Duc M Duong

List of Publications by Year
in descending order

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Version: 2024-02-01

144 papers	11,719 citations	36203 51 h-index	35952 97 g-index
176 all docs	176 docs citations	176 times ranked	14717 citing authors

#	Article	IF	Citations
1	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. Cell, 2009, 137, 133-145.	13.5	948
2	Large-scale proteomic analysis of Alzheimerâ€™s disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Nature Medicine, 2020, 26, 769-780.	15.2	547
3	Relative and Absolute Quantification of Postsynaptic Density Proteome Isolated from Rat Forebrain and Cerebellum. Molecular and Cellular Proteomics, 2006, 5, 1158-1170.	2.5	440
4	Semiquantitative Proteomic Analysis of Rat Forebrain Postsynaptic Density Fractions by Mass Spectrometry. Journal of Biological Chemistry, 2004, 279, 21003-21011.	1.6	417
5	TDP-43 pathology disrupts nuclear pore complexes and nucleocytoplasmic transport in ALS/FTD. Nature Neuroscience, 2018, 21, 228-239.	7.1	404
6	A Multi-network Approach Identifies Protein-Specific Co-expression in Asymptomatic and Symptomatic Alzheimerâ€™s Disease. Cell Systems, 2017, 4, 60-72.e4.	2.9	381
7	Cleavage of tau by asparagine endopeptidase mediates the neurofibrillary pathology in Alzheimer's disease. Nature Medicine, 2014, 20, 1254-1262.	15.2	367
8	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
9	Posttranslational Modifications Mediate the Structural Diversity of Tauopathy Strains. Cell, 2020, 180, 633-644.e12.	13.5	300
10	Glutamate Dehydrogenase 1 Signals through Antioxidant Glutathione Peroxidase 1 to Regulate Redox Homeostasis and Tumor Growth. Cancer Cell, 2015, 27, 257-270.	7.7	269
11	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16562-16567.	3.3	268
12	Proteomic Characterization of Postmortem Amyloid Plaques Isolated by Laser Capture Microdissection. Journal of Biological Chemistry, 2004, 279, 37061-37068.	1.6	267
13	Identification and therapeutic modulation of a pro-inflammatory subset of disease-associated-microglia in Alzheimerâ€™s disease. Molecular Neurodegeneration, 2018, 13, 24.	4.4	267
14	Delta-secretase cleaves amyloid precursor protein and regulates the pathogenesis in Alzheimerâ€™s disease. Nature Communications, 2015, 6, 8762.	5.8	210
15	Large-scale deep multi-layer analysis of Alzheimerâ€™s disease brain reveals strong proteomic disease-related changes not observed at the RNA level. Nature Neuroscience, 2022, 25, 213-225.	7.1	202
16	Integrated proteomics reveals brain-based cerebrospinal fluid biomarkers in asymptomatic and symptomatic Alzheimerâ€™s disease. Science Advances, 2020, 6, .	4.7	186
17	Global quantitative analysis of the human brain proteome in Alzheimerâ€™s and Parkinsonâ€™s Disease. Scientific Data, 2018, 5, 180036.	2.4	179
18	Deep proteomic network analysis of Alzheimerâ€™s disease brain reveals alterations in RNA binding proteins and RNA splicing associated with disease. Molecular Neurodegeneration, 2018, 13, 52.	4.4	178

