

Maximilian J Telford

List of Publications by Year in descending order

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Version: 2024-02-01

96
papers

8,870
citations

57631

44
h-index

46693

89
g-index

110
all docs

110
docs citations

110
times ranked

7544
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. <i>Nucleic Acids Research</i> , 2010, 38, W7-W13. | 6.5 | 1,238 |
| 2 | Deuterostome phylogeny reveals monophyletic chordates and the new phylum Xenoturbellida. <i>Nature</i> , 2006, 444, 85-88. | 13.7 | 528 |
| 3 | Acoelomorph flatworms are deuterostomes related to Xenoturbella. <i>Nature</i> , 2011, 470, 255-258. | 13.7 | 400 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444. | 7.7 | 226 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | The evolution of the Ecdysozoa. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1529-1537. | 1.8 | 203 |
| 12 | Xenoturbella is a deuterostome that eats molluscs. <i>Nature</i> , 2003, 424, 925-928. | 13.7 | 189 |
| 13 | Hox genes and the phylogeny of the arthropods. <i>Current Biology</i> , 2001, 11, 759-763. | 1.8 | 177 |
| 14 | 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 |
| 15 | Large-scale sequencing and the new animal phylogeny. <i>Trends in Ecology and Evolution</i> , 2006, 21, 614-620. | 4.2 | 164 |
| 16 | A Transcriptomic-Phylogenomic Analysis of the Evolutionary Relationships of Flatworms. <i>Current Biology</i> , 2015, 25, 1347-1353. | 1.8 | 160 |
| 17 | The origin and evolution of arthropods. <i>Nature</i> , 2009, 457, 812-817. | 13.7 | 159 |
| 18 | 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 |

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|----|--|-----|-----------|
| 19 | Phylogenomic Insights into Animal Evolution. <i>Current Biology</i> , 2015, 25, R876-R887. | 1.8 | 154 |
| 20 | 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 |
| 21 | Broad taxon and gene sampling indicate that chaetognaths are protostomes. <i>Current Biology</i> , 2006, 16, R575-R576. | 1.8 | 128 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Gnathostomulida—An Enigmatic Metazoan Phylum from both Morphological and Molecular Perspectives. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 72-79. | 1.2 | 111 |
| 26 | OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163. | 2.4 | 111 |
| 27 | 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 |
| 28 | 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 & Development</i> , 2004, 6, 164-169. | 1.1 | 104 |
| 29 | Phylogenomic analysis of echinoderm class relationships supports Asterozoa. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140479. | 1.2 | 102 |
| 30 | Topology-dependent asymmetry in systematic errors affects phylogenetic placement of Ctenophora and Xenacoelomorpha. <i>Science Advances</i> , 2020, 6, . | 4.7 | 102 |
| 31 | 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 |
| 32 | 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 |
| 33 | Mitogenomics and phylogenomics reveal priapulid worms as extant models of the ancestral Ecdysozoan. <i>Evolution & Development</i> , 2006, 8, 502-510. | 1.1 | 88 |
| 34 | A software tool—CroCo™ detects pervasive cross-species contamination in next generation sequencing data. <i>BMC Biology</i> , 2018, 16, 28. | 1.7 | 82 |
| 35 | 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 |
| 36 | Evidence for Multiple Independent Origins of trans-Splicing in Metazoa. <i>Molecular Biology and Evolution</i> , 2010, 27, 684-693. | 3.5 | 71 |

