Markus Majaneva

List of Publications by Year
in descending order

27	658	840776 11	677142 22
papers	citations	h-index	g-index

29	29	29	1211
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	First circumpolar assessment of Arctic freshwater phytoplankton and zooplankton diversity: Spatial patterns and environmental factors. Freshwater Biology, 2022, 67, 141-158.	2.4	13
2	DNA Metabarcoding of Preservative Ethanol Reveals Changes in Invertebrate Community Composition Following Rotenone Treatment. Frontiers in Environmental Science, 2022, 10, .	3.3	1
3	An urban Blitz with a twist: rapid biodiversity assessment using aquatic environmental DNA. Environmental DNA, 2021, 3, 200-213.	5.8	9
4	Group 2i Isochrysidales produce characteristic alkenones reflecting sea ice distribution. Nature Communications, 2021, 12, 15.	12.8	33
5	Multi-marker DNA metabarcoding reflects tardigrade diversity in different habitats. Genome, 2021, 64, 217-231.	2.0	9
6	Taxonomically and Functionally Distinct Ciliophora Assemblages Inhabiting Baltic Sea Ice. Microbial Ecology, 2021, , 1.	2.8	1
7	Deficiency syndromes in top predators associated with large-scale changes in the Baltic Sea ecosystem. PLoS ONE, 2020, 15, e0227714.	2.5	13
8	DNA metabarcoding adds valuable information for management of biodiversity in roadside stormwater ponds. Ecology and Evolution, 2019, 9, 9712-9722.	1.9	15
9	Environmental DNA filtration techniques affect recovered biodiversity. Scientific Reports, 2018, 8, 4682.	3.3	93
10	Phases of microalgal succession in sea ice and the water column in the Baltic Sea from autumn to spring. Marine Ecology - Progress Series, 2018, 599, 19-34.	1.9	17
11	Sea-ice eukaryotes of the Gulf of Finland, Baltic Sea, and evidence for herbivory on weakly shade-adapted ice algae. European Journal of Protistology, 2017, 57, 1-15.	1.5	12
12	Life associated with Baltic Sea ice. , 2017, , 333-357.		12
13	Primary production calculations for sea ice from bio-optical observations in the Baltic Sea. Elementa, 2016, 4, .	3.2	3
14	Bioinformatic Amplicon Read Processing Strategies Strongly Affect Eukaryotic Diversity and the Taxonomic Composition of Communities. PLoS ONE, 2015, 10, e0130035.	2.5	67
15	The contribution of mycosporine-like amino acids, chromophoric dissolved organic matter and particles to the UV protection of sea-ice organisms in the Baltic Sea. Photochemical and Photobiological Sciences, 2015, 14, 1025-1038.	2.9	25
16	Solar PAR and UVR modify the community composition and photosynthetic activity of sea ice algae. FEMS Microbiology Ecology, 2015, 91, fiv102.	2.7	11
17	Fast direct melting of brackish sea-ice samples results in biologically more accurate results than slow buffered melting. Polar Biology, 2014, 37, 1811-1822.	1.2	63
18	Rhinomonas nottbecki n. sp. (Cryptomonadales) and Molecular Phylogeny of the Family Pyrenomonadaceae. Journal of Eukaryotic Microbiology, 2014, 61, 480-492.	1.7	16

#	Article	IF	Citations
19	Cydippid ctenophores in the coastal waters of Svalbard: is it only Mertensia ovum?. Polar Biology, 2013, 36, 1681-1686.	1.2	11
20	The extensive bloom of alternate-stage Prymnesium polylepis (Haptophyta) in the Baltic Sea during autumnâ€“spring 2007â€“2008. European Journal of Phycology, 2012, 47, 310-320.	2.0	14
21	Comparison of wintertime eukaryotic community from sea ice and open water in the Baltic Sea, based on sequencing of the 18S rRNA gene. Polar Biology, 2012, 35, 875-889.	1.2	60
22	Molecular evidence for a diverse green algal community growing in the hair of sloths and a specific association with Trichophilus welckeri(Chlorophyta, Ulvophyceae). BMC Evolutionary Biology, 2010, 10, 86.	3.2	58
23	HETEROCAPSA ARCTICA SUBSP. FRIGIDA SUBSP. NOV. (PERIDINIALES, DINOPHYCEAE)-DESCRIPTION OF A NEW DINOFLAGELLATE AND ITS OCCURRENCE IN THE BALTIC SEA1. Journal of Phycology, 2010, 46, 751-762.	2.3	12
24	Technical challenges when scaling up macroinvertebrate DNA metabarcoding. ARPHA Conference Abstracts, 0, 4, .	0.0	0
25	The use of eDNA and DNA metabarcoding in monitoring the ecological condition of Norwegian lakes. ARPHA Conference Abstracts, 0, 4, .	0.0	0
26	Choice of DNA extraction method affects DNA metabarcoding of unsorted invertebrate bulk samples. Metabarcoding and Metagenomics, 0, 2, .	0.0	40
27	Advancing the use of molecular methods for routine freshwater macroinvertebrate biomonitoring â€“ the need for calibration experiments. Metabarcoding and Metagenomics, 0, 3, .	0.0	48