

# Yuji Inagaki

## List of Publications by Year in descending order

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111  
papers

3,707  
citations

126858

33  
h-index

168321

53  
g-index

122  
all docs

122  
docs citations

122  
times ranked

2958  
citing authors

#	ARTICLE	IF	CITATIONS
1	The closest lineage of Archaeplastida is revealed by phylogenomics analyses that include <i>Microheliella maris</i> . <i>Open Biology</i> , 2022, 12, 210376.	1.5	13
2	Phage Origin of Mitochondrion-Localized Family A DNA Polymerases in Kinetoplastids and Diplonemids. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
3	Signs of the plastid: Enzymes involved in plastid-localized metabolic pathways in a eugregarine species. <i>Parasitology International</i> , 2021, 83, 102364.	0.6	4
4	Ubiquity and Origins of Structural Maintenance of Chromosomes (SMC) Proteins in Eukaryotes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	20
5	Putative genome features of relic green alga-derived nuclei in dinoflagellates and future perspectives as model organisms. <i>Communicative and Integrative Biology</i> , 2020, 13, 84-88.	0.6	6
6	Experimental Analysis of Diurnal Variations in Humic-Like Fluorescent Dissolved Organic Matter in Surface Seawater. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	6
7	Barthelonids represent a deep-branching metamonad clade with mitochondrion-related organelles predicted to generate no ATP. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20201538.	1.2	13
8	Mitochondrial Genomes of <i>Hemiarma marina</i> and <i>Leucocryptos marina</i> Revised the Evolution of Cytochrome c Maturation in Cryptista. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	9
9	Dinoflagellates with relic endosymbiont nuclei as models for elucidating organellogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5364-5375.	3.3	36
10	Comparative Plastid Genomics of <i>Cryptomonas</i> Species Reveals Fine-Scale Genomic Responses to Loss of Photosynthesis. <i>Genome Biology and Evolution</i> , 2020, 12, 3926-3937.	1.1	27
11	Inventory and Evolution of Mitochondrion-localized Family A DNA Polymerases in Euglenozoa. <i>Pathogens</i> , 2020, 9, 257.	1.2	13
12	Single-cell genomics unveiled a cryptic cyanobacterial lineage with a worldwide distribution hidden by a dinoflagellate host. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15973-15978.	3.3	27
13	In Silico Structural Modeling and Analysis of Elongation Factor-1 Alpha and Elongation Factor-like Protein. <i>ACS Omega</i> , 2019, 4, 7308-7316.	1.6	5
14	Horizontally-acquired genetic elements in the mitochondrial genome of a centrohelid <i>Marophrys</i> sp. SRT127. <i>Scientific Reports</i> , 2019, 9, 4850.	1.6	16
15	Fates of Evolutionarily Distinct, Plastid- $\epsilon$ -type Glyceraldehyde 3-phosphate Dehydrogenase Genes in Kareniacean Dinoflagellates. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 669-678.	0.8	5
16	Extensive molecular tinkering in the evolution of the membrane attachment mode of the Rheb GTPase. <i>Scientific Reports</i> , 2018, 8, 5239.	1.6	9
17	Phylogenomics Places Orphan Protistan Lineages in a Novel Eukaryotic Super-Group. <i>Genome Biology and Evolution</i> , 2018, 10, 427-433.	1.1	112
18	Characterization of spliced leader trans-splicing in a photosynthetic rhizarian amoeba, <i>Paulinella micropora</i> , and its possible role in functional gene transfer. <i>PLoS ONE</i> , 2018, 13, e0200961.	1.1	8