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|----|---|------|-----------|
| 37 | Improving animal phylogenies with genomic data. Trends in Genetics, 2011, 27, 186-195. | 2.9 | 66 |
| 38 | Of mites and zen : expression studies in a chelicerate arthropod confirm zen is a divergent Hox gene. Development Genes and Evolution, 1998, 208, 591-594. | 0.4 | 64 |
| 39 | Is it possible to reconstruct an accurate cell lineage using CRISPR recorders?. ELife, 2019, 8, . | 2.8 | 62 |
| 40 | The multimeric beta-thymosin found in nematodes and arthropods is not a synapomorphy of the Ecdysozoa. Evolution & Development, 2004, 6, 90-94. | 1.1 | 60 |
| 41 | Lack of support for Deuterostomia prompts reinterpretation of the first Bilateria. Science Advances, 2021, 7, . | 4.7 | 60 |
| 42 | The complete mitochondrial genome of Flustrellidra hispida and the phylogenetic position of Bryozoa among the Metazoa. Molecular Phylogenetics and Evolution, 2006, 40, 195-207. | 1.2 | 57 |
| 43 | Identification of planarian homeobox sequences indicates the antiquity of most Hox/homeotic gene subclasses.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 7227-7231. | 3.3 | 56 |
| 44 | Demise of the Atelocerata?. Nature, 1995, 376, 123-124. | 13.7 | 56 |
| 45 | Elongation Factor 1-Alpha Sequences Alone Do Not Assist in Resolving the Position of the Acoela Within the Metazoa. Molecular Biology and Evolution, 2001, 18, 437-442. | 3.5 | 56 |
| 46 | A sisterly dispute. Nature, 2016, 529, 286-287. | 13.7 | 54 |
| 47 | Turning Hox "signatures" into synapomorphies. Evolution & Development, 2000, 2, 360-364. | 1.1 | 50 |
| 48 | Appendage development in embryos of the oribatid mite Archezogozetes longisetosus (Acari, Oribatei). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.56 45 | | |
| 49 | Animal phylogeny. Current Biology, 2006, 16, R981-R985. | 1.8 | 45 |
| 50 | Comparative gene expression supports the origin of the incisor and molar process from a single endite in the mandible of the red flour beetle Tribolium castaneum. EvoDevo, 2013, 4, 1. | 1.3 | 45 |
| 51 | Xenoturbella bocki exhibits direct development with similarities to Acoelomorpha. Nature Communications, 2013, 4, 1537. | 5.8 | 43 |
| 52 | The place of phylogeny and cladistics in Evo-Devo research. International Journal of Developmental Biology, 2003, 47, 479-90. | 0.3 | 40 |
| 53 | A parthenogenetic quasi-program causes teratoma-like tumors during aging in wild-type C. elegans. Npj Aging and Mechanisms of Disease, 2018, 4, 6. | 4.5 | 39 |
| 54 | Along came a sea spider. Nature, 2005, 437, 1099-1101. | 13.7 | 38 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | Benchmarked approaches for reconstruction of inÂvitro 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 |
| 57 | Resolving Animal Phylogeny: A Sledgehammer for a Tough Nut?. <i>Developmental Cell</i> , 2008, 14, 457-459. | 3.1 | 35 |
| 58 | 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 |
| 59 | Orthonectids Are Highly Degenerate Annelid Worms. <i>Current Biology</i> , 2018, 28, 1970-1974.e3. | 1.8 | 31 |
| 60 | Systematic errors in phylogenetic trees. <i>Current Biology</i> , 2021, 31, R59-R64. | 1.8 | 31 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | Systematic errors in orthology inference and their effects on evolutionary analyses. <i>IScience</i> , 2021, 24, 102110. | 1.9 | 27 |
| 65 | Extraocular, rod-like photoreceptors in a flatworm express xenopsin photopigment. <i>ELife</i> , 2019, 8, . | 2.8 | 27 |
| 66 | Animal Phylogeny: Back to the Coelomata?. <i>Current Biology</i> , 2004, 14, R274-R276. | 1.8 | 25 |
| 67 | 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 |
| 68 | Invertebrate Evolution: Bringing Order to the Molluscan Chaos. <i>Current Biology</i> , 2011, 21, R964-R966. | 1.8 | 24 |
| 69 | Xenoturbellida: The fourth deuterostome phylum and the diet of worms. <i>Genesis</i> , 2008, 46, 580-586. | 0.8 | 23 |
| 70 | 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 |
| 71 | 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 & Development</i> , 2009, 11, 88-96. | 1.1 | 22 |
| 72 | 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 |

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|----|--|------|-----------|
| 73 | Animal Phylogeny: Fatal Attraction. <i>Current Biology</i> , 2005, 15, R296-R299. | 1.8 | 21 |
| 74 | The mitochondrial genome of <i>Priapulus caudatus</i> Lamarck (Priapulida: Priapulidae). <i>Gene</i> , 2007, 389, 96-105. | 1.0 | 19 |
| 75 | 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 |
| 76 | 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 |
| 77 | Affinity for arrow worms. <i>Nature</i> , 2004, 431, 254-256. | 13.7 | 15 |
| 78 | Phylogenomics. <i>Current Biology</i> , 2007, 17, R945-R946. | 1.8 | 15 |
| 79 | Cellular dynamics during regeneration of the flatworm <i>Monocelis</i> sp. (Proseriata, Platyhelminthes). <i>EvoDevo</i> , 2014, 5, 37. | 1.3 | 14 |
| 80 | 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 |
| 81 | Zoology: War of the Worms. <i>Current Biology</i> , 2016, 26, R335-R337. | 1.8 | 13 |
| 82 | SALMFamide2 and serotonin immunoreactivity in the nervous system of some acoels (<sc>X</sc>enacoelomorpha). <i>Journal of Morphology</i> , 2018, 279, 589-597. | 0.6 | 13 |
| 83 | Animal Evolution: Once upon a Time. <i>Current Biology</i> , 2009, 19, R339-R341. | 1.8 | 11 |
| 84 | The Complete Mitochondrial Genome of the Geophilomorph Centipede <i>Strigamia maritima</i> . <i>PLoS ONE</i> , 2015, 10, e0121369. | 1.1 | 11 |
| 85 | Spermatozoon ultrastructure of <i>Xenoturbella bocki</i> (Westblad 1949). <i>Acta Zoologica</i> , 2011, 92, 109-115. | 0.6 | 10 |
| 86 | CeLaVi: an interactive cell lineage visualization tool. <i>Nucleic Acids Research</i> , 2021, 49, W80-W85. | 6.5 | 9 |
| 87 | A Single Origin of the Central Nervous System?. <i>Cell</i> , 2007, 129, 237-239. | 13.5 | 8 |
| 88 | 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 |
| 89 | Field et al. Redux.. <i>EvoDevo</i> , 2013, 4, 5. | 1.3 | 6 |
| 90 | Cladistic analyses of molecular characters: The good, the bad and the ugly. <i>Contributions To Zoology</i> , 2002, 71, 93-100. | 0.2 | 5 |

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|----|--|-----|-----------|
| 91 | Mollusc Evolution: Seven Shells on the Sea Shore. <i>Current Biology</i> , 2013, 23, R952-R954. | 1.8 | 5 |
| 92 | 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 |
| 93 | The Animal Tree of Life. <i>Science</i> , 2013, 339, 764-766. | 6.0 | 4 |
| 94 | 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 |
| 95 | Evolution: Arrow Worms Find Their Place on the Tree of Life. <i>Current Biology</i> , 2019, 29, R152-R154. | 1.8 | 1 |
| 96 | Nucleusâ€“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 |