Sophia Doll

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1124653/publications.pdf

Version: 2024-02-01

242 papers	51,033 citations	3930 88 h-index	1899 208 g-index
253 all docs	253 docs citations	253 times ranked	63471 citing authors

#	ARTICLE	IF	CITATIONS
1	AlphaMap: an open-source Python package for the visual annotation of proteomics data with sequence-specific knowledge. Bioinformatics, 2022, 38, 849-852.	1.8	12
2	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	0.6	16
3	Gene-selective transcription promotes the inhibition of tissue reparative macrophages by TNF. Life Science Alliance, 2022, 5, e202101315.	1.3	10
4	A knowledge graph to interpret clinical proteomics data. Nature Biotechnology, 2022, 40, 692-702.	9.4	97
5	Adverse stem cell clones within a single patientâ€™s tumor predict clinical outcome in AML patients. Journal of Hematology and Oncology, 2022, 15, 25.	6.9	1
6	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	7.7	43
7	OpenCell: Endogenous tagging for the cartography of human cellular organization. Science, 2022, 375, eabi6983.	6.0	174
8	Phosphorylation of serine-893 in CARD11 suppresses the formation and activity of the CARD11-BCL10-MALT1 complex in T and B cells. Science Signaling, 2022, 15, eabk3083.	1.6	3
9	Mast cells in lung damage of COVIDâ€•19 autopsies: A descriptive study. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 2237-2239.	2.7	13
10	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity. Life Science Alliance, 2022, 5, e202101185.	1.3	13
11	A GID E3 ligase assembly ubiquitinates an Rsp5 E3 adaptor and regulates plasma membrane transporters. EMBO Reports, 2022, 23, e53835.	2.0	9
12	Gelâ€•like inclusions of Câ€•terminal fragments of TDPâ€•43 sequester stalled proteasomes in neurons. EMBO Reports, 2022, 23, e53890.	2.0	28
13	HAX1-dependent control of mitochondrial proteostasis governs neutrophil granulocyte differentiation. Journal of Clinical Investigation, 2022, 132, .	3.9	18
14	The structural context of posttranslational modifications at a proteome-wide scale. PLoS Biology, 2022, 20, e3001636.	2.6	50
15	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
16	Deep Visual Proteomics defines single-cell identity and heterogeneity. Nature Biotechnology, 2022, 40, 1231-1240.	9.4	160
17	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	15.2	91
18	Cryo-EM structures of Gid12-bound GID E3 reveal steric blockade as a mechanism inhibiting substrate ubiquitylation. Nature Communications, 2022, 13, .	5.8	3

#	ARTICLE	IF	CITATIONS
19	Signatures of muscle disuse in spaceflight and bed rest revealed by single muscle fiber proteomics. , 2022, 1, .		22
20	Plasma proteome profiles treatment efficacy of incretin dual agonism in dietâ€induced obese female and male mice. Diabetes, Obesity and Metabolism, 2021, 23, 195-207.	2.2	12
21	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	3.9	26
22	Trapped Ion Mobility Spectrometry and Parallel Accumulationâ€“Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	2.5	84
23	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. Nature Communications, 2021, 12, 254.	5.8	71
24	A New Parallel High-Pressure Packing System Enables Rapid Multiplexed Production of Capillary Columns. Molecular and Cellular Proteomics, 2021, 20, 100082.	2.5	13
25	Urinary proteome profiling for stratifying patients with familial Parkinsonâ€™s disease. EMBO Molecular Medicine, 2021, 13, e13257.	3.3	88
26	Ethical Principles, Constraints, and Opportunities in Clinical Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100046.	2.5	33
27	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. ELife, 2021, 10, .	2.8	29
28	Plasma Proteomes Can Be Reidentifiable and Potentially Contain Personally Sensitive and Incidental Findings. Molecular and Cellular Proteomics, 2021, 20, 100035.	2.5	20
29	Interaction of 7SK with the Smn complex modulates snRNP production. Nature Communications, 2021, 12, 1278.	5.8	23
30	Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7.	3.1	38
31	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	5.8	81
32	DDRE-22. TARGETING SERINE SYNTHESIS IN BRAIN METASTASIS. Neuro-Oncology Advances, 2021, 3, i11-i11.	0.4	0
33	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STINGâ€“IFN-Î² pathway. Nature Immunology, 2021, 22, 485-496.	7.0	45
34	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	3.3	53
35	Tissue-specific modulation of gene expression in response to lowered insulin signalling in Drosophila. ELife, 2021, 10, .	2.8	12
36	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, .	3.3	41

