

# Gregory E Maes

## List of Publications by Year in descending order

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Version: 2024-02-01

93  
papers

4,344  
citations

109264

35  
h-index

118793

62  
g-index

102  
all docs

102  
docs citations

102  
times ranked

5802  
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. <i>Molecular Ecology Resources</i> , 2011, 11, 123-136.	2.2	391
2	The European eel ( <i>Anguilla anguilla</i> , Linnaeus), its Lifecycle, Evolution and Reproduction: A Literature Review. <i>Reviews in Fish Biology and Fisheries</i> , 2005, 15, 367-398.	2.4	251
3	Harnessing the Power of Genomics to Secure the Future of Seafood. <i>Trends in Ecology and Evolution</i> , 2017, 32, 665-680.	4.2	202
4	Gene-associated markers provide tools for tackling illegal fishing and false eco-certification. <i>Nature Communications</i> , 2012, 3, 851.	5.8	199
5	All roads lead to home: panmixia of European eel in the Sargasso Sea. <i>Molecular Ecology</i> , 2011, 20, 1333-1346.	2.0	176
6	Genome-wide single-generation signatures of local selection in the panmictic European eel. <i>Molecular Ecology</i> , 2014, 23, 2514-2528.	2.0	135
7	Panmixia in the European eel: a matter of time. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 1129-1137.	1.2	132
8	The catadromous European eel <i>Anguilla anguilla</i> (L.) as a model for freshwater evolutionary ecotoxicology: Relationship between heavy metal bioaccumulation, condition and genetic variability. <i>Aquatic Toxicology</i> , 2005, 73, 99-114.	1.9	127
9	Cracking behavior and mechanical properties of austenitic stainless steel parts produced by laser metal deposition. <i>Materials &amp; Design</i> , 2013, 45, 228-235.	5.1	124
10	Qualitative assessment of the diet of European eel larvae in the Sargasso Sea resolved by DNA barcoding. <i>Biology Letters</i> , 2010, 6, 819-822.	1.0	90
11	Oceanic fronts in the Sargasso Sea control the early life and drift of Atlantic eels. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3593-3599.	1.2	86
12	Sequencing, de novo annotation and analysis of the first <i>Anguilla anguilla</i> transcriptome: EeelBase opens new perspectives for the study of the critically endangered European eel. <i>BMC Genomics</i> , 2010, 11, 635.	1.2	83
13	Prebiotic effects of arabinoxylan oligosaccharides on juvenile Siberian sturgeon ( <i>Acipenser</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1 <i>Microbiology Ecology</i> , 2013, 86, 357-371.	1.3	80
14	Evidence for isolation by time in the European eel ( <i>Anguilla anguilla</i> L.). <i>Molecular Ecology</i> , 2006, 15, 2095-2107.	2.0	77
15	Genetic patchiness among recruits in the European eel <i>Anguilla anguilla</i> . <i>Marine Ecology - Progress Series</i> , 2006, 307, 209-217.	0.9	75
16	A resource of genome-wide single-nucleotide polymorphisms generated by RAD tag sequencing in the critically endangered European eel. <i>Molecular Ecology Resources</i> , 2013, 13, 706-714.	2.2	72
17	Clinal genetic variation and isolation by distance in the European eel <i>Anguilla anguilla</i> (L.). <i>Biological Journal of the Linnean Society</i> , 2002, 77, 509-521.	0.7	70
18	Modeling genetic connectivity in sticklebacks as a guideline for river restoration. <i>Evolutionary Applications</i> , 2008, 1, 475-488.	1.5	68

