Mark Collins

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Proximity-dependent biotin identification (BioID) reveals a dynamic LSD1–CoREST interactome during embryonic stem cell differentiation. Molecular Omics, 2022, 18, 31-44.	2.8	11
2	Transcriptional programs regulating neuronal differentiation are disrupted in DLG2 knockout human embryonic stem cells and enriched for schizophrenia and related disorders risk variants. Nature Communications, 2022, 13, 27.	12.8	8
3	Developmental disruption to the cortical transcriptome and synaptosome in a model of <i>SETD1A</i> loss-of-function. Human Molecular Genetics, 2022, 31, 3095-3106.	2.9	5
4	Altered subgenomic RNA abundance provides unique insight into SARS-CoV-2 B.1.1.7/Alpha variant infections. Communications Biology, 2022, 5, .	4.4	12
5	Proteomic Approaches to Study Cysteine Oxidation: Applications in Neurodegenerative Diseases. Frontiers in Molecular Neuroscience, 2021, 14, 678837.	2.9	10
6	PGFinder, a novel analysis pipeline for the consistent, reproducible, and high-resolution structural analysis of bacterial peptidoglycans. ELife, 2021, 10, .	6.0	6
7	Regulation and function of the palmitoylâ€acyltransferase ZDHHC5. FEBS Journal, 2021, 288, 6623-6634.	4.7	16
8	Cellâ€ŧypeâ€specific visualisation and biochemical isolation of endogenous synaptic proteins in mice. European Journal of Neuroscience, 2020, 51, 793-805.	2.6	18
9	Sâ€acylated Golga7b stabilises <scp>DHHC</scp> 5 at the plasma membrane to regulate cell adhesion. EMBO Reports, 2019, 20, e47472.	4.5	46
10	Apoptotic signalling targets the post-endocytic sorting machinery of the death receptor Fas/CD95. Nature Communications, 2019, 10, 3105.	12.8	20
11	Proteomic Profiling, Transcription Factor Modeling, and Genomics of Evolved Tolerant Strains Elucidate Mechanisms of Vanillin Toxicity in Escherichia coli. MSystems, 2019, 4, .	3.8	28
12	Quantitative Analysis of Protein S-Acylation Site Dynamics Using Site-Specific Acyl-Biotin Exchange (ssABE). Methods in Molecular Biology, 2019, 1977, 71-82.	0.9	4
13	S-acylation regulates the trafficking and stability of the unconventional Q-SNARE STX19. Journal of Cell Science, 2018, 131, .	2.0	8
14	Inhibition of somatosensory mechanotransduction by annexin A6. Science Signaling, 2018, 11, .	3.6	10
15	TBK1: a new player in ALS linking autophagy and neuroinflammation. Molecular Brain, 2017, 10, 5.	2.6	228
16	Evolution of complexity in the zebrafish synapse proteome. Nature Communications, 2017, 8, 14613.	12.8	112
17	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. Cell Reports, 2017, 21, 679-691.	6.4	79
18	Site Specific Modification of Adeno-Associated Virus Enables Both Fluorescent Imaging of Viral Particles and Characterization of the Capsid Interactome. Scientific Reports, 2017, 7, 14766.	3.3	15

