

# 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  
g-index

257  
all docs

257  
docs citations

257  
times ranked

23032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proximity labeling for investigating protein-protein interactions. <i>Methods in Cell Biology</i> , 2022, , 237-266.	1.1	7
2	Interrogating Kinase-Substrate Relationships with Proximity Labeling and Phosphorylation Enrichment. <i>Journal of Proteome Research</i> , 2022, 21, 494-506.	3.7	6
3	Assessing interference in isobaric tag-based sample multiplexing using an 18-plex interference standard. <i>Proteomics</i> , 2022, 22, e2100317.	2.2	5
4	Spatial Environment Affects <i>HNF4A</i> Mutation-Specific Proteome Signatures and Cellular Morphology in hiPSC-Derived $\beta$ -Like Cells. <i>Diabetes</i> , 2022, 71, 862-869.	0.6	4
5	Immune Checkpoint Blockade Augments Changes Within Oncolytic Virus-induced Cancer MHC-I Peptidome, Creating Novel Antitumor CD8 T Cell Reactivities. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100182.	3.8	3
6	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
7	Mapping Proteome Changes in Microsatellite Stable, Recurrent Colon Cancer Reveals a Significant Immune System Signature. <i>Cancer Genomics and Proteomics</i> , 2022, 19, 130-144.	2.0	0
8	Ribosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18
9	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. <i>Journal of Biological Chemistry</i> , 2022, 298, 101854.	3.4	6
10	Regulation of GTPase function by autophosphorylation. <i>Molecular Cell</i> , 2022, 82, 950-968.e14.	9.7	9
11	NAD <sup>+</sup> depletion enhances reovirus-induced oncolysis in multiple myeloma. <i>Molecular Therapy - Oncolytics</i> , 2022, 24, 695-706.	4.4	3
12	TrkB Receptor Agonist 7,8-Dihydroxyflavone is Protective Against the Inner Retinal Deficits Induced by Experimental Glaucoma. <i>Neuroscience</i> , 2022, 490, 36-48.	2.3	13
13	Fe <sup>3+</sup> -NTA magnetic beads as an alternative to spin column-based phosphopeptide enrichment. <i>Journal of Proteomics</i> , 2022, 260, 104561.	2.4	5
14	Profiling Yeast Deletion Strains Using Sample Multiplexing and Network-Based Analyses. <i>Journal of Proteome Research</i> , 2022, , .	3.7	1
15	$\beta$ Cell-specific deletion of Zfp148 improves nutrient-stimulated $\beta$ cell Ca <sup>2+</sup> responses. <i>JCI Insight</i> , 2022, 7, .	5.0	4
16	Time-resolved proximity labeling of protein networks associated with ligand-activated EGFR. <i>Cell Reports</i> , 2022, 39, 110950.	6.4	12
17	Disrupting the DREAM complex enables proliferation of adult human pancreatic $\beta$ cells. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	14
18	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. <i>Nature Communications</i> , 2022, 13, .	12.8	22

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19	A peroxisomal ubiquitin ligase complex forms a retrotranslocation channel. <i>Nature</i> , 2022, 607, 374-380.	27.8	36
20	Isobaric Tag-Based Protein Profiling across Eight Human Cell Lines Using High-Field Asymmetric Ion Mobility Spectrometry and Real-Time Database Searching. <i>Proteomics</i> , 2021, 21, e2000218.	2.2	4
21	Membrane skeleton modulates erythroid proteome remodeling and organelle clearance. <i>Blood</i> , 2021, 137, 398-409.	1.4	11
22	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
23	Growth media selection alters the proteome profiles of three model microorganisms. <i>Journal of Proteomics</i> , 2021, 231, 104006.	2.4	8
24	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
25	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
26	Categorization of Phosphorylation Site Behavior during the Diauxic Shift in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2021, 20, 2487-2496.	3.7	2
27	Rapid toxin sequestration modifies poison frog physiology. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	23
28	Targeting oncoproteins with a positive selection assay for protein degraders. <i>Science Advances</i> , 2021, 7, .	10.3	26
29	Dual DNA and protein tagging of open chromatin unveils dynamics of epigenomic landscapes in leukemia. <i>Nature Methods</i> , 2021, 18, 293-302.	19.0	9
30	Super Heavy TMTpro Labeling Reagent: An Alternative and Higher-Charge-State-Amenable Stable-Isotope-Labeled TMTpro Variant. <i>Journal of Proteome Research</i> , 2021, 20, 3009-3013.	3.7	1
31	DPP9 sequesters the C-terminus of NLRP1 to repress inflammasome activation. <i>Nature</i> , 2021, 592, 778-783.	27.8	114
32	Strain-Specific Peptide (SSP) Interference Reference Sample: A Genetically Encoded Quality Control for Isobaric Tagging Strategies. <i>Analytical Chemistry</i> , 2021, 93, 5241-5247.	6.5	8
33	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
34	Advances in quantitative high-throughput phosphoproteomics with sample multiplexing. <i>Proteomics</i> , 2021, 21, e2000140.	2.2	22
35	ORF10-Cullin-2-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
36	Iron Deficiency and Recovery in Yeast: A Quantitative Proteomics Approach. <i>Journal of Proteome Research</i> , 2021, 20, 2751-2761.	3.7	4

