J Mark Cock

List of Publications by Year in Descending Order

130 papers	5,573 citations	40 h-index	72 g-index
139 ext. papers	6,567 ext. citations	7.2 avg, IF	5.29 L-index

#	Paper	IF	Citations
130	Providing a phylogenetic framework for trait-based analyses in brown algae: Phylogenomic tree inferred from 32 nuclear protein-coding sequences.. *Molecular Phylogenetics and Evolution*, **2022**, 168, 107408	4.1	0
129	Chromatin landscape associated with sexual differentiation in a UV sex determination system.. *Nucleic Acids Research*, **2022**,	20.1	2
128	An Efficient Chromatin Immunoprecipitation Protocol for the Analysis of Histone Modification Distributions in the Brown Alga Ectocarpus. *Methods and Protocols*, **2022**, 5, 36	2.5	0
127	Biochemical characteristics of a diffusible factor that induces gametophyte to sporophyte switching in the brown alga Ectocarpus. *Journal of Phycology*, **2021**, 57, 742-753	3	1
126	Evolution of life cycles and reproductive traits: Insights from the brown algae. *Journal of Evolutionary Biology*, **2021**, 34, 992-1009	2.3	5
125	Alternation of Generations in Plants and Algae **2021**, 631-644		1
124	Histone modifications during the life cycle of the brown alga Ectocarpus. *Genome Biology*, **2021**, 22, 12	18.3	9
123	Role and Evolution of the Extracellular Matrix in the Acquisition of Complex Multicellularity in Eukaryotes: A Macroalgal Perspective. *Genes*, **2021**, 12,	4.2	6
122	Targeted CRISPR-Cas9-based gene knockouts in the model brown alga Ectocarpus. *New Phytologist*, **2021**, 231, 2077-2091	9.8	7
121	A partially sex-reversed giant kelp sheds light into the mechanisms of sexual differentiation in a UV sexual system. *New Phytologist*, **2021**, 232, 252-263	9.8	2
120	instaGRAAL: chromosome-level quality scaffolding of genomes using a proximity ligation-based scaffolder. *Genome Biology*, **2020**, 21, 148	18.3	11
119	Organelle inheritance and genome architecture variation in isogamous brown algae. *Scientific Reports*, **2020**, 10, 2048	4.9	7
118	Parallelisable non-invasive biomass, fitness and growth measurement of macroalgae and other protists with nephelometry. *Algal Research*, **2020**, 46, 101762	5	1
117	Production and Bioassay of a Diffusible Factor That Induces Gametophyte-to-Sporophyte Developmental Reprogramming in the Brown Alga. *Bio-protocol*, **2020**, 10, e3753	0.9	1
116	Brown Algal Model Organisms. *Annual Review of Genetics*, **2020**, 54, 71-92	14.5	7
115	Cytokinin and Ethylene Cell Signaling Pathways from Prokaryotes to Eukaryotes. *Cells*, **2020**, 9,	7.9	4
114	Phylogeny and Evolution of the Brown Algae. *Critical Reviews in Plant Sciences*, **2020**, 39, 281-321	5.6	31

