

James O Mcinerney

List of Publications by Year in descending order

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95
papers

6,704
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101543

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78
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101
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docs citations

101
times ranked

9386
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Assessment of methods for amino acid matrix selection and their use on empirical data shows that ad hoc assumptions for choice of matrix are not justified. <i>BMC Evolutionary Biology</i> , 2006, 6, 29. | 3.2 | 977 |
| 2 | Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794. | 28.9 | 363 |
| 3 | Why prokaryotes have pangenomes. <i>Nature Microbiology</i> , 2017, 2, 17040. | 13.3 | 327 |
| 4 | New approaches for unravelling reassortment pathways. <i>BMC Evolutionary Biology</i> , 2013, 13, 1. | 3.2 | 278 |
| 5 | Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015, 524, 427-432. | 27.8 | 251 |
| 6 | Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80. | 27.8 | 238 |
| 7 | Replicational and transcriptional selection on codon usage in <i>Borrelia burgdorferi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 10698-10703. | 7.1 | 223 |
| 8 | Acquisition of 1,000 eubacterial genes physiologically transformed a methanogen at the origin of Haloarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20537-20542. | 7.1 | 211 |
| 9 | Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280. | 3.5 | 177 |
| 10 | Networks: expanding evolutionary thinking. <i>Trends in Genetics</i> , 2013, 29, 439-441. | 6.7 | 176 |
| 11 | The Opisthokonta and the Ecdysozoa May Not Be Clades: Stronger Support for the Grouping of Plant and Animal than for Animal and Fungi and Stronger Support for the Coelomata than Ecdysozoa. <i>Molecular Biology and Evolution</i> , 2005, 22, 1175-1184. | 8.9 | 171 |
| 12 | Metazoan opsin evolution reveals a simple route to animal vision. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18868-18872. | 7.1 | 168 |
| 13 | Supertrees Disentangle the Chimerical Origin of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1752-1760. | 8.9 | 157 |
| 14 | Of clades and clans: terms for phylogenetic relationships in unrooted trees. <i>Trends in Ecology and Evolution</i> , 2007, 22, 114-115. | 8.7 | 145 |
| 15 | A Method for Inferring the Rate of Evolution of Homologous Characters that Can Potentially Improve Phylogenetic Inference, Resolve Deep Divergence and Correct Systematic Biases. <i>Systematic Biology</i> , 2011, 60, 833-844. | 5.6 | 134 |
| 16 | Genome Phylogenies Indicate a Meaningful $\hat{\pm}$ -Proteobacterial Phylogeny and Support a Grouping of the Mitochondria with the Rickettsiales. <i>Molecular Biology and Evolution</i> , 2006, 23, 74-85. | 8.9 | 133 |
| 17 | The hybrid nature of the Eukaryota and a consilient view of life on Earth. <i>Nature Reviews Microbiology</i> , 2014, 12, 449-455. | 28.6 | 124 |
| 18 | TOPD/FMTS: a new software to compare phylogenetic trees. <i>Bioinformatics</i> , 2007, 23, 1556-1558. | 4.1 | 120 |

