Eric B Dammer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

142 papers

4,685 citations

37 h-index 66 g-index

178 ext. papers

6,859 ext. citations

8.1 avg, IF

5.48 L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 142 | Identification of neuronal RNA targets of TDP-43-containing ribonucleoprotein complexes. <i>Journal of Biological Chemistry</i> , 2011 , 286, 1204-15 | 5.4 | 306 |
| 141 | The endosomal-lysosomal system: from acidification and cargo sorting to neurodegeneration. <i>Translational Neurodegeneration</i> , 2015 , 4, 18 | 10.3 | 269 |
| 140 | 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 | 50.5 | 226 |
| 139 | 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 | 10.6 | 219 |
| 138 | U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16562-7 | 11.5 | 200 |
| 137 | The cotranslational function of ribosome-associated Hsp70 in eukaryotic protein homeostasis. <i>Cell</i> , 2013 , 152, 196-209 | 56.2 | 177 |
| 136 | Evidence for brain glucose dysregulation in Alzheimer's disease. <i>Alzheimer and Dementia</i> , 2018 , 14, 318-329 | 1.2 | 161 |
| 135 | The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018 , 5, 180185 | 8.2 | 144 |
| 134 | Identification and therapeutic modulation of a pro-inflammatory subset of disease-associated-microglia in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2018 , 13, 24 | 19 | 138 |
| 133 | Polyubiquitin linkage profiles in three models of proteolytic stress suggest the etiology of Alzheimer disease. <i>Journal of Biological Chemistry</i> , 2011 , 286, 10457-65 | 5.4 | 128 |
| 132 | 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 | 19 | 94 |
| 131 | Coaggregation of RNA-binding proteins in a model of TDP-43 proteinopathy with selective RGG motif methylation and a role for RRM1 ubiquitination. <i>PLoS ONE</i> , 2012 , 7, e38658 | 3.7 | 85 |
| 130 | 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, 705-18 | 7.6 | 80 |
| 129 | SAT-LB138 The LncRNA Growth Arrest Specific 5 Regulates Cell Survival via Distinct Structural Modules With Independent Functions. <i>Journal of the Endocrine Society</i> , 2020 , 4, | 0.4 | 78 |
| 128 | Melatonin for sleep disorders and cognition in dementia: a meta-analysis of randomized controlled trials. <i>American Journal of Alzheimera Disease and Other Dementias</i> , 2015 , 30, 439-47 | 2.5 | 76 |
| 127 | Large-scale proteomic analysis of human brain identifies proteins associated with cognitive trajectory in advanced age. <i>Nature Communications</i> , 2019 , 10, 1619 | 17.4 | 72 |
| 126 | Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. <i>Alzheimer</i> and Dementia, 2018 , 14, 352-366 | 1.2 | 72 |