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19	Systematical Optimization of Reverse-Phase Chromatography for Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 3944-3950.	1.8	163
20	Asparagine endopeptidase cleaves Î±-synuclein and mediates pathologic activities in Parkinson's disease. Nature Structural and Molecular Biology, 2017, 24, 632-642.	3.6	159
21	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimerâ€™s disease pathogenesis. Nature Genetics, 2021, 53, 143-146.	9.4	158
22	Polyubiquitin Linkage Profiles in Three Models of Proteolytic Stress Suggest the Etiology of Alzheimer Disease. Journal of Biological Chemistry, 2011, 286, 10457-10465.	1.6	151
23	Large-scale proteomic analysis of human brain identifies proteins associated with cognitive trajectory in advanced age. Nature Communications, 2019, 10, 1619.	5.8	144
24	A proteomic network approach across the <scp>ALS</scp> â€•<scp>FTD</scp> disease spectrum resolves clinical phenotypes and genetic vulnerability in human brain. EMBO Molecular Medicine, 2018, 10, 48-62.	3.3	142
25	Proteomic identification of novel proteins associated with Lewy bodies. Frontiers in Bioscience - Landmark, 2008, Volume, 3850.	3.0	134
26	Pharmacologic Inhibition of ROCK2 Suppresses Amyloid-Î² Production in an Alzheimer's Disease Mouse Model. Journal of Neuroscience, 2013, 33, 19086-19098.	1.7	118
27	Differential Phagocytic Properties of CD45low Microglia and CD45high Brain Mononuclear Phagocytesâ€”Activation and Age-Related Effects. Frontiers in Immunology, 2018, 9, 405.	2.2	102
28	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimerâ€™s disease. Molecular Neurodegeneration, 2017, 12, 82.	4.4	100
29	Quantitative proteomics of acutely-isolated mouse microglia identifies novel immune Alzheimerâ€™s disease-related proteins. Molecular Neurodegeneration, 2018, 13, 34.	4.4	100
30	Coaggregation of RNA-Binding Proteins in a Model of TDP-43 Proteinopathy with Selective RGG Motif Methylation and a Role for RRM1 Ubiquitination. PLoS ONE, 2012, 7, e38658.	1.1	98
31	Multiscale causal networks identify VGF as a key regulator of Alzheimerâ€™s disease. Nature Communications, 2020, 11, 3942.	5.8	94
32	Multiplex SILAC Analysis of a Cellular TDP-43 Proteinopathy Model Reveals Protein Inclusions Associated with SUMOylation and Diverse Polyubiquitin Chains. Molecular and Cellular Proteomics, 2010, 9, 705-718.	2.5	92
33	Galectin-3 Is a Candidate Biomarker for Amyotrophic Lateral Sclerosis: Discovery by a Proteomics Approach. Journal of Proteome Research, 2010, 9, 5133-5141.	1.8	88
34	Phosphoproteomic Analysis of Human Brain by Calcium Phosphate Precipitation and Mass Spectrometry. Journal of Proteome Research, 2008, 7, 2845-2851.	1.8	87
35	SIRT2 directs the replication stress response through CDK9 deacetylation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13546-13551.	3.3	87
36	Shared proteomic effects of cerebral atherosclerosis and Alzheimerâ€™s disease on the human brain. Nature Neuroscience, 2020, 23, 696-700.	7.1	86

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37	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. Nature Neuroscience, 2021, 24, 810-817.	7.1	85
38	Selective Targeting of the Cysteine Proteome by Thioredoxin and Glutathione Redox Systems. Molecular and Cellular Proteomics, 2013, 12, 3285-3296.	2.5	81
39	Cellular O-Glycome Reporter/Amplification to explore O-glycans of living cells. Nature Methods, 2016, 13, 81-86.	9.0	81
40	Tissue-Type Plasminogen Activator Regulates the Neuronal Uptake of Glucose in the Ischemic Brain. Journal of Neuroscience, 2012, 32, 9848-9858.	1.7	79
41	Proteomics Analysis Reveals Novel Components in the Detergent-Insoluble Subproteome in Alzheimerâ€™s Disease. Journal of Proteome Research, 2009, 8, 5069-5079.	1.8	76
42	Stem cell-derived neurons reflect features of protein networks, neuropathology, and cognitive outcome of their aged human donors. Neuron, 2021, 109, 3402-3420.e9.	3.8	75
43	Global quantitative analysis of the human brain proteome and phosphoproteome in Alzheimerâ€™s disease. Scientific Data, 2020, 7, 315.	2.4	74
44	Analysis of a membraneâ€enriched proteome from postmortem human brain tissue in <scp>A</scp>lzheimer's disease. Proteomics - Clinical Applications, 2012, 6, 201-211.	0.8	72
45	Stress Induces p38 MAPK-Mediated Phosphorylation and Inhibition of Drosha-Dependent Cell Survival. Molecular Cell, 2015, 57, 721-734.	4.5	72
46	Phosphoproteomic Analysis Reveals Site-Specific Changes in GFAP and NDRG2 Phosphorylation in Frontotemporal Lobar Degeneration. Journal of Proteome Research, 2010, 9, 6368-6379.	1.8	71
47	Quantitative phosphoproteomics of Alzheimer's disease reveals crossâ€talk between kinases and small heat shock proteins. Proteomics, 2015, 15, 508-519.	1.3	70
48	Cortical Proteins Associated With Cognitive Resilience in Community-Dwelling Older Persons. JAMA Psychiatry, 2020, 77, 1172.	6.0	70
49	Changes in the detergent-insoluble brain proteome linked to amyloid and tau in Alzheimer's Disease progression. Proteomics, 2016, 16, 3042-3053.	1.3	69
50	Neuronal Morphogenesis Is Regulated by the Interplay between Cyclin-Dependent Kinase 5 and the Ubiquitin Ligase Mind Bomb 1. Journal of Neuroscience, 2007, 27, 9503-9512.	1.7	68
51	RNA-binding proteins with basic-acidic dipeptide (BAD) domains self-assemble and aggregate in Alzheimer's disease. Journal of Biological Chemistry, 2018, 293, 11047-11066.	1.6	66
52	Systematic Approach for Validating the Ubiquitinated Proteome. Analytical Chemistry, 2008, 80, 4161-4169.	3.2	65
53	Quantitative Analysis of the Detergent-Insoluble Brain Proteome in Frontotemporal Lobar Degeneration Using SILAC Internal Standards. Journal of Proteome Research, 2012, 11, 2721-2738.	1.8	61
54	Neuron Enriched Nuclear Proteome Isolated from Human Brain. Journal of Proteome Research, 2013, 12, 3193-3206.	1.8	60

