Zi-Min Hu

List of Publications by Year
in descending order

48	900	471509 17	526287 27
papers	citations	h-index	g-index

50	50	50	697
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Phylogeographic heterogeneity of the brown macroalgaSargassum horneri(Fucaceae) in the northwestern Pacific in relation to late Pleistocene glaciation and tectonic configurations. Molecular Ecology, 2011, 20, 3894-3909.	3.9	110
2	Kelp aquaculture in China: a retrospective and future prospects. Reviews in Aquaculture, 2021, 13, 1324-1351.	9.0	60
3	Hidden diversity and phylogeographic history provide conservation insights for the edible seaweed Sargassum fusiforme in the Northwest Pacific. Evolutionary Applications, 2017, 10, 366-378.	3.1	51
4	Oceanic currents drove population genetic connectivity of the brown alga Sargassum thunbergii in the northâ€west Pacific. Journal of Biogeography, 2017, 44, 230-242.	3.0	47
5	Inter-simple sequence repeat (ISSR) analysis of genetic variation of Chondrus crispus populations from North Atlantic. Aquatic Botany, 2008, 88, 154-159.	1.6	42
6	Asymmetric genetic exchange in the brown seaweed Sargassum fusiforme (Phaeophyceae) driven by oceanic currents. Marine Biology, 2013, 160, 1407-1414.	1.5	42
7	Adaptation mechanisms and ecological consequences of seaweed invasions: a review case of agarophyte Gracilaria vermiculophylla. Biological Invasions, 2014, 16, 967-976.	2.4	39
8	Phylogeographic structure and deep lineage diversification of the red alga Chondrus ocellatus Holmes in the Northwest Pacific. Molecular Ecology, 2015, 24, 5020-5033.	3.9	36
9	Intraspecific genetic variation matters when predicting seagrass distribution under climate change. Molecular Ecology, 2021, 30, 3840-3855.	3.9	30
10	An efficient method for DNA isolation from red algae. Journal of Applied Phycology, 2004, 16, 161-166.	2.8	29
11	Phylogeographic data revealed shallow genetic structure in the kelp Saccharina japonica (Laminariales, Phaeophyta). BMC Evolutionary Biology, 2015, 15, 237.	3.2	24
12	Genetic data from the red alga Palmaria palmata reveal a midâ€Pleistocene deep genetic split in the North Atlantic. Journal of Biogeography, 2015, 42, 902-913.	3.0	23
13	Historical isolation and contemporary gene flow drive population diversity of the brown alga Sargassum thunbergii along the coast of China. BMC Evolutionary Biology, 2017, 17, 246.	3.2	22
14	Phylogeographic diversification and postglacial range dynamics shed light on the conservation of the kelp Saccharina japonica. Evolutionary Applications, 2019, 12, 791-803.	3.1	22
15	Priming of Marine Macrophytes for Enhanced Restoration Success and Food Security in Future Oceans. Frontiers in Marine Science, 2021, 8, .	2.5	21
16	PHYLOGEOGRAPHIC PATTERNS INDICATE TRANSATLANTIC MIGRATION FROM EUROPE TO NORTH AMERICA IN THE RED SEAWEED CHONDRUS CRISPUS (GIGARTINALES, RHODOPHYTA)1. Journal of Phycology, 2010, 46, 889-900.	2.3	20
17	A late Pleistocene marine glacial refugium in the southâ€west of Hainan Island, China: Phylogeographical insights from the brown alga Sargassum polycystum. Journal of Biogeography, 2018, 45, 355-366.	3.0	20
18	Using the ribosomal internal transcribed spacer (ITS) as a complement marker for species identification of red macroalgae. Hydrobiologia, 2009, 635, 279-287.	2.0	18

