mass Tag-Synchronous Precursor Selection-MS3. <i>Journal of Proteome Research</i> , 2018, 17, 2226-2236.	3.7	245
10	Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6637-6642.	7.1	240
11	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. <i>Nature Communications</i> , 2017, 8, 15965.	12.8	231
12	Multidimensional Tracking of GPCR Signaling via Peroxidase-Catalyzed Proximity Labeling. <i>Cell</i> , 2017, 169, 338-349.e11.	28.9	221
13	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , 2020, 180, 968-983.e24.	28.9	220
14	TEX264 Is an Endoplasmic Reticulum-Resident ATG8-Interacting Protein Critical for ER Remodeling during Nutrient Stress. <i>Molecular Cell</i> , 2019, 74, 891-908.e10.	9.7	193
15	The Secreted Enzyme PM20D1 Regulates Lipidated Amino Acid Uncouplers of Mitochondria. <i>Cell</i> , 2016, 166, 424-435.	28.9	188
16	Diabetes relief in mice by glucose-sensing insulin-secreting human β -cells. <i>Nature</i> , 2019, 567, 43-48.	27.8	188
17	An Ancient, Unified Mechanism for Metformin Growth Inhibition in <i>C.Âlegans</i> and Cancer. <i>Cell</i> , 2016, 167, 1705-1718.e13.	28.9	181
18	Quantitative mass spectrometry-based multiplexing compares the abundance of 5000 <i>S. cerevisiae</i> proteins across 10 carbon sources. <i>Journal of Proteomics</i> , 2016, 148, 85-93.	2.4	173

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19	Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. <i>Cell</i> , 2016, 166, 1198-1214.e24.	28.9	172
20	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 2026-2034.	3.7	171
21	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019, 74, 32-44.e8.	9.7	170
22	TMTpro-18plex: The Expanded and Complete Set of TMTpro Reagents for Sample Multiplexing. <i>Journal of Proteome Research</i> , 2021, 20, 2964-2972.	3.7	158
23	Characterization and Optimization of Multiplexed Quantitative Analyses Using High-Field Asymmetric-Waveform Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 4010-4016.	6.5	155
24	A Triple Knockout (TKO) Proteomics Standard for Diagnosing Ion Interference in Isobaric Labeling Experiments. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1620-1625.	2.8	149
25	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. <i>Molecular Cell</i> , 2018, 70, 211-227.e8.	9.7	145
26	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	3.7	143
27	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. <i>Molecular Cell</i> , 2020, 77, 1124-1142.e10.	9.7	143
28	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. <i>ELife</i> , 2015, 4, .	6.0	141
29	pH-Gated Succinate Secretion Regulates Muscle Remodeling in Response to Exercise. <i>Cell</i> , 2020, 183, 62-75.e17.	28.9	129
30	RAB7A phosphorylation by TBK1 promotes mitophagy via the PINK-PARKIN pathway. <i>Science Advances</i> , 2018, 4, eaav0443.	10.3	128
31	Biallelic Mutations in DNAJC12 Cause Hyperphenylalaninemia, Dystonia, and Intellectual Disability. <i>American Journal of Human Genetics</i> , 2017, 100, 257-266.	6.2	127
32	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
33	UBE2O remodels the proteome during terminal erythroid differentiation. <i>Science</i> , 2017, 357, .	12.6	121
34	Epstein-Barr-Virus-Induced One-Carbon Metabolism Drives B Cell Transformation. <i>Cell Metabolism</i> , 2019, 30, 539-555.e11.	16.2	119
35	A Strategy to Combine Sample Multiplexing with Targeted Proteomics Assays for High-Throughput Protein Signature Characterization. <i>Molecular Cell</i> , 2017, 65, 361-370.	9.7	118
36	Structure-Based Evolution of Low Nanomolar O-GlcNAc Transferase Inhibitors. <i>Journal of the American Chemical Society</i> , 2018, 140, 13542-13545.	13.7	117

