

# Maximilian J Telford

## List of Publications by Year in descending order

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Version: 2024-02-01

96  
papers

8,870  
citations

57719

44  
h-index

46771

89  
g-index

110  
all docs

110  
docs citations

110  
times ranked

7544  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic errors in phylogenetic trees. <i>Current Biology</i> , 2021, 31, R59-R64.	1.8	31
2	Systematic errors in orthology inference and their effects on evolutionary analyses. <i>IScience</i> , 2021, 24, 102110.	1.9	27
3	Lack of support for Deuterostomia prompts reinterpretation of the first Bilateria. <i>Science Advances</i> , 2021, 7, .	4.7	60
4	CeLaVi: an interactive cell lineage visualization tool. <i>Nucleic Acids Research</i> , 2021, 49, W80-W85.	6.5	9
5	Benchmarked approaches for reconstruction of in vitro cell lineages and in silico models of <i>C. elegans</i> and <i>M. musculus</i> developmental trees. <i>Cell Systems</i> , 2021, 12, 810-826.e4.	2.9	36
6	Nucleus-Plasma Membrane Contact Sites Are Formed During Spermiogenesis in the Acoel <i>Symsagittifera roscoffensis</i> . <i>Contact (Thousand Oaks (Ventura County, Calif))</i> , 2020, 3, 251525642092635.	0.4	1
7	Topology-dependent asymmetry in systematic errors affects phylogenetic placement of Ctenophora and Xenacoelomorpha. <i>Science Advances</i> , 2020, 6, .	4.7	102
8	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
9	Reinvestigating the early embryogenesis in the flatworm <i>Maritigrella crozieri</i> highlights the unique spiral cleavage program found in polyclad flatworms. <i>EvoDevo</i> , 2019, 10, 12.	1.3	8
10	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	2.4	111
11	Mitigating Anticipated Effects of Systematic Errors Supports Sister-Group Relationship between Xenacoelomorpha and Ambulacraria. <i>Current Biology</i> , 2019, 29, 1818-1826.e6.	1.8	120
12	Evolution: Arrow Worms Find Their Place on the Tree of Life. <i>Current Biology</i> , 2019, 29, R152-R154.	1.8	1
13	Computational discovery of hidden breaks in 28S ribosomal RNAs across eukaryotes and consequences for RNA Integrity Numbers. <i>Scientific Reports</i> , 2019, 9, 19477.	1.6	29
14	Is it possible to reconstruct an accurate cell lineage using CRISPR recorders?. <i>ELife</i> , 2019, 8, .	2.8	62
15	Extraocular, rod-like photoreceptors in a flatworm express xenopsin photopigment. <i>ELife</i> , 2019, 8, .	2.8	27
16	SALMFamide2 and serotonin immunoreactivity in the nervous system of some acoels (Xenacoelomorpha). <i>Journal of Morphology</i> , 2018, 279, 589-597.	0.6	13
17	The mitochondrial genomes of the mesozoans <i>Intoshia linei</i> , <i>Dicyemasp.</i> and <i>Dicyema japonicum</i> . <i>Parasitology Open</i> , 2018, 4, .	0.9	2
18	Orthonectids Are Highly Degenerate Annelid Worms. <i>Current Biology</i> , 2018, 28, 1970-1974.e3.	1.8	31

