Martin J Lercher

List of Publications by Year
in descending order

105 papers	11,468 citations	57758 44 h-index	31849 101 g-index
122 all docs	122 docs citations	122 times ranked	15103 citing authors

#	ARTICLE	IF	CITATIONS
1	PopGenome: An Efficient Swiss Army Knife for Population Genomic Analyses in R. Molecular Biology and Evolution, 2014, 31, 1929-1936.	8.9	871
2	The evolutionary dynamics of eukaryotic gene order. Nature Reviews Genetics, 2004, 5, 299-310.	16.3	661
3	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. Nucleic Acids Research, 2016, 44, W236-W241.	14.5	610
4	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. Nucleic Acids Research, 2019, 47, W270-W275.	14.5	564
5	Clustering of housekeeping genes provides a unified model of gene order in the human genome. Nature Genetics, 2002, 31, 180-183.	21.4	496
6	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. Nature Genetics, 2005, 37, 1372-1375.	21.4	473
7	An integrated view of protein evolution. Nature Reviews Genetics, 2006, 7, 337-348.	16.3	460
8	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. Science, 2013, 339, 1207-1210.	12.6	439
9	EvolView, an online tool for visualizing, annotating and managing phylogenetic trees. Nucleic Acids Research, 2012, 40, W569-W572.	14.5	400
10	The ECAT HRRT: performance and first clinical application of the new high resolution research tomograph. IEEE Transactions on Nuclear Science, 2002, 49, 104-110.	2.0	364
11	Positron-emission tomography of vector-mediated gene expression in gene therapy for gliomas. Lancet, The, 2001, 358, 727-729.	13.7	356
12	Human SNP variability and mutation rate are higher in regions of high recombination. Trends in Genetics, 2002, 18, 337-340.	6.7	326
13	Prediction of effective genome size in metagenomic samples. Genome Biology, 2007, 8, R10.	9.6	281
14	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. Genome Research, 2006, 16, 1334-1338.	5.5	233
15	An mRNA Blueprint for C4 Photosynthesis Derived from Comparative Transcriptomics of Closely Related C3 and C4 Species Â Â. Plant Physiology, 2011, 155, 142-156.	4.8	222
16	Chance and necessity in the evolution of minimal metabolic networks. Nature, 2006, 440, 667-670.	27.8	219
17	Comparative Functional Analysis of the Caenorhabditis elegans and Drosophila melanogaster Proteomes. PLoS Biology, 2009, 7, e1000048.	5.6	208
18	Coexpression of Neighboring Genes in Caenorhabditis Elegans Is Mostly Due to Operons and Duplicate Genes. Genome Research, 2003, 13, 238-243.	5.5	194

