

Yuji Inagaki

List of Publications by Year in descending order

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| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Comprehensive Multigene Phylogenies of Excavate Protists Reveal the Evolutionary Positions of "Primitive" Eukaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 615-625. | 8.9 | 155 |
| 2 | 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. | 2.3 | 146 |
| 3 | Large-Scale Phylogenomic Analyses Reveal That Two Enigmatic Protist Lineages, <i>Telonemia</i> and <i>Centroheliozoa</i> , Are Related to Photosynthetic Chromalveolates. <i>Genome Biology and Evolution</i> , 2009, 1, 231-238. | 2.5 | 143 |
| 4 | 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. | 7.1 | 121 |
| 5 | Multiple Gene Phylogenies Support the Monophyly of Cryptomonad and Haptophyte Host Lineages. <i>Current Biology</i> , 2007, 17, 887-891. | 3.9 | 119 |
| 6 | Phylogenomics Places Orphan Protistan Lineages in a Novel Eukaryotic Super-Group. <i>Genome Biology and Evolution</i> , 2018, 10, 427-433. | 2.5 | 112 |
| 7 | 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. | 7.1 | 96 |
| 8 | Covariation Shifts Cause a Long-Branch Attraction Artifact That Unites Microsporidia and Archaeobacteria in EF-1 α Phylogenies. <i>Molecular Biology and Evolution</i> , 2004, 21, 1340-1349. | 8.9 | 93 |
| 9 | Organelles that illuminate the origins of <i>Trichomonas</i> hydrogenosomes and <i>Giardia</i> mitosomes. <i>Nature Ecology and Evolution</i> , 2017, 1, 0092. | 7.8 | 90 |
| 10 | <i>Capsaspora owczarzaki</i> is an independent opisthokont lineage. <i>Current Biology</i> , 2004, 14, R946-R947. | 3.9 | 82 |
| 11 | <i>Palpitomonas bilix</i> represents a basal cryptist lineage: insight into the character evolution in Cryptista. <i>Scientific Reports</i> , 2014, 4, 4641. | 3.3 | 80 |
| 12 | Evolution of the Eukaryotic Translation Termination System: Origins of Release Factors. <i>Molecular Biology and Evolution</i> , 2000, 17, 882-889. | 8.9 | 71 |
| 13 | <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. | 1.5 | 63 |
| 14 | 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 |
| 15 | 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. | 5.6 | 60 |
| 16 | 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. | 14.5 | 58 |
| 17 | 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. | 4.2 | 57 |
| 18 | Green-colored Plastids in the Dinoflagellate Genus <i>Lepidodinium</i> are of Core Chlorophyte Origin. <i>Protist</i> , 2011, 162, 268-276. | 1.5 | 56 |

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|----|---|------|-----------|
| 19 | 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. | 1.7 | 54 |
| 20 | A Non-photosynthetic Diatom Reveals Early Steps of Reductive Evolution in Plastids. <i>Molecular Biology and Evolution</i> , 2017, 34, 2355-2366. | 8.9 | 52 |
| 21 | Testing for Differences in Rates-Across-Sites Distributions in Phylogenetic Subtrees. <i>Molecular Biology and Evolution</i> , 2002, 19, 1514-1523. | 8.9 | 51 |
| 22 | 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. | 2.5 | 48 |
| 23 | Proposal of a Twin Aarginine Translocator System-Mediated Constraint against Loss of ATP Synthase Genes from Nonphotosynthetic Plastid Genomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 2598-2604. | 8.9 | 48 |
| 24 | 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. | 3.9 | 45 |
| 25 | A wide diversity of previously undetected free-living relatives of diplomonads isolated from marine/saline habitats. <i>Environmental Microbiology</i> , 2010, 12, 2700-2710. | 3.8 | 44 |
| 26 | Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. <i>Scientific Reports</i> , 2017, 7, 11688. | 3.3 | 44 |
| 27 | 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. | 8.9 | 43 |
| 28 | Multiple losses of photosynthesis in <i>Nitzschia</i> (<i>Bacillariophyceae</i>). <i>Phycological Research</i> , 2015, 63, 19-28. | 1.6 | 43 |
| 29 | Class I release factors in ciliates with variant genetic codes. <i>Nucleic Acids Research</i> , 2001, 29, 921-927. | 14.5 | 42 |
| 30 | 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. | 2.5 | 41 |
| 31 | Proposal of <i>Pseudochattonella verruculosa</i> gen. nov., comb. nov. (<i>Dictyochophyceae</i>) 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. | 1.6 | 37 |
| 32 | Ungulate malaria parasites. <i>Scientific Reports</i> , 2016, 6, 23230. | 3.3 | 37 |
| 33 | Directionally Evolving Genetic Code: The UGA Codon from Stop to Tryptophan in Mitochondria. <i>Journal of Molecular Evolution</i> , 1998, 47, 378-384. | 1.8 | 36 |
| 34 | 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. | 7.1 | 36 |
| 35 | 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. | 1.7 | 35 |
| 36 | Assessing functional divergence in EF-1 \hat{A} and its paralogs in eukaryotes and archaeobacteria. <i>Nucleic Acids Research</i> , 2003, 31, 4227-4237. | 14.5 | 33 |

