Angela Karp

List of Publications by Year
in descending order

98 papers	5,355 citations	81900 39 h-index	85541 71 g-index
99 all docs	99 docs citations	99 times ranked	4508 citing authors

#	Article	IF	Citations
1	Title is missing!. Molecular Breeding, 1997, 3, 381-390.	2.1	619
2	Bioenergy from plants and the sustainable yield challenge. New Phytologist, 2008, 179, 15-32.	7.3	427
3	Molecular Techniques in the Assessment of Botanical Diversity. Annals of Botany, 1996, 78, 143-149.	2.9	204
4	Somaclonal variation as a tool for crop improvement. Euphytica, 1995, 85, 295-302.	1.2	200
5	Genetic Improvement of Willow for Bioenergy and BiofuelsFree Access. Journal of Integrative Plant Biology, 2011, 53, 151-165.	8.5	172
6	Chromosome variation in wheat plants regenerated from cultured immature embryos. Theoretical and Applied Genetics, 1984, 67, 249-255.	3.6	153
7	Chromosome variation in protoplast-derived potato plants. Theoretical and Applied Genetics, 1982, 63, 265-272.	3.6	152
8	Molecular technologies for biodiversity evaluation: Opportunities and challenges. Nature Biotechnology, 1997, 15, 625-628.	17.5	147
9	An analysis of genetic diversity in coconut (Cocos nucifera) populations from across the geographic range using sequence-tagged microsatellites (SSRs) and AFLPs. Theoretical and Applied Genetics, 2000, 100, 764-771.	3.6	132
10	Land Use Implications of Increased Biomass Production Identified by GIS-Based Suitability and Yield Mapping for Miscanthus in England. Bioenergy Research, 2009, 2, 17-28.	3.9	126
11	Variation in oil palm (Elaeis guineensis Jacq.) tissue culture-derived regenerants revealed by AFLPs with methylation-sensitive enzymes. Theoretical and Applied Genetics, 2001, 102, 971-979.	3.6	125
12	A novel, integrated approach to assessing social, economic and environmental implications of changing rural landâ€use: a case study of perennial biomass crops. Journal of Applied Ecology, 2009, 46, 315-322.	4.0	117
13	Meeting the challenge of food and energy security. Journal of Experimental Botany, 2011, 62, 3263-3271.	4.8	97
14	AFLP analysis sheds light on distribution of two Salix species and their hybrid along a natural gradient. Molecular Ecology, 1997, 6, 989-993.	3.9	96
15	A study of genetic diversity in Populus nigra subsp. betulifolia in the Upper Severn area of the UK using AFLP markers. Molecular Ecology, 1998, 7, 3-10.	3.9	86
16	A genetic linkage map of willow (Salix viminalis) based on AFLP and microsatellite markers. Theoretical and Applied Genetics, 2002, 105, 1087-1096.	3.6	81
17	Invasive species ofHeracleumin Europe: an insight into genetic relationships and invasion history. Diversity and Distributions, 2007, 13, 99-114.	4.1	80
18	Alignment of a Salix linkage map to the Populus genomic sequence reveals macrosynteny between willow and poplar genomes. Tree Genetics and Genomes, 2006, 3, 35-48.	1.6	75

