Matthias Mann

List of Publications by Year
in descending order

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829
papers

259,066
citations

7
226
h-index

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475
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908
all docs

908
docs citations

908
times ranked

184144
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards Precision Dermatology: Emerging Role of Proteomic Analysis of the Skin. Dermatology, 2022, 238, 185-194.	0.9	9
2	YBX1 mediates translation of oncogenic transcripts to control cell competition in AML. Leukemia, 2022, 36, 426-437.	3.3	18
3	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
4	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	0.6	16
5	A20 and ABIN-1 cooperate in balancing CBM complex-triggered NF-ÎºB signaling in activated T cells. Cellular and Molecular Life Sciences, 2022, 79, 112.	2.4	11
6	Gene-selective transcription promotes the inhibition of tissue reparative macrophages by TNF. Life Science Alliance, 2022, 5, e202101315.	1.3	10
7	A knowledge graph to interpret clinical proteomics data. Nature Biotechnology, 2022, 40, 692-702.	9.4	97
8	Cotranslational N-degron masking by acetylation promotes proteome stability in plants. Nature Communications, 2022, 13, 810.	5.8	29
9	Association of Complement and MAPK Activation With SARS-CoV-2â€“Associated Myocardial Inflammation. JAMA Cardiology, 2022, 7, 286.	3.0	15
10	Ultraâ€high sensitivity mass spectrometry quantifies singleâ€cell proteome changes upon perturbation. Molecular Systems Biology, 2022, 18, e10798.	3.2	261
11	The emerging role of mass spectrometry-based proteomics in drug discovery. Nature Reviews Drug Discovery, 2022, 21, 637-654.	21.5	110
12	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	7.7	43
13	OpenCell: Endogenous tagging for the cartography of human cellular organization. Science, 2022, 375, eabi6983.	6.0	174
14	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
15	Amyloid-like aggregating proteins cause lysosomal defects in neurons via gain-of-function toxicity. Life Science Alliance, 2022, 5, e202101185.	1.3	13
16	A GID E3 ligase assembly ubiquitinates an Rsp5 E3 adaptor and regulates plasma membrane transporters. EMBO Reports, 2022, 23, e53835.	2.0	9
17	Gelâ€like inclusions of Câ€terminal fragments of TDPâ€43 sequester stalled proteasomes in neurons. EMBO Reports, 2022, 23, e53890.	2.0	28
18	HAX1-dependent control of mitochondrial proteostasis governs neutrophil granulocyte differentiation. Journal of Clinical Investigation, 2022, 132, .	3.9	18

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19	The structural context of posttranslational modifications at a proteome-wide scale. PLoS Biology, 2022, 20, e3001636.	2.6	50
20	Dynamic human liver proteome atlas reveals functional insights into disease pathways. Molecular Systems Biology, 2022, 18, e10947.	3.2	22
21	Deep Visual Proteomics defines single-cell identity and heterogeneity. Nature Biotechnology, 2022, 40, 1231-1240.	9.4	160
22	Noninvasive proteomic biomarkers for alcohol-related liver disease. Nature Medicine, 2022, 28, 1277-1287.	15.2	91
23	Cryo-EM structures of Gid12-bound GID E3 reveal steric blockade as a mechanism inhibiting substrate ubiquitylation. Nature Communications, 2022, 13, .	5.8	3
24	Identification of early neurodegenerative pathways in progressive multiple sclerosis. Nature Neuroscience, 2022, 25, 944-955.	7.1	55
25	Unbiased spatial proteomics with single-cell resolution in tissues. Molecular Cell, 2022, 82, 2335-2349.	4.5	85
26	HYPK promotes the activity of the <i>N</i> ^{Î±} -acetyltransferase A complex to determine proteostasis of nonAc-X ² /N-degronâ€“containing proteins. Science Advances, 2022, 8, .	4.7	11
27	Proteome profiling of cerebrospinal fluid reveals biomarker candidates for Parkinsonâ€™s disease. Cell Reports Medicine, 2022, 3, 100661.	3.3	48
28	Signatures of muscle disuse in spaceflight and bed rest revealed by single muscle fiber proteomics. , 2022, 1, .		22
29	Temporal resolution of gene derepression and proteome changes upon PROTAC-mediated degradation of BCL11A protein in erythroid cells. Cell Chemical Biology, 2022, 29, 1273-1287.e8.	2.5	14
30	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
31	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	3.9	26
32	Trapped Ion Mobility Spectrometry and Parallel Accumulationâ€“Serial Fragmentation in Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100138.	2.5	84
33	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. Nature Communications, 2021, 12, 254.	5.8	71
34	A New Parallel High-Pressure Packing System Enables Rapid Multiplexed Production of Capillary Columns. Molecular and Cellular Proteomics, 2021, 20, 100082.	2.5	13
35	Urinary proteome profiling for stratifying patients with familial Parkinsonâ€™s disease. EMBO Molecular Medicine, 2021, 13, e13257.	3.3	88
36	Ethical Principles, Constraints, and Opportunities in Clinical Proteomics. Molecular and Cellular Proteomics, 2021, 20, 100046.	2.5	33