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|----|---|------|-----------|
| 37 | Recombination between elongation factor 1A genes from distantly related archaeal lineages. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4528-4533. | 7.1 | 33 |
| 38 | Algae or Protozoa: Phylogenetic Position of Euglenophytes and Dinoflagellates as Inferred from Mitochondrial Sequences. Journal of Molecular Evolution, 1997, 45, 295-300. | 1.8 | 32 |
| 39 | Spheroid bodies in rhopalodiacean diatoms were derived from a single endosymbiotic cyanobacterium. Journal of Plant Research, 2011, 124, 93-97. | 2.4 | 32 |
| 40 | Multigene Phylogenies of Diverse Carpediemonas-like Organisms Identify the Closest Relatives of <i>Amitochondriate</i> Diplomonads and Retortamonads. Protist, 2012, 163, 344-355. | 1.5 | 32 |
| 41 | Origins of plastids and glyceraldehyde-3-phosphate dehydrogenase genes in the green-colored dinoflagellate <i>Lepidodinium chlorophorum</i> . Gene, 2008, 410, 26-36. | 2.2 | 31 |
| 42 | <i>Tsukubamonas globosa</i> n. gen., n. sp., A Novel Excavate Flagellate Possibly Holding a Key for the Early Evolution in <i>Discoba</i> . Journal of Eukaryotic Microbiology, 2011, 58, 319-331. | 1.7 | 30 |
| 43 | 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.. Journal of Eukaryotic Microbiology, 2015, 62, 532-542. | 1.7 | 30 |
| 44 | Lack of peptide-release activity responding to codon UGA in <i>Mycoplasma capricolum</i> . Nucleic Acids Research, 1993, 21, 1335-1338. | 14.5 | 29 |
| 45 | Lateral Transfer of an EF-1 Gene. Current Biology, 2002, 12, 772-776. | 3.9 | 29 |
| 46 | The Mitochondrial Genomes of a Myxozoan Genus <i>Kudoa</i> Are Extremely Divergent in Metazoa. PLoS ONE, 2015, 10, e0132030. | 2.5 | 29 |
| 47 | A deviant mitochondrial genetic code in prymnesiophytes (yellow-algae): UGA codon for tryptophan. Current Genetics, 1997, 32, 296-299. | 1.7 | 28 |
| 48 | Phylogenetic estimation under codon models can be biased by codon usage heterogeneity. Molecular Phylogenetics and Evolution, 2006, 40, 428-434. | 2.7 | 28 |
| 49 | Fragmentation of Mitochondrial Large Subunit rRNA in the Dinoflagellate <i>Alexandrium catenella</i> and the Evolution of rRNA structure in Alveolate Mitochondria. Protist, 2007, 158, 239-245. | 1.5 | 27 |
| 50 | Evolving genetic code. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2008, 84, 58-74. | 3.8 | 27 |
| 51 | 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. Genes and Genetic Systems, 2017, 92, 35-42. | 0.7 | 27 |
| 52 | Single-cell genomics unveiled a cryptic cyanobacterial lineage with a worldwide distribution hidden by a dinoflagellate host. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15973-15978. | 7.1 | 27 |
| 53 | Comparative Plastid Genomics of <i>Cryptomonas</i> Species Reveals Fine-Scale Genomic Responses to Loss of Photosynthesis. Genome Biology and Evolution, 2020, 12, 3926-3937. | 2.5 | 27 |
| 54 | The draft genome of <i>Kipferlia bialata</i> reveals reductive genome evolution in fornicate parasites. PLoS ONE, 2018, 13, e0194487. | 2.5 | 27 |

