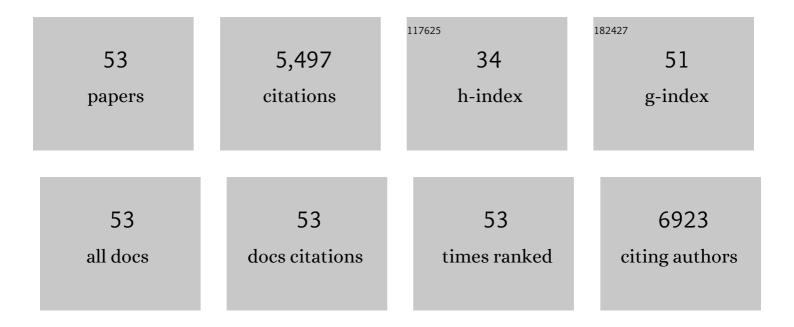
Richard Cooke

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome analysis of the smallest free-living eukaryote Ostreococcus tauri unveils many unique features. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11647-11652.	7.1	809
2	Extensive Duplication and Reshuffling in the Arabidopsis Genome. Plant Cell, 2000, 12, 1093-1101.	6.6	512
3	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
4	Identification and Characterization of Shared Duplications between Rice and Wheat Provide New Insight into Grass Genome Evolution. Plant Cell, 2008, 20, 11-24.	6.6	332
5	Reiterated WG/GW motifs form functionally and evolutionarily conserved ARGONAUTE-binding platforms in RNAi-related components. Genes and Development, 2007, 21, 2539-2544.	5.9	280
6	The Organization of Cytoplasmic Ribosomal Protein Genes in the Arabidopsis Genome. Plant Physiology, 2001, 127, 398-415.	4.8	272
7	Inventory, evolution and expression profiling diversity of the LEA (late embryogenesis abundant) protein gene family in Arabidopsis thaliana. Plant Molecular Biology, 2008, 67, 107-124.	3.9	272
8	An inventory of 1152 expressed sequence tags obtained by partial sequencing of cDNAs from Arabidopsis thaliana+. Plant Journal, 1993, 4, 1051-1061.	5.7	254
9	Further progress towards a catalogue of all Arabidopsis genes: analysis of a set of 5000 non-redundant ESTs. Plant Journal, 1996, 9, 101-124.	5.7	208
10	NERD, a Plant-Specific GW Protein, Defines an Additional RNAi-Dependent Chromatin-Based Pathway in Arabidopsis. Molecular Cell, 2012, 48, 121-132.	9.7	134
11	RNAâ€directed DNA methylation requires an AGO4â€interacting member of the SPT5 elongation factor family. EMBO Reports, 2009, 10, 649-654.	4.5	130
12	Nucleolin Is Required for DNA Methylation State and the Expression of rRNA Gene Variants in Arabidopsis thaliana. PLoS Genetics, 2010, 6, e1001225.	3.5	121
13	An Arabidopsis thaliana cDNA complementing a hamster apoptosis suppressor mutant. Plant Journal, 1997, 11, 1325-1331.	5.7	112
14	Palaeogenomics of plants: synteny-based modelling of extinct ancestors. Trends in Plant Science, 2010, 15, 479-487.	8.8	111
15	Life-Cycle and Genome of OtV5, a Large DNA Virus of the Pelagic Marine Unicellular Green Alga Ostreococcus tauri. PLoS ONE, 2008, 3, e2250.	2.5	107
16	The Arabidopsis Root Transcriptome by Serial Analysis of Gene Expression. Gene Identification Using the Genome Sequence. Plant Physiology, 2004, 134, 67-80.	4.8	90
17	Marine Prasinovirus Genomes Show Low Evolutionary Divergence and Acquisition of Protein Metabolism Genes by Horizontal Gene Transfer. Journal of Virology, 2010, 84, 12555-12563.	3.4	87
18	Newin silicoinsight into the synteny between rice (Oryza sativaL.) and maize (Zea maysL.) highlights reshuffling and identifies new duplications in the rice genome. Plant Journal, 2004, 38, 396-409.	5.7	86

