

Steven P Gygi

List of Publications by Year in descending order

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Version: 2024-02-01

393
papers

78,946
citations

764

119
h-index

567

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.	9.4	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.	9.0	3,547
3	Correlation between Protein and mRNA Abundance in Yeast. <i>Molecular and Cellular Biology</i> , 1999, 19, 1720-1730.	1.1	3,521
4	The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71.	13.7	3,270
5	Identification of a unique TGF- β -dependent molecular and functional signature in microglia. <i>Nature Neuroscience</i> , 2014, 17, 131-143.	7.1	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.	3.3	1,701
7	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	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.	1.8	1,557
9	A probability-based approach for high-throughput protein phosphorylation analysis and site localization. <i>Nature Biotechnology</i> , 2006, 24, 1285-1292.	9.4	1,482
10	A proteomics approach to understanding protein ubiquitination. <i>Nature Biotechnology</i> , 2003, 21, 921-926.	9.4	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.	3.3	1,434
12	Systematic and Quantitative Assessment of the Ubiquitin-Modified Proteome. <i>Molecular Cell</i> , 2011, 44, 325-340.	4.5	1,406
13	Network organization of the human autophagy system. <i>Nature</i> , 2010, 466, 68-76.	13.7	1,383
14	Defining the Human Deubiquitinating Enzyme Interaction Landscape. <i>Cell</i> , 2009, 138, 389-403.	13.5	1,354
15	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	13.5	1,241
16	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	13.7	1,190
17	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. <i>Nature</i> , 2014, 509, 105-109.	13.7	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.	3.2	1,130

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19	MS3 eliminates ratio distortion in isobaric multiplexed quantitative proteomics. <i>Nature Methods</i> , 2011, 8, 937-940.	9.0	928
20	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. <i>Nature</i> , 2013, 496, 372-376.	13.7	851
21	A Conserved MST-FOXO Signaling Pathway Mediates Oxidative-Stress Responses and Extends Life Span. <i>Cell</i> , 2006, 125, 987-1001.	13.5	758
22	Meteorin-like Is a Hormone that Regulates Immune-Adipose Interactions to Increase Beige Fat Thermogenesis. <i>Cell</i> , 2014, 157, 1279-1291.	13.5	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.	3.3	691
24	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <i>Nature Methods</i> , 2005, 2, 667-675.	9.0	664
25	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. <i>Cell</i> , 2016, 165, 153-164.	13.5	598
26	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	13.5	596
27	A Protein Complex Network of <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 690-703.	13.5	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.	2.5	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.	2.3	590
30	Proteomics: the move to mixtures. <i>Journal of Mass Spectrometry</i> , 2001, 36, 1083-1091.	0.7	586
31	The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 1630-1638.	5.5	566
32	Quantitative Proteomics Reveal a Feedforward Mechanism for Mitochondrial PARKIN Translocation and Ubiquitin Chain Synthesis. <i>Molecular Cell</i> , 2014, 56, 360-375.	4.5	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.	1.6	535
34	Target-Decoy Search Strategy for Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 55-71.	0.4	534
35	Increasing the Multiplexing Capacity of TMTs Using Reporter Ion Isotopologues with Isobaric Masses. <i>Analytical Chemistry</i> , 2012, 84, 7469-7478.	3.2	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.	1.9	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.	13.5	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.	5.8	436
39	Dual Inhibition of Sister Chromatid Separation at Metaphase. <i>Cell</i> , 2001, 107, 715-726.	13.5	417
40	Semiquantitative Proteomic Analysis of Rat Forebrain Postsynaptic Density Fractions by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 21003-21011.	1.6	417
41	Detection and Quantitation of Circulating Human Irisin by Tandem Mass Spectrometry. <i>Cell Metabolism</i> , 2015, 22, 734-740.	7.2	414
42	Quantitative Temporal Viromics: An Approach to Investigate Host-Pathogen Interaction. <i>Cell</i> , 2014, 157, 1460-1472.	13.5	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.	2.9	394
44	SAMTOR is an S-adenosylmethionine sensor for the mTORC1 pathway. <i>Science</i> , 2017, 358, 813-818.	6.0	384
45	Accumulation of succinate controls activation of adipose tissue thermogenesis. <i>Nature</i> , 2018, 560, 102-106.	13.7	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.	9.4	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.	3.3	364
48	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. <i>Cell</i> , 2020, 183, 1848-1866.e26.	13.5	347
49	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , 2016, 534, 500-505.	13.7	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.	1.8	329
51	Dynamics of Cullin-RING Ubiquitin Ligase Network Revealed by Systematic Quantitative Proteomics. <i>Cell</i> , 2010, 143, 951-965.	13.5	328
52	Proteomics of Primary Cilia by Proximity Labeling. <i>Developmental Cell</i> , 2015, 35, 497-512.	3.1	328
53	Purification and characterization of native spliceosomes suitable for three-dimensional structural analysis. <i>Rna</i> , 2002, 8, 426-439.	1.6	316
54	Intensity-based protein identification by machine learning from a library of tandem mass spectra. <i>Nature Biotechnology</i> , 2004, 22, 214-219.	9.4	294

