

Sophia Doll

List of Publications by Year in descending order

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242
papers

51,033
citations

3933

88
h-index

1900

208
g-index

253
all docs

253
docs citations

253
times ranked

63471
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass spectrometry-based proteomics. Nature, 2003, 422, 198-207.	27.8	6,282
2	The Perseus computational platform for comprehensive analysis of (prote)omics data. Nature Methods, 2016, 13, 731-740.	19.0	6,181
3	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. Molecular and Cellular Proteomics, 2014, 13, 2513-2526.	3.8	4,178
4	Mass-spectrometric exploration of proteome structure and function. Nature, 2016, 537, 347-355.	27.8	1,573
5	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. Nature Methods, 2014, 11, 319-324.	19.0	1,447
6	The growing landscape of lysine acetylation links metabolism and cell signalling. Nature Reviews Molecular Cell Biology, 2014, 15, 536-550.	37.0	1,153
7	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. Cell, 2015, 163, 712-723.	28.9	1,132
8	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. Cell, 2016, 167, 829-842.e13.	28.9	1,077
9	Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. Nature Communications, 2016, 7, 12429.	12.8	859
10	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. ELife, 2016, 5, .	6.0	766
11	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. Nature Biotechnology, 2003, 21, 315-318.	17.5	702
12	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. Nature Communications, 2016, 7, 13404.	12.8	613
13	Online Parallel Accumulationâ€Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Molecular and Cellular Proteomics, 2018, 17, 2534-2545.	3.8	602
14	Revisiting biomarker discovery by plasmaÂproteomics. Molecular Systems Biology, 2017, 13, 942.	7.2	597
15	Plasma Proteome Profiling to Assess Human Health and Disease. Cell Systems, 2016, 2, 185-195.	6.2	549
16	A Mammalian Organelle Map by Protein Correlation Profiling. Cell, 2006, 125, 187-199.	28.9	538
17	A â€Proteomic Rulerâ€for Protein Copy Number and Concentration Estimation without Spike-in Standards. Molecular and Cellular Proteomics, 2014, 13, 3497-3506.	3.8	530
18	Widespread Proteome Remodeling and Aggregation in Aging C.Âelegans. Cell, 2015, 161, 919-932.	28.9	478

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19	Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 658-673.	3.8	445
20	Uncovering global SUMOylation signaling networks in a site-specific manner. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 927-936.	8.2	408
21	High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. <i>Nature Biotechnology</i> , 2015, 33, 990-995.	17.5	408
22	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , 2019, 10, 963.	12.8	408
23	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 676-687.	7.1	402
24	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	12.6	400
25	The mitochondrial contact site complex, a determinant of mitochondrial architecture. <i>EMBO Journal</i> , 2011, 30, 4356-4370.	7.8	395
26	Precision proteomics: The case for high resolution and high mass accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18132-18138.	7.1	388
27	diaPASEF: parallel accumulation ⁺ serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	19.0	387
28	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. <i>ELife</i> , 2017, 6, .	6.0	344
29	Cytoplasmic protein aggregates interfere with nucleocytoplasmic transport of protein and RNA. <i>Science</i> , 2016, 351, 173-176.	12.6	336
30	Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts. <i>Nature</i> , 2019, 569, 723-728.	27.8	330
31	The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. <i>Molecular Cell</i> , 2013, 49, 583-590.	9.7	329
32	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. <i>Nature</i> , 2012, 488, 508-511.	27.8	323
33	A genome-wide resource for the analysis of protein localisation in <i>Drosophila</i> . <i>ELife</i> , 2016, 5, e12068.	6.0	315
34	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. <i>Nature Methods</i> , 2018, 15, 440-448.	19.0	303
35	Phosphorylation Is a Central Mechanism for Circadian Control of Metabolism and Physiology. <i>Cell Metabolism</i> , 2017, 25, 118-127.	16.2	297
36	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593.	14.5	296

