

Eric B Dammer

List of Publications by Year in Descending Order

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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	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
141	Quantitative proteomic analysis of the lysine acetylome reveals diverse SIRT2 substrates.. <i>Scientific Reports</i> , 2022 , 12, 3822	4.9	1
140	Adult-Onset Neuronal Ceroid Lipofuscinosis With a Novel Mutation Exhibits Aberrant Protein Palmitoylation.. <i>Frontiers in Aging Neuroscience</i> , 2022 , 14, 829573	5.3	0
139	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	0
138	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
137	Phosphorylation regulates arginine-rich RNA-binding protein solubility and oligomerization. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101306	5.4	0
136	Genetic control of the human brain proteome. <i>American Journal of Human Genetics</i> , 2021 , 108, 400-410	11	4
135	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
134	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
133	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021 , 24, 810-817	25.5	13
132	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
131	A proteomic network approach resolves stage-specific molecular phenotypes in chronic traumatic encephalopathy. <i>Molecular Neurodegeneration</i> , 2021 , 16, 40	19	1
130	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
129	Mass-Spectrometry-Based Near-Complete Draft of the Proteome. <i>Journal of Proteome Research</i> , 2021 , 20, 1328-1340	5.6	3
128	TBK1 interacts with tau and enhances neurodegeneration in tauopathy. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100760	5.4	2
127	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	1.2	9
126	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

125	microRNA-425 loss mediates amyloid plaque microenvironment heterogeneity and promotes neurodegenerative pathologies. <i>Aging Cell</i> , 2021 , 20, e13454	9.9	3
124	Association between Alzheimer's disease and risk of cancer: A retrospective cohort study in Shanghai, China. <i>Alzheimer's and Dementia</i> , 2021 ,	1.2	2
123	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
122	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
121	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
120	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 Suppl 3, e055041	1.2	1
119	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	1.2	
118	Proteomics identifies CSF biomarker panels reflective of pathological networks in the Alzheimer's disease brain. <i>Alzheimer's and Dementia</i> , 2020 , 16, e042227	1.2	
117	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	1.2	1
116	Network analysis of the brain proteome of GRN knockout mice reveals pathogenic mechanisms shared in human frontotemporal dementia caused by GRN mutations. <i>Alzheimer's and Dementia</i> , 2020 , 16, e047569	1.2	
115	Comparative proteomic analysis highlights metabolic dysfunction in Synucleinopathy. <i>Npj Parkinson's Disease</i> , 2020 , 6, 40	9.7	4
114	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
113	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
112	Targeted mass spectrometry to quantify brain-derived cerebrospinal fluid biomarkers in Alzheimer's disease. <i>Clinical Proteomics</i> , 2020 , 17, 19	5	22
111	Identification of Conserved Proteomic Networks in Neurodegenerative Dementia. <i>Cell Reports</i> , 2020 , 31, 107807	10.6	21
110	Molecular Signatures of Neuroinflammation Induced by Synuclein Aggregates in Microglial Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 33	8.4	31
109	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
108	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

107	Molecular signatures of neuroinflammation induced by β -synuclein aggregates in microglial cells. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	
106	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
105	Integrated analysis of the aging brain transcriptome and proteome in tauopathy. <i>Molecular Neurodegeneration</i> , 2020 , 15, 56	19	6
104	Integrated proteomics reveals brain-based cerebrospinal fluid biomarkers in asymptomatic and symptomatic Alzheimer's disease. <i>Science Advances</i> , 2020 , 6,	14.3	36
103	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
102	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020 , 7, 340	8.2	26
101	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
100	Activation of dopamine receptor D1 inhibits glioblastoma tumorigenicity by regulating autophagic activity. <i>Cellular Oncology (Dordrecht)</i> , 2020 , 43, 1175-1190	7.2	9
99	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020 , 11, 3942	17.4	28
98	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
97	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
96	Ionizing Radiation induction of cholesterol biosynthesis in Lung tissue. <i>Scientific Reports</i> , 2019 , 9, 12546	4.9	7
95	Network Analysis of a Membrane-Enriched Brain Proteome across Stages of Alzheimer's Disease. <i>Proteomes</i> , 2019 , 7,	4.6	12
94	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
93	Dysregulated Urinary Arginine Metabolism in Older Adults With Amnesic Mild Cognitive Impairment. <i>Frontiers in Aging Neuroscience</i> , 2019 , 11, 90	5.3	15
92	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
91	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
90	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. <i>Molecular Cell</i> , 2019 , 76, 126-137.e7	17.6	15