#	Article	IF	Citations
19	An integrated approach to characterize genetic interaction networks in yeast metabolism. Nature Genetics, 2011, 43, 656-662.	21.4	194
20	OGEE: an online gene essentiality database. Nucleic Acids Research, 2012, 40, D901-D906.	14.5	187
21	The role of photorespiration during the evolution of C4 photosynthesis in the genus Flaveria. ELife, 2014, 3, e02478.	6.0	182
22	Evidence for Widespread Degradation of Gene Control Regions in Hominid Genomes. PLoS Biology, 2005, 3, e42.	5.6	178
23	Predicting C4 Photosynthesis Evolution: Modular, Individually Adaptive Steps on a Mount Fuji Fitness Landscape. Cell, 2013, 153, 1579-1588.	28.9	173
24	Integration of Horizontally Transferred Genes into Regulatory Interaction Networks Takes Many Million Years. Molecular Biology and Evolution, 2008, 25, 559-567.	8.9	170
25	Distinct identities of leaf phloem cells revealed by single cell transcriptomics. Plant Cell, 2021, 33, 511-530.	6.6	162
26	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	12.8	151
27	Horizontal gene acquisitions by eukaryotes as drivers of adaptive evolution. BioEssays, 2014, 36, 9-20.	2.5	126
28	A unification of mosaic structures in the human genome. Human Molecular Genetics, 2003, 12, 2411-2415.	2.9	119
29	Evidence That the Human X Chromosome Is Enriched for Male-Specific but not Female-Specific Genes. Molecular Biology and Evolution, 2003, 20, 1113-1116.	8.9	112
30	sybil â€" Efficient constraint-based modelling in R. BMC Systems Biology, 2013, 7, 125.	3.0	110
31	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. Nature Communications, 2016, 7, 11334.	12.8	104
32	Local Similarity in Evolutionary Rates Extends over Whole Chromosomes in Human-Rodent and Mouse-Rat Comparisons: Implications for Understanding the Mechanistic Basis of the Male Mutation Bias. Molecular Biology and Evolution, 2001, 18, 2032-2039.	8.9	93
33	Younger Genes Are Less Likely to Be Essential than Older Genes, and Duplicates Are Less Likely to Be Essential than Singletons of the Same Age. Molecular Biology and Evolution, 2012, 29, 1703-1706.	8.9	90
34	X-chromosome-wide profiling of MSL-1 distribution and dosage compensation in Drosophila. Genes and Development, 2006, 20, 871-883.	5.9	88
35	Erroneous energy-generating cycles in published genome scale metabolic networks: Identification and removal. PLoS Computational Biology, 2017, 13, e1005494.	3.2	88
36	MVP: a microbeâ€"phage interaction database. Nucleic Acids Research, 2018, 46, D700-D707.	14.5	82

#	Article	IF	Citations
37	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. Nature Communications, 2016, 7, 11607.	12.8	60
38	Similar gene expression profiles do not imply similar tissue functions. Trends in Genetics, 2006, 22, 132-138.	6.7	59
39	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. Proteomics, 2010, 10, 1297-1306.	2.2	58
40	The Evolution of Isochores: Evidence From SNP Frequency Distributions. Genetics, 2002, 162, 1805-1810.	2.9	56
41	CycleFreeFlux: efficient removal of thermodynamically infeasible loops from flux distributions. Bioinformatics, 2015, 31, 2159-2165.	4.1	53
42	Transcriptional Coupling of Neighboring Genes and Gene Expression Noise: Evidence that Gene Orientation and Noncoding Transcripts Are Modulators of Noise. Genome Biology and Evolution, 2011, 3, 320-331.	2.5	52
43	Plant and Animal Glycolate Oxidases Have a Common Eukaryotic Ancestor and Convergently Duplicated to Evolve Long-Chain 2-Hydroxy Acid Oxidases. Molecular Biology and Evolution, 2014, 31, 1089-1101.	8.9	51
44	Genome-wide acceleration of protein evolution in flies (Diptera). BMC Evolutionary Biology, 2006, 6, 7.	3.2	47
45	Co-expression of neighbouring genes in Arabidopsis: separating chromatin effects from direct interactions. BMC Genomics, 2010, 11, 178.	2.8	47
46	The protein translation machinery is expressed for maximal efficiency in Escherichia coli. Nature Communications, 2020, 11, 5260.	12.8	47
47	Horizontal gene transfer depends on gene content of the host. Bioinformatics, 2005, 21, ii222-ii223.	4.1	45
48	A hypothesis is a liability. Genome Biology, 2020, 21, 231.	8.8	45
49	Interdependence of a mechanosensitive anion channel and glutamate receptors in distal wound signaling. Science Advances, 2021, 7, eabg4298.	10.3	45
50	Deep learning allows genome-scale prediction of Michaelis constants from structural features. PLoS Biology, 2021, 19, e3001402.	5.6	44
51	Genomic Regionality in Rates of Evolution Is Not Explained by Clustering of Genes of Comparable Expression Profile. Genome Research, 2004, 14, 1002-1013.	5.5	43
52	An analytical theory of balanced cellular growth. Nature Communications, 2020, 11, 1226.	12.8	41
53	Imprinted Chromosomal Regions of the Human Genome Have Unusually High Recombination Rates. Genetics, 2003, 165, 1629-1632.	2.9	39
54	Mitochondrial 2-hydroxyglutarate metabolism. Mitochondrion, 2014, 19, 275-281.	3.4	38