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55	A systems pharmacology-based approach to identify novel Kv1.3 channel-dependent mechanisms in microglial activation. Journal of Neuroinflammation, 2017, 14, 128.	3.1	58
56	Hectd3 promotes pathogenic Th17 lineage through Stat3 activation and Malt1 signaling in neuroinflammation. Nature Communications, 2019, 10, 701.	5.8	57
57	Effects of APOE Genotype on Brain Proteomic Network and Cell Type Changes in Alzheimer's Disease. Frontiers in Molecular Neuroscience, 2018, 11, 454.	1.4	55
58	ATRIP Deacetylation by SIRT2 Drives ATR Checkpoint Activation by Promoting Binding to RPA-ssDNA. Cell Reports, 2016, 14, 1435-1447.	2.9	54
59	Targeted mass spectrometry to quantify brain-derived cerebrospinal fluid biomarkers in Alzheimerâ€™s disease. Clinical Proteomics, 2020, 17, 19.	1.1	53
60	Asparaginyl endopeptidase cleaves TDPâ€43 in brain. Proteomics, 2012, 12, 2455-2463.	1.3	52
61	Genetic control of the human brain proteome. American Journal of Human Genetics, 2021, 108, 400-410.	2.6	52
62	Biochemical characterization of purified mammalian ARL13B protein indicates that it is an atypical GTPase and ARL3 guanine nucleotide exchange factor (GEF). Journal of Biological Chemistry, 2017, 292, 11091-11108.	1.6	51
63	Evolutionarily Conserved Polyadenosine RNA Binding Protein Nab2 Cooperates with Splicing Machinery To Regulate the Fate of Pre-mRNA. Molecular and Cellular Biology, 2016, 36, 2697-2714.	1.1	50
64	Quantitative Analysis of the Brain Ubiquitylome in Alzheimer's Disease. Proteomics, 2018, 18, e1800108.	1.3	50
65	Molecular Signatures of Neuroinflammation Induced by Î±Synuclein Aggregates in Microglial Cells. Frontiers in Immunology, 2020, 11, 33.	2.2	50
66	Acetylation regulates ribonucleotide reductase activity and cancer cell growth. Nature Communications, 2019, 10, 3213.	5.8	49
67	Network analysis of the progranulin-deficient mouse brain proteome reveals pathogenic mechanisms shared in human frontotemporal dementia caused by GRN mutations. Acta Neuropathologica Communications, 2020, 8, 163.	2.4	49
68	Identification of Conserved Proteomic Networks in Neurodegenerative Dementia. Cell Reports, 2020, 31, 107807.	2.9	49
69	Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain. Journal of Proteome Research, 2017, 16, 3336-3347.	1.8	48
70	U1 small nuclear ribonucleoproteins (snRNPs) aggregate in Alzheimerâ€™s disease due to autosomal dominant genetic mutations and trisomy 21. Molecular Neurodegeneration, 2014, 9, 15.	4.4	47
71	Proteomic analysis of postsynaptic density in Alzheimer's Disease. Clinica Chimica Acta, 2013, 420, 62-68.	0.5	42
72	Aggregation Properties of the Small Nuclear Ribonucleoprotein U1-70K in Alzheimer Disease. Journal of Biological Chemistry, 2014, 289, 35296-35313.	1.6	42