89	Transcriptional regulation of homeostatic and disease-associated-microglial genes by IRF1, LXR β and CEBP β <i>Glia</i> , 2019 , 67, 1958-1975	9	22
88	Transcriptome Network Analysis Identifies CXCL13-CXCR5 Signaling Modules in the Prostate Tumor Immune Microenvironment. <i>Scientific Reports</i> , 2019 , 9, 14963	4.9	10
87	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
86	Proteomic analysis of the poly-ubiquitin profiles in Alzheimer's Disease. <i>FASEB Journal</i> , 2019 , 33, 465.7	0.9	
85	INTEGRATIVE PROTEOMICS LINKS CEREBROSPINAL FLUID BIOMARKERS TO PATHOLOGICAL NETWORKS IN THE ALZHEIMER'S DISEASE BRAIN 2019 , 15, P191		
84	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
83	Characterization of Detergent Insoluble Proteome in Chronic Traumatic Encephalopathy. <i>Journal of Neuropathology and Experimental Neurology</i> , 2018 , 77, 40-49	3.1	10
82	Evidence for brain glucose dysregulation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2018 , 14, 318-329	1.2	161
81	Quantitative proteomics of acutely-isolated mouse microglia identifies novel immune Alzheimer's disease-related proteins. <i>Molecular Neurodegeneration</i> , 2018 , 13, 34	19	50
80	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
79	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
78	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
77	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
76	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. <i>Alzheimer's and Dementia</i> , 2018 , 14, 352-366	1.2	72
75	O2-01-01: A TRANSCRIPTOMIC LANDSCAPE OF MICROGLIAL ACTIVATION IN ALZHEIMER'S DISEASE 2018 , 14, P608-P608		
74	P2-217: INTEGRATED PROTEOMICS AND PHOSPHOPROTEOMICS REVEAL NETWORKS LINKED TO ALZHEIMER'S DISEASE RISK 2018 , 14, P752-P752		
73	P3-191: COMPREHENSIVE MAPPING OF ALZHEIMER'S DISEASE BRAIN UBIQUITYLOME 2018 , 14, P1140-P1140		
72	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

71	O2-02-05: RNA-BINDING PROTEINS WITH MIXED CHARGE DOMAINS SELF-ASSEMBLE AND AGGREGATE IN ALZHEIMER'S DISEASE 2018 , 14, P612-P612		
70	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
69	Quantitative Analysis of the Brain Ubiquitylome in Alzheimer's Disease. <i>Proteomics</i> , 2018 , 18, e1800108	4.8	31
68	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
67	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
66	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
65	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
64	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017 , 12, 82	19	61
63	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
62	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
61	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
60	[O20301]: PROTEIN CO-EXPRESSION NETWORK ANALYSIS IN ASYMPTOMATIC AND SYMPTOMATIC ALZHEIMER'S DISEASE 2017 , 13, P554-P555		
59	Osteopontin Is a Blood Biomarker for Microglial Activation and Brain Injury in Experimental Hypoxic-Ischemic Encephalopathy. <i>ENeuro</i> , 2017 , 4,	3.9	19
58	O5-06-02: Proteomic Network Analysis to Find Common Mechanisms Underlying Alzheimer's Disease and PD 2016 , 12, P390-P391		
57	F2-01-03: Discovery of Novel Proteomic Targets for Treatment of Alzheimer's Disease 2016 , 12, P215-P215		
56	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
55	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
54	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		

53	<i>Pseudomonas aeruginosa</i> EftM Is a Thermoregulated Methyltransferase. <i>Journal of Biological Chemistry</i> , 2016 , 291, 3280-90	5.4	8
52	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
51	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
50	The endosomal-lysosomal system: from acidification and cargo sorting to neurodegeneration. <i>Translational Neurodegeneration</i> , 2015 , 4, 18	10.3	269
49	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
48	O4-12-02: Protein co-expression network analysis in Alzheimer's disease 2015 , 11, P299-P299		
47	O4-12-03: Brain phosphoproteome network analysis discriminates Alzheimer's disease from other tauopathies 2015 , 11, P300-P300		
46	Melatonin for sleep disorders and cognition in dementia: a meta-analysis of randomized controlled trials. <i>American Journal of Alzheimer's Disease and Other Dementias</i> , 2015 , 30, 439-47	2.5	76
45	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
44	Aggregates of small nuclear ribonucleic acids (snRNAs) in Alzheimer's disease. <i>Brain Pathology</i> , 2014 , 24, 344-51	6	57
43	Proteomics of protein post-translational modifications implicated in neurodegeneration. <i>Translational Neurodegeneration</i> , 2014 , 3, 23	10.3	42
42	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
41	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, 5978-88	5.6	26
40	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
39	The cotranslational function of ribosome-associated Hsp70 in eukaryotic protein homeostasis. <i>Cell</i> , 2013 , 152, 196-209	56.2	177
38	Expression, purification and proteomic analysis of recombinant histone H4 acetylated at lysine 16. <i>Proteomics</i> , 2013 , 13, 1687-91	4.8	6
37	Neuron enriched nuclear proteome isolated from human brain. <i>Journal of Proteome Research</i> , 2013 , 12, 3193-206	5.6	52
36	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

