

J Mark Cock

List of Publications by Year in descending order

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127
papers

7,459
citations

53794

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62596

80
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139
all docs

139
docs citations

139
times ranked

5984
citing authors

#	ARTICLE	IF	CITATIONS
1	Providing a phylogenetic framework for trait-based analyses in brown algae: Phylogenomic tree inferred from 32 nuclear protein-coding sequences. <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107408.	2.7	2
2	Selection drives convergent gene expression changes during transitions to co-sexuality in haploid sexual systems. <i>Nature Ecology and Evolution</i> , 2022, 6, 579-589.	7.8	12
3	Chromatin landscape associated with sexual differentiation in a UV sex determination system. <i>Nucleic Acids Research</i> , 2022, 50, 3307-3322.	14.5	9
4	An Efficient Chromatin Immunoprecipitation Protocol for the Analysis of Histone Modification Distributions in the Brown Alga <i>Ectocarpus</i> . <i>Methods and Protocols</i> , 2022, 5, 36.	2.0	2
5	Alternation of Generations in Plants and Algae. , 2021, , 631-644.		2
6	Histone modifications during the life cycle of the brown alga <i>Ectocarpus</i> . <i>Genome Biology</i> , 2021, 22, 12.	8.8	29
7	Biochemical characteristics of a diffusible factor that induces gametophyte to sporophyte switching in the brown alga <i>Ectocarpus</i> . <i>Journal of Phycology</i> , 2021, 57, 742-753.	2.3	3
8	Priming of Marine Macrophytes for Enhanced Restoration Success and Food Security in Future Oceans. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	21
9	Evolution of life cycles and reproductive traits: Insights from the brown algae. <i>Journal of Evolutionary Biology</i> , 2021, 34, 992-1009.	1.7	35
10	Signatures of Transcription Factor Evolution and the Secondary Gain of Red Algae Complexity. <i>Genes</i> , 2021, 12, 1055.	2.4	9
11	Role and Evolution of the Extracellular Matrix in the Acquisition of Complex Multicellularity in Eukaryotes: A Macroalgal Perspective. <i>Genes</i> , 2021, 12, 1059.	2.4	34
12	Targeted CRISPR-Cas9-based gene knockouts in the model brown alga <i>Ectocarpus</i> . <i>New Phytologist</i> , 2021, 231, 2077-2091.	7.3	41
13	A partially sex-reversed giant kelp sheds light into the mechanisms of sexual differentiation in a UV sexual system. <i>New Phytologist</i> , 2021, 232, 252-263.	7.3	11
14	Evolution of Multicellularity. <i>Genes</i> , 2021, 12, 1532.	2.4	0
15	Brown Algal Model Organisms. <i>Annual Review of Genetics</i> , 2020, 54, 71-92.	7.6	16
16	Cytokinin and Ethylene Cell Signaling Pathways from Prokaryotes to Eukaryotes. <i>Cells</i> , 2020, 9, 2526.	4.1	14
17	Phylogeny and Evolution of the Brown Algae. <i>Critical Reviews in Plant Sciences</i> , 2020, 39, 281-321.	5.7	82
18	<i>Ectocarpus</i> : an evo-devo model for the brown algae. <i>EvoDevo</i> , 2020, 11, 19.	3.2	24

