

# Sara S Jawdy

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

2,265  
citations

201385

27  
h-index

223531

46  
g-index

50  
all docs

50  
docs citations

50  
times ranked

3382  
citing authors

#	ARTICLE	IF	CITATIONS
1	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. <i>Plant Physiology</i> , 2008, 148, 1189-1200.	2.3	125
2	Two Poplar-Associated Bacterial Isolates Induce Additive Favorable Responses in a Constructed Plant-Microbiome System. <i>Frontiers in Plant Science</i> , 2016, 7, 497.	1.7	113
3	<scp>Genome-wide association studies</scp> and expression-based quantitative trait loci analyses reveal roles of <scp>HCT</scp>2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in <i>Populus</i> . <i>New Phytologist</i> , 2018, 220, 502-516.	3.5	112
4	Leaf dynamics of a deciduous forest canopy: no response to elevated CO <sub>2</sub> . <i>Oecologia</i> , 2003, 136, 574-584.	0.9	106
5	High-resolution genetic mapping of allelic variants associated with cell wall chemistry in <i>Populus</i> . <i>BMC Genomics</i> , 2015, 16, 24.	1.2	106
6	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641.	2.4	105
7	<i>Pseudomonas fluorescens</i> Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 765-778.	1.4	100
8	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
9	The Ectomycorrhizal Fungus <i>Laccaria bicolor</i> Produces Lipochitooligosaccharides and Uses the Common Symbiosis Pathway to Colonize <i>Populus</i> Roots. <i>Plant Cell</i> , 2019, 31, 2386-2410.	3.1	73
10	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	1.2	72
11	Comparative physiology and transcriptional networks underlying the heat shock response in <i>Populus trichocarpa</i> , <i>Arabidopsis thaliana</i> and <i>Glycine max</i> . <i>Plant, Cell and Environment</i> , 2011, 34, 1488-1506.	2.8	71
12	Apoplast proteome reveals that extracellular matrix contributes to multistress response in poplar. <i>BMC Genomics</i> , 2010, 11, 674.	1.2	70
13	Genetic and physical mapping of <i>Melampsora</i> rust resistance genes in <i>Populus</i> and characterization of linkage disequilibrium and flanking genomic sequence. <i>New Phytologist</i> , 2004, 164, 95-105.	3.5	66
14	Knockdown of a laccase in <i>Populus deltoides</i> confers altered cell wall chemistry and increased sugar release. <i>Plant Biotechnology Journal</i> , 2016, 14, 2010-2020.	4.1	64
15	Root bacterial endophytes alter plant phenotype, but not physiology. <i>PeerJ</i> , 2016, 4, e2606.	0.9	64
16	Chemical, ultrastructural and supramolecular analysis of tension wood in <i>Populus tremula x alba</i> as a model substrate for reduced recalcitrance. <i>Energy and Environmental Science</i> , 2011, 4, 4962.	15.6	61
17	Metabolic profiling reveals altered sugar and secondary metabolism in response to UGPase overexpression in <i>Populus</i> . <i>BMC Plant Biology</i> , 2014, 14, 265.	1.6	61
18	Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11573-11578.	3.3	61

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19	Metabolic functions of <i>Pseudomonas fluorescens</i> strains from <i>Populus deltoides</i> depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , 2015, 6, 1118.	1.5	60
20	A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in <i>Populus</i> . <i>Plant Cell</i> , 2018, 30, 1645-1660.	3.1	56
21	Genome-wide identification of lineage-specific genes in <i>Arabidopsis</i> , <i>Oryza</i> and <i>Populus</i> . <i>Genomics</i> , 2009, 93, 473-480.	1.3	50
22	A Carotenoid-Deficient Mutant in <i>Pantoea</i> sp. YR343, a Bacteria Isolated from the Rhizosphere of <i>Populus deltoides</i> , Is Defective in Root Colonization. <i>Frontiers in Microbiology</i> , 2016, 7, 491.	1.5	48
23	The nature of the progression of drought stress drives differential metabolomic responses in <i>Populus deltoides</i> . <i>Annals of Botany</i> , 2019, 124, 617-626.	1.4	45
24	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
25	<i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. <i>Scientific Reports</i> , 2017, 7, 382.	1.6	36
26	Leaf endophytes and <i>Populus</i> genotype affect severity of damage from the necrotrophic leaf pathogen, <i>Drepanopeziza populi</i> . <i>Ecosphere</i> , 2013, 4, 1-12.	1.0	35
27	Down-Regulation of KORRIGAN-Like Endo-1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1455.	1.7	32
28	A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1669.	1.7	31
29	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207.	2.5	27
30	Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 311.	6.2	26
31	Bioinformatics-Based Identification of Candidate Genes from QTLs Associated with Cell Wall Traits in <i>Populus</i> . <i>Bioenergy Research</i> , 2010, 3, 172-182.	2.2	25
32	Initial characterization of shade avoidance response suggests functional diversity between <i>Populus</i> phytochrome B genes. <i>New Phytologist</i> , 2012, 196, 726-737.	3.5	25
33	Phytobiome and Transcriptional Adaptation of <i>Populus deltoides</i> to Acute Progressive Drought and Cyclic Drought. <i>Phytobiomes Journal</i> , 2018, 2, 249-260.	1.4	23
34	Overexpression of a Domain of Unknown Function 266-containing protein results in high cellulose content, reduced recalcitrance, and enhanced plant growth in the bioenergy crop <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 74.	6.2	22
35	Effects of Biomass Accessibility and Klason Lignin Contents during Consolidated Bioprocessing in <i>Populus trichocarpa</i> . <i>ACS Sustainable Chemistry and Engineering</i> , 2017, 5, 5075-5081.	3.2	20
36	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	3.5	18

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37	Quantitative proteome profile of water deficit stress responses in eastern cottonwood ( <i>Populus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	17
38	Identification of <i>Populus</i> Small RNAs Responsive to Mutualistic Interactions With Mycorrhizal Fungi, <i>Laccaria bicolor</i> and <i>Rhizophagus irregularis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 515.	1.5	17
39	Overexpression of a <i>Prefoldin 1</i> subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	17
40	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	1.7	17
41	Simultaneous knockdown of six non-family genes using a single synthetic RNAi fragment in <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2016, 12, 16.	1.9	12
42	Forest stand and canopy development unaltered by 12 years of CO <sub>2</sub> enrichment*. <i>Tree Physiology</i> , 2022, 42, 428-440.	1.4	12
43	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a <i>Populus</i> ANGUSTIFOLIA Protein. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2631-2641.	0.8	9
44	Relatively rare root endophytic bacteria drive plant resource allocation patterns and tissue nutrient concentration in unpredictable ways. <i>American Journal of Botany</i> , 2019, 106, 1423-1434.	0.8	9
45	Scaling nitrogen and carbon interactions: what are the consequences of biological buffering?. <i>Ecology and Evolution</i> , 2015, 5, 2839-2850.	0.8	4
46	Identification of functional single nucleotide polymorphism of <i>Populus trichocarpa</i> PtrEPSPâ€³TF and determination of its transcriptional effect. <i>Plant Direct</i> , 2020, 4, e00178.	0.8	4
47	Auxin Signaling and Response Mechanisms and Roles in Plant Growth and Development. , 2011, , 231-254.		3
48	Development of an Experimental Approach to Achieve Spatially Resolved Plant Root-Associated Metaproteomics Using an Agar-Plate System. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 639-649.	1.4	3