#	Article	IF	Citations
55	Scatter correction in 3-D PET. IEEE Transactions on Medical Imaging, 1994, 13, 649-657.	8.9	37
56	Co-expressed Yeast Genes Cluster Over a Long Range but are not Regularly Spaced. Journal of Molecular Biology, 2006, 359, 825-831.	4.2	36
57	Gene Expression, Synteny, and Local Similarity in Human Noncoding Mutation Rates. Molecular Biology and Evolution, 2004, 21, 1820-1830.	8.9	35
58	Molecular adaptations of NADP-malic enzyme for its function in C4 photosynthesis in grasses. Nature Plants, 2019, 5, 755-765.	9.3	35
59	HOTAIR rs7958904 polymorphism is associated with increased cervical cancer risk in a Chinese population. Scientific Reports, 2017, 7, 3144.	3.3	32
60	Night science. Genome Biology, 2019, 20, 179.	8.8	32
61	PET measurement of cerebral acetylcholine esterase activity without blood sampling. European Journal of Nuclear Medicine and Molecular Imaging, 2001, 28, 472-477.	2.1	29
62	On the optimality of the enzyme–substrate relationship in bacteria. PLoS Biology, 2021, 19, e3001416.	5.6	29
63	Each of 3,323 metabolic innovations in the evolution of <i>E. coli</i> arose through the horizontal transfer of a single DNA segment. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 187-192.	7.1	28
64	Freeze-quenched maize mesophyll and bundle sheath separation uncovers bias in previous tissue-specific RNA-Seq data. Journal of Experimental Botany, 2017, 68, 147-160.	4.8	26
65	The two languages of science. Genome Biology, 2020, 21, 147.	8.8	26
66	Amino acid composition in endothermic vertebrates is biased in the same direction as in thermophilic prokaryotes. BMC Evolutionary Biology, 2010, 10, 263.	3.2	24
67	Cellular export of sugars and amino acids: role in feeding other cells and organisms. Plant Physiology, 2021, 187, 1893-1914.	4.8	24
68	Improved Metabolic Models for E. coli and Mycoplasma genitalium from GlobalFit, an Algorithm That Simultaneously Matches Growth and Non-Growth Data Sets. PLoS Computational Biology, 2016, 12, e1005036.	3.2	24
69	Network reduction methods for genome-scale metabolic models. Cellular and Molecular Life Sciences, 2020, 77, 481-488.	5.4	22
70	Selection for energy efficiency drives strand-biased gene distribution in prokaryotes. Scientific Reports, 2017, 7, 10572.	3.3	20
71	Coexpression of Linked Gene Pairs Persists Long after Their Separation. Genome Biology and Evolution, 2011, 3, 565-570.	2.5	18
72	Novel predictions arise from contradictions. Genome Biology, 2021, 22, 153.	8.8	17

