

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
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459
all docs

459
docs citations

459
times ranked

84018
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Proximity labeling for investigating protein-protein interactions. <i>Methods in Cell Biology</i> , 2022, , 237-266.	1.1	7
4	APC7 mediates ubiquitin signaling in constitutive heterochromatin in the developing mammalian brain. <i>Molecular Cell</i> , 2022, 82, 90-105.e13.	9.7	4
5	Interrogating Kinase-Substrate Relationships with Proximity Labeling and Phosphorylation Enrichment. <i>Journal of Proteome Research</i> , 2022, 21, 494-506.	3.7	6
6	Assessing interference in isobaric tag-based sample multiplexing using an 18plex interference standard. <i>Proteomics</i> , 2022, 22, e2100317.	2.2	5
7	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
8	Enrichment of Tyrosine Phosphorylated Peptides for Quantitative Mass Spectrometry Analysis of RTK Signaling Dynamics. <i>Bio-protocol</i> , 2022, 12, e4311.	0.4	1
9	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
10	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
11	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
12	Ribosomal RNA degradation contributes to silencing of Polycomb target genes. <i>Nature</i> , 2022, 604, 167-174.	27.8	18
13	Functional mapping of PHF6 complexes in chromatin remodeling, replication dynamics, and DNA repair. <i>Blood</i> , 2022, 139, 3418-3429.	1.4	7
14	Kinase domain autophosphorylation rewrites the activity and substrate specificity of CK1 enzymes. <i>Molecular Cell</i> , 2022, 82, 2006-2020.e8.	9.7	12
15	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
16	NAD+ depletion enhances reovirus-induced oncolysis in multiple myeloma. <i>Molecular Therapy - Oncolytics</i> , 2022, 24, 695-706.	4.4	3
17	Fe ³⁺ -NTA magnetic beads as an alternative to spin column-based phosphopeptide enrichment. <i>Journal of Proteomics</i> , 2022, 260, 104561.	2.4	5
18	CDC7-independent G1/S transition revealed by targeted protein degradation. <i>Nature</i> , 2022, 605, 357-365.	27.8	38

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19	Profiling Yeast Deletion Strains Using Sample Multiplexing and Network-Based Analyses. <i>Journal of Proteome Research</i> , 2022, , .	3.7	1
20	Kinase Domain Autophosphorylation Rewires the Activity and Substrate Specificity of CK1 Enzymes. <i>FASEB Journal</i> , 2022, 36, .	0.5	1
21	Time-resolved proximity labeling of protein networks associated with ligand-activated EGFR. <i>Cell Reports</i> , 2022, 39, 110950.	6.4	12
22	A peroxisomal ubiquitin ligase complex forms a retrotranslocation channel. <i>Nature</i> , 2022, 607, 374-380.	27.8	36
23	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
24	Membrane skeleton modulates erythroid proteome remodeling and organelle clearance. <i>Blood</i> , 2021, 137, 398-409.	1.4	11
25	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
26	Growth media selection alters the proteome profiles of three model microorganisms. <i>Journal of Proteomics</i> , 2021, 231, 104006.	2.4	8
27	Improved Monoisotopic Mass Estimation for Deeper Proteome Coverage. <i>Journal of Proteome Research</i> , 2021, 20, 591-598.	3.7	52
28	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
29	Tetracyclines promote survival and fitness in mitochondrial disease models. <i>Nature Metabolism</i> , 2021, 3, 33-42.	11.9	37
30	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
31	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
32	Rapid toxin sequestration modifies poison frog physiology. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	23
33	Targeting oncoproteins with a positive selection assay for protein degraders. <i>Science Advances</i> , 2021, 7, .	10.3	26
34	Peroxisomal-derived ether phospholipids link nucleotides to respirasome assembly. <i>Nature Chemical Biology</i> , 2021, 17, 703-710.	8.0	28
35	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
36	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