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19	A parthenogenetic quasi-program causes teratoma-like tumors during aging in wild-type <i>C. elegans</i> . <i>Npj Aging and Mechanisms of Disease</i> , 2018, 4, 6.	4.5	39
20	A software tool <i>~CroCo~</i> <sup>™</sup> detects pervasive cross-species contamination in next generation sequencing data. <i>BMC Biology</i> , 2018, 16, 28.	1.7	82
21	The mitochondrial genomes of the acoelomorph worms <i>Paratomella rubra</i> , <i>Isodiametra pulchra</i> and <i>Archaphanostoma ylvae</i> . <i>Scientific Reports</i> , 2017, 7, 1847.	1.6	22
22	Zoology: War of the Worms. <i>Current Biology</i> , 2016, 26, R335-R337.	1.8	13
23	Light-sheet microscopy for everyone? Experience of building an OpenSPIM to study flatworm development. <i>BMC Developmental Biology</i> , 2016, 16, 22.	2.1	28
24	A sisterly dispute. <i>Nature</i> , 2016, 529, 286-287.	13.7	54
25	Regulatory circuit rewiring and functional divergence of the duplicate <i>admp</i> genes in dorsoventral axial patterning. <i>Developmental Biology</i> , 2016, 410, 108-118.	0.9	14
26	Molecular developmental evidence for a subcoxal origin of pleurites in insects and identity of the subcoxa in the gnathal appendages. <i>Scientific Reports</i> , 2015, 5, 15757.	1.6	18
27	A Transcriptomic-Phylogenomic Analysis of the Evolutionary Relationships of Flatworms. <i>Current Biology</i> , 2015, 25, 1347-1353.	1.8	160
28	Uncertainty in the Timing of Origin of Animals and the Limits of Precision in Molecular Timescales. <i>Current Biology</i> , 2015, 25, 2939-2950.	1.8	370
29	Phylogenomic Insights into Animal Evolution. <i>Current Biology</i> , 2015, 25, R876-R887.	1.8	154
30	The Complete Mitochondrial Genome of the Geophilomorph Centipede <i>Strigamia maritima</i> . <i>PLoS ONE</i> , 2015, 10, e0121369.	1.1	11
31	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221
32	Cellular dynamics during regeneration of the flatworm <i>Monocelis</i> sp. (Proseriata, Platyhelminthes). <i>EvoDevo</i> , 2014, 5, 37.	1.3	14
33	Phylogenomic analysis of echinoderm class relationships supports Asterozoa. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140479.	1.2	102
34	Field et al. Redux.. <i>EvoDevo</i> , 2013, 4, 5.	1.3	6
35	Comparative gene expression supports the origin of the incisor and molar process from a single endite in the mandible of the red flour beetle <i>Tribolium castaneum</i> . <i>EvoDevo</i> , 2013, 4, 1.	1.3	45
36	Mollusc Evolution: Seven Shells on the Sea Shore. <i>Current Biology</i> , 2013, 23, R952-R954.	1.8	5

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37	The Animal Tree of Life. <i>Science</i> , 2013, 339, 764-766.	6.0	4
38	<i>Xenoturbella bocki</i> exhibits direct development with similarities to Acoelomorpha. <i>Nature Communications</i> , 2013, 4, 1537.	5.8	43
39	Put a tiger in your tank: the polyclad flatworm <i>Maritigrella crozieri</i> as a proposed model for evo-devo. <i>EvoDevo</i> , 2013, 4, 29.	1.3	29
40	Cap'n'collar differentiates the mandible from the maxilla in the beetle <i>Tribolium castaneum</i> . <i>EvoDevo</i> , 2012, 3, 25.	1.3	18
41	A congruent solution to arthropod phylogeny: phylogenomics, microRNAs and morphology support monophyletic Mandibulata. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 298-306.	1.2	227
42	MicroRNAs and phylogenomics resolve the relationships of Tardigrada and suggest that velvet worms are the sister group of Arthropoda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15920-15924.	3.3	212
43	Spermatozoon ultrastructure of <i>Xenoturbella bocki</i> (Westblad 1949). <i>Acta Zoologica</i> , 2011, 92, 109-115.	0.6	10
44	Acoelomorph flatworms are deuterostomes related to <i>Xenoturbella</i> . <i>Nature</i> , 2011, 470, 255-258.	13.7	400
45	Improving animal phylogenies with genomic data. <i>Trends in Genetics</i> , 2011, 27, 186-195.	2.9	66
46	Invertebrate Evolution: Bringing Order to the Molluscan Chaos. <i>Current Biology</i> , 2011, 21, R964-R966.	1.8	24
47	Ecdysozoan Mitogenomics: Evidence for a Common Origin of the Legged Invertebrates, the Panarthropoda. <i>Genome Biology and Evolution</i> , 2010, 2, 425-440.	1.1	154
48	Evidence for Multiple Independent Origins of trans-Splicing in Metazoa. <i>Molecular Biology and Evolution</i> , 2010, 27, 684-693.	3.5	71
49	TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. <i>Nucleic Acids Research</i> , 2010, 38, W7-W13.	6.5	1,238
50	The mitochondrial genome structure of <i>Xenoturbella bocki</i> (phylum Xenoturbellida) is ancestral within the deuterostomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 107.	3.2	36
51	Animal Evolution: Once upon a Time. <i>Current Biology</i> , 2009, 19, R339-R341.	1.8	11
52	The origin and evolution of arthropods. <i>Nature</i> , 2009, 457, 812-817.	13.7	159
53	Comparative gene expression in the heads of <i>Drosophila melanogaster</i> and <i>Tribolium castaneum</i> and the segmental affinity of the <i>Drosophila</i> hypopharyngeal lobes. <i>Evolution &amp; Development</i> , 2009, 11, 88-96.	1.1	22
54	MtZoa: A general mitochondrial amino acid substitutions model for animal evolutionary studies. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 268-272.	1.2	105

