

# Martin J Lercher

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Improvisational science. <i>Genome Biology</i> , 2022, 23, 4.	8.8	14
2	Distinct identities of leaf phloem cells revealed by single cell transcriptomics. <i>Plant Cell</i> , 2021, 33, 511-530.	6.6	162
3	The data-hypothesis conversation. <i>Genome Biology</i> , 2021, 22, 58.	8.8	5
4	Cellular export of sugars and amino acids: role in feeding other cells and organisms. <i>Plant Physiology</i> , 2021, 187, 1893-1914.	4.8	24
5	Novel predictions arise from contradictions. <i>Genome Biology</i> , 2021, 22, 153.	8.8	17
6	Modeling photosynthetic resource allocation connects physiology with evolutionary environments. <i>Scientific Reports</i> , 2021, 11, 15979.	3.3	5
7	Interdependence of a mechanosensitive anion channel and glutamate receptors in distal wound signaling. <i>Science Advances</i> , 2021, 7, eabg4298.	10.3	45
8	Deep learning allows genome-scale prediction of Michaelis constants from structural features. <i>PLoS Biology</i> , 2021, 19, e3001402.	5.6	44
9	On the optimality of the enzyme-substrate relationship in bacteria. <i>PLoS Biology</i> , 2021, 19, e3001416.	5.6	29
10	An optimal growth law for RNA composition and its partial implementation through ribosomal and tRNA gene locations in bacterial genomes. <i>PLoS Genetics</i> , 2021, 17, e1009939.	3.5	13
11	Iterations of evolution <b>A (Very) Short History of Life on Earth</b> <i>Henry Gee</i> St. Martin's Press, 2021. 288 pp.. <i>Science</i> , 2021, 374, 828-828.	12.6	2
12	Network reduction methods for genome-scale metabolic models. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 481-488.	5.4	22
13	The protein translation machinery is expressed for maximal efficiency in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2020, 11, 5260.	12.8	47
14	A hypothesis is a liability. <i>Genome Biology</i> , 2020, 21, 231.	8.8	45
15	The two languages of science. <i>Genome Biology</i> , 2020, 21, 147.	8.8	26
16	An analytical theory of balanced cellular growth. <i>Nature Communications</i> , 2020, 11, 1226.	12.8	41
17	Renaissance minds in 21st century science. <i>Genome Biology</i> , 2020, 21, 67.	8.8	10
18	Molecular adaptations of NADP-malic enzyme for its function in C4 photosynthesis in grasses. <i>Nature Plants</i> , 2019, 5, 755-765.	9.3	35