113	: an evo-devo model for the brown algae. *EvoDevo*, **2020**, 11, 19	3.2	5
112	Unusual Patterns of Mitochondrial Inheritance in the Brown Alga Ectocarpus. *Molecular Biology and Evolution*, **2019**, 36, 2778-2789	8.3	3
111	Origin and evolution of sex-determination systems in the brown algae. *New Phytologist*, **2019**, 222, 1751-1756	9.8	10
110	A key role for sex chromosomes in the regulation of parthenogenesis in the brown alga Ectocarpus. *PLoS Genetics*, **2019**, 15, e1008211	6	11
109	Megaviruses: An involvement in phytohormone receptor gene transfer in brown algae?. *Gene*, **2019**, 704, 149-151	3.8	4
108	Rapid turnover of life-cycle-related genes in the brown algae. *Genome Biology*, **2019**, 20, 35	18.3	17
107	Convergent recruitment of TALE homeodomain life cycle regulators to direct sporophyte development in land plants and brown algae. *ELife*, **2019**, 8,	8.9	33
106	Diversity and Evolution of Sensor Histidine Kinases in Eukaryotes. *Genome Biology and Evolution*, **2019**, 11, 86-108	3.9	16
105	Genetic Diversity in the UV Sex Chromosomes of the Brown Alga. *Genes*, **2018**, 9,	4.2	10
104	UV Chromosomes and Haploid Sexual Systems. *Trends in Plant Science*, **2018**, 23, 794-807	13.1	34
103	The Ectocarpus IMMEDIATE UPRIGHT gene encodes a member of a novel family of cysteine-rich proteins with an unusual distribution across the eukaryotes. *Development (Cambridge)*, **2017**, 144, 409-418	6.6	18
102	Multiple gene movements into and out of haploid sex chromosomes. *Genome Biology*, **2017**, 18, 104	18.3	31
101	The Algal Revolution. *Trends in Plant Science*, **2017**, 22, 726-738	13.1	48
100	High-density genetic map and identification of QTLs for responses to temperature and salinity stresses in the model brown alga Ectocarpus. *Scientific Reports*, **2017**, 7, 43241	4.9	25
99	Biotic interactions as drivers of algal origin and evolution. *New Phytologist*, **2017**, 216, 670-681	9.8	18
98	DISTAG/TBCCd1 Is Required for Basal Cell Fate Determination in. *Plant Cell*, **2017**, 29, 3102-3122	11.6	12
97	Re-annotation, improved large-scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga Ectocarpus. *New Phytologist*, **2017**, 214, 219-232	9.8	46
96	Rapid Evolution of microRNA Loci in the Brown Algae. *Genome Biology and Evolution*, **2017**, 9, 740-749	3.9	15

95	Alternation of Generations in Plants and Algae **2017**, 1-14		
94	Characterization of newly developed expressed sequence tag-derived microsatellite markers revealed low genetic diversity within and low connectivity between European Saccharina latissima populations. *Journal of Applied Phycology*, **2016**, 28, 3057-3070	3.2	14
93	microRNAs and the evolution of complex multicellularity: identification of a large, diverse complement of microRNAs in the brown alga Ectocarpus. *Nucleic Acids Research*, **2015**, 43, 6384-98	20.1	28
92	Independent Emergence of Complex Multicellularity in the Brown and Red Algae. *Advances in Marine Genomics*, **2015**, 335-361		10
91	Sexual dimorphism and the evolution of sex-biased gene expression in the brown alga ectocarpus. *Molecular Biology and Evolution*, **2015**, 32, 1581-97	8.3	68
90	The Pseudoautosomal Regions of the U/V Sex Chromosomes of the Brown Alga Ectocarpus Exhibit Unusual Features. *Molecular Biology and Evolution*, **2015**, 32, 2973-85	8.3	16
89	Genome-wide comparison of ultraviolet and ethyl methanesulphonate mutagenesis methods for the brown alga Ectocarpus. *Marine Genomics*, **2015**, 24 Pt 1, 109-13	1.9	9
88	Evolution and maintenance of haploid-diploid life cycles in natural populations: The case of the marine brown alga Ectocarpus. *Evolution; International Journal of Organic Evolution*, **2015**, 69, 1808-22	3.8	36
87	Development of PCR-Based Markers to Determine the Sex of Kelps. *PLoS ONE*, **2015**, 10, e0140535	3.7	23
86	Emergence of Ectocarpus as a Model System to Study the Evolution of Complex Multicellularity in the Brown Algae. *Advances in Marine Genomics*, **2015**, 153-162		4
85	Proteomics analysis of heterogeneous flagella in brown algae (stramenopiles). *Protist*, **2014**, 165, 662-75	2.5	26
84	A haploid system of sex determination in the brown alga Ectocarpus sp. *Current Biology*, **2014**, 24, 1945-57	9.3	93
83	Evolution and regulation of complex life cycles: a brown algal perspective. *Current Opinion in Plant Biology*, **2014**, 17, 1-6	9.9	41
82	Gene silencing in Fucus embryos: developmental consequences of RNAi-mediated cytoskeletal disruption. *Journal of Phycology*, **2013**, 49, 819-29	3	20
81	Genome structure and metabolic features in the red seaweed Chondrus crispus shed light on evolution of the Archaeplastida. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 5247-52	11.5	239
80	Ecological and evolutionary genomics of marine photosynthetic organisms. *Molecular Ecology*, **2013**, 22, 867-907	5.7	27
79	Non-cell autonomous regulation of life cycle transitions in the model brown alga Ectocarpus. *New Phytologist*, **2013**, 197, 503-510	9.8	17
78	Genomics of brown algae: current advances and future prospects. *Genes and Genomics*, **2012**, 34, 1-5	2.1	6