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37	The Q Exactive HF, a Benchtop Mass Spectrometer with a Pre-filter, High-performance Quadrupole and an Ultra-high-field Orbitrap Analyzer. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3698-3708.	3.8	285
38	Parallel Accumulation-Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. <i>Journal of Proteome Research</i> , 2015, 14, 5378-5387.	3.7	281
39	Inflammatory signaling in human tuberculosis granulomas is spatially organized. <i>Nature Medicine</i> , 2016, 22, 531-538.	30.7	273
40	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2284-2296.	3.8	270
41	Proteomic maps of breast cancer subtypes. <i>Nature Communications</i> , 2016, 7, 10259.	12.8	256
42	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 132-144.	3.8	251
43	High-throughput and high-sensitivity phosphoproteomics with the EasyPhos platform. <i>Nature Protocols</i> , 2018, 13, 1897-1916.	12.0	238
44	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	17.5	237
45	Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 841-853.	3.8	234
46	Accurate Protein Complex Retrieval by Affinity Enrichment Mass Spectrometry (AE-MS) Rather than Affinity Purification Mass Spectrometry (AP-MS). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 120-135.	3.8	231
47	Functional classification of memory CD8+ T cells by CX3CR1 expression. <i>Nature Communications</i> , 2015, 6, 8306.	12.8	231
48	Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. <i>Cell Reports</i> , 2017, 19, 2396-2409.	6.4	213
49	Region and cell-type resolved quantitative proteomic map of the human heart. <i>Nature Communications</i> , 2017, 8, 1469.	12.8	213
50	Time- and compartment- resolved proteome profiling of the extracellular niche in lung injury and repair. <i>Molecular Systems Biology</i> , 2015, 11, 819.	7.2	211
51	Activation of the ATR kinase by the RPA-binding protein ETAA1. <i>Nature Cell Biology</i> , 2016, 18, 1196-1207.	10.3	208
52	Mass Spectrometry-Based Detection and Assignment of Protein Posttranslational Modifications. <i>ACS Chemical Biology</i> , 2015, 10, 63-71.	3.4	193
53	Circadian control of oscillations in mitochondrial rate-limiting enzymes and nutrient utilization by PERIOD proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1673-82.	7.1	190
54	Proteomics reveals the effects of sustained weight loss on the human plasma proteome. <i>Molecular Systems Biology</i> , 2016, 12, 901.	7.2	188

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55	Copy Number Analysis of the Murine Platelet Proteome Spanning the Complete Abundance Range. Molecular and Cellular Proteomics, 2014, 13, 3435-3445.	3.8	187
56	Novel and shared neoantigen derived from histone 3 variant H3.3K27M mutation for glioma T cell therapy. Journal of Experimental Medicine, 2018, 215, 141-157.	8.5	186
57	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. Science, 2015, 348, 1253671.	12.6	183
58	Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors. Molecular Cell, 2016, 63, 951-964.	9.7	181
59	Plasma proteome profiling discovers novel proteins associated with non-alcoholic fatty liver disease. Molecular Systems Biology, 2019, 15, e8793.	7.2	176
60	OpenCell: Endogenous tagging for the cartography of human cellular organization. Science, 2022, 375, eabi6983.	12.6	174
61	Plasma Proteome Profiling to detect and avoid sample-related biases in biomarker studies. EMBO Molecular Medicine, 2019, 11, e10427.	6.9	171
62	Loss-less Nano-fractionator for High Sensitivity, High Coverage Proteomics. Molecular and Cellular Proteomics, 2017, 16, 694-705.	3.8	169
63	The forebrain synaptic transcriptome is organized by clocks but its proteome is driven by sleep. Science, 2019, 366, .	12.6	169
64	Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. Molecular Cell, 2015, 59, 75-88.	9.7	166
65	Single muscle fiber proteomics reveals unexpected mitochondrial specialization. EMBO Reports, 2015, 16, 387-395.	4.5	163
66	Deep Visual Proteomics defines single-cell identity and heterogeneity. Nature Biotechnology, 2022, 40, 1231-1240.	17.5	160
67	Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. Molecular Systems Biology, 2020, 16, e9356.	7.2	157
68	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. Molecular and Cellular Proteomics, 2015, 14, 2014-2029.	3.8	150
69	Cell-Type- and Brain-Region-Resolved Mouse Brain Lipidome. Cell Reports, 2020, 32, 108132.	6.4	147
70	Limited Environmental Serine and Glycine Confer Brain Metastasis Sensitivity to PHGDH Inhibition. Cancer Discovery, 2020, 10, 1352-1373.	9.4	145
71	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. Cell Metabolism, 2014, 20, 1076-1087.	16.2	143
72	The CMG Helicase Bypasses DNA-Protein Cross-Links to Facilitate Their Repair. Cell, 2019, 176, 167-181.e21.	28.9	138

