

Steven P Gygi

List of Publications by Year in descending order

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Version: 2024-02-01

393
papers

78,946
citations

767

119
h-index

568

263
g-index

459
all docs

459
docs citations

459
times ranked

84018
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative analysis of complex protein mixtures using isotope-coded affinity tags. <i>Nature Biotechnology</i> , 1999, 17, 994-999.	17.5	4,673
2	Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry. <i>Nature Methods</i> , 2007, 4, 207-214.	19.0	3,547
3	Correlation between Protein and mRNA Abundance in Yeast. <i>Molecular and Cellular Biology</i> , 1999, 19, 1720-1730.	2.3	3,521
4	The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71.	27.8	3,270
5	Identification of a unique TGF- β dependent molecular and functional signature in microglia. <i>Nature Neuroscience</i> , 2014, 17, 131-143.	14.8	2,056
6	Absolute quantification of proteins and phosphoproteins from cell lysates by tandem MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6940-6945.	7.1	1,701
7	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	28.9	1,564
8	Evaluation of Multidimensional Chromatography Coupled with Tandem Mass Spectrometry (LC/LC-MS/MS) for Large-Scale Protein Analysis: The Yeast Proteome. <i>Journal of Proteome Research</i> , 2003, 2, 43-50.	3.7	1,557
9	A probability-based approach for high-throughput protein phosphorylation analysis and site localization. <i>Nature Biotechnology</i> , 2006, 24, 1285-1292.	17.5	1,482
10	A proteomics approach to understanding protein ubiquitination. <i>Nature Biotechnology</i> , 2003, 21, 921-926.	17.5	1,465
11	Large-scale characterization of HeLa cell nuclear phosphoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12130-12135.	7.1	1,434
12	Systematic and Quantitative Assessment of the Ubiquitin-Modified Proteome. <i>Molecular Cell</i> , 2011, 44, 325-340.	9.7	1,406
13	Network organization of the human autophagy system. <i>Nature</i> , 2010, 466, 68-76.	27.8	1,383
14	Defining the Human Deubiquitinating Enzyme Interaction Landscape. <i>Cell</i> , 2009, 138, 389-403.	28.9	1,354
15	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	28.9	1,241
16	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
17	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. <i>Nature</i> , 2014, 509, 105-109.	27.8	1,169
18	MultiNotch MS3 Enables Accurate, Sensitive, and Multiplexed Detection of Differential Expression across Cancer Cell Line Proteomes. <i>Analytical Chemistry</i> , 2014, 86, 7150-7158.	6.5	1,130

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19	MS3 eliminates ratio distortion in isobaric multiplexed quantitative proteomics. <i>Nature Methods</i> , 2011, 8, 937-940.	19.0	928
20	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. <i>Nature</i> , 2013, 496, 372-376.	27.8	851
21	A Conserved MST-FOXO Signaling Pathway Mediates Oxidative-Stress Responses and Extends Life Span. <i>Cell</i> , 2006, 125, 987-1001.	28.9	758
22	Meteorin-like Is a Hormone that Regulates Immune-Adipose Interactions to Increase Beige Fat Thermogenesis. <i>Cell</i> , 2014, 157, 1279-1291.	28.9	699
23	Large-scale phosphorylation analysis of mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1488-1493.	7.1	691
24	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <i>Nature Methods</i> , 2005, 2, 667-675.	19.0	664
25	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. <i>Cell</i> , 2016, 165, 153-164.	28.9	598
26	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	28.9	596
27	A Protein Complex Network of <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 690-703.	28.9	593
28	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2002, 1, 323-333.	3.8	591
29	Multi-omics analysis identifies ATF4 as a key regulator of the mitochondrial stress response in mammals. <i>Journal of Cell Biology</i> , 2017, 216, 2027-2045.	5.2	590
30	Proteomics: the move to mixtures. <i>Journal of Mass Spectrometry</i> , 2001, 36, 1083-1091.	1.6	586
31	The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 1630-1638.	12.0	566
32	Quantitative Proteomics Reveal a Feedforward Mechanism for Mitochondrial PARKIN Translocation and Ubiquitin Chain Synthesis. <i>Molecular Cell</i> , 2014, 56, 360-375.	9.7	550
33	Distinct Phosphorylation Sites on the β^2 -Adrenergic Receptor Establish a Barcode That Encodes Differential Functions of β^2 -Arrestin. <i>Science Signaling</i> , 2011, 4, ra51.	3.6	535
34	Target-Decoy Search Strategy for Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 55-71.	0.9	534
35	Increasing the Multiplexing Capacity of TMTs Using Reporter Ion Isotopologues with Isobaric Masses. <i>Analytical Chemistry</i> , 2012, 84, 7469-7478.	6.5	529
36	The absolute quantification strategy: a general procedure for the quantification of proteins and post-translational modifications. <i>Methods</i> , 2005, 35, 265-273.	3.8	518

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37	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
38	iPSC-derived neurons from GBA1-associated Parkinson's disease patients show autophagic defects and impaired calcium homeostasis. <i>Nature Communications</i> , 2014, 5, 4028.	12.8	436
39	Dual Inhibition of Sister Chromatid Separation at Metaphase. <i>Cell</i> , 2001, 107, 715-726.	28.9	417
40	Semiquantitative Proteomic Analysis of Rat Forebrain Postsynaptic Density Fractions by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 21003-21011.	3.4	417
41	Detection and Quantitation of Circulating Human Irisin by Tandem Mass Spectrometry. <i>Cell Metabolism</i> , 2015, 22, 734-740.	16.2	414
42	Quantitative Temporal Viromics: An Approach to Investigate Host-Pathogen Interaction. <i>Cell</i> , 2014, 157, 1460-1472.	28.9	409
43	The Sestrins Interact with GATOR2 to Negatively Regulate the Amino-Acid-Sensing Pathway Upstream of mTORC1. <i>Cell Reports</i> , 2014, 9, 1-8.	6.4	394
44	SAMTOR is an S-adenosylmethionine sensor for the mTORC1 pathway. <i>Science</i> , 2017, 358, 813-818.	12.6	384
45	Accumulation of succinate controls activation of adipose tissue thermogenesis. <i>Nature</i> , 2018, 560, 102-106.	27.8	380
46	A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides. <i>Nature Biotechnology</i> , 2015, 33, 743-749.	17.5	371
47	mTOR inhibition activates overall protein degradation by the ubiquitin proteasome system as well as by autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15790-15797.	7.1	364
48	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. <i>Cell</i> , 2020, 183, 1848-1866.e26.	28.9	347
49	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , 2016, 534, 500-505.	27.8	335
50	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2002, 1, 47-54.	3.7	329
51	Dynamics of Cullin-RING Ubiquitin Ligase Network Revealed by Systematic Quantitative Proteomics. <i>Cell</i> , 2010, 143, 951-965.	28.9	328
52	Proteomics of Primary Cilia by Proximity Labeling. <i>Developmental Cell</i> , 2015, 35, 497-512.	7.0	328
53	Purification and characterization of native spliceosomes suitable for three-dimensional structural analysis. <i>Rna</i> , 2002, 8, 426-439.	3.5	316
54	Intensity-based protein identification by machine learning from a library of tandem mass spectra. <i>Nature Biotechnology</i> , 2004, 22, 214-219.	17.5	294