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37	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. ELife, 2021, 10, .	2.8	29
38	Plasma Proteomes Can Be Reidentifiable and Potentially Contain Personally Sensitive and Incidental Findings. Molecular and Cellular Proteomics, 2021, 20, 100035.	2.5	20
39	Interaction of 7SK with the Smn complex modulates snRNP production. Nature Communications, 2021, 12, 1278.	5.8	23
40	Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7.	3.1	38
41	Deep learning the collisional cross sections of the peptide universe from a million experimental values. Nature Communications, 2021, 12, 1185.	5.8	81
42	DDRE-22. TARGETING SERINE SYNTHESIS IN BRAIN METASTASIS. Neuro-Oncology Advances, 2021, 3, i11-i11.	0.4	0
43	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STINGâ€"IFN-Î² pathway. Nature Immunology, 2021, 22, 485-496.	7.0	45
44	Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. EMBO Molecular Medicine, 2021, 13, e12871.	3.3	53
45	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. Nature, 2021, 594, 246-252.	13.7	475
46	Tissue-specific modulation of gene expression in response to lowered insulin signalling in Drosophila. ELife, 2021, 10, .	2.8	12
47	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
48	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie, 2021, 133, 17197-17206.	1.6	0
49	Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints**. Angewandte Chemie - International Edition, 2021, 60, 17060-17069.	7.2	13
50	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
51	InnenrÃ¼cktitelbild: Molecular Origin of Bloodâ€Based Infrared Spectroscopic Fingerprints (Angew.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.6	0
52	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
53	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
54	Identification of covalent modifications regulatingÂimmune signaling complex composition and phenotype. Molecular Systems Biology, 2021, 17, e10125.	3.2	6

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55	Highâ€resolution serum proteome trajectories in COVIDâ€19 reveal patientâ€specific seroconversion. EMBO Molecular Medicine, 2021, 13, e14167.	3.3	92
56	Reply to â€œQuality control requirements for the correct annotation of lipidomics dataâ€ Nature Communications, 2021, 12, 4772.	5.8	2
57	Artificial intelligence for proteomics and biomarker discovery. Cell Systems, 2021, 12, 759-770.	2.9	106
58	Identification of the transcription factor MAZ as a regulator of erythropoiesis. Blood Advances, 2021, 5, 3002-3015.	2.5	8
59	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
60	OS12.7.A Characterization of intra-tumoral heterogeneity and differential immune activation during malignant progression of meningiomas on single cell level. Neuro-Oncology, 2021, 23, ii15-ii16.	0.6	0
61	Signaling defects associated with insulin resistance in nondiabetic and diabetic individuals and modification by sex. Journal of Clinical Investigation, 2021, 131, .	3.9	27
62	Defining the RBPome of primary T helper cells to elucidate higher-order Roquin-mediated mRNA regulation. Nature Communications, 2021, 12, 5208.	5.8	23
63	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
64	Deep muscle-proteomic analysis of freeze-dried human muscle biopsies reveals fiber type-specific adaptations to exercise training. Nature Communications, 2021, 12, 304.	5.8	79
65	Sequential Defects in Cardiac Lineage Commitment and Maturation Cause Hypoplastic Left Heart Syndrome. Circulation, 2021, 144, 1409-1428.	1.6	29
66	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
67	Phosphoproteome profiling uncovers a key role for CDKs in TNF signaling. Nature Communications, 2021, 12, 6053.	5.8	31
68	Defining NASH from a Multi-Omics Systems Biology Perspective. Journal of Clinical Medicine, 2021, 10, 4673.	1.0	9
69	Protein profile of fiber types in human skeletal muscle: a single-fiber proteomics study. Skeletal Muscle, 2021, 11, 24.	1.9	65
70	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
71	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
72	Proteomic Analysis Identifies NDUFS1 and ATP5O as Novel Markers for Survival Outcome in Prostate Cancer. Cancers, 2021, 13, 6036.	1.7	7

