

# Nansheng Chen

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48  
papers

1,180  
citations

11  
h-index

34  
g-index

56  
ext. papers

1,825  
ext. citations

5  
avg, IF

4.79  
L-index

#	Paper	IF	Citations
48	Diatom Biodiversity and Speciation Revealed by Comparative Analysis of Mitochondrial Genomes.. <i>Frontiers in Plant Science</i> , <b>2022</b> , 13, 749982	6.2	
47	Metabarcoding analysis of microbiome dynamics during a <i>Phaeocystis globosa</i> bloom in the Beibu Gulf, China.. <i>Harmful Algae</i> , <b>2022</b> , 114, 102217	5.3	0
46	Comparative analysis of <i>Thalassionema</i> chloroplast genomes revealed hidden biodiversity.. <i>BMC Genomics</i> , <b>2022</b> , 23, 327	4.5	
45	Composition and spatial-temporal dynamics of phytoplankton community shaped by environmental selection and interactions in the Jiaozhou Bay.. <i>Water Research</i> , <b>2022</b> , 218, 118488	12.5	2
44	Biodiversity and Spatial-Temporal Dynamics of Species in Jiaozhou Bay, China. <i>International Journal of Environmental Research and Public Health</i> , <b>2021</b> , 18,	4.6	1
43	Comparative Analysis of Chloroplast Genomes of Seven Species Revealed Variation Hotspots and Speciation Time. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 742554	5.7	2
42	Improve hot region prediction by analyzing different machine learning algorithms. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 522	3.6	0
41	Comparative analysis of full-length mitochondrial genomes of five <i>Skeletonema</i> species reveals conserved genome organization and recent speciation. <i>BMC Genomics</i> , <b>2021</b> , 22, 746	4.5	2
40	Definition of a High-Resolution Molecular Marker for Tracking the Genetic Diversity of the Harmful Algal Species Through Comparative Analysis of Mitochondrial Genomes. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 631144	5.7	4
39	Development of a high-resolution molecular marker for tracking <i>Pseudo-nitzschia pungens</i> genetic diversity through comparative analysis of mitochondrial genomes. <i>Journal of Applied Phycology</i> , <b>2021</b> , 33, 2283-2298	3.2	0
38	Complete mitochondrial genome of the harmful algal bloom species (Mediophyceae, Bacillariophyta) from the east China sea.. <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 1421-1423	0.5	1
37	Complete mitochondrial genome of (Mediophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 1560-1562	0.5	1
36	The complete mitochondrial genome and phylogenetic analysis of (Coscinodiscophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 1849-1851	0.5	1
35	Mitochondrial genome and phylogenomic analysis of (Bacillariophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2035-2037	0.5	
34	Molecular characterization of harmful algal blooms in the Bohai Sea using metabarcoding analysis. <i>Harmful Algae</i> , <b>2021</b> , 106, 102066	5.3	1
33	Research on the biology and ecology of the harmful algal bloom species <i>Phaeocystis globosa</i> in China: Progresses in the last 20 years. <i>Harmful Algae</i> , <b>2021</b> , 107, 102057	5.3	6
32	Molecular cloning and transcriptional regulation of two $\Gamma$ -carbonic anhydrase genes in the green macroalga <i>Ulva prolifera</i> . <i>Genetica</i> , <b>2021</b> , 149, 63-72	1.5	0

