

# James O Mcinerney

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9579748/publications.pdf>

Version: 2024-02-01

95  
papers

6,704  
citations

101543

36  
h-index

66911

78  
g-index

101  
all docs

101  
docs citations

101  
times ranked

9386  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prokaryote pangenomes are dynamic entities. <i>Current Opinion in Microbiology</i> , 2022, 66, 73-78.	5.1	13
2	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
3	Mechanisms That Shape Microbial Pangenomes. <i>Trends in Microbiology</i> , 2021, 29, 493-503.	7.7	34
4	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
5	Horizontal Gene Transfer as a Source of Conflict and Cooperation in Prokaryotes. <i>Frontiers in Microbiology</i> , 2020, 11, 1569.	3.5	46
6	Pangenomes and Selection: The Public Goods Hypothesis. , 2020, , 151-167.		10
7	Coinfinder: detecting significant associations and dissociations in pangenomes. <i>Microbial Genomics</i> , 2020, 6, .	2.0	40
8	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
9	Eukaryote Genes Are More Likely than Prokaryote Genes to Be Composites. <i>Genes</i> , 2019, 10, 648.	2.4	2
10	Bipartite Network Analysis of Gene Sharings in the Microbial World. <i>Molecular Biology and Evolution</i> , 2018, 35, 899-913.	8.9	31
11	Formation of chimeric genes with essential functions at the origin of eukaryotes. <i>BMC Biology</i> , 2018, 16, 30.	3.8	19
12	Function-related replacement of bacterial siderophore pathways. <i>ISME Journal</i> , 2018, 12, 320-329.	9.8	66
13	Mind the gaps in cellular evolution. <i>Nature</i> , 2017, 541, 297-299.	27.8	8
14	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
15	Why prokaryotes have pangenomes. <i>Nature Microbiology</i> , 2017, 2, 17040.	13.3	327
16	Reply to "The population genetics of pangenomes"™. <i>Nature Microbiology</i> , 2017, 2, 1575-1575.	13.3	11
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	“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
21	Evolution: A four billion year old metabolism. <i>Nature Microbiology</i> , 2016, 1, 16139.	13.3	15
22	Evolution by Pervasive Gene Fusion in Antibiotic Resistance and Antibiotic Synthesizing Genes. <i>Computation</i> , 2015, 3, 114-127.	2.0	3
23	Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015, 524, 427-432.	27.8	251
24	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
25	Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80.	27.8	238
26	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
27	A Pluralistic Account of Homology: Adapting the Models to the Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 501-516.	8.9	37
28	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	28.9	363
29	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
30	Ghost locus appears. <i>Nature</i> , 2014, 514, 570-571.	27.8	2
31	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
32	EGN: a wizard for construction of gene and genome similarity networks. <i>BMC Evolutionary Biology</i> , 2013, 13, 146.	3.2	50
33	More than tree dimensions: inter-lineage evolution's ecological importance. <i>Trends in Ecology and Evolution</i> , 2013, 28, 624-625.	8.7	8
34	New approaches for unravelling reassortment pathways. <i>BMC Evolutionary Biology</i> , 2013, 13, 1.	3.2	278
35	Networks: expanding evolutionary thinking. <i>Trends in Genetics</i> , 2013, 29, 439-441.	6.7	176
36	Heterogeneous Models Place the Root of the Placental Mammal Phylogeny. <i>Molecular Biology and Evolution</i> , 2013, 30, 2145-2156.	8.9	115