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37	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
38	Proteomics of broad deubiquitylase inhibition unmasks redundant enzyme function to reveal substrates and assess enzyme specificity. <i>Cell Chemical Biology</i> , 2021, 28, 487-502.e5.	5.2	10
39	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
40	Chronically Elevated Exogenous Glucose Elicits Antipodal Effects on the Proteome Signature of Differentiating Human iPSC-Derived Pancreatic Progenitors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3698.	4.1	2
41	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
42	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
43	Mapping Angiotensin II Type 1 Receptor-Biased Signaling Using Proximity Labeling and Proteomics Identifies Diverse Actions of Biased Agonists. <i>Journal of Proteome Research</i> , 2021, 20, 3256-3267.	3.7	11
44	A Compendium of Murine (Phospho)Peptides Encompassing Different Isobaric Labeling and Data Acquisition Strategies. <i>Journal of Proteome Research</i> , 2021, 20, 3678-3688.	3.7	6
45	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
46	Temporal proteomic changes induced by nicotine in human cells: A quantitative proteomics approach. <i>Journal of Proteomics</i> , 2021, 241, 104244.	2.4	2
47	Crosstalk between repair pathways elicits double-strand breaks in alkylated DNA and implications for the action of temozolomide. <i>ELife</i> , 2021, 10, .	6.0	10
48	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
49	A Proteomic View of Cellular and Molecular Effects of Cannabis. <i>Biomolecules</i> , 2021, 11, 1411.	4.0	11
50	Filamin C Cardiomyopathy Variants Cause Protein and Lysosome Accumulation. <i>Circulation Research</i> , 2021, 129, 751-766.	4.5	25
51	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	6.5	27
52	Protein profiling in the habenula after chronic (±) menthol exposure in mice. <i>Journal of Neurochemistry</i> , 2021, 158, 1345-1358.	3.9	2
53	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
54	Development of a colorimetric $\alpha$ -ketoglutarate detection assay for prolyl hydroxylase domain (PHD) proteins. <i>Journal of Biological Chemistry</i> , 2021, 296, 100397.	3.4	10

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55	Global proteomics of Ubq1n2-based murine models of ALS. <i>Journal of Biological Chemistry</i> , 2021, 296, 100153.	3.4	17
56	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
57	Strategies for mass spectrometry-based phosphoproteomics using isobaric tagging. <i>Expert Review of Proteomics</i> , 2021, 18, 795-807.	3.0	6
58	The fission yeast FLCN/FNIP complex augments TORC1 repression or activation in response to amino acid (AA) availability. <i>IScience</i> , 2021, 24, 103338.	4.1	1
59	Proteome-wide mapping of short-lived proteins in human cells. <i>Molecular Cell</i> , 2021, 81, 4722-4735.e5.	9.7	64
60	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
61	Aging Predisposes B cells to Malignancy by Activating c-Myc and Perturbing the Genome and Epigenome. <i>Innovation in Aging</i> , 2021, 5, 560-561.	0.1	0
62	RNAmetasome network for macromolecule biogenesis in human cells. <i>Communications Biology</i> , 2021, 4, 1399.	4.4	2
63	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
64	Brain Region-Specific nAChR and Associated Protein Abundance Alterations Following Chronic Nicotine and/or Menthol Exposure. <i>Journal of Proteome Research</i> , 2020, 19, 36-48.	3.7	4
65	Quantitative Proteome Responses to Oncolytic Reovirus in GM-CSF- and M-CSF-Differentiated Bone Marrow-Derived Cells. <i>Journal of Proteome Research</i> , 2020, 19, 708-718.	3.7	4
66	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
67	Dynamic proteome profiling of human pluripotent stem cell-derived pancreatic progenitors. <i>Stem Cells</i> , 2020, 38, 542-555.	3.2	6
68	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
69	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
70	In vivo hyperglycaemia exposure elicits distinct periodâ€dependent effects on human pancreatic progenitor differentiation, conveyed by oxidative stress. <i>Acta Physiologica</i> , 2020, 228, e13433.	3.8	13
71	ADAM17 cytoplasmic domain modulates Thioredoxin-1 conformation and activity. <i>Redox Biology</i> , 2020, 37, 101735.	9.0	6
72	PHD3 Loss Promotes Exercise Capacity and Fat Oxidation in Skeletal Muscle. <i>Cell Metabolism</i> , 2020, 32, 215-228.e7.	16.2	22