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55	Amyloid-like Self-Assembly of a Cellular Compartment. <i>Cell</i> , 2016, 166, 637-650.	13.5	294
56	Quantitative Proteomic Atlas of Ubiquitination and Acetylation in the DNA Damage Response. <i>Molecular Cell</i> , 2015, 59, 867-881.	4.5	288
57	Cell-cycle-regulated activation of Akt kinase by phosphorylation at its carboxyl terminus. <i>Nature</i> , 2014, 508, 541-545.	13.7	285
58	Mitochondrial Biogenesis and Proteome Remodeling Promote One-Carbon Metabolism for T Cell Activation. <i>Cell Metabolism</i> , 2016, 24, 104-117.	7.2	282
59	BRCA1-Dependent Ubiquitination of β -Tubulin Regulates Centrosome Number. <i>Molecular and Cellular Biology</i> , 2004, 24, 8457-8466.	1.1	281
60	The metabolic function of cyclin D3 β -CDK6 kinase in cancer cell survival. <i>Nature</i> , 2017, 546, 426-430.	13.7	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.	9.0	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.	1.1	275
63	A large-scale method to measure absolute protein phosphorylation stoichiometries. <i>Nature Methods</i> , 2011, 8, 677-683.	9.0	264
64	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. <i>Cell</i> , 2016, 167, 985-1000.e21.	13.5	259
65	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1326-1337.	2.5	253
66	An ERK/Cdk5 axis controls the diabetogenic actions of PPAR γ . <i>Nature</i> , 2015, 517, 391-395.	13.7	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.	1.8	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.	1.4	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.	1.8	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.	4.5	232
71	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. <i>Nature Communications</i> , 2017, 8, 15965.	5.8	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.	11.6	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.	13.5	226
74	Multidimensional Tracking of GPCR Signaling via Peroxidase-Catalyzed Proximity Labeling. <i>Cell</i> , 2017, 169, 338-349.e11.	13.5	221
75	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , 2020, 180, 968-983.e24.	13.5	220
76	Quantitative proteomic analysis reveals posttranslational responses to aneuploidy in yeast. <i>ELife</i> , 2014, 3, e03023.	2.8	218
77	Differential Glutamate Metabolism in Proliferating and Quiescent Mammary Epithelial Cells. <i>Cell Metabolism</i> , 2016, 23, 867-880.	7.2	214
78	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , 2017, 548, 219-223.	13.7	211
79	Weighing in on ubiquitin: the expanding role of mass-spectrometry-based proteomics. <i>Nature Cell Biology</i> , 2005, 7, 750-757.	4.6	210
80	Structurally Distinct Ca ²⁺ Signaling Domains of Sperm Flagella Orchestrate Tyrosine Phosphorylation and Motility. <i>Cell</i> , 2014, 157, 808-822.	13.5	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.	2.5	202
82	Protein Profiling with Cleavable Isotope-coded Affinity Tag (cICAT) Reagents. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1198-1204.	2.5	201
83	Identification of a Protein Mediating Respiratory Supercomplex Stability. <i>Cell Metabolism</i> , 2012, 15, 348-360.	7.2	195
84	S-Nitrosylation links obesity-associated inflammation to endoplasmic reticulum dysfunction. <i>Science</i> , 2015, 349, 500-506.	6.0	189
85	Cdk1-Dependent Regulation of the Mitotic Inhibitor Wee1. <i>Cell</i> , 2005, 122, 407-420.	13.5	188
86	The Secreted Enzyme PM20D1 Regulates Lipidated Amino Acid Uncouplers of Mitochondria. <i>Cell</i> , 2016, 166, 424-435.	13.5	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.	3.1	186
88	On the Relationship of Protein and mRNA Dynamics in Vertebrate Embryonic Development. <i>Developmental Cell</i> , 2015, 35, 383-394.	3.1	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.	13.5	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.	4.6	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.	3.2	178
92	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , 2019, 75, 620-630.e9.	4.5	178
93	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
94	Phosphoproteome Analysis of Fission Yeast. <i>Journal of Proteome Research</i> , 2008, 7, 1088-1097.	1.8	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.	1.2	173
96	ATAD1 maintains mitochondrial function by facilitating the degradation of mislocalized tail-anchored proteins. <i>EMBO Journal</i> , 2014, 33, 1548-1564.	3.5	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.	1.8	171