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19	Identification of the E3900 family, a second family of rye B chromosome specific repeated sequences. Genome, 1993, 36, 706-711.	2.0	74
20	Chromosome doubling in monohaploid and dihaploid potatoes by regeneration from cultured leaf explants. Plant Cell, Tissue and Organ Culture, 1984, 3, 363-373.	2.3	72
21	Heritable somaclonal variation in wild barley (Hordeum spontaneum). Theoretical and Applied Genetics, 1987, 74, 104-112.	3.6	69
22	Characterisation of genetic diversity in potential biomass willows (Salix spp.) by RAPD and AFLP analyses. Genome, 1999, 42, 173-183.	2.0	69
23	Studies on the genetic basis of resistance to potato leaf roll virus, potato virus Y and potato virus X in Solanum brevidens using somatic hybrids of Solanum brevidens and Solanum tuberosum. Plant Science, 1990, 69, 95-101.	3.6	68
24	An anchored linkage map for sugar beet based on AFLP, SNP and RAPD markers and QTL mapping of a new source of resistance to Beet necrotic yellow vein virus. Theoretical and Applied Genetics, 2007, 114, 1151-1160.	3.6	64
25	High yielding biomass genotypes of willow (Salix spp.) show differences in below ground biomass allocation. Biomass and Bioenergy, 2015, 80, 114-127.	5.7	63
26	Chromosome variation in dividing protoplasts and cell suspensions of wheat. Theoretical and Applied Genetics, 1987, 74, 140-146.	3.6	61
27	Karyotypic changes in potato plants regenerated from protoplasts. Plant Cell, Tissue and Organ Culture, 1985, 4, 171-182.	2.3	60
28	Microsatellite markers for diverse Salix species. Molecular Ecology Notes, 2002, 3, 4-6.	1.7	57
29	Characterisation of genetic diversity in potential biomass willows (Salix spp.) by RAPD and AFLP analyses. Genome, 1999, 42, 173-183.	2.0	56
30	Genetic strategies for dissecting complex traits in biomass willows (Salix spp.). Tree Physiology, 2014, 34, 1167-1180.	3.1	54
31	Improvements in regeneration from protoplasts of potato and studies on chromosome stability. Theoretical and Applied Genetics, 1986, 72, 405-412.	3.6	51
32	Variation in Cell Wall Composition and Accessibility in Relation to Biofuel Potential of Short Rotation Coppice Willows. Bioenergy Research, 2012, 5, 685-698.	3.9	48
33	QTL Mapping of Enzymatic Saccharification in Short Rotation Coppice Willow and Its Independence from Biomass Yield. Bioenergy Research, 2010, 3, 251-261.	3.9	46
34	Analysis of rye B-chromosome structure using fluorescencein situ hybridization (FISH). Chromosome Research, 1995, 3, 466-472.	2.2	45
35	Learning How to Deal with Values, Frames and Governance in Sustainability Appraisal. Regional Studies, 2011, 45, 1157-1170.	4.4	45
36	Dedicated biomass crops can enhance biodiversity in the arable landscape. GCB Bioenergy, 2016, 8, 1071-1081.	5.6	45

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37	Genetic diversity, population structure and phenotypic variation in European Salix viminalis L. (Salicaceae). Tree Genetics and Genomes, 2014, 10, 1595-1610.	1.6	44
38	Somaclonal variation as a tool for crop improvement. Developments in Plant Breeding, 1995, , 295-302.	0.2	44
39	Characterisation of the willow phenylalanine ammonia-lyase (PAL) gene family reveals expression differences compared with poplar. Phytochemistry, 2015, 117, 90-97.	2.9	43
40	Genetic manipulation in potato withAgrobacterium rhizogenes. Potato Research, 1986, 29, 367-379.	2.7	40
41	Physical mapping of the B-hordein loci on barley chromosome 5 by in situ hybridization. Genome, 1989, 32, 925-929.	2.0	40
42	Genetic diversity in Echinochloa spp. collected from different geographic origins and within rice fields in Cote d'Ivoire. Weed Research, 2002, 42, 394-405.	1.7	40
43	Defining leaf traits linked to yield in short-rotation coppice Salix. Biomass and Bioenergy, 2004, 26, 417-431.	5.7	39
44	Microsatellite analysis of the inbreeding grass weed Barren Brome (Anisantha sterilis) reveals genetic diversity at the within- and between-farm scales. Molecular Ecology, 2001, 10, 1035-1045.	3.9	37
45	A Genetic Study of a Salix Germplasm Resource Reveals New Insights into Relationships Among Subgenera, Sections and Species. Bioenergy Research, 2008, 1, 67-79.	3.9	37
46	Reaction wood â€“ a key cause of variation in cell wall recalcitrance in willow. Biotechnology for Biofuels, 2012, 5, 83.	6.2	36
47	The environmental impacts of biomass crops: use by birds of miscanthus in summer and winter in southwestern England. Ibis, 2010, 152, 487-499.	1.9	35
48	G-fibre cell wall development in willow stems during tension wood induction. Journal of Experimental Botany, 2015, 66, 6447-6459.	4.8	34
49	A high degree of genetic diversity is revealed in Isatis spp. (dyer's woad) by amplified fragment length polymorphism (AFLP). Theoretical and Applied Genetics, 2002, 104, 1150-1156.	3.6	33
50	Differences in the molecular basis of resistance to the cyclohexanedione herbicide sethoxydim in Lolium multiflorum. Weed Research, 2005, 45, 440-448.	1.7	33
51	Investigation of tension wood formation and 2,6-dichlorbenzonitrile application in short rotation coppice willow composition and enzymatic saccharification. Biotechnology for Biofuels, 2011, 4, 13.	6.2	33
52	Association mapping in Salix viminalis L. (Salicaceae) â€“ identification of candidate genes associated with growth and phenology. GCB Bioenergy, 2016, 8, 670-685.	5.6	32
53	Variability in potato tissue culture. American Potato Journal, 1989, 66, 669-684.	0.3	30
54	X-ray micro-computed tomography in willow reveals tissue patterning of reaction wood and delay in programmed cell death. BMC Plant Biology, 2015, 15, 83.	3.6	30

