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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Peptide AS-48: Prototype of a New Class of Cyclic Bacteriocins. Current Protein and Peptide Science, 2004, 5, 399-416.	1.4	169
2	The Structure of the Arabidopsis thaliana SOS3: Molecular Mechanism of Sensing Calcium for Salt Stress Response. Journal of Molecular Biology, 2005, 345, 1253-1264.	4.2	166
3	Decoding of Methylated Histone H3 Tail by the Pygo-BCL9 Wnt Signaling Complex. Molecular Cell, 2008, 30, 507-518.	9.7	166
4	The Structure of the C-Terminal Domain of the Protein Kinase AtSOS2 Bound to the Calcium Sensor AtSOS3. Molecular Cell, 2007, 26, 427-435.	9.7	123
5	Structure of Bacteriocin AS-48: From Soluble State to Membrane Bound State. Journal of Molecular Biology, 2003, 334, 541-549.	4.2	92
6	Structural basis of the regulatory mechanism of the plant CIPK family of protein kinases controlling ion homeostasis and abiotic stress. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4532-41.	7.1	81
7	Structural Biology of a Major Signaling Network that Regulates Plant Abiotic Stress: The CBL-CIPK Mediated Pathway. International Journal of Molecular Sciences, 2013, 14, 5734-5749.	4.1	79
8	Calcium-dependent oligomerization of CAR proteins at cell membrane modulates ABA signaling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E396-405.	7.1	72
9	Recognition and Activation of the Plant AKT1 Potassium Channel by the Kinase CIPK23. Plant Physiology, 2020, 182, 2143-2153.	4.8	51
10	Structural Insights on the Plant Salt-Overly-Sensitive 1 (SOS1) Na+/H+ Antiporter. Journal of Molecular Biology, 2012, 424, 283-294.	4.2	49
11	Bin2 Is a Membrane Sculpting N-BAR Protein That Influences Leucocyte Podosomes, Motility and Phagocytosis. PLoS ONE, 2012, 7, e52401.	2.5	44
12	The bacteriocin AS-48 requires dimer dissociation followed by hydrophobic interactions with the membrane for antibacterial activity. Journal of Structural Biology, 2015, 190, 162-172.	2.8	40
13	Interference of the complex between NCS-1 and Ric8a with phenothiazines regulates synaptic function and is an approach for fragile X syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E999-E1008.	7.1	40
14	The guanine-exchange factor Ric8a binds the calcium sensor NCS-1 to regulate synapse number and probability of release. Journal of Cell Science, 2014, 127, 4246-59.	2.0	25
15	Evolutionary Adaptation of the Fly Pygo PHD Finger toward Recognizing Histone H3 Tail Methylated at Arginine 2. Structure, 2013, 21, 2208-2220.	3.3	16
16	Insights into real-time chemical processes in a calcium sensor protein-directed dynamic library. Nature Communications, 2019, 10, 2798.	12.8	16
17	Deciphering the Inhibition of the Neuronal Calcium Sensor 1 and the Guanine Exchange Factor Ric8a with a Small Phenothiazine Molecule for the Rational Generation of Therapeutic Synapse Function Regulators. Journal of Medicinal Chemistry, 2018, 61, 5910-5921.	6.4	10
18	The structure and flexibility analysis of the <i>Arabidopsis</i> synaptotagmin 1 reveal the basis of its regulation at membrane contact sites. Life Science Alliance, 2021, 4, e202101152.	2.8	9

#	Article	IF	CITATIONS
19	SOS3 (salt overly sensitive 3) fromArabidopsis thaliana: expression, purification, crystallization and preliminary X-ray analysis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1272-1274.	2.5	7
20	Frq2 from <i>Drosophila melanogaster</i> : cloning, expression, purification, crystallization and preliminary X-ray analysis. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 530-534.	0.8	6
21	The complex between SOS3 and SOS2 regulatory domain fromArabidopsis thaliana: cloning, expression, purification, crystallization and preliminary X-ray analysis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 568-570.	0.7	4
22	Preliminary crystallographic analysis of the ankyrin-repeat domain ofArabidopsis thalianaAKT1: identification of the domain boundaries for protein crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 509-512.	0.8	3