#	ARTICLE	IF	CITATIONS
37	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie, 2021, 133, 17197-17206.	1.6	0
38	Aggrecan: a new biomarker for acute type A aortic dissection. Scientific Reports, 2021, 11, 10371.	1.6	12
39	Insulin Resistance and Gender Define a Cell Autonomous Supernetworkof Protein Phosphorylation. Journal of the Endocrine Society, 2021, 5, A446-A446.	0.1	0
40	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie - International Edition, 2021, 60, 17060-17069.	7.2	13
41	Cohort profile: the MUNICH Preterm and Term Clinical study (MUNICH-PreTCl), a neonatal birth cohort with focus on prenatal and postnatal determinants of infant and childhood morbidity. BMJ Open, 2021, 11, e050652.	0.8	2
42	InnenrÃ¼cktitelbild: Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints (Angew.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	0
43	Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. Nature Metabolism, 2021, 3, 1017-1031.	5.1	76
44	GID E3 ligase supramolecular chelate assembly configures multipronged ubiquitin targeting of an oligomeric metabolic enzyme. Molecular Cell, 2021, 81, 2445-2459.e13.	4.5	44
45	Identification of covalent modifications regulatingÂimmune signaling complex composition and phenotype. Molecular Systems Biology, 2021, 17, e10125.	3.2	6
46	Highâ€resolution serum proteome trajectories in COVIDâ€19 reveal patientâ€specific seroconversion. EMBO Molecular Medicine, 2021, 13, e14167.	3.3	92
47	Reply to â€œQuality control requirements for the correct annotation of lipidomics dataâ€. Nature Communications, 2021, 12, 4772.	5.8	2
48	Artificial intelligence for proteomics and biomarker discovery. Cell Systems, 2021, 12, 759-770.	2.9	106
49	Identification of the transcription factor MAZ as a regulator of erythropoiesis. Blood Advances, 2021, 5, 3002-3015.	2.5	8
50	AlphaTims: Indexing Trapped Ion Mobility Spectrometryâ€“TOF Data for Fast and Easy Accession and Visualization. Molecular and Cellular Proteomics, 2021, 20, 100149.	2.5	23
51	SnapShot: Clinical proteomics. Cell, 2021, 184, 4840-4840.e1.	13.5	29
52	Signaling defects associated with insulin resistance in nondiabetic and diabetic individuals and modification by sex. Journal of Clinical Investigation, 2021, 131, .	3.9	27
53	Defining the RBPome of primary T helper cells to elucidate higher-order Roquin-mediated mRNA regulation. Nature Communications, 2021, 12, 5208.	5.8	23
54	JAZF1, A Novel p400/TIP60/NuA4 Complex Member, Regulates H2A.Z Acetylation at Regulatory Regions. International Journal of Molecular Sciences, 2021, 22, 678.	1.8	16

