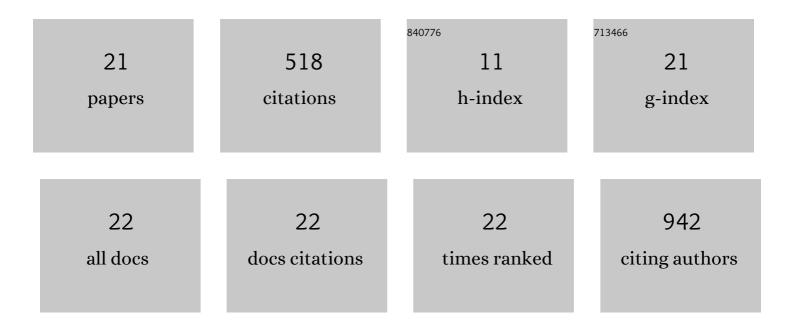
Matthew J Morgan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The role of predicted chemotactic and hydrocarbon degrading taxa in natural source zone depletion at a legacy petroleum hydrocarbon site. Journal of Hazardous Materials, 2022, 430, 128482.	12.4	8
2	Unravelling Microbial Communities Associated with Different Light Non-Aqueous Phase Liquid Types Undergoing Natural Source Zone Depletion Processes at a Legacy Petroleum Site. Water (Switzerland), 2021, 13, 898.	2.7	8
3	Genomics and transcriptomics yields a system-level view of the biology of the pathogen Naegleria fowleri. BMC Biology, 2021, 19, 142.	3.8	18
4	Biofilm and Related Amoebas in an UK Chlorinated Drinking Water System. Water (Switzerland), 2021, 13, 3069.	2.7	5
5	Investigation into the microbial communities and associated crude oil-contamination along a Gulf War impacted groundwater system in Kuwait. Water Research, 2020, 170, 115314.	11.3	19
6	Naegleria fowleri in drinking water distribution systems. Current Opinion in Environmental Science and Health, 2020, 16, 22-27.	4.1	12
7	Biodegradability of legacy crude oil contamination in Gulf War damaged groundwater wells in Northern Kuwait. Biodegradation, 2019, 30, 71-85.	3.0	9
8	Biodegradability of polar compounds formed from weathered diesel. Biodegradation, 2018, 29, 443-461.	3.0	10
9	Preferential feeding in Naegleria fowleri; intracellular bacteria isolated from amoebae in operational drinking water distribution systems. Water Research, 2018, 141, 126-134.	11.3	10
10	Comparison of biofilm ecology supporting growth of individual Naegleria species in a drinking water distribution system. FEMS Microbiology Ecology, 2017, 93, .	2.7	18
11	Elimination of Naegleria fowleri from bulk water and biofilm in an operational drinking water distribution system. Water Research, 2017, 110, 15-26.	11.3	23
12	Characterization of a Drinking Water Distribution Pipeline Terminally Colonized by <i>Naegleria fowleri</i> . Environmental Science & Technology, 2016, 50, 2890-2898.	10.0	36
13	Molecular homology and multiple-sequence alignment: an analysis of concepts and practice. Australian Systematic Botany, 2015, 28, 46.	0.9	30
14	Metabarcoding of benthic eukaryote communities predicts the ecological condition of estuaries. Environmental Pollution, 2015, 203, 165-174.	7.5	125
15	Impacts of inundation and drought on eukaryote biodiversity in semiâ€arid floodplain soils. Molecular Ecology, 2013, 22, 1746-1758.	3.9	54
16	Microeukaryote community composition assessed by pyrosequencing is associated with light availability and phytoplankton primary production along a lowland river. Freshwater Biology, 2013, 58, 2401-2413.	2.4	6
17	Improved Inference of Taxonomic Richness from Environmental DNA. PLoS ONE, 2013, 8, e71974.	2.5	33
18	Inference of molecular homology and sequence alignment by direct optimization. Molecular Phylogenetics and Evolution, 2010, 56, 305-311.	2.7	11

#	Article	IF	CITATIONS
19	Microsatellite markers in the endangered Australian northern corroboree frog, Pseudophryne pengilleyi (Anura: Myobatrachidae) and amplification in other Pseudophryne species. Conservation Genetics, 2008, 9, 1315-1317.	1.5	1
20	Assessment of genetic diversity in the critically endangered Australian corroboree frogs, <i>Pseudophryne corroboree</i> and <i>Pseudophryne pengilleyi</i> , identifies four evolutionarily significant units for conservation. Molecular Ecology, 2008, 17, 3448-3463.	3.9	27
21	Molecular phylogenetic dating supports an ancient endemic speciation model in Australia's biodiversity hotspot. Molecular Phylogenetics and Evolution, 2007, 44, 371-385.	2.7	43