77	The Ectocarpus Genome and Brown Algal Genomics: The Ectocarpus Genome Consortium. *Advances in Botanical Research*, **2012**, 64, 141-184	2.2	10
76	Extraction of high-quality genomic DNA from Ectocarpus. *Cold Spring Harbor Protocols*, **2012**, 2012, 365-8	1.2	2
75	Immunostaining of Ectocarpus cells. *Cold Spring Harbor Protocols*, **2012**, 2012, 369-72	1.2	5
74	Ectocarpus: a model organism for the brown algae. *Cold Spring Harbor Protocols*, **2012**, 2012, 193-8	1.2	33
73	Genetic crosses between Ectocarpus strains. *Cold Spring Harbor Protocols*, **2012**, 2012, 262-5	1.2	13
72	How to cultivate Ectocarpus. *Cold Spring Harbor Protocols*, **2012**, 2012, 258-61	1.2	39
71	In silico survey of the mitochondrial protein uptake and maturation systems in the brown alga Ectocarpus siliculosus. *PLoS ONE*, **2011**, 6, e19540	3.7	10
70	Brown algae. *Current Biology*, **2011**, 21, R573-5	6.3	21
69	Microarray estimation of genomic inter-strain variability in the genus Ectocarpus (Phaeophyceae). *BMC Molecular Biology*, **2011**, 12, 2	4.5	18
68	Genetic regulation of life cycle transitions in the brown alga Ectocarpus. *Plant Signaling and Behavior*, **2011**, 6, 1858-60	2.5	8
67	OUROBOROS is a master regulator of the gametophyte to sporophyte life cycle transition in the brown alga Ectocarpus. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 11518-23	11.5	69
66	Algal models in plant biology. *Journal of Experimental Botany*, **2011**, 62, 2425-30	7	25
65	Characterization of GDP-mannose dehydrogenase from the brown alga Ectocarpus siliculosus providing the precursor for the alginate polymer. *Journal of Biological Chemistry*, **2011**, 286, 16707-15	5.4	24
64	A sequence-tagged genetic map for the brown alga Ectocarpus siliculosus provides large-scale assembly of the genome sequence. *New Phytologist*, **2010**, 188, 42-51	9.8	51
63	Genetic diversity of Ectocarpus (Ectocarpales, Phaeophyceae) in Peru and northern Chile, the area of origin of the genome-sequenced strain. *New Phytologist*, **2010**, 188, 30-41	9.8	19
62	Central and storage carbon metabolism of the brown alga Ectocarpus siliculosus: insights into the origin and evolution of storage carbohydrates in Eukaryotes. *New Phytologist*, **2010**, 188, 67-81	9.8	129
61	Role of endoreduplication and apomeiosis during parthenogenetic reproduction in the model brown alga Ectocarpus. *New Phytologist*, **2010**, 188, 111-21	9.8	40
60	The cell wall polysaccharide metabolism of the brown alga Ectocarpus siliculosus. Insights into the evolution of extracellular matrix polysaccharides in Eukaryotes. *New Phytologist*, **2010**, 188, 82-97	9.8	297