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19	Surviving in a toxic world: transcriptomics and gene expression profiling in response to environmental pollution in the critically endangered European eel. BMC Genomics, 2012, 13, 507.	1.2	68
20	Adaptive and non-adaptive divergence in a common landscape. Nature Communications, 2017, 8, 267.	5.8	66
21	Assessing patterns of hybridization between North Atlantic eels using diagnostic single-nucleotide polymorphisms. Heredity, 2014, 112, 627-637.	1.2	65
22	Detecting Holocene divergence in the anadromous-freshwater three-spined stickleback ( <i>Gasterosteus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.6	61
23	The survey and reference assisted assembly of the Octopus vulgaris genome. Scientific Data, 2019, 6, 13.	2.4	60
24	Novel Tools for Conservation Genomics: Comparing Two High-Throughput Approaches for SNP Discovery in the Transcriptome of the European Hake. PLoS ONE, 2011, 6, e28008.	1.1	59
25	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2009â€“31 January 2010. Molecular Ecology Resources, 2010, 10, 576-579.	2.2	56
26	Genome-wide SNPs reveal low effective population size within confined management units of the highly vagile Galapagos shark ( <i>Carcharhinus galapagensis</i> ). Conservation Genetics, 2017, 18, 1151-1163.	0.8	55
27	Parallel evolution and adaptation to environmental factors in a marine flatfish: Implications for fisheries and aquaculture management of the turbot ( <i>Scophthalmus maximus</i> ). Evolutionary Applications, 2018, 11, 1322-1341.	1.5	54
28	SNP Discovery Using Next Generation Transcriptomic Sequencing in Atlantic Herring ( <i>Clupea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	1.1	53
29	De novo assembly, characterization, functional annotation and expression patterns of the black tiger shrimp ( <i>Penaeus monodon</i> ) transcriptome. Scientific Reports, 2018, 8, 13553.	1.6	48
30	Regional environmental pressure influences population differentiation in turbot ( <i>Scophthalmus maximus</i> ). Molecular Ecology, 2014, 23, 618-636.	2.0	43
31	Evidence for fine-scale genetic structure and estuarine colonisation in a potential high gene flow marine goby ( <i>Pomatoschistus minutus</i> ). Heredity, 2004, 92, 434-445.	1.2	42
32	High genetic diversity in cryptic populations of the migratory sutchi catfish <i>Pangasianodon hypophthalmus</i> in the Mekong River. Heredity, 2006, 96, 166-174.	1.2	42
33	A genome scan for candidate genes involved in the adaptation of turbot ( <i>Scophthalmus maximus</i> ). Marine Genomics, 2015, 23, 77-86.	0.4	41
34	Seascape genetics of a flatfish reveals local selection under high levels of gene flow. ICES Journal of Marine Science, 2018, 75, 675-689.	1.2	40
35	Modelling dispersal dynamics of the early life stages of a marine flatfish ( <i>Solea solea</i> L.). Journal of Sea Research, 2013, 84, 13-25.	0.6	39
36	Multi-marker estimate of genetic connectivity of sole ( <i>Solea solea</i> ) in the North-East Atlantic Ocean. Marine Biology, 2012, 159, 1239-1253.	0.7	38

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37	Integrating complementary methods to improve diet analysis in fishery-targeted species. <i>Ecology and Evolution</i> , 2018, 8, 9503-9515.	0.8	38
38	Temporal genetic stability and high effective population size despite fisheries-induced life-history trait evolution in the North Sea sole. <i>Molecular Ecology</i> , 2011, 20, no-no.	2.0	37
39	Strong trans-Pacific break and local conservation units in the Galapagos shark ( <i>Carcharhinus</i> ) Tj ETQq1 1 0.784314,rgBT /Overlock 10	1.2	37
40	Spatial dynamics and mixing of bluefin tuna in the Atlantic Ocean and Mediterranean Sea revealed using next-generation sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 620-638.	2.2	34
41	Challenges for genetic research in European eel management. <i>ICES Journal of Marine Science</i> , 2007, 64, 1463-1471.	1.2	32
42	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2011-30 September 2011. <i>Molecular Ecology Resources</i> , 2012, 12, 185-189.	2.2	32
43	Temperament traits and microhabitat use in bullhead, <i>Cottus perifretum</i> : fish associated with complex habitats are less aggressive. <i>Behaviour</i> , 2011, 148, 603-625.	0.4	31
44	Identification of neural progenitor cells and their progeny reveals long distance migration in the developing octopus brain. <i>ELife</i> , 2021, 10, .	2.8	29
45	Tracing the genetic impact of farmed turbot <i>Scophthalmus maximus</i> on wild populations. <i>Aquaculture Environment Interactions</i> , 2018, 10, 447-463.	0.7	29
46	Gene transcription reflects poor health status of resident European eel chronically exposed to environmental pollutants. <i>Aquatic Toxicology</i> , 2013, 126, 242-255.	1.9	28
47	How does marker choice affect your diet analysis: comparing genetic markers and digestion levels for diet metabarcoding of tropical-reef piscivores. <i>Marine and Freshwater Research</i> , 2019, 70, 8.	0.7	27
48	Microchemical variation in juvenile <i>Solea solea</i> otoliths as a powerful tool for studying connectivity in the North Sea. <i>Marine Ecology - Progress Series</i> , 2010, 401, 211-220.	0.9	27
49	Detecting genome-wide gene transcription profiles associated with high pollution burden in the critically endangered European eel. <i>Aquatic Toxicology</i> , 2013, 132-133, 157-164.	1.9	26
50	Indications for a recent Holarctic expansion of pike based on a preliminary study of mtDNA variation. <i>Journal of Fish Biology</i> , 2003, 63, 254-259.	0.7	24
51	An integrated genetic-demographic model to unravel the origin of genetic structure in European eel ( <i>Anguilla anguilla</i> L.). <i>Evolutionary Applications</i> , 2011, 4, 517-533.	1.5	23
52	Reconstructing Colonization Dynamics of the Human Parasite <i>Schistosoma mansoni</i> following Anthropogenic Environmental Changes in Northwest Senegal. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003998.	1.3	23
53	Performance and precision of double digestion RAD (ddRAD) genotyping in large multiplexed datasets of marine fish species. <i>Marine Genomics</i> , 2018, 39, 64-72.	0.4	21
54	Introgressive hybridisation between two widespread sharks in the east Pacific region. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 119-127.	1.2	21