98	Correct Interpretation of Comprehensive Phosphorylation Dynamics Requires Normalization by Protein Expression Changes. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009654.	2.5	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.	2.3	165
100	Mechanism of adrenergic CaV1.2 stimulation revealed by proximity proteomics. <i>Nature</i> , 2020, 577, 695-700.	13.7	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.	1.8	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.	1.8	158
103	Identification of Protein Components in vivo Human Acquired Enamel Pellicle Using LC-ESI-MS/MS. <i>Journal of Proteome Research</i> , 2007, 6, 2152-2160.	1.8	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.	3.2	155
105	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. <i>Cell Systems</i> , 2016, 3, 395-403.e4.	2.9	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.	3.3	151
107	USP14 deubiquitinates proteasome-bound substrates that are ubiquitinated at multiple sites. <i>Nature</i> , 2016, 532, 398-401.	13.7	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.	1.5	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.	1.2	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.	3.2	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.	4.5	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.	2.7	144
113	Autoubiquitination of the 26S Proteasome on Rpn13 Regulates Breakdown of Ubiquitin Conjugates. <i>EMBO Journal</i> , 2014, 33, 1159-1176.	3.5	143
114	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	1.8	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.	9.4	142
116	Proteome analysis: Biological assay or data archive?. <i>Electrophoresis</i> , 1998, 19, 1862-1871.	1.3	141
117	The mitochondrial acyl carrier protein (ACP) coordinates mitochondrial fatty acid synthesis with iron sulfur cluster biogenesis. <i>ELife</i> , 2016, 5, .	2.8	141
118	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. <i>ELife</i> , 2015, 4, .	2.8	141
119	An Integrated Microfluidics-Tandem Mass Spectrometry System for Automated Protein Analysis. <i>Analytical Chemistry</i> , 1998, 70, 3728-3734.	3.2	140
120	Accurate Multiplexed Proteomics at the MS2 Level Using the Complement Reporter Ion Cluster. <i>Analytical Chemistry</i> , 2012, 84, 9214-9221.	3.2	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.	1.6	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.	3.3	136
123	Latency-Associated Degradation of the MRP1 Drug Transporter During Latent Human Cytomegalovirus Infection. <i>Science</i> , 2013, 340, 199-202.	6.0	129
124	pH-Gated Succinate Secretion Regulates Muscle Remodeling in Response to Exercise. <i>Cell</i> , 2020, 183, 62-75.e17.	13.5	129
125	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	7.7	127
126	Hexameric assembly of the proteasomal ATPases is templated through their C termini. <i>Nature</i> , 2009, 459, 866-870.	13.7	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.	4.6	125
128	Cyclin C is a haploinsufficient tumour suppressor. <i>Nature Cell Biology</i> , 2014, 16, 1080-1091.	4.6	124
129	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	13.5	123
130	A Secreted Slit2 Fragment Regulates Adipose Tissue Thermogenesis and Metabolic Function. <i>Cell Metabolism</i> , 2016, 23, 454-466.	7.2	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.	1.1	121
132	UBE2O remodels the proteome during terminal erythroid differentiation. <i>Science</i> , 2017, 357, .	6.0	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.	4.5	120
134	Epstein-Barr-Virus-Induced One-Carbon Metabolism Drives B Cell Transformation. <i>Cell Metabolism</i> , 2019, 30, 539-555.e11.	7.2	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.	4.5	118
136	The Nuclear Proteome of a Vertebrate. <i>Current Biology</i> , 2015, 25, 2663-2671.	1.8	117
137	Structure-Based Evolution of Low Nanomolar O-GlcNAc Transferase Inhibitors. <i>Journal of the American Chemical Society</i> , 2018, 140, 13542-13545.	6.6	117
138	Dual Sensing of Physiologic pH and Calcium by EFCAB9 Regulates Sperm Motility. <i>Cell</i> , 2019, 177, 1480-1494.e19.	13.5	116
139	A Perturbed Ubiquitin Landscape Distinguishes Between Ubiquitin in Trafficking and in Proteolysis. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009753.	2.5	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.	7.2	114
141	DPP9 sequesters the CÂterminus of NLRP1 to repress inflammasome activation. <i>Nature</i> , 2021, 592, 778-783.	13.7	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.	1.8	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.	2.7	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.	4.5	110