59	The Ectocarpus genome sequence: insights into brown algal biology and the evolutionary diversity of the eukaryotes. *New Phytologist*, **2010**, 188, 1-4	9.8	32
58	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. *Nature*, **2010**, 465, 617-21	50.4	645
57	Reinstatement of Ectocarpus crouaniorum Thuret in Le Jolis as a third common species of Ectocarpus (Ectocarpales, Phaeophyceae) in Western Europe, and its phenology at Roscoff, Brittany. *Phycological Research*, **2010**, 58, 157-170	1.3	35
56	Cell cycles and endocycles in the model brown seaweed, Ectocarpus siliculosus. *Plant Signaling and Behavior*, **2010**, 5, 1473-5	2.5	5
55	Auxin metabolism and function in the multicellular brown alga Ectocarpus siliculosus. *Plant Physiology*, **2010**, 153, 128-44	6.6	76
54	Copper stress proteomics highlights local adaptation of two strains of the model brown alga Ectocarpus siliculosus. *Proteomics*, **2010**, 10, 2074-88	4.8	77
53	Genomics of Marine Algae **2010**, 179-211		2
52	03-P056 Molecular control of the alternation of generations in the brown alga Ectocarpus: The OUROBOROS mutant exhibits homeotic conversion of the sporophyte into a gametophyte. *Mechanisms of Development*, **2009**, 126, S83	1.7	
51	Plastid genomes of two brown algae, Ectocarpus siliculosus and Fucus vesiculosus: further insights on the evolution of red-algal derived plastids. *BMC Evolutionary Biology*, **2009**, 9, 253	3	71
50	Global expression analysis of the brown alga Ectocarpus siliculosus (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. *Genome Biology*, **2009**, 10, R66	18.3	113
49	EARLY DEVELOPMENT PATTERN OF THE BROWN ALGA ECTOCARPUS SILICULOSUS (ECTOCARPALES, PHAEOPHYCEAE) SPOROPHYTE(1). *Journal of Phycology*, **2008**, 44, 1269-81	3	21
48	Development and physiology of the brown alga Ectocarpus siliculosus: two centuries of research. *New Phytologist*, **2008**, 177, 319-332	9.8	103
47	HECTAR: a method to predict subcellular targeting in heterokonts. *BMC Bioinformatics*, **2008**, 9, 393	3.6	141
46	Scent evolution in Chinese roses. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 5927-32	11.5	68
45	Life-cycle-generation-specific developmental processes are modified in the immediate upright mutant of the brown alga Ectocarpus siliculosus. *Development (Cambridge)*, **2008**, 135, 1503-12	6.6	76
44	The FTO gene, implicated in human obesity, is found only in vertebrates and marine algae. *Journal of Molecular Evolution*, **2008**, 66, 80-4	3.1	50
43	Both the adaxial and abaxial epidermal layers of the rose petal emit volatile scent compounds. *Planta*, **2007**, 226, 853-66	4.7	80
42	Production and emission of volatile compounds by petal cells. *Plant Signaling and Behavior*, **2007**, 2, 525-6	2.5	18

41	Complex life cycles of multicellular eukaryotes: new approaches based on the use of model organisms. *Gene*, **2007**, 406, 152-70	3.8	92
40	Role of petal-specific orcinol O-methyltransferases in the evolution of rose scent. *Plant Physiology*, **2006**, 140, 18-29	6.6	55
39	BIGPETALp, a bHLH transcription factor is involved in the control of Arabidopsis petal size. *EMBO Journal*, **2006**, 25, 3912-20	13	142
38	A W-box is required for full expression of the SA-responsive gene SFR2. *Gene*, **2005**, 344, 181-92	3.8	22
37	Inheritance of organelles in artificial hybrids of the isogamous multicellular chromist alga Ectocarpus siliculosus (Phaeophyceae). *European Journal of Phycology*, **2004**, 39, 235-242	2.2	50
36	PROPOSAL OF ECTOCARPUS SILICULOSUS (ECTOCARPALES, PHAEOPHYCEAE) AS A MODEL ORGANISM FOR BROWN ALGAL GENETICS AND GENOMICS1,2. *Journal of Phycology*, **2004**, 40, 1079-1088	3	112
35	Antisense suppression of thioredoxin h mRNA in Brassica napus cv. Westar pistils causes a low level constitutive pollen rejection response. *Plant Molecular Biology*, **2004**, 55, 619-30	4.6	38
34	Making inroads into plant receptor kinase signalling pathways. *Trends in Plant Science*, **2003**, 8, 231-7	13.1	72
33	Interaction of calmodulin, a sorting nexin and kinase-associated protein phosphatase with the Brassica oleracea S locus receptor kinase. *Plant Physiology*, **2003**, 133, 919-29	6.6	96
32	Receptor kinase signalling in plants and animals: distinct molecular systems with mechanistic similarities. *Current Opinion in Cell Biology*, **2002**, 14, 230-6	9	69
31	Analysis of gene expression in rose petals using expressed sequence tags. *FEBS Letters*, **2002**, 515, 35-8	3.8	70
30	Biosynthesis of the major scent components 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene by novel rose O-methyltransferases. *FEBS Letters*, **2002**, 523, 113-8	3.8	60
29	Comparison of the expression patterns of two small gene families of S gene family receptor kinase genes during the defence response in Brassica oleracea and Arabidopsis thaliana. *Gene*, **2002**, 282, 215-25	2.8	35
28	Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the male component of the self-incompatibility response. *Plant Molecular Biology*, **2001**, 46, 17-34	4.6	61
27	Further analysis of the interactions between the Brassica S receptor kinase and three interacting proteins (ARC1, THL1 and THL2) in the yeast two-hybrid system. *Plant Molecular Biology*, **2001**, 45, 365-76	4.6	50
26	The S-locus receptor kinase is inhibited by thioredoxins and activated by pollen coat proteins. *Nature*, **2001**, 410, 220-3	50.4	208
25	A large family of genes that share homology with CLAVATA3. *Plant Physiology*, **2001**, 126, 939-42	6.6	282
24	Intrahaplotype polymorphism at the Brassica S locus. *Genetics*, **2001**, 159, 811-22	4	31