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19	Night science. <i>Genome Biology</i> , 2019, 20, 179.	8.8	32
20	Flux balance analysis with or without molecular crowding fails to predict two thirds of experimentally observed epistasis in yeast. <i>Scientific Reports</i> , 2019, 9, 11837.	3.3	8
21	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. <i>Nucleic Acids Research</i> , 2019, 47, W270-W275.	14.5	564
22	Prokaryotic Genome Expansion Is Facilitated by Phages and Plasmids but Impaired by CRISPR. <i>Frontiers in Microbiology</i> , 2019, 10, 2254.	3.5	6
23	What is the question?. <i>Genome Biology</i> , 2019, 20, 289.	8.8	9
24	Each of 3,323 metabolic innovations in the evolution of <i>E. coli</i> arose through the horizontal transfer of a single DNA segment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 187-192.	7.1	28
25	MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D700-D707.	14.5	82
26	BlockFeST: Bayesian calculation of region-specific <i>FST</i> to detect local adaptation. <i>Bioinformatics</i> , 2018, 34, 3205-3207.	4.1	2
27	Alleles of a gene differ in pleiotropy, often mediated through currency metabolite production, in <i>E. coli</i> and yeast metabolic simulations. <i>Scientific Reports</i> , 2018, 8, 17252.	3.3	4
28	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. <i>Nature Communications</i> , 2018, 9, 5252.	12.8	151
29	Supra-operonic clusters of functionally related genes (SOCs) are a source of horizontal gene co-transfers. <i>Scientific Reports</i> , 2017, 7, 40294.	3.3	11
30	The ancestors of diatoms evolved a unique mitochondrial dehydrogenase to oxidize photorespiratory glycolate. <i>Photosynthesis Research</i> , 2017, 132, 183-196.	2.9	9
31	HOTAIR rs7958904 polymorphism is associated with increased cervical cancer risk in a Chinese population. <i>Scientific Reports</i> , 2017, 7, 3144.	3.3	32
32	Freeze-quenched maize mesophyll and bundle sheath separation uncovers bias in previous tissue-specific RNA-Seq data. <i>Journal of Experimental Botany</i> , 2017, 68, 147-160.	4.8	26
33	Selection for energy efficiency drives strand-biased gene distribution in prokaryotes. <i>Scientific Reports</i> , 2017, 7, 10572.	3.3	20
34	Combining genetic and evolutionary engineering to establish C4 metabolism in C3 plants. <i>Journal of Experimental Botany</i> , 2017, 68, 117-125.	4.8	15
35	Erroneous energy-generating cycles in published genome scale metabolic networks: Identification and removal. <i>PLoS Computational Biology</i> , 2017, 13, e1005494.	3.2	88
36	Adaptive evolution of complex innovations through stepwise metabolic niche expansion. <i>Nature Communications</i> , 2016, 7, 11607.	12.8	60

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37	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016, 7, 11334.	12.8	104
38	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , 2016, 44, W236-W241.	14.5	610
39	Forty years of <i>The Selfish Gene</i> are not enough. <i>Genome Biology</i> , 2016, 17, 39.	8.8	3
40	Improved Metabolic Models for <i>E. coli</i> and <i>Mycoplasma genitalium</i> from GlobalFit, an Algorithm That Simultaneously Matches Growth and Non-Growth Data Sets. <i>PLoS Computational Biology</i> , 2016, 12, e1005036.	3.2	24
41	Horizontally transferred genes cluster spatially and metabolically. <i>Biology Direct</i> , 2015, 10, 72.	4.6	12
42	CycleFreeFlux: efficient removal of thermodynamically infeasible loops from flux distributions. <i>Bioinformatics</i> , 2015, 31, 2159-2165.	4.1	53
43	WhopGenome: high-speed access to whole-genome variation and sequence data in R. <i>Bioinformatics</i> , 2015, 31, 413-415.	4.1	4
44	The role of photorespiration during the evolution of C4 photosynthesis in the genus <i>Flaveria</i> . <i>ELife</i> , 2014, 3, e02478.	6.0	182
45	PopGenome: An Efficient Swiss Army Knife for Population Genomic Analyses in R. <i>Molecular Biology and Evolution</i> , 2014, 31, 1929-1936.	8.9	871
46	Horizontal gene acquisitions by eukaryotes as drivers of adaptive evolution. <i>BioEssays</i> , 2014, 36, 9-20.	2.5	126
47	Plant and Animal Glycolate Oxidases Have a Common Eukaryotic Ancestor and Convergently Duplicated to Evolve Long-Chain 2-Hydroxy Acid Oxidases. <i>Molecular Biology and Evolution</i> , 2014, 31, 1089-1101.	8.9	51
48	Mitochondrial 2-hydroxyglutarate metabolism. <i>Mitochondrion</i> , 2014, 19, 275-281.	3.4	38
49	sybil – Efficient constraint-based modelling in R. <i>BMC Systems Biology</i> , 2013, 7, 125.	3.0	110
50	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	12.6	439
51	Predicting C4 Photosynthesis Evolution: Modular, Individually Adaptive Steps on a Mount Fuji Fitness Landscape. <i>Cell</i> , 2013, 153, 1579-1588.	28.9	173
52	OGEE: an online gene essentiality database. <i>Nucleic Acids Research</i> , 2012, 40, D901-D906.	14.5	187
53	EvolView, an online tool for visualizing, annotating and managing phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 40, W569-W572.	14.5	400
54	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. <i>Molecular Biology and Evolution</i> , 2012, 29, 1703-1706.	8.9	90