#	Article	IF	Citations
19	Seaweed Phylogeography from 1994 to 2014: An Overview. , 2016, , 3-22.		17
20	Post-Pleistocene demographic history of the North Atlantic endemic Irish moss Chondrus crispus: glacial survival, spatial expansion and gene flow. Journal of Evolutionary Biology, 2011, 24, 505-517.	1.7	15
21	Linking Ecology to Genetics to Better Understand Adaptation and Evolution: A Review in Marine Macrophytes. Frontiers in Marine Science, 2020, 7, .	2.5	14
22	Identification of SCAR marker linking to longer frond length of Saccharina japonica (Laminariales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	12
23	Climateâ€induced range shifts shaped the present and threaten the future genetic variability of a marine brown alga in the Northwest Pacific. Evolutionary Applications, 2021, 14, 1867-1879.	3.1	12
24	Phylogeography of the Northern Atlantic species Chondrus crispus (Gigartinales, Rhodophyta) inferred from nuclear rDNA internal transcribed spacer sequences. Hydrobiologia, 2007, 575, 315-327.	2.0	11
25	Molecular analysis of Sargassum from the northern China seas. Phytotaxa, 2017, 319, 71.	0.3	11
26	MtDNA-Based Phylogeography of the Red Alga Agarophyton vermiculophyllum (Gigartinales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462	2.5	11
27	Delineation ofChondrus(Gigartinales, Florideophyceae) in China and the origin ofC. crispusinferred from molecular data. Marine Biology Research, 2007, 3, 145-154.	0.7	10
28	NrDNA internal transcribed spacer revealed molecular diversity in strains of red seaweed Porphyra yezoensis and genetic insights for commercial breeding. Genetic Resources and Crop Evolution, 2010, 57, 791-799.	1.6	10
29	Survival in Glacial Refugia Versus Postglacial Dispersal in the North Atlantic: The Cases of Red Seaweeds. , 2016, , 309-330.		10
30	AFLP analysis revealed a north to south genetic break in the brown alga Sargassum thunbergii along the coast of China. Journal of Applied Phycology, 2018, 30, 2697-2705.	2.8	10
31	PI signal transduction and ubiquitination respond to dehydration stress in the red seaweed Gloiopeltis furcata under successive tidal cycles. BMC Plant Biology, 2019, 19, 516.	3.6	10
32	Coastal upwelling areas as safe havens during climate warming. Journal of Biogeography, 2016, 43, 2513-2514.	3.0	8
33	Phylogeographic surveys and apomictic genetic connectivity in the North Atlantic red seaweed Mastocarpus stellatus. Molecular Phylogenetics and Evolution, 2016, 94, 463-472.	2.7	8
34	Genetic diversity of the habitat-forming red alga Gracilaria vermiculophylla along Chinese coasts. Biodiversity Science, 2016, 24, 781-790.	0.6	8
35	A unique genetic lineage at the southern coast of China in the agar-producing Gracilaria vermiculophylla (Gracilariales, Florideophyceae). Algae, 2018, 33, 269-278.	2.3	8
36	Molecular identification of Chinese cultivatedPorphyra(Bangiaceae, Rhodophyta) based on the rDNA internal transcribed spacer-1 sequence and random amplified polymorphic DNA markers. Marine Biology Research, 2007, 3, 20-28.	0.7	7

#	Article	IF	Citations
37	Species diversity and distribution of the genus <italic>Colpomenia</italic> (Scytosiphonaceae, Phaeophyceae) along the coast of China. Algae, 2019, 34, 217-228.	2.3	7
38	Identification and Assessing the Cultivars of Laminaria Lamx. (Phaeophyceae) with Molecular Markers. Journal of Integrative Plant Biology, 2005, 47, 283-291.	8.5	6
39	Insufficient geographical sampling could severely influence phylogeographic interpretations. Marine Biology, 2013, 160, 1521-1522.	1.5	6
40	A concise review of the brown seaweed Sargassum thunbergii â€" a knowledge base to inform large-scale cultivation efforts. Journal of Applied Phycology, 2021, 33, 3469-3482.	2.8	6
41	Adaptation of Temperate Seagrass to Arctic Light Relies on Seasonal Acclimatization of Carbon Capture and Metabolism. Frontiers in Plant Science, 2021, 12, 745855.	3.6	6
42	Growth, reproduction and recruitment of Silvetia siliquosa (Fucales, Phaeophyceae) transplants using polyethylene rope and natural rock methods. Algae, 2017, 32, 337-347.	2.3	5
43	Low genetic diversity in the endangered marine alga Silvetia siliquosa (Ochrophyta: Fucaceae) and the implication to conservation. Journal of Oceanology and Limnology, 2022, 40, 216-225.	1.3	4
44	Predicting macroalgal species distributions along the Thai-Malay Peninsula. Estuarine, Coastal and Shelf Science, 2022, 267, 107760.	2.1	4
45	Intertidal population genetic dynamics at a microgeographic seascape scale. Molecular Ecology, 2013, 22, 3191-3194.	3.9	3
46	Detecting no natural hybridization and predicting range overlap in Saccharina angustata and Saccharina japonica. Journal of Applied Phycology, 2021, 33, 693-702.	2.8	3
47	How to rectify the misuse of scientific names in bioscience?. Science Bulletin, 2014, 59, 1479-1481.	1.7	2
48	Primary species recognition and phylogeny of Chondrus (Gigartinales, Rhodophyta) using 18S rDNA sequence data. Chinese Journal of Oceanology and Limnology, 2007, 25, 174-183.	0.7	0