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19	The draft genome of <i>Kipferlia bialata</i> reveals reductive genome evolution in fornicate parasites. <i>PLoS ONE</i> , 2018, 13, e0194487.	1.1	27
20	Patterns in evolutionary origins of heme, chlorophyll <i>a</i> and isopentenyl diphosphate biosynthetic pathways suggest non-photosynthetic periods prior to plastid replacements in dinoflagellates. <i>PeerJ</i> , 2018, 6, e5345.	0.9	19
21	A Non-photosynthetic Diatom Reveals Early Steps of Reductive Evolution in Plastids. <i>Molecular Biology and Evolution</i> , 2017, 34, 2355-2366.	3.5	52
22	Organelles that illuminate the origins of <i>Trichomonas</i> hydrogenosomes and <i>Giardia</i> mitosomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 0092.	3.4	90
23	Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. <i>Scientific Reports</i> , 2017, 7, 13075.	1.6	17
24	Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. <i>Scientific Reports</i> , 2017, 7, 11688.	1.6	44
25	Global Kinetoplastea phylogeny inferred from a large-scale multigene alignment including parasitic species for better understanding transitions from a free-living to a parasitic lifestyle. <i>Genes and Genetic Systems</i> , 2017, 92, 35-42.	0.2	27
26	Mitochondrial Genome of <i>Palpitomonas bilix</i> : Derived Genome Structure and Ancestral System for Cytochrome <i>c</i> Maturation. <i>Genome Biology and Evolution</i> , 2016, 8, 3090-3098.	1.1	24
27	Ungulate malaria parasites. <i>Scientific Reports</i> , 2016, 6, 23230.	1.6	37
28	A System for Phylogenetic Analyses over Alignments of Next Generation Sequence Data. , 2016, , .		1
29	Multiple conversion between the genes encoding bacterial class-I release factors. <i>Scientific Reports</i> , 2015, 5, 12406.	1.6	1
30	The Mitochondrial Genomes of a Myxozoan Genus <i>Kudoa</i> Are Extremely Divergent in Metazoa. <i>PLoS ONE</i> , 2015, 10, e0132030.	1.1	29
31	Morphological Identities of Two Different Marine Stramenopile Environmental Sequence Clades: <i>Bicosoeca kenaiensis</i> (Hilliard, 1971) and <i>Cantina marsupialis</i> (Larsen and Patterson, 1990) gen. nov., comb. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 532-542.	0.8	30
32	Plastid Genome-Based Phylogeny Pinpointed the Origin of the Green-Colored Plastid in the Dinoflagellate <i>Lepidodinium chlorophorum</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1133-1140.	1.1	41
33	Proposal of a Twin Arginine Translocator System-Mediated Constraint against Loss of ATP Synthase Genes from Nonphotosynthetic Plastid Genomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 2598-2604.	3.5	48
34	Metabolic Capacity of Mitochondrion-related Organelles in the Free-living Anaerobic Stramenopile <i>Cantina marsupialis</i> . <i>Protist</i> , 2015, 166, 534-550.	0.6	12
35	Multiple losses of photosynthesis in <i>Nitzschia</i> ( <i>Bacillariophyceae</i> ). <i>Phycological Research</i> , 2015, 63, 19-28.	0.8	43
36	An intronic open reading frame was released from one of group II introns in the mitochondrial genome of the haptophyte <i>Chrysochromulina</i> sp. NIES-1333. <i>Mobile Genetic Elements</i> , 2014, 4, e29384.	1.8	13

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37	Gene Content Evolution in Discobid Mitochondria Deduced from the Phylogenetic Position and Complete Mitochondrial Genome of <i>Tsukubamonas globosa</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 306-315.	1.1	48
38	Unique genome evolution in an intracellular N <sub>2</sub> -fixing symbiont of a rhopalodiacean diatom. <i>Acta Societatis Botanicorum Poloniae</i> , 2014, 83, 409-413.	0.8	8
39	Complete genome of a nonphotosynthetic cyanobacterium in a diatom reveals recent adaptations to an intracellular lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11407-11412.	3.3	121
40	Secondary loss of a cis-spliced intron during the divergence of <i>Giardia intestinalis</i> assemblages. <i>BMC Research Notes</i> , 2014, 7, 413.	0.6	7
41	<i>Palpitomonas bilix</i> represents a basal cryptist lineage: insight into the character evolution in Cryptista. <i>Scientific Reports</i> , 2014, 4, 4641.	1.6	80
42	Parallel re-modeling of EF-1 $\alpha$ function: divergent EF-1 $\alpha$ genes co-occur with EFL genes in diverse distantly related eukaryotes. <i>BMC Evolutionary Biology</i> , 2013, 13, 131.	3.2	11
43	Identification of a Bacteria-Like Ferrochelatase in <i>Strongyloides venezuelensis</i> , an Animal Parasitic Nematode. <i>PLoS ONE</i> , 2013, 8, e58458.	1.1	12
44	RY-Coding and Non-Homogeneous Models Can Ameliorate the Maximum-Likelihood Inferences from Nucleotide Sequence Data with Parallel Compositional Heterogeneity. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9017.	0.6	26
45	An asynchronous parallel genetic algorithm for the maximum likelihood phylogenetic tree search. , 2012, , .		0
46	Prasinoxanthin is absent in the green-colored dinoflagellate <i>Lepidodinium chlorophorum</i> strain NIES-1868: pigment composition and 18S rRNA phylogeny. <i>Journal of Plant Research</i> , 2012, 125, 705-711.	1.2	13
47	Evolution of Elongation Factor- $\epsilon$ (EFL) Protein in Rhizaria is Revised by Radiolarian EFL Gene Sequences. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 367-373.	0.8	7
48	Multigene Phylogenies of Diverse Carpediemonas-like Organisms Identify the Closest Relatives of <i>Amitochondriate</i> Diplomonads and Retortamonads. <i>Protist</i> , 2012, 163, 344-355.	0.6	32
49	Separate Origins of Group I Introns in Two Mitochondrial Genes of the Katablepharid <i>Leucocryptos marina</i> . <i>PLoS ONE</i> , 2012, 7, e37307.	1.1	16
50	Mitochondrial genomes from two red tide forming raphidophycean algae <i>Heterosigma akashiwo</i> and <i>Chattonella marina</i> var. <i>marina</i> . <i>Harmful Algae</i> , 2011, 10, 130-137.	2.2	14
51	Splintrons in <i>Giardia intestinalis</i> . <i>Communicative and Integrative Biology</i> , 2011, 4, 454-456.	0.6	4
52	<i>Tsukubamonas globosa</i> n. gen., n. sp., A Novel Excavate Flagellate Possibly Holding a Key for the Early Evolution in <i>Discoba</i> . <i>Journal of Eukaryotic Microbiology</i> , 2011, 58, 319-331.	0.8	30
53	A deviant genetic code in the green alga-derived plastid in the dinoflagellate <i>Lepidodinium chlorophorum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 68-72.	1.2	18
54	Green-colored Plastids in the Dinoflagellate Genus <i>Lepidodinium</i> are of Core Chlorophyte Origin. <i>Protist</i> , 2011, 162, 268-276.	0.6	56