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73	Co-option of Plasmodium falciparum PP1 for egress from host erythrocytes. Nature Communications, 2020, 11, 3532.	12.8	37
74	pH-Gated Succinate Secretion Regulates Muscle Remodeling in Response to Exercise. Cell, 2020, 183, 62-75.e17.	28.9	129
75	Translation elongation factor 2 depletion by siRNA in mouse liver leads to mTOR-independent translational upregulation of ribosomal protein genes. Scientific Reports, 2020, 10, 15473.	3.3	10
76	Facultative protein selenation regulates redox sensitivity, adipose tissue thermogenesis, and obesity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10789-10796.	7.1	30
77	Selective Alanine Transporter Utilization Creates a Targetable Metabolic Niche in Pancreatic Cancer. Cancer Discovery, 2020, 10, 1018-1037.	9.4	104
78	High-Resolution In Vivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. Molecular Cell, 2020, 79, 167-179.e11.	9.7	36
79	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. Nature Methods, 2020, 17, 399-404.	19.0	276
80	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. Nature Communications, 2020, 11, 1406.	12.8	32
81	In vivo Environment Swiftly Restricts Human Pancreatic Progenitors Toward Mono-Hormonal Identity via a HNF1A/HNF4A Mechanism. Frontiers in Cell and Developmental Biology, 2020, 8, 109.	3.7	14
82	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. Molecular Cell, 2020, 77, 1124-1142.e10.	9.7	143
83	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. Nature Chemical Biology, 2020, 16, 546-555.	8.0	16
84	Targeting the cyclin-dependent kinase 5 in metastatic melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8001-8012.	7.1	21
85	A Triple Knockout Isobaric-Labeling Quality Control Platform with an Integrated Online Database Search. Journal of the American Society for Mass Spectrometry, 2020, 31, 1344-1349.	2.8	15
86	Selection of Heating Temperatures Improves the Sensitivity of the Proteome Integral Solubility Alteration Assay. Journal of Proteome Research, 2020, 19, 2159-2166.	3.7	36
87	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. Journal of Proteome Research, 2020, 19, 2026-2034.	3.7	171
88	Systematic quantitative analysis of ribosome inventory during nutrient stress. Nature, 2020, 583, 303-309.	27.8	78
89	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. Cell, 2020, 180, 968-983.e24.	28.9	220
90	Encapsulation boosts islet-cell signature in differentiating human induced pluripotent stem cells via integrin signalling. Scientific Reports, 2020, 10, 414.	3.3	33

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91	Loss of tumor suppressor inositol polyphosphate 4-phosphatase type B impairs DNA double-strand break repair by destabilization of DNA tethering protein Rad50. <i>Cell Death and Disease</i> , 2020, 11, 292.	6.3	6
92	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6478-6485.	6.5	44
93	O-GlcNAc regulates gene expression by controlling detained intron splicing. <i>Nucleic Acids Research</i> , 2020, 48, 5656-5669.	14.5	67
94	Autophagy promotes immune evasion of pancreatic cancer by degrading MHC-I. <i>Nature</i> , 2020, 581, 100-105.	27.8	628
95	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
96	Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. <i>ELife</i> , 2020, 9, .	6.0	62
97	EDF1 coordinates cellular responses to ribosome collisions. <i>ELife</i> , 2020, 9, .	6.0	96
98	TKO6: A Peptide Standard To Assess Interference for Unit-Resolved Isobaric Labeling Platforms. <i>Journal of Proteome Research</i> , 2019, 18, 565-570.	3.7	12
99	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019, 51, 1308-1314.	21.4	47
100	Epstein-Barr-Virus-Induced One-Carbon Metabolism Drives B Cell Transformation. <i>Cell Metabolism</i> , 2019, 30, 539-555.e11.	16.2	119
101	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
102	mTMT: An Alternative, Nonisobaric, Tandem Mass Tag Allowing for Precursor-Based Quantification. <i>Analytical Chemistry</i> , 2019, 91, 12167-12172.	6.5	8
103	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
104	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
105	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
106	Identification of Endogenous Adenomatous Polyposis Coli Interaction Partners and $\beta$ -Catenin-Independent Targets by Proteomics. <i>Molecular Cancer Research</i> , 2019, 17, 1828-1841.	3.4	5
107	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
108	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. <i>Genes and Development</i> , 2019, 33, 1031-1047.	5.9	83