31	Mitochondrial genome of the harmful algal bloom species <i>Odontella regia</i> (Mediophyceae, Bacillariophyta). <i>Journal of Applied Phycology</i> , <b>2021</b> , 33, 855-868	3.2	6
30	Large Differences in the Haptophyte Mitochondrial Genomes Driven by Repeat Amplifications. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 676447	5.7	2
29	High genetic diversity of the harmful algal bloom species <i>Phaeocystis globosa</i> revealed using the molecular marker COX1. <i>Harmful Algae</i> , <b>2021</b> , 107, 102065	5.3	4
28	Eight soybean reference genome resources from varying latitudes and agronomic traits. <i>Scientific Data</i> , <b>2021</b> , 8, 164	8.2	4
27	Complete chloroplast genome of (Mediophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2194-2197	0.5	1
26	Complete mitochondrial genome of (Coscinodiscophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2319-2321	0.5	1
25	Complete mitochondrial genome of (Coscinodiscophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2332-2334	0.5	0
24	Metabarcoding analysis of harmful algal bloom species in the Changjiang Estuary, China. <i>Science of the Total Environment</i> , <b>2021</b> , 782, 146823	10.2	4
23	Metabarcoding dissection of harmful algal bloom species in the East China Sea off Southern Zhejiang Province in late spring. <i>Marine Pollution Bulletin</i> , <b>2021</b> , 169, 112586	6.7	2
22	The Cardamine <i>enshiensis</i> genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. <i>Cell Discovery</i> , <b>2021</b> , 7, 62	22.3	2
21	Complete mitochondrial genome of the harmful algal bloom species (Bacillariophyceae, Bacillariophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 2541-2543	0.5	
20	Phylogenomic analysis of the chloroplast genome of the green-tide forming macroalga <i>Linnaeus</i> (Ulvophyceae, Chlorophyta). <i>Mitochondrial DNA Part B: Resources</i> , <b>2021</b> , 6, 3052-3054	0.5	0
19	Chloroplast Genomes for Five Species: Comparative and Phylogenetic Analysis.. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 774617	6.2	2
18	Comparative Analysis of Chloroplast Genomes of <i>Thalassiosira</i> Species. <i>Frontiers in Marine Science</i> , <b>2021</b> , 8,	4.5	1
17	Metabarcoding analysis of harmful algal species in Jiaozhou Bay. <i>Harmful Algae</i> , <b>2020</b> , 92, 101772	5.3	14
16	Metabolic analyses by metatranscriptomics highlight plasticity in phosphorus acquisition during monospecific and multispecies algal blooms. <i>Hydrobiologia</i> , <b>2020</b> , 847, 1071-1085	2.4	3
15	Development of a high-resolution molecular marker for tracking <i>Phaeocystis globosa</i> genetic diversity through comparative analysis of chloroplast genomes. <i>Harmful Algae</i> , <b>2020</b> , 99, 101911	5.3	15
14	Multiple Intraspecific Variations of Mitochondrial Genomes in the Green-Tide Forming Alga, <i>Ulva compressa</i> Linnaeus (Ulvophyceae, Chlorophyta). <i>Frontiers in Marine Science</i> , <b>2020</b> , 7,	4.5	1

13	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , <b>2020</b> , 9,	7.6	12
12	Construction and comparative analysis of mitochondrial genome in the brown tide forming alga <i>Aureococcus anophagefferens</i> (Pelagophyceae, Ochrophyta). <i>Journal of Applied Phycology</i> , <b>2020</b> , 32, 441-450	3.2	4
11	A chromosomal-level genome assembly for the insect vector for Chagas disease, <i>Triatoma rubrofasciata</i> . <i>GigaScience</i> , <b>2019</b> , 8,	7.6	11
10	Genomic Identification and Functional Characterization of Essential Genes in. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 981-997	3.2	13
9	A draft genome assembly of the Chinese sillago ( <i>Sillago sinica</i> ), the first reference genome for Sillaginidae fishes. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	22
8	Interplay between maternal <i>Slc6a4</i> mutation and prenatal stress: a possible mechanism for autistic behavior development. <i>Scientific Reports</i> , <b>2017</b> , 7, 8735	4.9	16
7	New observation of sialuria prompts detection of liver tumor in previously reported patient. <i>Molecular Genetics and Metabolism</i> , <b>2016</b> , 118, 92-9	3.7	2
6	Conservation of hot regions in protein-protein interaction in evolution. <i>Methods</i> , <b>2016</b> , 110, 73-80	4.6	11
5	Spectrum of variations in <i>dog-1/FANCJ</i> and <i>mdf-1/MAD1</i> defective <i>Caenorhabditis elegans</i> strains after long-term propagation. <i>BMC Genomics</i> , <b>2015</b> , 16, 210	4.5	6
4	Factor-induced Reprogramming and Zinc Finger Nuclease-aided Gene Targeting Cause Different Genome Instability in $\beta$ -Thalassemia Induced Pluripotent Stem Cells (iPSCs). <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 12079-89	5.4	27
3	Genome-wide variations in a natural isolate of the nematode <i>Caenorhabditis elegans</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 255	4.5	16
2	Mutational landscape of intrahepatic cholangiocarcinoma. <i>Nature Communications</i> , <b>2014</b> , 5, 5696	17.4	220
1	Using RepeatMasker to identify repetitive elements in genomic sequences. <i>Current Protocols in Bioinformatics</i> , <b>2009</b> , Chapter 4, Unit 4.10	24.2	733