

# Lars S Jermiin

## List of Publications by Year in descending order

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82  
papers

17,911  
citations

71102

41  
h-index

60623

81  
g-index

91  
all docs

91  
docs citations

91  
times ranked

22104  
citing authors

#	ARTICLE	IF	CITATIONS
1	ModelFinder: fast model selection for accurate phylogenetic estimates. <i>Nature Methods</i> , 2017, 14, 587-589.	19.0	9,486
2	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	12.6	2,096
3	Identification, Characterization, and Crystal Structure of the Omega Class Glutathione Transferases. <i>Journal of Biological Chemistry</i> , 2000, 275, 24798-24806.	3.4	625
4	Many Parallel Losses of <i>infA</i> from Chloroplast DNA during Angiosperm Evolution with Multiple Independent Transfers to the Nucleus. <i>Plant Cell</i> , 2001, 13, 645-658.	6.6	415
5	Characterization of an indoleamine 2,3-dioxygenase-like protein found in humans and mice. <i>Gene</i> , 2007, 396, 203-213.	2.2	400
6	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
7	Sensitivity and specificity of information criteria. <i>Briefings in Bioinformatics</i> , 2020, 21, 553-565.	6.5	257
8	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	3.8	238
9	The Biasing Effect of Compositional Heterogeneity on Phylogenetic Estimates May be Underestimated. <i>Systematic Biology</i> , 2004, 53, 638-643.	5.6	234
10	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	27.8	210
11	Characterization of the type I interferon locus and identification of novel genes. <i>Genomics</i> , 2004, 84, 331-345.	2.9	209
12	Genome-wide analysis of <i>MIKC</i> -type <i>MADS</i> -box genes in wheat: pervasive duplications, functional conservation and putative neofunctionalization. <i>New Phytologist</i> , 2020, 225, 511-529.	7.3	176
13	Nucleotide Composition Bias Affects Amino Acid Content in Proteins Coded by Animal Mitochondria. <i>Journal of Molecular Evolution</i> , 1997, 44, 282-288.	1.8	170
14	Megafaunal extinction in the late Quaternary and the global overkill hypothesis. <i>Alcheringa</i> , 2004, 28, 291-331.	1.2	159
15	Tracing the Decay of the Historical Signal in Biological Sequence Data. <i>Systematic Biology</i> , 2004, 53, 623-637.	5.6	154
16	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	2.7	154
17	Counterselection on sex chromosomes in the <i>Mus musculus</i> European hybrid zone. <i>Journal of Evolutionary Biology</i> , 1993, 6, 529-546.	1.7	153
18	Matched-pairs tests of homogeneity with applications to homologous nucleotide sequences. <i>Bioinformatics</i> , 2006, 22, 1225-1231.	4.1	124

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19	Mind the Gaps: Evidence of Bias in Estimates of Multiple Sequence Alignments. <i>Molecular Biology and Evolution</i> , 2007, 24, 2433-2442.	8.9	108
20	Gene Targeting of Desrt, a Novel ARID Class DNA-Binding Protein, Causes Growth Retardation and Abnormal Development of Reproductive Organs. <i>Genome Research</i> , 2001, 11, 1327-1334.	5.5	97
21	Fixed, free, and fixed: The fickle phylogeny of extant Crinoidea (Echinodermata) and their Permian–Triassic origin. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 161-181.	2.7	93
22	Evolutionary History of “Early-Diverging” Eukaryotes: The Excavate Taxon <i>Carpodidomonas</i> is a Close Relative of <i>Giardia</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 1782-1791.	8.9	90
23	Improving the Analysis of Dinoflagellate Phylogeny based on rDNA. <i>Protist</i> , 2005, 156, 269-286.	1.5	85
24	Analysis of directional mutation pressure and nucleotide content in mitochondrial cytochrome b genes. <i>Journal of Molecular Evolution</i> , 1994, 39, 160-173.	1.8	81
25	Are feeding preferences and insecticide resistance associated with the size of detoxifying enzyme families in insect herbivores?. <i>Current Opinion in Insect Science</i> , 2016, 13, 70-76.	4.4	80
26	A novel transcription factor, ELF5, belongs to the ELF subfamily of ETS genes and maps to human chromosome 11p13, a region subject to LOH and rearrangement in human carcinoma cell lines. <i>Oncogene</i> , 1998, 17, 2719-2732.	5.9	75
27	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. <i>Systematic Biology</i> , 2020, 69, 249-264.	5.6	75
28	Accelerated Evolution of Cytochrome b in Simian Primates: Adaptive Evolution in Concert with Other Mitochondrial Proteins?. <i>Journal of Molecular Evolution</i> , 1998, 47, 249-257.	1.8	71
29	Characterization and evolution of vertebrate indoleamine 2, 3-dioxygenases. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2009, 153, 137-144.	1.6	67
30	Mixture Models of Nucleotide Sequence Evolution that Account for Heterogeneity in the Substitution Process Across Sites and Across Lineages. <i>Systematic Biology</i> , 2014, 63, 726-742.	5.6	62
31	Mitochondrial DNA and trade data support multiple origins of <i>Helicoverpa armigera</i> (Lepidoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	3.3	61
32	Exaggeration and suppression of iridescence: the evolution of two-dimensional butterfly structural colours. <i>Journal of the Royal Society Interface</i> , 2006, 3, 99-109.	3.4	57
33	A comparative analysis of some life-history traits between cooperatively and non-cooperatively breeding Australian passerines. <i>Evolutionary Ecology</i> , 1994, 8, 471-488.	1.2	54
34	Phylogenetic Model Evaluation. <i>Methods in Molecular Biology</i> , 2008, 452, 331-364.	0.9	54
35	Molecular phylogeny reveals food plasticity in the evolution of true ladybird beetles (Coleoptera). <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	3.2	52
36	Majority-Rule Consensus of Phylogenetic Trees Obtained by Maximum-Likelihood Analysis. <i>Molecular Biology and Evolution</i> , 1997, 14, 1296-1302.	8.9	50