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55	Amyloid-like Self-Assembly of a Cellular Compartment. <i>Cell</i> , 2016, 166, 637-650.	28.9	294
56	Quantitative Proteomic Atlas of Ubiquitination and Acetylation in the DNA Damage Response. <i>Molecular Cell</i> , 2015, 59, 867-881.	9.7	288
57	Cell-cycle-regulated activation of Akt kinase by phosphorylation at its carboxyl terminus. <i>Nature</i> , 2014, 508, 541-545.	27.8	285
58	Mitochondrial Biogenesis and Proteome Remodeling Promote One-Carbon Metabolism for T Cell Activation. <i>Cell Metabolism</i> , 2016, 24, 104-117.	16.2	282
59	BRCA1-Dependent Ubiquitination of β -Tubulin Regulates Centrosome Number. <i>Molecular and Cellular Biology</i> , 2004, 24, 8457-8466.	2.3	281
60	The metabolic function of cyclin D3 β -CDK6 kinase in cancer cell survival. <i>Nature</i> , 2017, 546, 426-430.	27.8	276
61	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
62	Steps in Assembly of Silent Chromatin in Yeast: Sir3-Independent Binding of a Sir2/Sir4 Complex to Silencers and Role for Sir2-Dependent Deacetylation. <i>Molecular and Cellular Biology</i> , 2002, 22, 4167-4180.	2.3	275
63	A large-scale method to measure absolute protein phosphorylation stoichiometries. <i>Nature Methods</i> , 2011, 8, 677-683.	19.0	264
64	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. <i>Cell</i> , 2016, 167, 985-1000.e21.	28.9	259
65	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1326-1337.	3.8	253
66	An ERK/Cdk5 axis controls the diabetogenic actions of PPAR γ . <i>Nature</i> , 2015, 517, 391-395.	27.8	251
67	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
68	The Parkinson's disease-associated DJ-1 protein is a transcriptional co-activator that protects against neuronal apoptosis. <i>Human Molecular Genetics</i> , 2005, 14, 1231-1241.	2.9	234
69	Deep Proteomics of the <i>Xenopus laevis</i> Egg using an mRNA-Derived Reference Database. <i>Current Biology</i> , 2014, 24, 1467-1475.	3.9	234
70	Chemical Genetic Screen for AMPK α 2 Substrates Uncovers a Network of Proteins Involved in Mitosis. <i>Molecular Cell</i> , 2011, 44, 878-892.	9.7	232
71	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. <i>Nature Communications</i> , 2017, 8, 15965.	12.8	231
72	A human-airway-on-a-chip for the rapid identification of candidate antiviral therapeutics and prophylactics. <i>Nature Biomedical Engineering</i> , 2021, 5, 815-829.	22.5	228

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73	RNAi-Dependent and -Independent RNA Turnover Mechanisms Contribute to Heterochromatic Gene Silencing. <i>Cell</i> , 2007, 129, 707-721.	28.9	226
74	Multidimensional Tracking of GPCR Signaling via Peroxidase-Catalyzed Proximity Labeling. <i>Cell</i> , 2017, 169, 338-349.e11.	28.9	221
75	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , 2020, 180, 968-983.e24.	28.9	220
76	Quantitative proteomic analysis reveals posttranslational responses to aneuploidy in yeast. <i>ELife</i> , 2014, 3, e03023.	6.0	218
77	Differential Glutamate Metabolism in Proliferating and Quiescent Mammary Epithelial Cells. <i>Cell Metabolism</i> , 2016, 23, 867-880.	16.2	214
78	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017, 548, 219-223.	27.8	211
79	Weighing in on ubiquitin: the expanding role of mass-spectrometry-based proteomics. <i>Nature Cell Biology</i> , 2005, 7, 750-757.	10.3	210
80	Structurally Distinct Ca ²⁺ Signaling Domains of Sperm Flagella Orchestrate Tyrosine Phosphorylation and Motility. <i>Cell</i> , 2014, 157, 808-822.	28.9	210
81	Quantitative Cancer Proteomics: Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) as a Tool for Prostate Cancer Research. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 729-735.	3.8	202
82	Protein Profiling with Cleavable Isotope-coded Affinity Tag (cICAT) Reagents. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1198-1204.	3.8	201
83	Identification of a Protein Mediating Respiratory Supercomplex Stability. <i>Cell Metabolism</i> , 2012, 15, 348-360.	16.2	195
84	S-Nitrosylation links obesity-associated inflammation to endoplasmic reticulum dysfunction. <i>Science</i> , 2015, 349, 500-506.	12.6	189
85	Cdk1-Dependent Regulation of the Mitotic Inhibitor Wee1. <i>Cell</i> , 2005, 122, 407-420.	28.9	188
86	The Secreted Enzyme PM20D1 Regulates Lipidated Amino Acid Uncouplers of Mitochondria. <i>Cell</i> , 2016, 166, 424-435.	28.9	188
87	The Intraflagellar Transport Protein IFT27 Promotes BBSome Exit from Cilia through the GTPase ARL6/BBS3. <i>Developmental Cell</i> , 2014, 31, 265-278.	7.0	186
88	On the Relationship of Protein and mRNA Dynamics in Vertebrate Embryonic Development. <i>Developmental Cell</i> , 2015, 35, 383-394.	7.0	182
89	An Ancient, Unified Mechanism for Metformin Growth Inhibition in <i>C. elegans</i> and Cancer. <i>Cell</i> , 2016, 167, 1705-1718.e13.	28.9	181
90	Recruitment of <i>Xenopus</i> Scc2 and cohesin to chromatin requires the pre-replication complex. <i>Nature Cell Biology</i> , 2004, 6, 991-996.	10.3	180