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37	DPP9 sequesters the CÂterminus of NLRP1 to repress inflammasome activation. <i>Nature</i> , 2021, 592, 778-783.	27.8	114
38	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. <i>Journal of Proteome Research</i> , 2019, 18, 1299-1306.	3.7	109
39	A forward genetic screen identifies erythrocyte CD55 as essential for <i>Plasmodium falciparum</i> invasion. <i>Science</i> , 2015, 348, 711-714.	12.6	107
40	Selective Alanine Transporter Utilization Creates a Targetable Metabolic Niche in Pancreatic Cancer. <i>Cancer Discovery</i> , 2020, 10, 1018-1037.	9.4	104
41	A Survey and Classification of Storage Deduplication Systems. <i>ACM Computing Surveys</i> , 2014, 47, 1-30.	23.0	102
42	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. <i>Nature</i> , 2017, 547, 463-467.	27.8	96
43	EDF1 coordinates cellular responses to ribosome collisions. <i>ELife</i> , 2020, 9, .	6.0	96
44	Systematic Analysis of Human Cells Lacking ATG8 Proteins Uncovers Roles for GABARAPs and the CCZ1/MON1 Regulator C18orf8/RMC1 in Macroautophagic and Selective Autophagic Flux. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	95
45	Defective respiration and one-carbon metabolism contribute to impaired naïve T cell activation in aged mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13347-13352.	7.1	93
46	Comprehensive Temporal Protein Dynamics during the Diauxic Shift in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2454-2465.	3.8	84
47	A Temporal Proteomic Map of Epstein-Barr Virus Lytic Replication in B Cells. <i>Cell Reports</i> , 2017, 19, 1479-1493.	6.4	83
48	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. <i>Genes and Development</i> , 2019, 33, 1031-1047.	5.9	83
49	Proteomic Analysis of an $\hat{\pm}7$ Nicotinic Acetylcholine Receptor Interactome. <i>Journal of Proteome Research</i> , 2009, 8, 1849-1858.	3.7	82
50	Urine proteomics for discovery of improved diagnostic markers of Kawasaki disease. <i>EMBO Molecular Medicine</i> , 2013, 5, 210-220.	6.9	80
51	Blocking an N-terminal acetylationâ€dependent protein interaction inhibits an E3 ligase. <i>Nature Chemical Biology</i> , 2017, 13, 850-857.	8.0	80
52	<i>Plasmodium falciparum</i> CRK4 directs continuous rounds of DNA replication during schizogony. <i>Nature Microbiology</i> , 2017, 2, 17017.	13.3	79
53	TIMMDC1/C3orf1 Functions as a Membrane-Embedded Mitochondrial Complex I Assembly Factor through Association with the MCIA Complex. <i>Molecular and Cellular Biology</i> , 2014, 34, 847-861.	2.3	78
54	Systematic quantitative analysis of ribosome inventory during nutrient stress. <i>Nature</i> , 2020, 583, 303-309.	27.8	78

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55	Native Chromatin Proteomics Reveals a Role for Specific Nucleoporins in Heterochromatin Organization and Maintenance. <i>Molecular Cell</i> , 2020, 77, 51-66.e8.	9.7	75
56	Proteome of Human Perilymph. <i>Journal of Proteome Research</i> , 2011, 10, 3845-3851.	3.7	74
57	O-GlcNAc regulates gene expression by controlling detained intron splicing. <i>Nucleic Acids Research</i> , 2020, 48, 5656-5669.	14.5	67
58	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	6.0	67
59	Effects of MEK inhibitors GSK1120212 and PD0325901 in vivo using 10â€plex quantitative proteomics and phosphoproteomics. <i>Proteomics</i> , 2015, 15, 462-473.	2.2	64
60	Proteome-wide mapping of short-lived proteins in human cells. <i>Molecular Cell</i> , 2021, 81, 4722-4735.e5.	9.7	64
61	Proteome-wide quantitative multiplexed profiling of protein expression: carbon-source dependency in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2015, 26, 4063-4074.	2.1	62