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19	instaGRAAL: chromosome-level quality scaffolding of genomes using a proximity ligation-based scaffolder. <i>Genome Biology</i> , 2020, 21, 148.	8.8	38
20	Organelle inheritance and genome architecture variation in isogamous brown algae. <i>Scientific Reports</i> , 2020, 10, 2048.	3.3	12
21	Parallelisable non-invasive biomass, fitness and growth measurement of macroalgae and other protists with nephelometry. <i>Algal Research</i> , 2020, 46, 101762.	4.6	4
22	Production and Bioassay of a Diffusible Factor That Induces Gametophyte-to-Sporophyte Developmental Reprogramming in the Brown Alga <i>Ectocarpus</i> . <i>Bio-protocol</i> , 2020, 10, e3753.	0.4	1
23	Unusual Patterns of Mitochondrial Inheritance in the Brown Alga <i>Ectocarpus</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2778-2789.	8.9	5
24	Origin and evolution of sex-determination systems in the brown algae. <i>New Phytologist</i> , 2019, 222, 1751-1756.	7.3	34
25	A key role for sex chromosomes in the regulation of parthenogenesis in the brown alga <i>Ectocarpus</i> . <i>PLoS Genetics</i> , 2019, 15, e1008211.	3.5	26
26	Megaviruses: An involvement in phytohormone receptor gene transfer in brown algae?. <i>Gene</i> , 2019, 704, 149-151.	2.2	5
27	Rapid turnover of life-cycle-related genes in the brown algae. <i>Genome Biology</i> , 2019, 20, 35.	8.8	36
28	Diversity and Evolution of Sensor Histidine Kinases in Eukaryotes. <i>Genome Biology and Evolution</i> , 2019, 11, 86-108.	2.5	28
29	Convergent recruitment of TALE homeodomain life cycle regulators to direct sporophyte development in land plants and brown algae. <i>ELife</i> , 2019, 8, .	6.0	44
30	Genetic Diversity in the UV Sex Chromosomes of the Brown Alga <i>Ectocarpus</i> . <i>Genes</i> , 2018, 9, 286.	2.4	18
31	UV Chromosomes and Haploid Sexual Systems. <i>Trends in Plant Science</i> , 2018, 23, 794-807.	8.8	66
32	The <i>Ectocarpus</i> IMMEDIATE UPRIGHT gene encodes a member of a novel family of cysteine-rich proteins that have an unusual distribution across the eukaryotes. <i>Development (Cambridge)</i> , 2017, 144, 409-418.	2.5	27
33	Multiple gene movements into and out of haploid sex chromosomes. <i>Genome Biology</i> , 2017, 18, 104.	8.8	63
34	The Algal Revolution. <i>Trends in Plant Science</i> , 2017, 22, 726-738.	8.8	73
35	High-density genetic map and identification of QTLs for responses to temperature and salinity stresses in the model brown alga <i>Ectocarpus</i> . <i>Scientific Reports</i> , 2017, 7, 43241.	3.3	50
36	Biotic interactions as drivers of algal origin and evolution. <i>New Phytologist</i> , 2017, 216, 670-681.	7.3	25