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|----|--|-----|-----------|
| 55 | Direct phylogenetic evidence for lateral transfer of elongation factor-like gene. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6965-6969. | 7.1 | 26 |
| 56 | RY-Coding and Non-Homogeneous Models Can Ameliorate the Maximum-Likelihood Inferences from Nucleotide Sequence Data with Parallel Compositional Heterogeneity. Evolutionary Bioinformatics, 2012, 8, EBO.S9017. | 1.2 | 26 |
| 57 | Use of a deviant mitochondrial genetic code in yellow-green algae as a landmark for segregating members within the phylum. Journal of Molecular Evolution, 1997, 45, 119-124. | 1.8 | 25 |
| 58 | Plasticity of the domain structure in FlgJ, a bacterial protein involved in flagellar rod formation. Genes and Genetic Systems, 2006, 81, 381-389. | 0.7 | 25 |
| 59 | Phylogeny of Asian primate malaria parasites inferred from apicoplast genome-encoded genes with special emphasis on the positions of Plasmodium vivax and P. fragile. Gene, 2010, 450, 32-38. | 2.2 | 25 |
| 60 | A Hypothesis for the Evolution of Nuclear-Encoded, Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenase Genes in "Chromalveolate" Members. PLoS ONE, 2009, 4, e4737. | 2.5 | 25 |
| 61 | Mitochondrial Genome of <i>Palpitomonas bilix</i> : Derived Genome Structure and Ancestral System for Cytochrome <i>c</i> Maturation. Genome Biology and Evolution, 2016, 8, 3090-3098. | 2.5 | 24 |
| 62 | A close relationship between Cercozoa and Foraminifera supported by phylogenetic analyses based on combined amino acid sequences of three cytoskeletal proteins (actin, β -tubulin, and β -tubulin). Gene, 2005, 362, 153-160. | 2.2 | 22 |
| 63 | Assessing the monophyly of chlorophyll-c containing plastids by multi-gene phylogenies under the unlinked model conditions. Molecular Phylogenetics and Evolution, 2007, 45, 227-238. | 2.7 | 21 |
| 64 | Gene Sampling Can Bias Multi-Gene Phylogenetic Inferences: The Relationship between Red Algae and Green Plants as a Case Study. Molecular Biology and Evolution, 2009, 26, 1171-1178. | 8.9 | 21 |
| 65 | Tracing back EFL gene evolution in the cryptomonads "haptophytes assemblage: Separate origins of EFL genes in haptophytes, photosynthetic cryptomonads, and goniomonads. Gene, 2009, 441, 126-131. | 2.2 | 20 |
| 66 | Multigene phylogenetic analyses including diverse radiolarian species support the "Retaria" hypothesis " The sister relationship of Radiolaria and Foraminifera. Marine Micropaleontology, 2011, 81, 32-42. | 1.2 | 20 |
| 67 | Ubiquity and Origins of Structural Maintenance of Chromosomes (SMC) Proteins in Eukaryotes. Genome Biology and Evolution, 2021, 13, . | 2.5 | 20 |
| 68 | Distinctive origins of group I introns found in the COXI genes of three green algae. Gene, 1998, 213, 1-7. | 2.2 | 19 |
| 69 | Centrohelida is still searching for a phylogenetic home: Analyses of seven Raphidiphrys contractilis genes. Gene, 2007, 405, 47-54. | 2.2 | 19 |
| 70 | 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. PeerJ, 2018, 6, e5345. | 2.0 | 19 |
| 71 | A deviant genetic code in the green alga-derived plastid in the dinoflagellate <i>Lepidodinium chlorophorum</i> . Molecular Phylogenetics and Evolution, 2011, 60, 68-72. | 2.7 | 18 |
| 72 | 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. Journal of Eukaryotic Microbiology, 2010, 57, 554-561. | 1.7 | 17 |

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|----|--|-----|-----------|
| 73 | Genomic divergence within non-photosynthetic cyanobacterial endosymbionts in rhopalodiacean diatoms. <i>Scientific Reports</i> , 2017, 7, 13075. | 3.3 | 17 |
| 74 | Horizontally-acquired genetic elements in the mitochondrial genome of a centrohelid <i>Marophrys</i> sp. SRT127. <i>Scientific Reports</i> , 2019, 9, 4850. | 3.3 | 16 |
| 75 | Separate Origins of Group I Introns in Two Mitochondrial Genes of the Katablepharid <i>Leucocryptos marina</i> . <i>PLoS ONE</i> , 2012, 7, e37307. | 2.5 | 16 |
| 76 | 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. | 4.8 | 14 |
| 77 | 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. | 2.4 | 13 |
| 78 | 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 |
| 79 | 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. | 2.6 | 13 |
| 80 | Inventory and Evolution of Mitochondrion-localized Family A DNA Polymerases in Euglenozoa. <i>Pathogens</i> , 2020, 9, 257. | 2.8 | 13 |
| 81 | The closest lineage of Archaeplastida is revealed by phylogenomics analyses that include <i>Microheliella maris</i> . <i>Open Biology</i> , 2022, 12, 210376. | 3.6 | 13 |
| 82 | Rooting for the root of elongation factor-like protein phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1082-1088. | 2.7 | 12 |
| 83 | Cercozoa comprises both EF-1 α -containing and EFL-containing members. <i>European Journal of Protistology</i> , 2011, 47, 24-28. | 1.5 | 12 |
| 84 | Metabolic Capacity of Mitochondrion-related Organelles in the Free-living Anaerobic Stramenopile <i>Cantina marsupialis</i> . <i>Protist</i> , 2015, 166, 534-550. | 1.5 | 12 |
| 85 | Identification of a Bacteria-Like Ferrochelatase in <i>Strongyloides venezuelensis</i> , an Animal Parasitic Nematode. <i>PLoS ONE</i> , 2013, 8, e58458. | 2.5 | 12 |
| 86 | Parallel re-modeling of EF-1 α function: divergent EF-1 α genes co-occur with EFL genes in diverse distantly related eukaryotes. <i>BMC Evolutionary Biology</i> , 2013, 13, 131. | 3.2 | 11 |
| 87 | Cloning of the <i>Mycoplasma capricolum</i> gene encoding peptide-chain release factor. <i>Gene</i> , 1996, 169, 101-103. | 2.2 | 10 |
| 88 | 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. | 2.7 | 9 |
| 89 | Extensive molecular tinkering in the evolution of the membrane attachment mode of the Rheb GTPase. <i>Scientific Reports</i> , 2018, 8, 5239. | 3.3 | 9 |
| 90 | 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, . | 2.2 | 9 |