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55	TreeSnatcher plus: capturing phylogenetic trees from images. BMC Bioinformatics, 2012, 13, 110.	2.6	14
56	Horizontal gene transfers as metagenomic gene duplications. Molecular BioSystems, 2012, 8, 790.	2.9	11
57	A Gene's Ability to Buffer Variation Is Predicted by Its Fitness Contribution and Genetic Interactions. PLoS ONE, 2011, 6, e17650.	2.5	5
58	The Effects of Network Neighbours on Protein Evolution. PLoS ONE, 2011, 6, e18288.	2.5	8
59	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
60	Coexpression of Linked Gene Pairs Persists Long after Their Separation. Genome Biology and Evolution, 2011, 3, 565-570.	2.5	18
61	An integrated approach to characterize genetic interaction networks in yeast metabolism. Nature Genetics, 2011, 43, 656-662.	21.4	194
62	Minimal regulatory spaces in yeast genomes. BMC Genomics, 2011, 12, 320.	2.8	6
63	An mRNA Blueprint for C4 Photosynthesis Derived from Comparative Transcriptomics of Closely Related C3 and C4 Species. Plant Physiology, 2011, 155, 142-156.	4.8	222
64	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
65	Human functional genetic studies are biased against the medically most relevant primate-specific genes. BMC Evolutionary Biology, 2010, 10, 316.	3.2	16
66	Co-expression of neighbouring genes in Arabidopsis: separating chromatin effects from direct interactions. BMC Genomics, 2010, 11, 178.	2.8	47
67	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. Proteomics, 2010, 10, 1297-1306.	2.2	58
68	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
69	Does negative auto-regulation increase gene duplicability?. BMC Evolutionary Biology, 2009, 9, 193.	3.2	4
70	ColorTree: a batch customization tool for phylogenetic trees. BMC Research Notes, 2009, 2, 155.	1.4	12
71	Comparative Functional Analysis of the Caenorhabditis elegans and Drosophila melanogaster Proteomes. PLoS Biology, 2009, 7, e1000048.	5.6	208
72	Integration of Horizontally Transferred Genes into Regulatory Interaction Networks Takes Many Million Years. Molecular Biology and Evolution, 2008, 25, 559-567.	8.9	170