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55	Expression of homothorax and extradenticle mRNA in the legs of the crustacean <i>Parhyale hawaiiensis</i> : evidence for a reversal of gene expression regulation in the pancrustacean lineage. <i>Development Genes and Evolution</i> , 2008, 218, 333-339.	0.4	24
56	Xenoturbellida: The fourth deuterostome phylum and the diet of worms. <i>Genesis</i> , 2008, 46, 580-586.	0.8	23
57	A multi criterion approach for the selection of optimal outgroups in phylogeny: Recovering some support for Mandibulata over Myriochelata using mitogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 103-111.	1.2	117
58	Testing the new animal phylogeny: A phylum level molecular analysis of the animal kingdom. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 23-31.	1.2	121
59	Feeding ecology of <i>Xenoturbella bocki</i> (phylum Xenoturbellida) revealed by genetic barcoding. <i>Molecular Ecology Resources</i> , 2008, 8, 18-22.	2.2	23
60	Resolving Animal Phylogeny: A Sledgehammer for a Tough Nut?. <i>Developmental Cell</i> , 2008, 14, 457-459.	3.1	35
61	The evolution of the Ecdysozoa. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1529-1537.	1.8	203
62	The evolution of the animals: introduction to a Linnean tercentenary celebration. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1421-1424.	1.8	4
63	A Single Origin of the Central Nervous System?. <i>Cell</i> , 2007, 129, 237-239.	13.5	8
64	The mitochondrial genome of <i>Priapulius caudatus</i> Lamarck (Priapulida: Priapulidae). <i>Gene</i> , 2007, 389, 96-105.	1.0	19
65	Phylogenomics. <i>Current Biology</i> , 2007, 17, R945-R946.	1.8	15
66	Evolution of Hox3 and ftz in arthropods: insights from the crustacean <i>Daphnia pulex</i> . <i>Development Genes and Evolution</i> , 2007, 217, 315-322.	0.4	32
67	Large-scale sequencing and the new animal phylogeny. <i>Trends in Ecology and Evolution</i> , 2006, 21, 614-620.	4.2	164
68	Interrelationships of the Gastrotricha and their place among the Metazoa inferred from 18S rRNA genes. <i>Zoologica Scripta</i> , 2006, 35, 251-259.	0.7	88
69	Mitogenomics and phylogenomics reveal priapulid worms as extant models of the ancestral Ecdysozoan. <i>Evolution &amp; Development</i> , 2006, 8, 502-510.	1.1	88
70	Deuterostome phylogeny reveals monophyletic chordates and the new phylum Xenoturbellida. <i>Nature</i> , 2006, 444, 85-88.	13.7	528
71	The complete mitochondrial genome of <i>Flustrellidra hispida</i> and the phylogenetic position of Bryozoa among the Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 195-207.	1.2	57
72	Broad taxon and gene sampling indicate that chaetognaths are protostomes. <i>Current Biology</i> , 2006, 16, R575-R576.	1.8	128