| 125 | A proteomic network approach across the ALS-FTD disease spectrum resolves clinical phenotypes and genetic vulnerability in human brain. <i>EMBO Molecular Medicine</i> , 2018 , 10, 48-62 | 12 | 71 |
|-----|--|------|----|
| 124 | Sphingosine regulates the transcription of CYP17 by binding to steroidogenic factor-1. <i>Endocrinology</i> , 2006 , 147, 5249-58 | 4.8 | 70 |
| 123 | Tissue-type plasminogen activator regulates the neuronal uptake of glucose in the ischemic brain. Journal of Neuroscience, 2012 , 32, 9848-58 | 6.6 | 69 |
| 122 | Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020 , 32, 107908 | 10.6 | 68 |
| 121 | Alpha-2 macroglobulin in Alzheimer's disease: a marker of neuronal injury through the RCAN1 pathway. <i>Molecular Psychiatry</i> , 2017 , 22, 13-23 | 15.1 | 64 |
| 120 | Analysis of a membrane-enriched proteome from postmortem human brain tissue in Alzheimer's disease. <i>Proteomics - Clinical Applications</i> , 2012 , 6, 201-11 | 3.1 | 62 |
| 119 | Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017 , 12, 82 | 19 | 61 |
| 118 | Aggregates of small nuclear ribonucleic acids (snRNAs) in Alzheimer's disease. <i>Brain Pathology</i> , 2014 , 24, 344-51 | 6 | 57 |
| 117 | Neuron enriched nuclear proteome isolated from human brain. <i>Journal of Proteome Research</i> , 2013 , 12, 3193-206 | 5.6 | 52 |
| 116 | Quantitative analysis of the detergent-insoluble brain proteome in frontotemporal lobar degeneration using SILAC internal standards. <i>Journal of Proteome Research</i> , 2012 , 11, 2721-38 | 5.6 | 51 |
| 115 | Quantitative proteomics of acutely-isolated mouse microglia identifies novel immune Alzheimer's disease-related proteins. <i>Molecular Neurodegeneration</i> , 2018 , 13, 34 | 19 | 50 |
| 114 | Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA Splicing and Neurodegeneration in Alzheimer's Disease. <i>Cell Reports</i> , 2019 , 29, 301-316.e10 | 10.6 | 50 |
| 113 | Quantitative phosphoproteomics of Alzheimer's disease reveals cross-talk between kinases and small heat shock proteins. <i>Proteomics</i> , 2015 , 15, 508-519 | 4.8 | 48 |
| 112 | Steroidogenic factor-1 is a sphingolipid binding protein. <i>Molecular and Cellular Endocrinology</i> , 2007 , 265-266, 174-8 | 4.4 | 45 |
| 111 | Differential Phagocytic Properties of CD45 Microglia and CD45 Brain Mononuclear Phagocytes-Activation and Age-Related Effects. <i>Frontiers in Immunology</i> , 2018 , 9, 405 | 8.4 | 44 |
| 110 | Coregulator exchange and sphingosine-sensitive cooperativity of steroidogenic factor-1, general control nonderepressed 5, p54, and p160 coactivators regulate cyclic adenosine 3',5'-monophosphate-dependent cytochrome P450c17 transcription rate. <i>Molecular Endocrinology</i> , | | 44 |
| 109 | Proteomics of protein post-translational modifications implicated in neurodegeneration. Translational Neurodegeneration, 2014 , 3, 23 | 10.3 | 42 |
| 108 | Asparaginyl endopeptidase cleaves TDP-43 in brain. <i>Proteomics</i> , 2012 , 12, 2455-63 | 4.8 | 41 |

| 107 | Transcriptional regulation of adrenocortical steroidogenic gene expression. <i>Drug Metabolism Reviews</i> , 2007 , 39, 371-88 | 7 | 40 |
|-----|--|------|----|
| 106 | Changes in the detergent-insoluble brain proteome linked to amyloid and tau in Alzheimer's Disease progression. <i>Proteomics</i> , 2016 , 16, 3042-3053 | 4.8 | 39 |
| 105 | Integrated proteomics reveals brain-based cerebrospinal fluid biomarkers in asymptomatic and symptomatic Alzheimer's disease. <i>Science Advances</i> , 2020 , 6, | 14.3 | 36 |
| 104 | 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 | 36.3 | 36 |
| 103 | U1 small nuclear ribonucleoproteins (snRNPs) aggregate in Alzheimer's disease due to autosomal dominant genetic mutations and trisomy 21. <i>Molecular Neurodegeneration</i> , 2014 , 9, 15 | 19 | 34 |
| 102 | A systems pharmacology-based approach to identify novel Kv1.3 channel-dependent mechanisms in microglial activation. <i>Journal of Neuroinflammation</i> , 2017 , 14, 128 | 10.1 | 34 |
| 101 | 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 | 5.4 | 34 |
| 100 | Shared proteomic effects of cerebral atherosclerosis and Alzheimer's disease on the human brain. <i>Nature Neuroscience</i> , 2020 , 23, 696-700 | 25.5 | 33 |
| 99 | Molecular Signatures of Neuroinflammation Induced by Synuclein Aggregates in Microglial Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 33 | 8.4 | 31 |
| 98 | Peripheral Blood MicroRNA Expression Profiles in Alzheimer's Disease: Screening, Validation, Association with Clinical Phenotype and Implications for Molecular Mechanism. <i>Molecular Neurobiology</i> , 2016 , 53, 5772-81 | 6.2 | 31 |
| 97 | Effects of Genotype on Brain Proteomic Network and Cell Type Changes in Alzheimer's Disease. <i>Frontiers in Molecular Neuroscience</i> , 2018 , 11, 454 | 6.1 | 31 |
| 96 | Quantitative Analysis of the Brain Ubiquitylome in Alzheimer's Disease. <i>Proteomics</i> , 2018 , 18, e1800108 | 4.8 | 31 |
| 95 | Exploring the potential of the platelet membrane proteome as a source of peripheral biomarkers for Alzheimer's disease. <i>Alzheimer Research and Therapy</i> , 2013 , 5, 32 | 9 | 29 |
| 94 | 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 | 5.6 | 28 |
| 93 | Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020 , 11, 3942 | 17.4 | 28 |
| 92 | Quantitative proteomics reveals significant changes in cell shape and an energy shift after IPTG induction via an optimized SILAC approach for Escherichia coli. <i>Journal of Proteome Research</i> , 2013 , 12, 5978-88 | 5.6 | 26 |
| 91 | Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020 , 7, 340 | 8.2 | 26 |
| 90 | MicroRNA-146a represses LRP2 translation and leads to cell apoptosis in Alzheimer's disease. <i>FEBS Letters</i> , 2016 , 590, 2190-200 | 3.8 | 26 |