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91	Quantitative Proteomic Analysis Using a MALDI Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2001, 73, 978-986.	6.5	178
92	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , 2019, 75, 620-630.e9.	9.7	178
93	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
94	Phosphoproteome Analysis of Fission Yeast. <i>Journal of Proteome Research</i> , 2008, 7, 1088-1097.	3.7	173
95	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
96	ATAD1 maintains mitochondrial function by facilitating the degradation of mislocalized tail-anchored proteins. <i>EMBO Journal</i> , 2014, 33, 1548-1564.	7.8	172
97	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
98	Correct Interpretation of Comprehensive Phosphorylation Dynamics Requires Normalization by Protein Expression Changes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009654.	3.8	167
99	Ubiquitylation by Trim32 causes coupled loss of desmin, Z-bands, and thin filaments in muscle atrophy. <i>Journal of Cell Biology</i> , 2012, 198, 575-589.	5.2	165
100	Mechanism of adrenergic CaV1.2 stimulation revealed by proximity proteomics. <i>Nature</i> , 2020, 577, 695-700.	27.8	163
101	Global Analysis of Protein Expression and Phosphorylation of Three Stages of <i>Plasmodium falciparum</i> Intraerythrocytic Development. <i>Journal of Proteome Research</i> , 2013, 12, 4028-4045.	3.7	161
102	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
103	Identification of Protein Components in <i>in vivo</i> Human Acquired Enamel Pellicle Using LC-ESI-MS/MS. <i>Journal of Proteome Research</i> , 2007, 6, 2152-2160.	3.7	156
104	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
105	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. <i>Cell Systems</i> , 2016, 3, 395-403.e4.	6.2	153
106	A subset of membrane-associated proteins is ubiquitinated in response to mutations in the endoplasmic reticulum degradation machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12735-12740.	7.1	151
107	USP14 deubiquitinates proteasome-bound substrates that are ubiquitinated at multiple sites. <i>Nature</i> , 2016, 532, 398-401.	27.8	150
108	A Cullin E3 Ubiquitin Ligase Complex Associates with Rik1 and the Clr4 Histone H3-K9 Methyltransferase and is Required for RNAi-Mediated Heterochromatin Formation. <i>RNA Biology</i> , 2005, 2, 106-111.	3.1	149

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109	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
110	Evaluating Multiplexed Quantitative Phosphopeptide Analysis on a Hybrid Quadrupole Mass Filter/Linear Ion Trap/Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2015, 87, 1241-1249.	6.5	146
111	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
112	Inhibition of homologous recombination by a cohesin-associated clamp complex recruited to the rDNA recombination enhancer. <i>Genes and Development</i> , 2006, 20, 2887-2901.	5.9	144
113	Autoubiquitination of the 26S Proteasome on Rpn13 Regulates Breakdown of Ubiquitin Conjugates. <i>EMBO Journal</i> , 2014, 33, 1159-1176.	7.8	143
114	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	3.7	143
115	Reimagining high-throughput profiling of reactive cysteines for cell-based screening of large electrophile libraries. <i>Nature Biotechnology</i> , 2021, 39, 630-641.	17.5	142
116	Proteome analysis: Biological assay or data archive?. <i>Electrophoresis</i> , 1998, 19, 1862-1871.	2.4	141
117	The mitochondrial acyl carrier protein (ACP) coordinates mitochondrial fatty acid synthesis with iron sulfur cluster biogenesis. <i>ELife</i> , 2016, 5, .	6.0	141
118	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. <i>ELife</i> , 2015, 4, .	6.0	141
119	An Integrated Microfluidics-Tandem Mass Spectrometry System for Automated Protein Analysis. <i>Analytical Chemistry</i> , 1998, 70, 3728-3734.	6.5	140
120	Accurate Multiplexed Proteomics at the MS2 Level Using the Complement Reporter Ion Cluster. <i>Analytical Chemistry</i> , 2012, 84, 9214-9221.	6.5	138
121	Hyperplexing: A Method for Higher-Order Multiplexed Quantitative Proteomics Provides a Map of the Dynamic Response to Rapamycin in Yeast. <i>Science Signaling</i> , 2012, 5, rs2.	3.6	137
122	UCP1 deficiency causes brown fat respiratory chain depletion and sensitizes mitochondria to calcium overload-induced dysfunction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7981-7986.	7.1	136
123	Latency-Associated Degradation of the MRP1 Drug Transporter During Latent Human Cytomegalovirus Infection. <i>Science</i> , 2013, 340, 199-202.	12.6	129
124	pH-Gated Succinate Secretion Regulates Muscle Remodeling in Response to Exercise. <i>Cell</i> , 2020, 183, 62-75.e17.	28.9	129
125	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
126	Hexameric assembly of the proteasomal ATPases is templated through their C termini. <i>Nature</i> , 2009, 459, 866-870.	27.8	125

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127	APC/C-mediated multiple monoubiquitylation provides an alternative degradation signal for cyclin B1. <i>Nature Cell Biology</i> , 2012, 14, 168-176.	10.3	125
128	Cyclin C is a haploinsufficient tumour suppressor. <i>Nature Cell Biology</i> , 2014, 16, 1080-1091.	10.3	124
129	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	28.9	123
130	A Secreted Slit2 Fragment Regulates Adipose Tissue Thermogenesis and Metabolic Function. <i>Cell Metabolism</i> , 2016, 23, 454-466.	16.2	122
131	Mek1 Kinase Is Regulated To Suppress Double-Strand Break Repair between Sister Chromatids during Budding Yeast Meiosis. <i>Molecular and Cellular Biology</i> , 2007, 27, 5456-5467.	2.3	121
132	UBE2O remodels the proteome during terminal erythroid differentiation. <i>Science</i> , 2017, 357, .	12.6	121
133	PHD3 Loss in Cancer Enables Metabolic Reliance on Fatty Acid Oxidation via Deactivation of ACC2. <i>Molecular Cell</i> , 2016, 63, 1006-1020.	9.7	120
134	Epstein-Barr-Virus-Induced One-Carbon Metabolism Drives B Cell Transformation. <i>Cell Metabolism</i> , 2019, 30, 539-555.e11.	16.2	119
135	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
136	The Nuclear Proteome of a Vertebrate. <i>Current Biology</i> , 2015, 25, 2663-2671.	3.9	117
137	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
138	Dual Sensing of Physiologic pH and Calcium by EFCAB9 Regulates Sperm Motility. <i>Cell</i> , 2019, 177, 1480-1494.e19.	28.9	116
139	A Perturbed Ubiquitin Landscape Distinguishes Between Ubiquitin in Trafficking and in Proteolysis. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009753.	3.8	115
140	Cardiolipin Synthesis in Brown and Beige Fat Mitochondria Is Essential for Systemic Energy Homeostasis. <i>Cell Metabolism</i> , 2018, 28, 159-174.e11.	16.2	114
141	DPP9 sequesters the CÂterminus of NLRP1 to repress inflammasome activation. <i>Nature</i> , 2021, 592, 778-783.	27.8	114
142	The Impact of Peptide Abundance and Dynamic Range on Stable-Isotope-Based Quantitative Proteomic Analyses. <i>Journal of Proteome Research</i> , 2008, 7, 4756-4765.	3.7	111
143	Prolyl hydroxylation by EglN2 destabilizes FOXO3a by blocking its interaction with the USP9x deubiquitinase. <i>Genes and Development</i> , 2014, 28, 1429-1444.	5.9	111
144	3D Culture Models with CRISPR Screens Reveal Hyperactive NRF2 as a Prerequisite for Spheroid Formation via Regulation of Proliferation and Ferroptosis. <i>Molecular Cell</i> , 2020, 80, 828-844.e6.	9.7	110