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|----|--|------|-----------|
| 19 | Fatty acid biosynthesis in <i>Mycobacterium tuberculosis</i> : Lateral gene transfer, adaptive evolution, and gene duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10320-10325. | 7.1 | 119 |
| 20 | Heterogeneous Models Place the Root of the Placental Mammal Phylogeny. <i>Molecular Biology and Evolution</i> , 2013, 30, 2145-2156. | 8.9 | 115 |
| 21 | Does a tree-like phylogeny only exist at the tips in the prokaryotes?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 2551-2558. | 2.6 | 114 |
| 22 | Recovery and phylogenetic analysis of novel archaeal rRNA sequences from a deep-sea deposit feeder. <i>Applied and Environmental Microbiology</i> , 1995, 61, 1646-1648. | 3.1 | 92 |
| 23 | The Shape of Supertrees to Come: Tree Shape Related Properties of Fourteen Supertree Methods. <i>Systematic Biology</i> , 2005, 54, 419-431. | 5.6 | 88 |
| 24 | The prokaryotic tree of life: past, present and future?. <i>Trends in Ecology and Evolution</i> , 2008, 23, 276-281. | 8.7 | 82 |
| 25 | “Every Gene Is Everywhere but the Environment Selects” Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. <i>Genome Biology and Evolution</i> , 2016, 8, 1388-1400. | 2.5 | 82 |
| 26 | Planctomycetes and eukaryotes: A case of analogy not homology. <i>BioEssays</i> , 2011, 33, 810-817. | 2.5 | 79 |
| 27 | Eukaryotic genes of archaeobacterial origin are more important than the more numerous eubacterial genes, irrespective of function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17252-17255. | 7.1 | 74 |
| 28 | The public goods hypothesis for the evolution of life on Earth. <i>Biology Direct</i> , 2011, 6, 41. | 4.6 | 74 |
| 29 | Evolutionary analyses of non-genealogical bonds produced by introgressive descent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18266-18272. | 7.1 | 68 |
| 30 | Function-related replacement of bacterial siderophore pathways. <i>ISME Journal</i> , 2018, 12, 320-329. | 9.8 | 66 |
| 31 | MultiPhyl: a high-throughput phylogenomics webserver using distributed computing. <i>Nucleic Acids Research</i> , 2007, 35, W33-W37. | 14.5 | 59 |
| 32 | Gene similarity networks provide tools for understanding eukaryote origins and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1594-603. | 7.1 | 59 |
| 33 | EGN: a wizard for construction of gene and genome similarity networks. <i>BMC Evolutionary Biology</i> , 2013, 13, 146. | 3.2 | 50 |
| 34 | An algorithm for detecting directional and non-directional positive selection, neutrality and negative selection in protein coding DNA sequences. <i>Gene</i> , 2002, 300, 43-51. | 2.2 | 47 |
| 35 | Horizontal Gene Transfer as a Source of Conflict and Cooperation in Prokaryotes. <i>Frontiers in Microbiology</i> , 2020, 11, 1569. | 3.5 | 46 |
| 36 | Characterization of endospore-forming bacteria associated with entomopathogenic nematodes, <i>Heterorhabditis</i> spp., and description of <i>Paenibacillus nematophilus</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 435-441. | 1.7 | 44 |

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|----|--|-----|-----------|
| 37 | Coinfinder: detecting significant associations and dissociations in pangenomes. <i>Microbial Genomics</i> , 2020, 6, . | 2.0 | 40 |
| 38 | Timing and Reconstruction of the Most Recent Common Ancestor of the Subtype C Clade of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2004, 78, 10501-10506. | 3.4 | 39 |
| 39 | Molecular evidence for dim-light vision in the last common ancestor of the vertebrates. <i>Current Biology</i> , 2006, 16, R318-R319. | 3.9 | 39 |
| 40 | The causes of protein evolutionary rate variation. <i>Trends in Ecology and Evolution</i> , 2006, 21, 230-232. | 8.7 | 37 |
| 41 | A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516. | 8.9 | 37 |
| 42 | Molecular phylogeny of the <i>Drosophila tripunctata</i> and closely related species groups (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54 | 2.7 | 36 |
| 43 | Some Desiderata for Liberal Supertrees. <i>Computational Biology</i> , 2004, , 227-246. | 0.2 | 35 |
| 44 | Evidence for Heterogeneous Selective Pressures in the Evolution of the env Gene in Different Human Immunodeficiency Virus Type 1 Subtypes. <i>Journal of Virology</i> , 2005, 79, 1836-1841. | 3.4 | 34 |
| 45 | Translational Selection Frequently Overcomes Genetic Drift in Shaping Synonymous Codon Usage Patterns in Vertebrates. <i>Molecular Biology and Evolution</i> , 2013, 30, 2263-2267. | 8.9 | 34 |
| 46 | Mechanisms That Shape Microbial Pangenomes. <i>Trends in Microbiology</i> , 2021, 29, 493-503. | 7.7 | 34 |
| 47 | Bipartite Network Analysis of Gene Sharings in the Microbial World. <i>Molecular Biology and Evolution</i> , 2018, 35, 899-913. | 8.9 | 31 |
| 48 | The network of life: genome beginnings and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2169-2175. | 4.0 | 29 |
| 49 | Prokaryotic Genome Evolution as Assessed by Multivariate Analysis of Codon Usage Patterns. <i>Microbial & Comparative Genomics</i> , 1997, 2, 89-97. | 0.4 | 25 |
| 50 | Phylogenetic analysis of Group I marine archaeal rRNA sequences emphasizes the hidden diversity within the primary group Archaea. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997, 264, 1663-1669. | 2.6 | 25 |
| 51 | Gene prediction using the Self-Organizing Map: automatic generation of multiple gene models. <i>BMC Bioinformatics</i> , 2004, 5, 23. | 2.6 | 23 |
| 52 | Horizontal gene flow from Eubacteria to Archaeobacteria and what it means for our understanding of eukaryogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140337. | 4.0 | 23 |
| 53 | Trees from Trees: Construction of Phylogenetic Supertrees Using Clann. <i>Methods in Molecular Biology</i> , 2009, 537, 139-161. | 0.9 | 23 |
| 54 | Recurring cluster and operon assembly for Phenylacetate degradation genes. <i>BMC Evolutionary Biology</i> , 2009, 9, 36. | 3.2 | 21 |

