

# Cheong Xin Chan

## List of Publications by Year in descending order

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75  
papers

3,588  
citations

159358

30  
h-index

155451

55  
g-index

110  
all docs

110  
docs citations

110  
times ranked

3899  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tightly Constrained Genome Reduction and Relaxation of Purifying Selection during Secondary Plastid Endosymbiosis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
2	Nuclear genome of a pedinophyte pinpoints genomic innovation and streamlining in the green algae. <i>New Phytologist</i> , 2022, 233, 2144-2154.	3.5	5
3	Genome-powered classification of microbial eukaryotes: focus on coral algal symbionts. <i>Trends in Microbiology</i> , 2022, 30, 831-840.	3.5	17
4	Alignment-Free Analysis of Whole-Genome Sequences From Symbiodiniaceae Reveals Different Phylogenetic Signals in Distinct Regions. <i>Frontiers in Plant Science</i> , 2022, 13, 815714.	1.7	13
5	Transcriptome of the coralline alga <i>Calliarthron tuberculosum</i> (Corallinales, Rhodophyta) reveals convergent evolution of a partial lignin biosynthesis pathway. <i>PLoS ONE</i> , 2022, 17, e0266892.	1.1	4
6	Genomic adaptations to an endolithic lifestyle in the coral-associated alga <i>Ostreobium</i> . <i>Current Biology</i> , 2021, 31, 1393-1402.e5.	1.8	40
7	Comparative Genomics Supports That Brazilian Bioethanol <i>Saccharomyces cerevisiae</i> Comprise a Unified Group of Domesticated Strains Related to Cachaça Spirit Yeasts. <i>Frontiers in Microbiology</i> , 2021, 12, 644089.	1.5	16
8	Comparison of 15 dinoflagellate genomes reveals extensive sequence and structural divergence in family Symbiodiniaceae and genus <i>Symbiodinium</i> . <i>BMC Biology</i> , 2021, 19, 73.	1.7	65
9	Consensus Guidelines for Advancing Coral Holobiont Genome and Specimen Voucher Deposition. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	23
10	Inferring Phylogenomic Relationship of Microbes Using Scalable Alignment-Free Methods. <i>Methods in Molecular Biology</i> , 2021, 2242, 69-76.	0.4	4
11	Evidence That Inconsistent Gene Prediction Can Mislead Analysis of Dinoflagellate Genomes. <i>Journal of Phycology</i> , 2020, 56, 6-10.	1.0	37
12	Sex in Symbiodiniaceae dinoflagellates: genomic evidence for independent loss of the canonical synaptonemal complex. <i>Scientific Reports</i> , 2020, 10, 9792.	1.6	19
13	Dual RNA-seq analyses of a coral and its native symbiont during the establishment of symbiosis. <i>Molecular Ecology</i> , 2020, 29, 3921-3937.	2.0	26
14	Comparative transcriptomic analyses of <i>Chromera</i> and Symbiodiniaceae. <i>Environmental Microbiology Reports</i> , 2020, 12, 435-443.	1.0	4
15	Genomes of the dinoflagellate <i>Polarella glacialis</i> encode tandemly repeated single-exon genes with adaptive functions. <i>BMC Biology</i> , 2020, 18, 56.	1.7	64
16	Benchmarking of alignment-free sequence comparison methods. <i>Genome Biology</i> , 2019, 20, 144.	3.8	147
17	A genomic view of the reef-building coral <i>Porites lutea</i> and its microbial symbionts. <i>Nature Microbiology</i> , 2019, 4, 2090-2100.	5.9	160
18	Analysis of an improved <i>Cyanophora paradoxa</i> genome assembly. <i>DNA Research</i> , 2019, 26, 287-299.	1.5	35

