Thomas M Wishart

List of Publications by Year
in descending order

42	1,976	304743	302126
papers	citations	22 h-index	39 g-index

46	46	46	2959
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Training associated alterations in equine respiratory immunity using a multiomics comparative approach. Scientific Reports, 2022, 12, 427.	3.3	4
2	The mitochondrial protein Sideroflexin 3 (SFXN3) influences neurodegeneration pathways inÂvivo. FEBS Journal, 2022, 289, 3894-3914.	4.7	2
3	SMN Depleted Mice Offer a Robust and Rapid Onset Model of Nonalcoholic Fatty Liver Disease. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 354-377.e3.	4.5	16
4	Microarray profiling emphasizes transcriptomic differences between hippocampal in vivo tissue and in vitro cultures. Brain Communications, 2021, 3, fcab152.	3.3	0
5	Application across species of a one health approach to liquid sample handling for respiratory based -omics analysis. Scientific Reports, 2021, 11, 14292.	3.3	3
6	Confocal Endomicroscopy of Neuromuscular Junctions Stained with Physiologically Inert Protein Fragments of Tetanus Toxin. Biomolecules, 2021, 11, 1499.	4.0	0
7	Temporal Profiling of the Cortical Synaptic Mitochondrial Proteome Identifies Ageing Associated Regulators of Stability. Cells, 2021, 10, 3403.	4.1	0
8	Applying modern Omic technologies to the Neuronal Ceroid Lipofuscinoses. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165498.	3.8	17
9	Collateral Sprouting of Peripheral Sensory Neurons Exhibits a Unique Transcriptomic Profile. Molecular Neurobiology, 2020, 57, 4232-4249.	4.0	13
10	Comparative proteomic profiling reveals mechanisms for early spinal cord vulnerability in CLN1 disease. Scientific Reports, 2020, 10, 15157.	3.3	10
11	Pre-natal manifestation of systemic developmental abnormalities in spinal muscular atrophy. Human Molecular Genetics, 2020, 29, 2674-2683.	2.9	23
12	Altered mitochondrial bioenergetics are responsible for the delay in Wallerian degeneration observed in neonatal mice. Neurobiology of Disease, 2019, 130, 104496.	4.4	15
13	Regional Molecular Mapping of Primate Synapses during Normal Healthy Aging. Cell Reports, 2019, 27, 1018-1026.e4.	6.4	20
14	Comparative profiling of the synaptic proteome from Alzheimerâ€™s disease patients with focus on the APOE genotype. Acta Neuropathologica Communications, 2019, 7, 214.	5.2	63
15	Sideroflexin 3 is a Î±-synuclein-dependent mitochondrial protein that regulates synaptic morphology. Journal of Cell Science, 2017, 130, 325-331.	2.0	19
16	Proteomic mapping of differentially vulnerable pre-synaptic populations identifies regulators of neuronal stability in vivo. Scientific Reports, 2017, 7, 12412.	3.3	34
17	Cellular and Molecular Anatomy of the Human Neuromuscular Junction. Cell Reports, 2017, 21, 2348-2356.	6.4	158
18	Molecular analysis of axonal-intrinsic and glial-associated co-regulation of axon degeneration. Cell Death and Disease, 2017, 8, e3166-e3166.	6.3	41