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145	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways downstream of SDF-1/CXCR4 in breast cancer stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2182-90.	7.1	109
146	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
147	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
148	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. <i>Nature Cell Biology</i> , 2017, 19, 177-188.	10.3	107
149	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. <i>Scientific Reports</i> , 2017, 7, 12685.	3.3	105
150	Selective Alanine Transporter Utilization Creates a Targetable Metabolic Niche in Pancreatic Cancer. <i>Cancer Discovery</i> , 2020, 10, 1018-1037.	9.4	104
151	RFWD3-Dependent Ubiquitination of RPA Regulates Repair at Stalled Replication Forks. <i>Molecular Cell</i> , 2015, 60, 280-293.	9.7	103
152	Proteasomal Control of Cytokinin Synthesis Protects <i>Mycobacterium tuberculosis</i> against Nitric Oxide. <i>Molecular Cell</i> , 2015, 57, 984-994.	9.7	101
153	Protein analysis by mass spectrometry and sequence database searching: Tools for cancer research in the post-genomic era. <i>Electrophoresis</i> , 1999, 20, 310-319.	2.4	100
154	Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. <i>Nature Biotechnology</i> , 2009, 27, 933-940.	17.5	99
155	An inhibitor of the proteasomal deubiquitinating enzyme USP14 induces tau elimination in cultured neurons. <i>Journal of Biological Chemistry</i> , 2017, 292, 19209-19225.	3.4	98
156	Reuterin in the healthy gut microbiome suppresses colorectal cancer growth through altering redox balance. <i>Cancer Cell</i> , 2022, 40, 185-200.e6.	16.8	97
157	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. <i>Nature</i> , 2017, 547, 463-467.	27.8	96
158	G protein-coupled receptor 56 regulates mechanical overload-induced muscle hypertrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15756-15761.	7.1	95
159	PTP1B controls non-mitochondrial oxygen consumption by regulating RNF213 to promote tumour survival during hypoxia. <i>Nature Cell Biology</i> , 2016, 18, 803-813.	10.3	95
160	Toward a high-throughput approach to quantitative proteomic analysis: Expression-dependent protein identification by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1238-1246.	2.8	93
161	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
162	Expedited mapping of the ligandable proteome using fully functionalized enantiomeric probe pairs. <i>Nature Chemistry</i> , 2019, 11, 1113-1123.	13.6	93

#	ARTICLE	IF	CITATIONS
163	Promoter Decommissioning by the NuRD Chromatin Remodeling Complex Triggers Synaptic Connectivity in the Mammalian Brain. <i>Neuron</i> , 2014, 83, 122-134.	8.1	92
164	Electrophoresis combined with novel mass spectrometry techniques: Powerful tools for the analysis of proteins and proteomes. <i>Electrophoresis</i> , 1998, 19, 1811-1818.	2.4	91
165	Post-transcriptional regulation of meiotic genes by a nuclear RNA silencing complex. <i>Rna</i> , 2014, 20, 867-881.	3.5	90
166	SDHAF4 Promotes Mitochondrial Succinate Dehydrogenase Activity and Prevents Neurodegeneration. <i>Cell Metabolism</i> , 2014, 20, 241-252.	16.2	88
167	Evaluation of the utility of neutralâ€dependent MS3 strategies in largeâ€scale phosphorylation analysis. <i>Proteomics</i> , 2008, 8, 4444-4452.	2.2	85
168	Extraproteasomal Rpn10 Restricts Access of the Polyubiquitin-Binding Protein Dsk2 to Proteasome. <i>Molecular Cell</i> , 2008, 32, 415-425.	9.7	84
169	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
170	Transcription Factor Networks in <i>Drosophila melanogaster</i> . <i>Cell Reports</i> , 2014, 8, 2031-2043.	6.4	83
171	A Temporal Proteomic Map of Epstein-Barr Virus Lytic Replication in B Cells. <i>Cell Reports</i> , 2017, 19, 1479-1493.	6.4	83
172	Evidence that C9ORF72 Dipeptide Repeat Proteins Associate with U2 snRNP to Cause Mis-splicing in ALS/FTD Patients. <i>Cell Reports</i> , 2017, 19, 2244-2256.	6.4	82
173	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. <i>Cell Stem Cell</i> , 2019, 25, 622-638.e13.	11.1	82
174	UCP1 governs liver extracellular succinate and inflammatory pathogenesis. <i>Nature Metabolism</i> , 2021, 3, 604-617.	11.9	82
175	<i>Plasmodium falciparum</i> CRK4 directs continuous rounds of DNA replication during schizogony. <i>Nature Microbiology</i> , 2017, 2, 17017.	13.3	79
176	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. <i>Molecular Cell</i> , 2020, 78, 459-476.e13.	9.7	76
177	Targeting of AMSH to Endosomes Is Required for Epidermal Growth Factor Receptor Degradation. <i>Journal of Biological Chemistry</i> , 2007, 282, 9805-9812.	3.4	75
178	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
179	Proteomic Profiling of Extracellular Vesicles Derived from Cerebrospinal Fluid of Alzheimerâ€™s Disease Patients: A Pilot Study. <i>Cells</i> , 2020, 9, 1959.	4.1	75
180	Reduced MEK inhibition preserves genomic stability in naive human embryonic stem cells. <i>Nature Methods</i> , 2018, 15, 732-740.	19.0	74

#	ARTICLE	IF	CITATIONS
181	UHRF1 Is a Sensor for DNA Interstrand Crosslinks and Recruits FANCD2 to Initiate the Fanconi Anemia Pathway. <i>Cell Reports</i> , 2015, 10, 1947-1956.	6.4	73
182	Sample multiplexing for targeted pathway proteomics in aging mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9723-9732.	7.1	73
183	Enhanced Analysis of Metastatic Prostate Cancer Using Stable Isotopes and High Mass Accuracy Instrumentation. <i>Journal of Proteome Research</i> , 2006, 5, 1224-1231.	3.7	71
184	Phosphorylation of ETS1 by Src Family Kinases Prevents Its Recognition by the COP1 Tumor Suppressor. <i>Cancer Cell</i> , 2014, 26, 222-234.	16.8	71
185	ACP Acylation Is an Acetyl-CoA-Dependent Modification Required for Electron Transport Chain Assembly. <i>Molecular Cell</i> , 2018, 71, 567-580.e4.	9.7	71
186	Post-Translational Regulation via Clp Protease Is Critical for Survival of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2014, 10, e1003994.	4.7	69
187	Defective NADPH production in mitochondrial disease complex I causes inflammation and cell death. <i>Nature Communications</i> , 2020, 11, 2714.	12.8	69
188	The Proteasome Distinguishes between Heterotypic and Homotypic Lysine-11-Linked Polyubiquitin Chains. <i>Cell Reports</i> , 2015, 12, 545-553.	6.4	68
189	Increasing Throughput in Targeted Proteomics Assays: 54-Plex Quantitation in a Single Mass Spectrometry Run. <i>Analytical Chemistry</i> , 2013, 85, 5340-5346.	6.5	67
190	O-GlcNAc regulates gene expression by controlling detained intron splicing. <i>Nucleic Acids Research</i> , 2020, 48, 5656-5669.	14.5	67
191	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	6.0	67
192	OTUD4 Is a Phospho-Activated K63 Deubiquitinase that Regulates MyD88-Dependent Signaling. <i>Molecular Cell</i> , 2018, 69, 505-516.e5.	9.7	65
193	The effects of mass accuracy, data acquisition speed, and search algorithm choice on peptide identification rates in phosphoproteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1409-1419.	3.7	64
194	Combining Genetic Perturbations and Proteomics to Examine Kinase-Phosphatase Networks in <i>Drosophila</i> Embryos. <i>Developmental Cell</i> , 2014, 31, 114-127.	7.0	64
195	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
196	Proteome-wide mapping of short-lived proteins in human cells. <i>Molecular Cell</i> , 2021, 81, 4722-4735.e5.	9.7	64
197	DUSP9 Modulates DNA Hypomethylation in Female Mouse Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 706-719.e7.	11.1	63
198	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

