Jeffrey Fd Dean

List of Publications by Year
in descending order

37	2,533	304743 22	361022 35
papers	citations	h-index	g-index

39	39	39	3305
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	9.6	424
2	A fungal metabolite mediates degradation of non-phenolic lignin structures and synthetic lignin by laccase. FEBS Letters, 1996, 391, 144-148.	2.8	395
3	Laccase and the Deposition of Lignin in Vascular Plants. Holzforschung, 1994, 48, 21-33.	1.9	154
4	Oxidation of Phenolate Siderophores by the Multicopper Oxidase Encoded by the Escherichia coli yacK Gene. Journal of Bacteriology, 2001, 183, 4866-4875.	2.2	137
5	Laccase-mediated formation of the phenoxazinone derivative, cinnabarinic acid. FEBS Letters, 1995, 376, 202-206.	2.8	133
6	Forest tree biotechnology. Current Opinion in Biotechnology, 2000, 11, 298-302.	6.6	118
7	Microarray analysis and scale-free gene networks identify candidate regulators in drought-stressed roots of loblolly pine (P. taeda L.). BMC Genomics, 2011, 12, 264.	2.8	110
8	SAGE Analysis of Transcriptome Responses in Arabidopsis Roots Exposed to 2,4,6-Trinitrotoluene. Plant Physiology, 2003, 133, 1397-1406.	4.8	105
9	A laccase-like phenoloxidase is correlated with lignin biosynthesis in Zinnia elegans stem tissues. Plant Journal, 1994, 6, 213-224.	5.7	99
10	Ferroxidase activity in a laccase-like multicopper oxidase from Liriodendron tulipifera. Plant Physiology and Biochemistry, 2004, 42, 27-33.	5.8	99
11	Towards decoding the conifer giga-genome. Plant Molecular Biology, 2012, 80, 555-569.	3.9	91
12	Characterization and heterologous expression of laccase cDNAs from xylem tissues of yellow-poplar (Liriodendron tulipifera). Plant Molecular Biology, 1999, 40, 23-35.	3.9	75
13	The phenylalanine ammonia lyase (PAL) gene family shows a gymnosperm-specific lineage. BMC Genomics, 2012, 13, S1.	2.8	70
14	Release of lignin from kraft pulp by a hyperthermophilic xylanase from Thermatoga maritima. Enzyme and Microbial Technology, 1997, 20, 39-45.	3.2	55
15	A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. BMC Genomics, 2013, 14, 137.	2.8	55
16	Release of the FAD domain from cellobiose oxidase by proteases from cellulolytic cultures ofPhanerochaete chrysosporium. FEBS Letters, 1993, 327, 161-164.	2.8	54
17	Conifer DBMagic: a database housing multiple de novo transcriptome assemblies for 12 diverse conifer species. Tree Genetics and Genomes, 2012, 8, 1477-1485.	1.6	48
18	Transcriptomic analysis highlights epigenetic and transcriptional regulation during zygotic embryo development of Pinus pinaster. BMC Plant Biology, 2013, 13, 123.	3.6	37

#	Article	IF	Citations
19	Laccases Associated with Lignifying Vascular Tissues. ACS Symposium Series, 1998, , 96-108.	0.5	35
20	Activation of defence pathways in Scots pine bark after feeding by pine weevil (Hylobius abietis). BMC Genomics, 2015, 16, 352.	2.8	31
21	Noctilisin, a Venom Glycopeptide of <I>Sirex noctilio</I> (Hymenoptera: Siricidae), Causes Needle Wilt and Defense Gene Responses in Pines. Journal of Economic Entomology, 2014, 107, 1931-1945.	1.8	27
22	Characterization of a 1-aminocyclopropane-1-carboxylate synthase gene from loblolly pine (Pinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.2	25
23	Staining Electrophoretic Gels for Laccase and Peroxidase Activity Using 1,8-Diaminonaphthalene. Analytical Biochemistry, 2001, 293, 96-101.	2.4	19
24	Synthesis and spectroscopic characterization of p-hydroxyphenyl, guaiacyl and syringyl lignin polymer models (DHPs). Nordic Pulp and Paper Research Journal, 1993, 8, 344-349a.	0.7	17
25	Localization of hydrogen peroxide production in Zinnia elegans L. stems. Phytochemistry, 1999, 52, 545-554.	2.9	17
26	Forest biotechnology makes its position known. Nature Biotechnology, 1999, 17, 1145-1145.	17.5	16
27	Susceptibility and Response of Pines to Sirex noctilio. , 2012, , 31-50.		15
28	ConiferEST: an integrated bioinformatics system for data reprocessing and mining of conifer expressed sequence tags (ESTs). BMC Genomics, 2007, 8, 134.	2.8	14
29	Exploring the loblolly pine (Pinus taeda L.) genome by BAC sequencing and Cot analysis. Gene, 2018, 663, 165-177.	2.2	13
30	Colonization and Development of Sirex noctilio (Hymenoptera: Siricidae) in Bolts of a Native Pine Host and Six Species of Pine Grown in the Southeastern United States. Journal of Entomological Science, 2019, 54, 1-18.	0.3	12
31	Differential responses of the promoters from nearly identical paralogs of loblolly pine (Pinus taeda) Tj ETQq1 1 0.784314 rgBT /Overlo 873-886.	3.2	9
32	Forest tree biotechnology. Advances in Biochemical Engineering/Biotechnology, 1997, 57, 1-44.	1.1	8
33	An Improved Method of RNA Isolation from Loblolly Pine (P. taeda L.) and Other Conifer Species. Journal of Visualized Experiments, 2010, , .	0.3	5
34	Processing the Loblolly Pine PtGen2 cDNA Microarray. Journal of Visualized Experiments, 2009, , .	0.3	4
35	Tagging all genes. Nature Biotechnology, 2004, 22, 961-962.	17.5	2
36	Phylogenomic Analysis of the Phenylalanine Ammonia Lyase Gene Family in Loblolly Pine (Pinus Taeda) Tj ETQq0 0 0 rgBT /Overlock 10 T		0

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37	Generation of Internal Antino Acid Sequences without Peptide Purification. Amino Acid Sequencing of the Ethylene Biosynthesis Inducing Xylanase from Trichodernza viride. Protein and Peptide Letters, 1994, 1, 149-156.	0.9	0