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|----|---|------|-----------|
| 55 | Evidence for Selection in the Abundant Accessory Gene Content of a Prokaryote Pangenome. <i>Molecular Biology and Evolution</i> , 2021, 38, 3697-3708. | 8.9 | 21 |
| 56 | Formation of chimeric genes with essential functions at the origin of eukaryotes. <i>BMC Biology</i> , 2018, 16, 30. | 3.8 | 19 |
| 57 | Evidence of Positive Darwinian Selection in <i>Omp85</i> , a Highly Conserved Bacterial Outer Membrane Protein Essential for Cell Viability. <i>Journal of Molecular Evolution</i> , 2005, 60, 268-273. | 1.8 | 18 |
| 58 | The Molecular Phylogeny of a Nematode-Specific Clade of Heterotrimeric G-Protein β -Subunit Genes. <i>Journal of Molecular Evolution</i> , 2006, 63, 87-94. | 1.8 | 18 |
| 59 | The Human Genome Retains Relics of Its Prokaryotic Ancestry: Human Genes of Archaeobacterial and Eubacterial Origin Exhibit Remarkable Differences. <i>Genome Biology and Evolution</i> , 2011, 3, 782-790. | 2.5 | 18 |
| 60 | Paradigm for Life. <i>Science</i> , 2007, 318, 1390-1391. | 12.6 | 17 |
| 61 | Integration of Two Ancestral Chaperone Systems into One: The Evolution of Eukaryotic Molecular Chaperones in Light of Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2014, 31, 410-418. | 8.9 | 17 |
| 62 | Eukaryotic genes in <i>Mycobacterium tuberculosis</i> ? Possible alternative explanations. <i>Trends in Genetics</i> , 2003, 19, 687-689. | 6.7 | 15 |
| 63 | New methods ring changes for the tree of life. <i>Trends in Ecology and Evolution</i> , 2005, 20, 105-107. | 8.7 | 15 |
| 64 | Gene and genome trees conflict at many levels. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2209-2219. | 4.0 | 15 |
| 65 | Evolution: A four billion year old metabolism. <i>Nature Microbiology</i> , 2016, 1, 16139. | 13.3 | 15 |
| 66 | Gamma Chain Receptor Interleukins: Evidence for Positive Selection Driving the Evolution of Cell-to-Cell Communicators in the Mammalian Immune System. <i>Journal of Molecular Evolution</i> , 2005, 61, 608-619. | 1.8 | 14 |
| 67 | Horizontal gene transfer is less frequent in eukaryotes than prokaryotes but can be important (retrospective on DOI 10.1002/bies.201300095). <i>BioEssays</i> , 2017, 39, 1700002. | 2.5 | 14 |
| 68 | Analysis of gene expression in the bovine corpus luteum through generation and characterisation of 960 ESTs. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1679, 10-17. | 2.4 | 13 |
| 69 | Prokaryote pangenomes are dynamic entities. <i>Current Opinion in Microbiology</i> , 2022, 66, 73-78. | 5.1 | 13 |
| 70 | The tree of genomes: An empirical comparison of genome-phylogeny reconstruction methods. <i>BMC Evolutionary Biology</i> , 2008, 8, 312. | 3.2 | 12 |
| 71 | Reply to "The population genetics of pangenomes". <i>Nature Microbiology</i> , 2017, 2, 1575-1575. | 13.3 | 11 |
| 72 | Gene-gene relationships in an <i>Escherichia coli</i> accessory genome are linked to function and mobility. <i>Microbial Genomics</i> , 2021, 7, . | 2.0 | 11 |

