

Chloe Zubieta

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

5,269
citations

147801

31
h-index

110387

64
g-index

74
all docs

74
docs citations

74
times ranked

6640
citing authors

#	ARTICLE	IF	CITATIONS
1	Getting in phase- DNA damage repair mechanisms and liquid-liquid phase separation of the plant-specific histone methyltransferase MtSUVR2. <i>Molecular Plant</i> , 2022, , .	8.3	0
2	The LEAFY floral regulator displays pioneer transcription factor properties. <i>Molecular Plant</i> , 2021, 14, 829-837.	8.3	48
3	The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors. <i>Nature Communications</i> , 2021, 12, 4760.	12.8	29
4	Unraveling the role of MADS transcription factor complexes in apple tree dormancy. <i>New Phytologist</i> , 2021, 232, 2071-2088.	7.3	31
5	Genome-wide binding of SEPALLATA3 and AGAMOUS complexes determined by sequential DNA-affinity purification sequencing. <i>Nucleic Acids Research</i> , 2020, 48, 9637-9648.	14.5	39
6	A prion-like domain in ELF3 functions as a thermosensor in Arabidopsis. <i>Nature</i> , 2020, 585, 256-260.	27.8	337
7	Contrasted evolutionary trajectories of plant transcription factors. <i>Current Opinion in Plant Biology</i> , 2020, 54, 101-107.	7.1	26
8	Molecular mechanisms of Evening Complex activity in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6901-6909.	7.1	101
9	Structural Basis for Plant MADS Transcription Factor Oligomerization. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 946-953.	4.1	37
10	Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants. <i>Molecular Plant</i> , 2019, 12, 743-763.	8.3	71
11	CryoEM structure of adenovirus type 3 fibre with desmoglein 2 shows an unusual mode of receptor engagement. <i>Nature Communications</i> , 2019, 10, 1181.	12.8	24
12	Brassicaceae-specific Gretchen Hagen 3 acyl acid amido synthetases conjugate amino acids to chorismate, a precursor of aromatic amino acids and salicylic acid. <i>Journal of Biological Chemistry</i> , 2019, 294, 16855-16864.	3.4	18
13	MADS transcription factors cooperate: complexities of complex formation. <i>Journal of Experimental Botany</i> , 2018, 69, 1821-1823.	4.8	14
14	Tetramerization of MADS family transcription factors SEPALLATA3 and AGAMOUS is required for floral meristem determinacy in Arabidopsis. <i>Nucleic Acids Research</i> , 2018, 46, 4966-4977.	14.5	81
15	A multisubstrate reductase from <i>Plantago major</i> : structure-function in the short chain reductase superfamily. <i>Scientific Reports</i> , 2018, 8, 14796.	3.3	8
16	CircRNAs in Plants. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1087, 329-343.	1.6	37
17	Mapping of Adenovirus of serotype 3 fibre interaction to desmoglein 2 revealed a novel "non-classical" mechanism of viral receptor engagement. <i>Scientific Reports</i> , 2018, 8, 8381.	3.3	18
18	Pioneer Factors in Animals and Plants "Colonizing Chromatin for Gene Regulation. <i>Molecules</i> , 2018, 23, 1914.	3.8	18