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73	Protein Fold Classification with Backbone Torsional Characters Using Multi- Class Linear Discriminant Analysis. Journal of Proteomics and Bioinformatics, 2013, 06, 196-209.	0.4	42
74	Identifying the substrate proteins of U-box E3s E4B and CHIP by orthogonal ubiquitin transfer. Science Advances, 2018, 4, e1701393.	4.7	39
75	A phase II study repurposing atomoxetine for neuroprotection in mild cognitive impairment. Brain, 2022, 145, 1924-1938.	3.7	39
76	Flow-cytometric microglial sorting coupled with quantitative proteomics identifies moesin as a highly-abundant microglial protein with relevance to Alzheimerâ€™s disease. Molecular Neurodegeneration, 2020, 15, 28.	4.4	37
77	Identification and Characterization of Neuronal Mitogen-activated Protein Kinase Substrates Using a Specific Phosphomotif Antibody. Molecular and Cellular Proteomics, 2009, 8, 681-695.	2.5	35
78	Orthogonal ubiquitin transfer identifies ubiquitination substrates under differential control by the two ubiquitin activating enzymes. Nature Communications, 2017, 8, 14286.	5.8	35
79	Stable Isotope Labeling with Amino Acids in Drosophila for Quantifying Proteins and Modifications. Journal of Proteome Research, 2012, 11, 4403-4412.	1.8	34
80	Discovery of tear biomarkers in children with chronic non-infectious anterior uveitis: a pilot study. Journal of Ophthalmic Inflammation and Infection, 2018, 8, 17.	1.2	34
81	Quantitative Proteomics Reveals Significant Changes in Cell Shape and an Energy Shift after IPTG Induction via an Optimized SILAC Approach for Escherichia coli. Journal of Proteome Research, 2013, 12, 5978-5988.	1.8	32
82	Exploring the potential of the platelet membrane proteome as a source of peripheral biomarkers for Alzheimer's disease. Alzheimer's Research and Therapy, 2013, 5, 32.	3.0	32
83	Mice lacking Gpr37 exhibit decreased expression of the myelin-associated glycoprotein MAG and increased susceptibility to demyelination. Neuroscience, 2017, 358, 49-57.	1.1	32
84	Cell type-specific biotin labeling in vivo resolves regional neuronal and astrocyte proteomic differences in mouse brain. Nature Communications, 2022, 13, .	5.8	32
85	Systematic research on the pretreatment of peptides for quantitative proteomics using a <scp>C</scp>₁₈ microcolumn. Proteomics, 2013, 13, 2229-2237.	1.3	30
86	Identifying the ubiquitination targets of E6AP by orthogonal ubiquitin transfer. Nature Communications, 2017, 8, 2232.	5.8	30
87	Abnormal Gephyrin Immunoreactivity Associated With Alzheimer Disease Pathologic Changes. Journal of Neuropathology and Experimental Neurology, 2013, 72, 1009-1015.	0.9	29
88	EZH2 has a non-catalytic and PRC2-independent role in stabilizing DDB2 to promote nucleotide excision repair. Oncogene, 2020, 39, 4798-4813.	2.6	29
89	Merger of Laser Capture Microdissection and Mass Spectrometry: A Window into the Amyloid Plaque Proteome. Methods in Enzymology, 2006, 412, 77-93.	0.4	28
90	Osteopontin Is a Blood Biomarker for Microglial Activation and Brain Injury in Experimental Hypoxic-Ischemic Encephalopathy. ENeuro, 2017, 4, ENEURO.0253-16.2016.	0.9	28