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55	Multigene phylogenetic analyses including diverse radiolarian species support the “Retaria” hypothesis” The sister relationship of Radiolaria and Foraminifera. <i>Marine Micropaleontology</i> , 2011, 81, 32-42.	0.5	20
56	Split Introns in the Genome of <i>Giardia intestinalis</i> Are Excised by Spliceosome-Mediated trans-Splicing. <i>Current Biology</i> , 2011, 21, 311-315.	1.8	45
57	Cercozoa comprises both EF-1 $\alpha$ -containing and EFL-containing members. <i>European Journal of Protistology</i> , 2011, 47, 24-28.	0.5	12
58	Spheroid bodies in rhopalodiacean diatoms were derived from a single endosymbiotic cyanobacterium. <i>Journal of Plant Research</i> , 2011, 124, 93-97.	1.2	32
59	A novel spliceosome-mediated trans-splicing can change our view on genome complexity of the divergent eukaryote <i>Giardia intestinalis</i> . <i>Biophysical Reviews</i> , 2011, 3, 193-197.	1.5	6
60	Splintrons in <i>Giardia intestinalis</i> : Spliceosomal introns in a split form. <i>Communicative and Integrative Biology</i> , 2011, 4, 454-6.	0.6	3
61	<i>Palpitomonas bilix</i> gen. et sp. nov.: A Novel Deep-branching Heterotroph Possibly Related to Archaeplastida or Hacrobia. <i>Protist</i> , 2010, 161, 523-538.	0.6	63
62	A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate <i>Lepidodinium chlorophorum</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 191.	3.2	62
63	Rooting for the root of elongation factor-like protein phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1082-1088.	1.2	12
64	Cryptic Diversity of Free-Living Parabasalids, <i>Pseudotrichomonas keilini</i> and <i>Lacusteria cypriaca</i> n. g., n. sp., as Inferred from Small Subunit rDNA Sequences. <i>Journal of Eukaryotic Microbiology</i> , 2010, 57, 554-561.	0.8	17
65	A wide diversity of previously undetected free-living relatives of diplomonads isolated from marine/saline habitats. <i>Environmental Microbiology</i> , 2010, 12, 2700-2710.	1.8	44
66	Phylogeny of Asian primate malaria parasites inferred from apicoplast genome-encoded genes with special emphasis on the positions of <i>Plasmodium vivax</i> and <i>P. fragile</i> . <i>Gene</i> , 2010, 450, 32-38.	1.0	25
67	Large-Scale Phylogenomic Analyses Reveal That Two Enigmatic Protist Lineages, Telonemia and Centroheliozoa, Are Related to Photosynthetic Chromalveolates. <i>Genome Biology and Evolution</i> , 2009, 1, 231-238.	1.1	143
68	Gene Sampling Can Bias Multi-Gene Phylogenetic Inferences: The Relationship between Red Algae and Green Plants as a Case Study. <i>Molecular Biology and Evolution</i> , 2009, 26, 1171-1178.	3.5	21
69	Expanded phylogenies of canonical and non-canonical types of methionine adenosyltransferase reveal a complex history of these gene families in eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 565-570.	1.2	9
70	Eukaryotic origin of glyceraldehyde-3-phosphate dehydrogenase genes in <i>Clostridium thermocellum</i> and <i>Clostridium cellulolyticum</i> genomes and putative fates of the exogenous gene in the subsequent genome evolution. <i>Gene</i> , 2009, 441, 22-27.	1.0	7
71	Tracing back EFL gene evolution in the cryptomonads-haptophytes assemblage: Separate origins of EFL genes in haptophytes, photosynthetic cryptomonads, and goniomonads. <i>Gene</i> , 2009, 441, 126-131.	1.0	20
72	A Hypothesis for the Evolution of Nuclear-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase Genes in “Chromalveolate”-Members. <i>PLoS ONE</i> , 2009, 4, e4737.	1.1	25