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37	DISTAG/TBCCd1 Is Required for Basal Cell Fate Determination in <i>Ectocarpus</i> . <i>Plant Cell</i> , 2017, 29, 3102-3122.	6.6	22
38	Re-annotation, improved large-scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga <i>Ectocarpus</i> . <i>New Phytologist</i> , 2017, 214, 219-232.	7.3	65
39	Rapid Evolution of microRNA Loci in the Brown Algae. <i>Genome Biology and Evolution</i> , 2017, 9, 740-749.	2.5	22
40	Alternation of Generations in Plants and Algae. , 2017, , 1-14.		1
41	Characterization of newly developed expressed sequence tag-derived microsatellite markers revealed low genetic diversity within and low connectivity between European <i>Saccharina latissima</i> populations. <i>Journal of Applied Phycology</i> , 2016, 28, 3057-3070.	2.8	23
42	Evolution and maintenance of haploid-diploid life cycles in natural populations: The case of the marine brown alga <i>Ectocarpus</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1808-1822.	2.3	49
43	Development of PCR-Based Markers to Determine the Sex of Kelps. <i>PLoS ONE</i> , 2015, 10, e0140535.	2.5	36
44	microRNAs and the evolution of complex multicellularity: identification of a large, diverse complement of microRNAs in the brown alga <i>Ectocarpus</i> . <i>Nucleic Acids Research</i> , 2015, 43, 6384-6398.	14.5	40
45	Sexual Dimorphism and the Evolution of Sex-Biased Gene Expression in the Brown Alga <i>Ectocarpus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1581-1597.	8.9	111
46	The Pseudoautosomal Regions of the U/V Sex Chromosomes of the Brown Alga <i>Ectocarpus</i> Exhibit Unusual Features. <i>Molecular Biology and Evolution</i> , 2015, 32, 2973-2985.	8.9	25
47	Genome-wide comparison of ultraviolet and ethyl methanesulphonate mutagenesis methods for the brown alga <i>Ectocarpus</i> . <i>Marine Genomics</i> , 2015, 24, 109-113.	1.1	13
48	Emergence of <i>Ectocarpus</i> as a Model System to Study the Evolution of Complex Multicellularity in the Brown Algae. <i>Advances in Marine Genomics</i> , 2015, , 153-162.	1.2	9
49	Proteomics Analysis of Heterogeneous Flagella in Brown Algae (Stramenopiles). <i>Protist</i> , 2014, 165, 662-675.	1.5	32
50	A Haploid System of Sex Determination in the Brown Alga <i>Ectocarpus</i> sp.. <i>Current Biology</i> , 2014, 24, 1945-1957.	3.9	131
51	Evolution and regulation of complex life cycles: a brown algal perspective. <i>Current Opinion in Plant Biology</i> , 2014, 17, 1-6.	7.1	57
52	Gene silencing in <i>Fucus</i> embryos: developmental consequences of RNA-mediated cytoskeletal disruption. <i>Journal of Phycology</i> , 2013, 49, 819-829.	2.3	27
53	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	7.1	307
54	Ecological and evolutionary genomics of marine photosynthetic organisms. <i>Molecular Ecology</i> , 2013, 22, 867-907.	3.9	29

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55	Non-cell autonomous regulation of life cycle transitions in the model brown alga <i>Ectocarpus</i> . <i>New Phytologist</i> , 2013, 197, 503-510.	7.3	21
56	Immunostaining of <i>Ectocarpus</i> Cells. <i>Cold Spring Harbor Protocols</i> , 2012, 2012, pdb.prot067975-pdb.prot067975.	0.3	6
57	<i>Ectocarpus</i> : A Model Organism for the Brown Algae. <i>Cold Spring Harbor Protocols</i> , 2012, 2012, pdb.emo065821.	0.3	62
58	Genetic Crosses between <i>Ectocarpus</i> Strains: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2012, 2012, pdb.prot067942.	0.3	15
59	How to Cultivate <i>Ectocarpus</i> : Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2012, 2012, pdb.prot067934.	0.3	51
60	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18
61	Extraction of High-Quality Genomic DNA from <i>Ectocarpus</i> . <i>Cold Spring Harbor Protocols</i> , 2012, 2012, pdb.prot067967.	0.3	2
62	Genomics of brown algae: current advances and future prospects. <i>Genes and Genomics</i> , 2012, 34, 1-5.	1.4	6
63	In Silico Survey of the Mitochondrial Protein Uptake and Maturation Systems in the Brown Alga <i>Ectocarpus siliculosus</i> . <i>PLoS ONE</i> , 2011, 6, e19540.	2.5	10
64	Brown algae. <i>Current Biology</i> , 2011, 21, R573-R575.	3.9	23
65	Microarray estimation of genomic inter-strain variability in the genus <i>Ectocarpus</i> (Phaeophyceae). <i>BMC Molecular Biology</i> , 2011, 12, 2.	3.0	19
66	Genetic regulation of life cycle transitions in the brown alga <i>Ectocarpus</i> . <i>Plant Signaling and Behavior</i> , 2011, 6, 1858-1860.	2.4	11
67	<i>OUROBOROS</i> is a master regulator of the gametophyte to sporophyte life cycle transition in the brown alga <i>Ectocarpus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11518-11523.	7.1	88
68	Algal models in plant biology. <i>Journal of Experimental Botany</i> , 2011, 62, 2425-2430.	4.8	29
69	Characterization of GDP-mannose Dehydrogenase from the Brown Alga <i>Ectocarpus siliculosus</i> Providing the Precursor for the Alginate Polymer. <i>Journal of Biological Chemistry</i> , 2011, 286, 16707-16715.	3.4	29
70	Copper stress proteomics highlights local adaptation of two strains of the model brown alga <i>Ectocarpus siliculosus</i> . <i>Proteomics</i> , 2010, 10, 2074-2088.	2.2	85
71	A sequence-tagged genetic map for the brown alga <i>Ectocarpus siliculosus</i> provides large-scale assembly of the genome sequence. <i>New Phytologist</i> , 2010, 188, 42-51.	7.3	59
72	Genetic diversity of <i>Ectocarpus</i> (<i>Ectocarpales</i> , <i>Phaeophyceae</i>) in Peru and northern Chile, the area of origin of the genome-sequenced strain. <i>New Phytologist</i> , 2010, 188, 30-41.	7.3	20