#	ARTICLE	IF	CITATIONS
55	Molecular response to PARP1 inhibition in ovarian cancer cells as determined by mass spectrometry based proteomics. Journal of Ovarian Research, 2021, 14, 140.	1.3	8
56	Hippocampal disruptions of synaptic and astrocyte metabolism are primary events of early amyloid pathology in the 5xFAD mouse model of Alzheimerâ€™s disease. Cell Death and Disease, 2021, 12, 954.	2.7	41
57	Phosphoproteome profiling uncovers a key role for CDKs in TNF signaling. Nature Communications, 2021, 12, 6053.	5.8	31
58	Defining NASH from a Multi-Omics Systems Biology Perspective. Journal of Clinical Medicine, 2021, 10, 4673.	1.0	9
59	Protein profile of fiber types in human skeletal muscle: a single-fiber proteomics study. Skeletal Muscle, 2021, 11, 24.	1.9	65
60	Loss of full-length hnRNP R isoform impairs DNA damage response in motoneurons by inhibiting Yb1 recruitment to chromatin. Nucleic Acids Research, 2021, 49, 12284-12305.	6.5	10
61	Hepatocyte-specific perturbation of NAD+ biosynthetic pathways in mice induces reversible nonalcoholic steatohepatitisâ€“like phenotypes. Journal of Biological Chemistry, 2021, 297, 101388.	1.6	20
62	Proteomic Analysis Identifies NDUFS1 and ATP5O as Novel Markers for Survival Outcome in Prostate Cancer. Cancers, 2021, 13, 6036.	1.7	7
63	Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. Nature Communications, 2021, 12, 6761.	5.8	47
64	Interconversion between Anticipatory and Active GID E3ÂUbiquitin Ligase Conformations via Metabolically Driven Substrate Receptor Assembly. Molecular Cell, 2020, 77, 150-163.e9.	4.5	50
65	SHP1 regulates a STAT6â€“ITGB3 axis in FLT3ITD-positive AML cells. Leukemia, 2020, 34, 1444-1449.	3.3	7
66	Pharmacological and phosphoproteomic approaches to roles of protein kinase C in kappa opioid receptor-mediated effects in mice. Neuropharmacology, 2020, 181, 108324.	2.0	5
67	Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. Nature, 2020, 588, 157-163.	13.7	90
68	diaPASEF: parallel accumulationâ€“serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
69	DIA-based systems biology approach unveils E3 ubiquitin ligase-dependent responses to a metabolic shift. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32806-32815.	3.3	17
70	The Origins of Organellar Mapping by Protein Correlation Profiling. Proteomics, 2020, 20, 1900330.	1.3	9
71	MiT/ <scp>TFE</scp> factors control <scp>ER</scp> â€phagy via transcriptional regulation of <scp>FAM</scp> 134B. EMBO Journal, 2020, 39, e105696.	3.5	60
72	Cell-Type- and Brain-Region-Resolved Mouse Brain Lipidome. Cell Reports, 2020, 32, 108132.	2.9	147

#	ARTICLE	IF	CITATIONS
73	A Cell-Autonomous Signature of Dysregulated Protein Phosphorylation Underlies Muscle Insulin Resistance in Type 2 Diabetes. Cell Metabolism, 2020, 32, 844-859.e5.	7.2	68
74	Spatially and cell-type resolved quantitative proteomic atlas of healthy human skin. Nature Communications, 2020, 11, 5587.	5.8	72
75	Sequencing of the First Draft of the Human Acetylome. Clinical Chemistry, 2020, 66, 852-853.	1.5	1
76	Limited Environmental Serine and Glycine Confer Brain Metastasis Sensitivity to PHGDH Inhibition. Cancer Discovery, 2020, 10, 1352-1373.	7.7	145
77	Role for ribosome-associated quality control in sampling proteins for MHC class I-mediated antigen presentation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4099-4108.	3.3	27
78	The proteome landscape of the kingdoms of life. Nature, 2020, 582, 592-596.	13.7	128
79	A streamlined mass spectrometryâ€"based proteomics workflow for largeâ€scale FFPE tissue analysis. Journal of Pathology, 2020, 251, 100-112.	2.1	109
80	Pervasive functional translation of noncanonical human open reading frames. Science, 2020, 367, 1140-1146.	6.0	400
81	Accurate MS-based Rab10 Phosphorylation Stoichiometry Determination as Readout for LRRK2 Activity in Parkinson's Disease. Molecular and Cellular Proteomics, 2020, 19, 1546-1560.	2.5	45
82	Dynamics in protein translation sustaining T cell preparedness. Nature Immunology, 2020, 21, 927-937.	7.0	120
83	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. Nature Communications, 2020, 11, 331.	5.8	138
84	Quantitative and Dynamic Catalogs of Proteins Released during Apoptotic and Necroptotic Cell Death. Cell Reports, 2020, 30, 1260-1270.e5.	2.9	53
85	<i> <scp>STAT</scp> 3 </i> â€dependent analysis reveals <i> <scp>PDK</scp> 4 </i> as independent predictor of recurrence in prostate cancer. Molecular Systems Biology, 2020, 16, e9247.	3.2	38
86	A beginnerâ€™s guide to mass spectrometryâ€"based proteomics. Biochemist, 2020, 42, 64-69.	0.2	35
87	Fam20C regulates protein secretion by Cab45 phosphorylation. Journal of Cell Biology, 2020, 219, .	2.3	15
88	Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. Molecular Systems Biology, 2020, 16, e9356.	3.2	157
89	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. Molecular Systems Biology, 2020, 16, e9813.	3.2	21
90	Phosphoproteomic approach for agonist-specific signaling in mouse brains: mTOR pathway is involved in Îº opioid aversion. Neuropsychopharmacology, 2019, 44, 939-949.	2.8	74

