Maggie P Y Lam

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2149785/publications.pdf

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414414 471509 1,284 33 17 32 citations h-index g-index papers 37 37 37 2034 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
2	Metabolic Labeling Reveals Proteome Dynamics of Mouse Mitochondria. Molecular and Cellular Proteomics, 2012, 11, 1586-1594.	3.8	151
3	Dynamic Chromatin Targeting of BRD4 Stimulates Cardiac Fibroblast Activation. Circulation Research, 2019, 125, 662-677.	4.5	105
4	Protein kinetic signatures of the remodeling heart following isoproterenol stimulation. Journal of Clinical Investigation, 2014, 124, 1734-1744.	8.2	83
5	A large dataset of protein dynamics in the mammalian heart proteome. Scientific Data, 2016, 3, 160015.	5. 3	79
6	HDAC Inhibition Reverses Preexisting Diastolic Dysfunction and Blocks Covert Extracellular Matrix Remodeling. Circulation, 2021, 143, 1874-1890.	1.6	71
7	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. Circulation Research, 2013, 113, 1043-1053.	4.5	65
8	Proteomics Research in Cardiovascular Medicine and Biomarker Discovery. Journal of the American College of Cardiology, 2016, 68, 2819-2830.	2.8	64
9	Splice-Junction-Based Mapping of Alternative Isoforms in the Human Proteome. Cell Reports, 2019, 29, 3751-3765.e5.	6.4	64
10	Online coupling of reverse-phase and hydrophilic interaction liquid chromatography for protein and glycoprotein characterization. Analytical and Bioanalytical Chemistry, 2010, 398, 791-804.	3.7	50
11	Data-Driven Approach To Determine Popular Proteins for Targeted Proteomics Translation of Six Organ Systems. Journal of Proteome Research, 2016, 15, 4126-4134.	3.7	50
12	OsNOA1/RIF1 is a functional homolog of AtNOA1/RIF1: implication for a highly conserved plant cGTPase essential for chloroplast function. New Phytologist, 2010, 187, 83-105.	7.3	39
13	Identification of CD147 (basigin) as a mediator of trophoblast functions. Human Reproduction, 2013, 28, 2920-2929.	0.9	39
14	Combinatorial use of offline SCX and online RP–RP liquid chromatography for iTRAQ-based quantitative proteomics applications. Molecular BioSystems, 2011, 7, 1399.	2.9	37
15	Substrate- and Isoform-Specific Proteome Stability in Normal and Stressed Cardiac Mitochondria. Circulation Research, 2012, 110, 1174-1178.	4.5	29
16	Online combination of reversedâ€phase/reversedâ€phase and porous graphitic carbon liquid chromatography for multicomponent separation of proteomics and glycoproteomics samples. Electrophoresis, 2011, 32, 2930-2940.	2.4	27
17	Fully automatable twoâ€dimensional reversedâ€phase capillary liquid chromatography with online tandem mass spectrometry for shotgun proteomics. Proteomics, 2011, 11, 2308-2319.	2.2	26
18	Identifying High-Priority Proteins Across the Human Diseasome Using Semantic Similarity. Journal of Proteome Research, 2018, 17, 4267-4278.	3.7	21

#	Article	IF	CITATIONS
19	Prioritizing Proteomics Assay Development for Clinical Translation. Journal of the American College of Cardiology, 2015, 66, 202-204.	2.8	17
20	Working the literature harder: what can text mining and bibliometric analysis reveal?. Expert Review of Proteomics, 2019, 16, 871-873.	3.0	13
21	Proteomic signatures of acute oxidative stress response to paraquat in the mouse heart. Scientific Reports, 2020, 10, 18440.	3.3	12
22	HDAC6 modulates myofibril stiffness and diastolic function of the heart. Journal of Clinical Investigation, 2022, 132 , .	8.2	12
23	Mining the Proteome Associated with Rheumatic and Autoimmune Diseases. Journal of Proteome Research, 2019, 18, 4231-4239.	3.7	11
24	Spatial and temporal dynamics of the cardiac mitochondrial proteome. Expert Review of Proteomics, 2015, 12, 133-146.	3.0	9
25	Cardiovascular proteomics in the era of big data: experimental and computational advances. Clinical Proteomics, 2016, 13, 23.	2.1	9
26	Transcriptome features of striated muscle aging and predictability of protein level changes. Molecular Omics, 2021, 17, 796-808.	2.8	9
27	Computation-assisted targeted proteomics of alternative splicing protein isoforms in the human heart. Journal of Molecular and Cellular Cardiology, 2021, 154, 92-96.	1.9	9
28	Determining Alternative Protein Isoform Expression Using RNA Sequencing and Mass Spectrometry. STAR Protocols, 2020, 1, 100138.	1.2	8
29	Cyclophilin D and Acetylation. Circulation Research, 2013, 113, 1268-1269.	4.5	5
30	Harnessing the Power of Proteomics to Assess Drug Safety and Guide Clinical Trials. Circulation, 2018, 137, 1011-1014.	1.6	5
31	HUPO 2011: The New Cardiovascular Initiative ―Integrating Proteomics and Cardiovascular Biology in Health and Disease. Proteomics, 2012, 12, 749-751.	2.2	4
32	Shotgun Proteomics Sample Processing Automated by an Open-Source Lab Robot. Journal of Visualized Experiments, 2021, , .	0.3	3
33	Multi-omics approach to identify disease signatures in cardiac remodeling. Journal of Molecular and Cellular Cardiology, 2017, 112, 154-155.	1.9	О