

Duc M Duong

List of Publications by Year in descending order

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Version: 2024-02-01

144
papers

11,719
citations

36303

51
h-index

36028

97
g-index

176
all docs

176
docs citations

176
times ranked

14717
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. <i>Nature Neuroscience</i> , 2022, 25, 213-225.	14.8	202
2	A phase II study repurposing atomoxetine for neuroprotection in mild cognitive impairment. <i>Brain</i> , 2022, 145, 1924-1938.	7.6	39
3	Quantitative proteomic analysis of the lysine acetylome reveals diverse SIRT2 substrates. <i>Scientific Reports</i> , 2022, 12, 3822.	3.3	5
4	Genetic Evidence Supporting a Causal Role of Depression in Alzheimer's Disease. <i>Biological Psychiatry</i> , 2022, 92, 25-33.	1.3	18
5	APP and DYRK1A regulate axonal and synaptic vesicle protein networks and mediate Alzheimer's pathology in trisomy 21 neurons. <i>Molecular Psychiatry</i> , 2022, 27, 1970-1989.	7.9	14
6	Integrating human brain proteomes with genome-wide association data implicates novel proteins in post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2022, 27, 3075-3084.	7.9	13
7	Cell type-specific biotin labeling in vivo resolves regional neuronal and astrocyte proteomic differences in mouse brain. <i>Nature Communications</i> , 2022, 13, .	12.8	32
8	Signatures of glial activity can be detected in the CSF proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
9	Mass-Spectrometry-Based Near-Complete Draft of the <i>Saccharomyces cerevisiae</i> Proteome. <i>Journal of Proteome Research</i> , 2021, 20, 1328-1340.	3.7	13
10	Broad Kinase Inhibition Mitigates Early Neuronal Dysfunction in Tauopathy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1186.	4.1	6
11	TBK1 interacts with tau and enhances neurodegeneration in tauopathy. <i>Journal of Biological Chemistry</i> , 2021, 296, 100760.	3.4	14
12	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, 984-1004.	0.8	25
13	Genetic control of the human brain proteome. <i>American Journal of Human Genetics</i> , 2021, 108, 400-410.	6.2	52
14	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021, 24, 810-817.	14.8	85
15	Amphiphysin I cleavage by asparagine endopeptidase leads to tau hyperphosphorylation and synaptic dysfunction. <i>ELife</i> , 2021, 10, .	6.0	9
16	A proteomic network approach resolves stage-specific molecular phenotypes in chronic traumatic encephalopathy. <i>Molecular Neurodegeneration</i> , 2021, 16, 40.	10.8	4
17	Heterogeneous Expression of Nuclear Encoded Mitochondrial Genes Distinguishes Inhibitory and Excitatory Neurons. <i>ENeuro</i> , 2021, 8, ENEURO.0232-21.2021.	1.9	13
18	Mitochondrial Proteostasis Requires Genes Encoded in a Neurodevelopmental Syndrome Locus. <i>Journal of Neuroscience</i> , 2021, 41, 6596-6616.	3.6	18