#	ARTICLE	IF	CITATIONS
91	Quick and clean: Cracking sentences encoded in E. coli by LCâ€“MS/MS, de novo sequencing, and dictionary search. EuPA Open Proteomics, 2019, 22-23, 30-35.	2.5	2
92	Myosin binding protein H-like (MYBPHL): a promising biomarker to predict atrial damage. Scientific Reports, 2019, 9, 9986.	1.6	6
93	Catching Lipid Droplet Contacts by Proteomics. Contact (Thousand Oaks (Ventura County, Calif)), 2019, 2, 251525641985918.	0.4	6
94	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	10
95	The forebrain synaptic transcriptome is organized by clocks but its proteome is driven by sleep. Science, 2019, 366, .	6.0	169
96	Hepatic Rab24 controls blood glucose homeostasis via improving mitochondrial plasticity. Nature Metabolism, 2019, 1, 1009-1026.	5.1	27
97	Proteomics-Based Comparative Mapping of the Secretomes of Human Brown and White Adipocytes Reveals EPDR1 as a Novel Batokine. Cell Metabolism, 2019, 30, 963-975.e7.	7.2	109
98	Plasma Proteome Profiling to detect and avoid sampleâ€•related biases in biomarker studies. EMBO Molecular Medicine, 2019, 11, e10427.	3.3	171
99	Metallopeptidase inhibitor 1 (TIMPâ€•1) promotes receptor tyrosine kinase câ€•Kit signaling in colorectal cancer. Molecular Oncology, 2019, 13, 2646-2662.	2.1	11
100	The ever expanding scope of electrospray mass spectrometryâ€”a 30 year journey. Nature Communications, 2019, 10, 3744.	5.8	25
101	Key Features Relevant to Select Antigens and TCR From the MHC-Mismatched Repertoire to Treat Cancer. Frontiers in Immunology, 2019, 10, 1485.	2.2	8
102	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	2.9	111
103	Cortical circuit alterations precede motor impairments in Huntingtonâ€™s disease mice. Scientific Reports, 2019, 9, 6634.	1.6	53
104	Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts. Nature, 2019, 569, 723-728.	13.7	330
105	Plasma proteome profiling discovers novel proteins associated with nonâ€•alcoholic fatty liver disease. Molecular Systems Biology, 2019, 15, e8793.	3.2	176
106	FoxK1 and FoxK2 in insulin regulation of cellular and mitochondrial metabolism. Nature Communications, 2019, 10, 1582.	5.8	57
107	The Case for Proteomics and Phosphoâ€•Proteomics in Personalized Cancer Medicine. Proteomics - Clinical Applications, 2019, 13, e1800113.	0.8	88
108	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. Nature Communications, 2019, 10, 963.	5.8	408