#	ARTICLE	IF	CITATIONS
199	Regulation of MicroRNA Machinery and Development by Interspecies S-Nitrosylation. <i>Cell</i> , 2019, 176, 1014-1025.e12.	28.9	62
200	Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. <i>ELife</i> , 2021, 10, .	6.0	62
201	Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. <i>ELife</i> , 2020, 9, .	6.0	62
202	LIN28 phosphorylation by MAPK/ERK couples signalling to the post-transcriptional control of pluripotency. <i>Nature Cell Biology</i> , 2017, 19, 60-67.	10.3	59
203	BioPlex Display: An Interactive Suite for Large-Scale AP-MS Protein-Protein Interaction Data. <i>Journal of Proteome Research</i> , 2018, 17, 722-726.	3.7	59
204	Automethylation-induced conformational switch in Ctr4 (Suv39h) maintains epigenetic stability. <i>Nature</i> , 2018, 560, 504-508.	27.8	59
205	Interactome analyses revealed that the U1 snRNP machinery overlaps extensively with the RNAP II machinery and contains multiple ALS/SMA-causative proteins. <i>Scientific Reports</i> , 2018, 8, 8755.	3.3	59
206	Cdc28-Dependent Regulation of the Cdc5/Polo Kinase. <i>Current Biology</i> , 2005, 15, 2033-2037.	3.9	58
207	Quantitative Proteome Analysis: Methods and Applications. <i>Annals of the New York Academy of Sciences</i> , 2000, 919, 33-47.	3.8	57
208	Phosphorylation of Beta-3 adrenergic receptor at serine 247 by ERK MAP kinase drives lipolysis in obese adipocytes. <i>Molecular Metabolism</i> , 2018, 12, 25-38.	6.5	57
209	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
210	A solid phase extraction-based platform for rapid phosphoproteomic analysis. <i>Methods</i> , 2011, 54, 379-386.	3.8	56
211	Multiplexed, Proteome-Wide Protein Expression Profiling: Yeast Deubiquitylating Enzyme Knockout Strains. <i>Journal of Proteome Research</i> , 2015, 14, 5306-5317.	3.7	56
212	High-density chemical cross-linking for modeling protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 93-102.	7.1	56
213	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
214	Quantitative analysis of Y-Chromosome gene expression across 36 human tissues. <i>Genome Research</i> , 2020, 30, 860-873.	5.5	56
215	Development of a Multiplexed Microcapillary Liquid Chromatography System for High-Throughput Proteome Analysis. <i>Analytical Chemistry</i> , 2002, 74, 4353-4360.	6.5	55
216	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

#	ARTICLE	IF	CITATIONS
217	Human neural cell type-specific extracellular vesicle proteome defines disease-related molecules associated with activated astrocytes in Alzheimer's disease brain. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12183.	12.2	54
218	Thrap3 docks on phosphoserine 273 of PPAR β and controls diabetic gene programming. <i>Genes and Development</i> , 2014, 28, 2361-2369.	5.9	52
219	Profiling DNA damage-induced phosphorylation in budding yeast reveals diverse signaling networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3667-75.	7.1	52
220	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
221	Improved Monoisotopic Mass Estimation for Deeper Proteome Coverage. <i>Journal of Proteome Research</i> , 2021, 20, 591-598.	3.7	52
222	A cold-stress-inducible PERK/OGT axis controls TOM70-assisted mitochondrial protein import and cristae formation. <i>Cell Metabolism</i> , 2021, 33, 598-614.e7.	16.2	52
223	Proteomic insights into ubiquitin and ubiquitin-like proteins. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 69-75.	6.1	51
224	Selenoprotein S is involved in maintenance and transport of multiprotein complexes. <i>Biochemical Journal</i> , 2014, 462, 555-565.	3.7	51
225	Proteomic Analysis Identifies Ribosome Reduction as an Effective Proteotoxic Stress Response. <i>Journal of Biological Chemistry</i> , 2015, 290, 29695-29706.	3.4	51
226	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
227	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
228	Regulation of Cellular Levels of Sprouty2 Protein by Prolyl Hydroxylase Domain and von Hippel-Lindau Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 42027-42036.	3.4	50
229	Time-resolved proteomics profiling of the ciliary Hedgehog response. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	50
230	Regulation of microtubule-based transport by MAP4. <i>Molecular Biology of the Cell</i> , 2014, 25, 3119-3132.	2.1	49
231	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
232	A Critical Role for PKR Complexes with TRBP in Immunometabolic Regulation and eIF2 \pm Phosphorylation in Obesity. <i>Cell Reports</i> , 2015, 11, 295-307.	6.4	49
233	Role of Selenof as a Gatekeeper of Secreted Disulfide-Rich Glycoproteins. <i>Cell Reports</i> , 2018, 23, 1387-1398.	6.4	49
234	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