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19	Regulation of the endocytosis and prion-chaperoning machineries by yeast E3 ubiquitin ligase Rsp5 as revealed by orthogonal ubiquitin transfer. <i>Cell Chemical Biology</i> , 2021, 28, 1283-1297.e8.	5.2	9
20	Loss of the mitochondrial phosphate carrier SLC25A3 induces remodeling of the cardiac mitochondrial protein acylome. <i>American Journal of Physiology - Cell Physiology</i> , 2021, 321, C519-C534.	4.6	8
21	Stem cell-derived neurons reflect features of protein networks, neuropathology, and cognitive outcome of their aged human donors. <i>Neuron</i> , 2021, 109, 3402-3420.e9.	8.1	75
22	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis. <i>Nature Genetics</i> , 2021, 53, 143-146.	21.4	158
23	Extracellular calcium alters calcium-sensing receptor network integrating intracellular calcium-signaling and related key pathway. <i>Scientific Reports</i> , 2021, 11, 20576.	3.3	8
24	Phosphorylation regulates arginine-rich RNA-binding protein solubility and oligomerization. <i>Journal of Biological Chemistry</i> , 2021, 297, 101306.	3.4	9
25	Orthogonal ubiquitin transfer reveals human papillomavirus E6 downregulates nuclear transport to disarm interferon- β dependent apoptosis of cervical cancer cells. <i>FASEB Journal</i> , 2021, 35, e21986.	0.5	6
26	Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021, 12, 7035.	12.8	19
27	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. <i>Alzheimer's and Dementia</i> , 2021, 17, e055041.	0.8	1
28	Depression contributes to Alzheimer's disease through shared genetic risk.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e053251.	0.8	0
29	Quantitative Proteomics Reveal an Altered Pattern of Protein Expression in Brain Tissue from Mice Lacking GPR37 and GPR37L1. <i>Journal of Proteome Research</i> , 2020, 19, 744-755.	3.7	8
30	Integrated analysis of the aging brain transcriptome and proteome in tauopathy. <i>Molecular Neurodegeneration</i> , 2020, 15, 56.	10.8	22
31	Global quantitative analysis of the human brain proteome and phosphoproteome in Alzheimer's disease. <i>Scientific Data</i> , 2020, 7, 315.	5.3	74
32	Integrated proteomics reveals brain-based cerebrospinal fluid biomarkers in asymptomatic and symptomatic Alzheimer's disease. <i>Science Advances</i> , 2020, 6, .	10.3	186
33	Network analysis of the progranulin-deficient mouse brain proteome reveals pathogenic mechanisms shared in human frontotemporal dementia caused by GRN mutations. <i>Acta Neuropathologica Communications</i> , 2020, 8, 163.	5.2	49
34	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	12.8	94
35	A consensus proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Alzheimer's and Dementia</i> , 2020, 16, e039504.	0.8	0
36	Proteomics identifies CSF biomarker panels reflective of pathological networks in the Alzheimer's disease brain. <i>Alzheimer's and Dementia</i> , 2020, 16, e042227.	0.8	0

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37	Identifying novel causal genes and proteins in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e043523.	0.8	1
38	Integrating human brain proteomes and genome-wide association results implicates new genes in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e043865.	0.8	1
39	Hallmarks of late-onset Alzheimer's disease in a humanized mouse model. <i>Alzheimer's and Dementia</i> , 2020, 16, e045162.	0.8	0
40	Novel proteomic molecular signatures of brain endothelial cells and microglia in the aging mouse brain. <i>Alzheimer's and Dementia</i> , 2020, 16, e047549.	0.8	0
41	Shared proteomic effects of cerebral atherosclerosis and Alzheimer's disease on the human brain. <i>Nature Neuroscience</i> , 2020, 23, 696-700.	14.8	86
42	Flow-cytometric microglial sorting coupled with quantitative proteomics identifies moesin as a highly-abundant microglial protein with relevance to Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2020, 15, 28.	10.8	37
43	EZH2 has a non-catalytic and PRC2-independent role in stabilizing DDB2 to promote nucleotide excision repair. <i>Oncogene</i> , 2020, 39, 4798-4813.	5.9	29
44	Targeted mass spectrometry to quantify brain-derived cerebrospinal fluid biomarkers in Alzheimer's disease. <i>Clinical Proteomics</i> , 2020, 17, 19.	2.1	53
45	Cortical Proteins Associated With Cognitive Resilience in Community-Dwelling Older Persons. <i>JAMA Psychiatry</i> , 2020, 77, 1172.	11.0	70
46	Identification of Conserved Proteomic Networks in Neurodegenerative Dementia. <i>Cell Reports</i> , 2020, 31, 107807.	6.4	49
47	Molecular Signatures of Neuroinflammation Induced by \pm Synuclein Aggregates in Microglial Cells. <i>Frontiers in Immunology</i> , 2020, 11, 33.	4.8	50
48	Middle-Down Proteomics Reveals Dense Sites of Methylation and Phosphorylation in Arginine-Rich RNA-Binding Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 1574-1591.	3.7	10
49	Posttranslational Modifications Mediate the Structural Diversity of Tauopathy Strains. <i>Cell</i> , 2020, 180, 633-644.e12.	28.9	300
50	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Nature Medicine</i> , 2020, 26, 769-780.	30.7	547
51	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. <i>Molecular Cell</i> , 2019, 76, 126-137.e7.	9.7	24
52	Acetylation regulates ribonucleotide reductase activity and cancer cell growth. <i>Nature Communications</i> , 2019, 10, 3213.	12.8	49
53	Ionizing Radiation induction of cholesterol biosynthesis in Lung tissue. <i>Scientific Reports</i> , 2019, 9, 12546.	3.3	14
54	Network Analysis of a Membrane-Enriched Brain Proteome across Stages of Alzheimer's Disease. <i>Proteomes</i> , 2019, 7, 30.	3.5	18