62	Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. <i>ELife</i> , 2020, 9, .	6.0	62
63	Automethylation-induced conformational switch in Clr4 (Suv39h) maintains epigenetic stability. <i>Nature</i> , 2018, 560, 504-508.	27.8	59
64	Quantitative proteomics reveals the selectivity of ubiquitin-binding autophagy receptors in the turnover of damaged lysosomes by lysophagy. <i>ELife</i> , 2021, 10, .	6.0	59
65	Evaluating False Transfer Rates from the Match-between-Runs Algorithm with a Two-Proteome Model. <i>Journal of Proteome Research</i> , 2019, 18, 4020-4026.	3.7	57
66	Multiplexed, Proteome-Wide Protein Expression Profiling: Yeast Deubiquitylating Enzyme Knockout Strains. <i>Journal of Proteome Research</i> , 2015, 14, 5306-5317.	3.7	56
67	Optimized Workflow for Multiplexed Phosphorylation Analysis of TMT-Labeled Peptides Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 554-560.	3.7	56
68	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. <i>Science Advances</i> , 2019, 5, eaay4624.	10.3	55
69	Probing the missing mature $\hat{2}$ -cell proteomic landscape in differentiating patient iPSC-derived cells. <i>Scientific Reports</i> , 2017, 7, 4780.	3.3	54
70	Multiplexed Phosphoproteomic Profiling Using Titanium Dioxide and Immunoaffinity Enrichments Reveals Complementary Phosphorylation Events. <i>Journal of Proteome Research</i> , 2017, 16, 1506-1514.	3.7	52
71	Temporal proteomics during neurogenesis reveals large-scale proteome and organelle remodeling via selective autophagy. <i>Molecular Cell</i> , 2021, 81, 5082-5098.e11.	9.7	52
72	Global Analysis of Protein Expression and Phosphorylation Levels in Nicotine-Treated Pancreatic Stellate Cells. <i>Journal of Proteome Research</i> , 2015, 14, 4246-4256.	3.7	51

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73	Compositional Proteomics: Effects of Spatial Constraints on Protein Quantification Utilizing Isobaric Tags. <i>Journal of Proteome Research</i> , 2018, 17, 590-599.	3.7	51
74	Bromodomain Inhibitors Correct Bioenergetic Deficiency Caused by Mitochondrial Disease Complex I Mutations. <i>Molecular Cell</i> , 2016, 64, 163-175.	9.7	50
75	A comprehensive proteomic and phosphoproteomic analysis of yeast deletion mutants of 14 orthologs and associated effects of rapamycin. <i>Proteomics</i> , 2015, 15, 474-486.	2.2	49
76	Altered patterns of global protein synthesis and translational fidelity in RPS15-mutated chronic lymphocytic leukemia. <i>Blood</i> , 2018, 132, 2375-2388.	1.4	48
77	Autophagy is required for proper cysteine homeostasis in pancreatic cancer through regulation of SLC7A11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
78	Mammalian cell proliferation requires noncatalytic functions of O-GlcNAc transferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
79	The NAD ⁺ Salvage Pathway Supports PHGDH-Driven Serine Biosynthesis. <i>Cell Reports</i> , 2018, 24, 2381-2391.e5.	6.4	47
80	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019, 51, 1308-1314.	21.4	47
81	Merkel cell polyomavirus activates LSD1-mediated blockade of non-canonical BAF to regulate transformation and tumorigenesis. <i>Nature Cell Biology</i> , 2020, 22, 603-615.	10.3	47
82	QIL1 mutation causes MICOS disassembly and early onset fatal mitochondrial encephalopathy with liver disease. <i>ELife</i> , 2016, 5, .	6.0	46
83	Cdkal1, a type 2 diabetes susceptibility gene, regulates mitochondrial function in adipose tissue. <i>Molecular Metabolism</i> , 2017, 6, 1212-1225.	6.5	44
84	The effects of nonignorable missing data on label-free mass spectrometry proteomics experiments. <i>Annals of Applied Statistics</i> , 2018, 12, 2075-2095.	1.1	44