#	ARTICLE	IF	CITATIONS
235	MEKK2 mediates an alternative β -catenin pathway that promotes bone formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1226-35.	7.1	47
236	The NAD ⁺ Salvage Pathway Supports PHGDH-Driven Serine Biosynthesis. <i>Cell Reports</i> , 2018, 24, 2381-2391.e5.	6.4	47
237	Regulation of Selenocysteine Content of Human Selenoprotein P by Dietary Selenium and Insertion of Cysteine in Place of Selenocysteine. <i>PLoS ONE</i> , 2015, 10, e0140353.	2.5	45
238	Characterization of Mouse Spleen Cells by Subtractive Proteomics. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1459-1470.	3.8	44
239	Cdkal1, a type 2 diabetes susceptibility gene, regulates mitochondrial function in adipose tissue. <i>Molecular Metabolism</i> , 2017, 6, 1212-1225.	6.5	44
240	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
241	Proteomic Profiling of Extracellular Vesicles Isolated From Cerebrospinal Fluid of Former National Football League Players at Risk for Chronic Traumatic Encephalopathy. <i>Frontiers in Neuroscience</i> , 2019, 13, 1059.	2.8	44
242	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
243	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6478-6485.	6.5	44
244	Proteomics of phosphorylation and protein dynamics during fertilization and meiotic exit in the <i>Xenopus</i> egg. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10838-E10847.	7.1	43
245	A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.	27.8	43
246	Generation of Multiple Reporter Ions from a Single Isobaric Reagent Increases Multiplexing Capacity for Quantitative Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 9855-9863.	6.5	42
247	Proteomic and Metabolomic Characterization of a Mammalian Cellular Transition from Quiescence to Proliferation. <i>Cell Reports</i> , 2017, 20, 721-736.	6.4	41
248	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
249	An adenosine triphosphate-independent proteasome activator contributes to the virulence of <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1763-72.	7.1	40
250	SUMOylation of DNA topoisomerase III β regulates histone H3 kinase Haspin and H3 phosphorylation in mitosis. <i>Journal of Cell Biology</i> , 2016, 213, 665-678.	5.2	40
251	Cogenerating Synthetic Parts toward a Self-Replicating System. <i>ACS Synthetic Biology</i> , 2017, 6, 1327-1336.	3.8	40
252	Focal Adhesion- and IGF1R-Dependent Survival and Migratory Pathways Mediate Tumor Resistance to mTORC1/2 Inhibition. <i>Molecular Cell</i> , 2017, 67, 512-527.e4.	9.7	40

#	ARTICLE	IF	CITATIONS
253	Nicotine-induced protein expression profiling reveals mutually altered proteins across four human cell lines. <i>Proteomics</i> , 2017, 17, 1600319.	2.2	40
254	The neurodegenerative diseases ALS and SMA are linked at the molecular level via the ASC-1 complex. <i>Nucleic Acids Research</i> , 2018, 46, 11939-11951.	14.5	40
255	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
256	The Absolute Quantification Strategy. <i>Methods in Molecular Biology</i> , 2007, 359, 71-86.	0.9	40
257	Scaffold-mediated gating of Cdc42 signalling flux. <i>ELife</i> , 2017, 6, .	6.0	40
258	eIF1A augments Ago2-mediated Dicer-independent miRNA biogenesis and RNA interference. <i>Nature Communications</i> , 2015, 6, 7194.	12.8	39
259	Activation of PASK by mTORC1 is required for the onset of the terminal differentiation program. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10382-10391.	7.1	39
260	Mitotic regulators TPX2 and Aurora A protect DNA forks during replication stress by counteracting 53BP1 function. <i>Journal of Cell Biology</i> , 2019, 218, 422-432.	5.2	39
261	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
262	CDC7-independent G1/S transition revealed by targeted protein degradation. <i>Nature</i> , 2022, 605, 357-365.	27.8	38
263	<i>Pseudomonas aeruginosa</i> Proteome under Hypoxic Stress Conditions Mimicking the Cystic Fibrosis Lung. <i>Journal of Proteome Research</i> , 2017, 16, 3917-3928.	3.7	37
264	Co-option of <i>Plasmodium falciparum</i> PP1 for egress from host erythrocytes. <i>Nature Communications</i> , 2020, 11, 3532.	12.8	37
265	Tetracyclines promote survival and fitness in mitochondrial disease models. <i>Nature Metabolism</i> , 2021, 3, 33-42.	11.9	37
266	Ubiquilin1 promotes antigen-receptor mediated proliferation by eliminating mislocalized mitochondrial proteins. <i>ELife</i> , 2017, 6, .	6.0	37
267	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
268	A peroxisomal ubiquitin ligase complex forms a retrotranslocation channel. <i>Nature</i> , 2022, 607, 374-380.	27.8	36
269	Mechanism-based Proteomic Screening Identifies Targets of Thioredoxin-like Proteins. <i>Journal of Biological Chemistry</i> , 2015, 290, 5685-5695.	3.4	34
270	Enrichment of Neurodegenerative Microglia Signature in Brain-Derived Extracellular Vesicles Isolated from Alzheimer's Disease Mouse Models. <i>Journal of Proteome Research</i> , 2021, 20, 1733-1743.	3.7	34

#	ARTICLE	IF	CITATIONS
271	Kinesin superfamily protein Kif26b links Wnt5a-Ror signaling to the control of cell and tissue behaviors in vertebrates. <i>ELife</i> , 2017, 6, .	6.0	33
272	Assigning spectrum-specific P -values to protein identifications by mass spectrometry. <i>Bioinformatics</i> , 2011, 27, 1128-1134.	4.1	32
273	Kinase-independent function of E-type cyclins in liver cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1015-1020.	7.1	32
274	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. <i>Molecular Cell</i> , 2020, 79, 68-83.e7.	9.7	32
275	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32
276	Extended ubiquitin species are protein-based DUB inhibitors. <i>Nature Chemical Biology</i> , 2014, 10, 664-670.	8.0	31
277	The Methionine Transamination Pathway Controls Hepatic Glucose Metabolism through Regulation of the GCN5 Acetyltransferase and the PGC-1 β Transcriptional Coactivator. <i>Journal of Biological Chemistry</i> , 2016, 291, 10635-10645.	3.4	31
278	A conserved RNA degradation complex required for spreading and epigenetic inheritance of heterochromatin. <i>ELife</i> , 2020, 9, .	6.0	31
279	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
280	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
281	Phosphorylation of FANCD2 Inhibits the FANCD2/FANCI Complex and Suppresses the Fanconi Anemia Pathway in the Absence of DNA Damage. <i>Cell Reports</i> , 2019, 27, 2990-3005.e5.	6.4	29
282	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
283	A conserved signaling network monitors delivery of sphingolipids to the plasma membrane in budding yeast. <i>Molecular Biology of the Cell</i> , 2017, 28, 2589-2599.	2.1	28
284	Peroxisomal-derived ether phospholipids link nucleotides to respirasome assembly. <i>Nature Chemical Biology</i> , 2021, 17, 703-710.	8.0	28
285	The ubiquitin-proteasome system regulates membrane fusion of yeast vacuoles. <i>EMBO Journal</i> , 2007, 26, 275-287.	7.8	27
286	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
287	The biochemical basis of mitochondrial dysfunction in Zellweger Spectrum Disorder. <i>EMBO Reports</i> , 2021, 22, e51991.	4.5	27
288	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	6.5	27