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| 89 | Novel mouse models of oculopharyngeal muscular dystrophy (OPMD) reveal early onset mitochondrial defects and suggest loss of PABPN1 may contribute to pathology. <i>Human Molecular Genetics</i> , 2017 , 26, 3235-3252 | 5.6 | 22 |
|----|--|------|----|
| 88 | Targeted mass spectrometry to quantify brain-derived cerebrospinal fluid biomarkers in Alzheimer's disease. <i>Clinical Proteomics</i> , 2020 , 17, 19 | 5 | 22 |
| 87 | Transcriptional regulation of homeostatic and disease-associated-microglial genes by IRF1, LXR☐ and CEBP∄ <i>Glia</i> , 2019 , 67, 1958-1975 | 9 | 22 |
| 86 | Abnormal gephyrin immunoreactivity associated with Alzheimer disease pathologic changes. <i>Journal of Neuropathology and Experimental Neurology</i> , 2013 , 72, 1009-15 | 3.1 | 22 |
| 85 | Resveratrol stimulates cortisol biosynthesis by activating SIRT-dependent deacetylation of P450scc. <i>Endocrinology</i> , 2012 , 153, 3258-68 | 4.8 | 22 |
| 84 | Phosphorylation of CtBP1 by cAMP-dependent protein kinase modulates induction of CYP17 by stimulating partnering of CtBP1 and 2. <i>Journal of Biological Chemistry</i> , 2008 , 283, 6925-34 | 5.4 | 22 |
| 83 | Identification of Conserved Proteomic Networks in Neurodegenerative Dementia. <i>Cell Reports</i> , 2020 , 31, 107807 | 10.6 | 21 |
| 82 | Tissue-type plasminogen activator mediates neuronal detection and adaptation to metabolic stress. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2013 , 33, 1761-9 | 7.3 | 20 |
| 81 | Biochemical isolation of myonuclei employed to define changes to the myonuclear proteome that occur with aging. <i>Aging Cell</i> , 2017 , 16, 738-749 | 9.9 | 19 |
| 80 | Osteopontin Is a Blood Biomarker for Microglial Activation and Brain Injury in Experimental Hypoxic-Ischemic Encephalopathy. <i>ENeuro</i> , 2017 , 4, | 3.9 | 19 |
| 79 | 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 , | 25.5 | 18 |
| 78 | Mutation profile of APP, PSEN1, and PSEN2 in Chinese familial Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019 , 77, 154-157 | 5.6 | 17 |
| 77 | Dysregulated Urinary Arginine Metabolism in Older Adults With Amnestic Mild Cognitive Impairment. <i>Frontiers in Aging Neuroscience</i> , 2019 , 11, 90 | 5.3 | 15 |
| 76 | Interactome Analysis Reveals Regulator of G Protein Signaling 14 (RGS14) is a Novel Calcium/Calmodulin (Ca/CaM) and CaM Kinase II (CaMKII) Binding Partner. <i>Journal of Proteome Research</i> , 2018 , 17, 1700-1711 | 5.6 | 15 |
| 75 | Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. <i>Molecular Cell</i> , 2019 , 76, 126-137.e7 | 17.6 | 15 |
| 74 | Meta-analysis of the human brain transcriptome identifies heterogeneity across human AD coexpression modules robust to sample collection and methodological approach | | 14 |
| 73 | Proteomic analysis of hippocampal dentate granule cells in frontotemporal lobar degeneration: application of laser capture technology. <i>Frontiers in Neurology</i> , 2011 , 2, 24 | 4.1 | 13 |
| 72 | 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 | 7.3 | 13 |