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|-----|---|-----|-----------|
| 91 | Unique genome evolution in an intracellular N ₂ -fixing symbiont of a rhopalodiacean diatom. <i>Acta Societatis Botanicorum Poloniae</i> , 2014, 83, 409-413. | 0.8 | 8 |
| 92 | 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. | 2.5 | 8 |
| 93 | 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. | 2.2 | 7 |
| 94 | Evolution of Elongation Factor-Like (<sc>EFL</sc>) Protein in Rhizaria is Revised by Radiolarian <sc>EFL</sc> Gene Sequences. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 367-373. | 1.7 | 7 |
| 95 | Secondary loss of a cis-spliced intron during the divergence of <i>Giardia intestinalis</i> assemblages. <i>BMC Research Notes</i> , 2014, 7, 413. | 1.4 | 7 |
| 96 | Phage Origin of Mitochondrion-Localized Family A DNA Polymerases in Kinetoplastids and Diplonemids. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 7 |
| 97 | 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. | 3.2 | 6 |
| 98 | 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. | 1.4 | 6 |
| 99 | Experimental Analysis of Diurnal Variations in Humic-Like Fluorescent Dissolved Organic Matter in Surface Seawater. <i>Frontiers in Marine Science</i> , 2020, 7, . | 2.5 | 6 |
| 100 | Fates of Evolutionarily Distinct, Plastid-Type Glyceraldehyde 3-phosphate Dehydrogenase Genes in Kareniacean Dinoflagellates. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 669-678. | 1.7 | 5 |
| 101 | In Silico Structural Modeling and Analysis of Elongation Factor-1 Alpha and Elongation Factor-like Protein. <i>ACS Omega</i> , 2019, 4, 7308-7316. | 3.5 | 5 |
| 102 | DISTRIBUTION OF THE MITOCHONDRIAL DEVIANT GENETIC CODE AUA FOR METHIONINE IN HETEROKONT ALGAE. <i>Journal of Phycology</i> , 1998, 34, 1005-1008. | 2.3 | 4 |
| 103 | Splintrons in <i>Giardia intestinalis</i> . <i>Communicative and Integrative Biology</i> , 2011, 4, 454-456. | 1.4 | 4 |
| 104 | Signs of the plastid: Enzymes involved in plastid-localized metabolic pathways in a eugregarine species. <i>Parasitology International</i> , 2021, 83, 102364. | 1.3 | 4 |
| 105 | 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. | 1.6 | 4 |
| 106 | Comparative Plastid Genomics of Green-Colored Dinoflagellates Unveils Parallel Genome Compaction and RNA Editing. <i>Frontiers in Plant Science</i> , 0, 13, . | 3.6 | 4 |
| 107 | Splintrons in <i>Giardia intestinalis</i> : Spliceosomal introns in a split form. <i>Communicative and Integrative Biology</i> , 2011, 4, 454-6. | 1.4 | 3 |
| 108 | The evolutionary relationships amongst excavates: a concatenated protein analysis. <i>Journal of Eukaryotic Microbiology</i> , 2005, 52, 7S-27S. | 1.7 | 1 |

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|-----|---|-----|-----------|
| 109 | Multiple conversion between the genes encoding bacterial class-I release factors. Scientific Reports, 2015, 5, 12406. | 3.3 | 1 |
| 110 | A System for Phylogenetic Analyses over Alignments of Next Generation Sequence Data. , 2016, , . | | 1 |
| 111 | An asynchronous parallel genetic algorithm for the maximum likelihood phylogenetic tree search. , 2012, , . | | 0 |