#	ARTICLE	IF	CITATIONS
289	Cysteine 253 of UCP1 regulates energy expenditure and sex-dependent adipose tissue inflammation. <i>Cell Metabolism</i> , 2022, 34, 140-157.e8.	16.2	27
290	Mass Spectrometric Analysis of Type 1 Inositol 1,4,5-Trisphosphate Receptor Ubiquitination*. <i>Journal of Biological Chemistry</i> , 2008, 283, 35319-35328.	3.4	26
291	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
292	Targeting oncoproteins with a positive selection assay for protein degraders. <i>Science Advances</i> , 2021, 7, .	10.3	26
293	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
294	Multioomic analysis identifies CPT1A as a potential therapeutic target in platinum-refractory, high-grade serous ovarian cancer. <i>Cell Reports Medicine</i> , 2021, 2, 100471.	6.5	26
295	Neutral Loss Is a Very Common Occurrence in Phosphotyrosine-Containing Peptides Labeled with Isobaric Tags. <i>Journal of Proteome Research</i> , 2017, 16, 1069-1076.	3.7	25
296	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
297	Filamin C Cardiomyopathy Variants Cause Protein and Lysosome Accumulation. <i>Circulation Research</i> , 2021, 129, 751-766.	4.5	25
298	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
299	Ubiquitin-Dependent Modification of Skeletal Muscle by the Parasitic Nematode, <i>Trichinella spiralis</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005977.	4.7	24
300	Characterization of Plasmodium falciparum Atypical Kinase Pfpk7â€“ Dependent Phosphoproteome. <i>Journal of Proteome Research</i> , 2018, 17, 2112-2123.	3.7	24
301	ELAC1 Repairs tRNAs Cleaved during Ribosome-Associated Quality Control. <i>Cell Reports</i> , 2020, 30, 2106-2114.e5.	6.4	24
302	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
303	ERRÎ± Maintains Mitochondrial Oxidative Metabolism and Constitutes an Actionable Target in PGC1Î±-Elevated Melanomas. <i>Molecular Cancer Research</i> , 2017, 15, 1366-1375.	3.4	23
304	Rapid toxin sequestration modifies poison frog physiology. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	23
305	Proteomic Profiling of Paclitaxel Treated Cells Identifies a Novel Mechanism of Drug Resistance Mediated by PDCD4. <i>Journal of Proteome Research</i> , 2015, 14, 2480-2491.	3.7	22
306	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

#	ARTICLE	IF	CITATIONS
307	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
308	PHD3 Loss Promotes Exercise Capacity and Fat Oxidation in Skeletal Muscle. <i>Cell Metabolism</i> , 2020, 32, 215-228.e7.	16.2	22
309	Assessing target engagement using proteome-wide solvent shift assays. <i>ELife</i> , 2021, 10, .	6.0	22
310	CD22 Is a Functional Ligand for SH2 Domain-containing Protein-tyrosine Phosphatase-1 in Primary T Cells. <i>Journal of Biological Chemistry</i> , 2004, 279, 47783-47791.	3.4	21
311	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
312	Mechanism of p38 MAPK α -induced EGFR endocytosis and its crosstalk with ligand-induced pathways. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	19
313	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
314	Activated Inositol 1,4,5-Trisphosphate Receptors Are Modified by Homogeneous Lys-48- and Lys-63-linked Ubiquitin Chains, but Only Lys-48-linked Chains Are Required for Degradation. <i>Journal of Biological Chemistry</i> , 2011, 286, 1074-1082.	3.4	18
315	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
316	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
317	Rixosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18
318	Aminoglycoside-driven biosynthesis of selenium-deficient Selenoprotein P. <i>Scientific Reports</i> , 2017, 7, 4391.	3.3	17
319	Identification of UHRF2 as a novel DNA interstrand crosslink sensor protein. <i>PLoS Genetics</i> , 2018, 14, e1007643.	3.5	17
320	Erythrocytes lacking the Langereis blood group protein ABCB6 are resistant to the malaria parasite <i>Plasmodium falciparum</i> . <i>Communications Biology</i> , 2018, 1, 45.	4.4	17
321	Time-resolved phosphoproteomics reveals scaffolding and catalysis-responsive patterns of SHP2-dependent signaling. <i>ELife</i> , 2021, 10, .	6.0	17
322	Global proteomics of Ubqln2-based murine models of ALS. <i>Journal of Biological Chemistry</i> , 2021, 296, 100153.	3.4	17
323	Blood biomarkers in a mouse model of CADASIL. <i>Brain Research</i> , 2016, 1644, 118-126.	2.2	16
324	Targeted Degradation of Glucose Transporters Protects against Arsenic Toxicity. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	16

#	ARTICLE	IF	CITATIONS
325	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
326	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. <i>Nature Chemical Biology</i> , 2020, 16, 546-555.	8.0	16
327	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
328	WRNIP1 Is Recruited to DNA Interstrand Crosslinks and Promotes Repair. <i>Cell Reports</i> , 2020, 32, 107850.	6.4	15
329	A Triple Knockout Isobaric-Labeling Quality Control Platform with an Integrated Online Database Search. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1344-1349.	2.8	15
330	Boström et al. reply. <i>Nature</i> , 2012, 488, E10-E11.	27.8	14
331	TomahaqCompanion: A Tool for the Creation and Analysis of Isobaric Label Based Multiplexed Targeted Assays. <i>Journal of Proteome Research</i> , 2019, 18, 594-605.	3.7	14
332	SUMOylation of Psm1 Controls Adm1 Interaction with the Proteasome. <i>Cell Reports</i> , 2014, 7, 1842-1848.	6.4	13
333	Protein Kinase C Controls Binding of Igo/ENSA Proteins to Protein Phosphatase 2A in Budding Yeast. <i>Journal of Biological Chemistry</i> , 2017, 292, 4925-4941.	3.4	13
334	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
335	Cold Temperature Induces the Reprogramming of Proteolytic Pathways in Yeast. <i>Journal of Biological Chemistry</i> , 2016, 291, 1664-1675.	3.4	12
336	The skeletal phenotype of Achondrogenesis type 1A is caused exclusively by cartilage defects. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	12
337	Isobaric Tag-Based Protein Profiling of a Nicotine-Treated Alpha7 Nicotinic Receptor-Null Human Haploid Cell Line. <i>Proteomics</i> , 2018, 18, e1700475.	2.2	12
338	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
339	Quantitative multiplexed proteomics of <i>Taenia solium</i> cysts obtained from the skeletal muscle and central nervous system of pigs. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005962.	3.0	12
340	An expanded mouse testis transcriptome and mass spectrometry defines novel proteins. <i>Reproduction</i> , 2020, 159, 15-26.	2.6	12
341	Kinase domain autophosphorylation rewrites the activity and substrate specificity of CK1 enzymes. <i>Molecular Cell</i> , 2022, 82, 2006-2020.e8.	9.7	12
342	Genome-wide transcript and protein analysis highlights the role of protein homeostasis in the aging mouse heart. <i>Genome Research</i> , 2022, , .	5.5	12