| 71 | Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021 , 24, 810-817 | 25.5 | 13 |
|----|--|-------|----|
| 70 | Network Analysis of a Membrane-Enriched Brain Proteome across Stages of Alzheimer's Disease. <i>Proteomes</i> , 2019 , 7, | 4.6 | 12 |
| 69 | cAMP-stimulated phosphorylation of diaphanous 1 regulates protein stability and interaction with binding partners in adrenocortical cells. <i>Molecular Biology of the Cell</i> , 2013 , 24, 848-57 | 3.5 | 12 |
| 68 | The lncRNA Growth Arrest Specific 5 Regulates Cell Survival via Distinct Structural Modules with Independent Functions. <i>Cell Reports</i> , 2020 , 32, 107933 | 10.6 | 12 |
| 67 | 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 | 19 | 11 |
| 66 | Integrated Proteomics Reveals Brain-Based Cerebrospinal Fluid Biomarkers in Asymptomatic and Symptomatic Alzheimer Disease | | 11 |
| 65 | Extracellular signal-regulated kinase regulates microglial immune responses in Alzheimer's disease. <i>Journal of Neuroscience Research</i> , 2021 , 99, 1704-1721 | 4.4 | 11 |
| 64 | Characterization of Detergent Insoluble Proteome in Chronic Traumatic Encephalopathy. <i>Journal of Neuropathology and Experimental Neurology</i> , 2018 , 77, 40-49 | 3.1 | 10 |
| 63 | Transcriptome Network Analysis Identifies CXCL13-CXCR5 Signaling Modules in the Prostate Tumor Immune Microenvironment. <i>Scientific Reports</i> , 2019 , 9, 14963 | 4.9 | 10 |
| 62 | Protein profiling of active cysteine cathepsins in living cells using an activity-based probe containing a cell-penetrating peptide. <i>Journal of Proteome Research</i> , 2012 , 11, 5763-72 | 5.6 | 10 |
| 61 | 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 | 5.6 | 9 |
| 60 | Consequences of impaired purine recycling on the proteome in a cellular model of Lesch-Nyhan disease. <i>Molecular Genetics and Metabolism</i> , 2015 , 114, 570-579 | 3.7 | 9 |
| 59 | Activation of dopamine receptor D1 inhibits glioblastoma tumorigenicity by regulating autophagic activity. <i>Cellular Oncology (Dordrecht)</i> , 2020 , 43, 1175-1190 | 7.2 | 9 |
| 58 | Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. <i>Alzheimer</i> and Dementia, 2021 , 17, 984-1004 | 1.2 | 9 |
| 57 | 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 | 13.9 | 9 |
| 56 | Pseudomonas aeruginosa EftM Is a Thermoregulated Methyltransferase. <i>Journal of Biological Chemistry</i> , 2016 , 291, 3280-90 | 5.4 | 8 |
| 55 | Ionizing Radiation induction of cholesterol biosynthesis in Lung tissue. Scientific Reports, 2019, 9, 1254 | 6 4.9 | 7 |
| 54 | Microglial ERK signaling is a critical regulator of pro-inflammatory immune responses in Alzheimer dis | ease | 7 |