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37	Evolution of Vertebrate Genes Related to Prion and Shadoo Proteinsâ€”Clues from Comparative Genomic Analysis. <i>Molecular Biology and Evolution</i> , 2004, 21, 2210-2231.	8.9	50
38	SeqVis: Visualization of compositional heterogeneity in large alignments of nucleotides. <i>Bioinformatics</i> , 2006, 22, 2162-2163.	4.1	50
39	Intramolecular Epistasis and the Evolution of a New Enzymatic Function. <i>PLoS ONE</i> , 2012, 7, e39822.	2.5	49
40	A Molecular Framework for the Phylogeny of the Ant Subfamily Dolichoderinae. <i>Molecular Phylogenetics and Evolution</i> , 2000, 17, 108-116.	2.7	44
41	Multi-objective evolutionary algorithms and phylogenetic inference with multiple data sets. <i>Soft Computing</i> , 2006, 10, 359-368.	3.6	43
42	Estimation of Phylogeny Using a General Markov Model. <i>Evolutionary Bioinformatics</i> , 2005, 1, 117693430500100.	1.2	39
43	Molecular Evidence for a Jurassic Origin of Ants. <i>Die Naturwissenschaften</i> , 1997, 84, 22-23.	1.6	37
44	Reverse engineering: transaminase biocatalyst development using ancestral sequence reconstruction. <i>Green Chemistry</i> , 2017, 19, 5375-5380.	9.0	36
45	A minimum reporting standard for multiple sequence alignments. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa024.	3.2	36
46	TrExML: a maximum-likelihood approach for extensive tree-space exploration. <i>Bioinformatics</i> , 2000, 16, 383-394.	4.1	36
47	Molecular phylogeny of Australian Helicarionidae, Euconulidae and related groups (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 2007, 45, 792-812.	2.7	35
48	Improved Consensus Network Techniques for Genome-Scale Phylogeny. <i>Molecular Biology and Evolution</i> , 2006, 23, 848-855.	8.9	34
49	Estimation of Phylogeny and Invariant Sites under the General Markov Model of Nucleotide Sequence Evolution. <i>Systematic Biology</i> , 2007, 56, 155-162.	5.6	32
50	Serpins: Genome-Wide Characterisation and Expression Analysis of the Serine Protease Inhibitor Family in <i>Triticum aestivum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2709-2722.	1.8	29
51	Two Stationary Nonhomogeneous Markov Models of Nucleotide Sequence Evolution. <i>Systematic Biology</i> , 2011, 60, 74-86.	5.6	28
52	Reducing Model Complexity of the General Markov Model of Evolution. <i>Molecular Biology and Evolution</i> , 2011, 28, 3045-3059.	8.9	27
53	Markov invariants, plethysms, and phylogenetics. <i>Journal of Theoretical Biology</i> , 2008, 253, 601-615.	1.7	24
54	EVOLUTION: Is the "Big Bang" in Animal Evolution Real?. <i>Science</i> , 2005, 310, 1910-1911.	12.6	22

