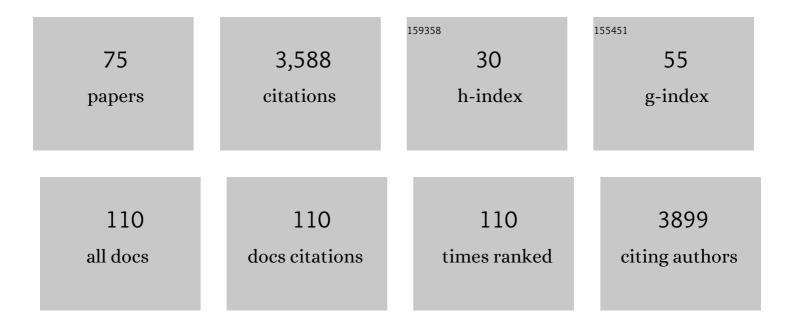
## **Cheong Xin Chan**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4181434/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	6.0	371
2	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	3.3	233
3	Genome of the red alga Porphyridium purpureum. Nature Communications, 2013, 4, 1941.	5.8	204
4	A genomic view of the reef-building coral Porites lutea and its microbial symbionts. Nature Microbiology, 2019, 4, 2090-2100.	5.9	160
5	Symbiodinium genomes reveal adaptive evolution of functions related to coral-dinoflagellate symbiosis. Communications Biology, 2018, 1, 95.	2.0	154
6	Benchmarking of alignment-free sequence comparison methods. Genome Biology, 2019, 20, 144.	3.8	147
7	Next-generation phylogenomics. Biology Direct, 2013, 8, 3.	1.9	122
8	Red and Green Algal Monophyly and Extensive Gene Sharing Found in a Rich Repertoire of Red Algal Genes. Current Biology, 2011, 21, 328-333.	1.8	101
9	A new species of <scp><i>B</i></scp> <i>urkholderia </i> isolated from sugarcane roots promotes plant growth. Microbial Biotechnology, 2014, 7, 142-154.	2.0	91
10	The transcriptomic response of the coral <i>Acropora digitifera</i> to a competent <i>Symbiodinium</i> strain: the symbiosome as an arrested early phagosome. Molecular Ecology, 2016, 25, 3127-3141.	2.0	88
11	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. Briefings in Bioinformatics, 2019, 20, 426-435.	3.2	74
12	The Algal Revolution. Trends in Plant Science, 2017, 22, 726-738.	4.3	73
13	Analysis of the Draft Genome of the Red Seaweed Gracilariopsis chorda Provides Insights into Genome Size Evolution in Rhodophyta. Molecular Biology and Evolution, 2018, 35, 1869-1886.	3.5	71
14	Plastid phylogenomics with broad taxon sampling further elucidates the distinct evolutionary origins and timing of secondary green plastids. Scientific Reports, 2018, 8, 1523.	1.6	66
15	Comparison of 15 dinoflagellate genomes reveals extensive sequence and structural divergence in family Symbiodiniaceae and genus Symbiodinium. BMC Biology, 2021, 19, 73.	1.7	65
16	Genomes of the dinoflagellate Polarella glacialis encode tandemly repeated single-exon genes with adaptive functions. BMC Biology, 2020, 18, 56.	1.7	64
17	Trends in seaweed research. Trends in Plant Science, 2006, 11, 165-166.	4.3	63
18	Inferring phylogenies of evolving sequences without multiple sequence alignment. Scientific Reports, 2014. 4. 6504.	1.6	62