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| 53 | 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 | 5.6 | 6 |
|----|--|------|---|
| 52 | Expression, purification and proteomic analysis of recombinant histone H4 acetylated at lysine 16. <i>Proteomics</i> , 2013 , 13, 1687-91 | 4.8 | 6 |
| 51 | Integrated analysis of the aging brain transcriptome and proteome in tauopathy. <i>Molecular Neurodegeneration</i> , 2020 , 15, 56 | 19 | 6 |
| 50 | Unique molecular characteristics and microglial origin of Kv1.3 channel-positive brain myeloid cells in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118, | 11.5 | 6 |
| 49 | Genetic control of the human brain proteome | | 5 |
| 48 | Association of plasma and CSF cytochrome P450, soluble epoxide hydrolase, and ethanolamide metabolism with Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2021 , 13, 149 | 9 | 5 |
| 47 | Comparative proteomic analysis highlights metabolic dysfunction in Bynucleinopathy. <i>Npj Parkinson Disease</i> , 2020 , 6, 40 | 9.7 | 4 |
| 46 | Multiple Signaling Pathways Coordinate CYP17 Gene Expression in the Human Adrenal Cortex. <i>Acta Chimica Slovenica</i> , 2008 , 55, 53-57 | 1.9 | 4 |
| 45 | Multiscale causal network models of Alzheimer∃ disease identify VGF as a key regulator of disease | | 4 |
| 44 | Genetic control of the human brain proteome. American Journal of Human Genetics, 2021, 108, 400-410 | 11 | 4 |
| 43 | At the crossroads of ubiquitin signaling and mass spectrometry. <i>Expert Review of Proteomics</i> , 2010 , 7, 643-5 | 4.2 | 3 |
| 42 | Cerebral atherosclerosis contributes to Alzheimer\(\mathbf{B}\) dementia independently of its hallmark amyloid and tau pathologies | | 3 |
| 41 | Mass-Spectrometry-Based Near-Complete Draft of the Proteome. <i>Journal of Proteome Research</i> , 2021 , 20, 1328-1340 | 5.6 | 3 |
| 40 | microRNA-425 loss mediates amyloid plaque microenvironment heterogeneity and promotes neurodegenerative pathologies. <i>Aging Cell</i> , 2021 , 20, e13454 | 9.9 | 3 |
| 39 | Insights into the changes in the proteome of Alzheimer disease elucidated by a meta-analysis. <i>Scientific Data</i> , 2021 , 8, 312 | 8.2 | 2 |
| 38 | Identification of conserved proteomic networks in neurodegenerative dementia | | 2 |
| 37 | TBK1 interacts with tau and enhances neurodegeneration in tauopathy. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100760 | 5.4 | 2 |
| 36 | Targeted Quantification of Detergent-Insoluble RNA-Binding Proteins in Human Brain Reveals Stage and Disease Specific Co-aggregation in Alzheimer's Disease. <i>Frontiers in Molecular Neuroscience</i> , 2021 , 14, 623659 | 6.1 | 2 |

| 35 | Association between Alzheimer's disease and risk of cancer: A retrospective cohort study in Shanghai, China. <i>Alzheimer</i> and <i>Dementia</i> , 2021 , | 1.2 | 2 |
|----|--|------|---|
| 34 | Integrating human brain proteomes and genome-wide association results implicates new genes in Alzheimer disease. <i>Alzheimer</i> and <i>Dementia</i> , 2020 , 16, e043865 | 1.2 | 1 |
| 33 | Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA-Splicing and Neurodegeneration in Alzheimer's Disease. <i>SSRN Electronic Journal</i> , | 1 | 1 |
| 32 | RNA-binding proteins with mixed charge domains self-assemble and aggregate in Alzheimer Disease | | 1 |
| 31 | Tau-mediated Disruption of the Spliceosome Triggers Cryptic RNA-splicing and Neurodegeneration in Alzheimer∄ Disease | | 1 |
| 30 | A Consensus Proteomic Analysis of Alzheimer Disease Brain and Cerebrospinal Fluid Reveals Early Changes in Energy Metabolism Associated with Microglia and Astrocyte Activation | | 1 |
| 29 | Flow-cytometric microglial sorting coupled with quantitative proteomics identifies moesin as a highly-abundant microglial protein with relevance to Alzheimer disease | | 1 |
| 28 | 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 | 5.6 | 1 |
| 27 | A network approach reveals driver genes associated with survival of patients with triple-negative breast cancer. <i>IScience</i> , 2021 , 24, 102451 | 6.1 | 1 |
| 26 | A proteomic network approach resolves stage-specific molecular phenotypes in chronic traumatic encephalopathy. <i>Molecular Neurodegeneration</i> , 2021 , 16, 40 | 19 | 1 |
| 25 | Multivariate transcriptome analysis identifies networks and key drivers of chronic lymphocytic leukemia relapse risk and patient survival. <i>BMC Medical Genomics</i> , 2021 , 14, 171 | 3.7 | 1 |
| 24 | Quantitative proteomic analysis of the lysine acetylome reveals diverse SIRT2 substrates <i>Scientific Reports</i> , 2022 , 12, 3822 | 4.9 | 1 |
| 23 | 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 and Dementia</i> , 2021 , 17 Suppl 3, e055041 | 1.2 | 1 |
| 22 | Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021 , 12, 7035 | 17.4 | O |
| 21 | Phosphorylation regulates arginine-rich RNA-binding protein solubility and oligomerization. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101306 | 5.4 | 0 |
| 20 | Adult-Onset Neuronal Ceroid Lipofuscinosis With a Novel Mutation Exhibits Aberrant Protein Palmitoylation <i>Frontiers in Aging Neuroscience</i> , 2022 , 14, 829573 | 5.3 | O |
| 19 | A consensus proteomic analysis of Alzheimer disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Alzheimer and Dementia</i> , 2020 , 16, e039504 | 1.2 | |
| 18 | Proteomics identifies CSF biomarker panels reflective of pathological networks in the Alzheimer's disease brain. <i>Alzheimer</i> and <i>Dementia</i> , 2020 , 16, e042227 | 1.2 | |