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91	An O2-sensing stressosome from a Gram-negative bacterium. Nature Communications, 2016, 7, 12381.	5.8	25
92	5-Aminolevulinic Acid Guided Sampling of Glioblastoma Microenvironments Identifies Pro-Survival Signaling at Infiltrative Margins. Scientific Reports, 2017, 7, 15593.	1.6	25
93	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, 984-1004.	0.4	25
94	GPRC5A suppresses protein synthesis at the endoplasmic reticulum to prevent radiation-induced lung tumorigenesis. Nature Communications, 2016, 7, 11795.	5.8	24
95	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. Molecular Cell, 2019, 76, 126-137.e7.	4.5	24
96	Tissue-Type Plasminogen Activator Mediates Neuronal Detection and Adaptation to Metabolic Stress. Journal of Cerebral Blood Flow and Metabolism, 2013, 33, 1761-1769.	2.4	22
97	Pseudomonas aeruginosa EftM Is a Thermoregulated Methyltransferase. Journal of Biological Chemistry, 2016, 291, 3280-3290.	1.6	22
98	Integrated analysis of the aging brain transcriptome and proteome in tauopathy. Molecular Neurodegeneration, 2020, 15, 56.	4.4	22
99	Interactome Analysis Reveals Regulator of G Protein Signaling 14 (RGS14) is a Novel Calcium/Calmodulin (Ca²⁺/CaM) and CaM Kinase II (CaMKII) Binding Partner. Journal of Proteome Research, 2018, 17, 1700-1711.	1.8	21
100	A Proteomic Strategy for Quantifying Polyubiquitin Chain Topologies. Israel Journal of Chemistry, 2006, 46, 171-182.	1.0	20
101	Characterization of Detergent Insoluble Proteome in Chronic Traumatic Encephalopathy. Journal of Neuropathology and Experimental Neurology, 2018, 77, 40-49.	0.9	19
102	Atlas of RNA editing events affecting protein expression in aged and Alzheimerâ€™s disease human brain tissue. Nature Communications, 2021, 12, 7035.	5.8	19
103	Proteomic Analysis of Hippocampal Dentate Granule Cells in Frontotemporal Lobar Degeneration: Application of Laser Capture Technology. Frontiers in Neurology, 2011, 2, 24.	1.1	18
104	Network Analysis of a Membrane-Enriched Brain Proteome across Stages of Alzheimerâ€™s Disease. Proteomes, 2019, 7, 30.	1.7	18
105	Specific Proteomes of Hippocampal Regions CA2 and CA1 Reveal Proteins Linked to the Unique Physiology of Area CA2. Journal of Proteome Research, 2019, 18, 2571-2584.	1.8	18
106	Mitochondrial Proteostasis Requires Genes Encoded in a Neurodevelopmental Syndrome Locus. Journal of Neuroscience, 2021, 41, 6596-6616.	1.7	18
107	Genetic Evidence Supporting a Causal Role of Depression in Alzheimerâ€™s Disease. Biological Psychiatry, 2022, 92, 25-33.	0.7	18
108	Aberrant septin 11 is associated with sporadic frontotemporal lobar degeneration. Molecular Neurodegeneration, 2011, 6, 82.	4.4	17

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109	Ionizing Radiation induction of cholesterol biosynthesis in Lung tissue. Scientific Reports, 2019, 9, 12546.	1.6	14
110	TBK1 interacts with tau and enhances neurodegeneration in tauopathy. Journal of Biological Chemistry, 2021, 296, 100760.	1.6	14
111	APP and DYRK1A regulate axonal and synaptic vesicle protein networks and mediate Alzheimerâ€™s pathology in trisomy 21 neurons. Molecular Psychiatry, 2022, 27, 1970-1989.	4.1	14
112	Mass-Spectrometry-Based Near-Complete Draft of theSaccharomyces cerevisiaeProteome. Journal of Proteome Research, 2021, 20, 1328-1340.	1.8	13
113	Heterogeneous Expression of Nuclear Encoded Mitochondrial Genes Distinguishes Inhibitory and Excitatory Neurons. ENeuro, 2021, 8, ENEURO.0232-21.2021.	0.9	13
114	Integrating human brain proteomes with genome-wide association data implicates novel proteins in post-traumatic stress disorder. Molecular Psychiatry, 2022, 27, 3075-3084.	4.1	13
115	Signatures of glial activity can be detected in the CSF proteome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	12
116	Protein Profiling of Active Cysteine Cathepsins in Living Cells Using an Activity-Based Probe Containing a Cell-Penetrating Peptide. Journal of Proteome Research, 2012, 11, 5763-5772.	1.8	11
117	Mass Spectrometry-Based Quantification of Tau in Human Cerebrospinal Fluid Using a Complementary Tryptic Peptide Standard. Journal of Proteome Research, 2019, 18, 2422-2432.	1.8	11
118	Consequences of impaired purine recycling on the proteome in a cellular model of Leschâ€“Nyhan disease. Molecular Genetics and Metabolism, 2015, 114, 570-579.	0.5	10
119	Middle-Down Proteomics Reveals Dense Sites of Methylation and Phosphorylation in Arginine-Rich RNA-Binding Proteins. Journal of Proteome Research, 2020, 19, 1574-1591.	1.8	10
120	Native low density lipoprotein promotes lipid raft formation in macrophages. Molecular Medicine Reports, 2016, 13, 2087-2093.	1.1	9
121	Amphiphysin I cleavage by asparagine endopeptidase leads to tau hyperphosphorylation and synaptic dysfunction. ELife, 2021, 10, .	2.8	9
122	Regulation of the endocytosis and prion-chaperoning machineries by yeast E3 ubiquitin ligase Rsp5 as revealed by orthogonal ubiquitin transfer. Cell Chemical Biology, 2021, 28, 1283-1297.e8.	2.5	9
123	Phosphorylation regulates arginine-rich RNA-binding protein solubility and oligomerization. Journal of Biological Chemistry, 2021, 297, 101306.	1.6	9
124	Quantitative Proteomics Reveal an Altered Pattern of Protein Expression in Brain Tissue from Mice Lacking GPR37 and GPR37L1. Journal of Proteome Research, 2020, 19, 744-755.	1.8	8
125	Loss of the mitochondrial phosphate carrier SLC25A3 induces remodeling of the cardiac mitochondrial protein acylome. American Journal of Physiology - Cell Physiology, 2021, 321, C519-C534.	2.1	8
126	Extracellular calcium alters calcium-sensing receptor network integrating intracellular calcium-signaling and related key pathway. Scientific Reports, 2021, 11, 20576.	1.6	8

