

# Maggie P Y Lam

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

1,284  
citations

471509

17  
h-index

414414

32  
g-index

37  
all docs

37  
docs citations

37  
times ranked

2034  
citing authors

#	ARTICLE	IF	CITATIONS
1	HDAC6 modulates myofibril stiffness and diastolic function of the heart. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	12
2	Transcriptome features of striated muscle aging and predictability of protein level changes. <i>Molecular Omics</i> , 2021, 17, 796-808.	2.8	9
3	Computation-assisted targeted proteomics of alternative splicing protein isoforms in the human heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 154, 92-96.	1.9	9
4	HDAC Inhibition Reverses Preexisting Diastolic Dysfunction and Blocks Covert Extracellular Matrix Remodeling. <i>Circulation</i> , 2021, 143, 1874-1890.	1.6	71
5	Shotgun Proteomics Sample Processing Automated by an Open-Source Lab Robot. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	3
6	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
7	Proteomic signatures of acute oxidative stress response to paraquat in the mouse heart. <i>Scientific Reports</i> , 2020, 10, 18440.	3.3	12
8	Determining Alternative Protein Isoform Expression Using RNA Sequencing and Mass Spectrometry. <i>STAR Protocols</i> , 2020, 1, 100138.	1.2	8
9	Dynamic Chromatin Targeting of BRD4 Stimulates Cardiac Fibroblast Activation. <i>Circulation Research</i> , 2019, 125, 662-677.	4.5	105
10	Mining the Proteome Associated with Rheumatic and Autoimmune Diseases. <i>Journal of Proteome Research</i> , 2019, 18, 4231-4239.	3.7	11
11	Splice-Junction-Based Mapping of Alternative Isoforms in the Human Proteome. <i>Cell Reports</i> , 2019, 29, 3751-3765.e5.	6.4	64
12	Working the literature harder: what can text mining and bibliometric analysis reveal?. <i>Expert Review of Proteomics</i> , 2019, 16, 871-873.	3.0	13
13	Harnessing the Power of Proteomics to Assess Drug Safety and Guide Clinical Trials. <i>Circulation</i> , 2018, 137, 1011-1014.	1.6	5
14	Identifying High-Priority Proteins Across the Human Diseasesome Using Semantic Similarity. <i>Journal of Proteome Research</i> , 2018, 17, 4267-4278.	3.7	21
15	Multi-omics approach to identify disease signatures in cardiac remodeling. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 112, 154-155.	1.9	0
16	Data-Driven Approach To Determine Popular Proteins for Targeted Proteomics Translation of Six Organ Systems. <i>Journal of Proteome Research</i> , 2016, 15, 4126-4134.	3.7	50
17	Cardiovascular proteomics in the era of big data: experimental and computational advances. <i>Clinical Proteomics</i> , 2016, 13, 23.	2.1	9
18	Proteomics Research in Cardiovascular Medicine and Biomarker Discovery. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2819-2830.	2.8	64

#	ARTICLE	IF	CITATIONS
19	A large dataset of protein dynamics in the mammalian heart proteome. <i>Scientific Data</i> , 2016, 3, 160015.	5.3	79
20	Spatial and temporal dynamics of the cardiac mitochondrial proteome. <i>Expert Review of Proteomics</i> , 2015, 12, 133-146.	3.0	9
21	Prioritizing Proteomics Assay Development for Clinical Translation. <i>Journal of the American College of Cardiology</i> , 2015, 66, 202-204.	2.8	17
22	Protein kinetic signatures of the remodeling heart following isoproterenol stimulation. <i>Journal of Clinical Investigation</i> , 2014, 124, 1734-1744.	8.2	83
23	Identification of CD147 (basigin) as a mediator of trophoblast functions. <i>Human Reproduction</i> , 2013, 28, 2920-2929.	0.9	39
24	Cyclophilin D and Acetylation. <i>Circulation Research</i> , 2013, 113, 1268-1269.	4.5	5
25	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. <i>Circulation Research</i> , 2013, 113, 1043-1053.	4.5	65
26	Metabolic Labeling Reveals Proteome Dynamics of Mouse Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1586-1594.	3.8	151
27	Substrate- and Isoform-Specific Proteome Stability in Normal and Stressed Cardiac Mitochondria. <i>Circulation Research</i> , 2012, 110, 1174-1178.	4.5	29
28	HUPO 2011: The New Cardiovascular Initiative – Integrating Proteomics and Cardiovascular Biology in Health and Disease. <i>Proteomics</i> , 2012, 12, 749-751.	2.2	4
29	Combinatorial use of offline SCX and online RP–RP liquid chromatography for iTRAQ-based quantitative proteomics applications. <i>Molecular BioSystems</i> , 2011, 7, 1399.	2.9	37
30	Fully automatable two-dimensional reversed-phase capillary liquid chromatography with online tandem mass spectrometry for shotgun proteomics. <i>Proteomics</i> , 2011, 11, 2308-2319.	2.2	26
31	Online combination of reversed-phase/reversed-phase and porous graphitic carbon liquid chromatography for multicomponent separation of proteomics and glycoproteomics samples. <i>Electrophoresis</i> , 2011, 32, 2930-2940.	2.4	27
32	Online coupling of reverse-phase and hydrophilic interaction liquid chromatography for protein and glycoprotein characterization. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 791-804.	3.7	50
33	OsNOA1/RIF1 is a functional homolog of AtNOA1/RIF1: implication for a highly conserved plant cGTPase essential for chloroplast function. <i>New Phytologist</i> , 2010, 187, 83-105.	7.3	39