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109	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
110	Lysine-specific demethylase 2A enhances binding of various nuclear factors to CpG-rich genomic DNAs by action of its CXXC-PHD domain. <i>Scientific Reports</i> , 2019, 9, 5496.	3.3	7
111	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
112	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019, 74, 32-44.e8.	9.7	170
113	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
114	Excessive Cell Growth Causes Cytoplasm Dilution And Contributes to Senescence. <i>Cell</i> , 2019, 176, 1083-1097.e18.	28.9	347
115	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
116	Diabetes relief in mice by glucose-sensing insulin-secreting human $\beta$ -cells. <i>Nature</i> , 2019, 567, 43-48.	27.8	188
117	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
118	Thiol-based direct threat sensing by the stress-activated protein kinase Hog1. <i>Science Signaling</i> , 2019, 12, .	3.6	10
119	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
120	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
121	MS3-IDQ: Utilizing MS3 Spectra beyond Quantification Yields Increased Coverage of the Phosphoproteome in Isobaric Tag Experiments. <i>Journal of Proteome Research</i> , 2018, 17, 1741-1747.	3.7	7
122	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
123	Isobaric Tagging-Based Protein Profiling of a Nicotine-Treated Alpha7 Nicotinic Receptor-Null Human Haploid Cell Line. <i>Proteomics</i> , 2018, 18, e1700475.	2.2	12
124	Multiplexed Isobaric Tagging-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
125	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	3.7	143
126	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

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127	Filter-Based Protein Digestion (FPD): A Detergent-Free and Scaffold-Based Strategy for TMT Workflows. <i>Journal of Proteome Research</i> , 2018, 17, 1227-1234.	3.7	13
128	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
129	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
130	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
131	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
132	RAB7A phosphorylation by TBK1 promotes mitophagy via the PINK-PARKIN pathway. <i>Science Advances</i> , 2018, 4, eaav0443.	10.3	128
133	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
134	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
135	Proteomic Investigation of Murine Neuronal $\alpha$ 7-Nicotinic Acetylcholine Receptor Interacting Proteins. <i>Journal of Proteome Research</i> , 2018, 17, 3959-3975.	3.7	8
136	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
137	The NAD <sup>+</sup> Salvage Pathway Supports PHGDH-Driven Serine Biosynthesis. <i>Cell Reports</i> , 2018, 24, 2381-2391.e5.	6.4	47
138	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
139	Automethylation-induced conformational switch in Clr4 (Suv39h) maintains epigenetic stability. <i>Nature</i> , 2018, 560, 504-508.	27.8	59
140	Biallelic Mutations in DNAJC12 Cause Hyperphenylalaninemia, Dystonia, and Intellectual Disability. <i>American Journal of Human Genetics</i> , 2017, 100, 257-266.	6.2	127
141	<i>Plasmodium falciparum</i> CRK4 directs continuous rounds of DNA replication during schizogony. <i>Nature Microbiology</i> , 2017, 2, 17017.	13.3	79
142	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
143	Proteome-Wide Protein Expression Profiling Across Five Pancreatic Cell Lines. <i>Pancreas</i> , 2017, 46, 690-698.	1.1	18
144	A Temporal Proteomic Map of Epstein-Barr Virus Lytic Replication in B Cells. <i>Cell Reports</i> , 2017, 19, 1479-1493.	6.4	83

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145	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
146	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. <i>Nature</i> , 2017, 547, 463-467.	27.8	96
147	Quantitative Phospho-proteomic Analysis of TNF $\alpha$ /NF $\kappa$ 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
148	Multidimensional Tracking of GPCR Signaling via Peroxidase-Catalyzed Proximity Labeling. <i>Cell</i> , 2017, 169, 338-349.e11.	28.9	221
149	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
150	Cdkal1, a type 2 diabetes susceptibility gene, regulates mitochondrial function in adipose tissue. <i>Molecular Metabolism</i> , 2017, 6, 1212-1225.	6.5	44
151	Quantitative Temporal in Vivo Proteomics Deciphers the Transition of Virus-Driven Myeloid Cells into M2 Macrophages. <i>Journal of Proteome Research</i> , 2017, 16, 3391-3406.	3.7	15
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