CHEONG XIN CHAN

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19	Are Protein Domains Modules of Lateral Genetic Transfer?. PLoS ONE, 2009, 4, e4524.	1.1	60
20	Optimisation of RNA extraction from Gracilaria changii (Gracilariales, Rhodophyta). Journal of Applied Phycology, 2004, 16, 297-301.	1.5	59
21	Lateral Transfer of Genes and Gene Fragments in Prokaryotes. Genome Biology and Evolution, 2009, 1, 429-438.	1.1	59
22	<i>Porphyra</i> (Bangiophyceae) Transcriptomes Provide Insights Into Red Algal Development And Metabolism. Journal of Phycology, 2012, 48, 1328-1342.	1.0	56
23	Deciphering the nature of the coral– <i>Chromera</i> association. ISME Journal, 2018, 12, 776-790.	4.4	56
24	Resolving structure and function of metaorganisms through a holistic framework combining reductionist and integrative approaches. Zoology, 2019, 133, 81-87.	0.6	53
25	Alignment-free microbial phylogenomics under scenarios of sequence divergence, genome rearrangement and lateral genetic transfer. Scientific Reports, 2016, 6, 28970.	1.6	51
26	Plastid Origin and Evolution: New Models Provide Insights into Old Problems. Plant Physiology, 2011, 155, 1552-1560.	2.3	48
27	Red and Green Algal Origin of Diatom Membrane Transporters: Insights into Environmental Adaptation and Cell Evolution. PLoS ONE, 2011, 6, e29138.	1.1	44
28	Detecting recombination in evolving nucleotide sequences. BMC Bioinformatics, 2006, 7, 412.	1.2	41
29	Core genes in diverse dinoflagellate lineages include a wealth of conserved dark genes with unknown functions. Scientific Reports, 2018, 8, 17175.	1.6	41
30	Genome Evolution of Coral Reef Symbionts as Intracellular Residents. Trends in Ecology and Evolution, 2019, 34, 799-806.	4.2	41
31	Genomic adaptations to an endolithic lifestyle in the coral-associated alga Ostreobium. Current Biology, 2021, 31, 1393-1402.e5.	1.8	40
32	Lateral Transfer of Genes and Gene Fragments in Staphylococcus Extends beyond Mobile Elements. Journal of Bacteriology, 2011, 193, 3964-3977.	1.0	38
33	Evidence That Inconsistent Gene Prediction Can Mislead Analysis of Dinoflagellate Genomes. Journal of Phycology, 2020, 56, 6-10.	1.0	37
34	Analysis of Porphyra Membrane Transporters Demonstrates Gene Transfer among Photosynthetic Eukaryotes and Numerous Sodium-Coupled Transport Systems   Â. Plant Physiology, 2012, 158, 2001-2012.	2.3	35
35	Signatures of adaptation and symbiosis in genomes and transcriptomes of Symbiodinium. Scientific Reports, 2017, 7, 15021.	1.6	35
36	Analysis of an improved Cyanophora paradoxa genome assembly. DNA Research, 2019, 26, 287-299.	1.5	35

CHEONG XIN CHAN

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37	Active Host Response to Algal Symbionts in the Sea Slug Elysia chlorotica. Molecular Biology and Evolution, 2018, 35, 1706-1711.	3.5	32
38	<i>k</i> -mer Similarity, Networks of Microbial Genomes, and Taxonomic Rank. MSystems, 2018, 3, .	1.7	30
39	ANALYSIS OF <i>ALEXANDRIUM TAMARENSE</i> (DINOPHYCEAE) GENES REVEALS THE COMPLEX EVOLUTIONARY HISTORY OF A MICROBIAL EUKARYOTE <sup>1</sup> . Journal of Phycology, 2012, 48, 1130-1142.	1.0	29
40	Dual RNAâ€sequencing analyses of a coral and its native symbiont during the establishment of symbiosis. Molecular Ecology, 2020, 29, 3921-3937.	2.0	26
41	Biotic interactions as drivers of algal origin and evolution. New Phytologist, 2017, 216, 670-681.	3.5	25
42	Consensus Guidelines for Advancing Coral Holobiont Genome and Specimen Voucher Deposition. Frontiers in Marine Science, 2021, 8, .	1.2	23
43	Commonly misunderstood parameters of NCBI BLAST and important considerations for users. Bioinformatics, 2019, 35, 2697-2698.	1.8	22
44	Recapitulating phylogenies using k-mers: from trees to networks. F1000Research, 2016, 5, 2789.	0.8	22
45	Porphyra: Complex Life Histories in a Harsh Environment: P. umbilicalis, an Intertidal Red Alga for Genomic Analysis. Cellular Origin and Life in Extreme Habitats, 2010, , 129-148.	0.3	21
46	Endosymbiotic and horizontal gene transfer in microbial eukaryotes. Mobile Genetic Elements, 2012, 2, 101-105.	1.8	19
47	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA) <sup>1</sup> . Journal of Phycology, 2012, 48, 883-896.	1.0	19
48	Sex in Symbiodiniaceae dinoflagellates: genomic evidence for independent loss of the canonical synaptonemal complex. Scientific Reports, 2020, 10, 9792.	1.6	19
49	PhySortR: a fast, flexible tool for sorting phylogenetic trees in R. PeerJ, 2016, 4, e2038.	0.9	17
50	Genome-powered classification of microbial eukaryotes: focus on coral algal symbionts. Trends in Microbiology, 2022, 30, 831-840.	3.5	17
51	A word-oriented approach to alignment validation. Bioinformatics, 2005, 21, 2230-2239.	1.8	16
52	Comparative Genomics Supports That Brazilian Bioethanol Saccharomyces cerevisiae Comprise a Unified Group of Domesticated Strains Related to Cachaça Spirit Yeasts. Frontiers in Microbiology, 2021, 12, 644089.	1.5	16
53	Biological Intuition in Alignment-Free Methods: Response to Posada. Journal of Molecular Evolution, 2013, 77, 1-2.	0.8	13
54	Molecular phylogenetics before sequences. RNA Biology, 2014, 11, 176-185.	1.5	13