85	Proteogenomic Network Analysis of Context-Specific KRAS Signaling in Mouse-to-Human Cross-Species Translation. <i>Cell Systems</i> , 2019, 9, 258-270.e6.	6.2	44
86	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6478-6485.	6.5	44
87	Brainstem Deficiency of the 14-3-3 Regulator of Serotonin Synthesis: A Proteomics Analysis in the Sudden Infant Death Syndrome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.009530.	3.8	42
88	Investigation of Proteomic and Phosphoproteomic Responses to Signaling Network Perturbations Reveals Functional Pathway Organizations in Yeast. <i>Cell Reports</i> , 2019, 29, 2092-2104.e4.	6.4	41
89	Nicotine-induced protein expression profiling reveals mutually altered proteins across four human cell lines. <i>Proteomics</i> , 2017, 17, 1600319.	2.2	40
90	Web-Based Search Tool for Visualizing Instrument Performance Using the Triple Knockout (TKO) Proteome Standard. <i>Journal of Proteome Research</i> , 2019, 18, 687-693.	3.7	40

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91	Mass Spectrometry-based Quantitative Proteomic Profiling of Human Pancreatic and Hepatic Stellate Cell Lines. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 105-113.	6.9	39
92	Sample preparation for proteomic analysis using a GeLC-MS/MS strategy. <i>Journal of Biological Methods</i> , 2016, 3, e45.	0.6	39
93	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
94	Pathogenic Pathways in Early-Onset Autosomal Recessive Parkinson's Disease Discovered Using Isogenic Human Dopaminergic Neurons. <i>Stem Cell Reports</i> , 2020, 14, 75-90.	4.8	37
95	Co-option of Plasmodium falciparum PP1 for egress from host erythrocytes. <i>Nature Communications</i> , 2020, 11, 3532.	12.8	37
96	Ubiquilin1 promotes antigen-receptor mediated proliferation by eliminating mislocalized mitochondrial proteins. <i>ELife</i> , 2017, 6, .	6.0	37
97	Proteomic Analysis of an Immortalized Mouse Pancreatic Stellate Cell Line Identifies Differentially-Expressed Proteins in Activated vs Nonproliferating Cell States. <i>Journal of Proteome Research</i> , 2011, 10, 4835-4844.	3.7	36
98	High-Resolution In Vivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. <i>Molecular Cell</i> , 2020, 79, 167-179.e11.	9.7	36
99	Selection of Heating Temperatures Improves the Sensitivity of the Proteome Integral Solubility Alteration Assay. <i>Journal of Proteome Research</i> , 2020, 19, 2159-2166.	3.7	36
100	A peroxisomal ubiquitin ligase complex forms a retrotranslocation channel. <i>Nature</i> , 2022, 607, 374-380.	27.8	36
101	The Effect of Wnt Pathway Modulators on Human iPSC-Derived Pancreatic Beta Cell Maturation. <i>Frontiers in Endocrinology</i> , 2019, 10, 293.	3.5	35
102	Encapsulation boosts islet-cell signature in differentiating human induced pluripotent stem cells via integrin signalling. <i>Scientific Reports</i> , 2020, 10, 414.	3.3	33
103	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32
104	Optimized sample preparation of endoscopic collected pancreatic fluid for SDS-PAGE analysis. <i>Electrophoresis</i> , 2010, 31, 2377-2387.	2.4	31
105	Proteomic analysis of a rat pancreatic stellate cell line using liquid chromatography tandem mass spectrometry (LC-MS/MS). <i>Journal of Proteomics</i> , 2011, 75, 708-717.	2.4	31
106	Proteomic Analysis of Formalin-Fixed Paraffin-Embedded Pancreatic Tissue Using Liquid Chromatography Tandem Mass Spectrometry. <i>Pancreas</i> , 2012, 41, 175-185.	1.1	30
107	Loss of the deubiquitinase USP36 destabilizes the RNA helicase DHX33 and causes preimplantation lethality in mice. <i>Journal of Biological Chemistry</i> , 2018, 293, 2183-2194.	3.4	30
