

Dominic Winter

List of Publications by Year in descending order

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57
papers

2,551
citations

304368

22
h-index

197535

49
g-index

60
all docs

60
docs citations

60
times ranked

5140
citing authors

#	ARTICLE	IF	CITATIONS
1	Age-Dependent Increase in Schmidt-Lanterman Incisures and a Cadm4-Associated Membrane Skeletal Complex in Fatty Acid 2-hydroxylase Deficient Mice: a Mouse Model of Spastic Paraplegia SPG35. <i>Molecular Neurobiology</i> , 2022, 59, 3969-3979.	1.9	2
2	Targeted Quantification of the Lysosomal Proteome in Complex Samples. <i>Proteomes</i> , 2021, 9, 4.	1.7	12
3	A proteomic view on lysosomes. <i>Molecular Omics</i> , 2021, 17, 842-859.	1.4	10
4	Generation of Antibodies Targeting Cleavable Cross-Linkers. <i>Analytical Chemistry</i> , 2021, 93, 3762-3769.	3.2	7
5	Proteomic Analysis of Niemann-Pick Type C Hepatocytes Reveals Potential Therapeutic Targets for Liver Damage. <i>Cells</i> , 2021, 10, 2159.	1.8	9
6	Pathogenic variants in GNPTAB and GNPTG encoding distinct subunits of GlcNAc-1-phosphotransferase differentially impact bone resorption in patients with mucopolidosis type II and III. <i>Genetics in Medicine</i> , 2021, 23, 2369-2377.	1.1	2
7	RapiGest precipitation depends on peptide concentration. <i>Proteomics</i> , 2021, 21, e2100129.	1.3	3
8	Effect of modulating glutamate signaling on myelinating oligodendrocytes and their developmentâ€”A study in the zebrafish model. <i>Journal of Neuroscience Research</i> , 2021, 99, 2774-2792.	1.3	4
9	Decreased turnover of the CNS myelin protein Opalin in a mouse model of hereditary spastic paraplegia 35. <i>Human Molecular Genetics</i> , 2021, 29, 3616-3630.	1.4	9
10	Surveying the mitochondrial proteome. <i>Nature Cell Biology</i> , 2021, 23, 1216-1217.	4.6	3
11	Systematic Comparison of Strategies for the Enrichment of Lysosomes by Data Independent Acquisition. <i>Journal of Proteome Research</i> , 2020, 19, 371-381.	1.8	25
12	c-Abl Inhibition Activates TFEB and Promotes Cellular Clearance in a Lysosomal Disorder. <i>iScience</i> , 2020, 23, 101691.	1.9	30
13	Comprehensive draft of the mouse embryonic fibroblast lysosomal proteome by mass spectrometry based proteomics. <i>Scientific Data</i> , 2020, 7, 68.	2.4	23
14	Identification of Antifungal Intracellular Proteins of Endophytic <i>Bacillus pumilus</i> by LCâ€”MS/MS Analysis. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2429-2435.	0.9	3
15	Proteophagy in Mammalian Cells Can Function Independent of ATG5/ATG7. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1120-1131.	2.5	11
16	Muscle regulates mTOR dependent axonal local translation in motor neurons via CTRP3 secretion: implications for a neuromuscular disorder, spinal muscular atrophy. <i>Acta Neuropathologica Communications</i> , 2019, 7, 154.	2.4	18
17	Front Cover: Investigation of Oligodendrocyte Precursor Cell Differentiation by Quantitative Proteomics. <i>Proteomics</i> , 2019, 19, 1970121.	1.3	0
18	Investigation of Oligodendrocyte Precursor Cell Differentiation by Quantitative Proteomics. <i>Proteomics</i> , 2019, 19, e1900057.	1.3	14

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19	A mouse model for SPG48 reveals a block of autophagic flux upon disruption of adaptor protein complex five. <i>Neurobiology of Disease</i> , 2019, 127, 419-431.	2.1	26
20	Identification of Unexpected Protein Modifications by Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1871, 225-251.	0.4	1
21	PINK1 Phosphorylates MIC60/Mitofilin to Control Structural Plasticity of Mitochondrial Crista Junctions. <i>Molecular Cell</i> , 2018, 69, 744-756.e6.	4.5	88
22	Identification of progesterone receptor membrane component-1 as an interaction partner and possible regulator of fatty acid 2-hydroxylase. <i>Biochemical Journal</i> , 2018, 475, 853-871.	1.7	11
23	Identification of Poly(ethylene glycol) and Poly(ethylene glycol)-Based Detergents Using Peptide Search Engines. <i>Analytical Chemistry</i> , 2018, 90, 6594-6600.	3.2	7
24	Phosphorylation of MCAD selectively rescues <i>PINK1</i> deficiencies in behavior and metabolism. <i>Molecular Biology of the Cell</i> , 2018, 29, 1219-1227.	0.9	12
25	Tip-Based Fractionation of Batch-Enriched Phosphopeptides Facilitates Easy and Robust Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 46-54.	1.8	17
26	Lysosomal Proteome and Secretome Analysis Identifies Missorted Enzymes and Their Nondegraded Substrates in Mucopolidosis III Mouse Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1612-1626.	2.5	24
27	SILAC-Based Comparative Proteomic Analysis of Lysosomes from Mammalian Cells Using LC-MS/MS. <i>Methods in Molecular Biology</i> , 2017, 1594, 1-18.	0.4	20
28	Systematic Evaluation of Protein Reduction and Alkylation Reveals Massive Unspecific Side Effects by Iodine-containing Reagents. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1173-1187.	2.5	122
29	A Comprehensive High-Resolution Targeted Workflow for the Deep Profiling of Sphingolipids. <i>Analytical Chemistry</i> , 2017, 89, 12480-12487.	3.2	32
30	Multifunctional Thioredoxin-Like Protein from the Gastrointestinal Parasitic Nematodes <i>Strongyloides ratti</i> and <i>Trichuris suis</i> Affects Mucosal Homeostasis. <i>Journal of Parasitology Research</i> , 2016, 2016, 1-17.	0.5	20
31	In vitro antihistamine-releasing activity of a peptide derived from wasp venom of <i>Vespa orientalis</i> . <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2016, 6, 259-264.	0.5	3
32	[Sec-to-Cys]selenoprotein " a novel type of recombinant, full-length selenoprotein standard for quantitative proteomics. <i>Journal of Analytical Atomic Spectrometry</i> , 2016, 31, 1929-1938.	1.6	7
33	Anti-inflammatory activity of low molecular weight polysialic acid on human macrophages. <i>Scientific Reports</i> , 2015, 5, 16800.	1.6	64
34	Optimization of Cell Lysis and Protein Digestion Protocols for Protein Analysis by LC-MS/MS. <i>Methods in Molecular Biology</i> , 2015, 1295, 259-273.	0.4	5
35	Quantitative profiling of peptides from RNAs classified as noncoding. <i>Nature Communications</i> , 2014, 5, 5429.	5.8	55
36	Co-regulation proteomics reveals substrates and mechanisms of APC/C-dependent degradation. <i>EMBO Journal</i> , 2014, 33, 385-399.	3.5	72