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73	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020, 11, 331.	12.8	138
74	Evidence of Extrapaneacretic Glucagon Secretion in Man. <i>Diabetes</i> , 2016, 65, 585-597.	0.6	136
75	Replication-Coupled DNA-Protein Crosslink Repair by SPRTN and the Proteasome in <i>Xenopus</i> Egg Extracts. <i>Molecular Cell</i> , 2019, 73, 574-588.e7.	9.7	135
76	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. <i>Developmental Cell</i> , 2018, 47, 205-221.e7.	7.0	132
77	C9ORF72 interaction with cofilin modulates actin dynamics in motor neurons. <i>Nature Neuroscience</i> , 2016, 19, 1610-1618.	14.8	131
78	Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4. <i>Molecular Cell</i> , 2014, 56, 43-54.	9.7	129
79	The proteome landscape of the kingdoms of life. <i>Nature</i> , 2020, 582, 592-596.	27.8	128
80	Multi-level Proteomics Identifies CT45 as a Chemosensitivity Mediator and Immunotherapy Target in Ovarian Cancer. <i>Cell</i> , 2018, 175, 159-170.e16.	28.9	127
81	Development of phospho-specific Rab protein antibodies to monitor <i>in vivo</i> activity of the LRRK2 Parkinson's disease kinase. <i>Biochemical Journal</i> , 2018, 475, 1-22.	3.7	123
82	The Proteome of Primary Prostate Cancer. <i>European Urology</i> , 2016, 69, 942-952.	1.9	122
83	Dynamics in protein translation sustaining T cell preparedness. <i>Nature Immunology</i> , 2020, 21, 927-937.	14.5	120
84	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10.	6.2	111
85	Proteomics-Based Comparative Mapping of the Secretomes of Human Brown and White Adipocytes Reveals EPDR1 as a Novel Adipokine. <i>Cell Metabolism</i> , 2019, 30, 963-975.e7.	16.2	109
86	A streamlined mass spectrometry-based proteomics workflow for large-scale FFPE tissue analysis. <i>Journal of Pathology</i> , 2020, 251, 100-112.	4.5	109
87	Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. <i>Cell Reports</i> , 2017, 21, 2291-2303.	6.4	107
88	Artificial intelligence for proteomics and biomarker discovery. <i>Cell Systems</i> , 2021, 12, 759-770.	6.2	106
89	In vivo brain GPCR signaling elucidated by phosphoproteomics. <i>Science</i> , 2018, 360, .	12.6	105
90	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 16575-16583.	3.4	98

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91	System-wide identification of wild-type SUMO-2 conjugation sites. Nature Communications, 2015, 6, 7289.	12.8	97
92	Deep Proteome Profiling Reveals Common Prevalence of MZB1-Positive Plasma B Cells in Human Lung and Skin Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 1298-1310.	5.6	97
93	A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. ELife, 2014, 3, e02975.	6.0	97
94	A knowledge graph to interpret clinical proteomics data. Nature Biotechnology, 2022, 40, 692-702.	17.5	97
95	T Cells Engineered to Express a T-Cell Receptor Specific for Glypican-3 to Recognize and Kill Hepatoma Cells In Vitro and In Mice. Gastroenterology, 2015, 149, 1042-1052.	1.3	96
96	Antisense-mediated exon skipping: a therapeutic strategy for titin-based dilated cardiomyopathy. EMBO Molecular Medicine, 2015, 7, 562-576.	6.9	94
97	C/EBPβ creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 and Brd4. Nature Cell Biology, 2016, 18, 371-381.	10.3	94
98	High-resolution serum proteome trajectories in COVID-19 reveal patient-specific seroconversion. EMBO Molecular Medicine, 2021, 13, e14167.	6.9	92
99	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	30.7	91
100	Quantitative shotgun proteomics: considerations for a high-quality workflow in immunology. Nature Immunology, 2014, 15, 112-117.	14.5	90
101	CRL2 ^{Lrr1} promotes unloading of the vertebrate replisome from chromatin during replication termination. Genes and Development, 2017, 31, 275-290.	5.9	90
102	Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. Nature, 2020, 588, 157-163.	27.8	90
103	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	19.0	88
104	The Case for Proteomics and Phospho-Proteomics in Personalized Cancer Medicine. Proteomics - Clinical Applications, 2019, 13, e1800113.	1.6	88
105	Urinary proteome profiling for stratifying patients with familial Parkinson's disease. EMBO Molecular Medicine, 2021, 13, e13257.	6.9	88
106	Proteomics and C9orf72 neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. Life Science Alliance, 2018, 1, e201800070.	2.8	88
107	Trapped Ion Mobility Spectrometry and Parallel Accumulation-Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	3.8	84
108	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	12.8	81