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73	Central and storage carbon metabolism of the brown alga <i>Ectocarpus siliculosus</i> : insights into the origin and evolution of storage carbohydrates in Eukaryotes. <i>New Phytologist</i> , 2010, 188, 67-81.	7.3	172
74	Role of endoreduplication and apomeiosis during parthenogenetic reproduction in the model brown alga <i>Ectocarpus</i> . <i>New Phytologist</i> , 2010, 188, 111-121.	7.3	54
75	The cell wall polysaccharide metabolism of the brown alga <i>Ectocarpus siliculosus</i> . Insights into the evolution of extracellular matrix polysaccharides in Eukaryotes. <i>New Phytologist</i> , 2010, 188, 82-97.	7.3	381
76	The <i>Ectocarpus</i> genome sequence: insights into brown algal biology and the evolutionary diversity of the eukaryotes. <i>New Phytologist</i> , 2010, 188, 1-4.	7.3	34
77	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
78	Reinstatement of <i>Ectocarpus crouaniorum</i> Thuret in Le Jolis as a third common species of <i>Ectocarpus</i> (Ectocarpales, Phaeophyceae) in Western Europe, and its phenology at Roscoff, Brittany. <i>Phycological Research</i> , 2010, 58, 157-170.	1.6	38
79	Cell cycles and endocycles in the model brown seaweed, <i>Ectocarpus siliculosus</i> . <i>Plant Signaling and Behavior</i> , 2010, 5, 1473-1475.	2.4	9
80	Auxin Metabolism and Function in the Multicellular Brown Alga <i>Ectocarpus siliculosus</i> . <i>Plant Physiology</i> , 2010, 153, 128-144.	4.8	103
81	Genomics of Marine Algae. , 2010, , 179-211.		2
82	03-P056 Molecular control of the alternation of generations in the brown alga <i>Ectocarpus</i> : The OUROBOROS mutant exhibits homeotic conversion of the sporophyte into a gametophyte. <i>Mechanisms of Development</i> , 2009, 126, S83.	1.7	0
83	Plastid genomes of two brown algae, <i>Ectocarpus siliculosus</i> and <i>Fucus vesiculosus</i> : further insights on the evolution of red-algal derived plastids. <i>BMC Evolutionary Biology</i> , 2009, 9, 253.	3.2	77
84	Global expression analysis of the brown alga <i>Ectocarpus siliculosus</i> (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. <i>Genome Biology</i> , 2009, 10, R66.	9.6	138
85	The FTO Gene, Implicated in Human Obesity, Is Found Only in Vertebrates and Marine Algae. <i>Journal of Molecular Evolution</i> , 2008, 66, 80-84.	1.8	59
86	EARLY DEVELOPMENT PATTERN OF THE BROWN ALGA <i>ECTOCARPUS SILICULOSUS</i> (ECTOCARPALES), Tj ETQg0 0 0 rgBT /Overlo	2.3	27
87	Development and physiology of the brown alga <i>Ectocarpus siliculosus</i> : two centuries of research. <i>New Phytologist</i> , 2008, 177, 319-332.	7.3	128
88	HECTAR: A method to predict subcellular targeting in heterokonts. <i>BMC Bioinformatics</i> , 2008, 9, 393.	2.6	197
89	Scent evolution in Chinese roses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5927-5932.	7.1	86
90	Life-cycle-generation-specific developmental processes are modified in the immediate upright mutant of the brown alga <i>Ectocarpus siliculosus</i> . <i>Development (Cambridge)</i> , 2008, 135, 1503-1512.	2.5	106