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73	Animal phylogeny. <i>Current Biology</i> , 2006, 16, R981-R985.	1.8	45
74	Along came a sea spider. <i>Nature</i> , 2005, 437, 1099-1101.	13.7	38
75	Animal Phylogeny: Fatal Attraction. <i>Current Biology</i> , 2005, 15, R296-R299.	1.8	21
76	Consideration of RNA Secondary Structure Significantly Improves Likelihood-Based Estimates of Phylogeny: Examples from the Bilateria. <i>Molecular Biology and Evolution</i> , 2005, 22, 1129-1136.	3.5	168
77	The multimeric beta-thymosin found in nematodes and arthropods is not a synapomorphy of the Ecdysozoa. <i>Evolution &amp; Development</i> , 2004, 6, 90-94.	1.1	60
78	Systematic searches for molecular synapomorphies in model metazoan genomes give some support for Ecdysozoa after accounting for the idiosyncrasies of <i>Caenorhabditis elegans</i> . <i>Evolution &amp; Development</i> , 2004, 6, 164-169.	1.1	104
79	Affinity for arrow worms. <i>Nature</i> , 2004, 431, 254-256.	13.7	15
80	Animal Phylogeny: Back to the Coelomata?. <i>Current Biology</i> , 2004, 14, R274-R276.	1.8	25
81	Xenoturbella is a deuterostome that eats molluscs. <i>Nature</i> , 2003, 424, 925-928.	13.7	189
82	Combined large and small subunit ribosomal RNA phylogenies support a basal position of the acoelomorph flatworms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1077-1083.	1.2	140
83	The place of phylogeny and cladistics in Evo-Devo research. <i>International Journal of Developmental Biology</i> , 2003, 47, 479-90.	0.3	40
84	Cladistic analyses of molecular characters: The good, the bad and the ugly. <i>Contributions To Zoology</i> , 2002, 71, 93-100.	0.2	5
85	Hox genes and the phylogeny of the arthropods. <i>Current Biology</i> , 2001, 11, 759-763.	1.8	177
86	Elongation Factor 1-Alpha Sequences Alone Do Not Assist in Resolving the Position of the Acoela Within the Metazoa. <i>Molecular Biology and Evolution</i> , 2001, 18, 437-442.	3.5	56
87	Turning Hox "signatures" into synapomorphies. <i>Evolution &amp; Development</i> , 2000, 2, 360-364.	1.1	50
88	Evidence for the derivation of the <i>Drosophila fushi tarazu</i> gene from a Hox gene orthologous to lophotrochozoan <i>Lox5</i> . <i>Current Biology</i> , 2000, 10, 349-352.	1.8	88
89	Changes in mitochondrial genetic codes as phylogenetic characters: Two examples from the flatworms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11359-11364.	3.3	223
90	Appendage development in embryos of the oribatid mite <i>Archezogozetes longisetosus</i> (Acari, Oribatei). <i>Trends in Ecology &amp; Evolution</i> , 2000, 15, 100-106.	0.6	45

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91	Gnathostomulida – An Enigmatic Metazoan Phylum from both Morphological and Molecular Perspectives. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 72-79.	1.2	111
92	Of mites and zen : expression studies in a chelicerate arthropod confirm zen is a divergent Hox gene. <i>Development Genes and Evolution</i> , 1998, 208, 591-594.	0.4	64
93	Expression of homeobox genes shows chelicerate arthropods retain their deutocerebral segment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 10671-10675.	3.3	241
94	Evolution of 28S Ribosomal DNA in Chaetognaths: Duplicate Genes and Molecular Phylogeny. <i>Journal of Molecular Evolution</i> , 1997, 44, 135-144.	0.8	77
95	Identification of planarian homeobox sequences indicates the antiquity of most Hox/homeotic gene subclasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7227-7231.	3.3	56
96	Demise of the Atelocerata?. <i>Nature</i> , 1995, 376, 123-124.	13.7	56