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109	Plasma Proteome Profiling Reveals Dynamics of Inflammatory and Lipid Homeostasis Markers after Roux-En-Y Gastric Bypass Surgery. <i>Cell Systems</i> , 2018, 7, 601-612.e3.	6.2	80
110	Molecular basis of PRC1 targeting to Polycomb response elements by PhoRC. <i>Genes and Development</i> , 2016, 30, 1116-1127.	5.9	78
111	Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. <i>Nature Metabolism</i> , 2021, 3, 1017-1031.	11.9	76
112	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591.	6.4	75
113	Absolute Proteome Analysis of Colorectal Mucosa, Adenoma, and Cancer Reveals Drastic Changes in Fatty Acid Metabolism and Plasma Membrane Transporters. <i>Journal of Proteome Research</i> , 2015, 14, 4005-4018.	3.7	74
114	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. <i>Nature Communications</i> , 2016, 7, 13250.	12.8	74
115	Phosphoproteomic approach for agonist-specific signaling in mouse brains: mTOR pathway is involved in μ opioid aversion. <i>Neuropsychopharmacology</i> , 2019, 44, 939-949.	5.4	74
116	Defective glycosylation and multisystem abnormalities characterize the primary immunodeficiency XMEN disease. <i>Journal of Clinical Investigation</i> , 2019, 130, 507-522.	8.2	74
117	Spatially and cell-type resolved quantitative proteomic atlas of healthy human skin. <i>Nature Communications</i> , 2020, 11, 5587.	12.8	72
118	A Stat6/Pten Axis Links Regulatory T Cells with Adipose Tissue Function. <i>Cell Metabolism</i> , 2017, 26, 475-492.e7.	16.2	71
119	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. <i>Nature Communications</i> , 2021, 12, 254.	12.8	71
120	Molecular and structural architecture of polyQ aggregates in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3446-E3453.	7.1	68
121	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. <i>Clinical Cancer Research</i> , 2018, 24, 5433-5444.	7.0	68
122	Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. <i>Translational Psychiatry</i> , 2018, 8, 160.	4.8	68
123	A Cell-Autonomous Signature of Dysregulated Protein Phosphorylation Underlies Muscle Insulin Resistance in Type 2 Diabetes. <i>Cell Metabolism</i> , 2020, 32, 844-859.e5.	16.2	68
124	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. <i>Journal of Proteome Research</i> , 2015, 14, 4885-4895.	3.7	66
125	TRAIPI is a PCNA-binding ubiquitin ligase that protects genome stability after replication stress. <i>Journal of Cell Biology</i> , 2016, 212, 63-75.	5.2	65
126	A Primer on Concepts and Applications of Proteomics in Neuroscience. <i>Neuron</i> , 2017, 96, 558-571.	8.1	65

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127	Protein profile of fiber types in human skeletal muscle: a single-fiber proteomics study. Skeletal Muscle, 2021, 11, 24.	4.2	65
128	Mit/ <scp>TFE</scp> factors control <scp>ER</scp> â€phagy via transcriptional regulation of <scp>FAM</scp> 134B. EMBO Journal, 2020, 39, e105696.	7.8	60
129	Parallel accumulation for 100% duty cycle trapped ion mobility-mass spectrometry. International Journal of Mass Spectrometry, 2017, 413, 168-175.	1.5	59
130	Comparative analysis to guide quality improvements in proteomics. Nature Methods, 2009, 6, 717-719.	19.0	58
131	<scp>PP</scp> 2A delays <scp>APC</scp> /Câ€dependent degradation of separaseâ€associated but not free securin. EMBO Journal, 2014, 33, 1134-1147.	7.8	57
132	FoxK1 and FoxK2 in insulin regulation of cellular and mitochondrial metabolism. Nature Communications, 2019, 10, 1582.	12.8	57
133	Efficient mitotic checkpoint signaling depends on integrated activities of Bub1 and the <scp>RZZ</scp> complex. EMBO Journal, 2019, 38, .	7.8	56
134	Oxyntomodulin Identified as a Marker of Type 2 Diabetes and Gastric Bypass Surgery by Mass-spectrometry Based Profiling of Human Plasma. EBioMedicine, 2016, 7, 112-120.	6.1	53
135	UBL3 modification influences protein sorting to small extracellular vesicles. Nature Communications, 2018, 9, 3936.	12.8	53
136	Cortical circuit alterations precede motor impairments in Huntingtonâ€™s disease mice. Scientific Reports, 2019, 9, 6634.	3.3	53
137	Quantitative and Dynamic Catalogs of Proteins Released during Apoptotic and Necroptotic Cell Death. Cell Reports, 2020, 30, 1260-1270.e5.	6.4	53
138	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	6.9	53
139	Overexpression of Q-rich prion-like proteins suppresses polyQ cytotoxicity and alters the polyQ interactome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18219-18224.	7.1	52
140	A Proteomics Approach to the Protein Normalization Problem: Selection of Unvarying Proteins for MS-Based Proteomics and Western Blotting. Journal of Proteome Research, 2016, 15, 2321-2326.	3.7	51
141	Quantitative Proteomics Identifies Serum Response Factor Binding Protein 1 as a Host Factor for Hepatitis C Virus Entry. Cell Reports, 2015, 12, 864-878.	6.4	50
142	Mechanisms Preserving Insulin Action during High Dietary Fat Intake. Cell Metabolism, 2019, 29, 50-63.e4.	16.2	50
143	Interconversion between Anticipatory and Active GID E3ÂUbiquitin Ligase Conformations via Metabolically Driven Substrate Receptor Assembly. Molecular Cell, 2020, 77, 150-163.e9.	9.7	50
144	The structural context of posttranslational modifications at a proteome-wide scale. PLoS Biology, 2022, 20, e3001636.	5.6	50