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55	Adverse effect of early-life high-fat/high-carbohydrate (Western) diet on bacterial community in the distal bowel of mice. <i>Nutrition Research</i> , 2018, 50, 25-36.	1.3	20
56	Conservation of the introgressed European water frog complex using molecular tools. <i>Molecular Ecology</i> , 2009, 18, 1071-1087.	2.0	19
57	High genetic diversity and connectivity in a common mesopelagic fish of the Southern Ocean: The myctophid <i>Electrona antarctica</i> . <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2012, 59-60, 199-207.	0.6	19
58	Differences in brain gene transcription profiles advocate for an important role of cognitive function in upstream migration and water obstacles crossing in European eel. <i>BMC Genomics</i> , 2015, 16, 378.	1.2	19
59	Genetic evidence challenges the native status of a threatened freshwater fish ( <i>Carassius</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	0.8	19
60	Evaluating genetic traceability methods for captive-bred marine fish and their applications in fisheries management and wildlife forensics. <i>Aquaculture Environment Interactions</i> , 2016, 8, 131-145.	0.7	18
61	Microsatellite conservation and Bayesian individual assignment in four <i>Anguilla</i> species. <i>Marine Ecology - Progress Series</i> , 2006, 319, 251-261.	0.9	18
62	Distribution of genetic variation in farmed and natural stocks of european eel. <i>Journal of Fish Biology</i> , 2004, 65, 333-334.	0.7	17
63	A Genetic Linkage Map of Sole ( <i>Solea solea</i> ): A Tool for Evolutionary and Comparative Analyses of Exploited (Flat)Fishes. <i>PLoS ONE</i> , 2014, 9, e115040.	1.1	17
64	The effect of ablation pattern on LA-ICPMS analysis of otolith element composition in hake, <i>Merluccius merluccius</i> . <i>Environmental Biology of Fishes</i> , 2012, 95, 509-520.	0.4	16
65	Comparative phylogeography of three trematomid fishes reveals contrasting genetic structure patterns in benthic and pelagic species. <i>Marine Genomics</i> , 2012, 8, 23-34.	0.4	16
66	Estimates of genetic variability and inbreeding in experimentally selected populations of European sea bass. <i>Aquaculture</i> , 2017, 479, 742-749.	1.7	16
67	Historical DNA Metabarcoding of the Prey and Microbiome of Trematomid Fishes Using Museum Samples. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	16
68	Preeclampsia is Associated with Sex-Specific Transcriptional and Proteomic Changes in Fetal Erythroid Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2038.	1.8	16
69	Differential timing of gene expression regulation between leptocephali of the two <i>Anguilla</i> eel species in the Sargasso Sea. <i>Ecology and Evolution</i> , 2011, 1, 459-467.	0.8	15
70	Identification and validation of single nucleotide polymorphisms in growth- and maturation-related candidate genes in sole ( <i>Solea solea</i> L.). <i>Marine Genomics</i> , 2013, 9, 33-38.	0.4	14
71	Bacterial signatures of productivity decay in <i>Penaeus monodon</i> ponds infected with PirA toxin. <i>Aquaculture</i> , 2019, 511, 734202.	1.7	14
72	Subtle population structure and male-biased dispersal in two <i>Copadichromis</i> species (Teleostei,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.0	12