RICHARD COOKE

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19	Gene expression profile in response to Xanthomonas axonopodis pv. manihotis infection in cassava using a cDNA microarray. Plant Molecular Biology, 2005, 57, 393-410.	3.9	86
20	Synteny between Arabidopsis thaliana and rice at the genome level: a tool to identify conservation in the ongoing rice genome sequencing project. Nucleic Acids Research, 2002, 30, 2316-2328.	14.5	81
21	Shared Subgenome Dominance Following Polyploidization Explains Grass Genome Evolutionary Plasticity from a Seven Protochromosome Ancestor with 16K Protogenes. Genome Biology and Evolution, 2014, 6, 12-33.	2.5	75
22	Evidence for ARGONAUTE4–DNA interactions in RNA-directed DNA methylation in plants. Genes and Development, 2016, 30, 2565-2570.	5.9	75
23	Rice genomics: Present and future. Plant Physiology and Biochemistry, 2001, 39, 323-334.	5.8	69
24	Sequence heterogeneity in radish nuclear ribosomal RNA genes. Plant Science Letters, 1983, 30, 107-119.	1.8	65
25	An update on nutrient transport processes in ectomycorrhizas. Plant and Soil, 2002, 244, 165-175.	3.7	62
26	A unigene catalogue of 5700 expressed genes in cassava. Plant Molecular Biology, 2004, 56, 541-554.	3.9	53
27	Genome-wide computational identification of WG/GW Argonaute-binding proteins in Arabidopsis. Nucleic Acids Research, 2010, 38, 4231-4245.	14.5	47
28	The Arabidopsis thaliana cDNA sequencing projects 1. FEBS Letters, 1997, 403, 221-224.	2.8	42
29	DNA LIBRARIES FOR SEQUENCING THE GENOME OFOSTREOCOCCUS TAURI(CHLOROPHYTA,) TJ ETQq1 1 0.784 1150-1156.	314 rgBT / 2.3	Overlock 10 42
30	A recent duplication revisited: phylogenetic analysis reveals an ancestral duplication highly-conserved throughout the Oryza genus and beyond. BMC Plant Biology, 2009, 9, 146.	3.6	41
31	Largeâ€scale identification of genes in the fungus Hebeloma cylindrosporum paves the way to molecular analyses of ectomycorrhizal symbiosis. New Phytologist, 2004, 164, 505-513.	7.3	40
32	Time course of hormonal control of the first mitosis in tobacco mesophyll protoplasts cultivated in vitro. Planta, 1979, 147, 181-185.	3.2	38
33	An EST resource for cassava and other species of Euphorbiaceae. Plant Molecular Biology, 2004, 56, 527-539.	3.9	38
34	Identification of members of gene families in Arabidopsis thaliana by contig construction from partial cDNA sequences: 106 genes encoding 50 cytoplasmic ribosomal proteins. Plant Journal, 1997, 11, 1127-1140.	5.7	35
35	Diversity of Viruses Infecting the Green Microalga Ostreococcus lucimarinus. Journal of Virology, 2015, 89, 5812-5821.	3.4	35
36	Identification of protein factors and U3 snoRNAs from a <i>Brassica oleracea</i> RNP complex involved in the processing of preâ€rRNA. Plant Journal, 2010, 61, 383-398.	5.7	30

RICHARD COOKE

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37	In vitro transcription from cauliflower mosaic virus promoters by a cell-free extract from tobacco cells. Plant Molecular Biology, 1990, 14, 391-405.	3.9	29
38	Variations in a team: Major and minor variants of <i>Arabidopsis</i> thaliana rDNA genes. Nucleus, 2011, 2, 294-299.	2.2	29
39	Structure, organization and expression of two closely related novel Lea (late-embryogenesis-abundant) genes in Arabidopsis thaliana. Plant Molecular Biology, 1999, 40, 153-165.	3.9	23
40	Taking RISCs with Ago hookers. Current Opinion in Plant Biology, 2011, 14, 594-600.	7.1	22
41	Restriction analysis of radish nuclear genes coding for rRNA: Evidence for heterogeneity. Biochemical and Biophysical Research Communications, 1979, 91, 540-547.	2.1	20
42	Flanking sequence tags in Arabidopsis thaliana T-DNA insertion lines: a pilot study. Comptes Rendus - Biologies, 2002, 325, 773-780.	0.2	18
43	Analysis of DNA associated with nucleosomes in pea chromatin. Planta, 1980, 148, 346-353.	3.2	17
44	GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. Nucleic Acids Research, 2004, 33, D641-D646.	14.5	16
45	Ribosomal RNA synthesis in imbibing radish (Raphanus sativus) embryo axes. Planta, 1980, 148, 17-23.	3.2	8
46	Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on chromosome III. Plant Molecular Biology, 1999, 41, 687-700.	3.9	8
47	The figwort mosaic virus gene VI promoter region contains a sequence highly homologous to the octopine synthase (ocs) enhancer element. Plant Molecular Biology, 1990, 15, 181-182.	3.9	6
48	The Arabidopsis thaliana genome project. Comptes Rendus De L'Académie Des Sciences Série 3, Sciences De La Vie, 1997, 320, 589-599.	0.8	6
49	Extensive Duplication and Reshuffling in the Arabidopsis Genome. Plant Cell, 2000, 12, 1093.	6.6	4
50	From Rice to Other Cereals: Comparative Genomics. , 2007, , 429-479.		3
51	Selective dinucleotide-primed in vitro transcription of a cloned fragment of cauliflower mosaic virus DNA is dependent on a limited region of the viral genome. FEBS Journal, 1986, 157, 83-89.	0.2	2
52	Detection of a potential transcription control sequene on the cauliflower mosaic virus oenome by dinuleotide primed "in vitro―transcription. Biochemical and Biophysical Research Communications, 1986, 138, 17-23.	2.1	1
53	In Vitro Transcription of Class II Promoters in Higher Plants. , 1995, 49, 271-290.		1