108	Facultative protein selenation regulates redox sensitivity, adipose tissue thermogenesis, and obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10789-10796.	7.1	30

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109	Structures of chaperone-associated assembly intermediates reveal coordinated mechanisms of proteasome biogenesis. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 418-425.	8.2	29
110	Identification of Pancreas-Specific Proteins in Endoscopically (Endoscopic Pancreatic Function Test) Collected Pancreatic Fluid with Liquid Chromatography- Tandem Mass Spectrometry. <i>Pancreas</i> , 2010, 39, 889-896.	1.1	27
111	Multiplexed Relative Quantitation with Isobaric Tagging Mass Spectrometry Reveals Class I Major Histocompatibility Complex Ligand Dynamics in Response to Doxorubicin. <i>Analytical Chemistry</i> , 2019, 91, 5106-5115.	6.5	27
112	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	6.5	27
113	Role of the B Allele of Influenza A Virus Segment 8 in Setting Mammalian Host Range and Pathogenicity. <i>Journal of Virology</i> , 2016, 90, 9263-9284.	3.4	26
114	Targeting oncoproteins with a positive selection assay for protein degraders. <i>Science Advances</i> , 2021, 7, .	10.3	26
115	ORF10â€“Cullin-2â€“ZYG11B complex is not required for SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
116	Proteomic Analysis (GeLCâ€“MS/MS) of ePFT-Collected Pancreatic Fluid in Chronic Pancreatitis. <i>Journal of Proteome Research</i> , 2012, 11, 1897-1912.	3.7	25
117	Genotypeâ€“phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. <i>Molecular BioSystems</i> , 2015, 11, 3101-3110.	2.9	25
118	An Internal Standard for Assessing Phosphopeptide Recovery from Metal Ion/Oxide Enrichment Strategies. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1505-1511.	2.8	25
119	Filamin C Cardiomyopathy Variants Cause Protein and Lysosome Accumulation. <i>Circulation Research</i> , 2021, 129, 751-766.	4.5	25
120	Improved Method for Determining Absolute Phosphorylation Stoichiometry Using Bayesian Statistics and Isobaric Labeling. <i>Journal of Proteome Research</i> , 2017, 16, 4217-4226.	3.7	25
121	Temporal Proteomic Profiling of SH-SY5Y Differentiation with Retinoic Acid Using FAIMS and Real-Time Searching. <i>Journal of Proteome Research</i> , 2021, 20, 704-714.	3.7	24
122	Rapid toxin sequestration modifies poison frog physiology. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	23
123	Proteomic analysis of endoscopically (endoscopic pancreatic function test) collected gastroduodenal fluid using inâ€“gel tryptic digestion followed by LCâ€“MS/MS. <i>Proteomics - Clinical Applications</i> , 2010, 4, 715-725.	1.6	22
124	Inflammatory protein profiling of pancreatic cyst fluid using EUS-FNA in tandem with cytokine microarray differentiates between branch duct IPMN and inflammatory cysts. <i>Journal of Immunological Methods</i> , 2012, 382, 142-149.	1.4	22
125	Multiplexed Isobaric Tagâ€“Based Profiling of Seven Murine Tissues Following In Vivo Nicotine Treatment Using a Minimalistic Proteomics Strategy. <i>Proteomics</i> , 2018, 18, e1700326.	2.2	22
126	Therapy-Induced MHC I Ligands Shape Neo-Antitumor CD8 T Cell Responses during Oncolytic Virus-Based Cancer Immunotherapy. <i>Journal of Proteome Research</i> , 2019, 18, 2666-2675.	3.7	22

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127	PHD3 Loss Promotes Exercise Capacity and Fat Oxidation in Skeletal Muscle. <i>Cell Metabolism</i> , 2020, 32, 215-228.e7.	16.2	22
