

Aoife McLysaght

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

24,941
citations

159358

30
h-index

205818

48
g-index

58
all docs

58
docs citations

58
times ranked

27596
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence from <i>Drosophila</i> Supports Higher Duplicability of Faster Evolving Genes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
2	Evidence for sponges as sister to all other animals from partitioned phylogenomics with mixture models and recoding. <i>Nature Communications</i> , 2021, 12, 1783.	5.8	70
3	Reconstruction of proto-vertebrate, proto-cyclostome and proto-gnathostome genomes provides new insights into early vertebrate evolution. <i>Nature Communications</i> , 2021, 12, 4489.	5.8	88
4	De novo emergence of adaptive membrane proteins from thymine-rich genomic sequences. <i>Nature Communications</i> , 2020, 11, 781.	5.8	84
5	Synteny-based analyses indicate that sequence divergence is not the main source of orphan genes. <i>ELife</i> , 2020, 9, .	2.8	104
6	Macrosynteny analysis shows the absence of ancient whole-genome duplication in lepidopteran insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1816-1818.	3.3	37
7	Evolutionary journey and characterisation of a novel panâ€šgene associated with beer strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2019, 36, 425-437.	0.8	2
8	Computational Prediction of De Novo Emerged Protein-Coding Genes. <i>Methods in Molecular Biology</i> , 2019, 1851, 63-81.	0.4	20
9	A Family of Vertebrate-Specific Polycombs Encoded by the LCOR/LCORL Genes Balance PRC2 Subtype Activities. <i>Molecular Cell</i> , 2018, 70, 408-421.e8.	4.5	121
10	Pseudogenes Provide Evolutionary Evidence for the Competitive Endogenous RNA Hypothesis. <i>Molecular Biology and Evolution</i> , 2018, 35, 2886-2899.	3.5	33
11	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	3.5	38
12	Dosage sensitivity is a major determinant of human copy number variant pathogenicity. <i>Nature Communications</i> , 2017, 8, 14366.	5.8	104
13	Dosage-sensitive genes in evolution and disease. <i>BMC Biology</i> , 2017, 15, 78.	1.7	79
14	Genomes as documents of evolutionary history: a probabilistic macrosynteny model for the reconstruction of ancestral genomes. <i>Bioinformatics</i> , 2017, 33, i369-i378.	1.8	24
15	Open questions in the study of de novo genes: what, how and why. <i>Nature Reviews Genetics</i> , 2016, 17, 567-578.	7.7	179
16	De Novo Genes Arise at a Slow but Steady Rate along the Primate Lineage and Have Been Subject to Incomplete Lineage Sorting. <i>Genome Biology and Evolution</i> , 2016, 8, 1222-1232.	1.1	45
17	Spatial Colocalization of Human Ohnolog Pairs Acts to Maintain Dosage-Balance. <i>Molecular Biology and Evolution</i> , 2016, 33, 2368-2375.	3.5	36
18	New genes from non-coding sequence: the role of de novo protein-coding genes in eukaryotic evolutionary innovation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140332.	1.8	136

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19	A chromatin-independent role of Polycomb-like 1 to stabilize p53 and promote cellular quiescence. <i>Genes and Development</i> , 2015, 29, 2231-2243.	2.7	32
20	Ohnologs are overrepresented in pathogenic copy number mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 361-366.	3.3	57
21	Genome-wide deserts for copy number variation in vertebrates. <i>Nature Communications</i> , 2013, 4, 2283.	5.8	40
22	A survey of host range genes in poxvirus genomes. <i>Infection, Genetics and Evolution</i> , 2013, 14, 406-425.	1.0	97
23	Positionally biased gene loss after whole genome duplication: Evidence from human, yeast, and plant. <i>Genome Research</i> , 2012, 22, 2427-2435.	2.4	32
24	Mammalian X chromosome inactivation evolved as a dosage-compensation mechanism for dosage-sensitive genes on the X chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5346-5351.	3.3	164
25	De Novo Origin of Protein-Coding Genes in Murine Rodents. <i>PLoS ONE</i> , 2012, 7, e48650.	1.1	45
26	Evolution of Vertebrate Tissues Driven by Differential Modes of Gene Duplication. <i>DNA Research</i> , 2012, 19, 305-316.	1.5	18
27	Patterns of indirect protein interactions suggest a spatial organization to metabolism. <i>Molecular BioSystems</i> , 2011, 7, 3056.	2.9	27
28	De Novo Origins of Human Genes. <i>PLoS Genetics</i> , 2011, 7, e1002381.	1.5	21
29	Duplicability of self-interacting human genes. <i>BMC Evolutionary Biology</i> , 2010, 10, 160.	3.2	18
30	Ohnologs in the human genome are dosage balanced and frequently associated with disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9270-9274.	3.3	245
31	Recent de novo origin of human protein-coding genes. <i>Genome Research</i> , 2009, 19, 1752-1759.	2.4	256
32	The complex relationship of gene duplication and essentiality. <i>Trends in Genetics</i> , 2009, 25, 152-155.	2.9	90
33	Evolutionary Analyses of Protein Interaction Networks. , 2009, , 169-181.		2
34	Identification of multiple independent horizontal gene transfers into poxviruses using a comparative genomics approach. <i>BMC Evolutionary Biology</i> , 2008, 8, 67.	3.2	61
35	Evolutionary steps of sex chromosomes are reflected in retrogenes. <i>Trends in Genetics</i> , 2008, 24, 478-481.	2.9	16
36	Interacting Gene Clusters and the Evolution of the Vertebrate Immune System. <i>Molecular Biology and Evolution</i> , 2008, 25, 1855-1862.	3.5	41

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37	High Rate of Recent Intron Gain and Loss in Simultaneously Duplicated Arabidopsis Genes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1548-1557.	3.5	59
38	Porter: a new, accurate server for protein secondary structure prediction. <i>Bioinformatics</i> , 2005, 21, 1719-1720.	1.8	428
39	Genomic features in the breakpoint regions between syntenic blocks. <i>Bioinformatics</i> , 2004, 20, i318-i325.	1.8	26
40	The 2R hypothesis and the human genome sequence. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 95-110.	1.2	59
41	Extensive gene gain associated with adaptive evolution of poxviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15655-15660.	3.3	161
42	The 2R hypothesis and the human genome sequence. , 2003, , 95-110.		4
43	LineUp: Statistical Detection of Chromosomal Homology With Application to Plant Comparative Genomics. <i>Genome Research</i> , 2003, 13, 999-1010.	2.4	45
44	The 2R hypothesis and the human genome sequence. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 95-110.	1.2	30
45	Extensive genomic duplication during early chordate evolution. <i>Nature Genetics</i> , 2002, 31, 200-204.	9.4	489
46	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
47	Estimation of Synteny Conservation and Genome Compaction Between Pufferfish (Fugu) and Human. <i>Yeast</i> , 2000, 1, 22-36.	0.8	64
48	High Frequency of Inversions During Eukaryote Gene Order Evolution. <i>Computational Biology</i> , 2000, , 47-58.	0.1	18