#	Article	IF	Citations
73	Human functional genetic studies are biased against the medically most relevant primate-specific genes. BMC Evolutionary Biology, 2010, 10, 316.	3.2	16
74	Combining genetic and evolutionary engineering to establish C4metabolism in C3plants. Journal of Experimental Botany, 2017, 68, 117-125.	4.8	15
75	Magnetic bilayer coupling inYBa2Cu3O7. Physical Review B, 1994, 49, 736-739.	3.2	14
76	Can mutation or fixation biases explain the allele frequency distribution of human single nucleotide polymorphisms (SNPs)?. Gene, 2002, 300, 53-58.	2.2	14
77	TreeSnatcher plus: capturing phylogenetic trees from images. BMC Bioinformatics, 2012, 13, 110.	2.6	14
78	Improvisational science. Genome Biology, 2022, 23, 4.	8.8	14
79	An optimal growth law for RNA composition and its partial implementation through ribosomal and tRNA gene locations in bacterial genomes. PLoS Genetics, 2021, 17, e1009939.	3.5	13
80	Regional similarities in polymorphism in the human genome extend over many megabases. Trends in Genetics, 2002, 18, 281-283.	6.7	12
81	Unusual linkage patterns of ligands and their cognate receptors indicate a novel reason for non-random gene order in the human genome. BMC Evolutionary Biology, 2005, 5, 62.	3.2	12
82	ColorTree: a batch customization tool for phylogenic trees. BMC Research Notes, 2009, 2, 155.	1.4	12
83	Horizontally transferred genes cluster spatially and metabolically. Biology Direct, 2015, 10, 72.	4.6	12
84	Horizontal gene transfers as metagenomic gene duplications. Molecular BioSystems, 2012, 8, 790.	2.9	11
85	Supra-operonic clusters of functionally related genes (SOCs) are a source of horizontal gene co-transfers. Scientific Reports, 2017, 7, 40294.	3.3	11
86	Renaissance minds in 21st century science. Genome Biology, 2020, 21, 67.	8.8	10
87	The ancestors of diatoms evolved a unique mitochondrial dehydrogenase to oxidize photorespiratory glycolate. Photosynthesis Research, 2017, 132, 183-196.	2.9	9
88	What is the question?. Genome Biology, 2019, 20, 289.	8.8	9
89	Magnetic properties of single layered Cu oxides in the extended tâˆ'J model. Physica C: Superconductivity and Its Applications, 1993, 215, 145-151.	1.2	8
90	Umklapp scattering from spin fluctuations in copper oxides. Physical Review B, 1995, 52, R7038-R7041.	3.2	8

#	Article	IF	Citations
91	The Effects of Network Neighbours on Protein Evolution. PLoS ONE, 2011, 6, e18288.	2.5	8
92	Flux balance analysis with or without molecular crowding fails to predict two thirds of experimentally observed epistasis in yeast. Scientific Reports, 2019, 9, 11837.	3.3	8
93	Understanding the Degradation of Hominid Gene Control. PLoS Computational Biology, 2006, 2, e19.	3.2	6
94	Minimal regulatory spaces in yeast genomes. BMC Genomics, 2011, 12, 320.	2.8	6
95	Prokaryotic Genome Expansion Is Facilitated by Phages and Plasmids but Impaired by CRISPR. Frontiers in Microbiology, 2019, 10, 2254.	3.5	6
96	A Gene's Ability to Buffer Variation Is Predicted by Its Fitness Contribution and Genetic Interactions. PLoS ONE, 2011, 6, e17650.	2.5	5
97	The data-hypothesis conversation. Genome Biology, 2021, 22, 58.	8.8	5
98	Modeling photosynthetic resource allocation connects physiology with evolutionary environments. Scientific Reports, 2021, 11, 15979.	3.3	5
99	Does negative auto-regulation increase gene duplicability?. BMC Evolutionary Biology, 2009, 9, 193.	3.2	4
100	Assessing the Influence of Adjacent Gene Orientation on the Evolution of Gene Upstream Regions in Arabidopsis thaliana. Genetics, 2010, 185, 695-701.	2.9	4
101	WhopGenome: high-speed access to whole-genome variation and sequence data in R. Bioinformatics, 2015, 31, 413-415.	4.1	4
102	Alleles of a gene differ in pleiotropy, often mediated through currency metabolite production, in E. coli and yeast metabolic simulations. Scientific Reports, 2018, 8, 17252.	3.3	4
103	Forty years of The Selfish Gene are not enough. Genome Biology, 2016, 17, 39.	8.8	3
104	<i>BlockFeST</i>: Bayesian calculation of region-specific <i>FST</i> to detect local adaptation. Bioinformatics, 2018, 34, 3205-3207.	4.1	2
105	Iterations of evolution A (Very) Short History of Life on Earth <i>Henry Gee</i> St. Martinâ€™s Press, 2021. 288 pp.. Science, 2021, 374, 828-828.	12.6	2