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55	Generation of the Exact Distribution and Simulation of Matched Nucleotide Sequences on a Phylogenetic Tree. <i>Mathematical Modelling and Algorithms</i> , 2006, 5, 291-308.	0.5	21
56	Evolution of the Inner Light-Harvesting Antenna Protein Family of Cyanobacteria, Algae, and Plants. <i>Journal of Molecular Evolution</i> , 2007, 64, 321-331.	1.8	19
57	Estimation of phylogeny using a general Markov model. <i>Evolutionary Bioinformatics</i> , 2007, 1, 62-80.	1.2	19
58	Polymorphism of phase II enzymes: identification of new enzymes and polymorphic variants by database analysis. <i>Toxicology Letters</i> , 1998, 102-103, 149-154.	0.8	18
59	Amylase and 16S rRNA genes from a hyperthermophilic archaeobacterium. <i>Journal of Applied Microbiology</i> , 1999, 86, 93-107.	3.1	18
60	Isolation and characterization of the mouse ubiquitin-specific protease Usp15. <i>Mammalian Genome</i> , 2003, 14, 31-46.	2.2	18
61	Response to Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	17
62	Identifying Optimal Models of Evolution. <i>Methods in Molecular Biology</i> , 2017, 1525, 379-420.	0.9	17
63	A new phylogenetic protocol: dealing with model misspecification and confirmation bias in molecular phylogenetics. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa041.	3.2	15
64	Population Genetic Structure and Potential Incursion Pathways of the Bluetongue Virus Vector <i>Culicoides brevitarsis</i> (Diptera: Ceratopogonidae) in Australia. <i>PLoS ONE</i> , 2016, 11, e0146699.	2.5	15
65	The molecular structure of the IsiA Photosystem I supercomplex, modelled from high-resolution, crystal structures of Photosystem I and the CP43 protein. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 457-465.	1.0	14
66	Unbiased estimation of symmetrical directional mutation pressure from protein-coding DNA. <i>Journal of Molecular Evolution</i> , 1996, 42, 476-480.	1.8	13
67	A modern soft-bottom, shallow-water crinoid fauna (Echinodermata) from the Great Barrier Reef, Australia. <i>Coral Reefs</i> , 2006, 25, 164-168.	2.2	11
68	SeqVis: A Tool for Detecting Compositional Heterogeneity Among Aligned Nucleotide Sequences. <i>Methods in Molecular Biology</i> , 2009, 537, 65-91.	0.9	11
69	Statistical tests to identify appropriate types of nucleotide sequence recoding in molecular phylogenetics. <i>BMC Bioinformatics</i> , 2014, 15, S8.	2.6	11
70	Hetero: a program to simulate the evolution of DNA on a four-taxon tree. <i>Applied Bioinformatics</i> , 2003, 2, 159-63.	1.6	11
71	Many Parallel Losses of <i>infA</i> from Chloroplast DNA during Angiosperm Evolution with Multiple Independent Transfers to the Nucleus. <i>Plant Cell</i> , 2001, 13, 645.	6.6	10
72	Analysis of Genomic Sequence Data Reveals the Origin and Evolutionary Separation of Hawaiian Hoary Bat Populations. <i>Genome Biology and Evolution</i> , 2020, 12, 1504-1514.	2.5	9

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73	A globally diverse reference alignment and panel for imputation of mitochondrial DNA variants. BMC Bioinformatics, 2021, 22, 417.	2.6	9
74	Unbiased Estimation of Symmetrical Directional Mutation Pressure from Protein-Coding DNA. Journal of Molecular Evolution, 1997, 44, 468-468.	1.8	7
75	Contradictory Phylogenetic Signals in the Laurasiatheria Anomaly Zone. Genes, 2022, 13, 766.	2.4	7
76	Lake Mungo 3: A response to recent critiques. Archaeology in Oceania, 2001, 36, 170-174.	0.7	6
77	A Likelihood-Ratio Test for Lumpability of Phylogenetic Data: Is the Markovian Property of an Evolutionary Process Retained in Recoded DNA?. Systematic Biology, 2021, , .	5.6	4
78	Parallel implementation of maximum likelihood methods for phylogenetic analysis. , 0, , .		3
79	Genetic and lipidomic analyses suggest that Nostoc punctiforme, a plant-symbiotic cyanobacterium, does not produce sphingolipids. Access Microbiology, 2022, 4, 000306.	0.5	2
80	AMID: autonomous modeler of intragenic duplication. Applied Bioinformatics, 2003, 2, 169-76.	1.6	2
81	Unbiased Estimation of Symmetrical Directional Mutation Pressure from Protein-Coding DNA. Journal of Molecular Evolution, 1996, 42, 476-480.	1.8	1
82	Changes in relative mobility of pancreatic amylase variants in isoelectric focusing. Primates, 1991, 32, 119-123.	1.1	0