LIST OF PUBLICATIONS

| 17 | Network analysis of the brain proteome of GRN knockout mice reveals pathogenic mechanisms shared in human frontotemporal dementia caused by GRN mutations. <i>Alzheimeros and Dementia</i> , 2020 , 16, e047569 | 1.2 |
|----|--|--------|
| 16 | O5-06-02: Proteomic Network Analysis to Find Common Mechanisms Underlying Alzheimer's Disease and PD 2016 , 12, P390-P391 | |
| 15 | F2-01-03: Discovery of Novel Proteomic Targets for Treatment of Alzheimer's Disease 2016 , 12, P215-P | 215 |
| 14 | [O2Ū3Ū1]: PROTEIN CO-EXPRESSION NETWORK ANALYSIS IN ASYMPTOMATIC AND SYMPTOMATIC ALZHEIMER'S DISEASE 2017 , 13, P554-P555 | |
| 13 | O4-12-02: Protein co-expression network analysis in Alzheimer's disease 2015 , 11, P299-P299 | |
| 12 | O4-12-03: Brain phosphoproteome network analysis discriminates Alzheimer's disease from other tauopathies 2015 , 11, P300-P300 | |
| 11 | Molecular signatures of neuroinflammation induced by Bynuclein aggregates in microglial cells. <i>FASEB Journal</i> , 2020 , 34, 1-1 | 0.9 |
| 10 | Temporal Analysis of Steroidogenic Factor-1 Binding to the human CYP17 Promoter: Roles of Ligand Binding, Coactivator Recruitment, and Phosphorylation. <i>FASEB Journal</i> , 2006 , 20, A969 | 0.9 |
| 9 | Post-Translational Regulation of Mitochondrial Steroidogenic Cytochrome P450s by NAD+-Dependent SIRT Deacetylases. <i>FASEB Journal</i> , 2008 , 22, 633.4 | 0.9 |
| 8 | Phosphorylation of CtBP1 by PKA Induces CYP17 by Promoting CtBP Heterooligomerization. <i>FASEB Journal</i> , 2008 , 22, 1016.1 | 0.9 |
| 7 | Proteomic analysis of the poly-ubiquitin profiles in Alzheimer's Disease. FASEB Journal, 2019, 33, 465.7 | 0.9 |
| 6 | P2-294: The Acute Phase Protein Alpha-2-Macroglobulin Predicts Risk of Incident Alzheimer's Disease and Modulates TAU Pathology through the RCAN1-Calcineurin Pathway 2016 , 12, P745-P745 | |
| 5 | INTEGRATIVE PROTEOMICS LINKS CEREBROSPINAL FLUID BIOMARKERS TO PATHOLOGICAL NETWORKS IN THE ALZHEIMER® DISEASE BRAIN 2019 , 15, P191 | |
| 4 | O2-01-01: A TRANSCRIPTOMIC LANDSCAPE OF MICROGLIAL ACTIVATION IN ALZHEIMER'S DISEASE 2018 , 14, P608-P608 | |
| 3 | P2-217: INTEGRATED PROTEOMICS AND PHOSPHOPROTEOMICS REVEAL NETWORKS LINKED TO ALZHEIMER'S DISEASE RISK 2018 , 14, P752-P752 | |
| 2 | P3-191: COMPREHENSIVE MAPPING OF ALZHEIMER'S DISEASE BRAIN UBIQUITYLOME 2018 , 14, P1140 | -P1140 |
| 1 | O2-02-05: RNA-BINDING PROTEINS WITH MIXED CHARGE DOMAINS SELF-ASSEMBLE AND AGGREGATE IN ALZHEIMER'S DISEASE 2018 , 14, P612-P612 | |