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55	Getting the most out of fluorescent amplified fragment length polymorphism. Canadian Journal of Botany, 2006, 84, 1347-1354.	1.1	29
56	Cytogenetics of Lolium perenne. Theoretical and Applied Genetics, 1983, 64, 137-145.	3.6	27
57	High Levels of Genetic Diversity in Salix viminalis of the Czech Republic as Revealed by Microsatellite Markers. Bioenergy Research, 2012, 5, 969-977.	3.9	27
58	Analysis off cereal chromosomes by atomic force microscopy. Genome, 1996, 39, 439-444.	2.0	25
59	Characterisation and inheritance of nuclear microsatellite loci for use in population studies of the allotetraploid Salix albaâ€“Salix fragilis complex. Tree Genetics and Genomes, 2010, 6, 247-258.	1.6	25
60	Isolation, culture, and regeneration of plants from potato protoplasts. Plant Cell Reports, 1989, 8, 307-11.	5.6	23
61	Expression of shoot-inducing Ti TL-DNA in differentiated tissues of potato (Solanum tuberosum cv) Tj ETQq1 1 0.784314 rgBT /Overlo	3.9	22
62	A comparison of chromosome instability in cell suspensions of diploid, tetraploid and hexaploid wheats. Heredity, 1993, 70, 187-194.	2.6	22
63	Using Arabidopsis to Study Shoot Branching in Biomass Willow Â Â Â. Plant Physiology, 2013, 162, 800-811.	4.8	22
64	Cytological and molecular evidence of deletion of ribosomal RNA genes in chromosome 6 of barley (Hordeum vulgare). Genome, 1994, 37, 419-425.	2.0	21
65	Genetic mapping of rust resistance loci in biomass willow. Tree Genetics and Genomes, 2011, 7, 597-608.	1.6	21
66	Cytogenetics of Lolium perenne. Theoretical and Applied Genetics, 1982, 62, 177-183.	3.6	18
67	Ploidy Variation inSolanum brevidensPlants Regenerated from Protoplasts Using an Improved Culture System. Journal of Experimental Botany, 1986, 37, 253-261.	4.8	18
68	Chromosomal assignment of genes in barley using telosomic wheatâ€“barley addition lines. Genome, 1992, 35, 17-23.	2.0	18
69	Insights into nitrogen allocation and recycling from nitrogen elemental analysis and 15N isotope labelling in 14 genotypes of willow. Tree Physiology, 2014, 34, 1252-1262.	3.1	17
70	Atomic force microscopy of plant chromosomes. Chromosome Research, 1995, 3, 128-131.	2.2	15
71	Development of a sinkâ€“source interaction model for the growth of short-rotation coppice willow andin silicoexploration of genotypeÃ—environment effects. Journal of Experimental Botany, 2016, 67, 961-977.	4.8	15
72	The effects of nucleotype and genotype upon pollen grain development in Hyacinth and Scilla. Heredity, 1982, 48, 251-261.	2.6	14