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55	Specific Proteomes of Hippocampal Regions CA2 and CA1 Reveal Proteins Linked to the Unique Physiology of Area CA2. <i>Journal of Proteome Research</i> , 2019, 18, 2571-2584.	3.7	18
56	Trimethylation of Elongation Factor-Tu by the Dual Thermoregulated Methyltransferase EftM Does Not Impact Its Canonical Function in Translation. <i>Scientific Reports</i> , 2019, 9, 3553.	3.3	5
57	Large-scale proteomic analysis of human brain identifies proteins associated with cognitive trajectory in advanced age. <i>Nature Communications</i> , 2019, 10, 1619.	12.8	144
58	Mass Spectrometry-Based Quantification of Tau in Human Cerebrospinal Fluid Using a Complementary Tryptic Peptide Standard. <i>Journal of Proteome Research</i> , 2019, 18, 2422-2432.	3.7	11
59	Hectd3 promotes pathogenic Th17 lineage through Stat3 activation and Malt1 signaling in neuroinflammation. <i>Nature Communications</i> , 2019, 10, 701.	12.8	57
60	Interactome Analysis Reveals Regulator of G Protein Signaling 14 (RGS14) is a Novel Calcium/Calmodulin (Ca ²⁺ /CaM) and CaM Kinase II (CaMKII) Binding Partner. <i>Journal of Proteome Research</i> , 2018, 17, 1700-1711.	3.7	21
61	Identifying the substrate proteins of U-box E3s E4B and CHIP by orthogonal ubiquitin transfer. <i>Science Advances</i> , 2018, 4, e1701393.	10.3	39
62	TDP-43 pathology disrupts nuclear pore complexes and nucleocytoplasmic transport in ALS/FTD. <i>Nature Neuroscience</i> , 2018, 21, 228-239.	14.8	404
63	Characterization of Detergent Insoluble Proteome in Chronic Traumatic Encephalopathy. <i>Journal of Neuropathology and Experimental Neurology</i> , 2018, 77, 40-49.	1.7	19
64	Global quantitative analysis of the human brain proteome in Alzheimer's and Parkinson's Disease. <i>Scientific Data</i> , 2018, 5, 180036.	5.3	179
65	A proteomic network approach across the <sc>ALS</sc> - <sc>FTD</sc> disease spectrum resolves clinical phenotypes and genetic vulnerability in human brain. <i>EMBO Molecular Medicine</i> , 2018, 10, 48-62.	6.9	142
66	Discovery of tear biomarkers in children with chronic non-infectious anterior uveitis: a pilot study. <i>Journal of Ophthalmic Inflammation and Infection</i> , 2018, 8, 17.	2.2	34
67	Effects of APOE Genotype on Brain Proteomic Network and Cell Type Changes in Alzheimer's Disease. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 454.	2.9	55
68	Deep proteomic network analysis of Alzheimer's disease brain reveals alterations in RNA binding proteins and RNA splicing associated with disease. <i>Molecular Neurodegeneration</i> , 2018, 13, 52.	10.8	178
69	Quantitative Analysis of the Brain Ubiquitylome in Alzheimer's Disease. <i>Proteomics</i> , 2018, 18, e1800108.	2.2	50
70	RNA-binding proteins with basic-acidic dipeptide (BAD) domains self-assemble and aggregate in Alzheimer's disease. <i>Journal of Biological Chemistry</i> , 2018, 293, 11047-11066.	3.4	66
71	Quantitative proteomics of acutely-isolated mouse microglia identifies novel immune Alzheimer's disease-related proteins. <i>Molecular Neurodegeneration</i> , 2018, 13, 34.	10.8	100
72	Differential Phagocytic Properties of CD45 ^{low} Microglia and CD45 ^{high} Brain Mononuclear Phagocytes - Activation and Age-Related Effects. <i>Frontiers in Immunology</i> , 2018, 9, 405.	4.8	102