#	Article	IF	Citations
109	Efficient mitotic checkpoint signaling depends on integrated activities of Bub1 and the <scp>RZZ</scp> complex. EMBO Journal, 2019, 38, .	3.5	56
110	Proteomics of Cytochrome c Oxidase-Negative versus -Positive Muscle Fiber Sections in Mitochondrial Myopathy. Cell Reports, 2019, 29, 3825-3834.e4.	2.9	17
111	Mesothelial Cell HIF1Î± Expression Is Metabolically Downregulated by Metformin to Prevent Oncogenic Tumor-Stromal Crosstalk. Cell Reports, 2019, 29, 4086-4098.e6.	2.9	26
112	The CMG Helicase Bypasses DNA-Protein Cross-Links to Facilitate Their Repair. Cell, 2019, 176, 167-181.e21.	13.5	138
113	Replication-Coupled DNA-Protein Crosslink Repair by SPRTN and the Proteasome in Xenopus Egg Extracts. Molecular Cell, 2019, 73, 574-588.e7.	4.5	135
114	Mechanisms Preserving Insulin Action during High Dietary Fat Intake. Cell Metabolism, 2019, 29, 50-63.e4.	7.2	50
115	Defective glycosylation and multisystem abnormalities characterize the primary immunodeficiency XMEN disease. Journal of Clinical Investigation, 2019, 130, 507-522.	3.9	74
116	Response to Raaijmakers & Medema. EMBO Journal, 2019, 38, e103547.	3.5	6
117	Metabolic reprogramming of the stromal epigenome in ovarian cancer metastasis. FASEB Journal, 2019, 33, lb240.	0.2	1
118	Molecular and structural architecture of polyQ aggregates in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3446-E3453.	3.3	68
119	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.	4.2	186
120	Development of phospho-specific Rab protein antibodies to monitor <i>in vivo</i> activity of the LRRK2 Parkinson's disease kinase. Biochemical Journal, 2018, 475, 1-22.	1.7	123
121	Online Parallel Accumulationâ€“Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Molecular and Cellular Proteomics, 2018, 17, 2534-2545.	2.5	602
122	Plasma Proteome Profiling Reveals Dynamics of Inflammatory and Lipid Homeostasis Markers after Roux-En-Y Gastric Bypass Surgery. Cell Systems, 2018, 7, 601-612.e3.	2.9	80
123	UBL3 modification influences protein sorting to small extracellular vesicles. Nature Communications, 2018, 9, 3936.	5.8	53
124	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. Nature Communications, 2018, 9, 4300.	5.8	46
125	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. Developmental Cell, 2018, 47, 205-221.e7.	3.1	132
126	High-throughput and high-sensitivity phosphoproteomics with the EasyPhos platform. Nature Protocols, 2018, 13, 1897-1916.	5.5	238

#	ARTICLE	IF	CITATIONS
127	Multi-level Proteomics Identifies CT45 as a Chemosensitivity Mediator and Immunotherapy Target in Ovarian Cancer. Cell, 2018, 175, 159-170.e16.	13.5	127
128	FRET Reagent Reveals the Intracellular Processing of Peptide-Linked Antibodyâ€"Drug Conjugates. Bioconjugate Chemistry, 2018, 29, 2468-2477.	1.8	29
129	The Transcription Factor ETV1 Induces Atrial Remodeling and Arrhythmia. Circulation Research, 2018, 123, 550-563.	2.0	40
130	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. Clinical Cancer Research, 2018, 24, 5433-5444.	3.2	68
131	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. Nature Methods, 2018, 15, 440-448.	9.0	303
132	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. Molecular and Cellular Proteomics, 2018, 17, 2284-2296.	2.5	270
133	Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. Translational Psychiatry, 2018, 8, 160.	2.4	68
134	Rapid proteomic analysis for solid tumors reveals <scp>LSD</scp>1 as a drug target in an endâ€stage cancer patient. Molecular Oncology, 2018, 12, 1296-1307.	2.1	25
135	In vivo brain GPCR signaling elucidated by phosphoproteomics. Science, 2018, 360, .	6.0	105
136	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	9.0	88
137	The non-classical nuclear import carrier Transportin 1 modulates circadian rhythms through its effect on PER1 nuclear localization. PLoS Genetics, 2018, 14, e1007189.	1.5	20
138	Proteomics and <i>C9orf72</i> neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. Life Science Alliance, 2018, 1, e201800070.	1.3	88
139	Parallel accumulation for 100% duty cycle trapped ion mobility-mass spectrometry. International Journal of Mass Spectrometry, 2017, 413, 168-175.	0.7	59
140	Loss-less Nano-fractionator for High Sensitivity, High Coverage Proteomics. Molecular and Cellular Proteomics, 2017, 16, 694-705.	2.5	169
141	CRL2^{Lrr1} promotes unloading of the vertebrate replisome from chromatin during replication termination. Genes and Development, 2017, 31, 275-290.	2.7	90
142	Phylointeractomics reconstructs functional evolution of protein binding. Nature Communications, 2017, 8, 14334.	5.8	26
143	Social network architecture of human immune cells unveiled by quantitative proteomics. Nature Immunology, 2017, 18, 583-593.	7.0	296
144	Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. Cell Reports, 2017, 19, 2396-2409.	2.9	213