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37	DPP9 sequesters the C-terminus of NLRP1 to repress inflammasome activation. <i>Nature</i> , 2021, 592, 778-783.	27.8	114
38	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
39	Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. <i>ELife</i> , 2021, 10, .	6.0	62
40	Time-resolved phosphoproteomics reveals scaffolding and catalysis-responsive patterns of SHP2-dependent signaling. <i>ELife</i> , 2021, 10, .	6.0	17
41	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
42	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
43	Iron Deficiency and Recovery in Yeast: A Quantitative Proteomics Approach. <i>Journal of Proteome Research</i> , 2021, 20, 2751-2761.	3.7	4
44	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
45	Proteomics of broad deubiquitylase inhibition unmask redundant enzyme function to reveal substrates and assess enzyme specificity. <i>Cell Chemical Biology</i> , 2021, 28, 487-502.e5.	5.2	10
46	Time-resolved proteomics profiling of the ciliary Hedgehog response. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	50
47	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
48	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
49	UCP1 governs liver extracellular succinate and inflammatory pathogenesis. <i>Nature Metabolism</i> , 2021, 3, 604-617.	11.9	82
50	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
51	Autophosphorylation of the CK1 Kinase Domain Regulates Enzyme Activity and Substrate Specificity. <i>FASEB Journal</i> , 2021, 35, .	0.5	2
52	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
53	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
54	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

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55	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
56	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
57	Temporal proteomic changes induced by nicotine in human cells: A quantitative proteomics approach. <i>Journal of Proteomics</i> , 2021, 241, 104244.	2.4	2
58	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
59	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
60	The biochemical basis of mitochondrial dysfunction in Zellweger Spectrum Disorder. <i>EMBO Reports</i> , 2021, 22, e51991.	4.5	27
61	Filamin C Cardiomyopathy Variants Cause Protein and Lysosome Accumulation. <i>Circulation Research</i> , 2021, 129, 751-766.	4.5	25
62	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	6.5	27
63	Global proteomics of Ubqln2-based murine models of ALS. <i>Journal of Biological Chemistry</i> , 2021, 296, 100153.	3.4	17
64	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
65	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
66	Proteome-wide mapping of short-lived proteins in human cells. <i>Molecular Cell</i> , 2021, 81, 4722-4735.e5.	9.7	64
67	A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.	27.8	43
68	Multiomic 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
69	Assessing target engagement using proteome-wide solvent shift assays. <i>ELife</i> , 2021, 10, .	6.0	22
70	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
71	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
72	Dynamic proteome profiling of human pluripotent stem cell-derived pancreatic progenitors. <i>Stem Cells</i> , 2020, 38, 542-555.	3.2	6

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73	High-density chemical cross-linking for modeling protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 93-102.	7.1	56
74	Optimized Workflow for Multiplexed Phosphorylation Analysis of TMT-Labeled Peptides Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. Journal of Proteome Research, 2020, 19, 554-560.	3.7	56
75	Native Chromatin Proteomics Reveals a Role for Specific Nucleoporins in Heterochromatin Organization and Maintenance. Molecular Cell, 2020, 77, 51-66.e8.	9.7	75
76	ADAM17 cytoplasmic domain modulates Thioredoxin-1 conformation and activity. Redox Biology, 2020, 37, 101735.	9.0	6
77	WRNIP1 Is Recruited to DNA Interstrand Crosslinks and Promotes Repair. Cell Reports, 2020, 32, 107850.	6.4	15
78	PHD3 Loss Promotes Exercise Capacity and Fat Oxidation in Skeletal Muscle. Cell Metabolism, 2020, 32, 215-228.e7.	16.2	22
79	Co-option of Plasmodium falciparum PP1 for egress from host erythrocytes. Nature Communications, 2020, 11, 3532.	12.8	37
80	The Arg/N-degron pathway targets transcription factors and regulates specific genes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31094-31104.	7.1	7
81	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
82	3D Culture Models with CRISPR Screens Reveal Hyperactive NRF2 as a Prerequisite for Spheroid Formation via Regulation of Proliferation and Ferroptosis. Molecular Cell, 2020, 80, 828-844.e6.	9.7	110
83	pH-Gated Succinate Secretion Regulates Muscle Remodeling in Response to Exercise. Cell, 2020, 183, 62-75.e17.	28.9	129
84	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
85	Proteomic Profiling of Extracellular Vesicles Derived from Cerebrospinal Fluid of Alzheimer's Disease Patients: A Pilot Study. Cells, 2020, 9, 1959.	4.1	75
86	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
87	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. Cell, 2020, 183, 1848-1866.e26.	28.9	347
88	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
89	Selective Alanine Transporter Utilization Creates a Targetable Metabolic Niche in Pancreatic Cancer. Cancer Discovery, 2020, 10, 1018-1037.	9.4	104
90	Defective NADPH production in mitochondrial disease complex I causes inflammation and cell death. Nature Communications, 2020, 11, 2714.	12.8	69