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73	Prediction of effective genome size in metagenomic samples. <i>Genome Biology</i> , 2007, 8, R10.	9.6	281
74	Co-expressed Yeast Genes Cluster Over a Long Range but are not Regularly Spaced. <i>Journal of Molecular Biology</i> , 2006, 359, 825-831.	4.2	36
75	An integrated view of protein evolution. <i>Nature Reviews Genetics</i> , 2006, 7, 337-348.	16.3	460
76	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	27.8	219
77	Similar gene expression profiles do not imply similar tissue functions. <i>Trends in Genetics</i> , 2006, 22, 132-138.	6.7	59
78	Genome-wide acceleration of protein evolution in flies (Diptera). <i>BMC Evolutionary Biology</i> , 2006, 6, 7.	3.2	47
79	Understanding the Degradation of Hominid Gene Control. <i>PLoS Computational Biology</i> , 2006, 2, e19.	3.2	6
80	Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of Holometabolous insects. <i>Genome Research</i> , 2006, 16, 1334-1338.	5.5	233
81	X-chromosome-wide profiling of MSL-1 distribution and dosage compensation in <i>Drosophila</i> . <i>Genes and Development</i> , 2006, 20, 871-883.	5.9	88
82	Adaptive evolution of bacterial metabolic networks by horizontal gene transfer. <i>Nature Genetics</i> , 2005, 37, 1372-1375.	21.4	473
83	Unusual linkage patterns of ligands and their cognate receptors indicate a novel reason for non-random gene order in the human genome. <i>BMC Evolutionary Biology</i> , 2005, 5, 62.	3.2	12
84	Horizontal gene transfer depends on gene content of the host. <i>Bioinformatics</i> , 2005, 21, ii222-ii223.	4.1	45
85	Evidence for Widespread Degradation of Gene Control Regions in Hominid Genomes. <i>PLoS Biology</i> , 2005, 3, e42.	5.6	178
86	Gene Expression, Synteny, and Local Similarity in Human Noncoding Mutation Rates. <i>Molecular Biology and Evolution</i> , 2004, 21, 1820-1830.	8.9	35
87	Genomic Regionality in Rates of Evolution Is Not Explained by Clustering of Genes of Comparable Expression Profile. <i>Genome Research</i> , 2004, 14, 1002-1013.	5.5	43
88	The evolutionary dynamics of eukaryotic gene order. <i>Nature Reviews Genetics</i> , 2004, 5, 299-310.	16.3	661
89	A unification of mosaic structures in the human genome. <i>Human Molecular Genetics</i> , 2003, 12, 2411-2415.	2.9	119
90	Coexpression of Neighboring Genes in <i>Caenorhabditis Elegans</i> Is Mostly Due to Operons and Duplicate Genes. <i>Genome Research</i> , 2003, 13, 238-243.	5.5	194

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91	Evidence That the Human X Chromosome Is Enriched for Male-Specific but not Female-Specific Genes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1113-1116.	8.9	112
92	Imprinted Chromosomal Regions of the Human Genome Have Unusually High Recombination Rates. <i>Genetics</i> , 2003, 165, 1629-1632.	2.9	39
93	The ECAT HRRT: performance and first clinical application of the new high resolution research tomograph. <i>IEEE Transactions on Nuclear Science</i> , 2002, 49, 104-110.	2.0	364
94	Can mutation or fixation biases explain the allele frequency distribution of human single nucleotide polymorphisms (SNPs)?. <i>Gene</i> , 2002, 300, 53-58.	2.2	14
95	Regional similarities in polymorphism in the human genome extend over many megabases. <i>Trends in Genetics</i> , 2002, 18, 281-283.	6.7	12
96	Human SNP variability and mutation rate are higher in regions of high recombination. <i>Trends in Genetics</i> , 2002, 18, 337-340.	6.7	326
97	Clustering of housekeeping genes provides a unified model of gene order in the human genome. <i>Nature Genetics</i> , 2002, 31, 180-183.	21.4	496
98	The Evolution of Isochores: Evidence From SNP Frequency Distributions. <i>Genetics</i> , 2002, 162, 1805-1810.	2.9	56
99	Positron-emission tomography of vector-mediated gene expression in gene therapy for gliomas. <i>Lancet</i> , The, 2001, 358, 727-729.	13.7	356
100	PET measurement of cerebral acetylcholine esterase activity without blood sampling. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2001, 28, 472-477.	2.1	29
101	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. <i>Molecular Biology and Evolution</i> , 2001, 18, 2032-2039.	8.9	93
102	Umklapp scattering from spin fluctuations in copper oxides. <i>Physical Review B</i> , 1995, 52, R7038-R7041.	3.2	8
103	Magnetic bilayer coupling in YBa <sub>2</sub> Cu <sub>3</sub> O <sub>7</sub> . <i>Physical Review B</i> , 1994, 49, 736-739.	3.2	14
104	Scatter correction in 3-D PET. <i>IEEE Transactions on Medical Imaging</i> , 1994, 13, 649-657.	8.9	37
105	Magnetic properties of single layered Cu oxides in the extended t <sup>2</sup> J model. <i>Physica C: Superconductivity and Its Applications</i> , 1993, 215, 145-151.	1.2	8