#	ARTICLE	IF	CITATIONS
145	H3.Y discriminates between HIRA and DAXX chaperone complexes and reveals unexpected insights into human DAXX-H3.3-H4 binding and deposition requirements. Nucleic Acids Research, 2017, 45, 5691-5706.	6.5	19
146	A Primer on Concepts and Applications of Proteomics in Neuroscience. Neuron, 2017, 96, 558-571.	3.8	65
147	Revisiting biomarker discovery by plasmaÂproteomics. Molecular Systems Biology, 2017, 13, 942.	3.2	597
148	A proteomic atlas of insulin signalling reveals tissueâ€•specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	3.2	42
149	A Stat6/Pten Axis Links Regulatory T Cells with Adipose Tissue Function. Cell Metabolism, 2017, 26, 475-492.e7.	7.2	71
150	Spatiotemporal Proteomic Profiling of Huntingtonâ€™s Disease Inclusions Reveals Widespread Loss of Protein Function. Cell Reports, 2017, 21, 2291-2303.	2.9	107
151	Region and cell-type resolved quantitative proteomic map of the human heart. Nature Communications, 2017, 8, 1469.	5.8	213
152	Circulating Glucagon 1-61 Regulates Blood Glucose by Increasing Insulin Secretion and Hepatic Glucose Production. Cell Reports, 2017, 21, 1452-1460.	2.9	28
153	Multivalent binding of PWWP2A to H2A.Z regulates mitosis and neural crest differentiation. EMBO Journal, 2017, 36, 2263-2279.	3.5	48
154	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.	2.5	97
155	Phosphorylation Is a Central Mechanism for Circadian Control of Metabolism and Physiology. Cell Metabolism, 2017, 25, 118-127.	7.2	297
156	Quantitative Proteomics Reveals Fundamental Regulatory Differences in Oncogenic HRAS and Isocitrate Dehydrogenase (IDH1) Driven Astrocytoma. Molecular and Cellular Proteomics, 2017, 16, 39-56.	2.5	23
157	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. ELife, 2017, 6, .	2.8	344
158	A genome-wide resource for the analysis of protein localisation in Drosophila. ELife, 2016, 5, e12068.	2.8	315
159	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. ELife, 2016, 5, .	2.8	766
160	Proteomics reveals the effects of sustained weight loss on the human plasma proteome. Molecular Systems Biology, 2016, 12, 901.	3.2	188
161	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.	2.7	53
162	Inflammatory signaling in human tuberculosis granulomas is spatially organized. Nature Medicine, 2016, 22, 531-538.	15.2	273

#	ARTICLE	IF	CITATIONS
163	Molecular basis of PRC1 targeting to Polycomb response elements by PhoRC. Genes and Development, 2016, 30, 1116-1127.	2.7	78
164	Activation of the ATR kinase by the RPA-binding protein ETAA1. Nature Cell Biology, 2016, 18, 1196-1207.	4.6	208
165	C9ORF72 interaction with cofilin modulates actin dynamics in motor neurons. Nature Neuroscience, 2016, 19, 1610-1618.	7.1	131
166	Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors. Molecular Cell, 2016, 63, 951-964.	4.5	181
167	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. Nature Communications, 2016, 7, 13404.	5.8	613
168	Mass-spectrometric exploration of proteome structure and function. Nature, 2016, 537, 347-355.	13.7	1,573
169	L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. Cell, 2016, 167, 829-842.e13.	13.5	1,077
170	Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. Nature Communications, 2016, 7, 12429.	5.8	859
171	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	5.8	74
172	The Perseus computational platform for comprehensive analysis of (prote)omics data. Nature Methods, 2016, 13, 731-740.	9.0	6,181
173	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.	1.8	51
174	Evidence of Extrapancreatic Glucagon Secretion in Man. Diabetes, 2016, 65, 585-597.	0.3	136
175	The Proteome of Primary Prostate Cancer. European Urology, 2016, 69, 942-952.	0.9	122
176	Cytoplasmic protein aggregates interfere with nucleocytoplasmic transport of protein and RNA. Science, 2016, 351, 173-176.	6.0	336
177	Plasma Proteome Profiling to Assess Human Health and Disease. Cell Systems, 2016, 2, 185-195.	2.9	549
178	Circadian control of oscillations in mitochondrial rate-limiting enzymes and nutrient utilization by PERIOD proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1673-82.	3.3	190
179	C/EBPÎ± creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 andÂBrd4. Nature Cell Biology, 2016, 18, 371-381.	4.6	94
180	Homology-driven assembly of NOn-redundant protEin sequence sets (NOmESS) for mass spectrometry. Bioinformatics, 2016, 32, 1417-1419.	1.8	9