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73	Identification and therapeutic modulation of a pro-inflammatory subset of disease-associated-microglia in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2018, 13, 24.	10.8	267
74	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	5.3	320
75	Orthogonal ubiquitin transfer identifies ubiquitination substrates under differential control by the two ubiquitin activating enzymes. <i>Nature Communications</i> , 2017, 8, 14286.	12.8	35
76	Biochemical characterization of purified mammalian ARL13B protein indicates that it is an atypical GTPase and ARL3 guanine nucleotide exchange factor (GEF). <i>Journal of Biological Chemistry</i> , 2017, 292, 11091-11108.	3.4	51
77	A Multi-network Approach Identifies Protein-Specific Co-expression in Asymptomatic and Symptomatic Alzheimer's Disease. <i>Cell Systems</i> , 2017, 4, 60-72.e4.	6.2	381
78	Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain. <i>Journal of Proteome Research</i> , 2017, 16, 3336-3347.	3.7	48
79	5-Aminolevulinic Acid Guided Sampling of Glioblastoma Microenvironments Identifies Pro-Survival Signaling at Infiltrative Margins. <i>Scientific Reports</i> , 2017, 7, 15593.	3.3	25
80	Mice lacking Gpr37 exhibit decreased expression of the myelin-associated glycoprotein MAG and increased susceptibility to demyelination. <i>Neuroscience</i> , 2017, 358, 49-57.	2.3	32
81	A systems pharmacology-based approach to identify novel Kv1.3 channel-dependent mechanisms in microglial activation. <i>Journal of Neuroinflammation</i> , 2017, 14, 128.	7.2	58
82	Asparagine endopeptidase cleaves α -synuclein and mediates pathologic activities in Parkinson's disease. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 632-642.	8.2	159
83	Identifying the ubiquitination targets of E6AP by orthogonal ubiquitin transfer. <i>Nature Communications</i> , 2017, 8, 2232.	12.8	30
84	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017, 12, 82.	10.8	100
85	Osteopontin Is a Blood Biomarker for Microglial Activation and Brain Injury in Experimental Hypoxic-Ischemic Encephalopathy. <i>ENeuro</i> , 2017, 4, ENEURO.0253-16.2016.	1.9	28
86	Native low density lipoprotein promotes lipid raft formation in macrophages. <i>Molecular Medicine Reports</i> , 2016, 13, 2087-2093.	2.4	9
87	GPRC5A suppresses protein synthesis at the endoplasmic reticulum to prevent radiation-induced lung tumorigenesis. <i>Nature Communications</i> , 2016, 7, 11795.	12.8	24
88	<i>Pseudomonas aeruginosa</i> EftM Is a Thermoregulated Methyltransferase. <i>Journal of Biological Chemistry</i> , 2016, 291, 3280-3290.	3.4	22
89	Changes in the detergent-insoluble brain proteome linked to amyloid and tau in Alzheimer's Disease progression. <i>Proteomics</i> , 2016, 16, 3042-3053.	2.2	69
90	Evolutionarily Conserved Polyadenosine RNA Binding Protein Nab2 Cooperates with Splicing Machinery To Regulate the Fate of Pre-mRNA. <i>Molecular and Cellular Biology</i> , 2016, 36, 2697-2714.	2.3	50