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19	Global, site-specific analysis of neuronal protein S-acylation. Scientific Reports, 2017, 7, 4683.	3.3	80
20	Phosphoinositide Metabolism Links cGMP-Dependent Protein Kinase G to Essential Ca2+ Signals at Key Decision Points in the Life Cycle of Malaria Parasites. PLoS Biology, 2014, 12, e1001806.	5.6	185
21	Human post-mortem synapse proteome integrity screening for proteomic studies of postsynaptic complexes. Molecular Brain, 2014, 7, 88.	2.6	49
22	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	27.8	1,305
23	AMPA Receptor Complex Dynamics in Time and Space. Neuron, 2014, 84, 1-3.	8.1	22
24	Confident and sensitive phosphoproteomics using combinations of collision induced dissociation and electron transfer dissociation. Journal of Proteomics, 2014, 103, 1-14.	2.4	34
25	Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. Molecular and Cellular Proteomics, 2012, 11, 478-491.	3.8	34
26	A Plasmodium Calcium-Dependent Protein Kinase Controls Zygote Development and Transmission by Translationally Activating Repressed mRNAs. Cell Host and Microbe, 2012, 12, 9-19.	11.0	163
27	Analysis of Protein Palmitoylation Reveals a Pervasive Role in Plasmodium Development and Pathogenesis. Cell Host and Microbe, 2012, 12, 246-258.	11.0	177
28	SynGAP isoforms exert opposing effects on synaptic strength. Nature Communications, 2012, 3, 900.	12.8	65
29	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. Molecular Psychiatry, 2012, 17, 142-153.	7.9	775
30	Comparative Study of Human and Mouse Postsynaptic Proteomes Finds High Compositional Conservation and Abundance Differences for Key Synaptic Proteins. PLoS ONE, 2012, 7, e46683.	2.5	179
31	APC15 drives the turnover of MCC-CDC20 to make the spindle assembly checkpoint responsive to kinetochore attachment. Nature Cell Biology, 2011, 13, 1234-1243.	10.3	139
32	Quantitative Proteomics Reveals the Basis for the Biochemical Specificity of the Cell-Cycle Machinery. Molecular Cell, 2011, 43, 406-417.	9.7	127
33	Characterization of the proteome, diseases and evolution of the human postsynaptic density. Nature Neuroscience, 2011, 14, 19-21.	14.8	449
34	Coordinating cell cycle progression via cyclin specificity. Cell Cycle, 2011, 10, 4195-4196.	2.6	6
35	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and "resurrected―pseudogenes in the mouse genome. Genome Research, 2011, 21, 756-767.	5.5	113
36	A comprehensive survey of protein palmitoylation in late blood-stage Plasmodium falciparum. Malaria Journal, 2010, 9, .	2.3	1

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37	A comprehensive survey of protein palmitoylation in late blood-stage Plasmodium falciparum. Malaria Journal, 2010, 9, .	2.3	1
38	Targeted tandem affinity purification of PSDâ€95 recovers core postsynaptic complexes and schizophrenia susceptibility proteins. Molecular Systems Biology, 2009, 5, 269.	7.2	245
39	Neurotransmitters Drive Combinatorial Multistate Postsynaptic Density Networks. Science Signaling, 2009, 2, ra19.	3.6	116
40	Evolving Cell Signals. Science, 2009, 325, 1635-1636.	12.6	10
41	Mapping multiprotein complexes by affinity purification and mass spectrometry. Current Opinion in Biotechnology, 2008, 19, 324-330.	6.6	118
42	Evolutionary expansion and anatomical specialization of synapse proteome complexity. Nature Neuroscience, 2008, 11, 799-806.	14.8	171
43	Phosphoproteomic Analysis of the Mouse Brain Cytosol Reveals a Predominance of Protein Phosphorylation in Regions of Intrinsic Sequence Disorder. Molecular and Cellular Proteomics, 2008, 7, 1331-1348.	3.8	157
44	Analysis of protein phosphorylation on a proteomeâ€scale. Proteomics, 2007, 7, 2751-2768.	2.2	153
45	Supramolecular Signalling Complexes in the Nervous System. , 2007, 43, 185-207.		22
46	Molecular characterization and comparison of the components and multiprotein complexes in the postsynaptic proteome. Journal of Neurochemistry, 2006, 97, 16-23.	3.9	397
47	Robust Enrichment of Phosphorylated Species in Complex Mixtures by Sequential Protein and Peptide Metal-Affinity Chromatography and Analysis by Tandem Mass Spectrometry. Science Signaling, 2005, 2005, pl6-pl6.	3.6	25
48	Proteomic Analysis of in Vivo Phosphorylated Synaptic Proteins. Journal of Biological Chemistry, 2005, 280, 5972-5982.	3.4	300
49	Polymorphisms in tumour necrosis factorâ€Î±, transforming growth factorâ€Î², interleukinâ€10, interleukinâ€6, interferonâ€Î³, and outcome of hepatitis C virus infection. Journal of Medical Virology, 2003, 71, 212-218.	5.0	112
50	Analysis protein complexes by 1D-SDS-PAGE and tandem mass spectrometry. Protocol Exchange, 0, , .	0.3	5