CHEONG XIN CHAN

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55	Recapitulating phylogenies using k-mers: from trees to networks. F1000Research, 2016, 5, 2789.	0.8	13
56	Alignment-Free Analysis of Whole-Genome Sequences From Symbiodiniaceae Reveals Different Phylogenetic Signals in Distinct Regions. Frontiers in Plant Science, 2022, 13, 815714.	1.7	13
57	Foreign gene recruitment to the fatty acid biosynthesis pathway in diatoms. Mobile Genetic Elements, 2013, 3, e27313.	1.8	10
58	Clustering evolving proteins into homologous families. BMC Bioinformatics, 2013, 14, 120.	1.2	9
59	Evidence for Widespread Exonic Small RNAs in the Glaucophyte Alga Cyanophora paradoxa. PLoS ONE, 2013, 8, e67669.	1.1	8
60	Analysis of the Genome of Cyanophora paradoxa: An Algal Model for Understanding Primary Endosymbiosis. , 2014, , 135-148.		7
61	Analysis of horizontal genetic transfer in red algae in the post-genomics age. Mobile Genetic Elements, 2013, 3, e27669.	1.8	5
62	Tightly Constrained Genome Reduction and Relaxation of Purifying Selection during Secondary Plastid Endosymbiosis. Molecular Biology and Evolution, 2022, 39, .	3.5	5
63	Nuclear genome of a pedinophyte pinpoints genomic innovation and streamlining in the green algae. New Phytologist, 2022, 233, 2144-2154.	3.5	5
64	Comparative transcriptomic analyses of Chromera and Symbiodiniaceae. Environmental Microbiology Reports, 2020, 12, 435-443.	1.0	4
65	Inferring Phylogenomic Relationship of Microbes Using Scalable Alignment-Free Methods. Methods in Molecular Biology, 2021, 2242, 69-76.	0.4	4
66	Transcriptome of the coralline alga Calliarthron tuberculosum (Corallinales, Rhodophyta) reveals convergent evolution of a partial lignin biosynthesis pathway. PLoS ONE, 2022, 17, e0266892.	1.1	4
67	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. Methods in Molecular Biology, 2017, 1525, 421-432.	0.4	2
68	A PHYLOGENOMIC APPROACH FOR STUDYING PLASTID ENDOSYMBIOSIS. , 2008, , .		2
69	A phylogenomic approach for studying plastid endosymbiosis. Genome Informatics, 2008, 21, 165-76.	0.4	2
70	Genome-Guided Analysis of Seven Weed Species Reveals Conserved Sequence and Structural Features of Key Gene Targets for Herbicide Development. Frontiers in Plant Science, 0, 13, .	1.7	2
71	Large-scale detection of recombination in nucleotide sequences. AIP Conference Proceedings, 2008, , .	0.3	1
72	Non-random sharing of Plantae genes. Communicative and Integrative Biology, 2011, 4, 361-363.	0.6	1

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73	Phylogenomics in Algal Research: Current Trends and Future Perspectives. Cellular Origin and Life in Extreme Habitats, 2015, , 501-517.	0.3	1
74	Selection of reference genes for transcript profiling of Sargassum polycystum by quantitative realâ€ŧime polymerase chain reaction. Phycological Research, 2018, 66, 247-252.	0.8	0
75	Phylogenomics of Marine Algae. Malaysian Journal of Science, 2013, 32, 11-18.	0.2	Ο