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91	Production and Emission of Volatile Compounds by Petal Cells. <i>Plant Signaling and Behavior</i> , 2007, 2, 525-526.	2.4	21
92	Complex life cycles of multicellular eukaryotes: New approaches based on the use of model organisms. <i>Gene</i> , 2007, 406, 152-170.	2.2	127
93	Both the adaxial and abaxial epidermal layers of the rose petal emit volatile scent compounds. <i>Planta</i> , 2007, 226, 853-866.	3.2	102
94	BIGPETALp, a bHLH transcription factor is involved in the control of Arabidopsis petal size. <i>EMBO Journal</i> , 2006, 25, 3912-3920.	7.8	188
95	Role of Petal-Specific Orcinol O-Methyltransferases in the Evolution of Rose Scent. <i>Plant Physiology</i> , 2006, 140, 18-29.	4.8	67
96	A W-box is required for full expression of the SA-responsive gene SFR2. <i>Gene</i> , 2005, 344, 181-192.	2.2	25
97	Inheritance of organelles in artificial hybrids of the isogamous multicellular chromist alga <i>Ectocarpus siliculosus</i> (Phaeophyceae). <i>European Journal of Phycology</i> , 2004, 39, 235-242.	2.0	53
98	PROPOSAL OF ECTOCARPUS SILICULOSUS (ECTOCARPALES, PHAEOPHYCEAE) AS A MODEL ORGANISM FOR BROWN ALGAL GENETICS AND GENOMICS. <i>Journal of Phycology</i> , 2004, 40, 1079-1088.	2.3	144
99	Antisense suppression of thioredoxin mRNA in <i>Brassica napus</i> cv.. <i>Plant Molecular Biology</i> , 2004, 55, 619-630.	3.9	59
100	Making inroads into plant receptor kinase signalling pathways. <i>Trends in Plant Science</i> , 2003, 8, 231-237.	8.8	77
101	Interaction of Calmodulin, a Sorting Nexin and Kinase-Associated Protein Phosphatase with the <i>Brassica oleracea</i> S Locus Receptor Kinase. <i>Plant Physiology</i> , 2003, 133, 919-929.	4.8	124
102	Analysis of gene expression in rose petals using expressed sequence tags. <i>FEBS Letters</i> , 2002, 515, 35-38.	2.8	78
103	Biosynthesis of the major scent components 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene by novel rose O-methyltransferases. <i>FEBS Letters</i> , 2002, 523, 113-118.	2.8	76
104	Comparison of the expression patterns of two small gene families of S gene family receptor kinase genes during the defence response in <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2002, 282, 215-225.	2.2	37
105	Receptor kinase signalling in plants and animals: distinct molecular systems with mechanistic similarities. <i>Current Opinion in Cell Biology</i> , 2002, 14, 230-236.	5.4	73
106	Two large <i>Arabidopsis thaliana</i> gene families are homologous to the <i>Brassica</i> gene superfamily that encodes pollen coat proteins and the male component of the self-incompatibility response. <i>Plant Molecular Biology</i> , 2001, 46, 17-34.	3.9	73
107	Further analysis of the interactions between the <i>Brassica</i> S receptor kinase and three interacting proteins (ARC1, THL1 and THL2) in the yeast two-hybrid system. <i>Plant Molecular Biology</i> , 2001, 45, 365-376.	3.9	81
108	The S-locus receptor kinase is inhibited by thioredoxins and activated by pollen coat proteins. <i>Nature</i> , 2001, 410, 220-223.	27.8	259