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|----|---|------|-----------|
| 73 | Pangenomes and Selection: The Public Goods Hypothesis. , 2020, , 151-167. | | 10 |
| 74 | Evidence of Positive Darwinian Selection in Putative Meningococcal Vaccine Antigens. <i>Journal of Molecular Evolution</i> , 2005, 61, 90-98. | 1.8 | 9 |
| 75 | Codon usage patterns in <i>Trichomonas vaginalis</i> . <i>European Journal of Protistology</i> , 1997, 33, 266-273. | 1.5 | 8 |
| 76 | More than tree dimensions: inter-lineage evolution's ecological importance. <i>Trends in Ecology and Evolution</i> , 2013, 28, 624-625. | 8.7 | 8 |
| 77 | Mind the gaps in cellular evolution. <i>Nature</i> , 2017, 541, 297-299. | 27.8 | 8 |
| 78 | On the desirability of models for inferring genome phylogenies. <i>Trends in Microbiology</i> , 2006, 14, 1-2. | 7.7 | 7 |
| 79 | Increased Genome Sampling Reveals a Dynamic Relationship between Gene Duplicability and the Structure of the Primate Protein-Protein Interaction Network. <i>Molecular Biology and Evolution</i> , 2012, 29, 3563-3573. | 8.9 | 7 |
| 80 | Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. <i>Genome Biology and Evolution</i> , 2019, 11, 2678-2690. | 2.5 | 7 |
| 81 | Bacteria and Archaea: Molecular techniques reveal astonishing diversity. <i>Biodiversity</i> , 2002, 3, 3-10. | 1.1 | 6 |
| 82 | Adaptive evolution of the human fatty acid synthase gene: Support for the cancer selection and fat utilization hypotheses?. <i>Gene</i> , 2005, 360, 151-159. | 2.2 | 6 |
| 83 | Goods-thinking vs. tree-thinking. <i>Mobile Genetic Elements</i> , 2011, 1, 304-343. | 1.8 | 6 |
| 84 | The role of public goods in planetary evolution. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2017, 375, 20160359. | 3.4 | 6 |
| 85 | Detecting Adaptive Molecular Evolution: Additional Tools for the Parasitologist. <i>Advances in Parasitology</i> , 2003, 54, 359-379. | 3.2 | 4 |
| 86 | Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. <i>Algorithmica</i> , 2006, 45, 285-300. | 1.3 | 4 |
| 87 | Extraction of Prokaryotic Genomic DNA from Marine Microbial Communities Suitable for Amplification Using the Polymerase Chain Reaction. <i>International Review of Hydrobiology</i> , 1995, 80, 351-360. | 0.6 | 3 |
| 88 | Evolution by Pervasive Gene Fusion in Antibiotic Resistance and Antibiotic Synthesizing Genes. <i>Computation</i> , 2015, 3, 114-127. | 2.0 | 3 |
| 89 | Re: Spectral Analysis of Echinoderm Small Subunit Ribosomal RNA Gene Sequence Data. <i>Molecular Phylogenetics and Evolution</i> , 2000, 15, 327-329. | 2.7 | 2 |
| 90 | Ghost locus appears. <i>Nature</i> , 2014, 514, 570-571. | 27.8 | 2 |

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|----|---|-----|-----------|
| 91 | Eukaryote Genes Are More Likely than Prokaryote Genes to Be Composites. <i>Genes</i> , 2019, 10, 648. | 2.4 | 2 |
| 92 | Gene Evolution and Drug Discovery. , 2006, 316, 87-109. | | 1 |
| 93 | Detection of micro-organisms in the environment. <i>Biochemical Society Transactions</i> , 1995, 23, 435-437. | 3.4 | 0 |
| 94 | Society for Molecular Biology and Evolution, Council and Business Meetings, 2013, Chicago, IL. <i>Genome Biology and Evolution</i> , 2013, 5, 2094-2095. | 2.5 | 0 |
| 95 | Society for <i>Molecular Biology and Evolution</i> , Council and Business Meetings, 2016, Gold Coast Australia. <i>Molecular Biology and Evolution</i> , 2017, 34, 243-244. | 8.9 | 0 |