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19	Genome Evolution of Coral Reef Symbionts as Intracellular Residents. Trends in Ecology and Evolution, 2019, 34, 799-806.	4.2	41
20	Resolving structure and function of metaorganisms through a holistic framework combining reductionist and integrative approaches. Zoology, 2019, 133, 81-87.	0.6	53
21	Commonly misunderstood parameters of NCBI BLAST and important considerations for users. Bioinformatics, 2019, 35, 2697-2698.	1.8	22
22	Alignment-free inference of hierarchical and reticulate phylogenomic relationships. Briefings in Bioinformatics, 2019, 20, 426-435.	3.2	74
23	Analysis of the Draft Genome of the Red Seaweed <i>Gracilariopsis chorda</i> Provides Insights into Genome Size Evolution in Rhodophyta. Molecular Biology and Evolution, 2018, 35, 1869-1886.	3.5	71
24	Active Host Response to Algal Symbionts in the Sea Slug <i>Elysia chlorotica</i> . Molecular Biology and Evolution, 2018, 35, 1706-1711.	3.5	32
25	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
26	Deciphering the nature of the coral- <i>Chromera</i> association. ISME Journal, 2018, 12, 776-790.	4.4	56
27	Core genes in diverse dinoflagellate lineages include a wealth of conserved dark genes with unknown functions. Scientific Reports, 2018, 8, 17175.	1.6	41
28	<i>k</i> -mer Similarity, Networks of Microbial Genomes, and Taxonomic Rank. MSystems, 2018, 3, .	1.7	30
29	Symbiodinium genomes reveal adaptive evolution of functions related to coral-dinoflagellate symbiosis. Communications Biology, 2018, 1, 95.	2.0	154
30	Selection of reference genes for transcript profiling of <i>Sargassum polycystum</i> by quantitative real-time polymerase chain reaction. Phycological Research, 2018, 66, 247-252.	0.8	0
31	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. Methods in Molecular Biology, 2017, 1525, 421-432.	0.4	2
32	The Algal Revolution. Trends in Plant Science, 2017, 22, 726-738.	4.3	73
33	Biotic interactions as drivers of algal origin and evolution. New Phytologist, 2017, 216, 670-681.	3.5	25
34	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
35	Signatures of adaptation and symbiosis in genomes and transcriptomes of Symbiodinium. Scientific Reports, 2017, 7, 15021.	1.6	35
36	Alignment-free microbial phylogenomics under scenarios of sequence divergence, genome rearrangement and lateral genetic transfer. Scientific Reports, 2016, 6, 28970.	1.6	51

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37	The transcriptomic response of the coral <i>Acropora digitifera</i> to a competent <i>Symbiodinium</i> strain: the symbiosome as an arrested early phagosome. <i>Molecular Ecology</i> , 2016, 25, 3127-3141.	2.0	88
38	Recapitulating phylogenies using k-mers: from trees to networks. <i>F1000Research</i> , 2016, 5, 2789.	0.8	22
39	PhySortR: a fast, flexible tool for sorting phylogenetic trees in R. <i>PeerJ</i> , 2016, 4, e2038.	0.9	17
40	Recapitulating phylogenies using k-mers: from trees to networks. <i>F1000Research</i> , 2016, 5, 2789.	0.8	13
41	Phylogenomics in Algal Research: Current Trends and Future Perspectives. <i>Cellular Origin and Life in Extreme Habitats</i> , 2015, , 501-517.	0.3	1
42	Molecular phylogenetics before sequences. <i>RNA Biology</i> , 2014, 11, 176-185.	1.5	13
43	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. <i>Microbial Biotechnology</i> , 2014, 7, 142-154.	2.0	91
44	Inferring phylogenies of evolving sequences without multiple sequence alignment. <i>Scientific Reports</i> , 2014, 4, 6504.	1.6	62
45	Analysis of the Genome of <i>Cyanophora paradoxa</i> : An Algal Model for Understanding Primary Endosymbiosis. , 2014, , 135-148.		7
46	Biological Intuition in Alignment-Free Methods: Response to Posada. <i>Journal of Molecular Evolution</i> , 2013, 77, 1-2.	0.8	13
47	Clustering evolving proteins into homologous families. <i>BMC Bioinformatics</i> , 2013, 14, 120.	1.2	9
48	Next-generation phylogenomics. <i>Biology Direct</i> , 2013, 8, 3.	1.9	122
49	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013, 4, 1941.	5.8	204
50	Analysis of horizontal genetic transfer in red algae in the post-genomics age. <i>Mobile Genetic Elements</i> , 2013, 3, e27669.	1.8	5
51	Foreign gene recruitment to the fatty acid biosynthesis pathway in diatoms. <i>Mobile Genetic Elements</i> , 2013, 3, e27313.	1.8	10
52	Evidence for Widespread Exonic Small RNAs in the Glaucophyte Alga <i>Cyanophora paradoxa</i> . <i>PLoS ONE</i> , 2013, 8, e67669.	1.1	8
53	Phylogenomics of Marine Algae. <i>Malaysian Journal of Science</i> , 2013, 32, 11-18.	0.2	0
54	Endosymbiotic and horizontal gene transfer in microbial eukaryotes. <i>Mobile Genetic Elements</i> , 2012, 2, 101-105.	1.8	19