#	ARTICLE	IF	CITATIONS
181	Proteomic maps of breast cancer subtypes. Nature Communications, 2016, 7, 10259.	5.8	256
182	TRAIP is a PCNA-binding ubiquitin ligase that protects genome stability after replication stress. Journal of Cell Biology, 2016, 212, 63-75.	2.3	65
183	The Rise of Mass Spectrometry and the Fall of Edman Degradation. Clinical Chemistry, 2016, 62, 293-294.	1.5	20
184	Minimal amounts of kindlin-3 suffice for basal platelet and leukocyte functions in mice. Blood, 2015, 126, 2592-2600.	0.6	45
185	Antisenseâ€•mediated exon skipping: a therapeutic strategy for titinâ€•based dilated cardiomyopathy. EMBO Molecular Medicine, 2015, 7, 562-576.	3.3	94
186	Timeâ€•and compartmentâ€•resolved proteome profiling of the extracellular niche in lung injury and repair. Molecular Systems Biology, 2015, 11, 819.	3.2	211
187	Systems Analyses Reveal Shared and Diverse Attributes of Oct4 Regulation in Pluripotent Cells. Cell Systems, 2015, 1, 141-151.	2.9	15
188	Parasiteâ€•induced <scp>ER</scp> stress response in hepatocytes facilitates <i>Plasmodium</i> liver stage infection. EMBO Reports, 2015, 16, 955-964.	2.0	46
189	T Cells Engineered to Express a T-Cell Receptor Specific for Glypican-3 to Recognize and Kill Hepatoma Cells InÂVitro and inÂMice. Gastroenterology, 2015, 149, 1042-1052.	0.6	96
190	Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. Molecular Cell, 2015, 59, 75-88.	4.5	166
191	Quantitative Proteomics Identifies Serum Response Factor Binding Protein 1 as a Host Factor for Hepatitis C Virus Entry. Cell Reports, 2015, 12, 864-878.	2.9	50
192	Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892.	2.9	47
193	Accurate Protein Complex Retrieval by Affinity Enrichment Mass Spectrometry (AE-MS) Rather than Affinity Purification Mass Spectrometry (AP-MS). Molecular and Cellular Proteomics, 2015, 14, 120-135.	2.5	231
194	Mass Spectrometry-Based Detection and Assignment of Protein Posttranslational Modifications. ACS Chemical Biology, 2015, 10, 63-71.	1.6	193
195	Single muscle fiber proteomics reveals unexpected mitochondrial specialization. EMBO Reports, 2015, 16, 387-395.	2.0	163
196	Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. Molecular and Cellular Proteomics, 2015, 14, 841-853.	2.5	234
197	The focal adhesion protein PINCH-1 associates with EPLIN at integrin adhesion sites. Journal of Cell Science, 2015, 128, 1023-33.	1.2	22
198	Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. Molecular and Cellular Proteomics, 2015, 14, 658-673.	2.5	445

#	ARTICLE	IF	CITATIONS
199	TLR3-Mediated CD8+ Dendritic Cell Activation Is Coupled with Establishment of a Cell-Intrinsic Antiviral State. Journal of Immunology, 2015, 195, 1025-1033.	0.4	26
200	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.	2.5	150
201	System-wide identification of wild-type SUMO-2 conjugation sites. Nature Communications, 2015, 6, 7289.	5.8	97
202	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. Science, 2015, 348, 1253671.	6.0	183
203	Acetylation site specificities of lysine deacetylase inhibitors in human cells. Nature Biotechnology, 2015, 33, 415-423.	9.4	237
204	Widespread Proteome Remodeling and Aggregation in Aging C.Âelegans. Cell, 2015, 161, 919-932.	13.5	478
205	Functional classification of memory CD8+ T cells by CX3CR1 expression. Nature Communications, 2015, 6, 8306.	5.8	231
206	Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. Trends in Endocrinology and Metabolism, 2015, 26, 676-687.	3.1	402
207	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. Cell, 2015, 163, 712-723.	13.5	1,132
208	Parallel Accumulationâ€"Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. Journal of Proteome Research, 2015, 14, 5378-5387.	1.8	281
209	Absolute Proteome Analysis of Colorectal Mucosa, Adenoma, and Cancer Reveals Drastic Changes in Fatty Acid Metabolism and Plasma Membrane Transporters. Journal of Proteome Research, 2015, 14, 4005-4018.	1.8	74
210	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. Journal of Proteome Research, 2015, 14, 4885-4895.	1.8	66
211	High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. Nature Biotechnology, 2015, 33, 990-995.	9.4	408
212	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.	3.3	52
213	<scp>PP</scp> 2A delays <scp>APC</scp> /Câ€dependent degradation of separaseâ€associated but not free securin. EMBO Journal, 2014, 33, 1134-1147.	3.5	57
214	Copy Number Analysis of the Murine Platelet Proteome Spanning the Complete Abundance Range. Molecular and Cellular Proteomics, 2014, 13, 3435-3445.	2.5	187
215	The Q Exactive HF, a Benchtop Mass Spectrometer with a Pre-filter, High-performance Quadrupole and an Ultra-high-field Orbitrap Analyzer. Molecular and Cellular Proteomics, 2014, 13, 3698-3708.	2.5	285
216	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. Molecular and Cellular Proteomics, 2014, 13, 2513-2526.	2.5	4,178