35	Abnormal gephyrin immunoreactivity associated with Alzheimer disease pathologic changes. <i>Journal of Neuropathology and Experimental Neurology</i> , 2013 , 72, 1009-15	3.1	22
34	Exploring the potential of the platelet membrane proteome as a source of peripheral biomarkers for Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2013 , 5, 32	9	29
33	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
32	Tissue-type plasminogen activator regulates the neuronal uptake of glucose in the ischemic brain. <i>Journal of Neuroscience</i> , 2012 , 32, 9848-58	6.6	69
31	Asparaginyl endopeptidase cleaves TDP-43 in brain. <i>Proteomics</i> , 2012 , 12, 2455-63	4.8	41
30	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
29	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
28	Resveratrol stimulates cortisol biosynthesis by activating SIRT-dependent deacetylation of P450 _{sc} . <i>Endocrinology</i> , 2012 , 153, 3258-68	4.8	22
27	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
26	Identification of neuronal RNA targets of TDP-43-containing ribonucleoprotein complexes. <i>Journal of Biological Chemistry</i> , 2011 , 286, 1204-15	5.4	306
25	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
24	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
23	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
22	At the crossroads of ubiquitin signaling and mass spectrometry. <i>Expert Review of Proteomics</i> , 2010 , 7, 643-5	4.2	3
21	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
20	Multiple Signaling Pathways Coordinate CYP17 Gene Expression in the Human Adrenal Cortex. <i>Acta Chimica Slovenica</i> , 2008 , 55, 53-57	1.9	4
19	Post-Translational Regulation of Mitochondrial Steroidogenic Cytochrome P450s by NAD ⁺ -Dependent SIRT Deacetylases. <i>FASEB Journal</i> , 2008 , 22, 633.4	0.9	
18	Phosphorylation of CtBP1 by PKA Induces CYP17 by Promoting CtBP Heterooligomerization. <i>FASEB Journal</i> , 2008 , 22, 1016.1	0.9	

17	Transcriptional regulation of adrenocortical steroidogenic gene expression. <i>Drug Metabolism Reviews</i> , 2007 , 39, 371-88	7	40
16	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> , 2007 , 21, 415-38		44
15	Steroidogenic factor-1 is a sphingolipid binding protein. <i>Molecular and Cellular Endocrinology</i> , 2007 , 265-266, 174-8	4.4	45
14	Sphingosine regulates the transcription of CYP17 by binding to steroidogenic factor-1. <i>Endocrinology</i> , 2006 , 147, 5249-58	4.8	70
13	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	
12	Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA-Splicing and Neurodegeneration in Alzheimer's Disease. <i>SSRN Electronic Journal</i> ,	1	1
11	RNA-binding proteins with mixed charge domains self-assemble and aggregate in Alzheimer's Disease		1
10	Tau-mediated Disruption of the Spliceosome Triggers Cryptic RNA-splicing and Neurodegeneration in Alzheimer's Disease		1
9	A Consensus Proteomic Analysis of Alzheimer's Disease Brain and Cerebrospinal Fluid Reveals Early Changes in Energy Metabolism Associated with Microglia and Astrocyte Activation		1
8	Multiscale causal network models of Alzheimer's disease identify VGF as a key regulator of disease		4
7	Meta-analysis of the human brain transcriptome identifies heterogeneity across human AD coexpression modules robust to sample collection and methodological approach		14
6	Cerebral atherosclerosis contributes to Alzheimer's dementia independently of its hallmark amyloid and tau pathologies		3
5	Microglial ERK signaling is a critical regulator of pro-inflammatory immune responses in Alzheimer's disease	7	
4	Flow-cytometric microglial sorting coupled with quantitative proteomics identifies moesin as a highly-abundant microglial protein with relevance to Alzheimer's disease		1
3	Integrated Proteomics Reveals Brain-Based Cerebrospinal Fluid Biomarkers in Asymptomatic and Symptomatic Alzheimer's Disease		11
2	Genetic control of the human brain proteome		5
1	Identification of conserved proteomic networks in neurodegenerative dementia		2