#	ARTICLE	IF	CITATIONS
343	Time-resolved proximity labeling of protein networks associated with ligand-activated EGFR. <i>Cell Reports</i> , 2022, 39, 110950.	6.4	12
344	Membrane skeleton modulates erythroid proteome remodeling and organelle clearance. <i>Blood</i> , 2021, 137, 398-409.	1.4	11
345	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
346	Thiol-based direct threat sensing by the stress-activated protein kinase Hog1. <i>Science Signaling</i> , 2019, 12, .	3.6	10
347	Translation elongation factor 2 depletion by siRNA in mouse liver leads to mTOR-independent translational upregulation of ribosomal protein genes. <i>Scientific Reports</i> , 2020, 10, 15473.	3.3	10
348	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
349	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
350	mTMT: An Alternative, Nonisobaric, Tandem Mass Tag Allowing for Precursor-Based Quantification. <i>Analytical Chemistry</i> , 2019, 91, 12167-12172.	6.5	8
351	Growth media selection alters the proteome profiles of three model microorganisms. <i>Journal of Proteomics</i> , 2021, 231, 104006.	2.4	8
352	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
353	The Arg/N-degron pathway targets transcription factors and regulates specific genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31094-31104.	7.1	7
354	Proximity labeling for investigating protein-protein interactions. <i>Methods in Cell Biology</i> , 2022, , 237-266.	1.1	7
355	Functional mapping of PHF6 complexes in chromatin remodeling, replication dynamics, and DNA repair. <i>Blood</i> , 2022, 139, 3418-3429.	1.4	7
356	Using mass spectrometry for quantitative proteomics. <i>Trends in Biotechnology</i> , 2000, 18, 31-36.	9.3	6
357	Dynamic proteome profiling of human pluripotent stem cell-derived pancreatic progenitors. <i>Stem Cells</i> , 2020, 38, 542-555.	3.2	6
358	ADAM17 cytoplasmic domain modulates Thioredoxin-1 conformation and activity. <i>Redox Biology</i> , 2020, 37, 101735.	9.0	6
359	The Insulin Receptor Adaptor IRS2 is an APC/C Substrate That Promotes Cell Cycle Protein Expression and a Robust Spindle Assembly Checkpoint. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1450-1467.	3.8	6
360	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

#	ARTICLE	IF	CITATIONS
361	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
362	Proteomic analysis identifies the E3 ubiquitin ligase Pdzn3 as a regulatory target of Wnt5a-Ror signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	6
363	Clonal populations of a human TNBC model display significant functional heterogeneity and divergent growth dynamics in distinct contexts. <i>Oncogene</i> , 2022, 41, 112-124.	5.9	6
364	Interrogating Kinase-Substrate Relationships with Proximity Labeling and Phosphorylation Enrichment. <i>Journal of Proteome Research</i> , 2022, 21, 494-506.	3.7	6
365	Apolipoprotein E is a pancreatic extracellular factor that maintains mature Î²-cell gene expression. <i>PLoS ONE</i> , 2018, 13, e0204595.	2.5	5
366	Assessing interference in isobaric tag-based sample multiplexing using an 18plex interference standard. <i>Proteomics</i> , 2022, 22, e2100317.	2.2	5
367	Fe3+-NTA magnetic beads as an alternative to spin column-based phosphopeptide enrichment. <i>Journal of Proteomics</i> , 2022, 260, 104561.	2.4	5
368	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
369	Parallel Notched Gas-Phase Enrichment for Improved Proteome Identification and Quantification with Fast Spectral Acquisition Rates. <i>Journal of Proteome Research</i> , 2020, 19, 2750-2757.	3.7	4
370	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
371	Iron Deficiency and Recovery in Yeast: A Quantitative Proteomics Approach. <i>Journal of Proteome Research</i> , 2021, 20, 2751-2761.	3.7	4
372	APC7 mediates ubiquitin signaling in constitutive heterochromatin in the developing mammalian brain. <i>Molecular Cell</i> , 2022, 82, 90-105.e13.	9.7	4
373	Structural Analysis of Mycobacterium tuberculosis Homologues of the Eukaryotic Proteasome Assembly Chaperone 2 (PAC2). <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	3
374	Proteomic profiling of yeast heterochromatin connects direct physical and genetic interactions. <i>Current Genetics</i> , 2019, 65, 495-505.	1.7	3
375	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
376	NAD+ depletion enhances reovirus-induced oncolysis in multiple myeloma. <i>Molecular Therapy - Oncolytics</i> , 2022, 24, 695-706.	4.4	3
377	Reply to "Phosphorylation sites of higher stoichiometry are more conserved". <i>Nature Methods</i> , 2012, 9, 318-318.	19.0	2
378	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

#	ARTICLE	IF	CITATIONS
379	Autophosphorylation of the CK1 Kinase Domain Regulates Enzyme Activity and Substrate Specificity. FASEB Journal, 2021, 35, .	0.5	2
380	Temporal proteomic changes induced by nicotine in human cells: A quantitative proteomics approach. Journal of Proteomics, 2021, 241, 104244.	2.4	2
381	ISDN2014_0027: REMOVED: Identification of a unique molecular and functional microglia signature in health and disease. International Journal of Developmental Neuroscience, 2015, 47, 5-5.	1.6	1
382	ISDN2014_0028: REMOVED: Targeting miRâ€155 restores dysfunctional microglia and ameliorates disease in the SOD1 model of ALS. International Journal of Developmental Neuroscience, 2015, 47, 5-5.	1.6	1
383	Super Heavy TMTpro Labeling Reagent: An Alternative and Higher-Charge-State-Amenable Stable-Isotope-Labeled TMTpro Variant. Journal of Proteome Research, 2021, 20, 3009-3013.	3.7	1
384	OR08-3 The Role Of Neuronal Plasticity In The Timing Of Puberty Onset: Insights From A Mkrn3 Deficient Mouse Model.. Journal of the Endocrine Society, 2019, 3, .	0.2	1
385	The fission yeast FLCN/FNIP complex augments TORC1 repression or activation in response to amino acid (AA) availability. IScience, 2021, 24, 103338.	4.1	1
386	Enrichment of Tyrosine Phosphorylated Peptides for Quantitative Mass Spectrometry Analysis of RTK Signaling Dynamics. Bio-protocol, 2022, 12, e4311.	0.4	1
387	Profiling Yeast Deletion Strains Using Sample Multiplexing and Network-Based Analyses. Journal of Proteome Research, 2022, , .	3.7	1
388	Kinase Domain Autophosphorylation Rewires the Activity and Substrate Specificity of CK1 Enzymes. FASEB Journal, 2022, 36, .	0.5	1
389	GENE-19. DEEP PROTEOMIC SURVEY ACROSS SEVEN CHILDHOOD BRAIN TUMORS. Neuro-Oncology, 2019, 21, ii85-ii85.	1.2	0
390	Evaluation of extracellular vesicles isolated from the cerebrospinal fluid and plasma from former National Football League players at risk for chronic traumatic encephalopathy. Alzheimer's and Dementia, 2020, 16, e042233.	0.8	0
391	Abstract 1426: Multiomic analysis identifies CPT1A and fatty acid oxidation as a potential therapeutic target in platinum-refractory high grade serous ovarian cancer. , 2021, , .		0
392	Landscape of the PARKINâ€dependent ubiquitin modified proteome in response to mitochondrial depolarization defined through quantitative proteomics. FASEB Journal, 2013, 27, 553.17.	0.5	0
393	Mechanisms of Wnt5aâ€Ror Signaling in Development and Disease. FASEB Journal, 2020, 34, 1-1.	0.5	0