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145	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways downstream of SDF-1/CXCR4 in breast cancer stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2182-90.	3.3	109
146	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. Journal of Proteome Research, 2019, 18, 1299-1306.	1.8	109
147	A forward genetic screen identifies erythrocyte CD55 as essential for <i>Plasmodium falciparum</i> invasion. Science, 2015, 348, 711-714.	6.0	107
148	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. Nature Cell Biology, 2017, 19, 177-188.	4.6	107
149	Age-related neurodegenerative disease associated pathways identified in retinal and vitreous proteome from human glaucoma eyes. Scientific Reports, 2017, 7, 12685.	1.6	105
150	Selective Alanine Transporter Utilization Creates a Targetable Metabolic Niche in Pancreatic Cancer. Cancer Discovery, 2020, 10, 1018-1037.	7.7	104
151	RFWD3-Dependent Ubiquitination of RPA Regulates Repair at Stalled Replication Forks. Molecular Cell, 2015, 60, 280-293.	4.5	103
152	Proteasomal Control of Cytokinin Synthesis Protects Mycobacterium tuberculosis against Nitric Oxide. Molecular Cell, 2015, 57, 984-994.	4.5	101
153	Protein analysis by mass spectrometry and sequence database searching: Tools for cancer research in the post-genomic era. Electrophoresis, 1999, 20, 310-319.	1.3	100
154	Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. Nature Biotechnology, 2009, 27, 933-940.	9.4	99
155	An inhibitor of the proteasomal deubiquitinating enzyme USP14 induces tau elimination in cultured neurons. Journal of Biological Chemistry, 2017, 292, 19209-19225.	1.6	98
156	Reuterin in the healthy gut microbiome suppresses colorectal cancer growth through altering redox balance. Cancer Cell, 2022, 40, 185-200.e6.	7.7	97
157	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. Nature, 2017, 547, 463-467.	13.7	96
158	G protein-coupled receptor 56 regulates mechanical overload-induced muscle hypertrophy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15756-15761.	3.3	95
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