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91	An O ₂ -sensing stressosome from a Gram-negative bacterium. <i>Nature Communications</i> , 2016, 7, 12381.	12.8	25
92	ATRIP Deacetylation by SIRT2 Drives ATR Checkpoint Activation by Promoting Binding to RPA-ssDNA. <i>Cell Reports</i> , 2016, 14, 1435-1447.	6.4	54
93	Cellular O-Glycome Reporter/Amplification to explore O-glycans of living cells. <i>Nature Methods</i> , 2016, 13, 81-86.	19.0	81
94	Consequences of impaired purine recycling on the proteome in a cellular model of Leschâ€™Nyhan disease. <i>Molecular Genetics and Metabolism</i> , 2015, 114, 570-579.	1.1	10
95	Delta-secretase cleaves amyloid precursor protein and regulates the pathogenesis in Alzheimerâ€™s disease. <i>Nature Communications</i> , 2015, 6, 8762.	12.8	210
96	O4-12-02: Protein co-expression network analysis in Alzheimer's disease. , 2015, 11, P299-P299.		0
97	O4-12-03: Brain phosphoproteome network analysis discriminates Alzheimer's disease from other tauopathies. , 2015, 11, P300-P300.		0
98	Stress Induces p38 MAPK-Mediated Phosphorylation and Inhibition of Drosha-Dependent Cell Survival. <i>Molecular Cell</i> , 2015, 57, 721-734.	9.7	72
99	Glutamate Dehydrogenase 1 Signals through Antioxidant Glutathione Peroxidase 1 to Regulate Redox Homeostasis and Tumor Growth. <i>Cancer Cell</i> , 2015, 27, 257-270.	16.8	269
100	Quantitative phosphoproteomics of Alzheimer's disease reveals crossâ€™talk between kinases and small heat shock proteins. <i>Proteomics</i> , 2015, 15, 508-519.	2.2	70
101	Tau phosphosignatures discriminate Alzheimer Disease from other tauopathies. <i>FASEB Journal</i> , 2015, 29, .	0.5	0
102	Aggregation Properties of the Small Nuclear Ribonucleoprotein U1-70K in Alzheimer Disease. <i>Journal of Biological Chemistry</i> , 2014, 289, 35296-35313.	3.4	42
103	Cleavage of tau by asparagine endopeptidase mediates the neurofibrillary pathology in Alzheimer's disease. <i>Nature Medicine</i> , 2014, 20, 1254-1262.	30.7	367
104	U1 small nuclear ribonucleoproteins (snRNPs) aggregate in Alzheimerâ€™s disease due to autosomal dominant genetic mutations and trisomy 21. <i>Molecular Neurodegeneration</i> , 2014, 9, 15.	10.8	47
105	Tissue-Type Plasminogen Activator Mediates Neuronal Detection and Adaptation to Metabolic Stress. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2013, 33, 1761-1769.	4.3	22
106	Quantitative Proteomics Reveals Significant Changes in Cell Shape and an Energy Shift after IPTG Induction via an Optimized SILAC Approach for <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2013, 12, 5978-5988.	3.7	32
107	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimerâ€™s disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16562-16567.	7.1	268
108	Pharmacologic Inhibition of ROCK2 Suppresses Amyloid-Î² Production in an Alzheimer's Disease Mouse Model. <i>Journal of Neuroscience</i> , 2013, 33, 19086-19098.	3.6	118

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109	Proteomic analysis of postsynaptic density in Alzheimer's Disease. Clinica Chimica Acta, 2013, 420, 62-68.	1.1	42
110	Expression, purification and proteomic analysis of recombinant histone <sc>H</sc>4 acetylated at lysine 16. Proteomics, 2013, 13, 1687-1691.	2.2	6
111	Neuron Enriched Nuclear Proteome Isolated from Human Brain. Journal of Proteome Research, 2013, 12, 3193-3206.	3.7	60
112	Systematic research on the pretreatment of peptides for quantitative proteomics using a <sc>C</sc> ₁₈ microcolumn. Proteomics, 2013, 13, 2229-2237.	2.2	30
113	Selective Targeting of the Cysteine Proteome by Thioredoxin and Glutathione Redox Systems. Molecular and Cellular Proteomics, 2013, 12, 3285-3296.	3.8	81
114	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.	7.1	87
115	Abnormal Gephyrin Immunoreactivity Associated With Alzheimer Disease Pathologic Changes. Journal of Neuropathology and Experimental Neurology, 2013, 72, 1009-1015.	1.7	29
116	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.	6.2	32
117	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.	0.3	2
118	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
119	Quantitative Analysis of the Detergent-Insoluble Brain Proteome in Frontotemporal Lobar Degeneration Using SILAC Internal Standards. Journal of Proteome Research, 2012, 11, 2721-2738.	3.7	61
120	Stable Isotope Labeling with Amino Acids in <i>Drosophila</i> for Quantifying Proteins and Modifications. Journal of Proteome Research, 2012, 11, 4403-4412.	3.7	34
121	Tissue-Type Plasminogen Activator Regulates the Neuronal Uptake of Glucose in the Ischemic Brain. Journal of Neuroscience, 2012, 32, 9848-9858.	3.6	79
122	Asparaginyl endopeptidase cleaves TDP+ in brain. Proteomics, 2012, 12, 2455-2463.	2.2	52
123	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.	3.7	11
124	Analysis of a membrane—enriched proteome from postmortem human brain tissue in <sc>A</sc> Alzheimer's disease. Proteomics - Clinical Applications, 2012, 6, 201-211.	1.6	72
125	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.	2.5	98
126	Proteomic Analysis of Hippocampal Dentate Granule Cells in Frontotemporal Lobar Degeneration: Application of Laser Capture Technology. Frontiers in Neurology, 2011, 2, 24.	2.4	18