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73	Origins of plastids and glyceraldehyde-3-phosphate dehydrogenase genes in the green-colored dinoflagellate <i>Lepidodinium chlorophorum</i> . <i>Gene</i> , 2008, 410, 26-36.	1.0	31
74	Direct phylogenetic evidence for lateral transfer of elongation factor-like gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6965-6969.	3.3	26
75	Evolving genetic code. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2008, 84, 58-74.	1.6	27
76	Centrohelida is still searching for a phylogenetic home: Analyses of seven <i>Raphidiophrys contractilis</i> genes. <i>Gene</i> , 2007, 405, 47-54.	1.0	19
77	Assessing the monophyly of chlorophyll-c containing plastids by multi-gene phylogenies under the unlinked model conditions. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 227-238.	1.2	21
78	Proposal of <i>Pseudochattonella verruculosa</i> gen. nov., comb. nov. (Dictyochophyceae) for a former raphidophycean alga <i>Chattonella verruculosa</i> , based on 18S rDNA phylogeny and ultrastructural characteristics. <i>Phycological Research</i> , 2007, 55, 185-192.	0.8	37
79	Ultrastructure and Ribosomal RNA Phylogeny of the Free-Living Heterotrophic Flagellate <i>Dysnectes brevis</i> n. gen., n. sp., a New Member of the Fornicata. <i>Journal of Eukaryotic Microbiology</i> , 2007, 54, 191-200.	0.8	35
80	Multiple Gene Phylogenies Support the Monophyly of Cryptomonad and Haptophyte Host Lineages. <i>Current Biology</i> , 2007, 17, 887-891.	1.8	119
81	Fragmentation of Mitochondrial Large Subunit rRNA in the Dinoflagellate <i>Alexandrium catenella</i> and the Evolution of rRNA structure in Alveolate Mitochondria. <i>Protist</i> , 2007, 158, 239-245.	0.6	27
82	Diversity of microbial eukaryotes in sediment at a deep-sea methane cold seep: surveys of ribosomal DNA libraries from raw sediment samples and two enrichment cultures. <i>Extremophiles</i> , 2007, 11, 563-576.	0.9	146
83	Plasticity of the domain structure in FliG, a bacterial protein involved in flagellar rod formation. <i>Genes and Genetic Systems</i> , 2006, 81, 381-389.	0.2	25
84	Phylogenetic estimation under codon models can be biased by codon usage heterogeneity. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 428-434.	1.2	28
85	Comprehensive Multigene Phylogenies of Excavate Protists Reveal the Evolutionary Positions of "Primitive" Eukaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 615-625.	3.5	155
86	Recombination between elongation factor 1A genes from distantly related archaeal lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4528-4533.	3.3	33
87	The evolutionary relationships amongst excavates: a concatenated protein analysis. <i>Journal of Eukaryotic Microbiology</i> , 2005, 52, 27S-27S.	0.8	1
88	A close relationship between Cercozoa and Foraminifera supported by phylogenetic analyses based on combined amino acid sequences of three cytoskeletal proteins (actin, $\beta$ -tubulin, and $\beta$ -tubulin). <i>Gene</i> , 2005, 362, 153-160.	1.0	22
89	On Inconsistency of the Neighbor-Joining, Least Squares, and Minimum Evolution Estimation When Substitution Processes Are Incorrectly Modeled. <i>Molecular Biology and Evolution</i> , 2004, 21, 1629-1642.	3.5	43
90	A class of eukaryotic GTPase with a punctate distribution suggesting multiple functional replacements of translation elongation factor 1A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15380-15385.	3.3	96