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109	A Large Family of Genes That Share Homology with CLAVATA3. <i>Plant Physiology</i> , 2001, 126, 939-942.	4.8	316
110	Intrahaplotype Polymorphism at the Brassica S Locus. <i>Genetics</i> , 2001, 159, 811-822.	2.9	34
111	The S15 Self-Incompatibility Haplotype in Brassica oleracea Includes Three S Gene Family Members Expressed in Stigmas. <i>Plant Cell</i> , 1999, 11, 971-986.	6.6	81
112	A Functional S Locus Anther Gene Is Not Required for the Self-Incompatibility Response in Brassica oleracea. <i>Plant Cell</i> , 1997, 9, 2065.	6.6	4
113	Rapid Induction by Wounding and Bacterial Infection of an S Gene Family Receptor-Like Kinase Gene in Brassica oleracea. <i>Plant Cell</i> , 1997, 9, 49.	6.6	28
114	Natural antisense transcripts of the S locus receptor kinase gene and related sequences in Brassica oleracea. <i>Molecular Genetics and Genomics</i> , 1997, 255, 514-524.	2.4	43
115	SLR3: A modified receptor kinase gene that has been adapted to encode a putative secreted glycoprotein similar to the S locus glycoprotein. <i>Molecular Genetics and Genomics</i> , 1995, 248, 151-161.	2.4	22
116	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. <i>Plant Journal</i> , 1995, 7, 429-440.	5.7	131
117	The S locus receptor kinase gene encodes a soluble glycoprotein corresponding to the SRK extracellular domain in Brassica oleracea. <i>Plant Journal</i> , 1995, 8, 827-834.	5.7	69
118	PCR-generated cDNA library of transition-stage maize embryos: cloning and expression of calmodulin genes during early embryogenesis. <i>Plant Molecular Biology</i> , 1995, 27, 105-113.	3.9	24
119	S-locus glycoproteins are expressed along the path of pollen tubes in Brassica pistils. <i>Planta</i> , 1995, 196, 614.	3.2	4
120	Characterization of three putative receptors homologous to genes of Brassica involved in self-incompatibility. <i>Biology of the Cell</i> , 1995, 84, 97-97.	2.0	0
121	Expression of the extracellular domain of a plant receptor in insect cells using different baculovirus vectors. <i>Biology of the Cell</i> , 1995, 84, 97-97.	2.0	0
122	Characterization of the gene encoding the plastid-located glutamine synthetase of Phaseolus vulgaris: regulation of β -glucuronidase gene fusions in transgenic tobacco. <i>Plant Molecular Biology</i> , 1992, 18, 1141-1149.	3.9	21
123	Regulation of glutamine synthetase genes in leaves of Phaseolus vulgaris. <i>Plant Molecular Biology</i> , 1991, 17, 761-771.	3.9	59
124	A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella sorokiniana. <i>Plant Molecular Biology</i> , 1991, 17, 1023-1044.	3.9	26
125	RESTRICTION ENZYME ANALYSIS AND CLONING OF HIGH MOLECULAR WEIGHT GENOMIC DNA ISOLATED FROM CHLORELLA SOROKINIANA (CHLOROPHYTA)1. <i>Journal of Phycology</i> , 1990, 26, 361-367.	2.3	10
126	Expression of glutamine synthetase genes in roots and nodules of Phaseolus vulgaris following changes in the ammonium supply and infection with various Rhizobium mutants. <i>Plant Molecular Biology</i> , 1990, 14, 549-560.	3.9	47

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127	A glutamate dehydrogenase gene sequence. <i>Nucleic Acids Research</i> , 1989, 17, 10500-10500.	14.5	5