#	ARTICLE	IF	CITATIONS
217	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. Cell Metabolism, 2014, 20, 1076-1087.	7.2	143
218	The ETS family member GABPÎ± modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. Nucleic Acids Research, 2014, 42, 6256-6269.	6.5	33
219	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF-Î². Science Signaling, 2014, 7, rs5.	1.6	39
220	Quantitative shotgun proteomics: considerations for a high-quality workflow in immunology. Nature Immunology, 2014, 15, 112-117.	7.0	90
221	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. Nature Methods, 2014, 11, 319-324.	9.0	1,447
222	A â€œProteomic Rulerâ€•for Protein Copy Number and Concentration Estimation without Spike-in Standards. Molecular and Cellular Proteomics, 2014, 13, 3497-3506.	2.5	530
223	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and proteinâ€“protein interactions. Molecular Biology of the Cell, 2014, 25, 3178-3194.	0.9	42
224	Uncovering global SUMOylation signaling networks in a site-specific manner. Nature Structural and Molecular Biology, 2014, 21, 927-936.	3.6	408
225	Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4. Molecular Cell, 2014, 56, 43-54.	4.5	129
226	The growing landscape of lysine acetylation links metabolism and cell signalling. Nature Reviews Molecular Cell Biology, 2014, 15, 536-550.	16.1	1,153
227	Immunoproteomics Using Polyclonal Antibodies and Stable Isotopeâ€“labeled Affinity-purified Recombinant Proteins. Molecular and Cellular Proteomics, 2014, 13, 1611-1624.	2.5	27
228	The<i>Caenorhabditis</i><i>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.	0.9	31
229	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. Cell Reports, 2014, 6, 578-591.	2.9	75
230	A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. ELife, 2014, 3, e02975.	2.8	97
231	The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. Molecular Cell, 2013, 49, 583-590.	4.5	329
232	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. Nature, 2012, 488, 508-511.	13.7	323
233	Proteomics for biomedicine: a halfâ€completed journey. EMBO Molecular Medicine, 2012, 4, 75-77.	3.3	7
234	John Bennett Fenn, 1917â€“2010. Journal of the American Society for Mass Spectrometry, 2011, 22, 602-603.	1.2	2

#	ARTICLE	IF	CITATIONS
235	The mitochondrial contact site complex, a determinant of mitochondrial architecture. EMBO Journal, 2011, 30, 4356-4370.	3.5	395
236	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. Journal of Biological Chemistry, 2009, 284, 16575-16583.	1.6	98
237	Comparative analysis to guide quality improvements in proteomics. Nature Methods, 2009, 6, 717-719.	9.0	58
238	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. Molecular and Cellular Proteomics, 2008, 7, 132-144.	2.5	251
239	Precision proteomics: The case for high resolution and high mass accuracy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18132-18138.	3.3	388
240	A Mammalian Organelle Map by Protein Correlation Profiling. Cell, 2006, 125, 187-199.	13.5	538
241	Mass spectrometry-based proteomics. Nature, 2003, 422, 198-207.	13.7	6,282
242	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. Nature Biotechnology, 2003, 21, 315-318.	9.4	702