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127	Expression, purification and proteomic analysis of recombinant histone <scp>H</scp>4 acetylated at lysine 16. Proteomics, 2013, 13, 1687-1691.	1.3	6
128	Broad Kinase Inhibition Mitigates Early Neuronal Dysfunction in Tauopathy. International Journal of Molecular Sciences, 2021, 22, 1186.	1.8	6
129	Orthogonal ubiquitin transfer reveals human papillomavirus E6 downregulates nuclear transport to disarm interferonâ€β dependent apoptosis of cervical cancer cells. FASEB Journal, 2021, 35, e21986.	0.2	6
130	Trimethylation of Elongation Factor-Tu by the Dual Thermoregulated Methyltransferase EftM Does Not Impact Its Canonical Function in Translation. Scientific Reports, 2019, 9, 3553.	1.6	5
131	Quantitative proteomic analysis of the lysine acetylome reveals diverse SIRT2 substrates. Scientific Reports, 2022, 12, 3822.	1.6	5
132	A proteomic network approach resolves stage-specific molecular phenotypes in chronic traumatic encephalopathy. Molecular Neurodegeneration, 2021, 16, 40.	4.4	4
133	Mycobacterium tuberculosis Biology Revealed by Proteome Profiling and Integration of Multi-omics Data—Proteomics Insight into M. tuberculosis Systems Biology. Current Proteomics, 2013, 10, 261-268.	0.1	2
134	Identifying novel causal genes and proteins in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043523.	0.4	1
135	Integrating human brain proteomes and genomeâ€wide association results implicates new genes in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043865.	0.4	1
136	Largeâ€scale deep multiâ€layer analysis of Alzheimerâ€™s disease brain reveals strong proteomic diseaseâ€related changes not observed at the RNA level. Alzheimer's and Dementia, 2021, 17, e055041.	0.4	1
137	O4-12-02: Protein co-expression network analysis in Alzheimer's disease. , 2015, 11, P299-P299.		0
138	O4-12-03: Brain phosphoproteome network analysis discriminates Alzheimer's disease from other tauopathies. , 2015, 11, P300-P300.		0
139	A consensus proteomic analysis of Alzheimerâ€™s disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Alzheimer's and Dementia, 2020, 16, e039504.	0.4	0
140	Proteomics identifies CSF biomarker panels reflective of pathological networks in the Alzheimer's disease brain. Alzheimer's and Dementia, 2020, 16, e042227.	0.4	0
141	Hallmarks of lateâ€onset Alzheimerâ€™s disease in a humanized mouse model. Alzheimer's and Dementia, 2020, 16, e045162.	0.4	0
142	Novel proteomic molecular signatures of brain endothelial cells and microglia in the aging mouse brain. Alzheimer's and Dementia, 2020, 16, e047549.	0.4	0
143	Tau phosphosignatures discriminate Alzheimer Disease from other tauopathies. FASEB Journal, 2015, 29, .	0.2	0
144	Depression contributes to Alzheimer's disease through shared genetic risk.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053251.	0.4	0