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73	Accounting for kin sampling reveals genetic connectivity in Tasmanian and New Zealand school sharks, <i>Galeorhinus galeus</i> . Ecology and Evolution, 2019, 9, 4465-4472.	0.8	12
74	Morphological and genetic seasonal dynamics of European eel <i>Anguilla anguilla</i> recruitment in southern France. Journal of Fish Biology, 2009, 74, 2047-2068.	0.7	10
75	Isolation and characterization of expressed sequence tag-linked microsatellite loci for the European eel ( <i>Anguilla anguilla</i> ). Molecular Ecology Resources, 2009, 9, 233-235.	2.2	10
76	Influence of DNA isolation from historical otoliths on nuclear mitochondrial marker amplification and age determination in an overexploited fish, the common sole ( <i>Solea solea</i> L.). Molecular Ecology Resources, 2009, 9, 725-732.	2.2	10
77	Differential gene expression in narrow and broad headed European glass eels ( <i>Anguilla</i> ) chemotaxis. Molecular Ecology, 2017, 26, 3943-3953.	2.0	10
78	Species identification in the trematomid family using nuclear genetic markers. Polar Biology, 2009, 32, 1731-1741.	0.5	9
79	Responses of mixed methanotrophic consortia to variable Cu <sup>2+</sup> /Fe <sup>2+</sup> ratios. Journal of Environmental Management, 2017, 197, 159-166.	3.8	9
80	Genome assembly of the Australian black tiger shrimp ( <i>Penaeus monodon</i> ) reveals a novel fragmented IHNV EVE sequence. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	9
81	Extracting a century of preserved molecular and population demographic data from archived otoliths in the endangered European eel ( <i>Anguilla anguilla</i> L.). Journal of Experimental Marine Biology and Ecology, 2011, 398, 56-62.	0.7	8
82	Integrating molecular identification of pelagic eggs with geostatistical mapping to improve the delineation of North Sea fish spawning grounds. Marine Ecology - Progress Series, 2012, 445, 161-172.	0.9	8
83	Assessment of the quality of European silver eels and tentative approach to trace the origin of contaminants – A European overview. Science of the Total Environment, 2020, 743, 140675.	3.9	7
84	Intra-annual genetic variation in the downstream larval drift of sutchi catfish ( <i>Pangasianodon</i> )	0.7	6
85	Restriction Fragment Length Analysis of the Cytochrome <i>b</i> Gene and Muscle Fatty Acid Composition Differentiate the Cryptic Flatfish Species <i>Solea solea</i> and <i>Solea aegyptiaca</i> . Journal of Agricultural and Food Chemistry, 2012, 60, 7941-7948.	2.4	6
86	Microsatellite Primers for the Gynodioecious Grassland Perennial <i>Saxifraga granulata</i> (Saxifragaceae). Applications in Plant Sciences, 2014, 2, 1400040.	0.8	6
87	Condition factor, Length – Weight relationship, and the fishery of <i>Barbus altianalis</i> (Boulenger 1900) in Lakes Victoria and Edward basins of Uganda. Environmental Biology of Fishes, 2017, 100, 99-110.	0.4	5
88	Microsatellite marker development and putative SNP detection for a northward expanding damselfly species using next generation sequencing. Conservation Genetics Resources, 2012, 4, 1079-1084.	0.4	4
89	Exploring Geovisualization Symbology for Landscape Genetics. Transactions in GIS, 2013, 17, 267-281.	1.0	4
90	Diet composition and gut microbiome of 0-group European plaice <i>Pleuronectes platessa</i> L. - Strong homogeneity and subtle spatial and temporal differences. Journal of Sea Research, 2019, 144, 67-77.	0.6	4

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91	Reconciling seascape genetics and fisheries science in three codistributed flatfishes. <i>Evolutionary Applications</i> , 2021, 14, 536-552.	1.5	4
92	Multi-species transcriptomics reveals evolutionary diversity in the mechanisms regulating shrimp tail muscle excitation-contraction coupling. <i>Gene</i> , 2020, 752, 144765.	1.0	4
93	Evolutionary Consequences of Eel Migration. , 2009, , 401-432.		1