128	Advances in quantitative high-throughput phosphoproteomics with sample multiplexing. <i>Proteomics</i> , 2021, 21, e2000140.	2.2	22
129	Mass spectrometry-based proteomics for translational research: a technical overview. <i>Yale Journal of Biology and Medicine</i> , 2012, 85, 59-73.	0.2	22
130	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. <i>Nature Communications</i> , 2022, 13, .	12.8	22
131	webmedcentral. , 2013, 4, .		21
132	Targeting the cyclin-dependent kinase 5 in metastatic melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8001-8012.	7.1	21
133	Cross-species analysis of nicotine-induced proteomic alterations in pancreatic cells. <i>Proteomics</i> , 2013, 13, 1499-1512.	2.2	20
134	Absence of Diabetes and Pancreatic Exocrine Dysfunction in a Transgenic Model of Carboxyl-Ester Lipase-MODY (Maturity-Onset Diabetes of the Young). <i>PLoS ONE</i> , 2013, 8, e60229.	2.5	20
135	Mass spectrometry-based proteomics of endoscopically collected pancreatic fluid in chronic pancreatitis research. <i>Proteomics - Clinical Applications</i> , 2011, 5, 109-120.	1.6	19
136	Mechanism of p38 MAPK-induced EGFR endocytosis and its crosstalk with ligand-induced pathways. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	19
137	A Semiautomated Paramagnetic Bead-Based Platform for Isobaric Tag Sample Preparation. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1519-1529.	2.8	19
138	Nicotine alters the proteome of two human pancreatic duct cell lines. <i>JOP: Journal of the Pancreas</i> , 2014, 15, 465-74.	1.5	19
139	Cytokine profiling of pancreatic fluid using the ePFT collection method in tandem with a multiplexed microarray assay. <i>Journal of Immunological Methods</i> , 2011, 369, 98-107.	1.4	18
140	Proteome-Wide Protein Expression Profiling Across Five Pancreatic Cell Lines. <i>Pancreas</i> , 2017, 46, 690-698.	1.1	18
141	Quantitative Phospho-proteomic Analysis of TNF α /NF κ B Signaling Reveals a Role for RIPK1 Phosphorylation in Suppressing Necrotic Cell Death. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1200-1216.	3.8	18
142	HYpro16: A Two-Proteome Mixture to Assess Interference in Isobaric Tag-Based Sample Multiplexing Experiments. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 247-254.	2.8	18
143	A composite DNA element that functions as a maintainer required for epigenetic inheritance of heterochromatin. <i>Molecular Cell</i> , 2021, 81, 3979-3991.e4.	9.7	18
144	Ribosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18

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145	Subcellular fractionation enhances proteome coverage of pancreatic duct cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 791-797.	2.3	17
146	Efficient Deduplication in a Distributed Primary Storage Infrastructure. <i>ACM Transactions on Storage</i> , 2016, 12, 1-35.	2.1	17
147	Global proteomics of Ubqln2-based murine models of ALS. <i>Journal of Biological Chemistry</i> , 2021, 296, 100153.	3.4	17
148	Multiplexed proteome profiling of carbon source perturbations in two yeast species with SL-SP3-TMT. <i>Journal of Proteomics</i> , 2020, 210, 103531.	2.4	16
149	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. <i>Nature Chemical Biology</i> , 2020, 16, 546-555.	8.0	16
150	Maternal Iron Deficiency Modulates Placental Transcriptome and Proteome in Mid-Gestation of Mouse Pregnancy. <i>Journal of Nutrition</i> , 2021, 151, 1073-1083.	2.9	16
151	Mass Spectrometry-Based (GeLC-MS/MS) Comparative Proteomic Analysis of Endoscopically (ePFT) Collected Pancreatic and Gastroduodenal Fluids. <i>Clinical and Translational Gastroenterology</i> , 2012, 3, e14.	2.5	15
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