23	The S15 self-incompatibility haplotype in Brassica oleracea includes three S gene family members expressed in stigmas. *Plant Cell*, **1999**, 11, 971-86	11.6	64
22	A Functional S Locus Anther Gene Is Not Required for the Self-Incompatibility Response in Brassica oleracea. *Plant Cell*, **1997**, 9, 2065	11.6	1
21	Rapid Induction by Wounding and Bacterial Infection of an S Gene Family Receptor-Like Kinase Gene in Brassica oleracea. *Plant Cell*, **1997**, 9, 49	11.6	11
20	Natural antisense transcripts of the S locus receptor kinase gene and related sequences in Brassica oleracea. *Molecular Genetics and Genomics*, **1997**, 255, 514-24		33
19	Characterization of the S locus genes, SLG and SRK, of the Brassica S3 haplotype: identification of a membrane-localized protein encoded by the S locus receptor kinase gene. *Plant Journal*, **1995**, 7, 429-40	6.9	114
18	The S locus receptor kinase gene encodes a soluble glycoprotein corresponding to the SKR extracellular domain in Brassica oleracea. *Plant Journal*, **1995**, 8, 827-34	6.9	59
17	PCR-generated cDNA library of transition-stage maize embryos: cloning and expression of calmodulin genes during early embryogenesis. *Plant Molecular Biology*, **1995**, 27, 105-13	4.6	18
16	S-locus glycoproteins are expressed along the path of pollen tubes in Brassica pistils. *Planta*, **1995**, 196, 614	4.7	3
15	Characterization of three putative receptors homologous to genes of Brassica involved in self-incompatibility. *Biology of the Cell*, **1995**, 84, 97-97	3.5	
14	Expression of the extracellular domain of a plant receptor in insect cells using different baculovirus vectors. *Biology of the Cell*, **1995**, 84, 97-97	3.5	
13	SLR3: a modified receptor kinase gene that has been adapted to encode a putative secreted glycoprotein similar to the S locus glycoprotein. *Molecular Genetics and Genomics*, **1995**, 248, 151-61		13
12	Characterization of the gene encoding the plastid-located glutamine synthetase of Phaseolus vulgaris: regulation of beta-glucuronidase gene fusions in transgenic tobacco. *Plant Molecular Biology*, **1992**, 18, 1141-9	4.6	16
11	Regulation of glutamine synthetase genes in leaves of Phaseolus vulgaris. *Plant Molecular Biology*, **1991**, 17, 761-71	4.6	51
10	A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella sorokiniana. *Plant Molecular Biology*, **1991**, 17, 1023-44	4.6	22
9	RESTRICTION ENZYME ANALYSIS AND CLONING OF HIGH MOLECULAR WEIGHT GENOMIC DNA ISOLATED FROM CHLORELLA SOROKINIANA (CHLOROPHYTA)1. *Journal of Phycology*, **1990**, 26, 361-367	3	7
8	Expression of glutamine synthetase genes in roots and nodules of Phaseolus vulgaris following changes in the ammonium supply and infection with various Rhizobium mutants. *Plant Molecular Biology*, **1990**, 14, 549-60	4.6	42
7	A glutamate dehydrogenase gene sequence. *Nucleic Acids Research*, **1989**, 17, 10500	20.1	4
6	Chromosome-level quality scaffolding of brown algal genomes using InstaGRAAL, a proximity ligation-based scaffolder		2

List of Publications

5	Histone modifications during the life cycle of the brown alga Ectocarpus		3
4	Rapid Turnover of Life-Cycle-Related Genes in the Brown Algae		2
3	Evolution of life cycles and reproductive traits: insights from the brown algae		5
2	Priming of Marine Macrophytes for Enhanced Restoration Success and Food Security in Future Oceans. *Frontiers in Marine Science*,8,	4.5	1
1	A partially sex-reversed giant kelp sheds light into the mechanisms of sexual differentiation in a UV sexual system		1