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91	Quantitative analysis of Y-Chromosome gene expression across 36 human tissues. <i>Genome Research</i> , 2020, 30, 860-873.	5.5	56
92	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
93	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
94	Chromatin accessibility promotes hematopoietic and leukemia stem cell activity. <i>Nature Communications</i> , 2020, 11, 1406.	12.8	32
95	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. <i>Nature Chemical Biology</i> , 2020, 16, 546-555.	8.0	16
96	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
97	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
98	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
99	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
100	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
101	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , 2020, 180, 968-983.e24.	28.9	220
102	ELAC1 Repairs tRNAs Cleaved during Ribosome-Associated Quality Control. <i>Cell Reports</i> , 2020, 30, 2106-2114.e5.	6.4	24
103	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	28.9	596
104	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
105	Mechanism of adrenergic CaV1.2 stimulation revealed by proximity proteomics. <i>Nature</i> , 2020, 577, 695-700.	27.8	163
106	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
107	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. <i>Molecular Cell</i> , 2020, 78, 459-476.e13.	9.7	76
108	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6478-6485.	6.5	44

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109	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
110	O-GlcNAc regulates gene expression by controlling detained intron splicing. <i>Nucleic Acids Research</i> , 2020, 48, 5656-5669.	14.5	67
111	An expanded mouse testis transcriptome and mass spectrometry defines novel proteins. <i>Reproduction</i> , 2020, 159, 15-26.	2.6	12
112	A conserved RNA degradation complex required for spreading and epigenetic inheritance of heterochromatin. <i>ELife</i> , 2020, 9, .	6.0	31
113	Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. <i>ELife</i> , 2020, 9, .	6.0	62
114	Mechanisms of Wnt5a- β -Catenin Signaling in Development and Disease. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
115	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
116	Epstein-Barr-Virus-Induced One-Carbon Metabolism Drives B Cell Transformation. <i>Cell Metabolism</i> , 2019, 30, 539-555.e11.	16.2	119
117	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , 2019, 75, 620-630.e9.	9.7	178
118	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
119	Expedited mapping of the ligandable proteome using fully functionalized enantiomeric probe pairs. <i>Nature Chemistry</i> , 2019, 11, 1113-1123.	13.6	93
120	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
121	mTMT: An Alternative, Nonisobaric, Tandem Mass Tag Allowing for Precursor-Based Quantification. <i>Analytical Chemistry</i> , 2019, 91, 12167-12172.	6.5	8
122	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
123	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
124	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
125	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
126	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

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127	GENE-19. DEEP PROTEOMIC SURVEY ACROSS SEVEN CHILDHOOD BRAIN TUMORS. <i>Neuro-Oncology</i> , 2019, 21, ii85-ii85.	1.2	0
128	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
129	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
130	Dual Sensing of Physiologic pH and Calcium by EFCAB9 Regulates Sperm Motility. <i>Cell</i> , 2019, 177, 1480-1494.e19.	28.9	116
131	Targeted Degradation of Glucose Transporters Protects against Arsenic Toxicity. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	16
132	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
133	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
134	Regulation of MicroRNA Machinery and Development by Interspecies S-Nitrosylation. <i>Cell</i> , 2019, 176, 1014-1025.e12.	28.9	62
135	Thiol-based direct threat sensing by the stress-activated protein kinase Hog1. <i>Science Signaling</i> , 2019, 12, .	3.6	10
136	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
137	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
138	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
139	Proteomic profiling of yeast heterochromatin connects direct physical and genetic interactions. <i>Current Genetics</i> , 2019, 65, 495-505.	1.7	3
140	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
141	OR08-3 The Role Of Neuronal Plasticity In The Timing Of Puberty Onset: Insights From A Mkrn3 Deficient Mouse Model.. <i>Journal of the Endocrine Society</i> , 2019, 3, .	0.2	1
142	The skeletal phenotype of Achondrogenesis type 1A is caused exclusively by cartilage defects. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	12
143	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
144	Characterization of Plasmodium falciparum Atypical Kinase Pfpk7â€œ Dependent Phosphoproteome. <i>Journal of Proteome Research</i> , 2018, 17, 2112-2123.	3.7	24

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145	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
146	Multiplexed Isobaric Tag-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
147	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	3.7	143
148	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
149	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
150	OTUD4 Is a Phospho-Activated K63 Deubiquitinase that Regulates MyD88-Dependent Signaling. <i>Molecular Cell</i> , 2018, 69, 505-516.e5.	9.7	65
151	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
152	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
153	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
154	Role of Selenof as a Gatekeeper of Secreted Disulfide-Rich Glycoproteins. <i>Cell Reports</i> , 2018, 23, 1387-1398.	6.4	49
155	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
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