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73	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
74	Ethical principles, opportunities and constraints in clinical proteomics. Molecular and Cellular Proteomics, 2021, , .	2.5	1
75	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
76	SHP1 regulates a STAT6â€“ITGB3 axis in FLT3ITD-positive AML cells. Leukemia, 2020, 34, 1444-1449.	3.3	7
77	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
78	Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. Nature, 2020, 588, 157-163.	13.7	90
79	diaPASEF: parallel accumulationâ€“serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
80	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
81	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
82	The Origins of Organellar Mapping by Protein Correlation Profiling. Proteomics, 2020, 20, 1900330.	1.3	9
83	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
84	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
85	Spatially and cell-type resolved quantitative proteomic atlas of healthy human skin. Nature Communications, 2020, 11, 5587.	5.8	72
86	Sequencing of the First Draft of the Human Acetylome. Clinical Chemistry, 2020, 66, 852-853.	1.5	1
87	Atomic-resolution mapping of transcription factor-DNA interactions by femtosecond laser crosslinking and mass spectrometry. Nature Communications, 2020, 11, 3019.	5.8	9
88	Limited Environmental Serine and Glycine Confer Brain Metastasis Sensitivity to PHGDH Inhibition. Cancer Discovery, 2020, 10, 1352-1373.	7.7	145
89	The proteome landscape of the kingdoms of life. Nature, 2020, 582, 592-596.	13.7	128
90	A Multi-Omics Approach to Liver Diseases: Integration of Single Nuclei Transcriptomics with Proteomics and HiCap Bulk Data in Human Liver. OMICS A Journal of Integrative Biology, 2020, 24, 180-194.	1.0	26

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91	A streamlined mass spectrometryâ€“based proteomics workflow for largeâ€scale FFPE tissue analysis. Journal of Pathology, 2020, 251, 100-112.	2.1	109
92	Pervasive functional translation of noncanonical human open reading frames. Science, 2020, 367, 1140-1146.	6.0	400
93	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
94	Dynamics in protein translation sustaining T cell preparedness. Nature Immunology, 2020, 21, 927-937.	7.0	120
95	Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. Nature Communications, 2020, 11, 331.	5.8	138
96	Quantitative and Dynamic Catalogs of Proteins Released during Apoptotic and Necroptotic Cell Death. Cell Reports, 2020, 30, 1260-1270.e5.	2.9	53
97	<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
98	Integrative Analysis Identifies Key Molecular Signatures Underlying Neurodevelopmental Deficits in Fragile X Syndrome. Biological Psychiatry, 2020, 88, 500-511.	0.7	33
99	A beginnerâ€™s guide to mass spectrometryâ€“based proteomics. Biochemist, 2020, 42, 64-69.	0.2	35
100	Fam20C regulates protein secretion by Cab45 phosphorylation. Journal of Cell Biology, 2020, 219, .	2.3	15
101	FAM111 protease activity undermines cellular fitness and is amplified by gainâ€ofâ€function mutations in human disease. EMBO Reports, 2020, 21, e50662.	2.0	37
102	Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. Molecular Systems Biology, 2020, 16, e9356.	3.2	157
103	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. Molecular Systems Biology, 2020, 16, e9813.	3.2	21
104	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
105	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
106	Myosin binding protein H-like (MYBPHL): a promising biomarker to predict atrial damage. Scientific Reports, 2019, 9, 9986.	1.6	6
107	Catching Lipid Droplet Contacts by Proteomics. Contact (Thousand Oaks (Ventura County, Calif)), 2019, 2, 251525641985918.	0.4	6
108	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