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91	Covariation Shifts Cause a Long-Branch Attraction Artifact That Unites Microsporidia and Archaeobacteria in EF-1 $\alpha$ Phylogenies. <i>Molecular Biology and Evolution</i> , 2004, 21, 1340-1349.	3.5	93
92	Phylogenetic Artifacts Can be Caused by Leucine, Serine, and Arginine Codon Usage Heterogeneity: Dinoflagellate Plastid Origins as a Case Study. <i>Systematic Biology</i> , 2004, 53, 582-593.	2.7	60
93	<i>Capsaspora owczarzaki</i> is an independent opisthokont lineage. <i>Current Biology</i> , 2004, 14, R946-R947.	1.8	82
94	Assessing functional divergence in EF-1 $\alpha$ and its paralogs in eukaryotes and archaeobacteria. <i>Nucleic Acids Research</i> , 2003, 31, 4227-4237.	6.5	33
95	Convergence and constraint in eukaryotic release factor 1 (eRF1) domain 1: the evolution of stop codon specificity. <i>Nucleic Acids Research</i> , 2002, 30, 532-544.	6.5	58
96	Testing for Differences in Rates-Across-Sites Distributions in Phylogenetic Subtrees. <i>Molecular Biology and Evolution</i> , 2002, 19, 1514-1523.	3.5	51
97	Lateral Transfer of an EF-1 $\alpha$ Gene. <i>Current Biology</i> , 2002, 12, 772-776.	1.8	29
98	Class I release factors in ciliates with variant genetic codes. <i>Nucleic Acids Research</i> , 2001, 29, 921-927.	6.5	42
99	Evolution of the Eukaryotic Translation Termination System: Origins of Release Factors. <i>Molecular Biology and Evolution</i> , 2000, 17, 882-889.	3.5	71
100	Phylogenetic analysis of diatom <i>cox1</i> genes and implications of a fluctuating GC content on mitochondrial genetic code evolution. <i>Current Genetics</i> , 2000, 37, 29-33.	0.8	54
101	Comprehensive molecular phylogenetic analysis of a heterokont alga (NIES 548) using genes from all three cellular compartments. <i>Phycological Research</i> , 1999, 47, 225-231.	0.8	4
102	Directionally Evolving Genetic Code: The UGA Codon from Stop to Tryptophan in Mitochondria. <i>Journal of Molecular Evolution</i> , 1998, 47, 378-384.	0.8	36
103	DISTRIBUTION OF THE MITOCHONDRIAL DEVIANT GENETIC CODE AUA FOR METHIONINE IN HETEROKONT ALGAE. <i>Journal of Phycology</i> , 1998, 34, 1005-1008.	1.0	4
104	Distinctive origins of group I introns found in the COXI genes of three green algae. <i>Gene</i> , 1998, 213, 1-7.	1.0	19
105	Algae or Protozoa: Phylogenetic Position of Euglenophytes and Dinoflagellates as Inferred from Mitochondrial Sequences. <i>Journal of Molecular Evolution</i> , 1997, 45, 295-300.	0.8	32
106	A deviant mitochondrial genetic code in prymnesiophytes (yellow-algae): UGA codon for tryptophan. <i>Current Genetics</i> , 1997, 32, 296-299.	0.8	28
107	Use of a deviant mitochondrial genetic code in yellow-green algae as a landmark for segregating members within the phylum. <i>Journal of Molecular Evolution</i> , 1997, 45, 119-124.	0.8	25
108	Cloning of the <i>Mycoplasma capricolum</i> gene encoding peptide-chain release factor. <i>Gene</i> , 1996, 169, 101-103.	1.0	10

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109	Translation of Synonymous Codons in Family Boxes by <i>Mycoplasma capricolum</i> tRNAs with Unmodified Uridine or Adenosine at the First Anticodon Position. <i>Journal of Molecular Biology</i> , 1995, 251, 486-492.	2.0	57
110	Lack of peptide-release activity responding to codon UGA in <i>Mycoplasma capricolum</i> . <i>Nucleic Acids Research</i> , 1993, 21, 1335-1338.	6.5	29
111	Comparative Plastid Genomics of Green-Colored Dinoflagellates Unveils Parallel Genome Compaction and RNA Editing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4