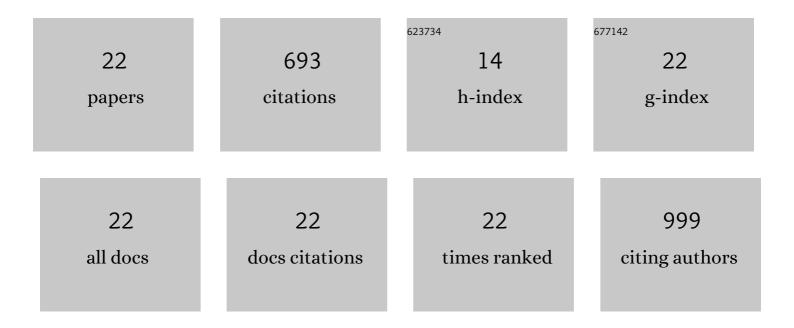
Tomoya Asano

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12062570/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Single-Molecule Imaging on Living Bacterial Cell Surface by High-Speed AFM. Journal of Molecular Biology, 2012, 422, 300-309.	4.2	114
2	A mutation of theCRUMPLED LEAFgene that encodes a protein localized in the outer envelope membrane of plastids affects the pattern of cell division, cell differentiation, and plastid division inArabidopsis. Plant Journal, 2004, 38, 448-459.	5.7	79
3	Plant Cells Without Detectable Plastids are Generated in the crumpled leaf Mutant of Arabidopsis thaliana. Plant and Cell Physiology, 2009, 50, 956-969.	3.1	63
4	Characterization of the chemical diversity of glycosylated mycosporine-like amino acids in the terrestrial cyanobacterium Nostoc commune. Journal of Photochemistry and Photobiology B: Biology, 2015, 142, 154-168.	3.8	62
5	Glycosylated Porphyra-334 and Palythine-Threonine from the Terrestrial Cyanobacterium Nostoc commune. Marine Drugs, 2013, 11, 3124-3154.	4.6	57
6	<i>AtNFXL1</i> , an Arabidopsis homologue of the human transcription factor NFâ€X1, functions as a negative regulator of the trichothecene phytotoxinâ€induced defense response. Plant Journal, 2008, 53, 450-464.	5.7	47
7	The Secreted Antifungal Protein Thionin 2.4 in Arabidopsis thaliana Suppresses the Toxicity of a Fungal Fruit Body Lectin from Fusarium graminearum. PLoS Pathogens, 2013, 9, e1003581.	4.7	39
8	Comparative Analysis of Phosphoprotein Expression Using 2D-DIGE. Methods in Molecular Biology, 2011, 744, 225-233.	0.9	28
9	Gene expression analysis of woundingâ€induced rootâ€toâ€shoot communication in <i>Arabidopsis thaliana</i> . Plant, Cell and Environment, 2011, 34, 705-716.	5.7	28
10	The defense response in Arabidopsis thaliana against Fusarium sporotrichioides. Proteome Science, 2012, 10, 61.	1.7	27
11	Lacking chloroplasts in guard cells of <i>crumpled leaf</i> attenuates stomatal opening: both guard cell chloroplasts and mesophyll contribute to guard cell <scp>ATP</scp> levels. Plant, Cell and Environment, 2014, 37, 2201-2210.	5.7	26
12	Arabidopsis MAPKKK δ-1 is required for full immunity against bacterial and fungal infection. Journal of Experimental Botany, 2020, 71, 2085-2097.	4.8	21
13	Identification of sperm equatorial segment protein 1 in the acrosome as the primary binding target of peanut agglutinin (PNA) in the mouse testis. Histochemistry and Cell Biology, 2017, 147, 27-38.	1.7	17
14	Visualization of wounding-induced root-to-shoot communication in arabidopsis. Plant Signaling and Behavior, 2011, 6, 1037-1039.	2.4	14
15	Role of the C-terminal extension stacked on the re-face of the isoalloxazine ring moiety of the flavin adenine dinucleotide prosthetic group in ferredoxin-NADP+ oxidoreductase from Bacillus subtilis. Plant Physiology and Biochemistry, 2014, 81, 143-148.	5.8	13
16	Characterization of mycosporine-like amino acids in the cyanobacterium <i>Nostoc verrucosum</i> . Journal of General and Applied Microbiology, 2018, 64, 203-211.	0.7	12
17	Characterization of extracellular matrix components from the desiccation-tolerant cyanobacterium <i>Nostoc commune</i> . Journal of General and Applied Microbiology, 2018, 64, 15-25.	0.7	12
18	A defect in atToc159 of Arabidopsis thaliana causes severe defects in leaf development. Genes and Genetic Systems, 2004, 79, 207-212.	0.7	11

Τομούα Asano

#	Article	IF	CITATIONS
19	Rice MEL2, the RNA recognition motif (RRM) protein, binds in vitro to meiosis-expressed genes containing U-rich RNA consensus sequences in the 3′-UTR. Plant Molecular Biology, 2015, 89, 293-307.	3.9	10
20	C-terminal residues of ferredoxin-NAD(P)+ reductase from Chlorobaculum tepidum are responsible for reaction dynamics in the hydride transfer and redox equilibria with NADP+/NADPH. Photosynthesis Research, 2018, 136, 275-290.	2.9	5
21	TheAtNFXL1gene functions as a signaling component of the type A trichothecene-dependent response. Plant Signaling and Behavior, 2008, 3, 991-992.	2.4	4
22	Quantitative Phosphoproteomic Analysis Using iTRAQ Method. Methods in Molecular Biology, 2014, 1171, 251-258.	0.9	4