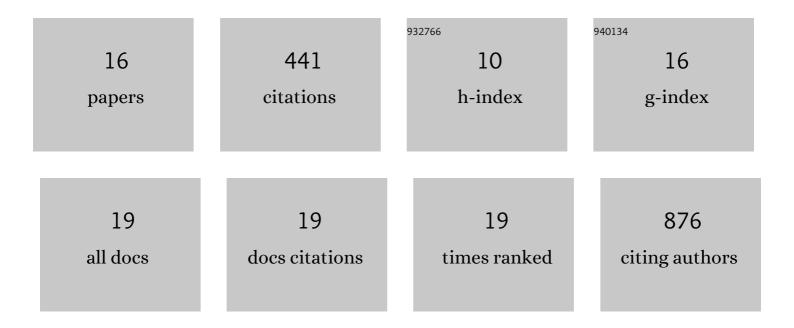
Ayako Takemori

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	H2 drives metabolic rearrangements in gas-fermenting Clostridium autoethanogenum. Biotechnology for Biofuels, 2018, 11, 55.	6.2	103
2	Bach2–Batf interactions control Th2-type immune response by regulating the IL-4 amplification loop. Nature Communications, 2016, 7, 12596.	5.8	73
3	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. Journal of Proteome Research, 2020, 19, 3779-3791.	1.8	49
4	The tumor suppressor menin prevents effector CD8 T-cell dysfunction by targeting mTORC1-dependent metabolic activation. Nature Communications, 2018, 9, 3296.	5.8	46
5	Targeted proteomics reveals promising biomarkers of disease activity and organ involvement in antineutrophil cytoplasmic antibody-associated vasculitis. Arthritis Research and Therapy, 2017, 19, 218.	1.6	40
6	MEERCAT: Multiplexed Efficient Cell Free Expression of Recombinant QconCATs For Large Scale Absolute Proteome Quantification. Molecular and Cellular Proteomics, 2017, 16, 2169-2183.	2.5	23
7	High-throughput synthesis of stable isotope-labeled transmembrane proteins for targeted transmembrane proteomics using a wheat germ cell-free protein synthesis system. Molecular BioSystems, 2015, 11, 361-365.	2.9	22
8	Top-down/Bottom-up Mass Spectrometry Workflow Using Dissolvable Polyacrylamide Gels. Analytical Chemistry, 2017, 89, 8244-8250.	3.2	18
9	BAC-DROP: Rapid Digestion of Proteome Fractionated via Dissolvable Polyacrylamide Gel Electrophoresis and Its Application to Bottom-Up Proteomics Workflow. Journal of Proteome Research, 2021, 20, 1535-1543.	1.8	13
10	Enzymatic protein digestion using a dissolvable polyacrylamide gel and its application to mass spectrometry-based proteomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 967, 36-40.	1.2	10
11	High-throughput production of a stable isotope-labeled peptide library for targeted proteomics using a wheat germ cell-free synthesis system. Molecular BioSystems, 2016, 12, 2389-2393.	2.9	10
12	Absolute Proteome Quantification in the Gas-Fermenting Acetogen <i>Clostridium autoethanogenum</i> . MSystems, 2022, 7, e0002622.	1.7	10
13	Construction of à la carte QconCAT protein standards for multiplexed quantification of user-specified target proteins. BMC Biology, 2021, 19, 195.	1.7	8
14	Usefulness of tissue inhibitor of metalloproteinase 1 as a predictor of sustained remission in patients with antineutrophil cytoplasmic antibody-associated vasculitis. Arthritis Research and Therapy, 2021, 23, 91.	1.6	5
15	Bottom-up/cross-linking mass spectrometry <i>via</i> simplified sample processing on anion-exchange solid-phase extraction spin column. Chemical Communications, 2022, 58, 775-778.	2.2	5
16	Quantitative assay of targeted proteome in tomato trichome glandular cells using a large-scale selected reaction monitoring strategy. Plant Methods, 2019, 15, 40.	1.9	4