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145	Multivalent binding of PWWP2A to H2A.Z regulates mitosis and neural crest differentiation. EMBO Journal, 2017, 36, 2263-2279.	7.8	48
146	Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892.	6.4	47
147	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. Nature Communications, 2021, 12, 6761.	12.8	47
148	Parasite-induced ER stress response in hepatocytes facilitates Plasmodium liver stage infection. EMBO Reports, 2015, 16, 955-964.	4.5	46
149	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. Nature Communications, 2018, 9, 4300.	12.8	46
150	Minimal amounts of kindlin-3 suffice for basal platelet and leukocyte functions in mice. Blood, 2015, 126, 2592-2600.	1.4	45
151	Accurate MS-based Rab10 Phosphorylation Stoichiometry Determination as Readout for LRRK2 Activity in Parkinson's Disease. Molecular and Cellular Proteomics, 2020, 19, 1546-1560.	3.8	45
152	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STING-IFN- λ pathway. Nature Immunology, 2021, 22, 485-496.	14.5	45
153	GID E3 ligase supramolecular chelate assembly configures multipronged ubiquitin targeting of an oligomeric metabolic enzyme. Molecular Cell, 2021, 81, 2445-2459.e13.	9.7	44
154	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	16.8	43
155	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and protein-protein interactions. Molecular Biology of the Cell, 2014, 25, 3178-3194.	2.1	42
156	A proteomic atlas of insulin signalling reveals tissue-specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	7.2	42
157	Distinct signaling by insulin and IGF-1 receptors and their extra- and intracellular domains. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	41
158	Hippocampal disruptions of synaptic and astrocyte metabolism are primary events of early amyloid pathology in the 5xFAD mouse model of Alzheimer's disease. Cell Death and Disease, 2021, 12, 954.	6.3	41
159	The Transcription Factor ETV1 Induces Atrial Remodeling and Arrhythmia. Circulation Research, 2018, 123, 550-563.	4.5	40
160	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- β . Science Signaling, 2014, 7, rs5.	3.6	39
161	STAT3 -dependent analysis reveals PDK4 as independent predictor of recurrence in prostate cancer. Molecular Systems Biology, 2020, 16, e9247.	7.2	38
162	Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7.	7.0	38

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163	A beginner's guide to mass spectrometry-based proteomics. Biochemist, 2020, 42, 64-69.	0.5	35
164	The ETS family member GABP \pm modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. Nucleic Acids Research, 2014, 42, 6256-6269.	14.5	33
165	Ethical Principles, Constraints, and Opportunities in Clinical Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100046.	3.8	33
166	The <i>Caenorhabditis elegans</i> pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. Molecular Biology of the Cell, 2014, 25, 2984-2992.	2.1	31
167	Phosphoproteome profiling uncovers a key role for CDKs in TNF signaling. Nature Communications, 2021, 12, 6053.	12.8	31
168	FRET Reagent Reveals the Intracellular Processing of Peptide-Linked Antibody-Drug Conjugates. Bioconjugate Chemistry, 2018, 29, 2468-2477.	3.6	29
169	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. ELife, 2021, 10, .	6.0	29
170	SnapShot: Clinical proteomics. Cell, 2021, 184, 4840-4840.e1.	28.9	29
171	Circulating Glucagon 1-61 Regulates Blood Glucose by Increasing Insulin Secretion and Hepatic Glucose Production. Cell Reports, 2017, 21, 1452-1460.	6.4	28
172	Gel-like inclusions of C-terminal fragments of TDP \pm 43 sequester stalled proteasomes in neurons. EMBO Reports, 2022, 23, e53890.	4.5	28
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