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19	Proteomic profiling of neuronal mitochondria reveals modulators of synaptic architecture. Molecular Neurodegeneration, 2017, 12, 77.	10.8	43
20	Bioenergetic status modulates motor neuron vulnerability and pathogenesis in a zebrafish model of spinal muscular atrophy. PLoS Genetics, 2017, 13, e1006744.	3.5	69
21	Systemic restoration of UBA1 ameliorates disease in spinal muscular atrophy. JCI Insight, 2016, 1, e87908.	5.0	65
22	Commonality amid diversity: Multi-study proteomic identification of conserved disease mechanisms in spinal muscular atrophy. Neuromuscular Disorders, 2016, 26, 560-569.	0.6	30
23	Quantitative imaging of tissue sections using infraredÂscanning technology. Journal of Anatomy, 2016, 228, 203-213.	1.5	10
24	Understanding the molecular consequences of inherited muscular dystrophies: advancements through proteomic experimentation. Expert Review of Proteomics, 2016, 13, 659-671.	3.0	19
25	Proteomic Profiling of Cranial (Superior) Cervical Ganglia Reveals Beta-Amyloid and Ubiquitin Proteasome System Perturbations in an Equine Multiple System Neuropathy. Molecular and Cellular Proteomics, 2015, 14, 3072-3086.	3.8	9
26	Increased levels of <scp>UCHL</scp>1 are a compensatory response to disrupted ubiquitin homeostasis in spinal muscular atrophy and do not represent a viable therapeutic target. Neuropathology and Applied Neurobiology, 2014, 40, 873-887.	3.2	23
27	A novel mouse model of Warburg Micro Syndrome reveals roles for RAB18 in eye development and organisation of the neuronal cytoskeleton. DMM Disease Models and Mechanisms, 2014, 7, 711-22.	2.4	38
28	Label-Free Quantitative Proteomic Profiling Identifies Disruption of Ubiquitin Homeostasis As a Key Driver of Schwann Cell Defects in Spinal Muscular Atrophy. Journal of Proteome Research, 2014, 13, 4546-4557.	3.7	39
29	Dysregulation of ubiquitin homeostasis and Î²-catenin signaling promote spinal muscular atrophy. Journal of Clinical Investigation, 2014, 124, 1821-1834.	8.2	151
30	A Guide to Modern Quantitative Fluorescent Western Blotting with Troubleshooting Strategies. Journal of Visualized Experiments, 2014, , e52099.	0.3	31
31	Label-free proteomics identifies Calreticulin and GRP75/Mortalin as peripherally accessible protein biomarkers for spinal muscular atrophy. Genome Medicine, 2013, 5, 95.	8.2	31
32	Total Protein Analysis as a Reliable Loading Control for Quantitative Fluorescent Western Blotting. PLoS ONE, 2013, 8, e72457.	2.5	300
33	Combining Comparative Proteomics and Molecular Genetics Uncovers Regulators of Synaptic and Axonal Stability and Degeneration In Vivo. PLoS Genetics, 2012, 8, e1002936.	3.5	54
34	ApoE isoform-specific regulation of regeneration in the peripheral nervous system. Human Molecular Genetics, 2011, 20, 2406-2421.	2.9	29
35	Reversible molecular pathology of skeletal muscle in spinal muscular atrophy. Human Molecular Genetics, 2011, 20, 4334-4344.	2.9	89
36	SMN deficiency disrupts brain development in a mouse model of severe spinal muscular atrophy. Human Molecular Genetics, 2010, 19, 4216-4228.	2.9	105

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37	Molecular correlates of axonal and synaptic pathology in mouse models of Batten disease. Human Molecular Genetics, 2009, 18, 4066-4080.	2.9	88
38	Expression of the neuroprotective slow Wallerian degeneration (Wld S) gene in non-neuronal tissues. BMC Neuroscience, 2009, 10, 148.	1.9	5
39	Modified cell cycle status in a mouse model of altered neuronal vulnerability (slow Wallerian) Tj ETQq1 1 0.784314 rgBT /Overlock 10	9.6	25
40	Differential Proteomics Analysis of Synaptic Proteins Identifies Potential Cellular Targets and Protein Mediators of Synaptic Neuroprotection Conferred by the Slow Wallerian Degeneration (Wld) Gene. Molecular and Cellular Proteomics, 2007, 6, 1318-1330.	3.8	82
41	Design of a novel quantitative PCR (QPCR)-based protocol for genotyping mice carrying the neuroprotective Wallerian degeneration slow (Wlds) gene. Molecular Neurodegeneration, 2007, 2, 21.	10.8	11
42	Synaptic Vulnerability in Neurodegenerative Disease. Journal of Neuropathology and Experimental Neurology, 2006, 65, 733-739.	1.7	189