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109	The forebrain synaptic transcriptome is organized by clocks but its proteome is driven by sleep. Science, 2019, 366, .	6.0	169
110	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. Science, 2019, 366, .	6.0	181
111	Hepatic Rab24 controls blood glucose homeostasis via improving mitochondrial plasticity. Nature Metabolism, 2019, 1, 1009-1026.	5.1	27
112	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
113	Plasma Proteome Profiling to detect and avoid sampleâ€related biases in biomarker studies. EMBO Molecular Medicine, 2019, 11, e10427.	3.3	171
114	Metallopeptidase inhibitor 1 (TIMPâ€1) promotes receptor tyrosine kinase câ€Kit signaling in colorectal cancer. Molecular Oncology, 2019, 13, 2646-2662.	2.1	11
115	The ever expanding scope of electrospray mass spectrometryâ€"a 30 year journey. Nature Communications, 2019, 10, 3744.	5.8	25
116	The Atherosclerosis Risk Variant rs2107595 Mediates Allele-Specific Transcriptional Regulation of <i>HDAC9</i> via E2F3 and Rb1. Stroke, 2019, 50, 2651-2660.	1.0	38
117	Functional identity of hypothalamic melanocortin neurons depends on Tbx3. Nature Metabolism, 2019, 1, 222-235.	5.1	27
118	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	2.9	111
119	Cortical circuit alterations precede motor impairments in Huntingtonâ€™s disease mice. Scientific Reports, 2019, 9, 6634.	1.6	53
120	Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts. Nature, 2019, 569, 723-728.	13.7	330
121	Plasma proteome profiling discovers novel proteins associated with nonâ€alcoholic fatty liver disease. Molecular Systems Biology, 2019, 15, e8793.	3.2	176
122	A protein-interaction network of interferon-stimulated genes extends the innate immune system landscape. Nature Immunology, 2019, 20, 493-502.	7.0	139
123	Phosphoproteomics Reveals the GSK3-PDX1 Axis as a Key Pathogenic Signaling Node in Diabetic Islets. Cell Metabolism, 2019, 29, 1422-1432.e3.	7.2	65
124	FoxK1 and FoxK2 in insulin regulation of cellular and mitochondrial metabolism. Nature Communications, 2019, 10, 1582.	5.8	57
125	Trends in trapped ion mobility â€" Mass spectrometry instrumentation. TrAC - Trends in Analytical Chemistry, 2019, 116, 324-331.	5.8	40
126	The Case for Proteomics and Phosphoâ€Proteomics in Personalized Cancer Medicine. Proteomics - Clinical Applications, 2019, 13, e1800113.	0.8	88

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127	An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. Nature Communications, 2019, 10, 963.	5.8	408
128	Efficient mitotic checkpoint signaling depends on integrated activities of Bub1 and the <scp>RZZ</scp> complex. EMBO Journal, 2019, 38, .	3.5	56
129	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. Molecular and Cellular Proteomics, 2019, 18, 982a-994.	2.5	91
130	Proteomics of Cytochrome c Oxidase-Negative versus -Positive Muscle Fiber Sections in Mitochondrial Myopathy. Cell Reports, 2019, 29, 3825-3834.e4.	2.9	17
131	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
132	A mass spectrometry guided approach for the identification of novel vaccine candidates in gram-negative pathogens. Scientific Reports, 2019, 9, 17401.	1.6	7
133	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
134	Proteomics in the Study of Liver Diseases. , 2019, , 165-193.		4
135	Defective glycosylation and multisystem abnormalities characterize the primary immunodeficiency XMEN disease. Journal of Clinical Investigation, 2019, 130, 507-522.	3.9	74
136	Response to Raaijmakers & Medema. EMBO Journal, 2019, 38, e103547.	3.5	6
137	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. Life Science Alliance, 2019, 2, e201900437.	1.3	41
138	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
139	Compartment-resolved Proteomic Analysis of Mouse Aorta during Atherosclerotic Plaque Formation Reveals Osteoclast-specific Protein Expression. Molecular and Cellular Proteomics, 2018, 17, 321-334.	2.5	40
140	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
141	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
142	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
143	UBL3 modification influences protein sorting to small extracellular vesicles. Nature Communications, 2018, 9, 3936.	5.8	53
144	Advocating for science progress as a human right. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10820-10823.	3.3	16