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37	Molecular interaction of artemisinin with translationally controlled tumor protein (TCTP) of <i>Plasmodium falciparum</i> . <i>Biochemical Pharmacology</i> , 2013, 85, 38-45.	2.0	61
38	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014167-1-M111.014167-12.	2.5	24
39	Enzyme-cleavable tandem peptides for quantitative studies in MS-based proteomics. <i>Proteomics</i> , 2012, 12, 3470-3474.	1.3	8
40	FLEXIQinase, a mass spectrometry-based assay, to unveil multikinase mechanisms. <i>Nature Methods</i> , 2012, 9, 504-508.	9.0	26
41	Pleiotropic effects of miR-183-96-182 converge to regulate cell survival, proliferation and migration in medulloblastoma. <i>Acta Neuropathologica</i> , 2012, 123, 539-552.	3.9	145
42	PINK1 and Parkin Target Miro for Phosphorylation and Degradation to Arrest Mitochondrial Motility. <i>Cell</i> , 2011, 147, 893-906.	13.5	997
43	Metal ion-mobilizing additives for comprehensive detection of femtomole amounts of phosphopeptides by reversed phase LC-MS. <i>Amino Acids</i> , 2011, 41, 311-320.	1.2	27
44	Optimization of cell lysis and protein digestion protocols for the analysis of HeLa S3 cells by LC-MS/MS. <i>Proteomics</i> , 2011, 11, 4726-4730.	1.3	41
45	Structural and mechanistic information on c_{1} ion formation in collision-induced fragmentation of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1814-1820.	1.2	6
46	Minimally permuted peptide analogs as internal standards for relative and absolute quantification of peptides and proteins. <i>Proteomics</i> , 2010, 10, 1510-1514.	1.3	15
47	Recombinant Isotope Labeled and Selenium Quantified Proteins for Absolute Protein Quantification. <i>Analytical Chemistry</i> , 2010, 82, 2334-2340.	3.2	33
48	Theoretical and experimental analysis links isoform-specific ERK signalling to cell fate decisions. <i>Molecular Systems Biology</i> , 2009, 5, 334.	3.2	72
49	Phosphorylation of CARMA1 by HPK1 is critical for NF- κ B activation in T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14508-14513.	3.3	60
50	Separation of peptide isomers and conformers by ultra performance liquid chromatography. <i>Journal of Separation Science</i> , 2009, 32, 1111-1119.	1.3	50
51	Individual b2 ion fragmentation profiles combined with AspN digestion improve N-terminal peptide sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 393, 1587-1591.	1.9	4
52	Sequencing of the thirteen structurally isomeric quartets of N-terminal dipeptide motifs in peptides by collision-induced dissociation. <i>Proteomics</i> , 2009, 9, 2076-2084.	1.3	7
53	When less can yield more - Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	1.3	73
54	Protein phosphorylation influences proteolytic cleavage and kinase substrate properties exemplified by analysis of in vitro phosphorylated <i>Plasmodium falciparum</i> glideosome-associated protein 45 by nano-ultra performance liquid chromatography-tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2009, 393, 41-47.	1.1	27

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55	Citrate Boosts the Performance of Phosphopeptide Analysis by UPLC-ESI-MS/MS. <i>Journal of Proteome Research</i> , 2009, 8, 418-424.	1.8	69
56	Simultaneous identification and quantification of proteins by differential (16)O/(18)O labeling and UPLC-MS/MS applied to mouse cerebellar phosphoproteome following irradiation. <i>Anticancer Research</i> , 2009, 29, 4949-58.	0.5	12
57	Raf kinase inhibitor protein affects activity of <i>Plasmodium falciparum</i> calcium-dependent protein kinase 1. <i>Molecular and Biochemical Parasitology</i> , 2007, 151, 111-117.	0.5	16