

# Rui Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3577116/publications.pdf>

Version: 2024-02-01

11  
papers

475  
citations

933447

10  
h-index

1281871

11  
g-index

11  
all docs

11  
docs citations

11  
times ranked

496  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chloroplast genomic data provide new and robust insights into the phylogeny and evolution of the Ranunculaceae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 12-21.	2.7	123
2	Disruption of the petal identity gene <i>APETALA3-3</i> is highly correlated with loss of petals within the buttercup family (Ranunculaceae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5074-5079.	7.1	88
3	Flexibility in the structure of spiral flowers and its underlying mechanisms. <i>Nature Plants</i> , 2016, 2, 15188.	9.3	88
4	Developmental mechanisms involved in the diversification of flowers. <i>Nature Plants</i> , 2019, 5, 917-923.	9.3	46
5	Identification of the Key Regulatory Genes Involved in Elaborate Petal Development and Specialized Character Formation in <i>Nigella damascena</i> (Ranunculaceae). <i>Plant Cell</i> , 2020, 32, 3095-3112.	6.6	27
6	The making of elaborate petals in <i>Nigella</i> through developmental repatterning. <i>New Phytologist</i> , 2019, 223, 385-396.	7.3	21
7	A role for the Auxin Response Factors <i>ARF6</i> and <i>ARF8</i> homologs in petal spur elongation and nectary maturation in <i>Aquilegia</i> . <i>New Phytologist</i> , 2020, 227, 1392-1405.	7.3	21
8	Prevalent Exon-Intron Structural Changes in the <i>APETALA1/FRUITFULL</i> , <i>SEPALLATA</i> , <i>AGAMOUS-LIKE6</i> , and <i>FLOWERING LOCUS C MADS-Box</i> Gene Subfamilies Provide New Insights into Their Evolution. <i>Frontiers in Plant Science</i> , 2016, 7, 598.	3.6	19
9	The morphology, molecular development and ecological function of pseudonectaries on <i>Nigella damascena</i> (Ranunculaceae) petals. <i>Nature Communications</i> , 2020, 11, 1777.	12.8	18
10	Interactions among proteins of floral MADS-box genes in <i>Nuphar pumila</i> (Nymphaeaceae) and the most recent common ancestor of extant angiosperms help understand the underlying mechanisms of the origin of the flower. <i>Journal of Systematics and Evolution</i> , 2015, 53, 285-296.	3.1	17
11	Identification of the target genes of <i>AqAPETALA3</i> ( <i>AqAP3</i> ) in <i>Aquilegia coerulea</i> (Ranunculaceae) helps understand the molecular bases of the conserved and nonconserved features of petals. <i>New Phytologist</i> , 2020, 227, 1235-1248.	7.3	7