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19	A circRNA from SEPALLATA3 regulates splicing of its cognate mRNA through R-loop formation. <i>Nature Plants</i> , 2017, 3, 17053.	9.3	434
20	Exploring the Multiligand Binding Specificity of Saposin B Reveals Two Binding Sites. <i>ACS Omega</i> , 2017, 2, 7141-7145.	3.5	4
21	The evening complex coordinates environmental and endogenous signals in Arabidopsis. <i>Nature Plants</i> , 2017, 3, 17087.	9.3	205
22	Plant SAM-Domain Proteins Start to Reveal Their Roles. <i>Trends in Plant Science</i> , 2017, 22, 718-725.	8.8	21
23	Merging of synchrotron serial crystallographic data by a genetic algorithm. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1026-1035.	2.3	26
24	Radiation-damage-induced phasing: a case study using UV irradiation with light-emitting diodes. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 395-402.	2.3	6
25	The Myb domain of LUX ARRHYTHMO in complex with DNA: expression, purification and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 356-361.	0.8	6
26	<i>Arabidopsis thaliana</i> GH3.5 acyl acid amido synthetase mediates metabolic crosstalk in auxin and salicylic acid homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13917-13922.	7.1	118
27	The Lysosomal Protein Saposin B Binds Chloroquine. <i>ChemMedChem</i> , 2016, 11, 277-282.	3.2	25
28	Practical Radiation Damage-Induced Phasing. <i>Methods in Molecular Biology</i> , 2016, 1320, 205-218.	0.9	3
29	Preclinical safety and efficacy studies with an affinity-enhanced epithelial junction opener and PEGylated liposomal doxorubicin. <i>Molecular Therapy - Methods and Clinical Development</i> , 2015, 2, 15005.	4.1	23
30	Intracellular Signaling and Desmoglein 2 Shedding Triggered by Human Adenoviruses Ad3, Ad14, and Ad14P1. <i>Journal of Virology</i> , 2015, 89, 10841-10859.	3.4	37
31	Evolution of the Plant Reproduction Master Regulators LFY and the MADS Transcription Factors: The Role of Protein Structure in the Evolutionary Development of the Flower. <i>Frontiers in Plant Science</i> , 2015, 6, 1193.	3.6	58
32	Biochemical and Biophysical Characterization of the Selenium-binding and Reducing Site in Arabidopsis thaliana Homologue to Mammals Selenium-binding Protein 1. <i>Journal of Biological Chemistry</i> , 2014, 289, 31765-31776.	3.4	29
33	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3603-3615.	6.6	97
34	Structural and Functional Studies on the Interaction of Adenovirus Fiber Knobs and Desmoglein 2. <i>Journal of Virology</i> , 2013, 87, 11346-11362.	3.4	32
35	Imaging material properties of biological samples with a force feedback microscope. <i>Journal of Molecular Recognition</i> , 2013, 26, 689-693.	2.1	13
36	Determination of the GH3.12 protein conformation through HPLC-integrated SAXS measurements combined with X-ray crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2072-2080.	2.5	37

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37	Crystallization studies of the keratin-like domain from <i>Arabidopsis thaliana</i> SEPALLATA 3. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 997-1000.	0.7	5
38	A Structural Basis for the Biosynthesis of the Major Chlorogenic Acids Found in Coffee. <i>Plant Physiology</i> , 2012, 160, 249-260.	4.8	120
39	Structural Basis for Prereceptor Modulation of Plant Hormones by GH3 Proteins. <i>Science</i> , 2012, 336, 1708-1711.	12.6	137
40	Structural Analysis of Specific Metal Chelating Inhibitor Binding to the Endonuclease Domain of Influenza pH1N1 (2009) Polymerase. <i>PLoS Pathogens</i> , 2012, 8, e1002831.	4.7	149
41	Macro-to-Micro Structural Proteomics: Native Source Proteins for High-Throughput Crystallization. <i>PLoS ONE</i> , 2012, 7, e32498.	2.5	36
42	The Structural Basis for the Integrity of Adenovirus Ad3 Dodecahedron. <i>PLoS ONE</i> , 2012, 7, e46075.	2.5	25
43	Conformational changes associated with the binding of zinc acetate at the putative active site of XcTcmJ, a cupin from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1347-1353.	0.7	5
44	Structural Basis for Evolution of Product Diversity in Soybean Glutathione Biosynthesis. <i>Plant Cell</i> , 2009, 21, 3450-3458.	6.6	22
45	Structural Basis of Murein Peptide Specificity of a $\hat{3}$ -D-Glutamyl-L-Diamino Acid Endopeptidase. <i>Structure</i> , 2009, 17, 303-313.	3.3	73
46	Crystal structures of MW1337R and lin2004: Representatives of a novel protein family that adopt a four-helical bundle fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1589-1596.	2.6	3
47	Cooperative Assembly of TGF- $\hat{2}$ Superfamily Signaling Complexes Is Mediated by Two Disparate Mechanisms and Distinct Modes of Receptor Binding. <i>Molecular Cell</i> , 2008, 29, 157-168.	9.7	247
48	A Single Amino Acid Change Is Responsible for Evolution of Acyltransferase Specificity in Bacterial Methionine Biosynthesis. <i>Journal of Biological Chemistry</i> , 2008, 283, 7561-7567.	3.4	21
49	<i>Arabidopsis</i> Isochorismate Synthase Functional in Pathogen-induced Salicylate Biosynthesis Exhibits Properties Consistent with a Role in Diverse Stress Responses. <i>Journal of Biological Chemistry</i> , 2007, 282, 5919-5933.	3.4	198
50	Crystal structure of homoserine O-succinyltransferase from <i>Bacillus cereus</i> at 2.4 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 999-1005.	2.6	13
51	Crystal structures of two novel dye-decolorizing peroxidases reveal a barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 223-233.	2.6	81
52	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 234-243.	2.6	67
53	Structural and biochemical characterization of a human adenovirus 2/12 penton base chimera. <i>FEBS Journal</i> , 2006, 273, 4336-4345.	4.7	16
54	A quasi-atomic model of human adenovirus type 5 capsid. <i>EMBO Journal</i> , 2005, 24, 1645-1654.	7.8	130