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145	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. Nature Communications, 2018, 9, 4300.	5.8	46
146	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. Developmental Cell, 2018, 47, 205-221.e7.	3.1	132
147	High-throughput and high-sensitivity phosphoproteomics with the EasyPhos platform. Nature Protocols, 2018, 13, 1897-1916.	5.5	238
148	Multi-level Proteomics Identifies CT45 as a Chemosensitivity Mediator and Immunotherapy Target in Ovarian Cancer. Cell, 2018, 175, 159-170.e16.	13.5	127
149	The Transcription Factor ETV1 Induces Atrial Remodeling and Arrhythmia. Circulation Research, 2018, 123, 550-563.	2.0	40
150	In-depth proteomic analyses of Haliotis laevigata (greenlip abalone) nacre and prismatic organic shell matrix. Proteome Science, 2018, 16, 11.	0.7	33
151	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. Clinical Cancer Research, 2018, 24, 5433-5444.	3.2	68
152	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
153	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
154	The hemicellulose-degrading enzyme system of the thermophilic bacterium Clostridium stercorarium: comparative characterisation and addition of new hemicellulolytic glycoside hydrolases. Biotechnology for Biofuels, 2018, 11, 229.	6.2	62
155	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
156	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
157	In vivo brain GPCR signaling elucidated by phosphoproteomics. Science, 2018, 360, .	6.0	105
158	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. Nature Methods, 2018, 15, 527-530.	9.0	88
159	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
160	Proteomics and <i>C9orf72</i> neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. Life Science Alliance, 2018, 1, e201800070.	1.3	88
161	Parallel accumulation for 100% duty cycle trapped ion mobility-mass spectrometry. International Journal of Mass Spectrometry, 2017, 413, 168-175.	0.7	59
162	Loss-less Nano-fractionator for High Sensitivity, High Coverage Proteomics. Molecular and Cellular Proteomics, 2017, 16, 694-705.	2.5	169

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163	CRL2^{Lrr1} promotes unloading of the vertebrate replisome from chromatin during replication termination. Genes and Development, 2017, 31, 275-290.	2.7	90
164	Phylointeractomics reconstructs functional evolution of protein binding. Nature Communications, 2017, 8, 14334.	5.8	26
165	Social network architecture of human immune cells unveiled by quantitative proteomics. Nature Immunology, 2017, 18, 583-593.	7.0	296
166	Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. Cell Reports, 2017, 19, 2396-2409.	2.9	213
167	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
168	Lysine acetylome profiling uncovers novel histone deacetylase substrate proteins in <i>Arabidopsis</i>. Molecular Systems Biology, 2017, 13, 949.	3.2	141
169	A Primer on Concepts and Applications of Proteomics in Neuroscience. Neuron, 2017, 96, 558-571.	3.8	65
170	Revisiting biomarker discovery by plasmaÂproteomics. Molecular Systems Biology, 2017, 13, 942.	3.2	597
171	Dimethyl-Labeling-Based Quantification of the Lysine Acetylome and Proteome of Plants. Methods in Molecular Biology, 2017, 1653, 65-81.	0.4	20
172	A proteomic atlas of insulin signalling reveals tissueâ€specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	3.2	42
173	A Stat6/Pten Axis Links Regulatory T Cells with Adipose Tissue Function. Cell Metabolism, 2017, 26, 475-492.e7.	7.2	71
174	Spatiotemporal Proteomic Profiling of Huntingtonâ€™s Disease Inclusions Reveals Widespread Loss of Protein Function. Cell Reports, 2017, 21, 2291-2303.	2.9	107
175	Region and cell-type resolved quantitative proteomic map of the human heart. Nature Communications, 2017, 8, 1469.	5.8	213
176	Multivalent binding of PWWP2A to H2A.Z regulates mitosis and neural crest differentiation. EMBO Journal, 2017, 36, 2263-2279.	3.5	48
177	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
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