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55	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	6.0	371
56	Analysis of Porphyra Membrane Transporters Demonstrates Gene Transfer among Photosynthetic Eukaryotes and Numerous Sodium-Coupled Transport Systems. <i>Plant Physiology</i> , 2012, 158, 2001-2012.	2.3	35
57	<i>Porphyra</i> (Bangiophyceae) Transcriptomes Provide Insights Into Red Algal Development And Metabolism. <i>Journal of Phycology</i> , 2012, 48, 1328-1342.	1.0	56
58	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA). <i>Journal of Phycology</i> , 2012, 48, 883-896.	1.0	19
59	ANALYSIS OF <i>ALEXANDRIUM TAMARENSE</i> (DINOPHYCEAE) GENES REVEALS THE COMPLEX EVOLUTIONARY HISTORY OF A MICROBIAL EUKARYOTE. <i>Journal of Phycology</i> , 2012, 48, 1130-1142.	1.0	29
60	Red and Green Algal Monophyly and Extensive Gene Sharing Found in a Rich Repertoire of Red Algal Genes. <i>Current Biology</i> , 2011, 21, 328-333.	1.8	101
61	Non-random sharing of Plantae genes. <i>Communicative and Integrative Biology</i> , 2011, 4, 361-363.	0.6	1
62	Plastid Origin and Evolution: New Models Provide Insights into Old Problems. <i>Plant Physiology</i> , 2011, 155, 1552-1560.	2.3	48
63	Lateral Transfer of Genes and Gene Fragments in <i>Staphylococcus</i> Extends beyond Mobile Elements. <i>Journal of Bacteriology</i> , 2011, 193, 3964-3977.	1.0	38
64	Red and Green Algal Origin of Diatom Membrane Transporters: Insights into Environmental Adaptation and Cell Evolution. <i>PLoS ONE</i> , 2011, 6, e29138.	1.1	44
65	Porphyra: Complex Life Histories in a Harsh Environment: <i>P. umbilicalis</i> , an Intertidal Red Alga for Genomic Analysis. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 129-148.	0.3	21
66	Are Protein Domains Modules of Lateral Genetic Transfer?. <i>PLoS ONE</i> , 2009, 4, e4524.	1.1	60
67	Lateral Transfer of Genes and Gene Fragments in Prokaryotes. <i>Genome Biology and Evolution</i> , 2009, 1, 429-438.	1.1	59
68	Large-scale detection of recombination in nucleotide sequences. <i>AIP Conference Proceedings</i> , 2008, , .	0.3	1
69	A PHYLOGENOMIC APPROACH FOR STUDYING PLASTID ENDOSYMBIOSIS. , 2008, , .		2
70	A phylogenomic approach for studying plastid endosymbiosis. <i>Genome Informatics</i> , 2008, 21, 165-76.	0.4	2
71	Trends in seaweed research. <i>Trends in Plant Science</i> , 2006, 11, 165-166.	4.3	63
72	Detecting recombination in evolving nucleotide sequences. <i>BMC Bioinformatics</i> , 2006, 7, 412.	1.2	41

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73	A word-oriented approach to alignment validation. <i>Bioinformatics</i> , 2005, 21, 2230-2239.	1.8	16
74	Optimisation of RNA extraction from <i>Gracilaria changii</i> (Gracilariales, Rhodophyta). <i>Journal of Applied Phycology</i> , 2004, 16, 297-301.	1.5	59
75	Genome-Guided Analysis of Seven Weed Species Reveals Conserved Sequence and Structural Features of Key Gene Targets for Herbicide Development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2