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	The public goods hypothesis for the evolution of life on Earth. <i>Biology Direct</i> , 2011, 6, 41.	4.6	74
45	Planctomycetes and eukaryotes: A case of analogy not homology. <i>BioEssays</i> , 2011, 33, 810-817.	2.5	79
46	Goods-thinking vs. tree-thinking. <i>Mobile Genetic Elements</i> , 2011, 1, 304-343.	1.8	6
47	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
48	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
49	Recurring cluster and operon assembly for Phenylacetate degradation genes. <i>BMC Evolutionary Biology</i> , 2009, 9, 36.	3.2	21
50	Molecular phylogeny of the <i>Drosophila tripunctata</i> and closely related species groups (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	2.7	36
51	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
52	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
53	Trees from Trees: Construction of Phylogenetic Supertrees Using Clann. <i>Methods in Molecular Biology</i> , 2009, 537, 139-161.	0.9	23
54	The tree of genomes: An empirical comparison of genome-phylogeny reconstruction methods. <i>BMC Evolutionary Biology</i> , 2008, 8, 312.	3.2	12

#	ARTICLE	IF	CITATIONS
55	The prokaryotic tree of life: past, present and future?. <i>Trends in Ecology and Evolution</i> , 2008, 23, 276-281.	8.7	82
56	MultiPhyl: a high-throughput phylogenomics webserver using distributed computing. <i>Nucleic Acids Research</i> , 2007, 35, W33-W37.	14.5	59
57	Paradigm for Life. <i>Science</i> , 2007, 318, 1390-1391.	12.6	17
58	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
59	Supertrees Disentangle the Chimerical Origin of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 1752-1760.	8.9	157
60	TOPD/FMTS: a new software to compare phylogenetic trees. <i>Bioinformatics</i> , 2007, 23, 1556-1558.	4.1	120
61	On the desirability of models for inferring genome phylogenies. <i>Trends in Microbiology</i> , 2006, 14, 1-2.	7.7	7
62	The causes of protein evolutionary rate variation. <i>Trends in Ecology and Evolution</i> , 2006, 21, 230-232.	8.7	37
63	Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. <i>Algorithmica</i> , 2006, 45, 285-300.	1.3	4
64	The Molecular Phylogeny of a Nematode-Specific Clade of Heterotrimeric G-Protein $\hat{\alpha}$ -Subunit Genes. <i>Journal of Molecular Evolution</i> , 2006, 63, 87-94.	1.8	18
65	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
66	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
67	Gene Evolution and Drug Discovery. , 2006, 316, 87-109.		1
68	Genome Phylogenies Indicate a Meaningful $\hat{\alpha}$ -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
69	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
70	Evidence of Positive Darwinian Selection in Putative Meningococcal Vaccine Antigens. <i>Journal of Molecular Evolution</i> , 2005, 61, 90-98.	1.8	9
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	New methods ring changes for the tree of life. <i>Trends in Ecology and Evolution</i> , 2005, 20, 105-107.	8.7	15
77	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
78	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
79	Gene prediction using the Self-Organizing Map: automatic generation of multiple gene models. <i>BMC Bioinformatics</i> , 2004, 5, 23.	2.6	23
80	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
81	Some Desiderata for Liberal Supertrees. <i>Computational Biology</i> , 2004, , 227-246.	0.2	35
82	Eukaryotic genes in <i>Mycobacterium tuberculosis</i> ? Possible alternative explanations. <i>Trends in Genetics</i> , 2003, 19, 687-689.	6.7	15
83	Detecting Adaptive Molecular Evolution: Additional Tools for the Parasitologist. <i>Advances in Parasitology</i> , 2003, 54, 359-379.	3.2	4
84	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
85	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
86	Bacteria and Archaea: Molecular techniques reveal astonishing diversity. <i>Biodiversity</i> , 2002, 3, 3-10.	1.1	6
87	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
88	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
89	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
90	Prokaryotic Genome Evolution as Assessed by Multivariate Analysis of Codon Usage Patterns. <i>Microbial &amp; Comparative Genomics</i> , 1997, 2, 89-97.	0.4	25

#	ARTICLE	IF	CITATIONS
91	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
92	Codon usage patterns in <i>Trichomonas vaginalis</i> . <i>European Journal of Protistology</i> , 1997, 33, 266-273.	1.5	8
93	Detection of micro-organisms in the environment. <i>Biochemical Society Transactions</i> , 1995, 23, 435-437.	3.4	0
94	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
95	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