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55	Crystal Structures of Alfalfa Caffeoyl Coenzyme A 3-O-Methyltransferase. <i>Plant Physiology</i> , 2005, 137, 1009-1017.	4.8	111
56	The Structure of the Human Adenovirus 2 Penton. <i>Molecular Cell</i> , 2005, 17, 121-135.	9.7	188
57	The Structure of the Human Adenovirus 2 Penton. <i>Molecular Cell</i> , 2005, 17, 319-320.	9.7	5
58	O-Methylation of benzaldehyde derivatives by α -lignin specific caffeic acid 3-O-methyltransferase. <i>Phytochemistry</i> , 2004, 65, 837-846.	2.9	32
59	Structural Basis for Substrate Recognition in the Salicylic Acid Carboxyl Methyltransferase Family. <i>Plant Cell</i> , 2003, 15, 1704-1716.	6.6	214
60	Chapter two Structural, functional, and evolutionary basis for methylation of plant small molecules. <i>Recent Advances in Phytochemistry</i> , 2003, 37, 37-58.	0.5	68
61	Structural Basis for the Modulation of Lignin Monomer Methylation by Caffeic Acid/5-Hydroxyferulic Acid 3/5-O-Methyltransferase. <i>Plant Cell</i> , 2002, 14, 1265-1277.	6.6	222
62	Characterization of Phenylpropene O-Methyltransferases from Sweet Basil. <i>Plant Cell</i> , 2002, 14, 505-519.	6.6	224
63	Chapter Seven Properties and metabolic engineering of alfalfa phenylpropanoid pathway O-methyltransferases. <i>Recent Advances in Phytochemistry</i> , 2001, , 131-154.	0.5	3
64	Structures of two natural product methyltransferases reveal the basis for substrate specificity in plant O-methyltransferases. <i>Nature Structural Biology</i> , 2001, 8, 271-279.	9.7	298
65	Composite Solids Constructed From One-Dimensional Coordination Polymer Matrices and Molybdenum Oxide Subunits: Polyoxomolybdate Clusters within $[\{Cu(4,4\text{-bpy})\}_4Mo_8O_{26}]$ and $[\{Ni(H_2O)_2(4,4\text{-bpy})_2\}_2Mo_8O_{26}]$ and One-Dimensional Oxide Chains in $[\{Cu(4,4\text{-bpy})\}_4Mo_{15}O_{47}] \cdot 8H_2O$. <i>Angewandte Chemie International Edition in English</i> , 1997, 36, 873-876.	4.4	438