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127	Aberrant septin 11 is associated with sporadic frontotemporal lobar degeneration. <i>Molecular Neurodegeneration</i> , 2011, 6, 82.	10.8	17
128	Polyubiquitin Linkage Profiles in Three Models of Proteolytic Stress Suggest the Etiology of Alzheimer Disease. <i>Journal of Biological Chemistry</i> , 2011, 286, 10457-10465.	3.4	151
129	Multiplex SILAC Analysis of a Cellular TDP-43 Proteinopathy Model Reveals Protein Inclusions Associated with SUMOylation and Diverse Polyubiquitin Chains. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 705-718.	3.8	92
130	Phosphoproteomic Analysis Reveals Site-Specific Changes in GFAP and NDRG2 Phosphorylation in Frontotemporal Lobar Degeneration. <i>Journal of Proteome Research</i> , 2010, 9, 6368-6379.	3.7	71
131	Galectin-3 Is a Candidate Biomarker for Amyotrophic Lateral Sclerosis: Discovery by a Proteomics Approach. <i>Journal of Proteome Research</i> , 2010, 9, 5133-5141.	3.7	88
132	Identification and Characterization of Neuronal Mitogen-activated Protein Kinase Substrates Using a Specific Phosphomotif Antibody. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 681-695.	3.8	35
133	Systematical Optimization of Reverse-Phase Chromatography for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2009, 8, 3944-3950.	3.7	163
134	Proteomics Analysis Reveals Novel Components in the Detergent-Insoluble Subproteome in Alzheimer's Disease. <i>Journal of Proteome Research</i> , 2009, 8, 5069-5079.	3.7	76
135	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. <i>Cell</i> , 2009, 137, 133-145.	28.9	948
136	Systematic Approach for Validating the Ubiquitinated Proteome. <i>Analytical Chemistry</i> , 2008, 80, 4161-4169.	6.5	65
137	Phosphoproteomic Analysis of Human Brain by Calcium Phosphate Precipitation and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 2845-2851.	3.7	87
138	Proteomic identification of novel proteins associated with Lewy bodies. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 3850.	3.0	134
139	Neuronal Morphogenesis Is Regulated by the Interplay between Cyclin-Dependent Kinase 5 and the Ubiquitin Ligase Mind Bomb 1. <i>Journal of Neuroscience</i> , 2007, 27, 9503-9512.	3.6	68
140	A Proteomic Strategy for Quantifying Polyubiquitin Chain Topologies. <i>Israel Journal of Chemistry</i> , 2006, 46, 171-182.	2.3	20
141	Relative and Absolute Quantification of Postsynaptic Density Proteome Isolated from Rat Forebrain and Cerebellum. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1158-1170.	3.8	440
142	Merger of Laser Capture Microdissection and Mass Spectrometry: A Window into the Amyloid Plaque Proteome. <i>Methods in Enzymology</i> , 2006, 412, 77-93.	1.0	28
143	Proteomic Characterization of Postmortem Amyloid Plaques Isolated by Laser Capture Microdissection. <i>Journal of Biological Chemistry</i> , 2004, 279, 37061-37068.	3.4	267
144	Semiquantitative Proteomic Analysis of Rat Forebrain Postsynaptic Density Fractions by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 21003-21011.	3.4	417