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73	Effect of genotype on chromosome variation in tissue culture of inbred and outbred rye. Heredity, 1993, 71, 138-144.	2.6	13
74	Functional screening of willow alleles in A rabidopsis combined with QTL mapping in willow (S alix) identifies S x MAX 4 as a coppicing response gene. Plant Biotechnology Journal, 2014, 12, 480-491.	8.3	13
75	A SNaPshot assay for the rapid and simple detection of known point mutations conferring resistance to ACCaseâ€inhibiting herbicides in Lolium spp.. Weed Research, 2013, 53, 12-20.	1.7	12
76	Photosynthesis and growth in diverse willow genotypes. Food and Energy Security, 2014, 3, 69-85.	4.3	12
77	Growing innovations for the bioeconomy. Nature Plants, 2015, 1, 15193.	9.3	12
78	Isolation, culture and morphogenesis from wheat protoplasts, and study of expression of DNA constructs by direct gene transfer. Plant Cell, Tissue and Organ Culture, 1988, 12, 223-226.	2.3	10
79	Isolation and characterization of polymorphic microsatellites in Cocos nucifera L.. Genome, 1999, 42, 668-675.	2.0	9
80	Potato Protoplasts and Tissue Culture in Crop Improvement. Biotechnology and Genetic Engineering Reviews, 1987, 5, 1-32.	6.2	8
81	Nonrandom chromosome variation and morphogenic potential in cell lines of bread wheat (Triticum aestivum L.). Genome, 1995, 38, 869-878.	2.0	8
82	Population structure of the beetle pests Phyllodecta vulgatissima and P.Âvitellinae on UK willow plantations. Insect Molecular Biology, 2004, 13, 413-421.	2.0	8
83	A pseudo-3D model to optimise the target traits of light interception in short-rotation coppice willow. Agricultural and Forest Meteorology, 2013, 173, 127-138.	4.8	8
84	Secondary cell wall composition and candidate gene expression in developing willow (Salix purpurea) stems. Planta, 2014, 239, 1041-1053.	3.2	8
85	Microsatellites for Barren Brome (Anisantha sterilis). Molecular Ecology, 2000, 9, 2195-2197.	3.9	7
86	Geographic variation in phenotypic traits in Phratora spp. and the effects of conditioning on feeding preference. Entomologia Experimentalis Et Applicata, 2003, 109, 31-37.	1.4	7
87	Chromosome 5D instability in cell lines of Triticum tauschii and morphological variation in regenerated plants. Genome, 1995, 38, 737-742.	2.0	6
88	A comparative study of interspecies mating of Phratora vulgatissima and P. vitellinae using behavioural tests and molecular markers. Entomologia Experimentalis Et Applicata, 2004, 110, 231-241.	1.4	6
89	Population genetics of Tuberolachnus salignus, an obligate parthenogenetic aphid. Agricultural and Forest Entomology, 2012, 14, 197-205.	1.3	6
90	Mendelian inheritance of rust resistance to Melampsora laricià€epitea in crosses between Salix sachalinensis and S.Âviminalis. Plant Pathology, 2010, 59, 862-872.	2.4	5

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91	Efficient method for rapid multiplication of clean and healthy willow clones via in vitro propagation with broad genotype applicability. Canadian Journal of Forest Research, 2015, 45, 1662-1667.	1.7	5
92	Willows as a Source of Renewable Fuels and Diverse Products. Forestry Sciences, 2014, , 617-641.	0.4	5
93	Cytogenetics of Lolium perenne. Theoretical and Applied Genetics, 1983, 65, 149-156.	3.6	3
94	Genetics, Genomics and Crop Modelling: Integrative Approaches to the Improvement of Biomass Willows. , 2014, , 107-130.		2
95	A comparative study of the mitochondrial genome organization in in vitro cultures of diploid, tetraploid, and hexaploid Triticum species. Theoretical and Applied Genetics, 1996, 93-93, 968-974.	3.6	1
96	Evidence of diversity within the SnRK1b gene family of Hordeum species. Genome, 2005, 48, 661-673.	2.0	1
97	Biotechnology, Biodiversity and Conservation. Nature Biotechnology, 1995, 13, 522-522.	17.5	0
98	Biodiversity in Agricultural Systems: New Challenges for Genome Diversity Studies. Stadler Genetics Symposia Series, 2000, , 99-108.	0.0	0