

# Eshchar Mizrachi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3892795/publications.pdf>

Version: 2024-02-01

38  
papers

3,274  
citations

361045

20  
h-index

315357

38  
g-index

39  
all docs

39  
docs citations

39  
times ranked

5268  
citing authors

#	ARTICLE	IF	CITATIONS
1	qtXplorer: an online systems genetics browser in the Eucalyptus Genome Integrative Explorer (EucGenIE). BMC Bioinformatics, 2021, 22, 595.	1.2	2
2	Analysis of Orthologous SECONDARY WALL-ASSOCIATED NAC DOMAIN1 (SND1) Promotor Activity in Herbaceous and Woody Angiosperms. International Journal of Molecular Sciences, 2019, 20, 4623.	1.8	2
3	A systems genetics analysis in <i>Eucalyptus</i> reveals coordination of metabolic pathways associated with xylan modification in wood-forming tissues. New Phytologist, 2019, 223, 1952-1972.	3.5	10
4	Loss of Wood Formation Genes in Monocot Genomes. Genome Biology and Evolution, 2019, 11, 1986-1996.	1.1	20
5	Systems and Synthetic Biology of Forest Trees: A Bioengineering Paradigm for Woody Biomass Feedstocks. Frontiers in Plant Science, 2019, 10, 775.	1.7	17
6	Identification and functional evaluation of accessible chromatin associated with wood formation in <i>Eucalyptus grandis</i> . New Phytologist, 2019, 223, 1937-1951.	3.5	10
7	Xylan in the Middle: Understanding Xylan Biosynthesis and Its Metabolic Dependencies Toward Improving Wood Fiber for Industrial Processing. Frontiers in Plant Science, 2019, 10, 176.	1.7	52
8	Organellar carbon metabolism is coordinated with distinct developmental phases of secondary xylem. New Phytologist, 2019, 222, 1832-1845.	3.5	11
9	The plastid and mitochondrial genomes of <i>Eucalyptus grandis</i> . BMC Genomics, 2019, 20, 132.	1.2	35
10	A Standardized Synthetic <i>Eucalyptus</i> Transcription Factor and Promoter Panel for Re-engineering Secondary Cell Wall Regulation in Biomass and Bioenergy Crops. ACS Synthetic Biology, 2019, 8, 463-465.	1.9	15
11	Unsung and understudied: plastids involved in secondary growth. Current Opinion in Plant Biology, 2018, 42, 30-36.	3.5	11
12	Carbohydrate active enzyme domains from extreme thermophiles: components of a modular toolbox for lignocellulose degradation. Extremophiles, 2018, 22, 1-12.	0.9	14
13	Network-based integration of systems genetics data reveals pathways associated with lignocellulosic biomass accumulation and processing. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1195-1200.	3.3	55
14	A Dual Laser Scanning Confocal and Transmission Electron Microscopy Analysis of the Intracellular Localization, Aggregation and Particle Formation of African Horse Sickness Virus Major Core Protein VP7. Microscopy and Microanalysis, 2017, 23, 56-68.	0.2	2
15	The evolutionary significance of polyploidy. Nature Reviews Genetics, 2017, 18, 411-424.	7.7	1,288
16	Integrated analysis and transcript abundance modelling of H3K4me3 and H3K27me3 in developing secondary xylem. Scientific Reports, 2017, 7, 3370.	1.6	32
17	In planta expression of hyperthermophilic enzymes as a strategy for accelerated lignocellulosic digestion. Scientific Reports, 2017, 7, 11462.	1.6	16
18	Evidence for an ancient whole genome duplication in the cycad lineage. PLoS ONE, 2017, 12, e0184454.	1.1	36

#	ARTICLE	IF	CITATIONS
19	Functional network analysis of genes differentially expressed during xylogenesis in woody Arabidopsis plants. <i>Plant Journal</i> , 2016, 86, 376-390.	2.8	27
20	Systems genetics of wood formation. <i>Current Opinion in Plant Biology</i> , 2016, 30, 94-100.	3.5	46
21	The Arabidopsis Domain of Unknown Function 1218 (DUF1218) Containing Proteins, MODIFYING WALL LIGNIN-1 and 2 (At1g31720/MWL-1 and At4g19370/MWL-2) Function Redundantly to Alter Secondary Cell Wall Lignin Content. <i>PLoS ONE</i> , 2016, 11, e0150254.	1.1	14
22	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . <i>Plant Cell</i> , 2015, 27, 1567-1578.	3.1	78
23	Comparative interrogation of the developing xylem transcriptomes of two wood-forming species: <i>Populus trichocarpa</i> and <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1391-1405.	3.5	47
24	Comparative analysis of plant carbohydrate active enzymes and their role in xylogenesis. <i>BMC Genomics</i> , 2015, 16, 402.	1.2	23
25	Genome-wide mapping of histone H3 lysine 4 trimethylation in <i>Eucalyptus grandis</i> developing xylem. <i>BMC Plant Biology</i> , 2015, 15, 117.	1.6	26
26	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1328-1336.	3.5	19
27	Investigating the molecular underpinnings underlying morphology and changes in carbon partitioning during tension wood formation in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1351-1363.	3.5	27
28	Cell Wall-Related Proteins of Unknown Function: Missing Links in Plant Cell Wall Development. <i>Plant and Cell Physiology</i> , 2014, 55, 1031-1043.	1.5	25
29	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
30	Recombinant hyperthermophilic enzyme expression in plants: a novel approach for lignocellulose digestion. <i>Trends in Biotechnology</i> , 2014, 32, 281-289.	4.9	21
31	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. <i>Frontiers in Plant Science</i> , 2013, 4, 325.	1.7	124
32	Cellulose factories: advancing bioenergy production from forest trees. <i>New Phytologist</i> , 2012, 194, 54-62.	3.5	82
33	SND2, a NAC transcription factor gene, regulates genes involved in secondary cell wall development in Arabidopsis fibres and increases fibre cell area in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2011, 11, 173.	1.6	164
34	The <i>Eucalyptus grandis</i> Genome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. <i>BMC Proceedings</i> , 2011, 5, .	1.8	25
35	The <i>Eucalyptus</i> genome integrative explorer (EucGenIE): a resource for <i>Eucalyptus</i> genomics and transcriptomics. <i>BMC Proceedings</i> , 2011, 5, .	1.8	18
36	Genetic dissection of transcript, metabolite, growth and wood property traits in an F2 pseudo-backcross pedigree of <i>Eucalyptus grandis</i> x <i>E. urophylla</i> . <i>BMC Proceedings</i> , 2011, 5, .	1.8	3

#	ARTICLE	IF	CITATIONS
37	In silico comparative analysis of glycoside hydrolase (GH) family 10 endo-(1-4)-beta-xylanase genes from <i>Eucalyptus grandis</i> and <i>Arabidopsis thaliana</i> . BMC Proceedings, 2011, 5, .	1.8	0
38	De novo assembled expressed gene catalog of a fast-growing <i>Eucalyptus</i> tree produced by Illumina mRNA-Seq. BMC Genomics, 2010, 11, 681.	1.2	150